

Danish data (–2016) and results for the Daffodil project

SDC

September 2018

<http://bendixcarstensen.com/SDC/daf>

Version 41

Compiled Sunday 16th September, 2018, 17:56
from: /home/bendix/sdc/proj/daffodil/rep/DKdat.tex

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Contents

1	Analysis of SGLT-2i vs. SU	1
1.1	Dataset for analysis od SGLT-2i vs SU	1
1.2	Baseline tables for all new-starters	3
1.2.1	Demographics	4
1.2.2	Comorbidities	6
1.2.3	Other medication	8
1.3	Propensity scoring	9
1.4	Propensity score matching	12
1.5	Baseline tables for propensity matched persons	17
1.5.1	Demographics	18
1.5.2	Comorbidities	19
1.5.3	Other medication	20
1.6	Overview of pre- and post matching	22
1.7	Survival analysis datasets: Lexis objects	25
1.8	Types of index drugs	25
1.9	Collecting analysis results and key data	27
1.10	Survival dataset: Lexis objects	27
1.10.1	Follow-up data and events	28
1.10.2	Analysis	29
1.11	Exposure tables by drug	37
1.12	Saving it all	38
1.13	Reformatting	38
1.13.1	Baseline tables	38
	Baseline pre-matching	39
	Baseline after matching	40
1.13.2	Treatment distribution	42
1.13.3	Events	43
1.13.4	Hazard ratios	45
1.13.5	Subgroup OT	46
1.13.6	Subgroup ITT	47
2	Analysis of SGLT-2i vs. DPP4	48
2.1	Dataset for analysis od SGLT-2i vs DPP-4	48
2.2	Baseline tables for all new-starters	50
2.2.1	Demographics	51
2.2.2	Comorbidities	53
2.2.3	Other medication	55

2.3	Propensity scoring	56
2.4	Propensity score matching	59
2.5	Baseline tables for propensity matched persons	63
2.5.1	Demographics	63
2.5.2	Comorbidities	66
2.5.3	Other medication	67
2.6	Overview of pre- and post matching	69
2.7	Survival analysis datasets: Lexis objects	72
2.8	Collecting analysis results and key data	72
2.9	Survival dataset: Lexis objects	73
2.9.1	Follow-up data and events	74
2.9.2	Analysis	75
2.10	Exposure tables by drug	83
2.11	Saving it all	84
2.12	Reformatting	84
2.12.1	Baseline tables	84
	Baseline pre-matching	85
	Baseline after matching	86
2.12.2	Treatment distribution	88
2.12.3	Events	89
2.12.4	Hazard ratios	91
2.12.5	Subgroup OT	92
2.12.6	Subgroup ITT	93
3	Analysis of SGLT-2i vs. any other drug	94
3.1	Dataset for analysis od SGLT-2i vs any other drug	94
3.1.1	Persons and episodes	98
3.2	Baseline tables for all new-starters	98
3.2.1	Demographics	99
3.2.2	Comorbidities	101
3.2.3	Other medication	103
3.3	Propensity scoring	105
3.4	Propensity score matching	108
3.5	Baseline tables for propensity matched persons	112
3.5.1	Demographics	113
3.5.2	Comorbidities	116
3.5.3	Other medication	117
3.6	Overview of pre- and post matching	118
3.7	Survival analysis datasets: Lexis objects	121
3.8	Collecting analysis results and key data	122
3.9	Survival dataset: Lexis objects	123
3.9.1	Follow-up data and events	124
3.9.2	Analysis	125
3.10	Exposure tables by drug	132
3.11	Saving it all	134
3.12	Reformatting	134
3.12.1	Baseline tables	134

	Baseline pre-matching	135
	Baseline after matching	136
3.12.2	Treatment distribution	138
3.12.3	Events	140
3.12.4	Hazard ratios	142
3.12.5	Subgroup OT	143
3.12.6	Subgroup ITT	144
4	SAS programs	145
4.1	Rationale and overview	145
4.2	Program documentation	146
4.2.1	optslibs.sas	146
4.3	01a-npr	147
4.3.1	01a-npr.lst	152
4.4	04a-rmps	156
4.4.1	04a-rmps.lst	160
4.5	04d-rmps	170
4.5.1	04d-rmps.lst	174
4.6	07-newuse	188
4.6.1	07-newuse.lst	221

Chapter 1

Analysis of SGLT-2i vs. SU

1.1 Dataset for analysis od SGLT-2i vs SU

First load the relevant package:

```
> options( width=95 )
> library( Epi )
> library( splines )
> library( haven )
> library( Matching )
> clear()
> print( sessionInfo(), l=F )
```

R version 3.5.0 (2018-04-23)

Platform: x86_64-w64-mingw32/x64 (64-bit)

Running under: Windows Server 2012 R2 x64 (build 9600)

Matrix products: default

attached base packages:

```
[1] splines    stats      graphics  grDevices  utils      datasets  methods    base
```

other attached packages:

```
[1] Matching_4.9-3 MASS_7.3-49    haven_1.1.1    Epi_2.30
```

loaded via a namespace (and not attached):

```
[1] Rcpp_0.12.16    lattice_0.20-35  zoo_1.8-1      grid_3.5.0      plyr_1.8.4
[6] magrittr_1.5    etm_0.6-2        pillar_1.2.2   rlang_0.2.0     Matrix_1.2-14
[11] forcats_0.3.0   tools_3.5.0      cmprsk_2.2-7   numDeriv_2016.8-1 survival_2.41-3
[16] parallel_3.5.0  compiler_3.5.0   tibble_1.4.2
```

Then we can read the data:

```
> system.time(
+ mset <- read_sas( "../data/episodes.sas7bdat" ) )
  user  system elapsed
 6.82    0.18   18.72

> dim( mset )

[1] 244715    98

> names( mset )
```

```

...now input from ../rep/matchSGSU.tex
[1] "druggr"      "pnr"         "eksd"        "ATC"         "doDM"        "epiN"
[7] "doIx"        "Ixdr"        "Ixatc"       "lastpr"     "doTm"        "doFL"
[13] "FLdr"       "FLatc"       "deCVDD"     "coD"        "doTIA"       "doAngina"
[19] "doBleed"    "doCOPD"     "doPAD"      "doHF"       "doCancer"    "doDMcompl"
[25] "doNeuro"    "doDKD"      "doDiaEye"   "doHypo"     "doAtrFib"    "doMI"
[31] "doUnstAng"  "doHmStr"    "doDiaFoot"  "doOther"    "doPeriAng"   "doIscStr"
[37] "doAmp"      "doCKD"      "doPCISTen"  "doCABG"     "doKeto"      "doDial"
[43] "doBari"     "sex"        "doBth"      "whBth"     "doDth"       "dSrc"
[49] "dolACE"     "dolSta"     "dolBBI"     "dolARB"     "dolA1A"      "dolDHP"
[55] "dolWtL"     "dolRPA"     "dolWrf"     "dolAsp"     "dolHCD"      "dolTHZ"
[61] "dolCcs"     "dolDXI"     "dolDgo"     "dolAP1"     "dolAmi"      "dolDTI"
[67] "dolNHP"     "dolFla"     "dolMetformin" "dolGLP1"    "dolMetxSGLT2" "dolMetxDPP4"
[73] "dolSGLT2"   "dolongIns"  "dolmixIns"  "dolDPP4"    "dolSU"       "dolintIns"
[79] "dolfastIns" "dolTZD"     "dolAcarbose" "dolTZDxDPP4" "maxH"        "frail"
[85] "recnum"     "C_ADIAAG"   "compl"      "C_OPR"     "D_INDDTO"    "V_SENGDAGE"
[91] "deHF"       "deMACE"     "deMI"       "deStr"     "deIscStr"    "deAF"
[97] "deHH"       "deDKD"

```

We subset to SGLT-2i / SU and on the fly convert all dates to fractions of years to facilitate programming:

```
> mset <- cal.yr( subset( as.data.frame( mset ), Ixdr %in% c("SGLT2","SU") ) )
```

We then select the first of these episodes from each person, and exclude those with the other in the baseline. Note that persons where both drugs are initiated the same day, will be excluded entirely, because drugs initiated on the index day are coded as baseline drug with the same date.

```

> nrow( mset )
[1] 36777
> mset <- mset[order(mset$pnr,mset$doIx),]
> mset <- mset[!duplicated(mset$pnr),]
> mset <- subset( mset, ( Ixdr=="SGLT2" & is.na(dolSU ) ) |
+                 ( Ixdr=="SU" & is.na(dolSGLT2) ) )
> with( mset, table(table(pnr)) )
1
29922

```

Thus we see that we have precisely one episode per person after these exclusions.

To make FLdr and Ixdr into factors we need some sensible levels:

```

> ( drlab <- read.table( "drlab.txt", header=TRUE, as.is=TRUE ) )
  gr  lab      longlab
1  11 Met    Metformin
2  12 SU  Sulfonylurea
3  13 TZD      TZD
4  14 DPP      DPP-4
5  15 GLP      GLP-1
6  16 SGL      SGLT2
7 fastIns fIns    fastIns
8 intIns  iIns    intIns
9 mixIns  mIns    mixIns
10 longIns lIns    longIns
11  18 Aca    Acarbose
12  19 Meg    Meglitinide

```

```

13      212  M+U      Met+SU
14      213  M+T      Met+TZD
15      214  M+D      Met+DPP4
16      216  M+S      Met+SGLT2
17      218  M+A      Met+Acarbose
18      223  U+T      SU+TZD
19      234  D+T      TZD+DPP4
20      246  D+S      DPP4+SGLT2

```

Then we can define the first line and the index drug variables as factors:

```

> mset <- transform( mset, FLdr = factor( FLdr,
+                                       levels = drlab$gr,
+                                       labels = drlab$lab ),
+                   Ixdr = factor( Ixdr ) )

```

We tabulate the index drug versus the first-line drug separately for those where the index date and first-line dates are the same:

```

> print( ftable( with( mset, addmargins(
+   table( "doIx=doFL"=abs(doIx-doFL)<0.1, FLdr, Ixdr ), 1:2 ) ),
+   col.vars=c(3,1) ),
+   zero = "." )

```

	Ixdr	SGLT2		SU			
	doIx=doFL	FALSE	TRUE	Sum	FALSE	TRUE	Sum
FLdr							
Met		9175	130	9305	12122	990	13112
SU		2311	.	2311	3078	892	3970
TZD		3	.	3	5	.	5
DPP		33	1	34	46	9	55
GLP		23	2	25	12	.	12
SGL		.	92	92	.	.	.
fIns		182	.	182	124	4	128
iIns		140	.	140	79	3	82
mIns		104	1	105	106	2	108
lIns		20	.	20	16	2	18
Aca		8	.	8	18	.	18
Meg		.	.	.	.	.	.
M+U		.	.	.	.	.	.
M+T		15	.	15	12	.	12
M+D		64	1	65	60	14	74
M+S		.	23	23	.	.	.
M+A		.	.	.	.	.	.
U+T		.	.	.	.	.	.
D+T		.	.	.	.	.	.
D+S		.	.	.	.	.	.
Sum		12078	250	12328	15678	1916	17594

We see that among those where the two dates are equal, there are still some where the first line and Index drug are not the same. This is because each initiating drug generates its own episode.

1.2 Baseline tables for all new-starters

We produce an overview of the the exposure status, but first we need a few derived variables, including the indicator of *any* previous CVD:

```
> mset <- transform( mset, age = doIx - doBth,
+                    tff = doIx - doFL,
+                    sex = factor( sex, labels=c("M","F") ),
+                    frail = pmax( frail, 0, na.rm=TRUE ),
+                    maxH = pmax( 0, maxH, na.rm=TRUE ) )
> with( mset, addmargins( table( Ixatc, Ixdr ), 1 ) )
```

	Ixdr	
Ixatc	SGLT2	SU
A10BB01	0	960
A10BB03	0	290
A10BB07	0	753
A10BB09	0	1753
A10BB12	0	13490
A10BD15	313	0
A10BD16	11	0
A10BD20	378	0
A10BK01	7238	0
A10BK02	357	0
A10BK03	4031	0
A10BX02	0	347
A10BX03	0	1
Sum	12328	17594

We now produce the baseline baseline tables for the entire set of new users, the result is in three tables, `dt.tab` (demographics for total sample), `ct.tab` (comobidites for total sample) and `mt.tab` (medication for total sample).

```
> ptab <- function( var ) cbind( tt <- table( var, mset$Ixdr ),
+                               round( prop.table( tt, 2 ) * 100, 1 ) )
```

1.2.1 Demographics

First the tabulations of the baseline demographics:

```
> t.sex <- with( mset, ptab(sex) )
> rownames( t.sex )[1] <- paste("Sex",rownames( t.sex )[1])
> t.fl0 <- with( mset, ptab( doIx-doFL==0 ) )[-1,,drop=F]
> rownames( t.fl0 )[1] <- "Index = First Line"
> t.fl0
```

	SGLT2	SU	SGLT2	SU
Index = First Line	156	1203	1.3	6.8

```
> m.fl0 <- with( subset(mset, doIx-doFL>0 ), round( c( tapply( doIx-doFL, Ixdr, mean ),
+                                                    tapply( doIx-doFL, Ixdr, sd ) ), 1 ) )
> dim( m.fl0 ) <- c(1,4)
> rownames( m.fl0 ) <- c("Index not FL: Mean / SD")
> m.fl0
```

	[,1]	[,2]	[,3]	[,4]
Index not FL: Mean / SD	8.5	6.2	5.3	5

```
> t.age <- with( mset, ptab( floor( pmin(pmax(age,30),89)/10 ) * 10 ) )
> rownames( t.age )[1] <- "Age at index <40"
> rownames( t.age )[nrow(t.age)] <- "80+"
> m.age <- with( mset, round( c( tapply( age, Ixdr, mean ),
+                               tapply( age, Ixdr, sd ) ), 1 ) )
> dim( m.age ) <- c(1,4)
> rownames( m.age ) <- c("Age: Mean / SD")
> m.age
```

```

      [,1] [,2] [,3] [,4]
Age: Mean / SD 59.8 63.9  11  13

> ## Date of index by 6 months and 1 year
> with( mset, ptab( floor( doIx*2 )/2 ) )

      SGLT2  SU SGLT2  SU
2012.5    11 412   0.1  2.3
2013     588 2800   4.8 15.9
2013.5    765 2330   6.2 13.2
2014     930 2486   7.5 14.1
2014.5   1139 1991   9.2 11.3
2015    1616 2229  13.1 12.7
2015.5   1717 1907  13.9 10.8
2016    2848 1927  23.1 11.0
2016.5   2714 1512  22.0  8.6

> t.dat <- with( mset, ptab( floor( doIx ) ) )
> rownames( t.dat )[1] <- paste("Index date",rownames( t.dat )[1])
> ## Date of First Line
> t.fl <- with( mset, ptab( floor( doFL ) ) )
> rownames( t.fl )[1] <- paste("Date of first line",rownames( t.fl )[1])
> ## Frailty
> t.fr <- with( mset, ptab( frail ) )
> rownames( t.fr )[1] <- paste("Frailty",rownames( t.fr )[1])
> dt.tab <- rbind( t.sex, t.fl0, m.fl0, t.age, m.age, t.dat, t.fl, t.fr )
> dt.tab

```

	SGLT2	SU	SGLT2	SU
Sex M	7525.0	10348.0	61.0	58.8
F	4803.0	7246.0	39.0	41.2
Index = First Line	156.0	1203.0	1.3	6.8
Index not FL: Mean / SD	8.5	6.2	5.3	5.0
Age at index <40	509.0	637.0	4.1	3.6
40	1782.0	1993.0	14.5	11.3
50	3787.0	3912.0	30.7	22.2
60	4007.0	5147.0	32.5	29.3
70	1960.0	4092.0	15.9	23.3
80+	283.0	1813.0	2.3	10.3
Age: Mean / SD	59.8	63.9	11.0	13.0
Index date 2012	11.0	412.0	0.1	2.3
2013	1353.0	5130.0	11.0	29.2
2014	2069.0	4477.0	16.8	25.4
2015	3333.0	4136.0	27.0	23.5
2016	5562.0	3439.0	45.1	19.5
Date of first line 1995	548.0	362.0	4.4	2.1
1996	196.0	157.0	1.6	0.9
1997	199.0	181.0	1.6	1.0
1998	257.0	247.0	2.1	1.4
1999	341.0	283.0	2.8	1.6
2000	358.0	329.0	2.9	1.9
2001	406.0	397.0	3.3	2.3
2002	421.0	470.0	3.4	2.7
2003	579.0	603.0	4.7	3.4
2004	602.0	698.0	4.9	4.0
2005	685.0	801.0	5.6	4.6
2006	760.0	879.0	6.2	5.0
2007	808.0	1004.0	6.6	5.7
2008	856.0	1151.0	6.9	6.5
2009	947.0	1218.0	7.7	6.9

2010	946.0	1345.0	7.7	7.6
2011	873.0	1515.0	7.1	8.6
2012	704.0	1533.0	5.7	8.7
2013	580.0	1720.0	4.7	9.8
2014	510.0	1239.0	4.1	7.0
2015	436.0	944.0	3.5	5.4
2016	316.0	518.0	2.6	2.9
Frailty 0	8283.0	12644.0	67.2	71.9
1	4045.0	4950.0	32.8	28.1

1.2.2 Comorbidities

The data frame contains the dates of the *earliest* recorded comorbidities from the NPR, hence the prefix `.prv`:

```
> wh <- grep( "do[A-Z]", names( mset ) )
> wh <- wh[4:30]
> names( mset )[wh]

 [1] "doFL"      "doTIA"      "doAngina"    "doBleed"    "doCOPD"     "doPAD"      "doHF"
 [8] "doCancer"  "doDMcompl"  "doNeuro"     "doDKD"      "doDiaEye"   "doHypo"     "doAtrFib"
[15] "doMI"      "doUnstAng"  "doHmStr"     "doDiaFoot"  "doOther"    "doPeriAng"  "doIscStr"
[22] "doAmp"     "doCKD"      "doPCIsten"   "doCABG"     "doKeto"     "doDial"

> comorb <- data.frame( pmax( mset[,wh] < mset[, "doIx"], 0, na.rm=TRUE ) )
> names( comorb ) <- gsub( "do", "prv.", names(comorb) )
> str( comorb )

'data.frame':      29922 obs. of  27 variables:
 $ prv.FL      : num  1 1 1 1 1 1 1 1 1 1 ...
 $ prv.TIA     : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.Angina  : num  0 1 0 0 0 0 0 1 0 0 ...
 $ prv.Bleed   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.COPD    : num  0 0 0 1 0 0 0 0 0 0 ...
 $ prv.PAD     : num  0 0 0 0 0 0 1 0 0 0 ...
 $ prv.HF      : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.Cancer  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.DMcompl: num  0 0 1 0 0 0 0 1 0 0 ...
 $ prv.Neuro   : num  1 0 0 1 0 0 0 1 0 0 ...
 $ prv.DKD     : num  0 0 0 1 0 0 0 0 0 0 ...
 $ prv.DiaEye  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.Hypo    : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.AtrFib  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.MI      : num  0 0 0 1 0 0 0 0 0 0 ...
 $ prv.UnstAng: num  0 0 0 1 0 0 0 0 0 0 ...
 $ prv.HmStr   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.DiaFoot: num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.Other   : num  0 0 0 0 0 0 1 0 0 0 ...
 $ prv.PeriAng: num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.IscStr  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.Amp     : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.CKD     : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.PCIsten: num  0 0 0 1 0 0 0 0 0 0 ...
 $ prv.CABG    : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.Keto    : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.Dial    : num  0 0 0 0 0 0 0 0 0 0 ...
```

Later, in the modeling we will need the indicator of *any* previous CVD as well as *any* type of stroke and micro-vascular complications:

```
> comorb$pre.CVD <- with( comorb, pmax( prv.MI,
+                                     prv.UnstAng,
+                                     prv.Angina,
+                                     prv.HF,
+                                     prv.AtrFib,
+                                     prv.HmStr,
+                                     prv.IscStr,
+                                     prv.TIA,
+                                     prv.PAD ) )
> comorb$pre.Str <- with( comorb, pmax( prv.HmStr,
+                                     prv.IscStr,
+                                     prv.TIA ) )
> comorb$pre.FPA <- with( comorb, pmax( prv.DiaFoot,
+                                     prv.PeriAng ) )
> comorb$pre.Mic <- with( comorb, pmax( prv.DiaEye,
+                                     prv.DMcompl,
+                                     prv.Neuro,
+                                     prv.DKD,
+                                     prv.DiaFoot,
+                                     prv.PeriAng ) )
```

Note that we name the columns `pre.` to avoid including these in the propensity score estimation.

```
> ct.tab <- cbind(
+ t( sapply( comorb,
+           function( x ) tapply( x, mset$Ixdr, sum ) ) ),
+ round(
+ t( sapply( comorb,
+           function( x ) tapply( x, mset$Ixdr, mean ) ) ) * 100, 1 ) )
> # remove the dates of recurrent HF
> # wh <- grep( "HF[1-9]", rownames(ct.tab) )
> # ct.tab <- ct.tab[-wh,]
> ct.tab
```

	SGLT2	SU	SGLT2	SU
prv.FL	12172	16391	98.7	93.2
prv.TIA	321	585	2.6	3.3
prv.Angina	1635	2219	13.3	12.6
prv.Bleed	522	894	4.2	5.1
prv.COPD	419	805	3.4	4.6
prv.PAD	599	1061	4.9	6.0
prv.HF	496	880	4.0	5.0
prv.Cancer	590	1284	4.8	7.3
prv.DMcompl	2291	1299	18.6	7.4
prv.Neuro	713	536	5.8	3.0
prv.DKD	461	420	3.7	2.4
prv.DiaEye	1501	1060	12.2	6.0
prv.Hypo	441	371	3.6	2.1
prv.AtrFib	740	1378	6.0	7.8
prv.MI	1003	1405	8.1	8.0
prv.UnstAng	470	640	3.8	3.6
prv.HmStr	96	163	0.8	0.9
prv.DiaFoot	121	98	1.0	0.6
prv.Other	554	791	4.5	4.5
prv.PeriAng	659	453	5.3	2.6

prv.IscStr	583	1028	4.7	5.8
prv.Amp	13	29	0.1	0.2
prv.CKD	69	434	0.6	2.5
prv.PCIsten	115	140	0.9	0.8
prv.CABG	326	451	2.6	2.6
prv.Keto	75	62	0.6	0.4
prv.Dial	0	8	0.0	0.0
pre.CVD	3681	5603	29.9	31.8
pre.Str	873	1535	7.1	8.7
pre.FPA	734	519	6.0	2.9
pre.Mic	4104	3035	33.3	17.3

1.2.3 Other medication

We have variables that hold the last date of dispensation before index for all drugs of interest, restricted to the period after 2011-12-01, one year prior to the first SGLT2 dispensation.

```
> wh <- grep( "dol", names(mset) )
> names( mset )[wh]
 [1] "dolACE"      "dolSta"      "dolBB1"      "dolARB"      "dolAlA"      "dolDHP"
 [7] "dolWtL"      "dolRPA"      "dolWrf"      "dolAsp"      "dolHCD"      "dolTHZ"
[13] "dolCcs"      "dolDXI"      "dolDgo"      "dolAP1"      "dolAmi"      "dolDTI"
[19] "dolNHP"      "dolFla"      "dolMetformin" "dolGLP1"     "dolMetxSGLT2" "dolMetxDPP4"
[25] "dolSGLT2"    "dolongIns"   "dolmixIns"   "dolDPP4"     "dolSU"       "dolintIns"
[31] "dolfastIns"  "dolTZD"      "dolAcarbose" "dolTZDxDPP4"

> codisp <- data.frame( pmax( mset[,wh] > ( mset[, "doIx"] - 1 ), 0, na.rm=TRUE ) )
> names( codisp ) <- gsub( "dol", "had.", names(codisp) )
> ( names( codisp )[wh.ins <- grep("Ins",names(codisp))] )
 [1] "had.longIns" "had.mixIns" "had.intIns" "had.fastIns"
> ( names( codisp )[wh.hyp <- c(1,4,6,12,3)] )
 [1] "had.ACE" "had.ARB" "had.DHP" "had.THZ" "had.BB1"
> ( names( codisp )[wh.cvd <- c(10,2,wh.hyp)] )
 [1] "had.Asp" "had.Sta" "had.ACE" "had.ARB" "had.DHP" "had.THZ" "had.BB1"
> codisp <- transform( codisp, got.Ins = apply( codisp[,wh.ins], 1, max ),
+                       got.Hyp = apply( codisp[,wh.hyp], 1, max ),
+                       got.CVD = apply( codisp[,wh.cvd], 1, max ) )
> names( codisp )
 [1] "had.ACE"      "had.Sta"      "had.BB1"      "had.ARB"      "had.AlA"
 [6] "had.DHP"      "had.WtL"      "had.RPA"      "had.Wrf"      "had.Asp"
[11] "had.HCD"      "had.THZ"      "had.Ccs"      "had.DXI"      "had.Dgo"
[16] "had.AP1"      "had.Ami"      "had.DTI"      "had.NHP"      "had.Fla"
[21] "had.Metformin" "had.GLP1"     "had.MetxSGLT2" "had.MetxDPP4" "had.SGLT2"
[26] "had.longIns"   "had.mixIns"   "had.DPP4"     "had.SU"       "had.intIns"
[31] "had.fastIns"   "had.TZD"      "had.Acarbose" "had.TZDxDPP4" "got.Ins"
[36] "got.Hyp"      "got.CVD"

> mt.tab <- cbind(
+ t( sapply( codisp,
+           function( x ) tapply( x, mset$Ixdr, sum ) ) ),
+ round(
+ t( sapply( codisp,
+           function( x ) tapply( x, mset$Ixdr, mean ) ) ) * 100, 1 ) )
> mt.tab
```

	SGLT2	SU	SGLT2	SU
had.ACE	4676	5886	37.9	33.5
had.Sta	9176	10956	74.4	62.3
had.BB1	3333	4769	27.0	27.1
had.ARB	4299	4459	34.9	25.3
had.A1A	644	896	5.2	5.1
had.DHP	3704	4613	30.0	26.2
had.WtL	89	77	0.7	0.4
had.RPA	791	1146	6.4	6.5
had.Wrf	508	1102	4.1	6.3
had.Asp	4301	5362	34.9	30.5
had.HCD	1703	2850	13.8	16.2
had.THZ	1877	2630	15.2	14.9
had.Ccs	662	1364	5.4	7.8
had.DXI	196	247	1.6	1.4
had.Dgo	307	762	2.5	4.3
had.AP1	122	285	1.0	1.6
had.Ami	30	71	0.2	0.4
had.DTI	153	263	1.2	1.5
had.NHP	212	256	1.7	1.5
had.Fla	10	19	0.1	0.1
had.Metformin	9881	14057	80.2	79.9
had.GLP1	4054	1332	32.9	7.6
had.MetxSGLT2	702	0	5.7	0.0
had.MetxDPP4	2702	2019	21.9	11.5
had.SGLT2	11626	0	94.3	0.0
had.longIns	2632	376	21.3	2.1
had.mixIns	1078	222	8.7	1.3
had.DPP4	2137	2264	17.3	12.9
had.SU	0	17594	0.0	100.0
had.intIns	935	332	7.6	1.9
had.fastIns	1052	229	8.5	1.3
had.TZD	28	27	0.2	0.2
had.Acarbose	15	35	0.1	0.2
had.TZDxDPP4	1	0	0.0	0.0
got.Ins	4147	952	33.6	5.4
got.Hyp	9593	12224	77.8	69.5
got.CVD	11229	14595	91.1	83.0

1.3 Propensity scoring

We now make a logistic regression of the indicator of SGLT2 assignment versus SU assignment. For convenience we append the just created data frames of the indicators we will use in the analysis:

```
> mset <- cbind( mset, comorb, codisp )
> names( mset )
 [1] "druggr"      "pnr"         "eksd"        "ATC"         "doDM"
 [6] "epiN"        "doIx"        "Ixdr"        "Ixatc"       "lastpr"
[11] "doTm"        "doFL"        "FLdr"        "FLatc"       "deCVDD"
[16] "coD"         "doTIA"       "doAngina"    "doBleed"     "doCOPD"
[21] "doPAD"       "doHF"        "doCancer"    "doDMcompl"   "doNeuro"
[26] "doDKD"       "doDiaEye"    "doHypo"      "doAtrFib"    "doMI"
[31] "doUnstAng"   "doHmStr"     "doDiaFoot"   "doOther"     "doPeriAng"
[36] "doIscStr"    "doAmp"       "doCKD"       "doPCIsten"   "doCABG"
```

[41]	"doKeto"	"doDial"	"doBari"	"sex"	"doBth"
[46]	"whBth"	"doDth"	"dSrc"	"dolACE"	"dolSta"
[51]	"dolBB1"	"dolARB"	"dolAlA"	"dolDHP"	"dolWtL"
[56]	"dolRPA"	"dolWrf"	"dolAsp"	"dolHCD"	"dolTHZ"
[61]	"dolCcs"	"dolDXI"	"dolDgo"	"dolAP1"	"dolAmi"
[66]	"dolDTI"	"dolNHP"	"dolFla"	"dolMetformin"	"dolGLP1"
[71]	"dolMetxSGLT2"	"dolMetxDPP4"	"dolSGLT2"	"dolongIns"	"dolmixIns"
[76]	"dolDPP4"	"dolSU"	"dolintIns"	"dolfastIns"	"dolTZD"
[81]	"dolAcarbose"	"dolTZDxDPP4"	"maxH"	"frail"	"recnum"
[86]	"C_ADIAG"	"compl"	"C_OPR"	"D_INDDTO"	"V_SENGDAGE"
[91]	"deHF"	"deMACE"	"deMI"	"deStr"	"deIscStr"
[96]	"deAF"	"deHH"	"deDKD"	"age"	"tff"
[101]	"prv.FL"	"prv.TIA"	"prv.Angina"	"prv.Bleed"	"prv.COPD"
[106]	"prv.PAD"	"prv.HF"	"prv.Cancer"	"prv.DMcompl"	"prv.Neuro"
[111]	"prv.DKD"	"prv.DiaEye"	"prv.Hypo"	"prv.AtrFib"	"prv.MI"
[116]	"prv.UnstAng"	"prv.HmStr"	"prv.DiaFoot"	"prv.Other"	"prv.PeriAng"
[121]	"prv.IscStr"	"prv.Amp"	"prv.CKD"	"prv.PCIsten"	"prv.CABG"
[126]	"prv.Keto"	"prv.Dial"	"pre.CVD"	"pre.Str"	"pre.FPA"
[131]	"pre.Mic"	"had.ACE"	"had.Sta"	"had.BB1"	"had.ARB"
[136]	"had.ALA"	"had.DHP"	"had.WtL"	"had.RPA"	"had.Wrf"
[141]	"had.Asp"	"had.HCD"	"had.THZ"	"had.Ccs"	"had.DXI"
[146]	"had.Dgo"	"had.AP1"	"had.Ami"	"had.DTI"	"had.NHP"
[151]	"had.Fla"	"had.Metformin"	"had.GLP1"	"had.MetxSGLT2"	"had.MetxDPP4"
[156]	"had.SGLT2"	"had.longIns"	"had.mixIns"	"had.DPP4"	"had.SU"
[161]	"had.intIns"	"had.fastIns"	"had.TZD"	"had.Acarbose"	"had.TZDxDPP4"
[166]	"got.Ins"	"got.Hyp"	"got.CVD"		

With this in place it is quite easy to fit a propensity score model because we can easily fish out the relevant variables:

```
> table( mset$Ixdr )
SGLT2    SU
12328 17594

> ( prv <- grep( "prv", names(mset) ) )
[1] 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122
[23] 123 124 125 126 127

> ( had <- grep( "had", names(mset) ) )
[1] 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153
[23] 154 155 156 157 158 159 160 161 162 163 164 165

> rmd <- c( grep( "SGL", names( mset ) [had] ),
+          grep( "SU" , names( mset ) [had] ) )
> had <- had[-rmd]
> names( mset ) [had]
[1] "had.ACE"      "had.Sta"      "had.BB1"      "had.ARB"      "had.ALA"
[6] "had.DHP"      "had.WtL"      "had.RPA"      "had.Wrf"      "had.Asp"
[11] "had.HCD"      "had.THZ"      "had.Ccs"      "had.DXI"      "had.Dgo"
[16] "had.AP1"      "had.Ami"      "had.DTI"      "had.NHP"      "had.Fla"
[21] "had.Metformin" "had.GLP1"     "had.MetxDPP4" "had.longIns"  "had.mixIns"
[26] "had.DPP4"      "had.intIns"   "had.fastIns"  "had.TZD"      "had.Acarbose"
[31] "had.TZDxDPP4"

> names( mset ) [prv]
[1] "prv.FL"      "prv.TIA"      "prv.Angina"   "prv.Bleed"    "prv.COPD"     "prv.PAD"
[7] "prv.HF"      "prv.Cancer"   "prv.DMcompl"  "prv.Neuro"    "prv.DKD"      "prv.DiaEye"
[13] "prv.Hypo"    "prv.AtrFib"   "prv.MI"       "prv.UnstAng"  "prv.HmStr"     "prv.DiaFoot"
[19] "prv.Other"   "prv.PeriAng"  "prv.IscStr"   "prv.Amp"      "prv.CKD"       "prv.PCIsten"
[25] "prv.CABG"    "prv.Keto"     "prv.Dial"
```

```

> system.time(
+ pr.0 <- glm( ( Ixdr == "SGLT2" ) ~
+             sex + age + frail + doIx + doFL +
+             as.matrix(mset[,prv]) + as.matrix(mset[,had]),
+             family = binomial,
+             data = mset, maxit = 100 ) )

   user  system elapsed 
   1.75    0.11    1.86 

> print( summary( pr.0 ), digits = 3 )

Call:
glm(formula = (Ixdr == "SGLT2") ~ sex + age + frail + doIx +
    doFL + as.matrix(mset[, prv]) + as.matrix(mset[, had]), family = binomial,
    data = mset, maxit = 100)

Deviance Residuals:
    Min       1Q   Median       3Q      Max 
-4.001  -0.751  -0.357   0.756   3.185 

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   -1.45e+03  2.78e+01  -52.23  < 2e-16 ***
sexF           -4.46e-02  3.09e-02   -1.44  0.14887
age            -2.92e-02  1.44e-03  -20.29  < 2e-16 ***
frail          -2.28e-03  3.46e-02   -0.07  0.94737
doIx             7.18e-01  1.40e-02   51.41  < 2e-16 ***
doFL             2.34e-03  3.58e-03    0.65  0.51351
as.matrix(mset[, prv])prv.FL    5.50e-01  9.91e-02   5.55  2.9e-08 ***
as.matrix(mset[, prv])prv.TIA  -6.98e-02  9.41e-02   -0.74  0.45811
as.matrix(mset[, prv])prv.Angina -4.17e-02  5.31e-02   -0.79  0.43235
as.matrix(mset[, prv])prv.Bleed -7.05e-02  7.21e-02   -0.98  0.32803
as.matrix(mset[, prv])prv.COPD  -9.39e-02  8.10e-02   -1.16  0.24689
as.matrix(mset[, prv])prv.PAD   -1.42e-01  7.05e-02   -2.02  0.04359 *
as.matrix(mset[, prv])prv.HF    -7.02e-02  8.47e-02   -0.83  0.40706
as.matrix(mset[, prv])prv.Cancer -1.17e-01  6.56e-02   -1.78  0.07531 .
as.matrix(mset[, prv])prv.DMcompl  1.92e-01  5.12e-02   3.75  0.00017 ***
as.matrix(mset[, prv])prv.Neuro   1.52e-01  7.83e-02   1.94  0.05216 .
as.matrix(mset[, prv])prv.DKD    -2.17e-01  9.35e-02   -2.33  0.02002 *
as.matrix(mset[, prv])prv.DiaEye   6.93e-02  5.78e-02   1.20  0.23035
as.matrix(mset[, prv])prv.Hypo   -8.65e-02  9.90e-02   -0.87  0.38250
as.matrix(mset[, prv])prv.AtrFib   4.82e-02  8.66e-02   0.56  0.57788
as.matrix(mset[, prv])prv.MI       2.46e-02  6.56e-02   0.38  0.70754
as.matrix(mset[, prv])prv.UnstAng -1.04e-01  8.80e-02   -1.19  0.23574
as.matrix(mset[, prv])prv.HmStr    3.29e-03  1.59e-01   0.02  0.98350
as.matrix(mset[, prv])prv.DiaFoot  2.00e-01  1.88e-01   1.07  0.28628
as.matrix(mset[, prv])prv.Other   -1.56e-01  8.13e-02   -1.92  0.05519 .
as.matrix(mset[, prv])prv.PeriAng  2.39e-01  8.58e-02   2.78  0.00537 **
as.matrix(mset[, prv])prv.IscStr  -1.43e-01  7.85e-02   -1.83  0.06762 .
as.matrix(mset[, prv])prv.Amp    -1.28e+00  4.88e-01   -2.62  0.00868 **
as.matrix(mset[, prv])prv.CKD    -1.33e+00  1.66e-01   -8.01  1.1e-15 ***
as.matrix(mset[, prv])prv.PCIsten  1.13e-01  1.71e-01   0.66  0.50765
as.matrix(mset[, prv])prv.CABG    6.18e-02  1.09e-01   0.57  0.56931
as.matrix(mset[, prv])prv.Keto     1.22e-03  2.32e-01   0.01  0.99582
as.matrix(mset[, prv])prv.Dial   -1.08e+01  9.06e+01  -0.12  0.90477
as.matrix(mset[, had])had.ACE     2.41e-01  3.54e-02   6.82  8.8e-12 ***
as.matrix(mset[, had])had.Sta     2.42e-01  3.41e-02   7.11  1.2e-12 ***
as.matrix(mset[, had])had.BB1     3.12e-03  3.99e-02   0.08  0.93778

```

```

as.matrix(mset[, had])had.ARB      4.27e-01  3.69e-02  11.57 < 2e-16 ***
as.matrix(mset[, had])had.ALA     -2.82e-03  7.41e-02  -0.04  0.96962
as.matrix(mset[, had])had.DHP      3.08e-02  3.55e-02   0.87  0.38689
as.matrix(mset[, had])had.WtL      6.42e-01  1.93e-01   3.32  0.00090 ***
as.matrix(mset[, had])had.RPA     -2.63e-02  6.99e-02  -0.38  0.70625
as.matrix(mset[, had])had.Wrf     -3.95e-02  9.00e-02  -0.44  0.66058
as.matrix(mset[, had])had.Asp      8.53e-02  3.71e-02   2.30  0.02130 *
as.matrix(mset[, had])had.HCD     -1.13e-01  4.99e-02  -2.26  0.02380 *
as.matrix(mset[, had])had.THZ      5.56e-02  4.28e-02   1.30  0.19406
as.matrix(mset[, had])had.Ccs     -3.34e-02  6.29e-02  -0.53  0.59499
as.matrix(mset[, had])had.DXI      1.85e-01  1.29e-01   1.44  0.14968
as.matrix(mset[, had])had.Dgo     -2.28e-01  1.09e-01  -2.09  0.03653 *
as.matrix(mset[, had])had.AP1     -1.33e-01  1.49e-01  -0.89  0.37461
as.matrix(mset[, had])had.Ami     -4.68e-01  2.81e-01  -1.66  0.09606 .
as.matrix(mset[, had])had.DTI      3.80e-02  1.40e-01   0.27  0.78610
as.matrix(mset[, had])had.NHP      3.05e-01  1.23e-01   2.48  0.01306 *
as.matrix(mset[, had])had.Fla     -1.62e-01  4.61e-01  -0.35  0.72505
as.matrix(mset[, had])had.Metformin -4.48e-02  4.33e-02  -1.03  0.30123
as.matrix(mset[, had])had.GLP1      1.65e+00  4.37e-02  37.73 < 2e-16 ***
as.matrix(mset[, had])had.MetxDPP4  1.24e+00  4.38e-02  28.25 < 2e-16 ***
as.matrix(mset[, had])had.longIns  2.19e+00  7.03e-02  31.22 < 2e-16 ***
as.matrix(mset[, had])had.mixIns   1.97e+00  9.15e-02  21.53 < 2e-16 ***
as.matrix(mset[, had])had.DPP4      7.66e-01  4.02e-02  19.05 < 2e-16 ***
as.matrix(mset[, had])had.intIns   1.31e+00  8.40e-02  15.55 < 2e-16 ***
as.matrix(mset[, had])had.fastIns  4.95e-01  1.01e-01   4.90  9.7e-07 ***
as.matrix(mset[, had])had.TZD      5.01e-01  3.39e-01   1.48  0.13957
as.matrix(mset[, had])had.Acarbose  2.43e-03  3.82e-01   0.01  0.99491
as.matrix(mset[, had])had.TZDxDPP4  9.98e+00  3.25e+02   0.03  0.97549
---

```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 40549 on 29921 degrees of freedom
Residual deviance: 28236 on 29858 degrees of freedom
AIC: 28364

Number of Fisher Scoring iterations: 11

With this fitted model we can now use the fitted values as propensity scores.

1.4 Propensity score matching

Based on this propensity score we take a matched sample of 1 per SGLT-2 user — note that we explicitly set a seed in order to get a fully reproducible code:

```

> set.seed( 1952 )
> system.time(
+ mt <- Match( Tr = (mset$Ixdr=="SGLT2"),
+             X = fitted( pr.0 ),
+             M = 1,
+             replace = FALSE,
+             exact = FALSE,
+             ties = FALSE,
+             caliper = 0.2 ) )

```

```

      user  system elapsed
    17.58    0.00   17.58
> str( mt )
List of 23
 $ est      : num [1, 1] 0
 $ se       : NULL
 $ est.noadj : num 0
 $ se.standard : num 0
 $ se.cond   : NULL
 $ mdata     :List of 4
 ..$ Y      : num [1:13712] 0 0 0 0 0 0 0 0 0 0 0 ...
 ..$ Tr     : num [1:13712] 1 1 1 1 1 1 1 1 1 1 1 ...
 ..$ X      : num [1:2, 1:6856] 0.823 0.822 0.982 0.981 0.982 ...
 .. ..- attr(*, "dimnames")=List of 2
 .. .. ..$ : NULL
 .. .. ..$ : chr [1:6856] "5" "7" "16" "19" ...
 ..$ orig.weighted.treated.nobs: num 12328
 $ index.treated : num [1:6856] 1 2 3 4 5 8 9 10 13 15 ...
 $ index.control : num [1:6856] 13743 7222 29782 3360 7498 ...
 $ index.dropped : int [1:5472] 1426 1620 1664 1667 1771 1824 1878 1929 1952 1984 ...
 $ weights       : num [1:6856] 1 1 1 1 1 1 1 1 1 1 ...
 $ orig.nobs      : int 29922
 $ orig.wnobs     : num 29922
 $ orig.treated.nobs: int 12328
 $ nobs           : int 29922
 $ wnobs          : num 6856
 $ caliper        : num 0.2
 $ ecaliper       : num 0.0591
 $ exact          : logi FALSE
 $ ndrops         : num 5472
 $ ndrops.matches : num 5472
 $ MatchLoopC     : num [1:6856, 1:6] 1 2 3 4 5 8 9 10 13 15 ...
 $ version        : chr "fast"
 $ estimand       : chr "ATT"
 - attr(*, "class")= chr "Match"

```

The resulting matching (`index.-variables`) refers to rows in `mset`:

```

> addmargins( rbind(
+ table( mset$Ixdr[unique(mt$index.treated)] ),
+ table( mset$Ixdr[unique(mt$index.control)] ) ), 2 )
      SGLT2  SU  Sum
[1,]  6856    0 6856
[2,]    0 6856 6856

```

We just use the index numbers for the treated as factor levels for the match-factor (we shall not use the factor though):

```

> tnum <- mt$index.treated
> cnum <- mt$index.control
> # a numeric with the index number of SGLT-2 for persons matched up
> mf <- rep( NA, nrow(mset) )
> mf[tnum] <- tnum
> mf[cnum] <- tnum
> # create a factor of this and tabulate
> mset <- transform( mset, mfac = factor(mf),
+                   psco = fitted(pr.0) )
> ( mtab <- with( mset, table( Ixdr, !is.na(mfac), useNA="ifany" ) ) )

```

```

Ixdr      FALSE  TRUE
SGLT2    5472  6856
SU       10738  6856

> round( cbind( rbind( cbind( mtab,
+                           pctab( mtab ) ),
+                           NA,
+                           NA),
+        pctab( mtab, margin=1 ) )[-3,], 1 )
Ixdr      FALSE  TRUE    All    N
SGLT2     44.4   55.6  100.0 12328.0
SU        61.0   39.0  100.0 17594.0

Ixdr      FALSE  TRUE
SGLT2     33.8   50.0
SU        66.2   50.0
All       100.0  100.0
N         16210.0 13712.0
FALSE TRUE FALSE TRUE All    N    FALSE  TRUE
SGLT2  5472 6856  44.4 55.6 100 12328    33.8    50
SU     10738 6856  61.0 39.0 100 17594    66.2    50
      NA   NA   NA   NA   NA   NA 16210.0 13712

```

We can see that not all persons can be matched with a caliper of 0.2; we can compare the propensity score among the matched and non-matched SGLT-2 patients:

```

> par( mar=c(3,3,1,1),mgp=c(3,1,0)/1.6,las=1,bty="n" )
> plot( mset$psco[mt$index.treated],
+       mset$psco[mt$index.control],
+       pch=16, cex=0.3 ,
+       xlim=0:1, xlab="SGLT-2i propensity score",
+       ylim=0:1, ylab="SU propensity score" )

```

For the use in further analyses we save a version for later use:

```

> oset <- mset
> pscore <- table( floor( oset$psco*100 ), oset$Ixdr )

```

Finally we make a dataset restricted to the matched persons:

```

> mset <- subset( oset, !is.na(mfac) )
> psmatch <- table( floor( mset$psco*100 ), mset$Ixdr )
> head( pscore )
      SGLT2  SU
0         2  64
1         2 218
2         4 382
3        14 519
4        29 625
5        31 678

> head( psmatch )
      SGLT2  SU
0         2  2
1         2  2
2         4  4
3        14 14
4        29 28
5        31 32

```

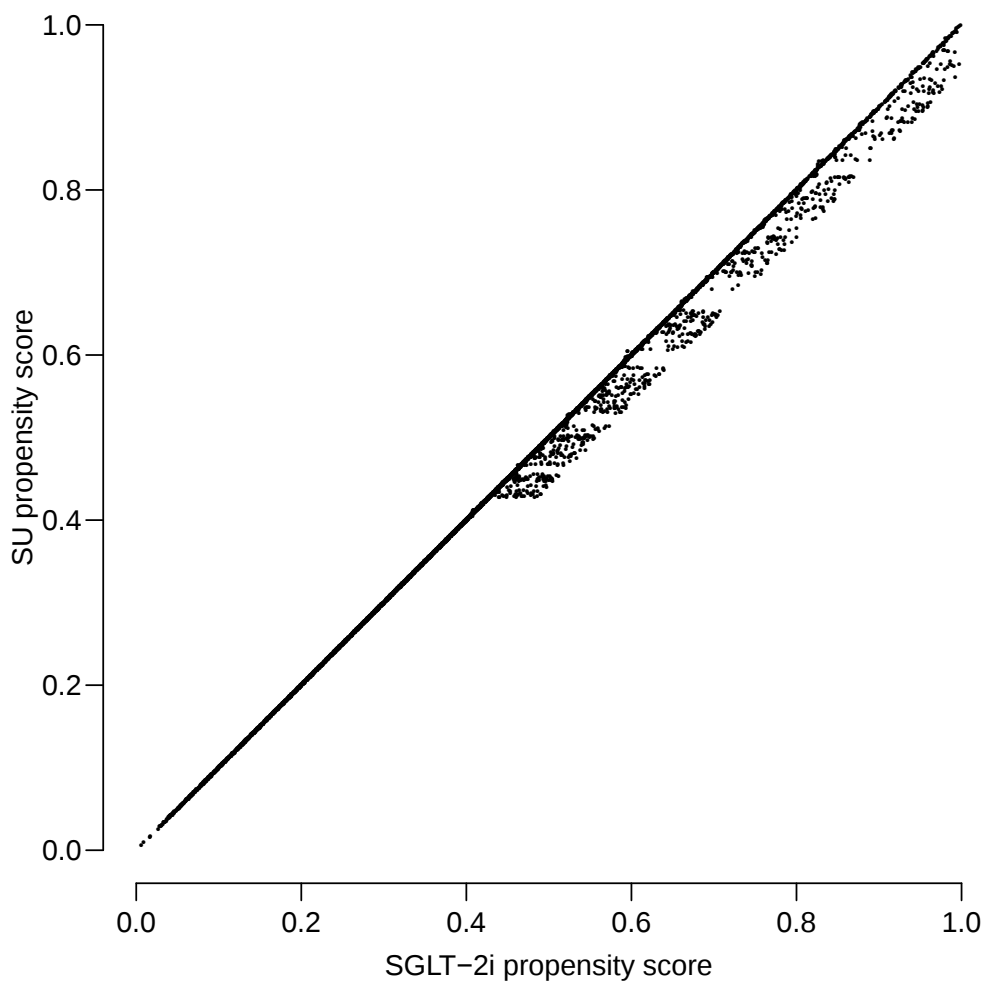


Figure 1.1: *Propensity scores from 1:1 matching; each matched set is represented by a dots.*
`./matchSGSU-cmp-ps`

```
> save( oset, mset, pscore, psmatch, file = "adatSGSU.Rda" )
> load( file = "adatSGSU.Rda" )
```

We also make histograms of the propensity scores, both for the original data and for the matched persons

```
> tt <- pscore
> tt[,1] <- tt[,1]/sum(tt[,1]) * 1000
> tt[,2] <- tt[,2]/sum(tt[,2]) * 1000
> tt <- cbind( -tt[,1], tt )
> head(tt)
```

	SGLT2		SU
0	-0.1622323	0.1622323	3.637604
1	-0.1622323	0.1622323	12.390588
2	-0.3244646	0.3244646	21.711947
3	-1.1356262	1.1356262	29.498693
4	-2.3523686	2.3523686	35.523474
5	-2.5146009	2.5146009	38.535864

```
> nam <- colnames( tt )[-1]
> clr <- c("transparent","red","blue")
```

```

> # we use the undocumented feature of boxplot that you can get stacked
> # bars starting in the negative by giving negative numbers to the first
> # column. But it will mysteriously ignore the first element of col...
> par( mar=c(3,3,1,1), mgp=c(3,1,0)/1.6, bty="n", las=1 )
> barplot( t(tt), space=0, col=clr, border="transparent", xlim=c(-65,65),
+         horiz=T, yaxt="n", ylab="Propensity score for SGLT-2 (%)", xaxt="n" )
> axis( side=2, at=seq(0,95,5), labels=NA, tcl=-0.3 )
> axis( side=2, at=0:9*10 )
> axis( side=1, at=-6:6*10, labels=NA, tcl=-0.3 )
> axis( side=1, at=-3:3*20, labels=abs(-3:3*20) )
> text( rep(60,2), 19:18*5, nam, col=clr[-1], font=2, adj=1 )
> # mtext( "%", side=1, font=2, line=1.5, at=-2.5 )
> mtext( "\211", side=1, font=2, line=1.5, at=0 )

```

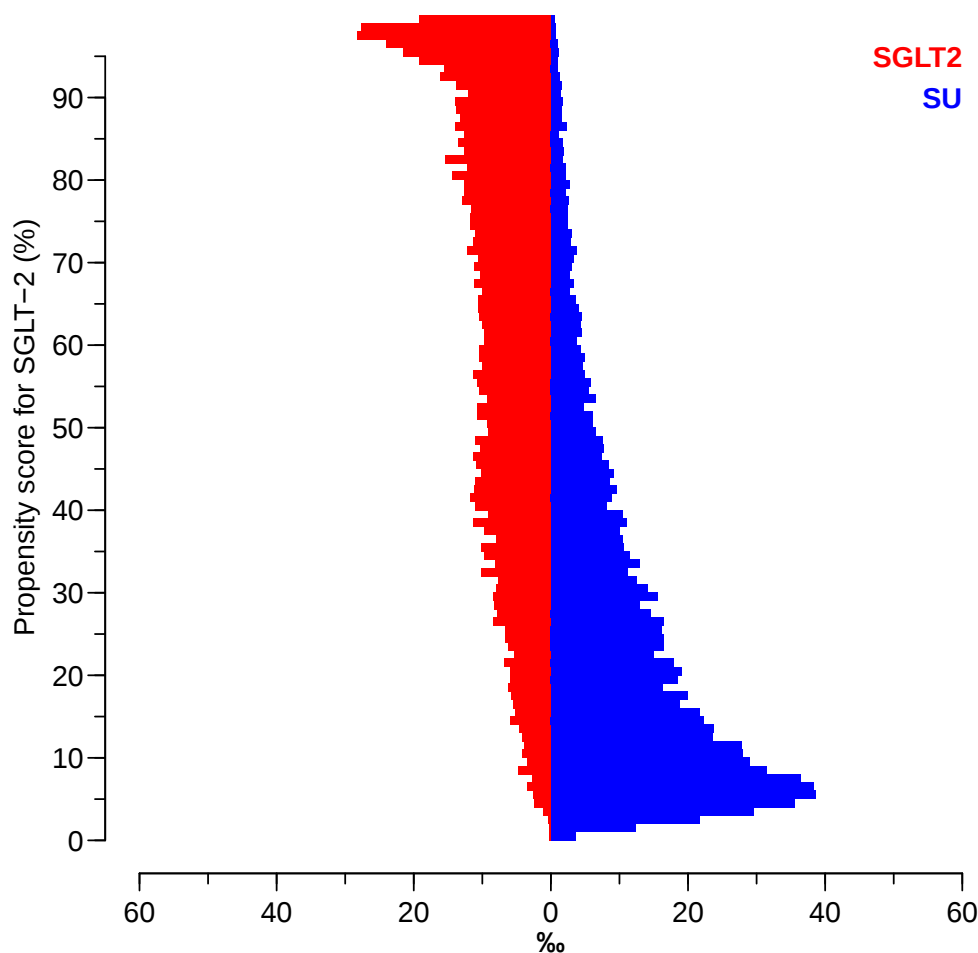


Figure 1.2: Propensity scores for the SGLT-2 group (left, percent) and other groups (right, %■) in the 1:3 propensity score matched study.

../matchSGSU-pscoreo

```

> tt <- psmatch
> tt[,1] <- tt[,1]/sum(tt[,1]) * 1000
> tt[,2] <- tt[,2]/sum(tt[,2]) * 1000
> tt <- cbind( -tt[,1], tt )

```

```

> par( mar=c(3,3,1,1), mgp=c(3,1,0)/1.6, bty="n", las=1 )
> barplot( t(tt), space=0, col=clr, border="transparent", xlim=c(-25,25),
+         horiz=T, yaxt="n", ylab="Propensity score for SGLT-2 (%)", xaxt="n" )
> axis( side=2, at=seq(0,95,5), labels=NA, tcl=-0.3 )
> axis( side=2, at=0:9*10 )
> axis( side=1, at=-6:6*10, labels=NA, tcl=-0.3 )
> axis( side=1, at=-3:3*20, labels=abs(-3:3*20) )
> text( rep(60,2), 19:18*5, nam, col=clr[-1], font=2, adj=1 )
> # mtext( "%", side=1, font=2, line=1.5, at=-2.5 )
> mtext( "\211", side=1, font=2, line=1.5, at=10 )

```

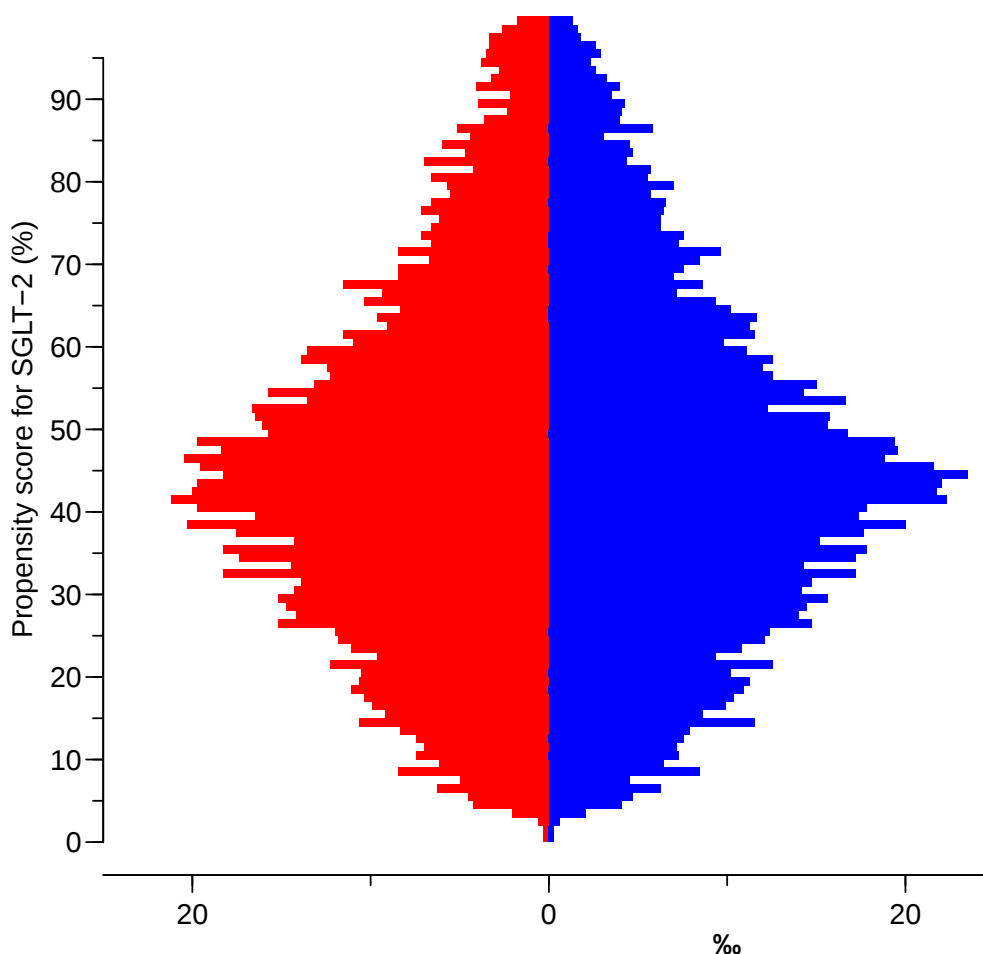


Figure 1.3: *Propensity scores for the SGLT-2 group resp. SU group in the 1:1 propensity score matched study.*

./matchSGSU-pscorem

1.5 Baseline tables for propensity matched persons

We have the matched sets in the dataframe `mset`, so we can almost verbatim reuse the code doing the tables for the original sample, except for the names of the resulting tables: `dm.tab` (demographics for matched sample), `cm.tab` (comobidites for matched sample) and `mm.tab` (medication for matched sample).

1.5.1 Demographics

First the tabulations of the baseline demographics:

```
> t.sex <- with( mset, ptab( sex ) )
> rownames( t.sex )[1] <- paste("Sex",rownames( t.sex )[1])
> t.age <- with( mset, ptab( floor( pmin(pmax(age,30),89)/10 ) * 10 ) )
> rownames( t.age )[1] <- "Age at index <40"
> rownames( t.age )[nrow(t.age)] <- "80+"
> t.fl0 <- with( mset, ptab( doIx-doFL==0 ) )[-1,,drop=F]
> rownames( t.fl0 )[1] <- "Index = First Line"
> t.fl0
```

	SGLT2	SU	SGLT2	SU
Index = First Line	154	128	2.2	1.9

```
> m.fl0 <- with( subset(mset, doIx-doFL>0 ), round( c( tapply( doIx-doFL, Ixdr, mean ),
+                                                     tapply( doIx-doFL, Ixdr, sd ) ), 1 ) )
> dim( m.fl0 ) <- c(1,4)
> rownames( m.fl0 ) <- c("Index not FL: Mean / SD")
> m.fl0
```

	[,1]	[,2]	[,3]	[,4]
Index not FL: Mean / SD	7	7	4.8	5.1

```
> m.age <- with( mset, round( c( tapply( age, Ixdr, mean ),
+                               tapply( age, Ixdr, sd ) ), 1 ) )
> dim( m.age ) <- c(1,4)
> rownames( m.age ) <- c("Age: Mean / SD")
> m.age
```

	[,1]	[,2]	[,3]	[,4]
Age: Mean / SD	60.8	60.7	11.2	12.5

```
> ## Date of index by 6 months and 1 year
> with( mset, ptab( floor( doIx*2 )/2 ) )
```

	SGLT2	SU	SGLT2	SU
2012.5	8	40	0.1	0.6
2013	458	430	6.7	6.3
2013.5	565	499	8.2	7.3
2014	665	666	9.7	9.7
2014.5	740	680	10.8	9.9
2015	965	986	14.1	14.4
2015.5	899	1004	13.1	14.6
2016	1376	1303	20.1	19.0
2016.5	1180	1248	17.2	18.2

```
> t.dat <- with( mset, ptab( floor( doIx ) ) )
> rownames( t.dat )[1] <- paste("Index date",rownames( t.dat )[1])
> ## Date of First Line
> t.fl <- with( mset, ptab( floor( doFL ) ) )
> rownames( t.fl )[1] <- paste("Date of first line",rownames( t.fl )[1])
> ## Frailty
> t.fr <- with( mset, ptab( frail ) )
> rownames( t.fr )[1] <- paste("Frailty",rownames( t.fr )[1])
> dm.tab <- rbind( t.sex, t.fl0, m.fl0, t.age, m.age, t.dat, t.fl, t.fr )
> dm.tab
```

	SGLT2	SU	SGLT2	SU
Sex M	4132.0	4111.0	60.3	60.0
F	2724.0	2745.0	39.7	40.0
Index = First Line	154.0	128.0	2.2	1.9
Index not FL: Mean / SD	7.0	7.0	4.8	5.1

Age at index <40	230.0	360.0	3.4	5.3
40	940.0	999.0	13.7	14.6
50	1950.0	1771.0	28.4	25.8
60	2285.0	2087.0	33.3	30.4
70	1226.0	1293.0	17.9	18.9
80+	225.0	346.0	3.3	5.0
Age: Mean / SD	60.8	60.7	11.2	12.5
Index date 2012	8.0	40.0	0.1	0.6
2013	1023.0	929.0	14.9	13.6
2014	1405.0	1346.0	20.5	19.6
2015	1864.0	1990.0	27.2	29.0
2016	2556.0	2551.0	37.3	37.2
Date of first line 1995	167.0	158.0	2.4	2.3
1996	68.0	73.0	1.0	1.1
1997	73.0	92.0	1.1	1.3
1998	87.0	107.0	1.3	1.6
1999	130.0	135.0	1.9	2.0
2000	133.0	149.0	1.9	2.2
2001	157.0	172.0	2.3	2.5
2002	157.0	194.0	2.3	2.8
2003	270.0	269.0	3.9	3.9
2004	291.0	296.0	4.2	4.3
2005	352.0	329.0	5.1	4.8
2006	407.0	375.0	5.9	5.5
2007	461.0	412.0	6.7	6.0
2008	490.0	467.0	7.1	6.8
2009	560.0	464.0	8.2	6.8
2010	616.0	548.0	9.0	8.0
2011	569.0	557.0	8.3	8.1
2012	496.0	501.0	7.2	7.3
2013	430.0	441.0	6.3	6.4
2014	362.0	395.0	5.3	5.8
2015	332.0	412.0	4.8	6.0
2016	248.0	310.0	3.6	4.5
Frailty 0	4934.0	4977.0	72.0	72.6
1	1922.0	1879.0	28.0	27.4

1.5.2 Comorbidities

The data frame contains the dates of the *earliest* recorded comorbidities from the NPR, hence the prefix `.prv`:

```
> wh <- match( rownames(ct.tab), names( mset ) )
> names( mset )[wh]
 [1] "prv.FL"      "prv.TIA"      "prv.Angina"    "prv.Bleed"    "prv.COPD"     "prv.PAD"
 [7] "prv.HF"      "prv.Cancer"   "prv.DMcompl"   "prv.Neuro"    "prv.DKD"      "prv.DiaEye"
[13] "prv.Hypo"    "prv.AtrFib"   "prv.MI"        "prv.UnstAng"  "prv.HmStr"    "prv.DiaFoot"
[19] "prv.Other"   "prv.PeriAng"  "prv.IscStr"    "prv.Amp"      "prv.CKD"      "prv.PCIsten"
[25] "prv.CABG"    "prv.Keto"     "prv.Dial"      "pre.CVD"      "pre.Str"       "pre.FPA"
[31] "pre.Mic"

> comorb <- mset[,wh]
> cm.tab <- cbind(
+ t( sapply( comorb,
+           function( x ) tapply( x, mset$Ixdr, sum ) ) ),
+ round(
```

```
+ t( supply( comorb,
+           function( x ) tapply( x, mset$Ixdr, mean ) ) ) * 100, 1 ) )
> cm.tab
```

	SGLT2	SU	SGLT2	SU
prv.FL	6702	6728	97.8	98.1
prv.TIA	184	175	2.7	2.6
prv.Angina	842	831	12.3	12.1
prv.Bleed	310	300	4.5	4.4
prv.COPD	252	263	3.7	3.8
prv.PAD	338	331	4.9	4.8
prv.HF	266	255	3.9	3.7
prv.Cancer	365	357	5.3	5.2
prv.DMcompl	760	722	11.1	10.5
prv.Neuro	270	254	3.9	3.7
prv.DKD	187	179	2.7	2.6
prv.DiaEye	543	532	7.9	7.8
prv.Hypo	161	163	2.3	2.4
prv.AtrFib	429	409	6.3	6.0
prv.MI	515	501	7.5	7.3
prv.UnstAng	228	245	3.3	3.6
prv.HmStr	56	50	0.8	0.7
prv.DiaFoot	40	39	0.6	0.6
prv.Other	283	286	4.1	4.2
prv.PeriAng	227	232	3.3	3.4
prv.IscStr	331	321	4.8	4.7
prv.Amp	6	7	0.1	0.1
prv.CKD	48	40	0.7	0.6
prv.PCIsten	52	49	0.8	0.7
prv.CABG	155	170	2.3	2.5
prv.Keto	30	33	0.4	0.5
prv.Dial	0	0	0.0	0.0
pre.CVD	2004	1907	29.2	27.8
pre.Str	499	482	7.3	7.0
pre.FPA	258	260	3.8	3.8
pre.Mic	1579	1500	23.0	21.9

1.5.3 Other medication

We have variables that hold the last date of dispensation before index for all drugs of interest — well, only in the period after 2011-12-01, one year prior to the first SGLT2 dispensation.

```
> wh <- grep( "had.", names( mset ) )
> names( mset )[wh]
 [1] "had.ACE"      "had.Sta"      "had.BB1"      "had.ARB"      "had.A1A"
 [6] "had.DHP"      "had.WtL"      "had.RPA"      "had.Wrf"      "had.Asp"
[11] "had.HCD"      "had.THZ"      "had.Ccs"      "had.DXI"      "had.Dgo"
[16] "had.AP1"      "had.Ami"      "had.DTI"      "had.NHP"      "had.Fla"
[21] "had.Metformin" "had.GLP1"     "had.MetxSGLT2" "had.MetxDPP4" "had.SGLT2"
[26] "had.longIns"  "had.mixIns"   "had.DPP4"      "had.SU"        "had.intIns"
[31] "had.fastIns"  "had.TZD"      "had.Acarbose"  "had.TZDxDPP4"

> codisp <- mset[,wh]
> ( names( codisp )[wh.ins <- grep("Ins",names(codisp))] )
 [1] "had.longIns" "had.mixIns" "had.intIns" "had.fastIns"

> ( names( codisp )[wh.hyp <- c(1,4,6,12,3)] )
```

```

[1] "had.ACE" "had.ARB" "had.DHP" "had.THZ" "had.BB1"
> ( names( codisp )[wh.cvd <- c(8,2,wh.hyp)] )
[1] "had.RPA" "had.Sta" "had.ACE" "had.ARB" "had.DHP" "had.THZ" "had.BB1"
> codisp <- transform( codisp, got.Ins = apply( codisp[,wh.ins], 1, max ),
+                       got.Hyp = apply( codisp[,wh.hyp], 1, max ),
+                       got.CVD = apply( codisp[,wh.cvd], 1, max ) )
> names( codisp )

[1] "had.ACE"      "had.Sta"      "had.BB1"      "had.ARB"      "had.A1A"
[6] "had.DHP"      "had.WtL"      "had.RPA"      "had.Wrf"      "had.Asp"
[11] "had.HCD"      "had.THZ"      "had.Ccs"      "had.DXI"      "had.Dgo"
[16] "had.AP1"      "had.Ami"      "had.DTI"      "had.NHP"      "had.Fla"
[21] "had.Metformin" "had.GLP1"     "had.MetxSGLT2" "had.MetxDPP4" "had.SGLT2"
[26] "had.longIns"  "had.mixIns"   "had.DPP4"      "had.SU"       "had.intIns"
[31] "had.fastIns"  "had.TZD"      "had.Acarbose"  "had.TZDxDPP4" "got.Ins"
[36] "got.Hyp"      "got.CVD"

> mm.tab <- cbind(
+ t( sapply( codisp,
+           function( x ) tapply( x, mset$Ixdr, sum ) ) ),
+ round(
+ t( sapply( codisp,
+           function( x ) tapply( x, mset$Ixdr, mean ) ) ) * 100, 1 ) )
+ mm.tab

```

	SGLT2	SU	SGLT2	SU
had.ACE	2467	2435	36.0	35.5
had.Sta	4779	4796	69.7	70.0
had.BB1	1759	1747	25.7	25.5
had.ARB	2083	2106	30.4	30.7
had.A1A	328	321	4.8	4.7
had.DHP	1897	1883	27.7	27.5
had.WtL	43	46	0.6	0.7
had.RPA	411	402	6.0	5.9
had.Wrf	293	264	4.3	3.9
had.Asp	2134	2117	31.1	30.9
had.HCD	891	862	13.0	12.6
had.THZ	977	1017	14.3	14.8
had.Ccs	432	437	6.3	6.4
had.DXI	118	108	1.7	1.6
had.Dgo	194	179	2.8	2.6
had.AP1	80	80	1.2	1.2
had.Ami	20	21	0.3	0.3
had.DTI	89	95	1.3	1.4
had.NHP	108	100	1.6	1.5
had.Fla	7	8	0.1	0.1
had.Metformin	5454	5484	79.6	80.0
had.GLP1	1194	1127	17.4	16.4
had.MetxSGLT2	418	0	6.1	0.0
had.MetxDPP4	1462	1464	21.3	21.4
had.SGLT2	6438	0	93.9	0.0
had.longIns	416	363	6.1	5.3
had.mixIns	227	192	3.3	2.8
had.DPP4	1306	1311	19.0	19.1
had.SU	0	6856	0.0	100.0
had.intIns	245	234	3.6	3.4
had.fastIns	182	164	2.7	2.4
had.TZD	16	14	0.2	0.2

had.Acarbose	10	10	0.1	0.1
had.TZDxDPP4	0	0	0.0	0.0
got.Ins	871	757	12.7	11.0
got.Hyp	5051	4976	73.7	72.6
got.CVD	6008	5899	87.6	86.0

1.6 Overview of pre- and post matching

The number of persons and episodes:

```
> addmargins( with( oset, table(table(pnr)) ) )
      1      Sum
29922 29922

> addmargins(
+ with( oset, table(DPP4=(tt<-table(pnr,Ixdr))[,1],SGLT2=tt[,2]) ) )

      SGLT2
DPP4      0      1      Sum
0          0 17594 17594
1    12328      0 12328
Sum 12328 17594 29922

> addmargins( with( mset, table(table(pnr)) ) )
      1      Sum
13712 13712

> addmargins(
+ with( mset, table(DPP4=(tt<-table(pnr,Ixdr))[,1],SGLT2=tt[,2]) ) )

      SGLT2
DPP4      0      1      Sum
0          0 6856 6856
1    6856      0 6856
Sum 6856 6856 13712
```

The best overview is created if we list the tables for the matched and un-matched next to each other. However we first check that that have the same sets of rows:

```
> identical( rownames(dt.tab), rownames(dm.tab) )
[1] TRUE

> identical( rownames(ct.tab), rownames(cm.tab) )
[1] TRUE

> identical( rownames(mt.tab), rownames(mm.tab) )
[1] TRUE

> cbind( dt.tab, dm.tab )

      SGLT2      SU SGLT2      SU SGLT2      SU SGLT2      SU
Sex M    7525.0 10348.0 61.0 58.8 4132.0 4111.0 60.3 60.0
F        4803.0 7246.0 39.0 41.2 2724.0 2745.0 39.7 40.0
Index = First Line    156.0 1203.0 1.3 6.8 154.0 128.0 2.2 1.9
Index not FL: Mean / SD    8.5 6.2 5.3 5.0 7.0 7.0 4.8 5.1
Age at index <40      509.0 637.0 4.1 3.6 230.0 360.0 3.4 5.3
40      1782.0 1993.0 14.5 11.3 940.0 999.0 13.7 14.6
50      3787.0 3912.0 30.7 22.2 1950.0 1771.0 28.4 25.8
```

60	4007.0	5147.0	32.5	29.3	2285.0	2087.0	33.3	30.4
70	1960.0	4092.0	15.9	23.3	1226.0	1293.0	17.9	18.9
80+	283.0	1813.0	2.3	10.3	225.0	346.0	3.3	5.0
Age: Mean / SD	59.8	63.9	11.0	13.0	60.8	60.7	11.2	12.5
Index date 2012	11.0	412.0	0.1	2.3	8.0	40.0	0.1	0.6
2013	1353.0	5130.0	11.0	29.2	1023.0	929.0	14.9	13.6
2014	2069.0	4477.0	16.8	25.4	1405.0	1346.0	20.5	19.6
2015	3333.0	4136.0	27.0	23.5	1864.0	1990.0	27.2	29.0
2016	5562.0	3439.0	45.1	19.5	2556.0	2551.0	37.3	37.2
Date of first line 1995	548.0	362.0	4.4	2.1	167.0	158.0	2.4	2.3
1996	196.0	157.0	1.6	0.9	68.0	73.0	1.0	1.1
1997	199.0	181.0	1.6	1.0	73.0	92.0	1.1	1.3
1998	257.0	247.0	2.1	1.4	87.0	107.0	1.3	1.6
1999	341.0	283.0	2.8	1.6	130.0	135.0	1.9	2.0
2000	358.0	329.0	2.9	1.9	133.0	149.0	1.9	2.2
2001	406.0	397.0	3.3	2.3	157.0	172.0	2.3	2.5
2002	421.0	470.0	3.4	2.7	157.0	194.0	2.3	2.8
2003	579.0	603.0	4.7	3.4	270.0	269.0	3.9	3.9
2004	602.0	698.0	4.9	4.0	291.0	296.0	4.2	4.3
2005	685.0	801.0	5.6	4.6	352.0	329.0	5.1	4.8
2006	760.0	879.0	6.2	5.0	407.0	375.0	5.9	5.5
2007	808.0	1004.0	6.6	5.7	461.0	412.0	6.7	6.0
2008	856.0	1151.0	6.9	6.5	490.0	467.0	7.1	6.8
2009	947.0	1218.0	7.7	6.9	560.0	464.0	8.2	6.8
2010	946.0	1345.0	7.7	7.6	616.0	548.0	9.0	8.0
2011	873.0	1515.0	7.1	8.6	569.0	557.0	8.3	8.1
2012	704.0	1533.0	5.7	8.7	496.0	501.0	7.2	7.3
2013	580.0	1720.0	4.7	9.8	430.0	441.0	6.3	6.4
2014	510.0	1239.0	4.1	7.0	362.0	395.0	5.3	5.8
2015	436.0	944.0	3.5	5.4	332.0	412.0	4.8	6.0
2016	316.0	518.0	2.6	2.9	248.0	310.0	3.6	4.5
Frailty 0	8283.0	12644.0	67.2	71.9	4934.0	4977.0	72.0	72.6
1	4045.0	4950.0	32.8	28.1	1922.0	1879.0	28.0	27.4

```
> cbind( ct.tab, cm.tab )
```

	SGLT2	SU	SGLT2	SU	SGLT2	SU	SGLT2	SU
prv.FL	12172	16391	98.7	93.2	6702	6728	97.8	98.1
prv.TIA	321	585	2.6	3.3	184	175	2.7	2.6
prv.Angina	1635	2219	13.3	12.6	842	831	12.3	12.1
prv.Bleed	522	894	4.2	5.1	310	300	4.5	4.4
prv.COPD	419	805	3.4	4.6	252	263	3.7	3.8
prv.PAD	599	1061	4.9	6.0	338	331	4.9	4.8
prv.HF	496	880	4.0	5.0	266	255	3.9	3.7
prv.Cancer	590	1284	4.8	7.3	365	357	5.3	5.2
prv.DMcompl	2291	1299	18.6	7.4	760	722	11.1	10.5
prv.Neuro	713	536	5.8	3.0	270	254	3.9	3.7
prv.DKD	461	420	3.7	2.4	187	179	2.7	2.6
prv.DiaEye	1501	1060	12.2	6.0	543	532	7.9	7.8
prv.Hypo	441	371	3.6	2.1	161	163	2.3	2.4
prv.AtrFib	740	1378	6.0	7.8	429	409	6.3	6.0
prv.MI	1003	1405	8.1	8.0	515	501	7.5	7.3
prv.UnstAng	470	640	3.8	3.6	228	245	3.3	3.6
prv.HmStr	96	163	0.8	0.9	56	50	0.8	0.7
prv.DiaFoot	121	98	1.0	0.6	40	39	0.6	0.6
prv.Other	554	791	4.5	4.5	283	286	4.1	4.2
prv.PeriAng	659	453	5.3	2.6	227	232	3.3	3.4
prv.IscStr	583	1028	4.7	5.8	331	321	4.8	4.7
prv.Amp	13	29	0.1	0.2	6	7	0.1	0.1

prv.CKD	69	434	0.6	2.5	48	40	0.7	0.6
prv.PCIsten	115	140	0.9	0.8	52	49	0.8	0.7
prv.CABG	326	451	2.6	2.6	155	170	2.3	2.5
prv.Keto	75	62	0.6	0.4	30	33	0.4	0.5
prv.Dial	0	8	0.0	0.0	0	0	0.0	0.0
pre.CVD	3681	5603	29.9	31.8	2004	1907	29.2	27.8
pre.Str	873	1535	7.1	8.7	499	482	7.3	7.0
pre.FPA	734	519	6.0	2.9	258	260	3.8	3.8
pre.Mic	4104	3035	33.3	17.3	1579	1500	23.0	21.9

```
> cbind( mt.tab, mm.tab )
```

	SGLT2	SU	SGLT2	SU	SGLT2	SU	SGLT2	SU
had.ACE	4676	5886	37.9	33.5	2467	2435	36.0	35.5
had.Sta	9176	10956	74.4	62.3	4779	4796	69.7	70.0
had.BBl	3333	4769	27.0	27.1	1759	1747	25.7	25.5
had.ARB	4299	4459	34.9	25.3	2083	2106	30.4	30.7
had.Ala	644	896	5.2	5.1	328	321	4.8	4.7
had.DHP	3704	4613	30.0	26.2	1897	1883	27.7	27.5
had.WtL	89	77	0.7	0.4	43	46	0.6	0.7
had.RPA	791	1146	6.4	6.5	411	402	6.0	5.9
had.Wrf	508	1102	4.1	6.3	293	264	4.3	3.9
had.Asp	4301	5362	34.9	30.5	2134	2117	31.1	30.9
had.HCD	1703	2850	13.8	16.2	891	862	13.0	12.6
had.THZ	1877	2630	15.2	14.9	977	1017	14.3	14.8
had.Ccs	662	1364	5.4	7.8	432	437	6.3	6.4
had.DXI	196	247	1.6	1.4	118	108	1.7	1.6
had.Dgo	307	762	2.5	4.3	194	179	2.8	2.6
had.APl	122	285	1.0	1.6	80	80	1.2	1.2
had.Ami	30	71	0.2	0.4	20	21	0.3	0.3
had.DTI	153	263	1.2	1.5	89	95	1.3	1.4
had.NHP	212	256	1.7	1.5	108	100	1.6	1.5
had.Fla	10	19	0.1	0.1	7	8	0.1	0.1
had.Metformin	9881	14057	80.2	79.9	5454	5484	79.6	80.0
had.GLP1	4054	1332	32.9	7.6	1194	1127	17.4	16.4
had.MetxSGLT2	702	0	5.7	0.0	418	0	6.1	0.0
had.MetxDPP4	2702	2019	21.9	11.5	1462	1464	21.3	21.4
had.SGLT2	11626	0	94.3	0.0	6438	0	93.9	0.0
had.longIns	2632	376	21.3	2.1	416	363	6.1	5.3
had.mixIns	1078	222	8.7	1.3	227	192	3.3	2.8
had.DPP4	2137	2264	17.3	12.9	1306	1311	19.0	19.1
had.SU	0	17594	0.0	100.0	0	6856	0.0	100.0
had.intIns	935	332	7.6	1.9	245	234	3.6	3.4
had.fastIns	1052	229	8.5	1.3	182	164	2.7	2.4
had.TZD	28	27	0.2	0.2	16	14	0.2	0.2
had.Acarbose	15	35	0.1	0.2	10	10	0.1	0.1
had.TZDxDPP4	1	0	0.0	0.0	0	0	0.0	0.0
got.Ins	4147	952	33.6	5.4	871	757	12.7	11.0
got.Hyp	9593	12224	77.8	69.5	5051	4976	73.7	72.6
got.CVD	11229	14595	91.1	83.0	6008	5899	87.6	86.0

```
> save( dt.tab, dm.tab,
+       ct.tab, cm.tab,
+       mt.tab, mm.tab, file="btabSGSU.Rda" )
```

...now input from ../rep/anaSGSU.tex

1.7 Survival analysis datasets: Lexis objects

In this section we take the original and the matched data and set up **Lexis**-objects for the survival analyses; we make separate objects for Death, heart failure (HF) and combined outcomes.

First get the relevant data:

```
> library( Epi )
> library( survival )
> print( sessionInfo(), l=F )
R version 3.5.0 (2018-04-23)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server 2012 R2 x64 (build 9600)

Matrix products: default

attached base packages:
[1] stats      graphics  grDevices  utils      datasets  methods   base

other attached packages:
[1] survival_2.41-3 Epi_2.30

loaded via a namespace (and not attached):
 [1] cmprsk_2.2-7      zoo_1.8-1         MASS_7.3-49       compiler_3.5.0
 [5] Matrix_1.2-14     plyr_1.8.4        parallel_3.5.0    tools_3.5.0
 [9] etm_0.6-2         Rcpp_0.12.16      splines_3.5.0     grid_3.5.0
[13] numDeriv_2016.8-1 lattice_0.20-35

> clear()
> load( file = "adatSGSU.Rda" )
> lls()

  name      mode      class      dim      size(Kb)
1 mset      list      data.frame 13712 170      20,004.8
2 oset      list      data.frame 29922 170      43,184.4
3 pscore    numeric table      100 2        8.1
4 psmatch   numeric table      100 2        8.1
```

We will follow persons from date of new use, `doIx`, till either date of event.

For later use we define both the time since index (`tfi`) and current date (period — `per`) and current age (`cua`) as timescales. The latter not to be confused with age at index date, `age`.

1.8 Types of index drugs

The datasets of all first users and all matched contain the variable `Ixatc`:

```
> tt <- cbind( table( oset$Ixatc ),
+             table( mset$Ixatc ) )
> tt <- data.frame( tt )
> str(tt)
'data.frame':    13 obs. of  2 variables:
 $ X1: int  960 290 753 1753 13490 313 11 378 7238 357 ...
 $ X2: int  380 119 290 685 5241 203 11 204 4481 204 ...

> tt$atc <- rownames(tt)
> str(tt)
```

```
'data.frame':      13 obs. of  3 variables:
 $ X1 : int  960 290 753 1753 13490 313 11 378 7238 357 ...
 $ X2 : int  380 119 290 685 5241 203 11 204 4481 204 ...
 $ atc: chr  "A10BB01" "A10BB03" "A10BB07" "A10BB09" ...
```

```
> head(tt)
      X1  X2   atc
A10BB01 960 380 A10BB01
A10BB03 290 119 A10BB03
A10BB07 753 290 A10BB07
A10BB09 1753 685 A10BB09
A10BB12 13490 5241 A10BB12
A10BD15  313 203 A10BD15
```

But we want a translation to text; this is in the file `atcnam.txt`:

```
> atc <- read.table( "atcnam.txt", header=TRUE )
> head(atc)
      atc                      drnam
1 A10BF01                      acarbose
2 A10BD07 metformin og sitagliptin
3 A10BD08 metformin og vildagliptin
4 A10BD09 pioglitazon og alogliptin
5 A10BD10 metformin og saxagliptin
6 A10BD11 metformin og linagliptin
> tt <- merge( tt, atc )
> tt
      atc  X1  X2                      drnam
1 A10BB01 960 380                      glibenclamid
2 A10BB03 290 119                      tolbutamid
3 A10BB07 753 290                      glipizid
4 A10BB09 1753 685                      gliclazid
5 A10BB12 13490 5241                    glimepirid
6 A10BD15  313 203 metformin og dapagliflozin
7 A10BD15  313 203 metformin og dapagliflozin
8 A10BD16  11  11 metformin og canagliflozin
9 A10BD16  11  11 metformin og canagliflozin
10 A10BD20 378 204 metformin og empagliflozin
11 A10BD20 378 204 metformin og empagliflozin
12 A10BK01 7238 4481                    dapagliflozin
13 A10BK02  357 204                    canagliflozin
14 A10BK03 4031 1753                    empagliflozin
15 A10BX02  347 141                      repaglinid
16 A10BX03   1 380                      nateglinid
> tt$drnam <- gsub( "metformin og ", "", tt$drnam )
> tt$drnam <- gsub( "pioglitazon og ", "", tt$drnam )
> aggregate( tt[,c("X1","X2")], tt[, "drnam", drop=FALSE], FUN=sum )
      drnam  X1  X2
1 canagliflozin 379 226
2 dapagliflozin 7864 4887
3 empagliflozin 4787 2161
4 glibenclamid 960 380
5 gliclazid 1753 685
6 glimepirid 13490 5241
7 glipizid 753 290
8 nateglinid 1 380
9 repaglinid 347 141
10 tolbutamid 290 119
```

1.9 Collecting analysis results and key data

We want to collect analysis results and background data for the analyses. The latter are classified by index drug and PY/events, the former by adjusted/non-adjusted analysis and HR/c.i./s.e. In addition both are classified by endpoint, data, and subset:

```
> lst <- list( endp = c("HF", "ACD", "ACD+HF", "CVDD", "MI", "Str", "IscStr",
+                      "CVDD+MI+Str", "ACD+MI+Str", "DKD"),
+             data = c("OnDr", "Total"),
+             sub = c("AllPtt", "preCVD", "noCVD") )
> dat <- NArray( c( lst, list( ix = c("SGLT2", "SU"),
+                               dat = c("N", "PY", "Event") ) ) )
> res <- NArray( c( lst, list( adj = c("Raw", "Adj"),
+                               res = c("HR", "lo", "up", "se") ) ) )
> length( dat ) ; str( dat )
[1] 360
logi [1:10, 1:2, 1:3, 1:2, 1:3] NA NA NA NA NA NA ...
- attr(*, "dimnames")=List of 5
..$ endp: chr [1:10] "HF" "ACD" "ACD+HF" "CVDD" ...
..$ data: chr [1:2] "OnDr" "Total"
..$ sub : chr [1:3] "AllPtt" "preCVD" "noCVD"
..$ ix : chr [1:2] "SGLT2" "SU"
..$ dat : chr [1:3] "N" "PY" "Event"
> length( res ) ; str( res )
[1] 480
logi [1:10, 1:2, 1:3, 1:2, 1:4] NA NA NA NA NA NA ...
- attr(*, "dimnames")=List of 5
..$ endp: chr [1:10] "HF" "ACD" "ACD+HF" "CVDD" ...
..$ data: chr [1:2] "OnDr" "Total"
..$ sub : chr [1:3] "AllPtt" "preCVD" "noCVD"
..$ adj : chr [1:2] "Raw" "Adj"
..$ res : chr [1:4] "HR" "lo" "up" "se"
```

1.10 Survival dataset: Lexis objects

Here is a definition of a function that produces a Lexis object with follow-up till `mset$doX` for the event D:

```
> mkLex <-
+ function( )
+ {
+   Lx <- Lexis( entry = list( per = doIx,
+                             cua = doIx-doBth,
+                             tfi = 0 ),
+               exit = list( per = doX ),
+               exit.status = factor( D, labels=c("OnDr", "Event") ),
+               data = subset( mset, is.na(doDth) | doIx < doDth ) )
+   Lx <- cutLexis( Lx, cut = Lx$doTm,
+                 new.state = "OffDr",
+                 pre = "OnDr" )
+   Lx
+ }
> mset$D <- with( mset, !is.na(deHF) & deHF<2017 )
> mset$doX <- with( mset, pmin( doDth, deHF, 2017, na.rm=TRUE ) )
> lxHF <- mkLex( )
```

NOTE: entry.status has been set to "OnDr" for all.

```
> summary( lxHF )
```

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
	OnDr	8987	4583	139	13709	4722	15816.17
	OffDr	0	4538	45	4583	45	5559.61
	Sum	8987	9121	184	18292	4767	21375.78

1.10.1 Follow-up data and events

First we devise a function to extract the person-years and events from the Lexis object:

```
> fill.dat <-
+ function( LexDat, outc )
+ {
+   whc <- c(" Persons:", "Risk time:", "Event")
+   cat( outc, ":\n" )
+   print( sm <- summary( LexDat, by="IxdR" ) )
+   s2 <- summary( LexDat, by=c("IxdR", "pre.CVD" ) )
+   for( ix in c("SU", "SGLT2") )
+   {
+     dat[outc,, "AllPtt", ix,] <- sm[[ix]][[1]][c(1,3), whc]
+     dat[outc,, "noCVD" , ix,] <- s2[[paste(ix,0, sep=".")]][[1]][c(1,3), whc]
+     dat[outc,, "preCVD", ix,] <- s2[[paste(ix,1, sep=".")]][[1]][c(1,3), whc]
+   }
+   invisible(NULL)
+ }
```

HF :

\$SGLT2

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
	OnDr	4634	2168	54	6856	2222	8139.88
	OffDr	0	2144	24	2168	24	2721.79
	Sum	4634	4312	78	9024	2246	10861.66

\$SU

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
	OnDr	4353	2415	85	6853	2500	7676.29
	OffDr	0	2394	21	2415	21	2837.82
	Sum	4353	4809	106	9268	2521	10514.11

```
> round( ftable( dat[1:2,,,], col.vars=c(4,5) ), 1 )
```

			ix	SGLT2		SU		
			dat	N	PY	Event	N	PY
endp data	sub							
HF	OnDr	AllPtt		6856.0	8139.9	54.0	6853.0	7676.3
		preCVD		2004.0	2295.0	43.0	1904.0	1982.7
		noCVD		4852.0	5844.8	11.0	4949.0	5693.6

	Total	AllPtt	6856.0	10861.7	78.0	6853.0	10514.1	106.0
		preCVD	2004.0	3049.5	58.0	1904.0	2769.7	79.0
		noCVD	4852.0	7812.2	20.0	4949.0	7744.4	27.0
ACD	OnDr	AllPtt	NA	NA	NA	NA	NA	NA
		preCVD	NA	NA	NA	NA	NA	NA
		noCVD	NA	NA	NA	NA	NA	NA
	Total	AllPtt	NA	NA	NA	NA	NA	NA
		preCVD	NA	NA	NA	NA	NA	NA
		noCVD	NA	NA	NA	NA	NA	NA

1.10.2 Analysis

Follow-up is now analysed by Cox-models adjusted and non-adjusted, total or on drug and separately for all persons and persons with and without prior CVD. These are named with an *m.* and combination of *r/a* (raw/adjusted), *t/d* (total/on drug) and *p/n/y* (patients/no CVD/yes CVD):

```
> m.tpr <- coxph( Surv( tfi, tfi+lex.dur, lex.Xst=="Event" ) ~
+               I(Ixdr=="SGLT2") + cluster(pnr),
+               data = lxHF )
> m.tpa <- update( m.tpr, . ~ . + I(doIx-doBth) + sex + I(doIx-doDM)
+               + prv.MI + prv.HF + prv.AtrFib + frail
+               + had.BBl + had.NHP + had.Ala + had.ACE )
> m.dpr <- update( m.tpr, data = subset( lxHF, lex.Cst=="OnDr" ) )
> m.dpa <- update( m.tpa, data = subset( lxHF, lex.Cst=="OnDr" ) )
> m.tnr <- update( m.tpr, data = subset( lxHF, pre.CVD==1 ) )
> m.tna <- update( m.tpa, data = subset( lxHF, pre.CVD==1 ) )
> m.dnr <- update( m.dpr, data = subset( lxHF, pre.CVD==1 & lex.Cst=="OnDr" ) )
> m.dna <- update( m.dpa, data = subset( lxHF, pre.CVD==1 & lex.Cst=="OnDr" ) )
> m.tyr <- update( m.tpr, data = subset( lxHF, pre.CVD==0 ) )
> m.tya <- update( m.tpa, data = subset( lxHF, pre.CVD==0 ) )
> m.dyr <- update( m.dpr, data = subset( lxHF, pre.CVD==0 & lex.Cst=="OnDr" ) )
> m.dya <- update( m.dpa, data = subset( lxHF, pre.CVD==0 & lex.Cst=="OnDr" ) )
```

With these models fitted we can now extract the HRs etc. and put into the right slots of *res*:

```
> get4 <- function( m ) ci.lin( m, subset="SGLT2", Exp=TRUE )[,c(5:7,2)]
> res["HF","Total","AllPtt","Raw",] <- get4( m.tpr )
> res["HF","Total","AllPtt","Adj",] <- get4( m.tpa )
> res["HF","OnDr","AllPtt","Raw",] <- get4( m.dpr )
> res["HF","OnDr","AllPtt","Adj",] <- get4( m.dpa )
> res["HF","Total","preCVD","Raw",] <- get4( m.tnr )
> res["HF","Total","preCVD","Adj",] <- get4( m.tna )
> res["HF","OnDr","preCVD","Raw",] <- get4( m.dnr )
> res["HF","OnDr","preCVD","Adj",] <- get4( m.dna )
> res["HF","Total","noCVD","Raw",] <- get4( m.tyr )
> res["HF","Total","noCVD","Adj",] <- get4( m.tya )
> res["HF","OnDr","noCVD","Raw",] <- get4( m.dyr )
> res["HF","OnDr","noCVD","Adj",] <- get4( m.dya )
```

This can now be packed into a function that does this for a given type of event:

```
> fill.res <- function( LexDat, outc )
+ {
+   m.tpr <- coxph( Surv( tfi, tfi+lex.dur, lex.Xst=="Event" ) ~
```

```

+           I(Ixdr=="SGLT2") + cluster(pnr),
+           data = LexDat )
+ m.tpa <- update( m.tpr, . ~ . + I(doIx-doBth) + sex + I(doIx-doDM)
+               + prv.MI + prv.HF + prv.AtrFib + frail
+               + had.BBl + had.NHP + had.Ala + had.ACE )
+ m.dpr <- update( m.tpr, data = subset( LexDat, lex.Cst=="OnDr" ) )
+ m.dpa <- update( m.tpa, data = subset( LexDat, lex.Cst=="OnDr" ) )
+
+ m.tnr <- update( m.tpr, data = subset( LexDat, pre.CVD==1 ) )
+ m.tna <- update( m.tpa, data = subset( LexDat, pre.CVD==1 ) )
+ m.dnr <- update( m.dpr, data = subset( LexDat, pre.CVD==1 & lex.Cst=="OnDr" ) )
+ m.dna <- update( m.dpa, data = subset( LexDat, pre.CVD==1 & lex.Cst=="OnDr" ) )
+
+ m.tyr <- update( m.tpr, data = subset( LexDat, pre.CVD==0 ) )
+ m.tya <- update( m.tpa, data = subset( LexDat, pre.CVD==0 ) )
+ m.dyr <- update( m.dpr, data = subset( LexDat, pre.CVD==0 & lex.Cst=="OnDr" ) )
+ m.dya <- update( m.dpa, data = subset( LexDat, pre.CVD==0 & lex.Cst=="OnDr" ) )
+
+ res[outc,"Total","AllPtt","Raw",] <- get4( m.tpr )
+ res[outc,"Total","AllPtt","Adj",] <- get4( m.tpa )
+ res[outc,"OnDr","AllPtt","Raw",] <- get4( m.dpr )
+ res[outc,"OnDr","AllPtt","Adj",] <- get4( m.dpa )
+
+ res[outc,"Total","preCVD","Raw",] <- get4( m.tnr )
+ res[outc,"Total","preCVD","Adj",] <- get4( m.tna )
+ res[outc,"OnDr","preCVD","Raw",] <- get4( m.dnr )
+ res[outc,"OnDr","preCVD","Adj",] <- get4( m.dna )
+
+ res[outc,"Total","noCVD","Raw",] <- get4( m.tyr )
+ res[outc,"Total","noCVD","Adj",] <- get4( m.tya )
+ res[outc,"OnDr","noCVD","Raw",] <- get4( m.dyr )
+ res[outc,"OnDr","noCVD","Adj",] <- get4( m.dya )
+ invisible( NULL )
+ }

```

So combining this with the function that constructs the Lexis object we get:

```

> mset$D <- with( mset, !is.na(deHF) & deHF<2017 )
> mset$doX <- with( mset, pmin( doDth, deHF, 2017, na.rm=TRUE ) )
> lxHF <- mkLex()

```

NOTE: entry.status has been set to "OnDr" for all.

```

> fill.res( lxHF, "HF" )
> round( ftable( res[1:2,,], col.vars=c(2,5) ), 3 )

```

			data	OnDr		Total					
			res	HR	lo	up	se	HR	lo	up	se
endp	sub	adj									
HF	AllPtt	Raw		0.608	0.432	0.854	0.174	0.714	0.533	0.956	0.149
		Adj		0.603	0.426	0.854	0.177	0.703	0.521	0.948	0.153
	preCVD	Raw		0.606	0.411	0.892	0.198	0.671	0.478	0.943	0.173
		Adj		0.616	0.415	0.913	0.201	0.667	0.472	0.942	0.176
	noCVD	Raw		0.490	0.238	1.008	0.368	0.730	0.411	1.298	0.293
		Adj		0.515	0.247	1.074	0.375	0.751	0.421	1.337	0.295
ACD	AllPtt	Raw		NA	NA	NA	NA	NA	NA	NA	NA
		Adj		NA	NA	NA	NA	NA	NA	NA	NA
	preCVD	Raw		NA	NA	NA	NA	NA	NA	NA	NA
		Adj		NA	NA	NA	NA	NA	NA	NA	NA
	noCVD	Raw		NA	NA	NA	NA	NA	NA	NA	NA
		Adj		NA	NA	NA	NA	NA	NA	NA	NA

So we just repeat this for all types of outcome:

```
> mset$D <- with( mset, !is.na(doDth) & doDth<2017 )
> mset$doX <- with( mset, pmin( doDth, 2017, na.rm=TRUE ) )
> lxACD <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxACD, "ACD" )
> fill.dat( lxACD, "ACD" )
```

ACD :
\$SGLT2

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	4601	2185	70	6856	2255	8182.18	6856
OffDr	0	2119	66	2185	66	2763.57	2185
Sum	4601	4304	136	9041	2321	10945.74	6856

\$SU

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	4247	2455	151	6853	2606	7750.92	6853
OffDr	0	2374	81	2455	81	2907.51	2455
Sum	4247	4829	232	9308	2687	10658.43	6853

```
> mset$D <- with( mset, ( !is.na(deHF) | !is.na(doDth) ) &
+ ( deHF<2017 | doDth<2017 ) )
> mset$doX <- with( mset, pmin( doDth, deHF, 2017, na.rm=TRUE ) )
> lxACDHF <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxACDHF, "ACD+HF" )
> fill.dat( lxACDHF, "ACD+HF" )
```

ACD+HF :
\$SGLT2

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	4566	2168	122	6856	2290	8139.88	6856
OffDr	0	2080	88	2168	88	2721.79	2168
Sum	4566	4248	210	9024	2378	10861.66	6856

\$SU

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	4212	2415	226	6853	2641	7676.29	6853
OffDr	0	2318	97	2415	97	2837.82	2415
Sum	4212	4733	323	9268	2738	10514.11	6853

```
> mset$D <- with( mset, !is.na(deCVDD) & deCVDD<2017 )
> mset$doX <- with( mset, pmin( doDth, deCVDD, 2017, na.rm=TRUE ) )
> lxCVDD <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxCVDD, "CVDD" )
> fill.dat( lxCVDD, "CVDD" )
```

CVDD :
\$SGLT2

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	4659	2185	12	6856	2197	8182.18	6856
OffDr	0	2177	8	2185	8	2763.57	2185
Sum	4659	4362	20	9041	2205	10945.74	6856

\$SU

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	4367	2455	31	6853	2486	7750.92	6853
OffDr	0	2436	19	2455	19	2907.51	2455
Sum	4367	4891	50	9308	2505	10658.43	6853

```
> mset$D <- with( mset, !is.na(deMI) & deMI<2017 )
> mset$doX <- with( mset, pmin( doDth, deMI, 2017, na.rm=TRUE ) )
> lxMI <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxMI, "MI" )
> fill.dat( lxMI, "MI" )
```

MI :
\$SGLT2

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	4640	2176	40	6856	2216	8151.09	6856
OffDr	0	2167	9	2176	9	2749.55	2176
Sum	4640	4343	49	9032	2225	10900.65	6856

\$SU

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	4362	2430	61	6853	2491	7703.40	6853
OffDr	0	2414	16	2430	16	2869.15	2430
Sum	4362	4844	77	9283	2507	10572.55	6853

```
> mset$D <- with( mset, !is.na(deStr) & deStr<2017 )
> mset$doX <- with( mset, pmin( doDth, deStr, 2017, na.rm=TRUE ) )
> lxStr <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxStr, "Str" )
> fill.dat( lxStr, "Str" )
```

Str :
\$SGLT2

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	4640	2163	53	6856	2216	8137.34	6856
OffDr	0	2146	17	2163	17	2732.69	2163
Sum	4640	4309	70	9019	2233	10870.03	6856

\$SU

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	4352	2431	70	6853	2501	7696.22	6853
OffDr	0	2406	25	2431	25	2857.20	2431
Sum	4352	4837	95	9284	2526	10553.42	6853

```
> mset$D <- with( mset, !is.na(deIscStr) & deIscStr<2017 )
> mset$doX <- with( mset, pmin( doDth, deIscStr, 2017, na.rm=TRUE ) )
> lxIstr <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxIstr, "IscStr" )
> fill.dat( lxIstr, "IscStr" )
```

IscStr :
\$SGLT2

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	4640	2166	50	6856	2216	8138.60	6856
OffDr	0	2152	14	2166	14	2736.75	2166
Sum	4640	4318	64	9022	2230	10875.36	6856

\$SU

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	4357	2432	64	6853	2496	7699.68	6853
OffDr	0	2416	16	2432	16	2867.21	2432
Sum	4357	4848	80	9285	2512	10566.89	6853

```
> mset$D <- with( mset, ( ( !is.na(deCVDD) & deCVDD < 2017 ) |
+ ( !is.na(deMI) & deMI < 2017 ) |
+ ( !is.na(deStr) & deStr < 2017 ) ) )
> mset$doX <- with( mset, pmin( doDth, deCVDD, deMI, deStr, 2017, na.rm=TRUE ) )
> lxCVDDx <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxCVDDx, "CVDD+MI+Str" )
> fill.dat( lxCVDDx, "CVDD+MI+Str" )
```

CVDD+MI+Str :
\$SGLT2

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	4599	2154	103	6856	2257	8106.84	6856

OffDr	0	2123	31	2154	31	2718.67	2154
Sum	4599	4277	134	9010	2288	10825.51	6856

\$SU

Transitions:

		To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:	
	OnDr	4296	2406	151	6853	2557	7650.81	6853
	OffDr	0	2353	53	2406	53	2818.85	2406
	Sum	4296	4759	204	9259	2610	10469.65	6853

```
> mset$D <- with( mset, ( ( !is.na(doDth) & doDth < 2017 ) |
+                      ( !is.na(deMI) & deMI < 2017 ) |
+                      ( !is.na(deStr) & deStr < 2017 ) ) )
> mset$doX <- with( mset, pmin( doDth, deMI, deStr, 2017, na.rm=TRUE ) )
> lxACDx <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxACDx, "ACD+MI+Str" )
> fill.dat( lxACDx, "ACD+MI+Str" )
```

ACD+MI+Str :
\$SGLT2

Transitions:

		To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:	
	OnDr	4544	2154	158	6856	2312	8106.84	6856
	OffDr	0	2072	82	2154	82	2718.67	2154
	Sum	4544	4226	240	9010	2394	10825.51	6856

\$SU

Transitions:

		To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:	
	OnDr	4180	2406	267	6853	2673	7650.81	6853
	OffDr	0	2294	112	2406	112	2818.85	2406
	Sum	4180	4700	379	9259	2785	10469.65	6853

```
> mset$D <- with( mset, !is.na(deDKD) & deDKD<2017 )
> mset$doX <- with( mset, pmin( doDth, deDKD, 2017, na.rm=TRUE ) )
> lxKid <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxKid, "DKD" )
> fill.dat( lxKid, "DKD" )
```

DKD :
\$SGLT2

Transitions:

		To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:	
	OnDr	4647	2161	48	6856	2209	8141.67	6856
	OffDr	0	2140	21	2161	21	2715.16	2161
	Sum	4647	4301	69	9017	2230	10856.83	6856

\$SU

Transitions:

From	To			Records:	Events:	Risk time:	Persons:
OnDr	OnDr	OffDr	Event	6853	2498	7682.32	6853
OffDr	0	2382	34	2416	34	2844.94	2416
Sum	4355	4798	116	9269	2532	10527.26	6853

So we can summarize results:

```
> round( ftable( dat, col.vars=c(2,4,5) ), 0 )
```

endp	sub	data			OnDr			Total			SU		
		ix	SGLT2		N	PY	Event	N	PY	Event	N	PY	Event
HF	AllPtt				6856	8140	54	6853	7676	85	6856	10862	78
	preCVD				2004	2295	43	1904	1983	63	2004	3049	58
	noCVD				4852	5845	11	4949	5694	22	4852	7812	20
ACD	AllPtt				6856	8182	70	6853	7751	151	6856	10946	136
	preCVD				2004	2328	35	1904	2038	86	2004	3115	73
	noCVD				4852	5854	35	4949	5713	65	4852	7831	63
ACD+HF	AllPtt				6856	8140	122	6853	7676	226	6856	10862	210
	preCVD				2004	2295	76	1904	1983	140	2004	3049	127
	noCVD				4852	5845	46	4949	5694	86	4852	7812	83
CVDD	AllPtt				6856	8182	12	6853	7751	31	6856	10946	20
	preCVD				2004	2328	8	1904	2038	25	2004	3115	13
	noCVD				4852	5854	4	4949	5713	6	4852	7831	7
MI	AllPtt				6856	8151	40	6853	7703	61	6856	10901	49
	preCVD				2004	2312	20	1904	2007	34	2004	3090	26
	noCVD				4852	5839	20	4949	5696	27	4852	7811	23
Str	AllPtt				6856	8137	53	6853	7696	70	6856	10870	70
	preCVD				2004	2312	27	1904	2010	35	2004	3082	34
	noCVD				4852	5825	26	4949	5686	35	4852	7788	36
IscStr	AllPtt				6856	8139	50	6853	7700	64	6856	10875	64
	preCVD				2004	2313	24	1904	2011	33	2004	3088	29
	noCVD				4852	5825	26	4949	5689	31	4852	7788	35
CVDD+MI+Str	AllPtt				6856	8107	103	6853	7651	151	6856	10826	134
	preCVD				2004	2295	54	1904	1981	87	2004	3058	70
	noCVD				4852	5812	49	4949	5670	64	4852	7768	64
ACD+MI+Str	AllPtt				6856	8107	158	6853	7651	267	6856	10826	240
	preCVD				2004	2295	79	1904	1981	146	2004	3058	124
	noCVD				4852	5812	79	4949	5670	121	4852	7768	116
DKD	AllPtt				6856	8142	48	6853	7682	82	6856	10857	69
	preCVD				2004	2314	19	1904	2017	29	2004	3079	27
	noCVD				4852	5827	29	4949	5666	53	4852	7778	42

```
> round( ftable( res, col.vars=c(2,5) ), 3 )
```

endp	sub	adj	data			OnDr			Total		
			res	HR	lo	up	se	HR	lo	up	se
HF	AllPtt	Raw		0.608	0.432	0.854	0.174	0.714	0.533	0.956	0.149
		Adj		0.603	0.426	0.854	0.177	0.703	0.521	0.948	0.153
	preCVD	Raw		0.606	0.411	0.892	0.198	0.671	0.478	0.943	0.173
		Adj		0.616	0.415	0.913	0.201	0.667	0.472	0.942	0.176
	noCVD	Raw		0.490	0.238	1.008	0.368	0.730	0.411	1.298	0.293
		Adj		0.515	0.247	1.074	0.375	0.751	0.421	1.337	0.295
ACD	AllPtt	Raw		0.442	0.333	0.587	0.144	0.570	0.462	0.705	0.108
		Adj		0.506	0.381	0.674	0.146	0.614	0.497	0.759	0.108

ACD+HF	preCVD	Raw	0.359	0.243	0.532	0.200	0.541	0.405	0.721	0.147
		Adj	0.418	0.282	0.620	0.201	0.601	0.450	0.803	0.148
	noCVD	Raw	0.530	0.352	0.798	0.209	0.584	0.428	0.797	0.159
		Adj	0.603	0.398	0.913	0.212	0.623	0.456	0.852	0.160
	AllPtt	Raw	0.515	0.414	0.642	0.112	0.629	0.529	0.749	0.089
		Adj	0.562	0.450	0.702	0.114	0.659	0.553	0.785	0.090
CVDD	preCVD	Raw	0.480	0.363	0.634	0.142	0.600	0.480	0.750	0.114
		Adj	0.526	0.397	0.698	0.144	0.642	0.512	0.806	0.116
	noCVD	Raw	0.525	0.367	0.750	0.182	0.631	0.480	0.831	0.140
		Adj	0.585	0.407	0.841	0.185	0.663	0.503	0.874	0.141
	AllPtt	Raw	0.373	0.192	0.722	0.338	0.392	0.234	0.658	0.264
		Adj	0.424	0.214	0.841	0.349	0.427	0.253	0.721	0.267
MI	preCVD	Raw	0.287	0.130	0.631	0.402	0.312	0.167	0.583	0.319
		Adj	0.318	0.143	0.708	0.408	0.334	0.177	0.629	0.324
	noCVD	Raw	0.665	0.189	2.337	0.642	0.643	0.250	1.650	0.481
		Adj	0.835	0.215	3.238	0.692	0.692	0.270	1.776	0.481
	AllPtt	Raw	0.629	0.421	0.938	0.204	0.622	0.434	0.890	0.183
		Adj	0.628	0.419	0.941	0.206	0.619	0.432	0.887	0.184
Str	preCVD	Raw	0.521	0.299	0.906	0.283	0.582	0.356	0.950	0.251
		Adj	0.552	0.313	0.974	0.290	0.606	0.369	0.995	0.253
	noCVD	Raw	0.735	0.411	1.317	0.297	0.640	0.378	1.083	0.269
		Adj	0.735	0.410	1.316	0.297	0.640	0.378	1.082	0.268
	AllPtt	Raw	0.726	0.507	1.038	0.183	0.718	0.527	0.978	0.157
		Adj	0.750	0.524	1.074	0.183	0.727	0.533	0.990	0.158
IscStr	preCVD	Raw	0.690	0.417	1.141	0.256	0.684	0.439	1.065	0.226
		Adj	0.726	0.437	1.206	0.259	0.698	0.446	1.090	0.228
	noCVD	Raw	0.729	0.438	1.214	0.260	0.730	0.475	1.122	0.219
		Adj	0.730	0.438	1.216	0.260	0.728	0.473	1.120	0.220
	AllPtt	Raw	0.747	0.516	1.083	0.189	0.781	0.563	1.085	0.167
		Adj	0.773	0.534	1.120	0.189	0.788	0.568	1.094	0.167
CVDD+MI+Str	preCVD	Raw	0.648	0.383	1.097	0.269	0.689	0.427	1.113	0.245
		Adj	0.674	0.398	1.142	0.269	0.695	0.430	1.122	0.244
	noCVD	Raw	0.822	0.487	1.388	0.267	0.849	0.541	1.333	0.230
		Adj	0.826	0.489	1.397	0.268	0.846	0.538	1.329	0.231
	AllPtt	Raw	0.653	0.508	0.839	0.128	0.639	0.514	0.795	0.111
		Adj	0.674	0.523	0.868	0.129	0.648	0.521	0.806	0.111
ACD+MI+Str	preCVD	Raw	0.549	0.391	0.770	0.173	0.568	0.422	0.765	0.152
		Adj	0.591	0.419	0.834	0.176	0.593	0.440	0.800	0.153
	noCVD	Raw	0.757	0.521	1.100	0.191	0.701	0.509	0.966	0.163
		Adj	0.764	0.525	1.111	0.191	0.701	0.509	0.966	0.163
	AllPtt	Raw	0.564	0.464	0.687	0.100	0.614	0.522	0.722	0.082
		Adj	0.607	0.498	0.740	0.101	0.639	0.543	0.751	0.083
DKD	preCVD	Raw	0.475	0.361	0.625	0.140	0.584	0.466	0.731	0.115
		Adj	0.534	0.405	0.705	0.141	0.633	0.505	0.794	0.115
	noCVD	Raw	0.643	0.484	0.854	0.145	0.622	0.493	0.784	0.119
		Adj	0.672	0.506	0.893	0.145	0.633	0.502	0.799	0.119
	AllPtt	Raw	0.555	0.388	0.794	0.183	0.576	0.427	0.776	0.152
		Adj	0.567	0.396	0.811	0.183	0.585	0.434	0.788	0.152
	preCVD	Raw	0.580	0.323	1.040	0.298	0.527	0.328	0.846	0.242
		Adj	0.651	0.353	1.200	0.312	0.557	0.339	0.913	0.253
	noCVD	Raw	0.532	0.338	0.838	0.232	0.601	0.409	0.882	0.196
		Adj	0.537	0.341	0.845	0.231	0.611	0.417	0.896	0.195

1.11 Exposure tables by drug

We can then produce an overview of the number of persons, risk time and events by index medication; to this end we define functions that uses the `by` argument of the `summary.Lexis` to classify events and follow-up by index drug in various groupings:

```
> tabFU <- ZArray( list( Ix = c("SU", "SGLT2", "Dapa", "Empa", "Cana"),
+                        wh = c("nPers", "FU", "meanfu", "sdFU", "maxFU") ) )
> getFU <-
+ function( lx ) c( length( unique( lx$lex.id ) ),
+                  sum( lx$lex.dur ),
+                  mean( lx$lex.dur ),
+                  sd( lx$lex.dur ),
+                  max( lx$lex.dur ) )
> mset$D <- 0
> mset$doX <- with( mset, pmin( doDth, 2017, na.rm=TRUE ) )
> Lx <- Lexis( entry = list( per = doIx,
+                           cua = doIx-doBth,
+                           tfi = 0 ),
+             exit = list( per = doX ),
+             exit.status = factor( D, levels=0:1, labels=c("OnDr", "Event") ),
+             data = subset( mset, is.na(doDth) | doIx < doDth ) )
NOTE: entry.status has been set to "OnDr" for all.
> summary( Lx, by="Ixdr" , simplify=FALSE )
```

\$SGLT2

Transitions:

	To					
From	OnDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	6856	0	6856	0	10945.74	6856
Event	0	0	0	0	NA	NA
Sum	6856	0	6856	0	10945.74	6856

\$SU

Transitions:

	To					
From	OnDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	6853	0	6853	0	10658.43	6853
Event	0	0	0	0	NA	NA
Sum	6853	0	6853	0	10658.43	6853

```
> tabFU["SU" ,] <- getFU( subset( Lx, Ixdr=="SU" ) )
> tabFU["SGLT2",] <- getFU( subset( Lx, Ixdr=="SGLT2" ) )
> tabFU["Dapa" ,] <- getFU( subset( Lx, Ixatc %in% c("A10BD15", "A10BK01") ) )
> tabFU["Cana" ,] <- getFU( subset( Lx, Ixatc %in% c("A10BD16", "A10BK02") ) )
> tabFU["Empa" ,] <- getFU( subset( Lx, Ixatc %in% c("A10BD20", "A10BK03") ) )
> round( tabFU, 2 )
```

	wh					
Ix	nPers	FU	meanfu	sdFU	maxFU	
SU	6853	10658.43	1.56	1.09	4.08	
SGLT2	6856	10945.74	1.60	1.09	4.05	
Dapa	4684	9145.68	1.95	1.09	4.05	
Empa	1957	1495.64	0.76	0.54	2.33	
Cana	215	304.42	1.42	0.65	2.54	

1.12 Saving it all

Fially we save all results:

```
> save( res, dat, tabFU, file = "resSGSU.Rda" )
```

1.13 Reformatting

The results are here reformatted to Excel-format, `xlsx`, by the `xlsx` package of R, so we load that concomitantly with the data.

```
> library( Epi )
> library( xlsx )
> clear()
> load( "btabsGSU.Rda" )
> load( "resSGSU.Rda" )
> lls()
```

	name	mode	class	dim	size(Kb)
1	cm.tab	numeric	matrix	31 4	3.4
2	ct.tab	numeric	matrix	31 4	3.4
3	dat	numeric	array	10 2 3 2 3	5.5
4	dm.tab	numeric	matrix	40 4	3.9
5	dt.tab	numeric	matrix	40 4	3.9
6	mm.tab	numeric	matrix	37 4	3.8
7	mt.tab	numeric	matrix	37 4	3.8
8	res	numeric	array	10 2 3 2 4	6.4
9	tabFU	numeric	matrix	5 5	1.7

With this in place we can now construct the tables wanted for the sheet in the desired order.

1.13.1 Baseline tables

In order to check that we get the rows correct we read the row-names from the supplied spreadsheet, in order to put these in as a column in the new sheet for control:

```
> cat("Sample size
+ Age, years
+ Women
+ CV-history
+ Myocardial infarction
+ Unstable angina
+ Heart failure
+ Atrial fibrillation
+ Stroke
+ PAD
+ Microvascular disease
+ CKD
+ Frailty (yes)
+ Metformin
+ DPP4
+ TZD
+ GLP1
+ Insulin
+ Anti hypertensive therapy
```

```

...now input from ../rep/2xlSGSU.tex
+ LOOP diuretics
+ Low ceiling diuretics
+ ACE Inhibitors
+ ARBs
+ Statin therapy
+ Beta blockers
+ Aldosterone antagonists
+ Index year
+ 2012
+ 2013
+ 2014
+ 2015
+ 2016
+ 2017
+ ", file='ol.txt' )
> ol <- read.table('ol.txt',header=FALSE,sep='\t',as.is=TRUE)

```

Baseline pre-matching

We can now construct the pre-matching table

```

> bt <- rbind( "Sample size"= dt.tab[1,2:1]+dt.tab[2,2:1],
+             "Age" = NA,
+             dt.tab["F",2:1,drop=FALSE],
+             ct.tab["pre.CVD",2:1,drop=FALSE],
+             ct.tab["prv.MI",2:1,drop=FALSE],
+             ct.tab["prv.UnstAng",2:1,drop=FALSE],
+             ct.tab["prv.HF",2:1,drop=FALSE],
+             ct.tab["prv.AtrFib",2:1,drop=FALSE],
+             ct.tab["pre.Str",2:1,drop=FALSE],
+             ct.tab["prv.PAD",2:1,drop=FALSE],
+             ct.tab["pre.Mic",2:1,drop=FALSE],
+             ct.tab["prv.CKD",2:1,drop=FALSE],
+             "Frail"=dt.tab["1",2:1],
+             mt.tab["had.Metformin",2:1,drop=FALSE],
+             mt.tab["had.DPP4",2:1,drop=FALSE],
+             mt.tab["had.TZD",2:1,drop=FALSE],
+             mt.tab["had.GLP1",2:1,drop=FALSE],
+             mt.tab["got.Ins",2:1,drop=FALSE],
+             mt.tab["got.Hyp",2:1,drop=FALSE],
+             mt.tab["had.HCD",2:1,drop=FALSE],
+             mt.tab["had.THZ",2:1,drop=FALSE],
+             mt.tab["had.ACE",2:1,drop=FALSE],
+             mt.tab["had.ARB",2:1,drop=FALSE],
+             mt.tab["had.Sta",2:1,drop=FALSE],
+             mt.tab["had.BB1",2:1,drop=FALSE],
+             mt.tab["had.A1A",2:1,drop=FALSE],
+             "Index year"=NA,
+             dt.tab["Index date 2012",2:1,drop=FALSE],
+             dt.tab["2013",2:1,drop=FALSE],
+             dt.tab["2014",2:1,drop=FALSE],
+             dt.tab["2015",2:1,drop=FALSE],
+             dt.tab["2016",2:1,drop=FALSE],
+             '2017'=NA)
> str(ol)

```

```

'data.frame':      33 obs. of  1 variable:
 $ V1: chr  "Sample size" "Age, years" "Women" "CV-history" ...

> bt <- cbind(bt[,1],NA,NA,NA,NA)
> bt["Age",c(2,3,5,6)] <- dt.tab["Age: Mean / SD",c(1,3,2,4)]
> colnames( bt ) <- c("SGLT-2","mean","sd","SU","mean","sd")
> cbind( ol, bt )

      Sample size      Sample size      V1 SGLT-2 mean sd      SU mean sd
Sample size      Sample size      17594      NA NA 12328      NA NA
Age      Age, years      NA 59.8 11      NA 63.9 13
F      Women      7246      NA NA 4803      NA NA
pre.CVD      CV-history      5603      NA NA 3681      NA NA
prv.MI      Myocardial infarction      1405      NA NA 1003      NA NA
prv.UnstAng      Unstable angina      640      NA NA 470      NA NA
prv.HF      Heart failure      880      NA NA 496      NA NA
prv.AtrFib      Atrial fibrillation      1378      NA NA 740      NA NA
pre.Str      Stroke      1535      NA NA 873      NA NA
prv.PAD      PAD      1061      NA NA 599      NA NA
pre.Mic      Microvascular disease      3035      NA NA 4104      NA NA
prv.CKD      CKD      434      NA NA 69      NA NA
Frail      Frailty (yes)      4950      NA NA 4045      NA NA
had.Metformin      Metformin      14057      NA NA 9881      NA NA
had.DPP4      DPP4      2264      NA NA 2137      NA NA
had.TZD      TZD      27      NA NA 28      NA NA
had.GLP1      GLP1      1332      NA NA 4054      NA NA
got.Ins      Insulin      952      NA NA 4147      NA NA
got.Hyp      Anti hypertensive therapy      12224      NA NA 9593      NA NA
had.HCD      LOOP diuretics      2850      NA NA 1703      NA NA
had.THZ      Low ceiling diuretics      2630      NA NA 1877      NA NA
had.ACE      ACE Inhibitors      5886      NA NA 4676      NA NA
had.ARB      ARBs      4459      NA NA 4299      NA NA
had.Sta      Statin therapy      10956      NA NA 9176      NA NA
had.BB1      Beta blockers      4769      NA NA 3333      NA NA
had.A1A      Aldosterone antagonists      896      NA NA 644      NA NA
Index year      Index year      NA      NA NA      NA      NA NA
Index date 2012      2012      412      NA NA      11      NA NA
2013      2013      5130      NA NA      1353      NA NA
2014      2014      4477      NA NA      2069      NA NA
2015      2015      4136      NA NA      3333      NA NA
2016      2016      3439      NA NA      5562      NA NA
2017      2017      NA      NA NA      NA      NA NA

> write.xlsx( cbind( 'Org. labs'=ol, bt ),
+             "SGSU.xlsx",
+             sheetName = "Baseline pre-matching",
+             append = FALSE,
+             showNA = FALSE )

```

Baseline after matching

The data for post matching have exactly the same structure; the tables are just called 'm.tab' instead of 't.tab':

```

> bm <- rbind( "Sample size"= dm.tab[1,2:1]+dm.tab[2,2:1],
+             "Age" = NA,
+             dm.tab["F",2:1,drop=FALSE],
+             cm.tab["pre.CVD",2:1,drop=FALSE],
+             cm.tab["prv.MI",2:1,drop=FALSE],
+             cm.tab["prv.UnstAng",2:1,drop=FALSE],
+             cm.tab["prv.HF",2:1,drop=FALSE],
+             cm.tab["prv.AtrFib",2:1,drop=FALSE],
+             cm.tab["pre.Str",2:1,drop=FALSE],
+             cm.tab["prv.PAD",2:1,drop=FALSE],
+             cm.tab["pre.Mic",2:1,drop=FALSE],
+             cm.tab["prv.CKD",2:1,drop=FALSE],
+             "Frail"=dm.tab["1",2:1],
+             mm.tab["had.Metformin",2:1,drop=FALSE],
+             mm.tab["had.DPP4",2:1,drop=FALSE],
+             mm.tab["had.TZD",2:1,drop=FALSE],
+             mm.tab["had.GLP1",2:1,drop=FALSE],
+             mm.tab["got.Ins",2:1,drop=FALSE],
+             mm.tab["got.Hyp",2:1,drop=FALSE],
+             mm.tab["had.HCD",2:1,drop=FALSE],
+             mm.tab["had.THZ",2:1,drop=FALSE],
+             mm.tab["had.ACE",2:1,drop=FALSE],
+             mm.tab["had.ARB",2:1,drop=FALSE],
+             mm.tab["had.Sta",2:1,drop=FALSE],
+             mm.tab["had.BB1",2:1,drop=FALSE],
+             mm.tab["had.A1A",2:1,drop=FALSE],
+             "Index year"=NA,
+             dm.tab["Index date 2012",2:1,drop=FALSE],
+             dm.tab["2013",2:1,drop=FALSE],
+             dm.tab["2014",2:1,drop=FALSE],
+             dm.tab["2015",2:1,drop=FALSE],
+             dm.tab["2016",2:1,drop=FALSE],
+             '2017'=NA)
> str(ol)
'data.frame':      33 obs. of  1 variable:
 $ V1: chr  "Sample size" "Age, years" "Women" "CV-history" ...
> bm <- cbind(bm[,1],NA,NA,bm[,2],NA,NA)
> bm["Age",c(2,3,5,6)] <- dm.tab["Age: Mean / SD",c(1,3,2,4)]
> colnames( bm ) <- c("SGLT-2","mean","sd","SU","mean","sd")
> cbind( ol, bm )

```

	V1	SGLT-2	mean	sd	SU	mean	sd
Sample size	Sample size	6856	NA	NA	6856	NA	NA
Age	Age, years	NA	60.8	11.2	NA	60.7	12.5
F	Women	2745	NA	NA	2724	NA	NA
pre.CVD	CV-history	1907	NA	NA	2004	NA	NA
prv.MI	Myocardial infarction	501	NA	NA	515	NA	NA
prv.UnstAng	Unstable angina	245	NA	NA	228	NA	NA
prv.HF	Heart failure	255	NA	NA	266	NA	NA
prv.AtrFib	Atrial fibrillation	409	NA	NA	429	NA	NA
pre.Str	Stroke	482	NA	NA	499	NA	NA
prv.PAD	PAD	331	NA	NA	338	NA	NA
pre.Mic	Microvascular disease	1500	NA	NA	1579	NA	NA
prv.CKD	CKD	40	NA	NA	48	NA	NA
Frail	Frailty (yes)	1879	NA	NA	1922	NA	NA
had.Metformin	Metformin	5484	NA	NA	5454	NA	NA
had.DPP4	DPP4	1311	NA	NA	1306	NA	NA
had.TZD	TZD	14	NA	NA	16	NA	NA

```

had.GLP1          GLP1      1127  NA  NA 1194  NA  NA
got.Ins           Insulin    757  NA  NA  871  NA  NA
got.Hyp           Anti hypertensive therapy 4976 NA  NA 5051 NA  NA
had.HCD           LOOP diuretics 862  NA  NA  891  NA  NA
had.THZ           Low ceiling diuretics 1017 NA  NA  977  NA  NA
had.ACE           ACE Inhibitors 2435 NA  NA 2467  NA  NA
had.ARB           ARBs      2106  NA  NA 2083  NA  NA
had.Sta           Statin therapy 4796 NA  NA 4779  NA  NA
had.BBl           Beta blockers 1747 NA  NA 1759  NA  NA
had.Ala           Aldosterone antagonists 321  NA  NA  328  NA  NA
Index year        Index year  NA  NA  NA  NA  NA  NA
Index date 2012   2012       40  NA  NA   8  NA  NA
2013              2013      929  NA  NA 1023  NA  NA
2014              2014     1346  NA  NA 1405  NA  NA
2015              2015     1990  NA  NA 1864  NA  NA
2016              2016     2551  NA  NA 2556  NA  NA
2017              2017       NA  NA  NA  NA  NA  NA

> write.xlsx( cbind( 'Org. labs'=ol, bm ),
+             "SGSU.xlsx",
+             sheetName = "Baseline after matching",
+             append = TRUE,
+             showNA = FALSE )

```

1.13.2 Treatment distribution

```

> ( FUt看 <- tabFU[c(2:5,rep(NA,4),1),] )

      wh
Ix      nPers      FU      meanfu      sdFU      maxFU
SGLT2  6856 10945.7413 1.5965200 1.0895279 4.051335
Dapa   4684  9145.6769 1.9525356 1.0852049 4.051335
Empa   1957 1495.6441 0.7642535 0.5430833 2.331964
Cana    215  304.4203 1.4159082 0.6456059 2.540041
<NA>     NA      NA      NA      NA      NA
<NA>     NA      NA      NA      NA      NA
<NA>     NA      NA      NA      NA      NA
<NA>     NA      NA      NA      NA      NA
SU      6853 10658.4278 1.5552937 1.0900305 4.078713

> colnames(FUt看) <- c(
+ 'Number of patients',
+ 'Total follow-up time',
+ 'Mean follow-up time',
+ 'Sd follow-up time',
+ 'maximum follow-up time')
> rownames( FUt看 ) <- c(
+ 'SGLT-2',
+ ' Dapagliflozin',
+ ' Empagliflozin',
+ ' Canagliflozin',
+ ' Ipragliflozin',
+ ' Luseogliflozin',
+ ' Tofugliflozin',
+ '-',
+ 'SU')
> FUt看

```

```

                                wh
Ix      Number of patients Total follow-up time Mean follow-up time Sd follow-up t
  SGLT-2      6856      10945.7413      1.5965200      1.0895
    Dapagliflozin      4684      9145.6769      1.9525356      1.0852
    Empagliflozin      1957      1495.6441      0.7642535      0.5430
    Canagliflozin      215      304.4203      1.4159082      0.6456
    Ipragliflozin      NA      NA      NA
    Luseogliflozin      NA      NA      NA
    Tofugliflozin      NA      NA      NA
  -      NA      NA      NA
  SU      6853      10658.4278      1.5552937      1.0900

                                wh
Ix      maximum follow-up time
  SGLT-2      4.051335
    Dapagliflozin      4.051335
    Empagliflozin      2.331964
    Canagliflozin      2.540041
    Ipragliflozin      NA
    Luseogliflozin      NA
    Tofugliflozin      NA
  -      NA
  SU      4.078713

> write.xlsx( FUt看,
+           "SGSU.xlsx",
+ sheetName = "Treatment distribution",
+   append = TRUE,
+   showNA = FALSE )

```

1.13.3 Events

```

> cat(
+ 'Number of patients
+ Total follow-up time - on treatment
+ Number of patients with event - on treatment
+ Total follow-up time - ITT
+ Number of patients with event - ITT
+ ', file='oc' )
> ( oc <- read.table('oc',header=FALSE,sep='\t',as.is=TRUE)[,1] )

[1] "Number of patients" "Total follow-up time - on treatment"
[3] "Number of patients with event - on treatment" "Total follow-up time - ITT"
[5] "Number of patients with event - ITT"

> cat(
+ 'HHF
+ All-cause death
+ All-cause death or HHF
+ Cardiavascular death
+ Myocardial infarction
+ Stroke
+ Ischemic stroke
+ MACE (cardiavascular death, MI or stroke)
+ modified MACE (All-cause death, MI or stroke)
+ Kidney disease
+ ', file='ol' )
> ( ol <- read.table('ol',header=FALSE,sep='\t',as.is=TRUE)[,1] )

```

```

[1] "HHF" "All-cause death"
[3] "All-cause death or HHF" "Cardiavascular death"
[5] "Myocardial infarction" "Stroke"
[7] "Ischemic stroke" "MACE (cardiovascular death, MI or stroke)"
[9] "modified MACE (All-cause death, MI or stroke)" "Kidney disease"

```

The data for this is in the `dat` object:

```

> str( dat )
num [1:10, 1:2, 1:3, 1:2, 1:3] 6856 6856 6856 6856 6856 ...
- attr(*, "dimnames")=List of 5
 ..$ endp: chr [1:10] "HF" "ACD" "ACD+HF" "CVDD" ...
 ..$ data: chr [1:2] "OnDr" "Total"
 ..$ sub : chr [1:3] "AllPtt" "preCVD" "noCVD"
 ..$ ix  : chr [1:2] "SGLT2" "SU"
 ..$ dat : chr [1:3] "N" "PY" "Event"

> cbind( ol, dimnames(dat)[[1]] )
      ol
[1,] "HHF" "HF"
[2,] "All-cause death" "ACD"
[3,] "All-cause death or HHF" "ACD+HF"
[4,] "Cardiavascular death" "CVDD"
[5,] "Myocardial infarction" "MI"
[6,] "Stroke" "Str"
[7,] "Ischemic stroke" "IscStr"
[8,] "MACE (cardiovascular death, MI or stroke)" "CVDD+MI+Str"
[9,] "modified MACE (All-cause death, MI or stroke)" "ACD+MI+Str"
[10,] "Kidney disease" "DKD"

> ft <- ftable( dat[,1,1:2,,drop=FALSE], col.vars=c(4,2,5) )
> round( ft, 1 )

```

		ix	SGLT2					SU			
		data	OnDr			Total		OnDr			
		dat	N	PY	Event	N	PY	Event	N	PY	Event
endp	sub										
HF	AllPtt		6856.0	8139.9	54.0	6856.0	10861.7	78.0	6853.0	7676.3	85.0
ACD	AllPtt		6856.0	8182.2	70.0	6856.0	10945.7	136.0	6853.0	7750.9	151.0
ACD+HF	AllPtt		6856.0	8139.9	122.0	6856.0	10861.7	210.0	6853.0	7676.3	226.0
CVDD	AllPtt		6856.0	8182.2	12.0	6856.0	10945.7	20.0	6853.0	7750.9	31.0
MI	AllPtt		6856.0	8151.1	40.0	6856.0	10900.6	49.0	6853.0	7703.4	61.0
Str	AllPtt		6856.0	8137.3	53.0	6856.0	10870.0	70.0	6853.0	7696.2	70.0
IscStr	AllPtt		6856.0	8138.6	50.0	6856.0	10875.4	64.0	6853.0	7699.7	64.0
CVDD+MI+Str	AllPtt		6856.0	8106.8	103.0	6856.0	10825.5	134.0	6853.0	7650.8	151.0
ACD+MI+Str	AllPtt		6856.0	8106.8	158.0	6856.0	10825.5	240.0	6853.0	7650.8	267.0
DKD	AllPtt		6856.0	8141.7	48.0	6856.0	10856.8	69.0	6853.0	7682.3	82.0

This is the table needed (except for the column on persons, which should not be repeated):

```

> py <- data.frame( as.matrix(ft) )[-c(4,10)]
> py

```

	SGLT2_OnDr_N	SGLT2_OnDr_PY	SGLT2_OnDr_Event	SGLT2_Total_PY	SGLT2_Total_Event
HF_AllPtt	6856	8139.875	54	10861.66	78
ACD_AllPtt	6856	8182.176	70	10945.74	136
ACD+HF_AllPtt	6856	8139.875	122	10861.66	210
CVDD_AllPtt	6856	8182.176	12	10945.74	20
MI_AllPtt	6856	8151.094	40	10900.65	49
Str_AllPtt	6856	8137.341	53	10870.03	70

IscStr_AllPtt	6856	8138.600	50	10875.36	6
CVDD+MI+Str_AllPtt	6856	8106.839	103	10825.51	13
ACD+MI+Str_AllPtt	6856	8106.839	158	10825.51	24
DKD_AllPtt	6856	8141.666	48	10856.83	6
	SU_OnDr_N	SU_OnDr_PY	SU_OnDr_Event	SU_Total_PY	SU_Total_Event
HF_AllPtt	6853	7676.290	85	10514.11	106
ACD_AllPtt	6853	7750.916	151	10658.43	232
ACD+HF_AllPtt	6853	7676.290	226	10514.11	323
CVDD_AllPtt	6853	7750.916	31	10658.43	50
MI_AllPtt	6853	7703.396	61	10572.55	77
Str_AllPtt	6853	7696.223	70	10553.42	95
IscStr_AllPtt	6853	7699.676	64	10566.89	80
CVDD+MI+Str_AllPtt	6853	7650.806	151	10469.65	204
ACD+MI+Str_AllPtt	6853	7650.806	267	10469.65	379
DKD_AllPtt	6853	7682.322	82	10527.26	116

```
> colnames( py )
[1] "SGLT2_OnDr_N"      "SGLT2_OnDr_PY"      "SGLT2_OnDr_Event"   "SGLT2_Total_PY"
[5] "SGLT2_Total_Event" "SU_OnDr_N"          "SU_OnDr_PY"         "SU_OnDr_Event"
[9] "SU_Total_PY"       "SU_Total_Event"

> colnames(py) <- c(oc,oc[-1])
> rownames(py) <- ol
```

With this in order we can now write it to the excel sheet:

```
> write.xlsx( py,
+            "SGSU.xlsx",
+            sheetName = "Events",
+            append = TRUE,
+            showNA = FALSE )
```

1.13.4 Hazard ratios

```
> ft <- ftable((dat[c(1:3,9,5,6),1:2,1,"SGLT2",,drop=FALSE])+
+             dat[c(1:3,9,5,6),1:2,1,"SU" ,,drop=FALSE]),,c(1,1),,row.vars=c(1,2,3))
> YD <- data.frame(as.matrix(ft))
> HR <- data.frame(as.matrix(ftable(res[c(1:3,9,5,6),1:2,1,1:2,c(1,4)],row.vars=c(1,2,3))))
> Endpoint <- sapply( strsplit( rownames(HR), "_" ), FUN=function(x) x[1] )
> Adjusted <- sapply( strsplit( rownames(HR), "_" ), FUN=function(x) x[3] )
> Analysis <- sapply( strsplit( rownames(HR), "_" ), FUN=function(x) x[2] )
> ( HR <- cbind(Endpoint,Adjusted,Analysis,HR,YD)[,c(1:3,6:8,4:5)] )
```

	Endpoint	Adjusted	Analysis	N	PY	Event	HR	se
HF_OnDr_Raw	HF	Raw	OnDr	13709	15816.17	139	0.6077071	0.17365434
HF_OnDr_Adj	HF	Adj	OnDr	13709	15816.17	139	0.6031188	0.17739474
HF_Total_Raw	HF	Raw	Total	13709	21375.78	184	0.7140715	0.14897696
HF_Total_Adj	HF	Adj	Total	13709	21375.78	184	0.7027171	0.15289665
ACD_OnDr_Raw	ACD	Raw	OnDr	13709	15933.09	221	0.4422793	0.14420681
ACD_OnDr_Adj	ACD	Adj	OnDr	13709	15933.09	221	0.5064158	0.14558176
ACD_Total_Raw	ACD	Raw	Total	13709	21604.17	368	0.5702962	0.10783769
ACD_Total_Adj	ACD	Adj	Total	13709	21604.17	368	0.6140819	0.10825180
ACD+HF_OnDr_Raw	ACD+HF	Raw	OnDr	13709	15816.17	348	0.5154844	0.11198305
ACD+HF_OnDr_Adj	ACD+HF	Adj	OnDr	13709	15816.17	348	0.5619028	0.11374067
ACD+HF_Total_Raw	ACD+HF	Raw	Total	13709	21375.78	533	0.6293378	0.08850966
ACD+HF_Total_Adj	ACD+HF	Adj	Total	13709	21375.78	533	0.6590630	0.08951955
ACD+MI+Str_OnDr_Raw	ACD+MI+Str	Raw	OnDr	13709	15757.65	425	0.5644601	0.10046010

ACD+MI+Str_OnDr_Adj	ACD+MI+Str	Adj	OnDr	13709	15757.65	425	0.6072930	0.10086093
ACD+MI+Str_Total_Raw	ACD+MI+Str	Raw	Total	13709	21295.16	619	0.6138429	0.08247205
ACD+MI+Str_Total_Adj	ACD+MI+Str	Adj	Total	13709	21295.16	619	0.6387273	0.08263003
MI_OnDr_Raw	MI	Raw	OnDr	13709	15854.49	101	0.6287445	0.20433098
MI_OnDr_Adj	MI	Adj	OnDr	13709	15854.49	101	0.6278277	0.20632178
MI_Total_Raw	MI	Raw	Total	13709	21473.19	126	0.6216086	0.18332122
MI_Total_Adj	MI	Adj	Total	13709	21473.19	126	0.6186374	0.18365548
Str_OnDr_Raw	Str	Raw	OnDr	13709	15833.56	123	0.7255626	0.18254770
Str_OnDr_Adj	Str	Adj	OnDr	13709	15833.56	123	0.7498096	0.18327263
Str_Total_Raw	Str	Raw	Total	13709	21423.45	165	0.7180294	0.15741846
Str_Total_Adj	Str	Adj	Total	13709	21423.45	165	0.7265511	0.15777364

```
> write.xlsx( HR,
+           "SGSU.xlsx",
+ sheetName = "Hazard ratios",
+   append = TRUE,
+   showNA = FALSE )
```

1.13.5 Subgroup OT

This is same as above, except the we restrict to “OnDr”, and subclassify by previous CVD:

```
> str(dat)
num [1:10, 1:2, 1:3, 1:2, 1:3] 6856 6856 6856 6856 6856 ...
- attr(*, "dimnames")=List of 5
 ..$ endp: chr [1:10] "HF" "ACD" "ACD+HF" "CVDD" ...
 ..$ data: chr [1:2] "OnDr" "Total"
 ..$ sub : chr [1:3] "AllPtt" "preCVD" "noCVD"
 ..$ ix : chr [1:2] "SGLT2" "SU"
 ..$ dat : chr [1:3] "N" "PY" "Event"

> YD <-
+   data.frame(as.matrix(ftable(dat[c(1:3,9,5,6),"OnDr",,"SGLT2",] +
+                               dat[c(1:3,9,5,6),"OnDr",,"SU" ],row.vars=c(1,2))))
> str( YD )

'data.frame':      18 obs. of  3 variables:
 $ N      : num  13709 3908 9801 13709 3908 ...
 $ PY     : num  15816 4278 11538 15933 4366 ...
 $ Event: num  139 106 33 221 121 100 348 216 132 425 ...

> HR <-
+   data.frame(as.matrix(ftable(res[c(1:3,9,5,6),"OnDr",,"Adj",c(1,4)],row.vars=c(1,2))))
```

With this fixed we can now write the table:

```
> write.xlsx( cbind(YD,HR),
+           "SGSU.xlsx",
+ sheetName = "Subgroups OT",
+   append = TRUE,
+   showNA = FALSE )
```

1.13.6 Subgroup ITT

This is same as above, except the we restrict to “Total”, and subclassify by previous CVD:

```
> YD <-
+   data.frame(as.matrix(ftable(dat[c(1:3,9,5,6),"Total",,"SGLT2",] +
+                               dat[c(1:3,9,5,6),"Total",,"SU"    ,],row.vars=c(1,2))))
> HR <-
+   data.frame(as.matrix(ftable(res[c(1:3,9,5,6),"Total",,"Adj",c(1,4)],row.vars=c(1,2))))
```

With this fixed we can now write the table:

```
> write.xlsx( cbind(YD,HR),
+             "SGSU.xlsx",
+             sheetName = "Subgroups ITT",
+             append = TRUE,
+             showNA = FALSE )
```

Chapter 2

Analysis of SGLT-2i vs. DPP4

2.1 Dataset for analysis of SGLT-2i vs DPP-4

First load the relevant package:

```
> options( width=95 )
> library( Epi )
> library( splines )
> library( haven )
> library( Matching )
> clear()
> print( sessionInfo(), l=F )
```

R version 3.4.1 (2017-06-30)

Platform: x86_64-w64-mingw32/x64 (64-bit)

Running under: Windows Server 2012 R2 x64 (build 9600)

Matrix products: default

attached base packages:

```
[1] splines    stats      graphics  grDevices  utils      datasets  methods    base
```

other attached packages:

```
[1] Matching_4.9-2 MASS_7.3-47    haven_1.1.0    Epi_2.26
```

loaded via a namespace (and not attached):

```
[1] Rcpp_0.12.12    lattice_0.20-35  zoo_1.8-0       grid_3.4.1      plyr_1.8.4
[6] magrittr_1.5    etm_0.6-2        rlang_0.1.2     Matrix_1.2-11   forcats_0.2.0
[11] tools_3.4.1     cmprsk_2.2-7     numDeriv_2016.8-1 survival_2.41-3  parallel_3.4.1
[16] compiler_3.4.1  tibble_1.3.4
```

Then we can read the data:

```
> system.time(
+ mset <- read_sas( "../data/episodes.sas7bdat" ) )
      user system elapsed
      8.39    0.26    24.04

> dim( mset )

[1] 244715    98

> names( mset )
```

```

...now input from ../rep/matchSGDP.tex
[1] "druggr"      "pnr"         "eksd"        "ATC"         "doDM"        "epiN"
[7] "doIx"        "Ixdr"        "Ixatc"       "lastpr"      "doTm"        "doFL"
[13] "FLdr"        "FLatc"       "deCVDD"     "coD"         "doTIA"       "doAngina"
[19] "doBleed"     "doCOPD"      "doPAD"       "doHF"        "doCancer"    "doDMcompl"
[25] "doNeuro"     "doDKD"       "doDiaEye"    "doHypo"      "doAtrFib"    "doMI"
[31] "doUnstAng"   "doHmStr"     "doDiaFoot"   "doOther"     "doPeriAng"   "doIscStr"
[37] "doAmp"       "doCKD"       "doPCIsTen"   "doCABG"      "doKeto"      "doDial"
[43] "doBari"      "sex"         "doBth"       "whBth"       "doDth"       "dSrc"
[49] "dolACE"      "dolSta"      "dolBB1"      "dolARB"      "dolA1A"      "dolDHP"
[55] "dolWtL"      "dolRPA"      "dolWrf"      "dolAsp"      "dolHCD"      "dolTHZ"
[61] "dolCcs"      "dolDXI"      "dolDgo"      "dolAP1"      "dolAmi"      "dolDTI"
[67] "dolNHP"      "dolFla"      "dolMetformin" "dolGLP1"     "dolMetxSGLT2" "dolMetxDPP4"
[73] "dolSGLT2"    "dolongIns"   "dolmixIns"   "dolDPP4"     "dolSU"       "dolintIns"
[79] "dolfastIns"  "dolTZD"      "dolAcarbose" "dolTZDxDPP4" "maxH"        "frail"
[85] "recnum"      "C_ADIAAG"    "compl"       "C_OPR"       "D_INDDTO"    "V_SENGDAGE"
[91] "deHF"        "deMACE"      "deMI"        "deStr"       "deIscStr"    "deAF"
[97] "deHH"        "deDKD"

```

We subset to SGLT-2i / DPP-4 and on the fly convert all dates to fractions of years to facilitate programming:

```
> mset <- cal.yr( subset( as.data.frame( mset ), Ixdr %in% c("SGLT2","DPP4") ) )
```

We then select the first of these episodes from each person, and exclude those with the other in the baseline. Note that persons where both drugs are initiated the same day, will be excluded entirely, because drugs initiated on the index day are coded as baseline drug with the same date.

```

> nrow( mset )
[1] 56984
> mset <- mset[order(mset$pnr,mset$doIx),]
> mset <- mset[!duplicated(mset$pnr),]
> mset <- subset( mset, ( Ixdr=="SGLT2" & is.na(dolDPP4) ) |
+                 ( Ixdr=="DPP4" & is.na(dolSGLT2) ) )
> with( mset, table(table(pnr)) )
1
48140

```

Thus we see that we have precisely one episode per person after these exclusions.

To make FLdr and Ixdr into factors we need some sensible levels:

```

> ( drlab <- read.table( "drlab.txt", header=TRUE, as.is=TRUE ) )
  gr  lab      longlab
1  11 Met    Metformin
2  12 SU  Sulfonylurea
3  13 TZD      TZD
4  14 DPP      DPP-4
5  15 GLP      GLP-1
6  16 SGL      SGLT2
7 fastIns fIns    fastIns
8 intIns  iIns    intIns
9 mixIns  mIns    mixIns
10 longIns lIns    longIns
11  18 Aca    Acarbose
12  19 Meg  Meglitinide

```

```

13      212  M+U      Met+SU
14      213  M+T      Met+TZD
15      214  M+D      Met+DPP4
16      216  M+S      Met+SGLT2
17      218  M+A  Met+Acarbose
18      223  U+T      SU+TZD
19      234  D+T      TZD+DPP4
20      246  D+S      DPP4+SGLT2

```

Then we can define the first line and the index drug variables as factors:

```

> mset <- transform( mset, FLdr = factor( FLdr,
+                                       levels = drlab$gr,
+                                       labels = drlab$lab ),
+                   Ixdr = factor( Ixdr ) )

```

We tabulate the index drug versus the first-line drug separately for those where the index date and first-line dates are the same:

```

> print( ftable( with( mset, addmargins(
+   table( "doIx=doFL"=abs(doIx-doFL)<0.1, FLdr, Ixdr ), 1:2 ) ),
+   col.vars=c(3,1) ),
+   zero = "." )

```

	Ixdr	DPP4		SGLT2			
	doIx=doFL	FALSE	TRUE	Sum	FALSE	TRUE	Sum
FLdr							
Met		25926	1074	27000	7973	123	8096
SU		7763	30	7793	2588	1	2589
TZD		5	.	5	2	.	2
DPP		34	676	710	9	.	9
GLP		25	3	28	21	1	22
SGL		.	.	.	.	90	90
fIns		259	4	263	165	.	165
iIns		246	3	249	125	.	125
mIns		229	1	230	92	1	93
lIns		43	5	48	16	.	16
Aca		33	1	34	12	.	12
Meg		.	.	.	.	.	.
M+U		.	.	.	.	.	.
M+T		24	.	24	12	.	12
M+D		43	422	465	37	.	37
M+S		.	.	.	.	23	23
M+A		.	.	.	.	.	.
U+T		.	.	.	.	.	.
D+T		.	.	.	.	.	.
D+S		.	.	.	.	.	.
Sum		34630	2219	36849	11052	239	11291

We see that among those where the two dates are equal, there are still some where the first line and Index drug are not the same. This is because each initiating drug generates its own episode.

2.2 Baseline tables for all new-starters

We produce an overview of the the exposure status, but first we need a few derived variables, including the indicator of *any* previous CVD:

```
> mset <- transform( mset, age = doIx - doBth,
+                    tff = doIx - doFL,
+                    sex = factor( sex, labels=c("M","F") ),
+                    frail = pmax( frail, 0, na.rm=TRUE ),
+                    maxH = pmax( 0, maxH, na.rm=TRUE ) )
> with( mset, addmargins( table( Ixatc, Ixdr ), 1 ) )
```

	Ixdr	
Ixatc	DPP4	SGLT2
A10BD07	7110	0
A10BD08	6427	0
A10BD09	5	0
A10BD10	15	0
A10BD11	99	0
A10BD13	316	0
A10BD15	0	309
A10BD16	0	11
A10BD20	0	372
A10BH01	13719	0
A10BH02	2752	0
A10BH03	826	0
A10BH04	651	0
A10BH05	4929	0
A10BK01	0	6665
A10BK02	0	321
A10BK03	0	3613
Sum	36849	11291

We now produce the baseline baseline tables for the entire set of new users, the result is in three tables, `dt.tab` (demographics for total sample), `ct.tab` (comobidites for total sample) and `mt.tab` (medication for total sample).

```
> ptab <- function( var ) cbind( tt <- table( var, mset$Ixdr ),
+                               round( prop.table( tt, 2 ) * 100, 1 ) )
```

2.2.1 Demographics

First the tabulations of the baseline demographics:

```
> t.sex <- with( mset, ptab(sex) )
> rownames( t.sex )[1] <- paste("Sex",rownames( t.sex )[1])
> t.fl0 <- with( mset, ptab( doIx-doFL==0 ) )[-1,,drop=F]
> rownames( t.fl0 )[1] <- "Index = First Line"
> t.fl0
```

	DPP4	SGLT2	DPP4	SGLT2
Index = First Line	1383	152	3.8	1.3

```
> m.fl0 <- with( subset(mset, doIx-doFL>0 ), round( c( tapply( doIx-doFL, Ixdr, mean ),
+                                                    tapply( doIx-doFL, Ixdr, sd ) ), 1 ) )
> dim( m.fl0 ) <- c(1,4)
> rownames( m.fl0 ) <- c("Index not FL: Mean / SD")
> m.fl0
```

	[,1]	[,2]	[,3]	[,4]
Index not FL: Mean / SD	6.9	9.2	5.2	5.4

```

> t.age <- with( mset, ptab( floor( pmin(pmax(age,30),89)/10 ) * 10 ) )
> rownames( t.age )[1] <- "Age at index <40"
> rownames( t.age )[nrow(t.age)] <- "80+"
> m.age <- with( mset, round( c( tapply( age, lxd, mean ),
+                               tapply( age, lxd, sd ) ), 1 ) )
> dim( m.age ) <- c(1,4)
> rownames( m.age ) <- c("Age: Mean / SD")
> m.age
      [,1] [,2] [,3] [,4]
Age: Mean / SD 64.6 60.1 12.6 10.9

> ## Date of index by 6 months and 1 year
> with( mset, ptab( floor( doIx*2 )/2 ) )
      DPP4  SGLT2  DPP4  SGLT2
2012.5  673    18  1.8   0.2
2013    4468   665 12.1   5.9
2013.5  4216   829 11.4   7.3
2014    4864   983 13.2   8.7
2014.5  4033  1108 10.9   9.8
2015    5043  1438 13.7  12.7
2015.5  4349  1493 11.8  13.2
2016    5031  2467 13.7  21.8
2016.5  4172  2290 11.3  20.3

> t.dat <- with( mset, ptab( floor( doIx ) ) )
> rownames( t.dat )[1] <- paste("Index date",rownames( t.dat )[1])
> ## Date of First Line
> t.fl <- with( mset, ptab( floor( doFL ) ) )
> rownames( t.fl )[1] <- paste("Date of first line",rownames( t.fl )[1])
> ## Frailty
> t.fr <- with( mset, ptab( frail ) )
> rownames( t.fr )[1] <- paste("Frailty",rownames( t.fr )[1])
> dt.tab <- rbind( t.sex, t.fl0, m.fl0, t.age, m.age, t.dat, t.fl, t.fr )
> dt.tab
      Sex M      DPP4  SGLT2  DPP4  SGLT2
      F      14603.0 4387.0 39.6  38.9
Index = First Line      1383.0 152.0 3.8  1.3
Index not FL: Mean / SD      6.9  9.2 5.2  5.4
Age at index <40      1147.0 431.0 3.1  3.8
40      3772.0 1555.0 10.2 13.8
50      7959.0 3405.0 21.6 30.2
60     10916.0 3760.0 29.6 33.3
70      9037.0 1892.0 24.5 16.8
80+     4018.0  248.0 10.9  2.2
Age: Mean / SD      64.6  60.1 12.6 10.9
Index date 2012      673.0   18.0 1.8  0.2
2013     8684.0 1494.0 23.6 13.2
2014     8897.0 2091.0 24.1 18.5
2015     9392.0 2931.0 25.5 26.0
2016     9203.0 4757.0 25.0 42.1
Date of first line 1995 1200.0  560.0 3.3  5.0
1996      457.0  202.0 1.2  1.8
1997      491.0  226.0 1.3  2.0
1998      633.0  288.0 1.7  2.6
1999      716.0  384.0 1.9  3.4
2000      812.0  411.0 2.2  3.6
2001      952.0  449.0 2.6  4.0

```

2002	1129.0	499.0	3.1	4.4
2003	1447.0	612.0	3.9	5.4
2004	1512.0	634.0	4.1	5.6
2005	1717.0	688.0	4.7	6.1
2006	1862.0	731.0	5.1	6.5
2007	2082.0	760.0	5.7	6.7
2008	2509.0	780.0	6.8	6.9
2009	2551.0	816.0	6.9	7.2
2010	2942.0	760.0	8.0	6.7
2011	3090.0	660.0	8.4	5.8
2012	2897.0	461.0	7.9	4.1
2013	2698.0	384.0	7.3	3.4
2014	2181.0	357.0	5.9	3.2
2015	1922.0	344.0	5.2	3.0
2016	1049.0	285.0	2.8	2.5
Frailty 0	25973.0	7459.0	70.5	66.1
1	10876.0	3832.0	29.5	33.9

2.2.2 Comorbidities

The data frame contains the dates of the *earliest* recorded comorbidities from the NPR, hence the prefix `.prv`:

```
> wh <- grep( "do[A-Z]", names( mset ) )
> wh <- wh[4:30]
> names( mset )[wh]
[1] "doFL"      "doTIA"      "doAngina"   "doBleed"    "doCOPD"     "doPAD"      "doHF"
[8] "doCancer"  "doDMcompl"  "doNeuro"    "doDKD"      "doDiaEye"   "doHypo"     "doAtrFib"
[15] "doMI"      "doUnstAng"  "doHmStr"    "doDiaFoot"  "doOther"    "doPeriAng"  "doIscStr"
[22] "doAmp"     "doCKD"      "doPCIsTen"  "doCABG"     "doKeto"     "doDial"

> comorb <- data.frame( pmax( mset[,wh] < mset[, "doIx"], 0, na.rm=TRUE ) )
> names( comorb ) <- gsub( "do", "prv.", names(comorb) )
> str( comorb )

'data.frame':      48140 obs. of  27 variables:
 $ prv.FL      : num  1 1 1 1 1 1 1 1 0 1 ...
 $ prv.TIA     : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.Angina  : num  0 0 0 1 1 0 0 0 0 0 ...
 $ prv.Bleed   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.COPD    : num  0 0 0 0 0 0 1 0 0 0 ...
 $ prv.PAD     : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.HF      : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.Cancer  : num  1 0 0 0 0 0 0 0 0 0 ...
 $ prv.DMcompl: num  1 0 0 0 0 1 0 0 0 0 ...
 $ prv.Neuro   : num  0 1 0 0 0 0 1 0 0 0 ...
 $ prv.DKD     : num  0 0 0 0 0 0 1 0 0 0 ...
 $ prv.DiaEye  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.Hypo    : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.AtrFib  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.MI      : num  0 0 0 0 1 0 1 0 0 0 ...
 $ prv.UnstAng: num  0 0 0 0 1 0 1 0 0 0 ...
 $ prv.HmStr   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.DiaFoot: num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.Other   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.PeriAng: num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.IscStr  : num  0 0 0 0 0 0 0 0 0 0 ...
```

```

$ prv.Amp      : num  0 0 0 0 0 0 0 0 0 0 0 ...
$ prv.CKD      : num  0 0 0 0 0 0 0 0 0 0 0 ...
$ prv.PCIsten: num  0 0 0 0 0 0 1 0 0 0 0 ...
$ prv.CABG     : num  0 0 0 0 0 0 0 0 0 0 0 ...
$ prv.Keto     : num  0 0 0 0 0 0 0 0 0 0 0 ...
$ prv.Dial     : num  0 0 0 0 0 0 0 0 0 0 0 ...

```

Later, in the modeling we will need the indicator of *any* previous CVD as well as *any* type of stroke and micro-vascular complications:

```

> comorb$pre.CVD <- with( comorb, pmax( prv.MI,
+                                     prv.UnstAng,
+                                     prv.Angina,
+                                     prv.HF,
+                                     prv.AtrFib,
+                                     prv.HmStr,
+                                     prv.IscStr,
+                                     prv.TIA,
+                                     prv.PAD ) )
> comorb$pre.Str <- with( comorb, pmax( prv.HmStr,
+                                     prv.IscStr,
+                                     prv.TIA ) )
> comorb$pre.FPA <- with( comorb, pmax( prv.DiaFoot,
+                                     prv.PeriAng ) )
> comorb$pre.Mic <- with( comorb, pmax( prv.DiaEye,
+                                     prv.DMcompl,
+                                     prv.Neuro,
+                                     prv.DKD,
+                                     prv.DiaFoot,
+                                     prv.PeriAng ) )

```

Note that we name the columns `pre.` to avoid including these in the propensity score estimation.

```

> ct.tab <- cbind(
+ t( sapply( comorb,
+           function( x ) tapply( x, mset$Ixdr, sum ) ) ),
+ round(
+ t( sapply( comorb,
+           function( x ) tapply( x, mset$Ixdr, mean ) ) ) * 100, 1 ) )
> # remove the dates of recurrent HF
> # wh <- grep( "HF[1-9]", rownames(ct.tab) )
> # ct.tab <- ct.tab[-wh,]
> ct.tab

```

	DPP4	SGLT2	DPP4	SGLT2
prv.FL	35466	11139	96.2	98.7
prv.TIA	1254	301	3.4	2.7
prv.Angina	4864	1574	13.2	13.9
prv.Bleed	1827	493	5.0	4.4
prv.COPD	1841	386	5.0	3.4
prv.PAD	2311	562	6.3	5.0
prv.HF	2080	475	5.6	4.2
prv.Cancer	2648	558	7.2	4.9
prv.DMcompl	3563	2307	9.7	20.4
prv.Neuro	1278	724	3.5	6.4
prv.DKD	1383	445	3.8	3.9
prv.DiaEye	2798	1569	7.6	13.9

prv.Hypo	1040	425	2.8	3.8
prv.AtrFib	3134	677	8.5	6.0
prv.MI	3253	956	8.8	8.5
prv.UnstAng	1403	440	3.8	3.9
prv.HmStr	411	85	1.1	0.8
prv.DiaFoot	285	112	0.8	1.0
prv.Other	1855	533	5.0	4.7
prv.PeriAng	1266	637	3.4	5.6
prv.IscStr	2443	535	6.6	4.7
prv.Amp	58	13	0.2	0.1
prv.CKD	1131	56	3.1	0.5
prv.PCIsten	383	105	1.0	0.9
prv.CABG	1128	314	3.1	2.8
prv.Keto	155	67	0.4	0.6
prv.Dial	9	1	0.0	0.0
pre.CVD	12424	3445	33.7	30.5
pre.Str	3551	802	9.6	7.1
pre.FPA	1470	703	4.0	6.2
pre.Mic	7800	4132	21.2	36.6

2.2.3 Other medication

We have variables that hold the last date of dispensation before index for all drugs of interest, restricted to the period after 2011-12-01, one year prior to the first SGLT2 dispensation.

```
> wh <- grep( "dol", names(mset) )
> names( mset )[wh]
[1] "dolACE"      "dolSta"      "dolBB1"      "dolARB"      "dolAlA"      "dolDHP"
[7] "dolWtL"      "dolRPA"      "dolWrf"      "dolAsp"      "dolHCD"      "dolTHZ"
[13] "dolCcs"      "dolDXI"      "dolDgo"      "dolAP1"      "dolAmi"      "dolDTI"
[19] "dolNHP"      "dolFla"      "dolMetformin" "dolGLP1"      "dolMetxSGLT2" "dolMetxDPP4"
[25] "dolSGLT2"    "dolongIns"   "dolmixIns"   "dolDPP4"     "dolSU"       "dolintIns"
[31] "dolfastIns"  "dolTZD"      "dolAcarbose" "dolTZDxDPP4"

> codisp <- data.frame( pmax( mset[,wh] > ( mset[, "doIx"] - 1 ), 0, na.rm=TRUE ) )
> names( codisp ) <- gsub( "dol", "had.", names(codisp) )
> ( names( codisp )[wh.ins <- grep("Ins",names(codisp))] )
[1] "had.longIns" "had.mixIns" "had.intIns" "had.fastIns"
> ( names( codisp )[wh.hyp <- c(1,4,6,12,3)] )
[1] "had.ACE" "had.ARB" "had.DHP" "had.THZ" "had.BB1"
> ( names( codisp )[wh.cvd <- c(10,2,wh.hyp)] )
[1] "had.Asp" "had.Sta" "had.ACE" "had.ARB" "had.DHP" "had.THZ" "had.BB1"
> codisp <- transform( codisp, got.Ins = apply( codisp[,wh.ins], 1, max ),
+                       got.Hyp = apply( codisp[,wh.hyp], 1, max ),
+                       got.CVD = apply( codisp[,wh.cvd], 1, max ) )
> names( codisp )
[1] "had.ACE"      "had.Sta"      "had.BB1"      "had.ARB"      "had.AlA"
[6] "had.DHP"      "had.WtL"      "had.RPA"      "had.Wrf"      "had.Asp"
[11] "had.HCD"      "had.THZ"      "had.Ccs"      "had.DXI"      "had.Dgo"
[16] "had.AP1"      "had.Ami"      "had.DTI"      "had.NHP"      "had.Fla"
[21] "had.Metformin" "had.GLP1"     "had.MetxSGLT2" "had.MetxDPP4" "had.SGLT2"
[26] "had.longIns"   "had.mixIns"   "had.DPP4"     "had.SU"       "had.intIns"
[31] "had.fastIns"   "had.TZD"      "had.Acarbose" "had.TZDxDPP4" "got.Ins"
[36] "got.Hyp"      "got.CVD"
```

```
> mt.tab <- cbind(
+ t( sapply( codisp,
+           function( x ) tapply( x, mset$Ixdr, sum ) ) ),
+ round(
+ t( sapply( codisp,
+           function( x ) tapply( x, mset$Ixdr, mean ) ) ) * 100, 1 ) )
> mt.tab
```

	DPP4	SGLT2	DPP4	SGLT2
had.ACE	13775	4463	37.4	39.5
had.Sta	25543	8459	69.3	74.9
had.BB1	10977	3124	29.8	27.7
had.ARB	10731	3954	29.1	35.0
had.A1A	2169	607	5.9	5.4
had.DHP	11043	3529	30.0	31.3
had.WtL	109	91	0.3	0.8
had.RPA	2664	716	7.2	6.3
had.Wrf	2498	460	6.8	4.1
had.Asp	12479	4159	33.9	36.8
had.HCD	6956	1577	18.9	14.0
had.THZ	5651	1735	15.3	15.4
had.Ccs	2803	569	7.6	5.0
had.DXI	754	174	2.0	1.5
had.Dgo	1723	277	4.7	2.5
had.APl	645	121	1.8	1.1
had.Ami	240	27	0.7	0.2
had.DTI	592	139	1.6	1.2
had.NHP	620	197	1.7	1.7
had.Fla	48	9	0.1	0.1
had.Metformin	32241	9074	87.5	80.4
had.GLP1	1567	4516	4.3	40.0
had.MetxSGLT2	0	693	0.0	6.1
had.MetxDPP4	14134	1601	38.4	14.2
had.SGLT2	0	10599	0.0	93.9
had.longIns	1934	2438	5.2	21.6
had.mixIns	1109	994	3.0	8.8
had.DPP4	22733	0	61.7	0.0
had.SU	9683	2622	26.3	23.2
had.intIns	1207	890	3.3	7.9
had.fastIns	1002	979	2.7	8.7
had.TZD	54	44	0.1	0.4
had.Acarbose	53	19	0.1	0.2
had.TZDxDPP4	5	0	0.0	0.0
got.Ins	4009	3859	10.9	34.2
got.Hyp	27580	8930	74.8	79.1
got.CVD	32539	10313	88.3	91.3

2.3 Propensity scoring

We now make a logistic regression of the indicator of SGLT2 assignment versus DPP4 assignment. For convenience we append the just created data frames of the indicators we will use in the analysis:

```
> mset <- cbind( mset, comorb, codisp )
> names( mset )
```

[1]	"druggr"	"pnr"	"eksd"	"ATC"	"doDM"
[6]	"epiN"	"doIx"	"Ixdr"	"Ixatc"	"lastpr"
[11]	"doTm"	"doFL"	"FLdr"	"FLatc"	"deCVDD"
[16]	"coD"	"doTIA"	"doAngina"	"doBleed"	"doCOPD"
[21]	"doPAD"	"doHF"	"doCancer"	"doDMcompl"	"doNeuro"
[26]	"doDKD"	"doDiaEye"	"doHypo"	"doAtrFib"	"doMI"
[31]	"doUnstAng"	"doHmStr"	"doDiaFoot"	"doOther"	"doPeriAng"
[36]	"doIscStr"	"doAmp"	"doCKD"	"doPCIsten"	"doCABG"
[41]	"doKeto"	"doDial"	"doBari"	"sex"	"doBth"
[46]	"whBth"	"doDth"	"dSrc"	"dolACE"	"dolSta"
[51]	"dolBB1"	"dolARB"	"dolAlA"	"dolDHP"	"dolWtL"
[56]	"dolRPA"	"dolWrf"	"dolAsp"	"dolHCD"	"dolTHZ"
[61]	"dolCcs"	"dolDXI"	"dolDgo"	"dolAP1"	"dolAmi"
[66]	"dolDTI"	"dolNHP"	"dolFla"	"dolMetformin"	"dolGLP1"
[71]	"dolMetxSGLT2"	"dolMetxDPP4"	"dolSGLT2"	"dolongIns"	"dolmixIns"
[76]	"dolDPP4"	"dolSU"	"dolintIns"	"dolfastIns"	"dolTZD"
[81]	"dolAcarbose"	"dolTZDxDPP4"	"maxH"	"frail"	"recnum"
[86]	"C_ADIAG"	"compl"	"C_OPR"	"D_INDDTO"	"V_SENGDAGE"
[91]	"deHF"	"deMACE"	"deMI"	"deStr"	"deIscStr"
[96]	"deAF"	"deHH"	"deDKD"	"age"	"tff"
[101]	"prv.FL"	"prv.TIA"	"prv.Angina"	"prv.Bleed"	"prv.COPD"
[106]	"prv.PAD"	"prv.HF"	"prv.Cancer"	"prv.DMcompl"	"prv.Neuro"
[111]	"prv.DKD"	"prv.DiaEye"	"prv.Hypo"	"prv.AtrFib"	"prv.MI"
[116]	"prv.UnstAng"	"prv.HmStr"	"prv.DiaFoot"	"prv.Other"	"prv.PeriAng"
[121]	"prv.IscStr"	"prv.Amp"	"prv.CKD"	"prv.PCIsten"	"prv.CABG"
[126]	"prv.Keto"	"prv.Dial"	"pre.CVD"	"pre.Str"	"pre.FPA"
[131]	"pre.Mic"	"had.ACE"	"had.Sta"	"had.BB1"	"had.ARB"
[136]	"had.ALA"	"had.DHP"	"had.WtL"	"had.RPA"	"had.Wrf"
[141]	"had.Asp"	"had.HCD"	"had.THZ"	"had.Ccs"	"had.DXI"
[146]	"had.Dgo"	"had.AP1"	"had.Ami"	"had.DTI"	"had.NHP"
[151]	"had.Fla"	"had.Metformin"	"had.GLP1"	"had.MetxSGLT2"	"had.MetxDPP4"
[156]	"had.SGLT2"	"had.longIns"	"had.mixIns"	"had.DPP4"	"had.SU"
[161]	"had.intIns"	"had.fastIns"	"had.TZD"	"had.Acarbose"	"had.TZDxDPP4"
[166]	"got.Ins"	"got.Hyp"	"got.CVD"		

With this in place it is quite easy to fit a propensity score model because we can easily fish out the relevant variables:

```
> table( mset$Ixdr )
DPP4 SGLT2
36849 11291

> ( prv <- grep( "prv", names(mset) ) )
[1] 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122
[23] 123 124 125 126 127

> ( had <- grep( "had", names(mset) ) )
[1] 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153
[23] 154 155 156 157 158 159 160 161 162 163 164 165

> rmd <- c( grep( "SGL", names( mset ) [had] ),
+          grep( "DPP", names( mset ) [had] ) )
> had <- had[-rmd]
> names( mset ) [had]
```

[1]	"had.ACE"	"had.Sta"	"had.BB1"	"had.ARB"	"had.ALA"
[6]	"had.DHP"	"had.WtL"	"had.RPA"	"had.Wrf"	"had.Asp"
[11]	"had.HCD"	"had.THZ"	"had.Ccs"	"had.DXI"	"had.Dgo"
[16]	"had.AP1"	"had.Ami"	"had.DTI"	"had.NHP"	"had.Fla"
[21]	"had.Metformin"	"had.GLP1"	"had.longIns"	"had.mixIns"	"had.SU"
[26]	"had.intIns"	"had.fastIns"	"had.TZD"	"had.Acarbose"	

```

> names( mset )[prv]
 [1] "prv.FL"      "prv.TIA"      "prv.Angina"    "prv.Bleed"    "prv.COPD"     "prv.PAD"
 [7] "prv.HF"      "prv.Cancer"   "prv.DMcompl"   "prv.Neuro"    "prv.DKD"      "prv.DiaEye"
[13] "prv.Hypo"    "prv.AtrFib"   "prv.MI"        "prv.UnstAng"  "prv.HmStr"     "prv.DiaFoot"
[19] "prv.Other"   "prv.PeriAng"  "prv.IscStr"    "prv.Amp"      "prv.CKD"       "prv.PCIsten"
[25] "prv.CABG"    "prv.Keto"     "prv.Dial"

> system.time(
+ pr.0 <- glm( ( Ixdr == "SGLT2" ) ~
+             sex + age + frail + doIx + doFL +
+             as.matrix(mset[,prv]) + as.matrix(mset[,had]),
+             family = binomial,
+             data = mset, maxit = 100 ) )

   user  system elapsed
   2.22    0.11    2.33

> print( summary( pr.0 ), digits = 3 )

Call:
glm(formula = (Ixdr == "SGLT2") ~ sex + age + frail + doIx +
    doFL + as.matrix(mset[, prv]) + as.matrix(mset[, had]), family = binomial,
    data = mset, maxit = 100)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.784  -0.603  -0.409  -0.170   3.560

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    -1.04e+03   2.46e+01  -42.29 < 2e-16 ***
sexF            -8.64e-02   2.75e-02   -3.14  0.00171 **
age            -3.40e-02   1.29e-03  -26.38 < 2e-16 ***
frail           8.74e-02   3.05e-02    2.87  0.00417 **
doIx           5.52e-01   1.24e-02   44.53 < 2e-16 ***
doFL          -3.55e-02   3.10e-03  -11.44 < 2e-16 ***
as.matrix(mset[, prv])prv.FL    9.31e-01   9.74e-02    9.55 < 2e-16 ***
as.matrix(mset[, prv])prv.TIA   3.79e-02   8.21e-02    0.46  0.64445
as.matrix(mset[, prv])prv.Angina 1.59e-02   4.57e-02    0.35  0.72778
as.matrix(mset[, prv])prv.Bleed -5.10e-02   6.34e-02   -0.81  0.42060
as.matrix(mset[, prv])prv.COPD  -1.64e-01   7.19e-02   -2.29  0.02226 *
as.matrix(mset[, prv])prv.PAD   -1.21e-01   6.14e-02   -1.98  0.04793 *
as.matrix(mset[, prv])prv.HF    -7.85e-02   7.31e-02   -1.07  0.28281
as.matrix(mset[, prv])prv.Cancer -1.23e-01   5.80e-02   -2.12  0.03438 *
as.matrix(mset[, prv])prv.DMcompl 1.11e-01   4.15e-02    2.68  0.00729 **
as.matrix(mset[, prv])prv.Neuro  1.93e-01   6.29e-02    3.07  0.00216 **
as.matrix(mset[, prv])prv.DKD   -6.28e-01   7.41e-02   -8.47 < 2e-16 ***
as.matrix(mset[, prv])prv.DiaEye  9.77e-02   4.54e-02    2.15  0.03144 *
as.matrix(mset[, prv])prv.Hypo  -2.54e-01   7.68e-02   -3.30  0.00096 ***
as.matrix(mset[, prv])prv.AtrFib 1.08e-01   7.50e-02    1.44  0.14914
as.matrix(mset[, prv])prv.MI     1.10e-01   5.61e-02    1.95  0.05059 .
as.matrix(mset[, prv])prv.UnstAng -9.04e-02   7.65e-02   -1.18  0.23731
as.matrix(mset[, prv])prv.HmStr  -4.34e-02   1.41e-01   -0.31  0.75750
as.matrix(mset[, prv])prv.DiaFoot -2.07e-01   1.49e-01   -1.39  0.16419
as.matrix(mset[, prv])prv.Other  -2.31e-01   6.89e-02   -3.35  0.00080 ***
as.matrix(mset[, prv])prv.PeriAng 2.78e-02   6.78e-02    0.41  0.68244
as.matrix(mset[, prv])prv.IscStr -2.55e-01   6.79e-02   -3.76  0.00017 ***
as.matrix(mset[, prv])prv.Amp    -1.03e+00   4.13e-01   -2.51  0.01218 *
as.matrix(mset[, prv])prv.CKD    -2.23e+00   1.58e-01  -14.14 < 2e-16 ***
as.matrix(mset[, prv])prv.PCIsten -1.83e-01   1.45e-01   -1.27  0.20490

```

```

as.matrix(mset[, prv])prv.CABG      -1.01e-01  9.06e-02  -1.11  0.26567
as.matrix(mset[, prv])prv.Keto      -1.90e-01  1.89e-01  -1.00  0.31639
as.matrix(mset[, prv])prv.Dial      -1.34e-01  1.22e+00  -0.11  0.91250
as.matrix(mset[, had])had.ACE        1.96e-01  3.13e-02   6.26  3.9e-10 ***
as.matrix(mset[, had])had.Sta        1.90e-01  3.10e-02   6.13  8.5e-10 ***
as.matrix(mset[, had])had.BB1        2.08e-02  3.46e-02   0.60  0.54800
as.matrix(mset[, had])had.ARB        2.86e-01  3.27e-02   8.74  < 2e-16 ***
as.matrix(mset[, had])had.A1A        3.55e-02  6.37e-02   0.56  0.57687
as.matrix(mset[, had])had.DHP        3.38e-03  3.08e-02   0.11  0.91253
as.matrix(mset[, had])had.WtL        8.78e-01  1.74e-01   5.05  4.5e-07 ***
as.matrix(mset[, had])had.RPA       -1.35e-01  6.12e-02  -2.21  0.02736 *
as.matrix(mset[, had])had.Wrf       -1.62e-01  7.97e-02  -2.04  0.04164 *
as.matrix(mset[, had])had.Asp        9.37e-02  3.20e-02   2.92  0.00346 **
as.matrix(mset[, had])had.HCD       -3.80e-01  4.42e-02  -8.60  < 2e-16 ***
as.matrix(mset[, had])had.THZ        7.31e-02  3.76e-02   1.94  0.05201 .
as.matrix(mset[, had])had.Ccs       -8.56e-02  5.78e-02  -1.48  0.13909
as.matrix(mset[, had])had.DXI       -1.82e-01  1.12e-01  -1.63  0.10226
as.matrix(mset[, had])had.Dgo       -1.30e-01  9.57e-02  -1.36  0.17406
as.matrix(mset[, had])had.APl       -3.24e-02  1.26e-01  -0.26  0.79641
as.matrix(mset[, had])had.Ami       -7.29e-01  2.45e-01  -2.97  0.00296 **
as.matrix(mset[, had])had.DTI        1.30e-01  1.25e-01   1.04  0.29979
as.matrix(mset[, had])had.NHP        2.29e-01  1.05e-01   2.17  0.02981 *
as.matrix(mset[, had])had.Fla       -6.11e-01  4.41e-01  -1.38  0.16609
as.matrix(mset[, had])had.Metformin -1.26e+00  3.72e-02 -33.94  < 2e-16 ***
as.matrix(mset[, had])had.GLP1       2.56e+00  3.72e-02  68.77  < 2e-16 ***
as.matrix(mset[, had])had.longIns    9.45e-01  4.68e-02  20.20  < 2e-16 ***
as.matrix(mset[, had])had.mixIns     6.00e-01  6.04e-02   9.94  < 2e-16 ***
as.matrix(mset[, had])had.SU         2.82e-02  3.23e-02   0.87  0.38287
as.matrix(mset[, had])had.intIns     4.72e-01  6.04e-02   7.81  5.7e-15 ***
as.matrix(mset[, had])had.fastIns    1.28e-01  6.70e-02   1.91  0.05605 .
as.matrix(mset[, had])had.TZD        6.36e-01  2.67e-01   2.38  0.01721 *
as.matrix(mset[, had])had.Acarbose   3.03e-01  3.30e-01   0.92  0.35811
---

```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

```

Null deviance: 52445  on 48139  degrees of freedom
Residual deviance: 38085  on 48078  degrees of freedom
AIC: 38209

```

Number of Fisher Scoring iterations: 6

With this fitted model we can now use the fitted values as propensity scores.

2.4 Propensity score matching

Based on this propensity score we take a matched sample of 1 per SGLT-2 user — note that we explicitly set a seed in order to get a fully reproducible code:

```

> set.seed( 1952 )
> system.time(
+ mt <- Match( Tr = (mset$Ixdr=="SGLT2"),
+             X = fitted( pr.0 ),
+             M = 1,
+             replace = FALSE,

```

```

+         exact = FALSE,
+         ties = FALSE,
+         caliper = 0.2 ) )
  user  system elapsed
26.74   1.15   27.89

> str( mt )
List of 23
 $ est          : num [1, 1] 0
 $ se           : NULL
 $ est.noadj    : num 0
 $ se.standard  : num 0
 $ se.cond      : NULL
 $ mdata        :List of 4
 ..$ Y          : num [1:15774] 0 0 0 0 0 0 0 0 0 0 ...
 ..$ Tr         : num [1:15774] 1 1 1 1 1 1 1 1 1 1 ...
 ..$ X          : num [1:2, 1:7887] 0.872 0.872 0.813 0.813 0.957 ...
 .. ..- attr(*, "dimnames")=List of 2
 .. .. ..$ : NULL
 .. .. ..$ : chr [1:7887] "5" "7" "16" "19" ...
 ..$ orig.weighted.treated.nobs: num 11291
 $ index.treated   : num [1:7887] 2 4 6 7 14 17 19 20 24 25 ...
 $ index.control   : num [1:7887] 3883 25566 639 8785 14347 ...
 $ index.dropped   : int  [1:3404] 5303 5653 5839 5877 5967 6167 6343 6355 6358 6445 ...
 $ weights         : num [1:7887] 1 1 1 1 1 1 1 1 1 1 ...
 $ orig.nobs       : int 48140
 $ orig.wnobs      : num 48140
 $ orig.treated.nobs: int 11291
 $ nobs           : int 48140
 $ wnobs          : num 7887
 $ caliper        : num 0.2
 $ ecaliper       : num 0.0477
 $ exact          : logi FALSE
 $ ndrops         : num 3404
 $ ndrops.matches : num 3404
 $ MatchLoopC     : num [1:7887, 1:6] 2 4 6 7 14 17 19 20 24 25 ...
 $ version        : chr "fast"
 $ estimand       : chr "ATT"
 - attr(*, "class")= chr "Match"

```

The resulting matching (`index.-variables`) refers to rows in `mset`:

```

> addmargins( rbind(
+ table( mset$Ixdr[unique(mt$index.treated)] ),
+ table( mset$Ixdr[unique(mt$index.control)] ) ), 2 )
      DPP4 SGLT2 Sum
[1,]    0  7887 7887
[2,] 7887    0 7887

```

We just use the index numbers for the treated as factor levels for the match-factor (we shall not use the factor though):

```

> tnum <- mt$index.treated
> cnum <- mt$index.control
> # a numeric with the index number of SGLT-2 for persons matched up
> mf <- rep( NA, nrow(mset) )
> mf[tnum] <- tnum

```

```

> mf[cnum] <- tnum
> # create a factor of this and tabulate
> mset <- transform( mset, mfac = factor(mf),
+                   psc = fitted(pr.0) )
> ( mtab <- with( mset, table( Ixdr, !is.na(mfac), useNA="ifany" ) ) )
Ixdr      FALSE  TRUE
DPP4    28962  7887
SGLT2   3404  7887

> round( cbind( rbind( cbind( mtab,
+                           pscab( mtab ) ),
+                           NA,
+                           NA),
+         pscab( mtab, margin=1 ) )[-3,], 1 )
Ixdr      FALSE  TRUE    All    N
DPP4      78.6   21.4  100.0 36849.0
SGLT2     30.1   69.9  100.0 11291.0

Ixdr      FALSE  TRUE
DPP4      89.5   50.0
SGLT2     10.5   50.0
All       100.0  100.0
N        32366.0 15774.0
      FALSE TRUE FALSE TRUE All    N    FALSE TRUE
DPP4  28962 7887  78.6 21.4 100 36849   89.5   50
SGLT2  3404 7887  30.1 69.9 100 11291   10.5   50
      NA  NA   NA  NA  NA   NA 32366.0 15774

```

We can see that not all persons can be matched with a caliper of 0.2; we can compare the propensity score among the matched and non-matched SGLT-2 patients:

```

> par( mar=c(3,3,1,1),mgp=c(3,1,0)/1.6,las=1,bty="n" )
> plot( mset$psco[mt$index.treated],
+       mset$psco[mt$index.control],
+       pch=16, cex=0.3 ,
+       xlim=0:1, xlab="SGLT-2i propensity score",
+       ylim=0:1, ylab="DPP-4 propensity score" )

```

For the use in further analyses we save a version for later use:

```

> oset <- mset
> pscore <- table( floor( oset$psco*100 ), oset$Ixdr )

```

Finally we make a dataset restricted to the matched persons:

```

> mset <- subset( oset, !is.na(mfac) )
> psmatch <- table( floor( mset$psco*100 ), mset$Ixdr )
> head( psmatch )
      DPP4 SGLT2
0  468      5
1  779     13
2 1289     41
3 1860     71
4 2146    117
5 2186    131

> head( psmatch )

```

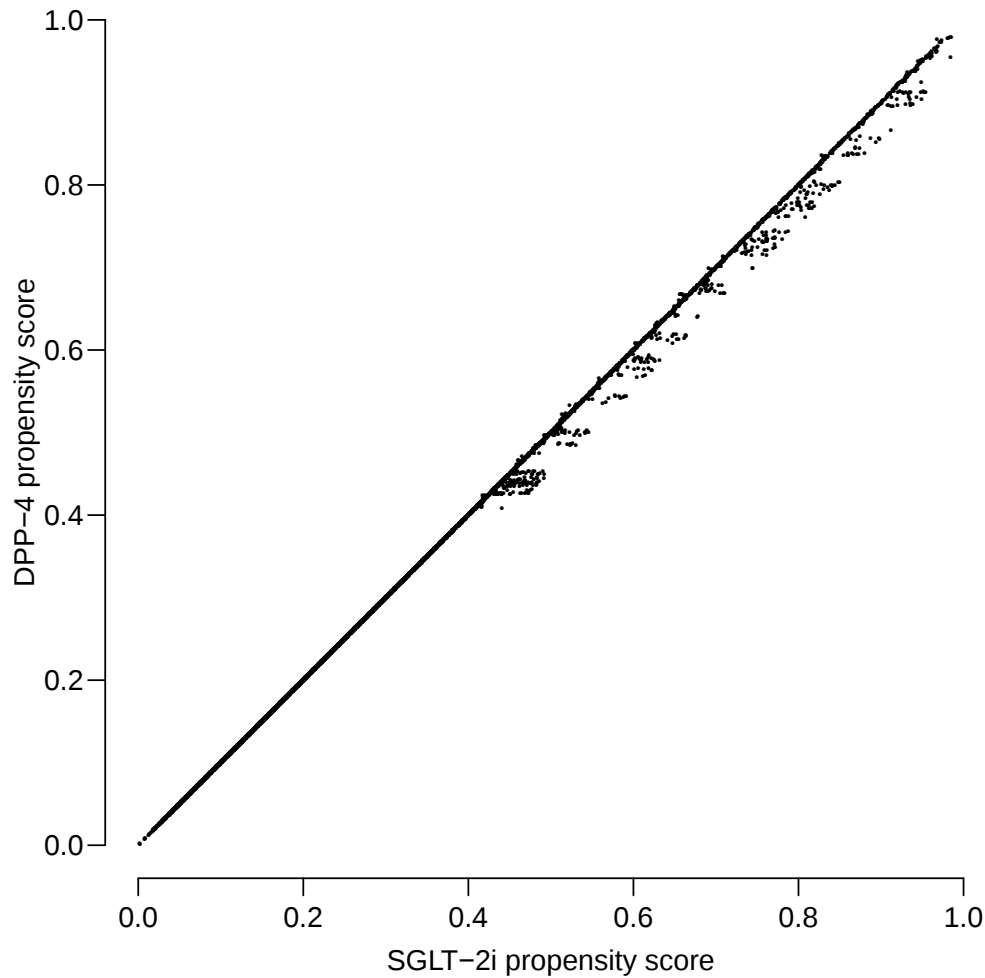


Figure 2.1: *Propensity scores from 1:1 matching; each matched set is represented by a dots.*
`./matchSGDP-cmp-ps`

	DPP4	SGLT2
0	5	5
1	13	13
2	40	41
3	74	71
4	117	117
5	128	131

```
> save( oset, mset, pscore, psmatch, file = "adatSGDP.Rda" )
> load( file = "adatSGDP.Rda" )
```

We also make histograms of the propensity scores, both for the original data and for the matched persons

```
> tt <- pscore
> tt[,1] <- tt[,1]/sum(tt[,1]) * 1000
> tt[,2] <- tt[,2]/sum(tt[,2]) * 1000
> tt <- cbind( -tt[,1], tt )
> head(tt)
```

	DPP4	SGLT2
0	-12.70048 12.70048	0.4428306

```

1 -21.14033 21.14033 1.1513595
2 -34.98060 34.98060 3.6312107
3 -50.47627 50.47627 6.2881941
4 -58.23767 58.23767 10.3622354
5 -59.32318 59.32318 11.6021610

> nam <- colnames( tt )[-1]
> clr <- c("transparent","red","blue")
> # we use the undocumented feature of boxplot that you can get stacked
> # bars starting in the negative by giving negative numbers to the first
> # column. But it will mysteriously ignore the first element of col...
> par( mar=c(3,3,1,1), mgp=c(3,1,0)/1.6, bty="n", las=1 )
> barplot( t(tt), space=0, col=clr, border="transparent", xlim=c(-65,65),
+         horiz=T, yaxt="n", ylab="Propensity score for SGLT-2 (%)", xaxt="n" )
> axis( side=2, at=seq(0,95,5), labels=NA, tcl=-0.3 )
> axis( side=2, at=0:9*10 )
> axis( side=1, at=-6:6*10, labels=NA, tcl=-0.3 )
> axis( side=1, at=-3:3*20, labels=abs(-3:3*20) )
> text( rep(60,2), 19:18*5, nam, col=clr[-1], font=2, adj=1 )
> # mtext( "%", side=1, font=2, line=1.5, at=-2.5 )
> mtext( "\211", side=1, font=2, line=1.5, at=0 )

> tt <- psmatch
> tt[,1] <- tt[,1]/sum(tt[,1]) * 1000
> tt[,2] <- tt[,2]/sum(tt[,2]) * 1000
> tt <- cbind( -tt[,1], tt )
> par( mar=c(3,3,1,1), mgp=c(3,1,0)/1.6, bty="n", las=1 )
> barplot( t(tt), space=0, col=clr, border="transparent", xlim=c(-65,65),
+         horiz=T, yaxt="n", ylab="Propensity score for SGLT-2 (%)", xaxt="n" )
> axis( side=2, at=seq(0,95,5), labels=NA, tcl=-0.3 )
> axis( side=2, at=0:9*10 )
> axis( side=1, at=-6:6*10, labels=NA, tcl=-0.3 )
> axis( side=1, at=-3:3*20, labels=abs(-3:3*20) )
> text( rep(60,2), 19:18*5, nam, col=clr[-1], font=2, adj=1 )
> # mtext( "%", side=1, font=2, line=1.5, at=-2.5 )
> mtext( "\211", side=1, font=2, line=1.5, at=10 )

```

2.5 Baseline tables for propensity matched persons

We have the matched sets in the dataframe `mset`, so we can almost verbatim reuse the code doing the tables for the original sample, except for the names of the resulting tables: `dm.tab` (demographics for matched sample), `cm.tab` (comorbidities for matched sample) and `mm.tab` (medication for matched sample).

2.5.1 Demographics

First the tabulations of the baseline demographics:

```

> t.sex <- with( mset, ptab( sex ) )
> rownames( t.sex )[1] <- paste("Sex",rownames( t.sex )[1])
> t.age <- with( mset, ptab( floor( pmin(pmax(age,30),89)/10 ) * 10 ) )
> rownames( t.age )[1] <- "Age at index <40"
> rownames( t.age )[nrow(t.age)] <- "80+"

```

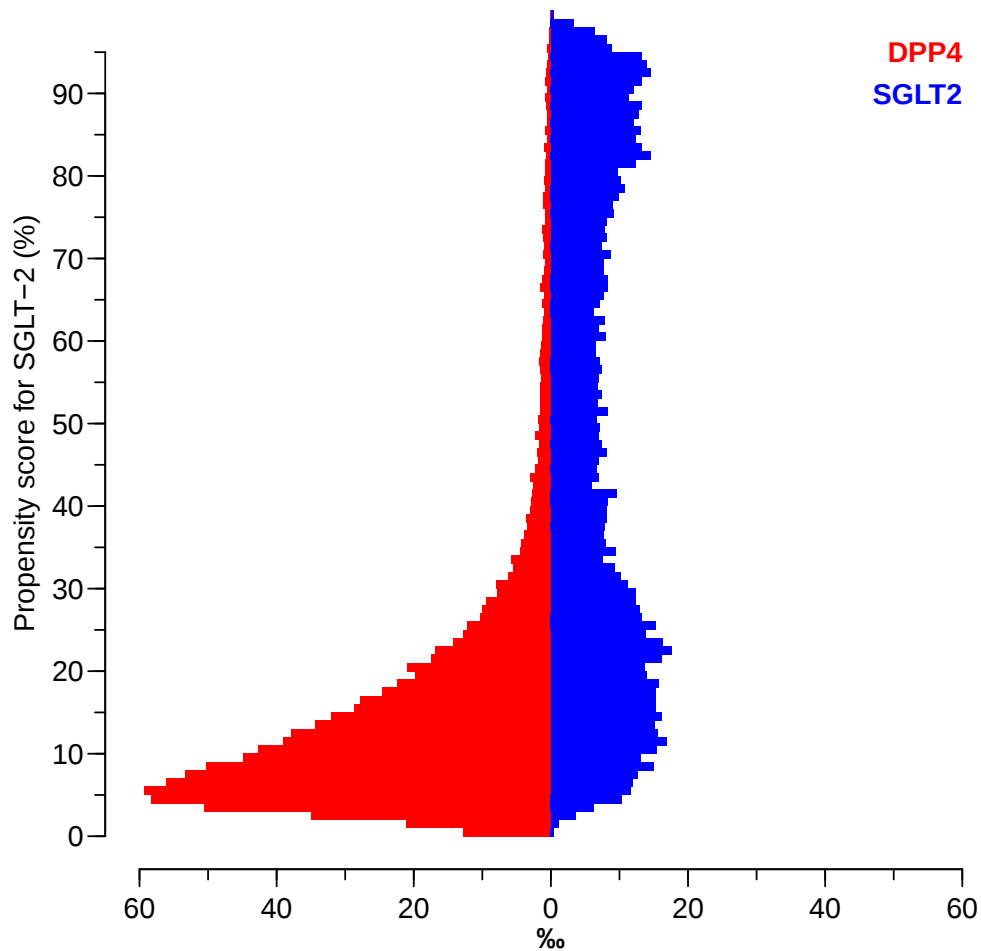


Figure 2.2: Propensity scores for the SGLT-2 group (left, percent) and other groups (right, %) in the 1:3 propensity score matched study.

./matchSGDP-pscoreo

```
> t.fl0 <- with( mset, ptab( doIx-doFL==0 ) )[-1,,drop=F]
> rownames( t.fl0 )[1] <- "Index = First Line"
> t.fl0

          DPP4 SGLT2 DPP4 SGLT2
Index = First Line 157  151    2   1.9
> m.fl0 <- with( subset(mset, doIx-doFL>0 ), round( c( tapply( doIx-doFL, Ixdr, mean ),
+                                                     tapply( doIx-doFL, Ixdr, sd ) ), 1 ) )
> dim( m.fl0 ) <- c(1,4)
> rownames( m.fl0 ) <- c("Index not FL: Mean / SD")
> m.fl0

          [,1] [,2] [,3] [,4]
Index not FL: Mean / SD  8.4  8.3  5.6  5.3
> m.age <- with( mset, round( c( tapply( age, Ixdr, mean ),
+                               tapply( age, Ixdr, sd ) ), 1 ) )
> dim( m.age ) <- c(1,4)
> rownames( m.age ) <- c("Age: Mean / SD")
> m.age

          [,1] [,2] [,3] [,4]
Age: Mean / SD  61 61.1 12.9 11.1
```

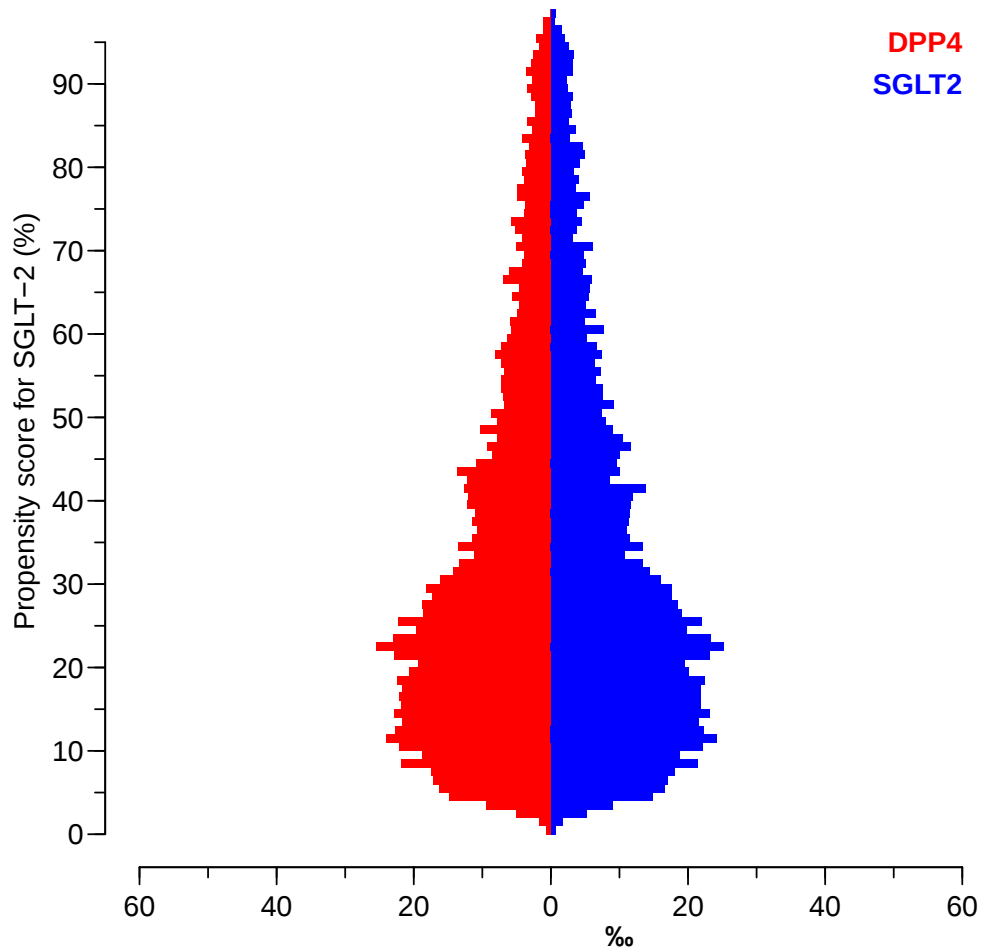


Figure 2.3: Propensity scores for the SGLT-2 group (left, percent) and other groups in the 1:1 propensity score matched study.

./matchSGDP-pscorem

```
> ## Date of index by 6 months and 1 year
> with( mset, ptab( floor( doIx*2 )/2 ) )

      DPP4 SGLT2 DPP4 SGLT2
2012.5   64   15  0.8  0.2
2013    505  556  6.4  7.0
2013.5  592  637  7.5  8.1
2014    787  720 10.0  9.1
2014.5  712  794  9.0 10.1
2015   1055  993 13.4 12.6
2015.5 1124  988 14.3 12.5
2016   1499 1659 19.0 21.0
2016.5 1549 1525 19.6 19.3

> t.dat <- with( mset, ptab( floor( doIx ) ) )
> rownames( t.dat )[1] <- paste("Index date",rownames( t.dat )[1])
> ## Date of First Line
> t.fl <- with( mset, ptab( floor( doFL ) ) )
> rownames( t.fl )[1] <- paste("Date of first line",rownames( t.fl )[1])
> ## Frailty
> t.fr <- with( mset, ptab( frail ) )
```

```
> rownames( t.fr )[1] <- paste("Frailty",rownames( t.fr )[1])
> dm.tab <- rbind( t.sex, t.fl0, m.fl0, t.age, m.age, t.dat, t.fl, t.fr )
> dm.tab
```

	DPP4	SGLT2	DPP4	SGLT2
Sex M	4795.0	4818.0	60.8	61.1
F	3092.0	3069.0	39.2	38.9
Index = First Line	157.0	151.0	2.0	1.9
Index not FL: Mean / SD	8.4	8.3	5.6	5.3
Age at index <40	442.0	257.0	5.6	3.3
40	1147.0	1010.0	14.5	12.8
50	2021.0	2198.0	25.6	27.9
60	2233.0	2674.0	28.3	33.9
70	1558.0	1518.0	19.8	19.2
80+	486.0	230.0	6.2	2.9
Age: Mean / SD	61.0	61.1	12.9	11.1
Index date 2012	64.0	15.0	0.8	0.2
2013	1097.0	1193.0	13.9	15.1
2014	1499.0	1514.0	19.0	19.2
2015	2179.0	1981.0	27.6	25.1
2016	3048.0	3184.0	38.6	40.4
Date of first line 1995	410.0	307.0	5.2	3.9
1996	153.0	111.0	1.9	1.4
1997	144.0	130.0	1.8	1.6
1998	184.0	161.0	2.3	2.0
1999	198.0	240.0	2.5	3.0
2000	250.0	248.0	3.2	3.1
2001	259.0	251.0	3.3	3.2
2002	297.0	299.0	3.8	3.8
2003	368.0	369.0	4.7	4.7
2004	363.0	403.0	4.6	5.1
2005	408.0	435.0	5.2	5.5
2006	400.0	511.0	5.1	6.5
2007	450.0	520.0	5.7	6.6
2008	533.0	547.0	6.8	6.9
2009	495.0	585.0	6.3	7.4
2010	567.0	575.0	7.2	7.3
2011	573.0	526.0	7.3	6.7
2012	463.0	404.0	5.9	5.1
2013	380.0	343.0	4.8	4.3
2014	367.0	325.0	4.7	4.1
2015	375.0	323.0	4.8	4.1
2016	250.0	274.0	3.2	3.5
Frailty 0	5482.0	5474.0	69.5	69.4
1	2405.0	2413.0	30.5	30.6

2.5.2 Comorbidities

The data frame contains the dates of the *earliest* recorded comorbidities from the NPR, hence the prefix `.prv`:

```
> wh <- match( rownames(ct.tab), names( mset ) )
> names( mset )[wh]
```

[1] "prv.FL"	"prv.TIA"	"prv.Angina"	"prv.Bleed"	"prv.COPD"	"prv.PAD"
[7] "prv.HF"	"prv.Cancer"	"prv.DMcompl"	"prv.Neuro"	"prv.DKD"	"prv.DiaEye"
[13] "prv.Hypo"	"prv.AtrFib"	"prv.MI"	"prv.UnstAng"	"prv.HmStr"	"prv.DiaFoot"

```

[19] "prv.Other"      "prv.PeriAng"  "prv.IscStr"   "prv.Amp"      "prv.CKD"      "prv.PCIsten"
[25] "prv.CABG"       "prv.Keto"     "prv.Dial"     "pre.CVD"      "pre.Str"      "pre.FPA"
[31] "pre.Mic"

> comorb <- mset[,wh]
> cm.tab <- cbind(
+ t( sapply( comorb,
+           function( x ) tapply( x, mset$Ixdr, sum ) ) ),
+ round(
+ t( sapply( comorb,
+           function( x ) tapply( x, mset$Ixdr, mean ) ) ) * 100, 1 ) )
> cm.tab

```

	DPP4	SGLT2	DPP4	SGLT2
prv.FL	7730	7736	98.0	98.1
prv.TIA	220	222	2.8	2.8
prv.Angina	1046	1061	13.3	13.5
prv.Bleed	367	369	4.7	4.7
prv.COPD	269	285	3.4	3.6
prv.PAD	431	413	5.5	5.2
prv.HF	351	364	4.5	4.6
prv.Cancer	448	443	5.7	5.6
prv.DMcompl	1259	1218	16.0	15.4
prv.Neuro	405	395	5.1	5.0
prv.DKD	320	292	4.1	3.7
prv.DiaEye	916	893	11.6	11.3
prv.Hypo	260	268	3.3	3.4
prv.AtrFib	475	486	6.0	6.2
prv.MI	647	655	8.2	8.3
prv.UnstAng	279	285	3.5	3.6
prv.HmStr	62	67	0.8	0.8
prv.DiaFoot	65	62	0.8	0.8
prv.Other	388	379	4.9	4.8
prv.PeriAng	363	378	4.6	4.8
prv.IscStr	394	399	5.0	5.1
prv.Amp	8	7	0.1	0.1
prv.CKD	66	55	0.8	0.7
prv.PCIsten	74	63	0.9	0.8
prv.CABG	211	225	2.7	2.9
prv.Keto	42	37	0.5	0.5
prv.Dial	1	1	0.0	0.0
pre.CVD	2378	2419	30.2	30.7
pre.Str	606	596	7.7	7.6
pre.FPA	410	417	5.2	5.3
pre.Mic	2283	2385	28.9	30.2

2.5.3 Other medication

We have variables that hold the last date of dispensation before index for all drugs of interest — well, only in the period after 2011-12-01, one year prior to the first SGLT2 dispensation.

```

> wh <- grep( "had.", names( mset ) )
> names( mset )[wh]

```

[1] "had.ACE"	"had.Sta"	"had.BB1"	"had.ARB"	"had.A1A"
[6] "had.DHP"	"had.WtL"	"had.RPA"	"had.Wrf"	"had.Asp"
[11] "had.HCD"	"had.THZ"	"had.Ccs"	"had.DXI"	"had.Dgo"
[16] "had.APl"	"had.Ami"	"had.DTI"	"had.NHP"	"had.Fla"

```

[21] "had.Metformin" "had.GLP1"      "had.MetxSGLT2" "had.MetxDPP4"  "had.SGLT2"
[26] "had.longIns"   "had.mixIns"     "had.DPP4"      "had.SU"        "had.intIns"
[31] "had.fastIns"   "had.TZD"        "had.Acarbose"  "had.TZDxDPP4"

> codisp <- mset[,wh]
> ( names( codisp )[wh.ins <- grep("Ins",names(codisp))]) )
[1] "had.longIns" "had.mixIns" "had.intIns" "had.fastIns"
> ( names( codisp )[wh.hyp <- c(1,4,6,12,3)] )
[1] "had.ACE" "had.ARB" "had.DHP" "had.THZ" "had.BB1"
> ( names( codisp )[wh.cvd <- c(8,2,wh.hyp)] )
[1] "had.RPA" "had.Sta" "had.ACE" "had.ARB" "had.DHP" "had.THZ" "had.BB1"
> codisp <- transform( codisp, got.Ins = apply( codisp[,wh.ins], 1, max ),
+                       got.Hyp = apply( codisp[,wh.hyp], 1, max ),
+                       got.CVD = apply( codisp[,wh.cvd], 1, max ) )
> names( codisp )
[1] "had.ACE"      "had.Sta"      "had.BB1"      "had.ARB"      "had.A1A"
[6] "had.DHP"      "had.WtL"      "had.RPA"      "had.Wrf"      "had.Asp"
[11] "had.HCD"      "had.THZ"      "had.Ccs"      "had.DXI"      "had.Dgo"
[16] "had.AP1"      "had.Ami"      "had.DTI"      "had.NHP"      "had.Fla"
[21] "had.Metformin" "had.GLP1"     "had.MetxSGLT2" "had.MetxDPP4" "had.SGLT2"
[26] "had.longIns"   "had.mixIns"   "had.DPP4"      "had.SU"        "had.intIns"
[31] "had.fastIns"   "had.TZD"      "had.Acarbose"  "had.TZDxDPP4" "got.Ins"
[36] "got.Hyp"      "got.CVD"

> mm.tab <- cbind(
+ t( sapply( codisp,
+           function( x ) tapply( x, mset$Ixdr, sum ) ) ),
+ round(
+ t( sapply( codisp,
+           function( x ) tapply( x, mset$Ixdr, mean ) ) ) * 100, 1 ) )
+ mm.tab

```

	DPP4	SGLT2	DPP4	SGLT2
had.ACE	2942	3034	37.3	38.5
had.Sta	5641	5716	71.5	72.5
had.BB1	2159	2178	27.4	27.6
had.ARB	2624	2613	33.3	33.1
had.A1A	424	428	5.4	5.4
had.DHP	2378	2405	30.2	30.5
had.WtL	57	51	0.7	0.6
had.RPA	527	520	6.7	6.6
had.Wrf	353	353	4.5	4.5
had.Asp	2706	2722	34.3	34.5
had.HCD	1150	1116	14.6	14.1
had.THZ	1161	1146	14.7	14.5
had.Ccs	424	434	5.4	5.5
had.DXI	110	130	1.4	1.6
had.Dgo	218	211	2.8	2.7
had.AP1	94	101	1.2	1.3
had.Ami	26	23	0.3	0.3
had.DTI	84	97	1.1	1.2
had.NHP	146	132	1.9	1.7
had.Fla	4	8	0.1	0.1
had.Metformin	6181	6267	78.4	79.5
had.GLP1	1477	1516	18.7	19.2
had.MetxSGLT2	0	536	0.0	6.8
had.MetxDPP4	3029	1349	38.4	17.1

had.SGLT2	0	7352	0.0	93.2
had.longIns	1121	1113	14.2	14.1
had.mixIns	533	539	6.8	6.8
had.DPP4	4857	0	61.6	0.0
had.SU	1980	1907	25.1	24.2
had.intIns	493	483	6.3	6.1
had.fastIns	490	467	6.2	5.9
had.TZD	18	22	0.2	0.3
had.Acarbose	15	13	0.2	0.2
had.TZDxDPP4	3	0	0.0	0.0
got.Ins	1896	1954	24.0	24.8
got.Hyp	5956	6097	75.5	77.3
got.CVD	6930	7055	87.9	89.5

2.6 Overview of pre- and post matching

The number of persons and episodes:

```
> addmargins( with( oset, table(table(pnr)) ) )
      1      Sum
48140 48140

> addmargins(
+ with( oset, table(DPP4=(tt<-table(pnr,Ixdr))[,1],SGLT2=tt[,2]) ) )
      SGLT2
DPP4      0      1      Sum
0          0 11291 11291
1    36849      0 36849
Sum 36849 11291 48140

> addmargins( with( mset, table(table(pnr)) ) )
      1      Sum
15774 15774

> addmargins(
+ with( mset, table(DPP4=(tt<-table(pnr,Ixdr))[,1],SGLT2=tt[,2]) ) )
      SGLT2
DPP4      0      1      Sum
0          0  7887  7887
1    7887      0  7887
Sum  7887  7887 15774
```

The best overview is created if we list the tables for the matched and un-matched next to each other. However we first check that that have the same sets of rows:

```
> identical( rownames(dt.tab), rownames(dm.tab) )
[1] TRUE

> identical( rownames(ct.tab), rownames(cm.tab) )
[1] TRUE

> identical( rownames(mt.tab), rownames(mm.tab) )
[1] TRUE

> cbind( dt.tab, dm.tab )
```

	DPP4	SGLT2	DPP4	SGLT2	DPP4	SGLT2	DPP4	SGLT2
Sex M	22246.0	6904.0	60.4	61.1	4795.0	4818.0	60.8	61.1
F	14603.0	4387.0	39.6	38.9	3092.0	3069.0	39.2	38.9
Index = First Line	1383.0	152.0	3.8	1.3	157.0	151.0	2.0	1.9
Index not FL: Mean / SD	6.9	9.2	5.2	5.4	8.4	8.3	5.6	5.3
Age at index <40	1147.0	431.0	3.1	3.8	442.0	257.0	5.6	3.3
40	3772.0	1555.0	10.2	13.8	1147.0	1010.0	14.5	12.8
50	7959.0	3405.0	21.6	30.2	2021.0	2198.0	25.6	27.9
60	10916.0	3760.0	29.6	33.3	2233.0	2674.0	28.3	33.9
70	9037.0	1892.0	24.5	16.8	1558.0	1518.0	19.8	19.2
80+	4018.0	248.0	10.9	2.2	486.0	230.0	6.2	2.9
Age: Mean / SD	64.6	60.1	12.6	10.9	61.0	61.1	12.9	11.1
Index date 2012	673.0	18.0	1.8	0.2	64.0	15.0	0.8	0.2
2013	8684.0	1494.0	23.6	13.2	1097.0	1193.0	13.9	15.1
2014	8897.0	2091.0	24.1	18.5	1499.0	1514.0	19.0	19.2
2015	9392.0	2931.0	25.5	26.0	2179.0	1981.0	27.6	25.1
2016	9203.0	4757.0	25.0	42.1	3048.0	3184.0	38.6	40.4
Date of first line 1995	1200.0	560.0	3.3	5.0	410.0	307.0	5.2	3.9
1996	457.0	202.0	1.2	1.8	153.0	111.0	1.9	1.4
1997	491.0	226.0	1.3	2.0	144.0	130.0	1.8	1.6
1998	633.0	288.0	1.7	2.6	184.0	161.0	2.3	2.0
1999	716.0	384.0	1.9	3.4	198.0	240.0	2.5	3.0
2000	812.0	411.0	2.2	3.6	250.0	248.0	3.2	3.1
2001	952.0	449.0	2.6	4.0	259.0	251.0	3.3	3.2
2002	1129.0	499.0	3.1	4.4	297.0	299.0	3.8	3.8
2003	1447.0	612.0	3.9	5.4	368.0	369.0	4.7	4.7
2004	1512.0	634.0	4.1	5.6	363.0	403.0	4.6	5.1
2005	1717.0	688.0	4.7	6.1	408.0	435.0	5.2	5.5
2006	1862.0	731.0	5.1	6.5	400.0	511.0	5.1	6.5
2007	2082.0	760.0	5.7	6.7	450.0	520.0	5.7	6.6
2008	2509.0	780.0	6.8	6.9	533.0	547.0	6.8	6.9
2009	2551.0	816.0	6.9	7.2	495.0	585.0	6.3	7.4
2010	2942.0	760.0	8.0	6.7	567.0	575.0	7.2	7.3
2011	3090.0	660.0	8.4	5.8	573.0	526.0	7.3	6.7
2012	2897.0	461.0	7.9	4.1	463.0	404.0	5.9	5.1
2013	2698.0	384.0	7.3	3.4	380.0	343.0	4.8	4.3
2014	2181.0	357.0	5.9	3.2	367.0	325.0	4.7	4.1
2015	1922.0	344.0	5.2	3.0	375.0	323.0	4.8	4.1
2016	1049.0	285.0	2.8	2.5	250.0	274.0	3.2	3.5
Frailty 0	25973.0	7459.0	70.5	66.1	5482.0	5474.0	69.5	69.4
1	10876.0	3832.0	29.5	33.9	2405.0	2413.0	30.5	30.6

```
> cbind( ct.tab, cm.tab )
```

	DPP4	SGLT2	DPP4	SGLT2	DPP4	SGLT2	DPP4	SGLT2
prv.FL	35466	11139	96.2	98.7	7730	7736	98.0	98.1
prv.TIA	1254	301	3.4	2.7	220	222	2.8	2.8
prv.Angina	4864	1574	13.2	13.9	1046	1061	13.3	13.5
prv.Bleed	1827	493	5.0	4.4	367	369	4.7	4.7
prv.COPD	1841	386	5.0	3.4	269	285	3.4	3.6
prv.PAD	2311	562	6.3	5.0	431	413	5.5	5.2
prv.HF	2080	475	5.6	4.2	351	364	4.5	4.6
prv.Cancer	2648	558	7.2	4.9	448	443	5.7	5.6
prv.DMcompl	3563	2307	9.7	20.4	1259	1218	16.0	15.4
prv.Neuro	1278	724	3.5	6.4	405	395	5.1	5.0
prv.DKD	1383	445	3.8	3.9	320	292	4.1	3.7
prv.DiaEye	2798	1569	7.6	13.9	916	893	11.6	11.3
prv.Hypo	1040	425	2.8	3.8	260	268	3.3	3.4
prv.AtrFib	3134	677	8.5	6.0	475	486	6.0	6.2

prv.MI	3253	956	8.8	8.5	647	655	8.2	8.3
prv.UnstAng	1403	440	3.8	3.9	279	285	3.5	3.6
prv.HmStr	411	85	1.1	0.8	62	67	0.8	0.8
prv.DiaFoot	285	112	0.8	1.0	65	62	0.8	0.8
prv.Other	1855	533	5.0	4.7	388	379	4.9	4.8
prv.PeriAng	1266	637	3.4	5.6	363	378	4.6	4.8
prv.IscStr	2443	535	6.6	4.7	394	399	5.0	5.1
prv.Amp	58	13	0.2	0.1	8	7	0.1	0.1
prv.CKD	1131	56	3.1	0.5	66	55	0.8	0.7
prv.PCIsten	383	105	1.0	0.9	74	63	0.9	0.8
prv.CABG	1128	314	3.1	2.8	211	225	2.7	2.9
prv.Keto	155	67	0.4	0.6	42	37	0.5	0.5
prv.Dial	9	1	0.0	0.0	1	1	0.0	0.0
pre.CVD	12424	3445	33.7	30.5	2378	2419	30.2	30.7
pre.Str	3551	802	9.6	7.1	606	596	7.7	7.6
pre.FPA	1470	703	4.0	6.2	410	417	5.2	5.3
pre.Mic	7800	4132	21.2	36.6	2283	2385	28.9	30.2

```
> cbind( mt.tab, mm.tab )
```

	DPP4	SGLT2	DPP4	SGLT2	DPP4	SGLT2	DPP4	SGLT2
had.ACE	13775	4463	37.4	39.5	2942	3034	37.3	38.5
had.Sta	25543	8459	69.3	74.9	5641	5716	71.5	72.5
had.BBl	10977	3124	29.8	27.7	2159	2178	27.4	27.6
had.ARB	10731	3954	29.1	35.0	2624	2613	33.3	33.1
had.Ala	2169	607	5.9	5.4	424	428	5.4	5.4
had.DHP	11043	3529	30.0	31.3	2378	2405	30.2	30.5
had.WtL	109	91	0.3	0.8	57	51	0.7	0.6
had.RPA	2664	716	7.2	6.3	527	520	6.7	6.6
had.Wrf	2498	460	6.8	4.1	353	353	4.5	4.5
had.Asp	12479	4159	33.9	36.8	2706	2722	34.3	34.5
had.HCD	6956	1577	18.9	14.0	1150	1116	14.6	14.1
had.THZ	5651	1735	15.3	15.4	1161	1146	14.7	14.5
had.Ccs	2803	569	7.6	5.0	424	434	5.4	5.5
had.DXI	754	174	2.0	1.5	110	130	1.4	1.6
had.Dgo	1723	277	4.7	2.5	218	211	2.8	2.7
had.APl	645	121	1.8	1.1	94	101	1.2	1.3
had.Ami	240	27	0.7	0.2	26	23	0.3	0.3
had.DTI	592	139	1.6	1.2	84	97	1.1	1.2
had.NHP	620	197	1.7	1.7	146	132	1.9	1.7
had.Fla	48	9	0.1	0.1	4	8	0.1	0.1
had.Metformin	32241	9074	87.5	80.4	6181	6267	78.4	79.5
had.GLP1	1567	4516	4.3	40.0	1477	1516	18.7	19.2
had.MetxSGLT2	0	693	0.0	6.1	0	536	0.0	6.8
had.MetxDPP4	14134	1601	38.4	14.2	3029	1349	38.4	17.1
had.SGLT2	0	10599	0.0	93.9	0	7352	0.0	93.2
had.longIns	1934	2438	5.2	21.6	1121	1113	14.2	14.1
had.mixIns	1109	994	3.0	8.8	533	539	6.8	6.8
had.DPP4	22733	0	61.7	0.0	4857	0	61.6	0.0
had.SU	9683	2622	26.3	23.2	1980	1907	25.1	24.2
had.intIns	1207	890	3.3	7.9	493	483	6.3	6.1
had.fastIns	1002	979	2.7	8.7	490	467	6.2	5.9
had.TZD	54	44	0.1	0.4	18	22	0.2	0.3
had.Acarbose	53	19	0.1	0.2	15	13	0.2	0.2
had.TZDxDPP4	5	0	0.0	0.0	3	0	0.0	0.0
got.Ins	4009	3859	10.9	34.2	1896	1954	24.0	24.8
got.Hyp	27580	8930	74.8	79.1	5956	6097	75.5	77.3
got.CVD	32539	10313	88.3	91.3	6930	7055	87.9	89.5

```
> save( dt.tab, dm.tab,
+       ct.tab, cm.tab,
+       mt.tab, mm.tab, file="btabSGDP.Rda" )
```

2.7 Survival analysis datasets: Lexis objects

In this section we take the original and the matched data and set up Lexis-objects for the survival analyses; we make separate objects for Death, heart failure (HF) and combined outcomes.

First get the relevant data:

```
> library( Epi )
> library( survival )
> print( sessionInfo(), l=F )
R version 3.4.1 (2017-06-30)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server 2012 R2 x64 (build 9600)

Matrix products: default

attached base packages:
[1] stats      graphics  grDevices  utils      datasets  methods   base

other attached packages:
[1] survival_2.41-3 Epi_2.26

loaded via a namespace (and not attached):
 [1] cmprsk_2.2-7      zoo_1.8-0         MASS_7.3-47       compiler_3.4.1
 [5] Matrix_1.2-11     plyr_1.8.4        parallel_3.4.1    tools_3.4.1
 [9] etm_0.6-2         Rcpp_0.12.12      splines_3.4.1     grid_3.4.1
[13] numDeriv_2016.8-1 lattice_0.20-35

> clear()
> load( file = "adatSGDP.Rda" )
> lls()

  name    mode    class      dim          size(Kb)
1 mset    list     data.frame 15774 170      22,785.3
2 oset    list     data.frame 48140 170      68,613.9
3 pscore  numeric table      100 2         7.2
4 psmatch numeric table      99 2         7.1
```

We will follow persons from date of new use, `do1x`, till either date of event.

For later use we define both the time since index (`tfi`) and current date (period — `per`) and current age (`cua`) as timescales. The latter not to be confused with age at index date, `age`.

2.8 Collecting analysis results and key data

We want to collect analysis results and background data for the analyses. The latter are classified by index drug and PY/events, the former by adjusted/non-adjusted analysis and HR/c.i./s.e. In addition both are classified by endpoint, data, and subset:

```

...now input from ../rep/anaSGDP.tex
> lst <- list( endp = c("HF", "ACD", "ACD+HF", "CVDD", "MI", "Str", "IscStr",
+                      "CVDD+MI+Str", "ACD+MI+Str", "DKD"),
+            data = c("OnDr", "Total"),
+            sub = c("AllPtt", "preCVD", "noCVD") )
> dat <- NArray( c( lst, list( ix = c("SGLT2", "DPP4"),
+                               dat = c("N", "PY", "Event") ) ) )
> res <- NArray( c( lst, list( adj = c("Raw", "Adj"),
+                               res = c("HR", "lo", "up", "se") ) ) )
> length( dat ) ; str( dat )
[1] 360

logi [1:10, 1:2, 1:3, 1:2, 1:3] NA NA NA NA NA NA ...
- attr(*, "dimnames")=List of 5
..$ endp: chr [1:10] "HF" "ACD" "ACD+HF" "CVDD" ...
..$ data: chr [1:2] "OnDr" "Total"
..$ sub : chr [1:3] "AllPtt" "preCVD" "noCVD"
..$ ix : chr [1:2] "SGLT2" "DPP4"
..$ dat : chr [1:3] "N" "PY" "Event"
> length( res ) ; str( res )
[1] 480

logi [1:10, 1:2, 1:3, 1:2, 1:4] NA NA NA NA NA NA ...
- attr(*, "dimnames")=List of 5
..$ endp: chr [1:10] "HF" "ACD" "ACD+HF" "CVDD" ...
..$ data: chr [1:2] "OnDr" "Total"
..$ sub : chr [1:3] "AllPtt" "preCVD" "noCVD"
..$ adj : chr [1:2] "Raw" "Adj"
..$ res : chr [1:4] "HR" "lo" "up" "se"

```

2.9 Survival dataset: Lexis objects

Here is a definition of a function that produces a Lexis object with follow-up till `mset$doX` for the event D:

```

> mkLex <-
+ function( )
+ {
+   Lx <- Lexis( entry = list( per = doIx,
+                             cua = doIx-doBth,
+                             tfi = 0 ),
+               exit = list( per = doX ),
+               exit.status = factor( D, labels=c("OnDr", "Event") ),
+               data = subset( mset, is.na(doDth) | doIx < doDth ) )
+   Lx <- cutLexis( Lx, cut = Lx$doTm,
+                  new.state = "OffDr",
+                  pre = "OnDr" )
+   Lx
+ }
> mset$D <- with( mset, !is.na(deHF) & deHF<2017 )
> mset$doX <- with( mset, pmin( doDth, deHF, 2017, na.rm=TRUE ) )
> lxHF <- mkLex( )
NOTE: entry.status has been set to "OnDr" for all.
> summary( lxHF )

```

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	10873	4704	197	15774	4901	18245.92	15774
OffDr	0	4641	63	4704	63	5824.28	4704
Sum	10873	9345	260	20478	4964	24070.19	15774

2.9.1 Follow-up data and events

First we devise a function to extract the person-years and events from the *Lexis* object:

```
> fill.dat <-
+ function( LexDat, outc )
+ {
+   whc <- c(" Persons:", "Risk time:", "Event")
+   cat( outc, ":\n" )
+   print( sm <- summary( LexDat, by="IxdR" ) )
+   s2 <- summary( LexDat, by=c("IxdR", "pre.CVD") )
+   for( ix in c("DPP4", "SGLT2") )
+   {
+     dat[outc, "AllPtt", ix,] <- sm[[ix]][[1]][c(1,3), whc]
+     dat[outc, "noCVD", ix,] <- s2[[paste(ix, 0, sep=".")]][[1]][c(1,3), whc]
+     dat[outc, "preCVD", ix,] <- s2[[paste(ix, 1, sep=".")]][[1]][c(1,3), whc]
+   }
+   invisible(NULL)
+ }
```

```
HF :
$DPP4
```

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	5495	2268	124	7887	2392	9170.43	7887
OffDr	0	2245	23	2268	23	2775.33	2268
Sum	5495	4513	147	10155	2415	11945.76	7887

\$SGLT2

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	5378	2436	73	7887	2509	9075.48	7887
OffDr	0	2396	40	2436	40	3048.95	2436
Sum	5378	4832	113	10323	2549	12124.43	7887

```
> round( ftable( dat[1:2,,,], col.vars=c(4,5) ), 1 )
```

			ix	SGLT2		DPP4			
			dat	N	PY	Event	N	PY	Event
endp	data	sub							
HF	OnDr	AllPtt		7887.0	9075.5	73.0	7887.0	9170.4	124.0
		preCVD		2419.0	2668.1	60.0	2378.0	2625.3	103.0
		noCVD		5468.0	6407.4	13.0	5509.0	6545.1	21.0
	Total	AllPtt		7887.0	12124.4	113.0	7887.0	11945.8	147.0
		preCVD		2419.0	3520.0	87.0	2378.0	3401.4	120.0
		noCVD		5468.0	8604.4	26.0	5509.0	8544.4	27.0

ACD	OnDr	AllPtt	NA	NA	NA	NA	NA	NA
		preCVD	NA	NA	NA	NA	NA	NA
		noCVD	NA	NA	NA	NA	NA	NA
	Total	AllPtt	NA	NA	NA	NA	NA	NA
		preCVD	NA	NA	NA	NA	NA	NA
		noCVD	NA	NA	NA	NA	NA	NA

2.9.2 Analysis

Follow-up is now analysed by Cox-models adjusted and non-adjusted, total or on drug and separately for all persons and persons with and without prior CVD. These are named with an *m.* and combination of *r/a* (raw/adjusted), *t/d* (total/on drug) and *p/n/y* (patients/no CVD/yes CVD):

```
> m.tpr <- coxph( Surv( tfi, tfi+lex.dur, lex.Xst=="Event" ) ~
+               I(Ixdr=="SGLT2") + cluster(pnr),
+               data = lxHF )
> m.tpa <- update( m.tpr, . ~ . + I(doIx-doBth) + sex + I(doIx-doDM)
+               + prv.MI + prv.HF + prv.AtrFib + frail
+               + had.BBl + had.NHP + had.Ala + had.ACE )
> m.dpr <- update( m.tpr, data = subset( lxHF, lex.Cst=="OnDr" ) )
> m.dpa <- update( m.tpa, data = subset( lxHF, lex.Cst=="OnDr" ) )
> m.tnr <- update( m.tpr, data = subset( lxHF, pre.CVD==1 ) )
> m.tna <- update( m.tpa, data = subset( lxHF, pre.CVD==1 ) )
> m.dnr <- update( m.dpr, data = subset( lxHF, pre.CVD==1 & lex.Cst=="OnDr" ) )
> m.dna <- update( m.dpa, data = subset( lxHF, pre.CVD==1 & lex.Cst=="OnDr" ) )
> m.tyr <- update( m.tpr, data = subset( lxHF, pre.CVD==0 ) )
> m.tya <- update( m.tpa, data = subset( lxHF, pre.CVD==0 ) )
> m.dyr <- update( m.dpr, data = subset( lxHF, pre.CVD==0 & lex.Cst=="OnDr" ) )
> m.dya <- update( m.dpa, data = subset( lxHF, pre.CVD==0 & lex.Cst=="OnDr" ) )
```

With these models fitted we can now extract the HRs etc. and put into the right slots of *res*:

```
> get4 <- function( m ) ci.lin( m, subset="SGLT2", Exp=TRUE )[,c(5:7,2)]
> res["HF","Total","AllPtt","Raw",] <- get4( m.tpr )
> res["HF","Total","AllPtt","Adj",] <- get4( m.tpa )
> res["HF","OnDr","AllPtt","Raw",] <- get4( m.dpr )
> res["HF","OnDr","AllPtt","Adj",] <- get4( m.dpa )
> res["HF","Total","preCVD","Raw",] <- get4( m.tnr )
> res["HF","Total","preCVD","Adj",] <- get4( m.tna )
> res["HF","OnDr","preCVD","Raw",] <- get4( m.dnr )
> res["HF","OnDr","preCVD","Adj",] <- get4( m.dna )
> res["HF","Total","noCVD","Raw",] <- get4( m.tyr )
> res["HF","Total","noCVD","Adj",] <- get4( m.tya )
> res["HF","OnDr","noCVD","Raw",] <- get4( m.dyr )
> res["HF","OnDr","noCVD","Adj",] <- get4( m.dya )
```

This can now be packed into a function that does this for a given type of event:

```
> fill.res <- function( LexDat, outc )
+ {
+   m.tpr <- coxph( Surv( tfi, tfi+lex.dur, lex.Xst=="Event" ) ~
+               I(Ixdr=="SGLT2") + cluster(pnr),
+               data = LexDat )
+   m.tpa <- update( m.tpr, . ~ . + I(doIx-doBth) + sex + I(doIx-doDM)
```

```

+               + prv.MI + prv.HF + prv.AtrFib + frail
+               + had.BBl + had.NHP + had.ALA + had.ACE )
+ m.dpr <- update( m.tpr, data = subset( LexDat, lex.Cst=="OnDr" ) )
+ m.dpa <- update( m.tpa, data = subset( LexDat, lex.Cst=="OnDr" ) )
+
+ m.tnr <- update( m.tpr, data = subset( LexDat, pre.CVD==1 ) )
+ m.tna <- update( m.tpa, data = subset( LexDat, pre.CVD==1 ) )
+ m.dnr <- update( m.dpr, data = subset( LexDat, pre.CVD==1 & lex.Cst=="OnDr" ) )
+ m.dna <- update( m.dpa, data = subset( LexDat, pre.CVD==1 & lex.Cst=="OnDr" ) )
+
+ m.tyr <- update( m.tpr, data = subset( LexDat, pre.CVD==0 ) )
+ m.tya <- update( m.tpa, data = subset( LexDat, pre.CVD==0 ) )
+ m.dyr <- update( m.dpr, data = subset( LexDat, pre.CVD==0 & lex.Cst=="OnDr" ) )
+ m.dya <- update( m.dpa, data = subset( LexDat, pre.CVD==0 & lex.Cst=="OnDr" ) )
+
+ res[outc,"Total","AllPtt","Raw",] <- get4( m.tpr )
+ res[outc,"Total","AllPtt","Adj",] <- get4( m.tpa )
+ res[outc,"OnDr","AllPtt","Raw",] <- get4( m.dpr )
+ res[outc,"OnDr","AllPtt","Adj",] <- get4( m.dpa )
+
+ res[outc,"Total","preCVD","Raw",] <- get4( m.tnr )
+ res[outc,"Total","preCVD","Adj",] <- get4( m.tna )
+ res[outc,"OnDr","preCVD","Raw",] <- get4( m.dnr )
+ res[outc,"OnDr","preCVD","Adj",] <- get4( m.dna )
+
+ res[outc,"Total","noCVD","Raw",] <- get4( m.tyr )
+ res[outc,"Total","noCVD","Adj",] <- get4( m.tya )
+ res[outc,"OnDr","noCVD","Raw",] <- get4( m.dyr )
+ res[outc,"OnDr","noCVD","Adj",] <- get4( m.dya )
+ invisible( NULL )
+ }

```

So combining this with the function that constructs the Lexis object we get:

```

> mset$D <- with( mset, !is.na(deHF) & deHF<2017 )
> mset$dOx <- with( mset, pmin( doDth, deHF, 2017, na.rm=TRUE ) )
> lxHF <- mkLex()
NOTE: entry.status has been set to "OnDr" for all.
> fill.res( lxHF, "HF" )
> round( ftable( res[1:2,,,], col.vars=c(2,5) ), 3 )

```

			data	OnDr		Total				
		res	HR	lo	up	se	HR	lo	up	se
endp	sub	adj								
HF	AllPtt	Raw	0.593	0.444	0.792	0.148	0.758	0.593	0.969	0.125
		Adj	0.568	0.425	0.760	0.148	0.748	0.585	0.957	0.126
	preCVD	Raw	0.574	0.417	0.788	0.162	0.703	0.533	0.926	0.141
		Adj	0.556	0.405	0.762	0.161	0.704	0.536	0.923	0.139
	noCVD	Raw	0.633	0.317	1.267	0.354	0.953	0.557	1.630	0.274
		Adj	0.643	0.314	1.316	0.365	0.944	0.544	1.636	0.281
ACD	AllPtt	Raw	NA	NA	NA	NA	NA	NA	NA	NA
		Adj	NA	NA	NA	NA	NA	NA	NA	NA
	preCVD	Raw	NA	NA	NA	NA	NA	NA	NA	NA
		Adj	NA	NA	NA	NA	NA	NA	NA	NA
	noCVD	Raw	NA	NA	NA	NA	NA	NA	NA	NA
		Adj	NA	NA	NA	NA	NA	NA	NA	NA

So we just repeat this for all types of outcome:

```
> mset$D <- with( mset, !is.na(doDth) & doDth<2017 )
> mset$doX <- with( mset, pmin( doDth, 2017, na.rm=TRUE ) )
> lxACD <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxACD, "ACD" )
> fill.dat( lxACD, "ACD" )
```

ACD :
\$DPP4

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	5337	2297	253	7887	2550	9269.42	7887
OffDr	0	2218	79	2297	79	2826.14	2297
Sum	5337	4515	332	10184	2629	12095.56	7887

\$SGLT2

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	5335	2459	93	7887	2552	9133.55	7887
OffDr	0	2384	75	2459	75	3111.51	2459
Sum	5335	4843	168	10346	2627	12245.06	7887

```
> mset$D <- with( mset, ( !is.na(deHF) | !is.na(doDth) ) &
+ ( deHF<2017 | doDth<2017 ) )
> mset$doX <- with( mset, pmin( doDth, deHF, 2017, na.rm=TRUE ) )
> lxACDHF <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxACDHF, "ACD+HF" )
> fill.dat( lxACDHF, "ACD+HF" )
```

ACD+HF :
\$DPP4

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	5263	2268	356	7887	2624	9170.43	7887
OffDr	0	2176	92	2268	92	2775.33	2268
Sum	5263	4444	448	10155	2716	11945.76	7887

\$SGLT2

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	5287	2436	164	7887	2600	9075.48	7887
OffDr	0	2326	110	2436	110	3048.95	2436
Sum	5287	4762	274	10323	2710	12124.43	7887

```
> mset$D <- with( mset, !is.na(deCVDD) & deCVDD<2017 )
> mset$doX <- with( mset, pmin( doDth, deCVDD, 2017, na.rm=TRUE ) )
> lxCVDD <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxCVDD, "CVDD" )
> fill.dat( lxCVDD, "CVDD" )
```

```
CVDD :
$DPP4
```

```
Transitions:
  To
```

From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	5533	2297	57	7887	2354	9269.42	7887
OffDr	0	2281	16	2297	16	2826.14	2297
Sum	5533	4578	73	10184	2370	12095.56	7887

```
$SGLT2
```

```
Transitions:
  To
```

From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	5411	2459	17	7887	2476	9133.55	7887
OffDr	0	2445	14	2459	14	3111.51	2459
Sum	5411	4904	31	10346	2490	12245.06	7887

```
> mset$D <- with( mset, !is.na(deMI) & deMI<2017 )
> mset$doX <- with( mset, pmin( doDth, deMI, 2017, na.rm=TRUE ) )
> lxMI <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxMI, "MI" )
> fill.dat( lxMI, "MI" )
```

```
MI :
$DPP4
```

```
Transitions:
  To
```

From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	5533	2276	78	7887	2354	9204.19	7887
OffDr	0	2251	25	2276	25	2775.85	2276
Sum	5533	4527	103	10163	2379	11980.04	7887

```
$SGLT2
```

```
Transitions:
  To
```

From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	5388	2445	54	7887	2499	9093.07	7887
OffDr	0	2427	18	2445	18	3084.42	2445
Sum	5388	4872	72	10332	2517	12177.49	7887

```
> mset$D <- with( mset, !is.na(deStr) & deStr<2017 )
> mset$doX <- with( mset, pmin( doDth, deStr, 2017, na.rm=TRUE ) )
> lxStr <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxStr, "Str" )
> fill.dat( lxStr, "Str" )
```

```
Str :
$DPP4
```

```
Transitions:
```

```

      To
From   OnDr OffDr Event Records: Events: Risk time: Persons:
  OnDr  5523  2279   85     7887    2364    9203.86     7887
  OffDr   0   2267   12     2279     12    2804.17     2279
  Sum    5523  4546   97    10166    2376   12008.03     7887

```

\$SGLT2

Transitions:

```

      To
From   OnDr OffDr Event Records: Events: Risk time: Persons:
  OnDr  5393  2439   55     7887    2494    9086.79     7887
  OffDr   0   2418   21     2439     21    3071.02     2439
  Sum    5393  4857   76    10326    2515   12157.81     7887

```

```

> mset$D <- with( mset, !is.na(deIscStr) & deIscStr<2017 )
> mset$doX <- with( mset, pmin( doDth, deIscStr, 2017, na.rm=TRUE ) )
> lxIStr <- mkLex()

```

NOTE: entry.status has been set to "OnDr" for all.

```

> fill.res( lxIStr, "IscStr" )
> fill.dat( lxIStr, "IscStr" )

```

IscStr :

\$DPP4

Transitions:

```

      To
From   OnDr OffDr Event Records: Events: Risk time: Persons:
  OnDr  5532  2280   75     7887    2355    9211.97     7887
  OffDr   0   2270   10     2280     10    2806.66     2280
  Sum    5532  4550   85    10167    2365   12018.63     7887

```

\$SGLT2

Transitions:

```

      To
From   OnDr OffDr Event Records: Events: Risk time: Persons:
  OnDr  5394  2441   52     7887    2493    9088.84     7887
  OffDr   0   2423   18     2441     18    3074.45     2441
  Sum    5394  4864   70    10328    2511   12163.29     7887

```

```

> mset$D <- with( mset, ( ( !is.na(deCVDD) & deCVDD < 2017 ) |
+                       ( !is.na(deMI) & deMI < 2017 ) |
+                       ( !is.na(deStr) & deStr < 2017 ) ) )
> mset$doX <- with( mset, pmin( doDth, deCVDD, deMI, deStr, 2017, na.rm=TRUE ) )
> lxCVDDx <- mkLex()

```

NOTE: entry.status has been set to "OnDr" for all.

```

> fill.res( lxCVDDx, "CVDD+MI+Str" )
> fill.dat( lxCVDDx, "CVDD+MI+Str" )

```

CVDD+MI+Str :

\$DPP4

Transitions:

```

      To
From   OnDr OffDr Event Records: Events: Risk time: Persons:
  OnDr  5426  2258   203     7887    2461    9138.64     7887
  OffDr   0   2212    46     2258     46    2754.63     2258

```

Sum	5426	4470	249	10145	2507	11893.27	7887
-----	------	------	-----	-------	------	----------	------

\$SGLT2

Transitions:

To

From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	5342	2425	120	7887	2545	9047.82	7887
OffDr	0	2380	45	2425	45	3043.94	2425
Sum	5342	4805	165	10312	2590	12091.76	7887

```
> mset$D <- with( mset, ( ( !is.na(doDth) & doDth < 2017 ) |
+                      ( !is.na(deMI) & deMI < 2017 ) |
+                      ( !is.na(deStr) & deStr < 2017 ) ) )
> mset$doX <- with( mset, pmin( doDth, deMI, deStr, 2017, na.rm=TRUE ) )
> lxACDx <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxACDx, "ACD+MI+Str" )
> fill.dat( lxACDx, "ACD+MI+Str" )
```

ACD+MI+Str :

\$DPP4

Transitions:

To

From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	5246	2258	383	7887	2641	9138.64	7887
OffDr	0	2154	104	2258	104	2754.63	2258
Sum	5246	4412	487	10145	2745	11893.27	7887

\$SGLT2

Transitions:

To

From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	5269	2425	193	7887	2618	9047.82	7887
OffDr	0	2323	102	2425	102	3043.94	2425
Sum	5269	4748	295	10312	2720	12091.76	7887

```
> mset$D <- with( mset, !is.na(deDKD) & deDKD<2017 )
> mset$doX <- with( mset, pmin( doDth, deDKD, 2017, na.rm=TRUE ) )
> lxKid <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxKid, "DKD" )
> fill.dat( lxKid, "DKD" )
```

DKD :

\$DPP4

Transitions:

To

From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	5460	2238	189	7887	2427	9093.73	7887
OffDr	0	2209	29	2238	29	2732.94	2238
Sum	5460	4447	218	10125	2456	11826.67	7887

\$SGLT2

Transitions:

From	To		Event	Records:	Events:	Risk time:	Persons:
OnDr	OnDr	OffDr	55	7887	2488	9081.69	7887
OffDr	0	2407	26	2433	26	3054.16	2433
Sum	5399	4840	81	10320	2514	12135.85	7887

So we can summarize results:

```
> round( ftable( dat, col.vars=c(2,4,5) ), 0 )
```

		data			OnDr			Total			DPP4			
		ix	SGLT2					SGLT2					DPP4	
		dat	N	PY	Event	N	PY	Event	N	PY	Event	N	PY	Event
endp	sub													
HF	AllPtt		7887	9075	73	7887	9170	124	7887	12124	113	7887	11946	14
	preCVD		2419	2668	60	2378	2625	103	2419	3520	87	2378	3401	12
	noCVD		5468	6407	13	5509	6545	21	5468	8604	26	5509	8544	2
ACD	AllPtt		7887	9134	93	7887	9269	253	7887	12245	168	7887	12096	33
	preCVD		2419	2714	45	2378	2709	142	2419	3615	90	2378	3526	18
	noCVD		5468	6420	48	5509	6560	111	5468	8630	78	5509	8570	14
ACD+HF	AllPtt		7887	9075	164	7887	9170	356	7887	12124	274	7887	11946	44
	preCVD		2419	2668	103	2378	2625	225	2419	3520	171	2378	3401	27
	noCVD		5468	6407	61	5509	6545	131	5468	8604	103	5509	8544	17
CVDD	AllPtt		7887	9134	17	7887	9269	57	7887	12245	31	7887	12096	7
	preCVD		2419	2714	14	2378	2709	41	2419	3615	23	2378	3526	5
	noCVD		5468	6420	3	5509	6560	16	5468	8630	8	5509	8570	1
MI	AllPtt		7887	9093	54	7887	9204	78	7887	12177	72	7887	11980	10
	preCVD		2419	2692	28	2378	2659	54	2419	3579	39	2378	3440	6
	noCVD		5468	6401	26	5509	6546	24	5468	8599	33	5509	8540	3
Str	AllPtt		7887	9087	55	7887	9204	85	7887	12158	76	7887	12008	9
	preCVD		2419	2696	28	2378	2676	47	2419	3570	41	2378	3480	5
	noCVD		5468	6391	27	5509	6528	38	5468	8588	35	5509	8528	4
IscStr	AllPtt		7887	9089	52	7887	9212	75	7887	12163	70	7887	12019	8
	preCVD		2419	2696	26	2378	2680	42	2419	3574	36	2378	3484	4
	noCVD		5468	6392	26	5509	6532	33	5468	8589	34	5509	8535	3
CVDD+MI+Str	AllPtt		7887	9048	120	7887	9139	203	7887	12092	165	7887	11893	24
	preCVD		2419	2674	66	2378	2625	132	2419	3534	94	2378	3395	16
	noCVD		5468	6374	54	5509	6513	71	5468	8558	71	5509	8498	8
ACD+MI+Str	AllPtt		7887	9048	193	7887	9139	383	7887	12092	295	7887	11893	48
	preCVD		2419	2674	95	2378	2625	222	2419	3534	156	2378	3395	27
	noCVD		5468	6374	98	5509	6513	161	5468	8558	139	5509	8498	20
DKD	AllPtt		7887	9082	55	7887	9094	189	7887	12136	81	7887	11827	21
	preCVD		2419	2698	21	2378	2634	83	2419	3573	33	2378	3407	9
	noCVD		5468	6384	34	5509	6460	106	5468	8563	48	5509	8420	11

```
> round( ftable( res, col.vars=c(2,5) ), 3 )
```

			data	OnDr	Total						
			res	HR	lo	up	se	HR	lo	up	se
endp	sub	adj									
HF	AllPtt	Raw	0.593	0.444	0.792	0.148	0.758	0.593	0.969	0.125	
		Adj	0.568	0.425	0.760	0.148	0.748	0.585	0.957	0.126	
	preCVD	Raw	0.574	0.417	0.788	0.162	0.703	0.533	0.926	0.141	
		Adj	0.556	0.405	0.762	0.161	0.704	0.536	0.923	0.139	
	noCVD	Raw	0.633	0.317	1.267	0.354	0.953	0.557	1.630	0.274	
		Adj	0.643	0.314	1.316	0.365	0.944	0.544	1.636	0.281	
ACD	AllPtt	Raw	0.372	0.293	0.472	0.121	0.499	0.414	0.600	0.095	
		Adj	0.471	0.369	0.600	0.124	0.588	0.487	0.711	0.096	
	preCVD	Raw	0.314	0.224	0.439	0.171	0.471	0.366	0.606	0.128	
		Adj	0.314	0.224	0.439	0.171	0.471	0.366	0.606	0.128	

ACD+HF	noCVD	Adj	0.408	0.290	0.575	0.174	0.581	0.450	0.751	0.131
		Raw	0.442	0.315	0.620	0.173	0.531	0.403	0.698	0.140
	AllPtt	Adj	0.544	0.383	0.772	0.179	0.591	0.447	0.781	0.142
		Raw	0.464	0.386	0.559	0.094	0.602	0.518	0.700	0.077
	preCVD	Adj	0.528	0.438	0.638	0.096	0.669	0.575	0.779	0.078
		Raw	0.450	0.356	0.568	0.119	0.597	0.494	0.722	0.097
CVDD	noCVD	Adj	0.503	0.399	0.635	0.119	0.672	0.555	0.813	0.098
		Raw	0.476	0.351	0.645	0.155	0.598	0.468	0.763	0.125
	AllPtt	Adj	0.560	0.409	0.767	0.160	0.647	0.505	0.829	0.127
		Raw	0.301	0.175	0.518	0.276	0.418	0.275	0.637	0.214
	preCVD	Adj	0.430	0.248	0.745	0.280	0.539	0.353	0.825	0.217
		Raw	0.336	0.183	0.617	0.310	0.412	0.253	0.672	0.249
MI	noCVD	Adj	0.495	0.266	0.923	0.318	0.545	0.330	0.901	0.256
		Raw	0.191	0.056	0.654	0.628	0.415	0.182	0.945	0.420
	AllPtt	Adj	0.265	0.079	0.882	0.614	0.489	0.222	1.076	0.402
		Raw	0.700	0.494	0.991	0.178	0.692	0.512	0.936	0.154
	preCVD	Adj	0.738	0.522	1.044	0.177	0.723	0.535	0.977	0.153
		Raw	0.510	0.323	0.806	0.233	0.564	0.380	0.836	0.201
Str	noCVD	Adj	0.551	0.346	0.878	0.238	0.598	0.402	0.889	0.202
		Raw	1.125	0.643	1.969	0.286	0.915	0.569	1.472	0.242
	AllPtt	Adj	1.130	0.651	1.959	0.281	0.926	0.578	1.483	0.240
		Raw	0.656	0.467	0.920	0.173	0.775	0.574	1.047	0.153
	preCVD	Adj	0.689	0.491	0.967	0.173	0.810	0.599	1.094	0.154
		Raw	0.588	0.368	0.939	0.239	0.725	0.484	1.086	0.206
IscStr	noCVD	Adj	0.626	0.388	1.008	0.243	0.770	0.510	1.162	0.210
		Raw	0.729	0.445	1.195	0.252	0.830	0.530	1.300	0.229
	AllPtt	Adj	0.743	0.453	1.219	0.252	0.835	0.533	1.308	0.229
		Raw	0.703	0.493	1.001	0.180	0.815	0.594	1.118	0.161
	preCVD	Adj	0.737	0.518	1.049	0.180	0.849	0.619	1.166	0.162
		Raw	0.611	0.374	0.997	0.250	0.715	0.465	1.099	0.219
CVDD+MI+Str	noCVD	Adj	0.644	0.393	1.055	0.252	0.758	0.490	1.171	0.222
		Raw	0.809	0.483	1.354	0.263	0.941	0.589	1.504	0.239
	AllPtt	Adj	0.823	0.490	1.381	0.264	0.945	0.590	1.512	0.240
		Raw	0.596	0.476	0.747	0.115	0.654	0.537	0.797	0.100
	preCVD	Adj	0.643	0.513	0.806	0.115	0.697	0.573	0.849	0.100
		Raw	0.489	0.364	0.657	0.151	0.562	0.436	0.725	0.130
ACD+MI+Str	noCVD	Adj	0.545	0.403	0.737	0.154	0.618	0.478	0.799	0.131
		Raw	0.781	0.548	1.115	0.181	0.803	0.587	1.099	0.160
	AllPtt	Adj	0.802	0.564	1.141	0.180	0.816	0.597	1.114	0.159
		Raw	0.508	0.427	0.604	0.088	0.597	0.516	0.689	0.074
	preCVD	Adj	0.576	0.484	0.686	0.089	0.658	0.569	0.761	0.074
		Raw	0.419	0.329	0.532	0.123	0.540	0.444	0.657	0.100
DKD	noCVD	Adj	0.485	0.380	0.619	0.125	0.618	0.506	0.753	0.101
		Raw	0.623	0.485	0.802	0.128	0.662	0.534	0.820	0.110
	AllPtt	Adj	0.683	0.530	0.880	0.130	0.693	0.559	0.860	0.110
		Raw	0.291	0.216	0.393	0.153	0.363	0.281	0.468	0.130
	preCVD	Adj	0.305	0.225	0.412	0.154	0.378	0.293	0.488	0.130
		Raw	0.248	0.154	0.401	0.245	0.318	0.215	0.471	0.200
	noCVD	Adj	0.278	0.171	0.454	0.250	0.352	0.235	0.528	0.206
		Raw	0.324	0.220	0.477	0.197	0.398	0.285	0.556	0.171
		Adj	0.326	0.222	0.479	0.197	0.398	0.285	0.555	0.170

2.10 Exposure tables by drug

We can then produce an overview of the number of persons, risk time and events by index medication; to this end we define functions that uses the `by` argument of the `summary.Lexis` to classify events and follow-up by index drug in various groupings:

```
> tabFU <- ZArray( list( Ix = c("DPP4", "SGLT2", "Dapa", "Empa", "Cana"),
+                          wh = c("nPers", "FU", "meanfu", "sdFU", "maxFU") ) )
> getFU <-
+ function( lx ) c( length( unique( lx$lex.id ) ),
+                   sum( lx$lex.dur ),
+                   mean( lx$lex.dur ),
+                   sd( lx$lex.dur ),
+                   max( lx$lex.dur ) )
> mset$D <- 0
> mset$doX <- with( mset, pmin( doDth, 2017, na.rm=TRUE ) )
> Lx <- Lexis( entry = list( per = doIx,
+                           cua = doIx-doBth,
+                           tfi = 0 ),
+             exit = list( per = doX ),
+             exit.status = factor( D, levels=0:1, labels=c("OnDr", "Event") ),
+             data = subset( mset, is.na(doDth) | doIx < doDth ) )
NOTE: entry.status has been set to "OnDr" for all.
> summary( Lx, by="Ixdr" , simplify=FALSE )
```

\$DPP4

Transitions:

	To					
From	OnDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	7887	0	7887	0	12095.56	7887
Event	0	0	0	0	NA	NA
Sum	7887	0	7887	0	12095.56	7887

\$SGLT2

Transitions:

	To					
From	OnDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	7887	0	7887	0	12245.06	7887
Event	0	0	0	0	NA	NA
Sum	7887	0	7887	0	12245.06	7887

```
> tabFU["DPP4",] <- getFU( subset( Lx, Ixdr=="DPP4" ) )
> tabFU["SGLT2",] <- getFU( subset( Lx, Ixdr=="SGLT2" ) )
> tabFU["Dapa",] <- getFU( subset( Lx, Ixatc %in% c("A10BD15", "A10BK01") ) )
> tabFU["Cana",] <- getFU( subset( Lx, Ixatc %in% c("A10BD16", "A10BK02") ) )
> tabFU["Empa",] <- getFU( subset( Lx, Ixatc %in% c("A10BD20", "A10BK03") ) )
> round( tabFU, 2 )
```

	wh					
Ix	nPers	FU	meanfu	sdFU	maxFU	
DPP4	7887	12095.56	1.53	1.11	4.08	
SGLT2	7887	12245.06	1.55	1.11	4.05	
Dapa	5094	10088.15	1.98	1.11	4.05	
Empa	2556	1839.65	0.72	0.53	2.35	
Cana	237	317.25	1.34	0.66	2.54	

2.11 Saving it all

Fially we save all results:

```
> save( res, dat, tabFU, file = "resSGDP.Rda" )
```

2.12 Reformatting

The results are here reformatted to Excel-format, `xlsx`, by the `xlsx` package of R, so we load that concomitantly with the data.

```
> library( Epi )
> library( xlsx )
> clear()
> load( "btabsGDP.Rda" )
> load( "resSGDP.Rda" )
> lls()
```

	name	mode	class	dim	size(Kb)
1	cm.tab	numeric	matrix	31 4	3.4
2	ct.tab	numeric	matrix	31 4	3.4
3	dat	numeric	array	10 2 3 2 3	5.5
4	dm.tab	numeric	matrix	40 4	3.9
5	dt.tab	numeric	matrix	40 4	3.9
6	mm.tab	numeric	matrix	37 4	3.8
7	mt.tab	numeric	matrix	37 4	3.8
8	res	numeric	array	10 2 3 2 4	6.4
9	tabFU	numeric	matrix	5 5	1.7

With this in place we can now construct the tables wanted for the sheet in th desided order.

2.12.1 Baseline tables

In order to chack that we get the rows correct we read the rownames from the supplied spreadsheet, in ordet to put these in as a column in the new sheet for control:

```
> cat("Sample size
+ Age, years
+ Women
+ CV-history
+ Myocardial infarction
+ Unstable angina
+ Heart failure
+ Atrial fibrillation
+ Stroke
+ PAD
+ Microvascular disease
+ CKD
+ Frailty (yes)
+ Metformin
+ SU
+ TZD
+ GLP1
+ Insulin
+ Anti hypertensive therapy
```

```

...now input from ../rep/2xlSGDP.tex
+ LOOP diuretics
+ Low ceiling diuretics
+ ACE Inhibitors
+ ARBs
+ Statin therapy
+ Beta blockers
+ Aldosterone antagonists
+ Index year
+ 2012
+ 2013
+ 2014
+ 2015
+ 2016
+ 2017
+ ", file='ol.txt' )
> ol <- read.table('ol.txt',header=FALSE,sep='\t',as.is=TRUE)

```

Baseline pre-matching

We can now construct the pre-matching table

```

> bt <- rbind( "Sample size"= dt.tab[1,2:1]+dt.tab[2,2:1],
+             "Age" = NA,
+             dt.tab["F",2:1,drop=FALSE],
+             ct.tab["pre.CVD",2:1,drop=FALSE],
+             ct.tab["prv.MI",2:1,drop=FALSE],
+             ct.tab["prv.UnstAng",2:1,drop=FALSE],
+             ct.tab["prv.HF",2:1,drop=FALSE],
+             ct.tab["prv.AtrFib",2:1,drop=FALSE],
+             ct.tab["pre.Str",2:1,drop=FALSE],
+             ct.tab["prv.PAD",2:1,drop=FALSE],
+             ct.tab["pre.Mic",2:1,drop=FALSE],
+             ct.tab["prv.CKD",2:1,drop=FALSE],
+             "Frail"=dt.tab["1",2:1],
+             mt.tab["had.Metformin",2:1,drop=FALSE],
+             mt.tab["had.SU",2:1,drop=FALSE],
+             mt.tab["had.TZD",2:1,drop=FALSE],
+             mt.tab["had.GLP1",2:1,drop=FALSE],
+             mt.tab["got.Ins",2:1,drop=FALSE],
+             mt.tab["got.Hyp",2:1,drop=FALSE],
+             mt.tab["had.HCD",2:1,drop=FALSE],
+             mt.tab["had.THZ",2:1,drop=FALSE],
+             mt.tab["had.ACE",2:1,drop=FALSE],
+             mt.tab["had.ARB",2:1,drop=FALSE],
+             mt.tab["had.Sta",2:1,drop=FALSE],
+             mt.tab["had.BB1",2:1,drop=FALSE],
+             mt.tab["had.A1A",2:1,drop=FALSE],
+             "Index year"=NA,
+             dt.tab["Index date 2012",2:1,drop=FALSE],
+             dt.tab["2013",2:1,drop=FALSE],
+             dt.tab["2014",2:1,drop=FALSE],
+             dt.tab["2015",2:1,drop=FALSE],
+             dt.tab["2016",2:1,drop=FALSE],
+             '2017'=NA)
> str(ol)

```

```

'data.frame':      33 obs. of  1 variable:
 $ V1: chr  "Sample size" "Age, years" "Women" "CV-history" ...

> bt <- cbind(bt[,1],NA,NA,NA,NA)
> bt["Age",c(2,3,5,6)] <- dt.tab["Age: Mean / SD",c(1,3,2,4)]
> colnames( bt ) <- c("SGLT-2","mean","sd","DPP4","mean","sd")
> cbind( ol, bt )

      V1 SGLT-2 mean  sd DPP4 mean  sd
Sample size      Sample size 11291  NA  NA 36849  NA  NA
Age              Age, years    NA 64.6 12.6    NA 60.1 10.9
F                Women      4387  NA  NA 14603  NA  NA
pre.CVD          CV-history   3445  NA  NA 12424  NA  NA
prv.MI            Myocardial infarction 956  NA  NA 3253  NA  NA
prv.UnstAng       Unstable angina    440  NA  NA 1403  NA  NA
prv.HF            Heart failure     475  NA  NA 2080  NA  NA
prv.AtrFib        Atrial fibrillation 677  NA  NA 3134  NA  NA
pre.Str           Stroke           802  NA  NA 3551  NA  NA
prv.PAD           PAD             562  NA  NA 2311  NA  NA
pre.Mic           Microvascular disease 4132  NA  NA 7800  NA  NA
prv.CKD           CKD             56  NA  NA 1131  NA  NA
Frail             Frailty (yes)    3832  NA  NA 10876  NA  NA
had.Metformin     Metformin       9074  NA  NA 32241  NA  NA
had.SU            SU             2622  NA  NA 9683  NA  NA
had.TZD           TZD            44  NA  NA 54  NA  NA
had.GLP1          GLP1          4516  NA  NA 1567  NA  NA
got.Ins           Insulin       3859  NA  NA 4009  NA  NA
got.Hyp           Anti hypertensive therapy 8930  NA  NA 27580  NA  NA
had.HCD           LOOP diuretics 1577  NA  NA 6956  NA  NA
had.THZ           Low ceiling diuretics 1735  NA  NA 5651  NA  NA
had.ACE           ACE Inhibitors 4463  NA  NA 13775  NA  NA
had.ARB           ARBs          3954  NA  NA 10731  NA  NA
had.Sta           Statin therapy 8459  NA  NA 25543  NA  NA
had.BB1           Beta blockers 3124  NA  NA 10977  NA  NA
had.A1A           Aldosterone antagonists 607  NA  NA 2169  NA  NA
Index year        Index year    NA  NA  NA    NA  NA  NA
Index date 2012   2012         18  NA  NA 673  NA  NA
2013              2013        1494  NA  NA 8684  NA  NA
2014              2014        2091  NA  NA 8897  NA  NA
2015              2015        2931  NA  NA 9392  NA  NA
2016              2016       4757  NA  NA 9203  NA  NA
2017              2017         NA  NA  NA    NA  NA  NA

> write.xlsx( cbind( 'Org. labs'=ol, bt ),
+             "SGDP.xlsx",
+             sheetName = "Baseline pre-matching",
+             append = FALSE,
+             showNA = FALSE )

```

Baseline after matching

The data for post matching have exactly the same structure; the tables are just called 'm.tab' instead of 't.tab':

```

> bm <- rbind( "Sample size"= dm.tab[1,2:1]+dm.tab[2,2:1],
+             "Age" = NA,
+             dm.tab["F",2:1,drop=FALSE],
+             cm.tab["pre.CVD",2:1,drop=FALSE],
+             cm.tab["prv.MI",2:1,drop=FALSE],
+             cm.tab["prv.UnstAng",2:1,drop=FALSE],
+             cm.tab["prv.HF",2:1,drop=FALSE],
+             cm.tab["prv.AtrFib",2:1,drop=FALSE],
+             cm.tab["pre.Str",2:1,drop=FALSE],
+             cm.tab["prv.PAD",2:1,drop=FALSE],
+             cm.tab["pre.Mic",2:1,drop=FALSE],
+             cm.tab["prv.CKD",2:1,drop=FALSE],
+             "Frail"=dm.tab["1",2:1],
+             mm.tab["had.Metformin",2:1,drop=FALSE],
+             mm.tab["had.SU",2:1,drop=FALSE],
+             mm.tab["had.TZD",2:1,drop=FALSE],
+             mm.tab["had.GLP1",2:1,drop=FALSE],
+             mm.tab["got.Ins",2:1,drop=FALSE],
+             mm.tab["got.Hyp",2:1,drop=FALSE],
+             mm.tab["had.HCD",2:1,drop=FALSE],
+             mm.tab["had.THZ",2:1,drop=FALSE],
+             mm.tab["had.ACE",2:1,drop=FALSE],
+             mm.tab["had.ARB",2:1,drop=FALSE],
+             mm.tab["had.Sta",2:1,drop=FALSE],
+             mm.tab["had.BB1",2:1,drop=FALSE],
+             mm.tab["had.A1A",2:1,drop=FALSE],
+             "Index year"=NA,
+             dm.tab["Index date 2012",2:1,drop=FALSE],
+             dm.tab["2013",2:1,drop=FALSE],
+             dm.tab["2014",2:1,drop=FALSE],
+             dm.tab["2015",2:1,drop=FALSE],
+             dm.tab["2016",2:1,drop=FALSE],
+             '2017'=NA)
> str(ol)
'data.frame':      33 obs. of  1 variable:
 $ V1: chr  "Sample size" "Age, years" "Women" "CV-history" ...
> bm <- cbind(bm[,1],NA,NA,bm[,2],NA,NA)
> bm["Age",c(2,3,5,6)] <- dm.tab["Age: Mean / SD",c(1,3,2,4)]
> colnames( bm ) <- c("SGLT-2","mean","sd","DPP4","mean","sd")
> cbind( ol, bm )

```

	V1	SGLT-2	mean	sd	DPP4	mean	sd
Sample size	Sample size	7887	NA	NA	7887	NA	NA
Age	Age, years	NA	61	12.9	NA	61.1	11.1
F	Women	3069	NA	NA	3092	NA	NA
pre.CVD	CV-history	2419	NA	NA	2378	NA	NA
prv.MI	Myocardial infarction	655	NA	NA	647	NA	NA
prv.UnstAng	Unstable angina	285	NA	NA	279	NA	NA
prv.HF	Heart failure	364	NA	NA	351	NA	NA
prv.AtrFib	Atrial fibrillation	486	NA	NA	475	NA	NA
pre.Str	Stroke	596	NA	NA	606	NA	NA
prv.PAD	PAD	413	NA	NA	431	NA	NA
pre.Mic	Microvascular disease	2385	NA	NA	2283	NA	NA
prv.CKD	CKD	55	NA	NA	66	NA	NA
Frail	Frailty (yes)	2413	NA	NA	2405	NA	NA
had.Metformin	Metformin	6267	NA	NA	6181	NA	NA
had.SU	SU	1907	NA	NA	1980	NA	NA
had.TZD	TZD	22	NA	NA	18	NA	NA

```

had.GLP1          GLP1      1516  NA  NA 1477  NA  NA
got.Ins           Insulin   1954  NA  NA 1896  NA  NA
got.Hyp           Anti hypertensive therapy 6097  NA  NA 5956  NA  NA
had.HCD           LOOP diuretics 1116  NA  NA 1150  NA  NA
had.THZ           Low ceiling diuretics 1146  NA  NA 1161  NA  NA
had.ACE           ACE Inhibitors 3034  NA  NA 2942  NA  NA
had.ARB           ARBs      2613  NA  NA 2624  NA  NA
had.Sta           Statin therapy 5716  NA  NA 5641  NA  NA
had.BBl           Beta blockers 2178  NA  NA 2159  NA  NA
had.Ala           Aldosterone antagonists 428  NA  NA 424  NA  NA
Index year        Index year  NA  NA  NA  NA  NA  NA
Index date 2012   2012       15  NA  NA  64  NA  NA
2013              2013      1193  NA  NA 1097  NA  NA
2014              2014      1514  NA  NA 1499  NA  NA
2015              2015      1981  NA  NA 2179  NA  NA
2016              2016      3184  NA  NA 3048  NA  NA
2017              2017       NA  NA  NA  NA  NA  NA

> write.xlsx( cbind( 'Org. labs'=ol, bm ),
+             "SGDP.xlsx",
+ sheetName = "Baseline after matching",
+   append = TRUE,
+   showNA = FALSE )

```

2.12.2 Treatment distribution

```

> ( FUt看ab <- tabFU[c(2:5,rep(NA,4),1),] )

      wh
Ix    nPers    FU    meanfu    sdFU    maxFU
SGLT2  7887 12245.0575 1.5525621 1.1144939 4.051335
Dapa   5094 10088.1533 1.9803992 1.1089062 4.051335
Empa   2556 1839.6496 0.7197377 0.5286949 2.348392
Cana   237  317.2546 1.3386271 0.6579770 2.542779
<NA>    NA      NA      NA      NA      NA
<NA>    NA      NA      NA      NA      NA
<NA>    NA      NA      NA      NA      NA
<NA>    NA      NA      NA      NA      NA
DPP4   7887 12095.5599 1.5336072 1.1129297 4.078713

> colnames(FUt看ab) <- c(
+ 'Number of patients',
+ 'Total follow-up time',
+ 'Mean follow-up time',
+ 'Sd follow-up time',
+ 'maximum follow-up time')
> rownames( FUt看ab ) <- c(
+ 'SGLT-2',
+ '  Dapagliflozin',
+ '  Empagliflozin',
+ '  Canagliflozin',
+ '  Ipragliflozin',
+ '  Luseogliflozin',
+ '  Tofugliflozin',
+ '-',
+ 'DPP4')
> FUt看ab

```

```

      wh
Ix      Number of patients Total follow-up time Mean follow-up time Sd follow-up t
  SGLT-2      7887      12245.0575      1.5525621      1.1144
    Dapagliflozin      5094      10088.1533      1.9803992      1.1089
    Empagliflozin      2556      1839.6496      0.7197377      0.5286
    Canagliflozin      237      317.2546      1.3386271      0.6579
    Ipragliflozin      NA      NA      NA
    Luseogliflozin      NA      NA      NA
    Tofugliflozin      NA      NA      NA
  -      NA      NA      NA
DPP4      7887      12095.5599      1.5336072      1.1129
      wh
Ix      maximum follow-up time
  SGLT-2      4.051335
    Dapagliflozin      4.051335
    Empagliflozin      2.348392
    Canagliflozin      2.542779
    Ipragliflozin      NA
    Luseogliflozin      NA
    Tofugliflozin      NA
  -      NA
DPP4      4.078713

```

```

> write.xlsx( FUt看,
+           "SGDP.xlsx",
+ sheetName = "Treatment distribution",
+   append = TRUE,
+   showNA = FALSE )

```

2.12.3 Events

```

> cat(
+ 'Number of patients
+ Total follow-up time - on treatment
+ Number of patients with event - on treatment
+ Total follow-up time - ITT
+ Number of patients with event - ITT
+ ', file='oc' )
> ( oc <- read.table('oc',header=FALSE,sep='\t',as.is=TRUE)[,1] )

[1] "Number of patients" "Total follow-up time - on treatment"
[3] "Number of patients with event - on treatment" "Total follow-up time - ITT"
[5] "Number of patients with event - ITT"

> cat(
+ 'HHF
+ All-cause death
+ All-cause death or HHF
+ Cardiavascular death
+ Myocardial infarction
+ Stroke
+ Ischemic stroke
+ MACE (cardiavascular death, MI or stroke)
+ modified MACE (All-cause death, MI or stroke)
+ Kidney disease
+ ', file='ol' )
> ( ol <- read.table('ol',header=FALSE,sep='\t',as.is=TRUE)[,1] )

```

```

[1] "HHF" "All-cause death"
[3] "All-cause death or HHF" "Cardiavascular death"
[5] "Myocardial infarction" "Stroke"
[7] "Ischemic stroke" "MACE (cardiavascular death, MI or stroke)"
[9] "modified MACE (All-cause death, MI or stroke)" "Kidney disease"

```

The data for this is in the `dat` object:

```

> str( dat )
num [1:10, 1:2, 1:3, 1:2, 1:3] 7887 7887 7887 7887 7887 ...
- attr(*, "dimnames")=List of 5
 ..$ endp: chr [1:10] "HF" "ACD" "ACD+HF" "CVDD" ...
 ..$ data: chr [1:2] "OnDr" "Total"
 ..$ sub : chr [1:3] "AllPtt" "preCVD" "noCVD"
 ..$ ix  : chr [1:2] "SGLT2" "DPP4"
 ..$ dat : chr [1:3] "N" "PY" "Event"

> cbind( ol, dimnames(dat)[[1]] )
      ol
[1,] "HHF" "HF"
[2,] "All-cause death" "ACD"
[3,] "All-cause death or HHF" "ACD+HF"
[4,] "Cardiavascular death" "CVDD"
[5,] "Myocardial infarction" "MI"
[6,] "Stroke" "Str"
[7,] "Ischemic stroke" "IsCStr"
[8,] "MACE (cardiavascular death, MI or stroke)" "CVDD+MI+Str"
[9,] "modified MACE (All-cause death, MI or stroke)" "ACD+MI+Str"
[10,] "Kidney disease" "DKD"

> ft <- ftable( dat[,1,1:2,,drop=FALSE], col.vars=c(4,2,5) )
> round( ft, 1 )

```

		ix data dat	SGLT2 OnDr N	PY	Event	Total N	PY	Event	DPP4 OnDr N	PY	Event
endp	sub										
HF	AllPtt	7887.0	9075.5	73.0	7887.0	12124.4	113.0	7887.0	9170.4	124.0	7887.0
ACD	AllPtt	7887.0	9133.6	93.0	7887.0	12245.1	168.0	7887.0	9269.4	253.0	7887.0
ACD+HF	AllPtt	7887.0	9075.5	164.0	7887.0	12124.4	274.0	7887.0	9170.4	356.0	7887.0
CVDD	AllPtt	7887.0	9133.6	17.0	7887.0	12245.1	31.0	7887.0	9269.4	57.0	7887.0
MI	AllPtt	7887.0	9093.1	54.0	7887.0	12177.5	72.0	7887.0	9204.2	78.0	7887.0
Str	AllPtt	7887.0	9086.8	55.0	7887.0	12157.8	76.0	7887.0	9203.9	85.0	7887.0
IsCStr	AllPtt	7887.0	9088.8	52.0	7887.0	12163.3	70.0	7887.0	9212.0	75.0	7887.0
CVDD+MI+Str	AllPtt	7887.0	9047.8	120.0	7887.0	12091.8	165.0	7887.0	9138.6	203.0	7887.0
ACD+MI+Str	AllPtt	7887.0	9047.8	193.0	7887.0	12091.8	295.0	7887.0	9138.6	383.0	7887.0
DKD	AllPtt	7887.0	9081.7	55.0	7887.0	12135.8	81.0	7887.0	9093.7	189.0	7887.0

This is the table needed (except for the column on persons, which should not be repeated):

```

> py <- data.frame( as.matrix(ft) )[-c(4,10)]
> py

```

	SGLT2_OnDr_N	SGLT2_OnDr_PY	SGLT2_OnDr_Event	SGLT2_Total_PY	SGLT2_Total_Event
HF_AllPtt	7887	9075.483	73	12124.43	113
ACD_AllPtt	7887	9133.550	93	12245.06	168
ACD+HF_AllPtt	7887	9075.483	164	12124.43	274
CVDD_AllPtt	7887	9133.550	17	12245.06	31
MI_AllPtt	7887	9093.067	54	12177.49	72
Str_AllPtt	7887	9086.789	55	12157.81	76

IscStr_AllPtt	7887	9088.836	52	12163.29	7
CVDD+MI+Str_AllPtt	7887	9047.824	120	12091.76	16
ACD+MI+Str_AllPtt	7887	9047.824	193	12091.76	29
DKD_AllPtt	7887	9081.685	55	12135.85	8
	DPP4_OnDr_N	DPP4_OnDr_PY	DPP4_OnDr_Event	DPP4_Total_PY	DPP4_Total_Event
HF_AllPtt	7887	9170.435	124	11945.76	147
ACD_AllPtt	7887	9269.423	253	12095.56	332
ACD+HF_AllPtt	7887	9170.435	356	11945.76	448
CVDD_AllPtt	7887	9269.423	57	12095.56	73
MI_AllPtt	7887	9204.194	78	11980.04	103
Str_AllPtt	7887	9203.862	85	12008.03	97
IscStr_AllPtt	7887	9211.971	75	12018.63	85
CVDD+MI+Str_AllPtt	7887	9138.635	203	11893.27	249
ACD+MI+Str_AllPtt	7887	9138.635	383	11893.27	487
DKD_AllPtt	7887	9093.732	189	11826.67	218

```

> colnames( py )
[1] "SGLT2_OnDr_N"      "SGLT2_OnDr_PY"      "SGLT2_OnDr_Event"   "SGLT2_Total_PY"
[5] "SGLT2_Total_Event" "DPP4_OnDr_N"         "DPP4_OnDr_PY"       "DPP4_OnDr_Event"
[9] "DPP4_Total_PY"     "DPP4_Total_Event"

> colnames(py) <- c(oc,oc[-1])
> rownames(py) <- ol

```

With this in order we can now write it to the excel sheet:

```

> write.xlsx( py,
+            "SGDP.xlsx",
+            sheetName = "Events",
+            append = TRUE,
+            showNA = FALSE )

```

2.12.4 Hazard ratios

```

> ft <- ftable((dat[c(1:3,9,5,6),1:2,1,"SGLT2",,drop=FALSE]+
+             dat[c(1:3,9,5,6),1:2,1,"DPP4" ,,drop=FALSE]))[, ,c(1,1),,row.vars=c(1,2,3))
> YD <- data.frame(as.matrix(ft))
> HR <- data.frame(as.matrix(ftable(res[c(1:3,9,5,6),1:2,1,1:2,c(1,4)],row.vars=c(1,2,3))))
> Endpoint <- sapply( strsplit( rownames(HR), "_" ), FUN=function(x) x[1] )
> Adjusted <- sapply( strsplit( rownames(HR), "_" ), FUN=function(x) x[3] )
> Analysis <- sapply( strsplit( rownames(HR), "_" ), FUN=function(x) x[2] )
> ( HR <- cbind(Endpoint,Adjusted,Analysis,HR,YD)[,c(1:3,6:8,4:5)] )

```

	Endpoint	Adjusted	Analysis	N	PY	Event	HR	se
HF_OnDr_Raw	HF	Raw	OnDr	15774	18245.92	197	0.5927892	0.14755802
HF_OnDr_Adj	HF	Adj	OnDr	15774	18245.92	197	0.5683430	0.14812834
HF_Total_Raw	HF	Raw	Total	15774	24070.19	260	0.7582214	0.12508638
HF_Total_Adj	HF	Adj	Total	15774	24070.19	260	0.7481364	0.12563777
ACD_OnDr_Raw	ACD	Raw	OnDr	15774	18402.97	346	0.3719135	0.12136017
ACD_OnDr_Adj	ACD	Adj	OnDr	15774	18402.97	346	0.4705849	0.12416019
ACD_Total_Raw	ACD	Raw	Total	15774	24340.62	500	0.4988829	0.09458513
ACD_Total_Adj	ACD	Adj	Total	15774	24340.62	500	0.5883592	0.09624492
ACD+HF_OnDr_Raw	ACD+HF	Raw	OnDr	15774	18245.92	520	0.4641810	0.09443447
ACD+HF_OnDr_Adj	ACD+HF	Adj	OnDr	15774	18245.92	520	0.5284903	0.09581194
ACD+HF_Total_Raw	ACD+HF	Raw	Total	15774	24070.19	722	0.6023997	0.07662925
ACD+HF_Total_Adj	ACD+HF	Adj	Total	15774	24070.19	722	0.6692084	0.07769434
ACD+MI+Str_OnDr_Raw	ACD+MI+Str	Raw	OnDr	15774	18186.46	576	0.5082130	0.08835286

ACD+MI+Str_OnDr_Adj	ACD+MI+Str	Adj	OnDr	15774	18186.46	576	0.5760822	0.08900205
ACD+MI+Str_Total_Raw	ACD+MI+Str	Raw	Total	15774	23985.03	782	0.5966130	0.07373626
ACD+MI+Str_Total_Adj	ACD+MI+Str	Adj	Total	15774	23985.03	782	0.6578412	0.07426376
MI_OnDr_Raw	MI	Raw	OnDr	15774	18297.26	132	0.6999601	0.17752253
MI_OnDr_Adj	MI	Adj	OnDr	15774	18297.26	132	0.7383851	0.17686639
MI_Total_Raw	MI	Raw	Total	15774	24157.53	175	0.6924864	0.15378461
MI_Total_Adj	MI	Adj	Total	15774	24157.53	175	0.7230674	0.15346243
Str_OnDr_Raw	Str	Raw	OnDr	15774	18290.65	140	0.6556483	0.17297282
Str_OnDr_Adj	Str	Adj	OnDr	15774	18290.65	140	0.6887783	0.17301996
Str_Total_Raw	Str	Raw	Total	15774	24165.84	173	0.7752544	0.15310089
Str_Total_Adj	Str	Adj	Total	15774	24165.84	173	0.8096341	0.15351589

```
> write.xlsx( HR,
+           "SGDP.xlsx",
+ sheetName = "Hazard ratios",
+   append = TRUE,
+   showNA = FALSE )
```

2.12.5 Subgroup OT

This is same as above, except the we restrict to “OnDr”, and subclassify by previous CVD:

```
> str(dat)
num [1:10, 1:2, 1:3, 1:2, 1:3] 7887 7887 7887 7887 7887 ...
- attr(*, "dimnames")=List of 5
 ..$ endp: chr [1:10] "HF" "ACD" "ACD+HF" "CVDD" ...
 ..$ data: chr [1:2] "OnDr" "Total"
 ..$ sub : chr [1:3] "AllPtt" "preCVD" "noCVD"
 ..$ ix : chr [1:2] "SGLT2" "DPP4"
 ..$ dat : chr [1:3] "N" "PY" "Event"

> YD <-
+   data.frame(as.matrix(ftable(dat[c(1:3,9,5,6),"OnDr",,"SGLT2",] +
+                               dat[c(1:3,9,5,6),"OnDr",,"DPP4" ],row.vars=c(1,2))))
> str( YD )

'data.frame':      18 obs. of  3 variables:
 $ N      : num  15774 4797 10977 15774 4797 ...
 $ PY     : num  18246 5293 12953 18403 5423 ...
 $ Event: num  197 163 34 346 187 159 520 328 192 576 ...

> HR <-
+   data.frame(as.matrix(ftable(res[c(1:3,9,5,6),"OnDr",,"Adj",c(1,4)],row.vars=c(1,2))))
```

With this fixed we can now write the table:

```
> write.xlsx( cbind(YD,HR),
+           "SGDP.xlsx",
+ sheetName = "Subgroups OT",
+   append = TRUE,
+   showNA = FALSE )
```

2.12.6 Subgroup ITT

This is same as above, except the we restrict to “Total”, and subclassify by previous CVD:

```
> YD <-
+   data.frame(as.matrix(ftable(dat[c(1:3,9,5,6),"Total",,"SGLT2",] +
+                               dat[c(1:3,9,5,6),"Total",,"DPP4" ],row.vars=c(1,2))))
> HR <-
+   data.frame(as.matrix(ftable(res[c(1:3,9,5,6),"Total",,"Adj",c(1,4)],row.vars=c(1,2))))
```

With this fixed we can now write the table:

```
> write.xlsx( cbind(YD,HR),
+             "SGDP.xlsx",
+             sheetName = "Subgroups ITT",
+             append = TRUE,
+             showNA = FALSE )
```

Chapter 3

Analysis of SGLT-2i vs. any other drug

3.1 Dataset for analysis od SGLT-2i vs any other drug

First load the relevant package:

```
> options( width=95 )
> library( Epi )
> library( splines )
> library( haven )
> library( Matching )
> clear()
> print( sessionInfo(), l=F )
R version 3.5.0 (2018-04-23)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server 2012 R2 x64 (build 9600)
```

Matrix products: default

attached base packages:

```
[1] splines      stats      graphics  grDevices  utils      datasets  methods    base
```

other attached packages:

```
[1] Matching_4.9-3 MASS_7.3-49      haven_1.1.1      Epi_2.30
```

loaded via a namespace (and not attached):

```
[1] Rcpp_0.12.16      lattice_0.20-35    zoo_1.8-1          grid_3.5.0         plyr_1.8.4
[6] magrittr_1.5      etm_0.6-2          pillar_1.2.2       rlang_0.2.0        Matrix_1.2-14
[11] forcats_0.3.0     tools_3.5.0        cmprsk_2.2-7       numDeriv_2016.8-1 survival_2.41-3
[16] parallel_3.5.0    compiler_3.5.0     tibble_1.4.2
```

Then we can read the data:

```
> system.time(
+ mset <- read_sas( "../data/episodes.sas7bdat" ) )
      user system elapsed
      7.14    0.03    22.25
> dim( mset )
[1] 244715      98
> mset <- subset( mset, is.na(doDth) | doIx<doDth )
> dim( mset )
[1] 244662      98
```

```

...now input from ../rep/matchSGoth.tex

> names( mset )

[1] "druggr"      "pnr"          "eksd"          "ATC"           "doDM"          "epiN"
[7] "doIx"        "IxdR"          "Ixatc"          "lastpr"         "doTm"          "doFL"
[13] "FLdr"        "FLatc"         "deCVDD"         "coD"           "doTIA"         "doAngina"
[19] "doBleed"     "doCOPD"        "doPAD"          "doHF"           "doCancer"      "doDMcompl"
[25] "doNeuro"     "doDKD"         "doDiaEye"       "doHypo"         "doAtrFib"      "doMI"
[31] "doUnstAng"   "doHmStr"       "doDiaFoot"      "doOther"        "doPeriAng"     "doIscStr"
[37] "doAmp"       "doCKD"         "doPCIsten"      "doCABG"         "doKeto"         "doDial"
[43] "doBari"      "sex"           "doBth"          "whBth"          "doDth"          "dSrc"
[49] "dolACE"      "dolSta"        "dolBB1"         "dolARB"         "dolA1A"         "dolDHP"
[55] "dolWtL"      "dolRPA"        "dolWrf"         "dolAsp"         "dolHCD"         "dolTHZ"
[61] "dolCcs"      "dolDXI"        "dolDgo"         "dolAP1"         "dolAmi"         "dolDTI"
[67] "dolNHP"      "dolFla"        "dolMetformin"   "dolGLP1"        "dolMetxSGLT2"   "dolMetxDPP4"
[73] "dolSGLT2"    "dolongIns"     "dolmixIns"      "dolDPP4"        "dolSU"          "dolintIns"
[79] "dolfastIns"  "dolTZD"        "dolAcarbose"    "dolTZDxDPP4"    "maxH"           "frail"
[85] "recnum"      "C_ADIAg"       "compl"          "C_OPR"          "D_INDDTO"       "V_SENGDAGE"
[91] "deHF"        "deMACE"        "deMI"           "deStr"          "deIscStr"       "deAF"
[97] "deHH"        "deDKD"

> addmargins( table( table( mset$pnr ) ) )

      1      2      3      4      5      6      7      8      9     10     11     Sum
99132 36028 13706  5015  1596   464   143   49    12     2     1 156148

```

We convert all dates to fractions of years to facilitate programming:

```
> mset <- cal.yr( as.data.frame(mset) )
```

To make FLdr and IxdR into factors we need some sensible levels:

```

> ( drlab <- read.table( "drlab.txt", header=TRUE, as.is=TRUE ) )

      gr  lab      longlab
1      11  Met    Metformin
2      12  SU    Sulfonylurea
3      13  TZD           TZD
4      14  DPP      DPP-4
5      15  GLP      GLP-1
6      16  SGL      SGLT2
7 fastIns fIns    fastIns
8  intIns iIns    intIns
9  mixIns mIns    mixIns
10 longIns lIns    longIns
11      18  Aca    Acarbose
12      19  Meg  Meglitinide
13     212  M+U      Met+SU
14     213  M+T      Met+TZD
15     214  M+D      Met+DPP4
16     216  M+S      Met+SGLT2
17     218  M+A  Met+Acarbose
18     223  U+T      SU+TZD
19     234  D+T      TZD+DPP4
20     246  D+S      DPP4+SGLT2

```

Then we can define the first line and the index drug variables as factors:

```
> mset <- transform( mset, doFL = pmax( doFL, 1995 ),
+                      FLdr = factor( FLdr,
+                      levels = drlab$gr,
+                      labels = drlab$lab ),
+                      Ixdr = factor( ifelse( is.na(ii<-match(Ixdr,drlab$longlab)),
+                      Ixdr,
+                      drlab$lab[ii] ) ) )
> with( mset, table(FLdr, Ixdr) )
```

	Ixdr										
FLdr	Aca	DPP4	fIns	GLP1	iIns	lIns	Met	mIns	SGL	SU	TZD
Met	76	28839	8370	12121	6250	12547	79299	2751	12880	14189	99
SU	31	8282	7332	3349	3377	7422	7635	1849	3947	4346	43
TZD	0	6	2	9	4	8	16	0	4	5	9
DPP	0	727	61	38	56	74	232	17	42	60	0
GLP	0	30	10	1044	7	22	133	3	31	13	0
SGL	0	11	2	4	2	3	26	0	94	1	0
fIns	1	280	2296	302	812	1255	749	245	213	140	2
iIns	1	265	1118	207	1139	631	590	182	167	91	1
mIns	1	257	549	175	150	439	569	551	134	116	2
lIns	1	52	291	26	9	733	177	25	21	18	0
Aca	68	35	41	23	22	28	49	8	16	18	0
Meg	0	0	0	0	0	0	0	0	0	0	0
M+U	0	0	0	0	0	0	0	0	0	0	0
M+T	0	25	16	21	8	31	21	5	23	13	0
M+D	0	489	37	51	17	48	498	13	82	84	0
M+S	0	2	0	0	0	0	23	0	24	0	0
M+A	0	0	0	0	0	0	0	0	0	0	0
U+T	0	0	0	0	0	0	0	0	0	0	0
D+T	0	0	0	0	0	0	0	0	0	0	0
D+S	0	0	0	0	0	0	0	0	0	0	0

We shall use all *episodes*, which means that some persons will contribute more episodes, some of the same type of matching drug (which here is either SGLT2 or Other), so we move the Ixdr to the variable Epdr (Episode drug), and relevel the Ixdr to only two levels:

```
> mset$Epdr <- mset$Ixdr
> mset$Ixdr <- factor( 1-(mset$Ixdr=="SGL"), labels=c("SGLT2","Other") )
> with( mset, table( Epdr, Ixdr ) )
```

	Ixdr	
Epdr	SGLT2	Other
Aca	0	179
DPP4	0	39300
fIns	0	20125
GLP1	0	17370
iIns	0	11853
lIns	0	23241
Met	0	90017
mIns	0	5649
SGL	17678	0
SU	0	19094
TZD	0	156

We tabulate the index drug versus the first-line drug separately for those where the index date and first-line dates are the same:

```
> print( ftable( with( mset, addmargins(
+               table( "Ix=FL"=abs(doIx-doFL)<0.1, FLdr, E=Epdr ), 2:3 ) ),
+       col.vars=c(3) ),
+       zero = "." )
```

	E	Aca	DPP4	fIns	GLP1	iIns	lIns	Met	mIns	SGL	SU	TZD	S
Ix=FL FLdr													
FALSE Met		75	27758	7918	11901	5606	11833	18599	2605	12748	13198	95	1123
SU		30	8252	7317	3347	3372	7418	7565	1844	3946	3453	41	465
TZD		.	6	1	9	4	7	15	.	4	5	1	
DPP		.	51	34	37	40	57	187	14	41	51	.	5
GLP		.	27	8	73	7	17	118	3	29	13	.	2
SGL		.	8	1	3	1	2	16	.	2	1	.	
fIns		1	276	758	302	368	784	666	134	213	136	2	36
iIns		1	262	1056	207	345	625	526	167	167	88	1	34
mIns		1	256	524	175	148	433	548	166	133	114	2	25
lIns		1	47	203	25	8	72	113	15	21	16	.	5
Aca		7	34	41	23	22	28	48	8	16	18	.	2
Meg		.	.	.	.	.	.	.	.	.	.	.	
M+U		.	.	.	.	.	.	.	.	.	.	.	
M+T		.	25	16	21	8	31	21	5	23	13	.	1
M+D		.	67	36	50	15	42	76	12	81	70	.	4
M+S		.	2	.	.	.	.	.	.	1	.	.	
M+A		.	.	.	.	.	.	.	.	.	.	.	
U+T		.	.	.	.	.	.	.	.	.	.	.	
D+T		.	.	.	.	.	.	.	.	.	.	.	
D+S		.	.	.	.	.	.	.	.	.	.	.	
Sum		116	37071	17913	16173	9944	21349	28498	4973	17425	17176	142	1707
TRUE Met		1	1081	452	220	644	714	60700	146	132	991	4	650
SU		1	30	15	2	5	4	70	5	1	893	2	10
TZD		.	.	1	.	.	1	1	.	.	.	8	
DPP		.	676	27	1	16	17	45	3	1	9	.	7
GLP		.	3	2	971	.	5	15	.	2	.	.	9
SGL		.	3	1	1	1	1	10	.	92	.	.	1
fIns		.	4	1538	.	444	471	83	111	.	4	.	26
iIns		.	3	62	.	794	6	64	15	.	3	.	9
mIns		.	1	25	.	2	6	21	385	1	2	.	4
lIns		.	5	88	1	1	661	64	10	.	2	.	8
Aca		61	1	.	.	.	.	1	.	.	.	.	
Meg		.	.	.	.	.	.	.	.	.	.	.	
M+U		.	.	.	.	.	.	.	.	.	.	.	
M+T		.	.	.	.	.	.	.	.	.	.	.	
M+D		.	422	1	1	2	6	422	1	1	14	.	8
M+S		.	.	.	.	.	.	23	.	23	.	.	
M+A		.	.	.	.	.	.	.	.	.	.	.	
U+T		.	.	.	.	.	.	.	.	.	.	.	
D+T		.	.	.	.	.	.	.	.	.	.	.	
D+S		.	.	.	.	.	.	.	.	.	.	.	
Sum		63	2229	2212	1197	1909	1892	61519	676	253	1918	14	738

We see that among those where the two dates are equal, there are still some where the first line and Index drug are not the same. This is because each initiating *drug* generates its own episode, so they represent episodes where people start more than one drug, or rather different episodes that start the same day.

3.1.1 Persons and episodes

Since we have more episodes for each person we also want to see how many persons contribute how many episodes on index drug SGLT2 resp. Other:

```
> tt <- with( mset, table( pnr, Ixdr ) )
> addmargins( table( SGLT2=tt[, "SGLT2"], Other=tt[, "Other"] ) )
```

	Other											
SGLT2	0	1	2	3	4	5	6	7	8	9	10	Sum
0	0	94727	30195	9798	3142	847	227	61	12	4	0	139013
1	4405	5720	3758	1746	678	205	64	24	4	1	1	16606
2	113	148	124	69	31	15	11	3	1	0	0	515
3	2	3	2	1	3	2	1	0	0	0	0	14
Sum	4520	100598	34079	11614	3854	1069	303	88	17	5	1	156148

```
> addmargins( table( table( mset$pnr ) ) )
```

	1	2	3	4	5	6	7	8	9	10	11	Sum
99132	36028	13706	5015	1596	464	143	49	12	2	1	156148	

Note that the latter table is a tabulation of the diagonals in the former table.

3.2 Baseline tables for all new-starters

We produce an overview of the the exposure status, but first we need a few derived variables, including the indicator of *any* previous CVD:

```
> mset <- transform( mset, age = doIx - doBth,
+                    tff = doIx - doFL,
+                    sex = factor( sex, labels=c("M","F") ),
+                    frail = pmax( frail, 0, na.rm=TRUE ),
+                    maxH = pmax( 0, maxH, na.rm=TRUE ) )
> with( mset, addmargins( table( Ixatc, Ixdr ), 1 ) )
```

	Ixdr	
Ixatc	SGLT2	Other
A10AB01	0	7136
A10AB04	0	67
A10AB05	0	12589
A10AB06	0	333
A10AC01	0	11853
A10AD01	0	642
A10AD04	0	22
A10AD05	0	4980
A10AD06	0	5
A10AE04	0	15608
A10AE05	0	5574
A10AE06	0	2059
A10BA02	0	89236
A10BB01	0	1086
A10BB03	0	326
A10BB07	0	821
A10BB09	0	1915
A10BB12	0	14570
A10BD03	0	71
A10BD07	0	7899
A10BD08	0	7153
A10BD09	0	15

A10BD10	0	22
A10BD11	0	108
A10BD13	0	353
A10BD15	407	12
A10BD16	13	1
A10BD20	487	14
A10BF01	0	179
A10BG02	0	15
A10BG03	0	121
A10BH01	0	14762
A10BH02	0	2930
A10BH03	0	908
A10BH04	0	727
A10BH05	0	5126
A10BJ01	0	502
A10BJ02	0	16499
A10BJ03	0	79
A10BJ05	0	290
A10BK01	10684	0
A10BK02	465	0
A10BK03	5622	0
A10BX02	0	375
A10BX03	0	1
Sum	17678	226984

We now produce the baseline tables for the entire set of new user episodess; the result is in three tables, `dt.tab` (demographics for total sample), `ct.tab` (comobidites for total sample) and `mt.tab` (medication for total sample).

```
> ptab <- function( var ) cbind( tt <- table( var, mset$Ixdr ),
+                               round( prop.table( tt, 2 ) * 100, 1 ) )
```

3.2.1 Demographics

First the tabulations of the baseline demographics:

```
> t.sex <- with( mset, ptab(sex) )
> rownames( t.sex )[1] <- paste("Sex",rownames( t.sex )[1])
> t.fl0 <- with( mset, ptab( doIx-doFL==0 ) )[-1,,drop=F]
> rownames( t.fl0 )[1] <- "Index = First Line"
> t.fl0
```

	SGLT2	Other	SGLT2	Other
Index = First Line	157	70185	0.9	30.9

```
> m.fl0 <- with( subset(mset, doIx-doFL>0 ), round( c( tapply( doIx-doFL, Ixdr, mean ),
+                                                     tapply( doIx-doFL, Ixdr, sd ) ), 1 ) )
> dim( m.fl0 ) <- c(1,4)
> rownames( m.fl0 ) <- c("Index not FL: Mean / SD")
> m.fl0
```

	[,1]	[,2]	[,3]	[,4]
Index not FL: Mean / SD	8.9	8.4	5.2	5.7

```
> t.age <- with( mset, ptab( floor( pmin(pmax(age,30),89)/10 ) * 10 ) )
> rownames( t.age )[1] <- "Age at index <40"
> rownames( t.age )[nrow(t.age)] <- "80+"
> m.age <- with( mset, round( c( tapply( age, Ixdr, mean ),
```

```

+                                     tapply( age, lxd, sd ) ), 1 ) )
> dim( m.age ) <- c(1,4)
> rownames( m.age ) <- c("Age: Mean / SD")
> m.age

      [,1] [,2] [,3] [,4]
Age: Mean / SD 60.4 63.2  11 13.6

> ## Date of index by 6 months and 1 year
> with( mset, ptab( floor( doIx*2 )/2 ) )

      SGLT2 Other SGLT2 Other
2012.5    20  4468    0.1   2.0
2013      870 28592    4.9  12.6
2013.5   1059 24531    6.0  10.8
2014     1383 27503    7.8  12.1
2014.5   1655 24758    9.4  10.9
2015     2285 29637   12.9  13.1
2015.5   2476 27216   14.0  12.0
2016     4043 32204   22.9  14.2
2016.5   3887 28075   22.0  12.4

> t.dat <- with( mset, ptab( floor( doIx ) ) )
> rownames( t.dat )[1] <- paste("Index date",rownames( t.dat )[1])
> ## Date of First Line
> t.fl <- with( mset, ptab( floor( doFL ) ) )
> rownames( t.fl )[1] <- paste("Date of first line",rownames( t.fl )[1])
> ## Frailty
> t.fr <- with( mset, ptab( frail ) )
> rownames( t.fr )[1] <- paste("Frailty",rownames( t.fr )[1])
> dt.tab <- rbind( t.sex, t.fl0, m.fl0, t.age, m.age, t.dat, t.fl, t.fr )
> dt.tab

```

	SGLT2	Other	SGLT2	Other
Sex M	10822.0	132244.0	61.2	58.3
F	6856.0	94740.0	38.8	41.7
Index = First Line	157.0	70185.0	0.9	30.9
Index not FL: Mean / SD	8.9	8.4	5.2	5.7
Age at index <40	630.0	11106.0	3.6	4.9
40	2379.0	27582.0	13.5	12.2
50	5310.0	50352.0	30.0	22.2
60	5838.0	63988.0	33.0	28.2
70	3028.0	50123.0	17.1	22.1
80+	493.0	23833.0	2.8	10.5
Age: Mean / SD	60.4	63.2	11.0	13.6
Index date 2012	20.0	4468.0	0.1	2.0
2013	1929.0	53123.0	10.9	23.4
2014	3038.0	52261.0	17.2	23.0
2015	4761.0	56853.0	26.9	25.0
2016	7930.0	60279.0	44.9	26.6
Date of first line 1995	739.0	10675.0	4.2	4.7
1996	294.0	3164.0	1.7	1.4
1997	306.0	3145.0	1.7	1.4
1998	415.0	4008.0	2.3	1.8
1999	525.0	4604.0	3.0	2.0
2000	564.0	4963.0	3.2	2.2
2001	652.0	5527.0	3.7	2.4
2002	753.0	5860.0	4.3	2.6
2003	919.0	7273.0	5.2	3.2
2004	953.0	7504.0	5.4	3.3
2005	1048.0	8005.0	5.9	3.5

2006	1173.0	8560.0	6.6	3.8
2007	1242.0	9342.0	7.0	4.1
2008	1288.0	10100.0	7.3	4.4
2009	1315.0	10342.0	7.4	4.6
2010	1301.0	11079.0	7.4	4.9
2011	1158.0	11679.0	6.6	5.1
2012	900.0	11901.0	5.1	5.2
2013	725.0	25332.0	4.1	11.2
2014	593.0	21549.0	3.4	9.5
2015	481.0	21609.0	2.7	9.5
2016	334.0	20763.0	1.9	9.1
Frailty 0	11663.0	145101.0	66.0	63.9
1	6015.0	81883.0	34.0	36.1

3.2.2 Comorbidities

The data frame contains the dates of the *earliest* recorded comorbidities from the NPR, hence the prefix `.prv`:

```
> wh <- grep( "do[A-Z]", names( mset ) )
> wh <- wh[4:30]
> names( mset )[wh]
 [1] "doFL"      "doTIA"      "doAngina"    "doBleed"    "doCOPD"    "doPAD"      "doHF"
 [8] "doCancer"  "doDMcompl"  "doNeuro"     "doDKD"      "doDiaEye"   "doHypo"     "doAtrFib"
[15] "doMI"      "doUnstAng"  "doHmStr"     "doDiaFoot"  "doOther"    "doPeriAng"  "doIscStr"
[22] "doAmp"     "doCKD"      "doPCIsten"   "doCABG"     "doKeto"     "doDial"

> comorb <- data.frame( pmax( mset[,wh] < mset[, "doIx"], 0, na.rm=TRUE ) )
> names( comorb ) <- gsub( "do", ".prv.", names(comorb) )
> str( comorb )

'data.frame':      244662 obs. of  27 variables:
 $ prv.FL      : num  1 1 1 1 1 1 1 1 1 1 ...
 $ prv.TIA     : num  0 0 0 0 0 0 0 0 1 1 ...
 $ prv.Angina  : num  0 0 0 0 0 0 1 1 0 0 ...
 $ prv.Bleed   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.COPD    : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.PAD     : num  0 0 0 0 0 0 0 0 1 1 ...
 $ prv.HF      : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.Cancer  : num  1 1 1 1 0 0 0 0 0 0 ...
 $ prv.DMcompl: num  1 1 1 1 0 0 0 0 0 0 ...
 $ prv.Neuro   : num  0 0 0 0 1 0 0 0 0 0 ...
 $ prv.DKD     : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.DiaEye  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.Hypo    : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.AtrFib  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.MI      : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.UnstAng: num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.HmStr   : num  0 0 0 0 0 0 0 0 1 1 ...
 $ prv.DiaFoot: num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.Other   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.PeriAng: num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.IscStr  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.Amp     : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.CKD     : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.PCIsten: num  0 0 0 0 0 0 0 0 0 0 ...
 $ prv.CABG    : num  0 0 0 0 0 0 0 0 0 0 ...
```

```
$ prv.Keto    : num  0 0 0 0 0 0 0 0 0 0 ...
$ prv.Dial    : num  0 0 0 0 0 0 0 0 0 0 ...
```

Later, in the modeling we will need the indicator of *any* previous CVD as well as *any* type of stroke and micro-vascular complications:

```
> comorb$pre.CVD <- with( comorb, pmax( prv.MI,
+                                     prv.UnstAng,
+                                     prv.Angina,
+                                     prv.HF,
+                                     prv.AtrFib,
+                                     prv.HmStr,
+                                     prv.IscStr,
+                                     prv.TIA,
+                                     prv.PAD ) )
> comorb$pre.Str <- with( comorb, pmax( prv.HmStr,
+                                     prv.IscStr,
+                                     prv.TIA ) )
> comorb$pre.FPA <- with( comorb, pmax( prv.DiaFoot,
+                                     prv.PeriAng ) )
> comorb$pre.Mic <- with( comorb, pmax( prv.DiaEye,
+                                     prv.DMcompl,
+                                     prv.Neuro,
+                                     prv.DKD,
+                                     prv.DiaFoot,
+                                     prv.PeriAng ) )
```

Note that we name the columns `pre.` to avoid including these in the propensity score estimation.

```
> ct.tab <- cbind(
+ t( sapply( comorb,
+           function( x ) tapply( x, mset$Ixdr, sum ) ) ),
+ round(
+ t( sapply( comorb,
+           function( x ) tapply( x, mset$Ixdr, mean ) ) ) * 100, 1 ) )
> # remove the dates of recurrent HF
> # wh <- grep( "HF[1-9]", rownames(ct.tab) )
> # ct.tab <- ct.tab[-wh,]
> ct.tab
```

	SGLT2	Other	SGLT2	Other
prv.FL	17521	156799	99.1	69.1
prv.TIA	480	7881	2.7	3.5
prv.Angina	2348	29626	13.3	13.1
prv.Bleed	737	13032	4.2	5.7
prv.COPD	584	12222	3.3	5.4
prv.PAD	861	15553	4.9	6.9
prv.HF	702	13182	4.0	5.8
prv.Cancer	862	20305	4.9	8.9
prv.DMcompl	3297	27477	18.7	12.1
prv.Neuro	1032	9309	5.8	4.1
prv.DKD	671	8484	3.8	3.7
prv.DiaEye	2204	20020	12.5	8.8
prv.Hypo	613	8993	3.5	4.0
prv.AtrFib	1042	18499	5.9	8.1
prv.MI	1412	19911	8.0	8.8
prv.UnstAng	653	8459	3.7	3.7

prv.HmStr	144	2642	0.8	1.2
prv.DiaFoot	156	2295	0.9	1.0
prv.Other	814	11625	4.6	5.1
prv.PeriAng	902	10607	5.1	4.7
prv.IscStr	828	15774	4.7	6.9
prv.Amp	17	543	0.1	0.2
prv.CKD	101	6537	0.6	2.9
prv.PCIsten	156	2317	0.9	1.0
prv.CABG	477	6534	2.7	2.9
prv.Keto	95	2156	0.5	0.9
prv.Dial	1	80	0.0	0.0
pre.CVD	5268	76805	29.8	33.8
pre.Str	1263	22710	7.1	10.0
pre.FPA	1001	12080	5.7	5.3
pre.Mic	6021	53275	34.1	23.5

3.2.3 Other medication

We have variables that hold the last date of dispensation before index for all drugs of interest, restricted to the period after 2011-12-01, one year prior to the first SGLT2 dispensation. We of course also only count the drugs dispensed *before* the index date and not *on* it:

```
> wh <- grep( "dol", names(mset) )
> names( mset )[wh]
[1] "dolACE"      "dolSta"      "dolBB1"      "dolARB"      "dolAlA"      "dolDHP"
[7] "dolWtL"      "dolRPA"      "dolWrf"      "dolAsp"      "dolHCD"      "dolTHZ"
[13] "dolCcs"      "dolDXI"      "dolDgo"      "dolAP1"      "dolAmi"      "dolDTI"
[19] "dolNHP"      "dolFla"      "dolMetformin" "dolGLP1"      "dolMetxSGLT2" "dolMetxDPP4"
[25] "dolSGLT2"    "dolongIns"   "dolmixIns"   "dolDPP4"      "dolSU"        "dolintIns"
[31] "dolfastIns"  "dolTZD"      "dolAcarbose" "dolTZDxDPP4"

> codisp <- data.frame( pmax( mset[,wh] > ( mset[, "doIx"] - 1 ) &
+                           mset[,wh] < mset[, "doIx"] ,
+                           0, na.rm=TRUE ) )
> names( codisp ) <- gsub( "dol", "had.", names(codisp) )
> ( names( codisp )[wh.ins <- grep("Ins",names(codisp))] )
[1] "had.longIns" "had.mixIns" "had.intIns" "had.fastIns"
> ( names( codisp )[wh.hyp <- c(1,4,6,12,3)] )
[1] "had.ACE" "had.ARB" "had.DHP" "had.THZ" "had.BB1"
> ( names( codisp )[wh.cvd <- c(10,2,wh.hyp)] )
[1] "had.Asp" "had.Sta" "had.ACE" "had.ARB" "had.DHP" "had.THZ" "had.BB1"
> codisp <- transform( codisp, got.Ins = apply( codisp[,wh.ins], 1, max ),
+                       got.Hyp = apply( codisp[,wh.hyp], 1, max ),
+                       got.CVD = apply( codisp[,wh.cvd], 1, max ) )
> names( codisp )
[1] "had.ACE"      "had.Sta"      "had.BB1"      "had.ARB"      "had.AlA"
[6] "had.DHP"      "had.WtL"      "had.RPA"      "had.Wrf"      "had.Asp"
[11] "had.HCD"      "had.THZ"      "had.Ccs"      "had.DXI"      "had.Dgo"
[16] "had.AP1"      "had.Ami"      "had.DTI"      "had.NHP"      "had.Fla"
[21] "had.Metformin" "had.GLP1"      "had.MetxSGLT2" "had.MetxDPP4" "had.SGLT2"
[26] "had.longIns"   "had.mixIns"   "had.DPP4"      "had.SU"        "had.intIns"
[31] "had.fastIns"   "had.TZD"      "had.Acarbose" "had.TZDxDPP4" "got.Ins"
[36] "got.Hyp"      "got.CVD"
```

```
> mt.tab <- cbind(
+ t( sapply( codisp,
+           function( x ) tapply( x, mset$Ixdr, sum ) ) ),
+ round(
+ t( sapply( codisp,
+           function( x ) tapply( x, mset$Ixdr, mean ) ) ) * 100, 1 ) )
> mt.tab
```

	SGLT2	Other	SGLT2	Other
had.ACE	6830	72133	38.6	31.8
had.Sta	13263	126144	75.0	55.6
had.BB1	4771	63033	27.0	27.8
had.ARB	6104	56367	34.5	24.8
had.A1A	883	14102	5.0	6.2
had.DHP	5354	59189	30.3	26.1
had.WtL	120	1029	0.7	0.5
had.RPA	1134	16626	6.4	7.3
had.Wrf	721	14724	4.1	6.5
had.Asp	6226	68351	35.2	30.1
had.HCD	2330	44177	13.2	19.5
had.THZ	2697	33724	15.3	14.9
had.Ccs	925	21060	5.2	9.3
had.DXI	288	4525	1.6	2.0
had.Dgo	434	10410	2.5	4.6
had.AP1	175	3882	1.0	1.7
had.Ami	39	1328	0.2	0.6
had.DTI	218	3451	1.2	1.5
had.NHP	297	3665	1.7	1.6
had.Fla	15	200	0.1	0.1
had.Metformin	11391	80273	64.4	35.4
had.GLP1	4470	13314	25.3	5.9
had.MetxSGLT2	0	215	0.0	0.1
had.MetxDPP4	3192	8967	18.1	4.0
had.SGLT2	0	5432	0.0	2.4
had.longIns	2375	11834	13.4	5.2
had.mixIns	984	11555	5.6	5.1
had.DPP4	3085	14701	17.5	6.5
had.SU	4095	30627	23.2	13.5
had.intIns	932	13647	5.3	6.0
had.fastIns	1034	7846	5.8	3.5
had.TZD	58	224	0.3	0.1
had.Acarbose	32	229	0.2	0.1
had.TZDxDPP4	1	1	0.0	0.0
got.Ins	4067	36359	23.0	16.0
got.Hyp	13819	152904	78.2	67.4
got.CVD	16183	176968	91.5	78.0

We also check that there are no episodes with the index drug in the baseline:

```
> print( as.table( t( sapply( codisp,
+                             function( x ) tapply( x, mset$Epdr, sum ) ) ) ),
+        zero.print="-" )
```

	Aca	DPP4	fIns	GLP1	iIns	lIns	Met	mIns	SGL	SU	TZD
had.ACE	42	14599	7260	6555	4482	8863	21794	2106	6830	6366	66
had.Sta	79	27158	12584	12073	7349	15818	35551	3501	13263	11936	95
had.BB1	40	11633	7023	4756	3857	7615	21127	1825	4771	5106	51
had.ARB	36	11503	5228	5464	2999	6834	17943	1443	6104	4875	42
had.A1A	8	2294	2231	1138	972	1905	4090	506	883	950	8

had.DHP	27	11676	6133	5080	3529	7225	18853	1653	5354	4975	38
had.WtL	2	118	50	229	26	67	434	16	120	87	-
had.RPA	11	2834	2435	1024	1063	2139	5354	523	1134	1233	10
had.Wrf	11	2621	1869	857	1017	1796	4932	445	721	1167	9
had.Asp	40	13219	8059	5756	4455	8894	19837	2230	6226	5818	43
had.HCD	22	7314	7484	2978	3414	6240	12040	1659	2330	3003	23
had.THZ	28	5939	2917	2788	1811	3404	13202	807	2697	2808	20
had.Ccs	13	2956	3589	1031	1685	2205	7280	849	925	1443	9
had.DXI	-	810	678	252	278	640	1466	121	288	278	2
had.Dgo	6	1796	1448	471	738	1285	3517	341	434	801	7
had.APl	1	665	541	204	325	464	1242	137	175	301	2
had.Ami	-	252	224	90	89	200	341	61	39	70	1
had.DTI	1	621	379	210	210	397	1271	88	218	273	1
had.NHP	10	651	427	256	208	447	1276	100	297	286	4
had.Fla	2	49	13	15	8	13	80	-	15	20	-
had.Metformin	51	29442	8472	10287	5889	12291	-	2814	11391	10939	88
had.GLP1	6	1713	2222	-	1477	4666	1190	834	4470	1176	30
had.MetxSGLT2	-	59	10	45	7	68	-	5	-	21	-
had.MetxDPP4	11	-	783	2631	981	2422	-	368	3192	1759	12
had.SGLT2	3	821	519	1068	388	1615	386	148	-	471	13
had.longIns	6	1622	4592	2115	483	-	1575	1092	2375	333	16
had.mixIns	2	1011	3382	1231	845	3607	1271	-	984	203	3
had.DPP4	18	-	1722	3226	1892	3562	1529	672	3085	2051	29
had.SU	34	9035	2687	3816	3378	5573	4772	1283	4095	-	49
had.intIns	2	1100	3224	1313	-	5068	1496	1134	932	300	10
had.fastIns	6	877	-	1290	825	2482	1468	699	1034	188	11
had.TZD	-	56	15	27	23	34	34	11	58	24	-
had.Acarbose	-	51	17	30	17	25	51	7	32	30	1
had.TZDxDPP4	-	-	-	1	-	-	-	-	1	-	-
got.Ins	11	3643	9882	4457	1854	8949	4340	2342	4067	854	27
got.Hyp	100	29327	14888	12944	8691	17636	51872	4076	13819	13249	121
got.CVD	120	34640	17099	15051	9908	20181	59344	4648	16183	15845	132

3.3 Propensity scoring

We now make a logistic regression of the indicator of SGLT2 assignment versus Other assignment. For convenience we append the just created data frames of the indicators we will use in the analysis:

```
> mset <- cbind( mset, comorb, codisp )
> names( mset )
 [1] "druggr"      "pnr"          "eksd"          "ATC"           "doDM"
 [6] "epiN"        "doIx"         "Ixdr"          "Ixatc"         "lastpr"
[11] "doTm"        "doFL"         "FLdr"          "FLatc"         "deCVDD"
[16] "coD"         "doTIA"        "doAngina"      "doBleed"       "doCOPD"
[21] "doPAD"       "doHF"         "doCancer"      "doDMcompl"     "doNeuro"
[26] "doDKD"       "doDiaEye"     "doHypo"        "doAtrFib"      "doMI"
[31] "doUnstAng"   "doHmStr"      "doDiaFoot"     "doOther"       "doPeriAng"
[36] "doIscStr"    "doAmp"        "doCKD"         "doPCIsTen"     "doCABG"
[41] "doKeto"      "doDial"       "doBari"        "sex"           "doBth"
[46] "whBth"      "doDth"        "dSrc"          "dolACE"        "dolSta"
[51] "dolBB1"     "dolARB"       "dolA1A"        "dolDHP"        "dolWtL"
[56] "dolRPA"     "dolWrf"       "dolAsp"        "dolHCD"        "dolTHZ"
[61] "dolCcs"     "dolDXI"       "dolDgo"        "dolAP1"        "dolAmi"
[66] "dolDTI"     "dolNHP"       "dolFla"        "dolMetformin"  "dolGLP1"
```

[71]	"dolMetxSGLT2"	"dolMetxDPP4"	"dolSGLT2"	"dolongIns"	"dolmixIns"
[76]	"dolDPP4"	"dolSU"	"dolintIns"	"dolfastIns"	"dolTZD"
[81]	"dolAcarbose"	"dolTZDxDPP4"	"maxH"	"frail"	"recnum"
[86]	"C_ADIAG"	"compl"	"C_OPR"	"D_INDDTO"	"V_SENGDAGE"
[91]	"deHF"	"deMACE"	"deMI"	"deStr"	"deIscStr"
[96]	"deAF"	"deHH"	"deDKD"	"Epdr"	"age"
[101]	"tff"	"prv.FL"	"prv.TIA"	"prv.Angina"	"prv.Bleed"
[106]	"prv.COPD"	"prv.PAD"	"prv.HF"	"prv.Cancer"	"prv.DMcompl"
[111]	"prv.Neuro"	"prv.DKD"	"prv.DiaEye"	"prv.Hypo"	"prv.AtrFib"
[116]	"prv.MI"	"prv.UnstAng"	"prv.HmStr"	"prv.DiaFoot"	"prv.Other"
[121]	"prv.PeriAng"	"prv.IscStr"	"prv.Amp"	"prv.CKD"	"prv.PCIsten"
[126]	"prv.CABG"	"prv.Keto"	"prv.Dial"	"pre.CVD"	"pre.Str"
[131]	"pre.FPA"	"pre.Mic"	"had.ACE"	"had.Sta"	"had.BB1"
[136]	"had.ARB"	"had.A1A"	"had.DHP"	"had.WtL"	"had.RPA"
[141]	"had.Wrf"	"had.Asp"	"had.HCD"	"had.THZ"	"had.Ccs"
[146]	"had.DXI"	"had.Dgo"	"had.AP1"	"had.Ami"	"had.DTI"
[151]	"had.NHP"	"had.Fla"	"had.Metformin"	"had.GLP1"	"had.MetxSGLT2"
[156]	"had.MetxDPP4"	"had.SGLT2"	"had.longIns"	"had.mixIns"	"had.DPP4"
[161]	"had.SU"	"had.intIns"	"had.fastIns"	"had.TZD"	"had.Acarbose"
[166]	"had.TZDxDPP4"	"got.Ins"	"got.Hyp"	"got.CVD"	

With this in place it is quite easy to fit a propensity score model because we can easily fish out the relevant variables:

```
> table( mset$Ixdr )
SGLT2  Other
17678 226984

> ( prv <- grep( "prv", names(mset) ) )
[1] 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123
[23] 124 125 126 127 128

> ( had <- grep( "had", names(mset) ) )
[1] 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154
[23] 155 156 157 158 159 160 161 162 163 164 165 166

> # rmd <- grep( "SGL", names( mset ) [had] )
> # had <- had[-rmd]
> names( mset ) [had]
[1] "had.ACE"      "had.Sta"      "had.BB1"      "had.ARB"      "had.A1A"
[6] "had.DHP"      "had.WtL"      "had.RPA"      "had.Wrf"      "had.Asp"
[11] "had.HCD"      "had.THZ"      "had.Ccs"      "had.DXI"      "had.Dgo"
[16] "had.AP1"      "had.Ami"      "had.DTI"      "had.NHP"      "had.Fla"
[21] "had.Metformin" "had.GLP1"     "had.MetxSGLT2" "had.MetxDPP4" "had.SGLT2"
[26] "had.longIns"  "had.mixIns"   "had.DPP4"      "had.SU"       "had.intIns"
[31] "had.fastIns"  "had.TZD"      "had.Acarbose"  "had.TZDxDPP4"

> names( mset ) [prv]
[1] "prv.FL"      "prv.TIA"      "prv.Angina"   "prv.Bleed"    "prv.COPD"     "prv.PAD"
[7] "prv.HF"      "prv.Cancer"   "prv.DMcompl"  "prv.Neuro"    "prv.DKD"      "prv.DiaEye"
[13] "prv.Hypo"    "prv.AtrFib"   "prv.MI"       "prv.UnstAng"  "prv.HmStr"    "prv.DiaFoot"
[19] "prv.Other"   "prv.PeriAng"  "prv.IscStr"   "prv.Amp"      "prv.CKD"      "prv.PCIsten"
[25] "prv.CABG"    "prv.Keto"     "prv.Dial"

> system.time(
+ pr.0 <- glm( ( Ixdr == "SGLT2" ) ~
+             sex + age + frail + doIx + doFL +
+             as.matrix(mset[,prv]) + as.matrix(mset[,had]),
+             family = binomial,
+             data = mset, maxit = 100 ) )
```

```

      user  system elapsed
    25.75    2.01    27.77
> print( summary( pr.0 ), digits = 3 )
Call:
glm(formula = (Ixdr == "SGLT2") ~ sex + age + frail + doIx +
     doFL + as.matrix(mset[, prv]) + as.matrix(mset[, had]), family = binomial,
     data = mset, maxit = 100)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.554  -0.393  -0.217  -0.061   4.273

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   -1.05e+03   1.61e+01  -64.78 < 2e-16 ***
sexF           -1.05e-01   1.80e-02   -5.85 5.0e-09 ***
age            -2.06e-02   8.14e-04  -25.34 < 2e-16 ***
frail          -2.31e-01   1.93e-02  -11.92 < 2e-16 ***
doIx           5.30e-01   8.07e-03   65.61 < 2e-16 ***
doFL          -1.31e-02   1.95e-03   -6.72 1.8e-11 ***
as.matrix(mset[, prv])prv.FL      3.01e+00   8.28e-02   36.31 < 2e-16 ***
as.matrix(mset[, prv])prv.TIA    -2.40e-02   5.39e-02   -0.45 0.65580
as.matrix(mset[, prv])prv.Angina -5.66e-04   2.97e-02   -0.02 0.98479
as.matrix(mset[, prv])prv.Bleed  -1.65e-01   4.21e-02   -3.93 8.5e-05 ***
as.matrix(mset[, prv])prv.COPD   -1.68e-01   4.78e-02   -3.52 0.00043 ***
as.matrix(mset[, prv])prv.PAD    -2.39e-01   4.03e-02   -5.93 3.1e-09 ***
as.matrix(mset[, prv])prv.HF     -1.05e-01   4.81e-02   -2.18 0.02910 *
as.matrix(mset[, prv])prv.Cancer -3.98e-01   3.90e-02  -10.22 < 2e-16 ***
as.matrix(mset[, prv])prv.DMcompl 1.55e-01   2.46e-02    6.32 2.6e-10 ***
as.matrix(mset[, prv])prv.Neuro   1.39e-01   3.82e-02    3.65 0.00026 ***
as.matrix(mset[, prv])prv.DKD    -2.54e-01   4.56e-02   -5.56 2.6e-08 ***
as.matrix(mset[, prv])prv.DiaEye  1.72e-02   2.80e-02    0.61 0.53927
as.matrix(mset[, prv])prv.Hypo   -2.28e-01   4.70e-02   -4.85 1.2e-06 ***
as.matrix(mset[, prv])prv.AtrFib  4.93e-02   4.90e-02    1.01 0.31487
as.matrix(mset[, prv])prv.MI      7.01e-03   3.69e-02    0.19 0.84944
as.matrix(mset[, prv])prv.UnstAng -2.68e-02   4.94e-02   -0.54 0.58823
as.matrix(mset[, prv])prv.HmStr  -1.18e-01   9.29e-02   -1.27 0.20367
as.matrix(mset[, prv])prv.DiaFoot -1.26e-01   9.14e-02   -1.38 0.16893
as.matrix(mset[, prv])prv.Other  -1.37e-01   4.41e-02   -3.11 0.00187 **
as.matrix(mset[, prv])prv.PeriAng -4.37e-02   4.13e-02   -1.06 0.29015
as.matrix(mset[, prv])prv.IscStr  -2.17e-01   4.44e-02   -4.88 1.0e-06 ***
as.matrix(mset[, prv])prv.Amp    -8.48e-01   2.60e-01   -3.27 0.00109 **
as.matrix(mset[, prv])prv.CKD    -1.47e+00   1.05e-01  -14.04 < 2e-16 ***
as.matrix(mset[, prv])prv.PCIsten -1.58e-01   9.35e-02   -1.69 0.09064 .
as.matrix(mset[, prv])prv.CABG   1.51e-02   5.93e-02    0.25 0.79929
as.matrix(mset[, prv])prv.Keto   -6.59e-01   1.12e-01   -5.91 3.5e-09 ***
as.matrix(mset[, prv])prv.Dial  -3.16e-01   1.03e+00   -0.31 0.75799
as.matrix(mset[, had])had.ACE    1.82e-01   2.08e-02    8.77 < 2e-16 ***
as.matrix(mset[, had])had.Sta    3.26e-01   2.08e-02   15.68 < 2e-16 ***
as.matrix(mset[, had])had.BB1    1.28e-02   2.27e-02    0.56 0.57389
as.matrix(mset[, had])had.ARB    3.31e-01   2.15e-02   15.40 < 2e-16 ***
as.matrix(mset[, had])had.ALA    -2.58e-02   4.17e-02   -0.62 0.53584
as.matrix(mset[, had])had.DHP    5.88e-04   2.03e-02    0.03 0.97689
as.matrix(mset[, had])had.WtL    5.03e-01   1.09e-01    4.61 4.0e-06 ***
as.matrix(mset[, had])had.RPA    -6.52e-02   3.93e-02   -1.66 0.09721 .
as.matrix(mset[, had])had.Wrf    -1.29e-01   5.24e-02   -2.46 0.01394 *
as.matrix(mset[, had])had.Asp    7.68e-02   2.09e-02    3.67 0.00025 ***

```

```

as.matrix(mset[, had])had.HCD      -3.02e-01  2.85e-02 -10.59 < 2e-16 ***
as.matrix(mset[, had])had.THZ       6.77e-02  2.46e-02   2.75 0.00591 **
as.matrix(mset[, had])had.Ccs      -2.72e-01  3.81e-02  -7.15 8.6e-13 ***
as.matrix(mset[, had])had.DXI      -1.27e-01  7.09e-02  -1.79 0.07408 .
as.matrix(mset[, had])had.Dgo      -1.43e-01  6.37e-02  -2.24 0.02531 *
as.matrix(mset[, had])had.APl      -2.28e-01  8.80e-02  -2.59 0.00962 **
as.matrix(mset[, had])had.Ami      -5.90e-01  1.73e-01  -3.41 0.00064 ***
as.matrix(mset[, had])had.DTI       1.68e-04  8.39e-02   0.00 0.99840
as.matrix(mset[, had])had.NHP       1.90e-01  6.84e-02   2.78 0.00546 **
as.matrix(mset[, had])had.Fla       8.10e-02  2.91e-01   0.28 0.78059
as.matrix(mset[, had])had.Metformin 4.52e-01  1.86e-02  24.25 < 2e-16 ***
as.matrix(mset[, had])had.GLP1      1.32e+00  2.25e-02  58.50 < 2e-16 ***
as.matrix(mset[, had])had.MetxSGLT2 -1.60e+01  2.40e+02  -0.07 0.94688
as.matrix(mset[, had])had.MetxDPP4  1.49e+00  2.54e-02  58.44 < 2e-16 ***
as.matrix(mset[, had])had.SGLT2     -1.64e+01  4.96e+01  -0.33 0.74047
as.matrix(mset[, had])had.longIns   5.57e-01  2.86e-02  19.45 < 2e-16 ***
as.matrix(mset[, had])had.mixIns   -1.67e-01  3.84e-02  -4.34 1.4e-05 ***
as.matrix(mset[, had])had.DPP4      8.77e-01  2.42e-02  36.18 < 2e-16 ***
as.matrix(mset[, had])had.SU        2.20e-01  2.17e-02  10.14 < 2e-16 ***
as.matrix(mset[, had])had.intIns   -5.69e-01  3.84e-02 -14.81 < 2e-16 ***
as.matrix(mset[, had])had.fastIns   3.32e-01  4.01e-02   8.29 < 2e-16 ***
as.matrix(mset[, had])had.TZD       1.01e+00  1.65e-01   6.12 9.5e-10 ***
as.matrix(mset[, had])had.Acarbose  3.04e-01  2.05e-01   1.48 0.13892
as.matrix(mset[, had])had.TZDxDPP4  1.19e+00  1.45e+00   0.82 0.41059
---

```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

```

Null deviance: 126947  on 244661  degrees of freedom
Residual deviance: 95983  on 244595  degrees of freedom
AIC: 96117

```

Number of Fisher Scoring iterations: 16

With this fitted model we can now use the fitted values as propensity scores.

3.4 Propensity score matching

Based on this propensity score we take a matched sample of 1 per SGLT-2 user — note that we explicitly set a seed in order to get a fully reproducible code:

```

> set.seed( 1952 )
> system.time(
+ mt <- Match( Tr = (mset$Ixdr=="SGLT2"),
+             X = fitted( pr.0 ),
+             M = 1,
+             replace = FALSE,
+             exact = FALSE,
+             ties = FALSE,
+             caliper = 0.2 ) )
   user  system elapsed
198.84  131.68   330.56
> str( mt )

```

```

List of 23
 $ est          : num [1, 1] 0
 $ se           : NULL
 $ est.noadj    : num 0
 $ se.standard  : num 0
 $ se.cond      : NULL
 $ mdata        :List of 4
 ..$ Y          : num [1:35220] 0 0 0 0 0 0 0 0 0 0 ...
 ..$ Tr         : num [1:35220] 1 1 1 1 1 1 1 1 1 1 ...
 ..$ X          : num [1:2, 1:17610] 0.479 0.479 0.178 0.179 0.46 ...
 .. ..- attr(*, "dimnames")=List of 2
 .. .. ..$ : NULL
 .. .. ..$ : chr [1:17610] "5" "7" "16" "19" ...
 ..$ orig.weighted.treated.nobs: num 17678
 $ index.treated : num [1:17610] 5 7 16 19 37 56 61 69 77 83 ...
 $ index.control : num [1:17610] 153842 133038 87125 108397 113006 ...
 $ index.dropped : int [1:68] 124432 144439 184560 185280 198909 200020 200851 201996 202700 ...
 $ weights       : num [1:17610] 1 1 1 1 1 1 1 1 1 1 ...
 $ orig.nobs     : int 244662
 $ orig.wnobs    : num 244662
 $ orig.treated.nobs: int 17678
 $ nobs         : int 244662
 $ wnobs        : num 17610
 $ caliper       : num 0.2
 $ ecaliper      : num 0.0211
 $ exact         : logi FALSE
 $ ndrops        : num 68
 $ ndrops.matches : num 68
 $ MatchLoopC    : num [1:17610, 1:6] 5 7 16 19 37 56 61 69 77 83 ...
 $ version       : chr "fast"
 $ estimand      : chr "ATT"
 - attr(*, "class")= chr "Match"
> save( mt, file='mtSGoth.Rda' )

> load( file='mtSGoth.Rda' )

```

The resulting matching (`index.-`variables) refers to rows in `mset`:

```

> addmargins( rbind(
+ table( mset$Ixdr[unique(mt$index.treated)] ),
+ table( mset$Ixdr[unique(mt$index.control)] ) ), 2 )
      SGLT2 Other Sum
[1,] 17610      0 17610
[2,]      0 17610 17610

```

We just use the index numbers for the treated as factor levels for the match-factor (we shall not use the factor though):

```

> tnum <- mt$index.treated
> cnum <- mt$index.control
> # a numeric with the index number of SGLT-2 for persons matched up
> mf <- rep( NA, nrow(mset) )
> mf[tnum] <- tnum
> mf[cnum] <- tnum
> # create a factor of this and tabulate
> mset <- transform( mset, mfac = factor(mf),
+                   psco = fitted(pr.0) )
> ( mtab <- with( mset, table( Ixdr, !is.na(mfac), useNA="ifany" ) ) )

```

```

Ixdr      FALSE    TRUE
SGLT2      68    17610
Other 209374    17610

> round( cbind( rbind( cbind( mtab,
+                               pctab( mtab ) ),
+                               NA,
+                               NA),
+                               pctab( mtab, margin=1 ) )[-3,], 1 )
Ixdr      FALSE    TRUE    All    N
SGLT2      0.4    99.6    100.0 17678.0
Other     92.2     7.8    100.0 226984.0

Ixdr      FALSE    TRUE
SGLT2      0      50
Other     100     50
All       100     100
N       209442  35220

      FALSE TRUE FALSE TRUE All    N FALSE TRUE
SGLT2   68 17610   0.4 99.6 100  17678     0   50
Other 209374 17610 92.2  7.8 100 226984    100   50
      NA    NA    NA    NA  NA    NA 209442 35220

```

We can see that we did match all persons, presumably because a lot of persons were matched to themselves:

```

> par( mar=c(3,3,1,1),mgp=c(3,1,0)/1.6,las=1,bty="n" )
> plot( mset$psco[mt$index.treated],
+       mset$psco[mt$index.control],
+       pch=16, cex=0.3 ,
+       xlim=0:1, xlab="SGLT-2i propensity score",
+       ylim=0:1, ylab="Other-drug propensity score" )

```

For the use in further analyses we save a version of the original data for later use:

```

> oset <- mset
> pscore <- table( floor( oset$psco*100 ), oset$Ixdr )

```

Finally we make a dataset restricted to the matched persons:

```

> mset <- subset( oset, !is.na(mfac) )
> psmatch <- table( floor( mset$psco*100 ), mset$Ixdr )
> head( pscore )
      SGLT2 Other
0      181 83655
1      170 15493
2      373 16538
3      456 14788
4      517 12308
5      560 10494

> head( psmatch )
      SGLT2 Other
0      181   179
1      170   169
2      373   370
3      456   463
4      517   516
5      560   563

```

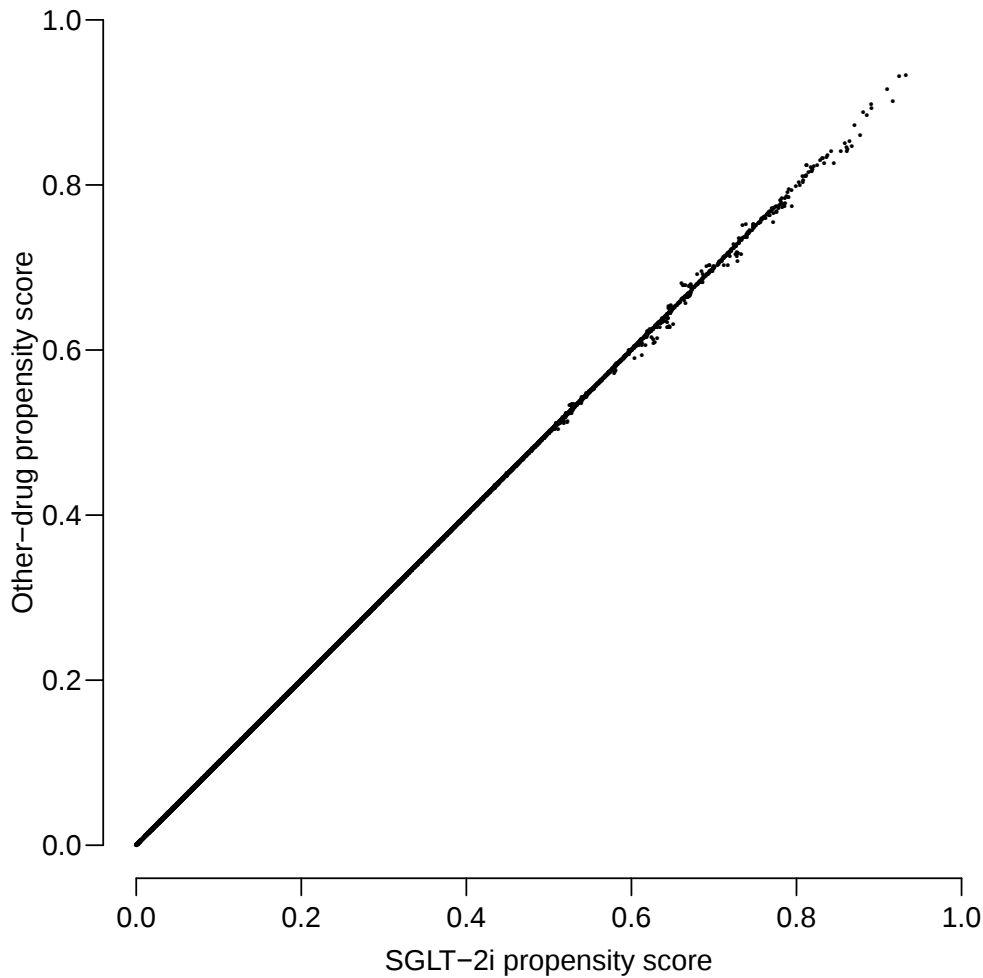


Figure 3.1: *Propensity scores from 1:1 matching; each matched set is represented by a dot.*
`./matchSGoth-cmp-ps`

```
> save( oset, mset, pscore, psmatch, file = "adatSGoth.Rda" )
> load( file = "adatSGoth.Rda" )

> tt <- with( mset, table( pnr, lxd ) )
> addmargins( gg <- table( SGLT2=tt[, "SGLT2"], Other=tt[, "Other"] ) )
```

	Other						
SGLT2	0	1	2	3	4	5	Sum
0	0	12165	1261	137	12	1	13576
1	14460	1826	228	29	2	1	16546
2	443	62	6	0	0	0	511
3	12	1	1	0	0	0	14
Sum	14915	14054	1496	166	14	2	30647

```
> sum( gg[-1,-1] )
[1] 2156

> addmargins( table( table( mset$pnr ) ) )
```

	1	2	3	4	5	6	Sum
26625	3530	439	48	4	1		30647

Thus there are 30,647 persons with a total of 2 episodes. Of these persons 2,156 contribute episodes in both groups.

We also make histograms of the propensity scores, both for the original data and for the matched persons

```
> tt <- pscore
> tt[,1] <- tt[,1]/sum(tt[,1]) * 1000
> tt[,2] <- tt[,2]/sum(tt[,2]) * 1000
> tt <- cbind( -tt[,1], tt )
> head(tt)
      SGLT2      Other
0 -10.238715 10.238715 368.55021
1  -9.616472  9.616472  68.25591
2 -21.099672 21.099672  72.85976
3 -25.794773 25.794773  65.14997
4 -29.245390 29.245390  54.22409
5 -31.677792 31.677792  46.23233

> nam <- colnames( tt )[-1]
> clr <- c("transparent","red","blue")
> # we use the undocumented feature of boxplot that you can get stacked
> # bars starting in the negative by giving negative numbers to the first
> # column. But it will mysteriously ignore the first element of col...
> par( mar=c(3,3,1,1), mgp=c(3,1,0)/1.6, bty="n", las=1 )
> barplot( t(tt), space=0, col=clr, border="transparent", xlim=c(-65,65),
+         horiz=T, yaxt="n", ylab="Propensity score for SGLT-2 (%)", xaxt="n" )
> axis( side=2, at=seq(0,95,5), labels=NA, tcl=-0.3 )
> axis( side=2, at=0:9*10 )
> axis( side=1, at=-6:6*10, labels=NA, tcl=-0.3 )
> axis( side=1, at=-3:3*20, labels=abs(-3:3*20) )
> text( rep(60,2), 19:18*5, nam, col=clr[-1], font=2, adj=1 )
> # mtext( "%", side=1, font=2, line=1.5, at=-2.5 )
> mtext( "\211", side=1, font=2, line=1.5, at=0 )

> tt <- psmatch
> tt[,1] <- tt[,1]/sum(tt[,1]) * 1000
> tt[,2] <- tt[,2]/sum(tt[,2]) * 1000
> tt <- cbind( -tt[,1], tt )
> par( mar=c(3,3,1,1), mgp=c(3,1,0)/1.6, bty="n", las=1 )
> barplot( t(tt), space=0, col=clr, border="transparent", xlim=c(-65,65),
+         horiz=T, yaxt="n", ylab="Propensity score for SGLT-2 (%)", xaxt="n" )
> axis( side=2, at=seq(0,95,5), labels=NA, tcl=-0.3 )
> axis( side=2, at=0:9*10 )
> axis( side=1, at=-6:6*10, labels=NA, tcl=-0.3 )
> axis( side=1, at=-3:3*20, labels=abs(-3:3*20) )
> text( rep(60,2), 19:18*5, nam, col=clr[-1], font=2, adj=1 )
> # mtext( "%", side=1, font=2, line=1.5, at=-2.5 )
> mtext( "\211", side=1, font=2, line=1.5, at=10 )
```

3.5 Baseline tables for propensity matched persons

We have the matched sets in the dataframe `mset`, so we can almost verbatim reuse the code doing the tables for the original sample, except for the names of the resulting tables: `dm.tab` (demographics for matched sample), `cm.tab` (comobidites for matched sample) and `mm.tab` (medication for matched sample).

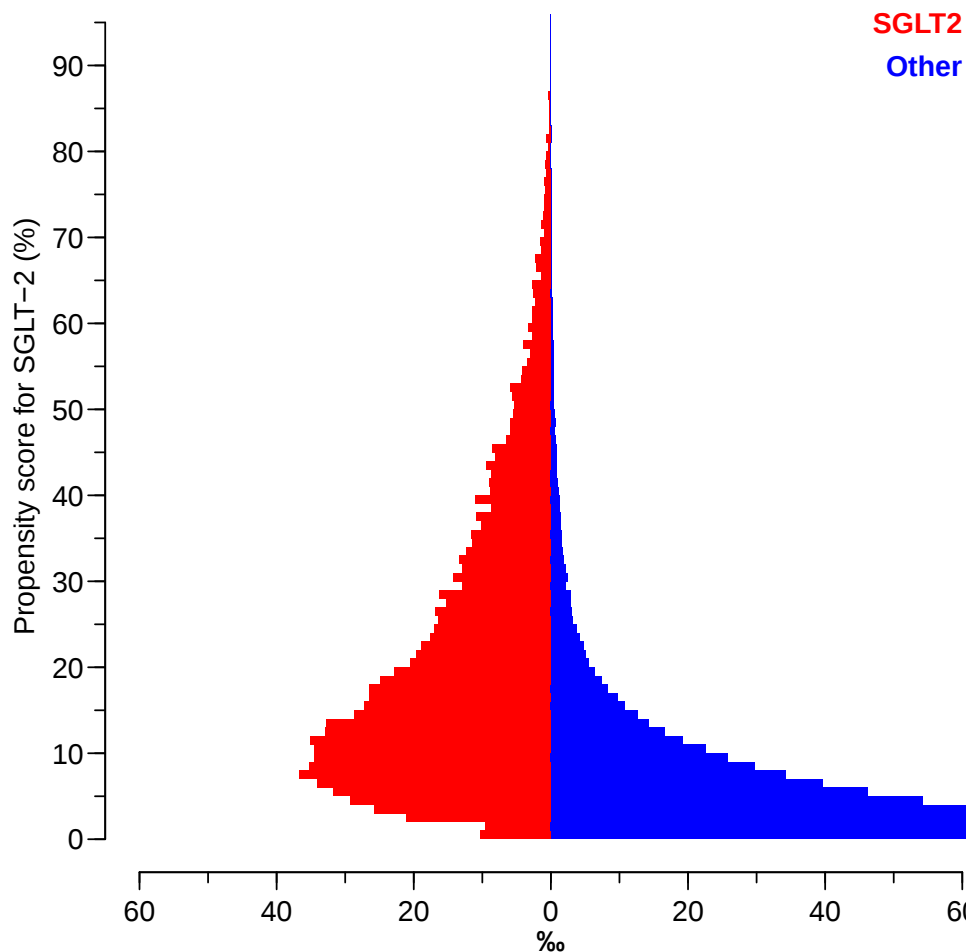


Figure 3.2: Propensity scores for the SGLT-2 group (left, percent) and other groups (right, %) in the 1:3 propensity score matched study.

3.5.1 Demographics

First the tabulations of the baseline demographics for the included *episodes*:

```
> t.sex <- with( mset, ptab( sex ) )
> rownames( t.sex )[1] <- paste("Sex",rownames( t.sex )[1])
> t.age <- with( mset, ptab( floor( pmin(pmax(age,30),89)/10 ) * 10 ) )
> rownames( t.age )[1] <- "Age at index <40"
> rownames( t.age )[nrow(t.age)] <- "80+"
> t.fl0 <- with( mset, ptab( doIx-doFL==0 ) )[-1,,drop=F]
> rownames( t.fl0 )[1] <- "Index = First Line"
> t.fl0
```

	SGLT2	Other	SGLT2	Other
Index = First Line	157	146	0.9	0.8

```
> m.fl0 <- with( subset(mset, doIx-doFL>0 ), round( c( tapply( doIx-doFL, lxd, mean ),
+                                                     tapply( doIx-doFL, lxd, sd ) ), 1 ) )
> dim( m.fl0 ) <- c(1,4)
> rownames( m.fl0 ) <- c("Index not FL: Mean / SD")
> m.fl0
```

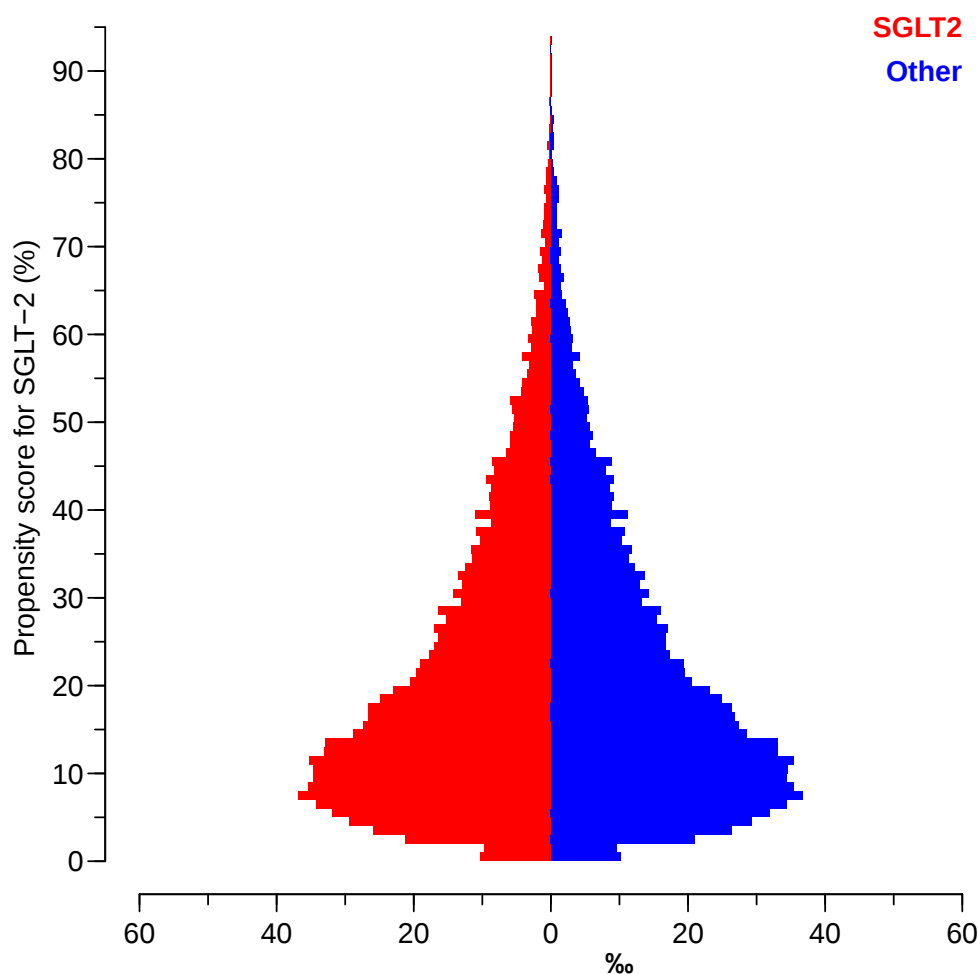


Figure 3.3: Propensity scores for the SGLT-2 group (left, percent) and other groups in the 1:1 propensity score matched study.

```

      [,1] [,2] [,3] [,4]
Index not FL: Mean / SD  8.9  8.9  5.2  5.6

> m.age <- with( mset, round( c( tapply( age, lxdx, mean ),
+                               tapply( age, lxdx, sd ) ), 1 ) )
> dim( m.age ) <- c(1,4)
> rownames( m.age ) <- c("Age: Mean / SD")
> m.age

      [,1] [,2] [,3] [,4]
Age: Mean / SD 60.4 60.4  11 12.7

> ## Date of index by 6 months and 1 year
> with( mset, ptab( floor( doIx*2 )/2 ) )

      SGLT2 Other SGLT2 Other
2012.5    20   109    0.1   0.6
2013     870   868    4.9   4.9
2013.5   1059  1007    6.0   5.7
2014     1383  1396    7.9   7.9
2014.5   1655  1485    9.4   8.4
2015     2280  2385   12.9  13.5

```

```
2015.5  2467  2555  14.0  14.5
2016    4020  3745  22.8  21.3
2016.5  3856  4060  21.9  23.1
```

```
> t.dat <- with( mset, ptab( floor( doIx ) ) )
> rownames( t.dat )[1] <- paste("Index date",rownames( t.dat )[1])
> ## Date of First Line
> t.fl <- with( mset, ptab( floor( doFL ) ) )
> rownames( t.fl )[1] <- paste("Date of first line",rownames( t.fl )[1])
> ## Frailty
> t.fr <- with( mset, ptab( frail ) )
> rownames( t.fr )[1] <- paste("Frailty",rownames( t.fr )[1])
> dm.tab <- rbind( t.sex, t.fl0, m.fl0, t.age, m.age, t.dat, t.fl, t.fr )
> dm.tab
```

	SGLT2	Other	SGLT2	Other
Sex M	10777.0	10801.0	61.2	61.3
F	6833.0	6809.0	38.8	38.7
Index = First Line	157.0	146.0	0.9	0.8
Index not FL: Mean / SD	8.9	8.9	5.2	5.6
Age at index <40	627.0	1023.0	3.6	5.8
40	2371.0	2600.0	13.5	14.8
50	5279.0	4704.0	30.0	26.7
60	5817.0	5160.0	33.0	29.3
70	3023.0	3153.0	17.2	17.9
80+	493.0	970.0	2.8	5.5
Age: Mean / SD	60.4	60.4	11.0	12.7
Index date 2012	20.0	109.0	0.1	0.6
2013	1929.0	1875.0	11.0	10.6
2014	3038.0	2881.0	17.3	16.4
2015	4747.0	4940.0	27.0	28.1
2016	7876.0	7805.0	44.7	44.3
Date of first line 1995	736.0	965.0	4.2	5.5
1996	293.0	330.0	1.7	1.9
1997	306.0	308.0	1.7	1.7
1998	412.0	433.0	2.3	2.5
1999	525.0	508.0	3.0	2.9
2000	562.0	595.0	3.2	3.4
2001	649.0	657.0	3.7	3.7
2002	750.0	695.0	4.3	3.9
2003	912.0	870.0	5.2	4.9
2004	945.0	893.0	5.4	5.1
2005	1044.0	943.0	5.9	5.4
2006	1171.0	1022.0	6.6	5.8
2007	1235.0	1096.0	7.0	6.2
2008	1284.0	1238.0	7.3	7.0
2009	1307.0	1190.0	7.4	6.8
2010	1299.0	1219.0	7.4	6.9
2011	1155.0	1191.0	6.6	6.8
2012	895.0	1060.0	5.1	6.0
2013	724.0	805.0	4.1	4.6
2014	591.0	664.0	3.4	3.8
2015	481.0	563.0	2.7	3.2
2016	334.0	365.0	1.9	2.1
Frailty 0	11622.0	11660.0	66.0	66.2
1	5988.0	5950.0	34.0	33.8

3.5.2 Comorbidities

The data frame contains the dates of the *earliest* recorded comorbidities from the NPR, hence the prefix `.prv`:

```
> wh <- match( rownames(ct.tab), names( mset ) )
> names( mset )[wh]

[1] "prv.FL"      "prv.TIA"      "prv.Angina"   "prv.Bleed"    "prv.COPD"     "prv.PAD"
[7] "prv.HF"      "prv.Cancer"   "prv.DMcompl"  "prv.Neuro"    "prv.DKD"      "prv.DiaEye"
[13] "prv.Hypo"    "prv.AtrFib"   "prv.MI"       "prv.UnstAng"  "prv.HmStr"     "prv.DiaFoot"
[19] "prv.Other"   "prv.PeriAng"  "prv.IscStr"   "prv.Amp"      "prv.CKD"       "prv.PCIsten"
[25] "prv.CABG"    "prv.Keto"     "prv.Dial"     "pre.CVD"      "pre.Str"       "pre.FPA"
[31] "pre.Mic"

> comorb <- mset[,wh]
> cm.tab <- cbind(
+ t( sapply( comorb,
+           function( x ) tapply( x, mset$Idxr, sum ) ) ),
+ round(
+ t( sapply( comorb,
+           function( x ) tapply( x, mset$Idxr, mean ) ) ) * 100, 1 ) )
> cm.tab
```

	SGLT2	Other	SGLT2	Other
prv.FL	17453	17464	99.1	99.2
prv.TIA	479	434	2.7	2.5
prv.Angina	2336	2371	13.3	13.5
prv.Bleed	731	692	4.2	3.9
prv.COPD	584	566	3.3	3.2
prv.PAD	861	839	4.9	4.8
prv.HF	701	737	4.0	4.2
prv.Cancer	861	906	4.9	5.1
prv.DMcompl	3274	3272	18.6	18.6
prv.Neuro	1027	998	5.8	5.7
prv.DKD	670	710	3.8	4.0
prv.DiaEye	2191	2271	12.4	12.9
prv.Hypo	613	594	3.5	3.4
prv.AtrFib	1039	991	5.9	5.6
prv.MI	1406	1399	8.0	7.9
prv.UnstAng	647	628	3.7	3.6
prv.HmStr	144	147	0.8	0.8
prv.DiaFoot	156	135	0.9	0.8
prv.Other	811	773	4.6	4.4
prv.PeriAng	898	894	5.1	5.1
prv.IscStr	824	825	4.7	4.7
prv.Amp	17	12	0.1	0.1
prv.CKD	101	81	0.6	0.5
prv.PCIsten	156	167	0.9	0.9
prv.CABG	475	464	2.7	2.6
prv.Keto	95	102	0.5	0.6
prv.Dial	1	0	0.0	0.0
pre.CVD	5248	5195	29.8	29.5
pre.Str	1258	1251	7.1	7.1
pre.FPA	997	975	5.7	5.5
pre.Mic	5988	5899	34.0	33.5

3.5.3 Other medication

We have variables that hold the last date of dispensation before index for all drugs of interest — well, only in the period after 2011-12-01, one year prior to the first SGLT2 dispensation.

```
> wh <- grep( "had.", names( mset ) )
> names( mset )[wh]
 [1] "had.ACE"      "had.Sta"      "had.BB1"      "had.ARB"      "had.A1A"
 [6] "had.DHP"      "had.WtL"      "had.RPA"      "had.Wrf"      "had.Asp"
[11] "had.HCD"      "had.THZ"      "had.Ccs"      "had.DXI"      "had.Dgo"
[16] "had.AP1"      "had.Ami"      "had.DTI"      "had.NHP"      "had.Fla"
[21] "had.Metformin" "had.GLP1"     "had.MetxSGLT2" "had.MetxDPP4" "had.SGLT2"
[26] "had.longIns"  "had.mixIns"   "had.DPP4"     "had.SU"       "had.intIns"
[31] "had.fastIns"  "had.TZD"      "had.Acarbose" "had.TZDxDPP4"

> codisp <- mset[,wh]
> ( names( codisp )[wh.ins <- grep("Ins",names(codisp))] )
 [1] "had.longIns" "had.mixIns" "had.intIns" "had.fastIns"
> ( names( codisp )[wh.hyp <- c(1,4,6,12,3)] )
 [1] "had.ACE" "had.ARB" "had.DHP" "had.THZ" "had.BB1"
> ( names( codisp )[wh.cvd <- c(8,2,wh.hyp)] )
 [1] "had.RPA" "had.Sta" "had.ACE" "had.ARB" "had.DHP" "had.THZ" "had.BB1"
> codisp <- transform( codisp, got.Ins = apply( codisp[,wh.ins], 1, max ),
+                       got.Hyp = apply( codisp[,wh.hyp], 1, max ),
+                       got.CVD = apply( codisp[,wh.cvd], 1, max ) )
> names( codisp )
 [1] "had.ACE"      "had.Sta"      "had.BB1"      "had.ARB"      "had.A1A"
 [6] "had.DHP"      "had.WtL"      "had.RPA"      "had.Wrf"      "had.Asp"
[11] "had.HCD"      "had.THZ"      "had.Ccs"      "had.DXI"      "had.Dgo"
[16] "had.AP1"      "had.Ami"      "had.DTI"      "had.NHP"      "had.Fla"
[21] "had.Metformin" "had.GLP1"     "had.MetxSGLT2" "had.MetxDPP4" "had.SGLT2"
[26] "had.longIns"  "had.mixIns"   "had.DPP4"     "had.SU"       "had.intIns"
[31] "had.fastIns"  "had.TZD"      "had.Acarbose" "had.TZDxDPP4" "got.Ins"
[36] "got.Hyp"      "got.CVD"

> mm.tab <- cbind(
+ t( sapply( codisp,
+           function( x ) tapply( x, mset$Ixdr, sum ) ) ),
+ round(
+ t( sapply( codisp,
+           function( x ) tapply( x, mset$Ixdr, mean ) ) ) * 100, 1 ) )
> mm.tab
```

	SGLT2	Other	SGLT2	Other
had.ACE	6802	6962	38.6	39.5
had.Sta	13204	13336	75.0	75.7
had.BB1	4755	4740	27.0	26.9
had.ARB	6072	6075	34.5	34.5
had.A1A	883	898	5.0	5.1
had.DHP	5337	5354	30.3	30.4
had.WtL	120	129	0.7	0.7
had.RPA	1131	1165	6.4	6.6
had.Wrf	719	687	4.1	3.9
had.Asp	6205	6309	35.2	35.8
had.HCD	2321	2313	13.2	13.1
had.THZ	2684	2717	15.2	15.4
had.Ccs	925	923	5.3	5.2

had.DXI	287	274	1.6	1.6
had.Dgo	433	424	2.5	2.4
had.APl	174	182	1.0	1.0
had.Ami	39	36	0.2	0.2
had.DTI	216	213	1.2	1.2
had.NHP	292	269	1.7	1.5
had.Fla	15	13	0.1	0.1
had.Metformin	11333	11345	64.4	64.4
had.GLP1	4419	4296	25.1	24.4
had.MetxSGLT2	0	0	0.0	0.0
had.MetxDPP4	3149	3174	17.9	18.0
had.SGLT2	0	1	0.0	0.0
had.longIns	2351	2315	13.4	13.1
had.mixIns	984	1023	5.6	5.8
had.DPP4	3060	3115	17.4	17.7
had.SU	4074	4116	23.1	23.4
had.intIns	928	939	5.3	5.3
had.fastIns	1027	1008	5.8	5.7
had.TZD	56	58	0.3	0.3
had.Acarbose	32	35	0.2	0.2
had.TZDxDPP4	1	0	0.0	0.0
got.Ins	4042	4241	23.0	24.1
got.Hyp	13759	13641	78.1	77.5
got.CVD	16016	15743	90.9	89.4

3.6 Overview of pre- and post matching

The number of persons and episodes:

```
> addmargins( with( oset, table(table(pnr)) ) )
```

	1	2	3	4	5	6	7	8	9	10	11	Sum
	99132	36028	13706	5015	1596	464	143	49	12	2	1	156148

```
> addmargins(
+ with( oset, table(DPP4=(tt<-table(pnr,Ixdr))[,1],SGLT2=tt[,2]) ) )
```

	SGLT2											
DPP4	0	1	2	3	4	5	6	7	8	9	10	Sum
0	0	94727	30195	9798	3142	847	227	61	12	4	0	139013
1	4405	5720	3758	1746	678	205	64	24	4	1	1	16606
2	113	148	124	69	31	15	11	3	1	0	0	515
3	2	3	2	1	3	2	1	0	0	0	0	14
Sum	4520	100598	34079	11614	3854	1069	303	88	17	5	1	156148

```
> addmargins( with( mset, table(table(pnr)) ) )
```

	1	2	3	4	5	6	Sum
	26625	3530	439	48	4	1	30647

```
> addmargins(
+ with( mset, table(DPP4=(tt<-table(pnr,Ixdr))[,1],SGLT2=tt[,2]) ) )
```

	SGLT2						
DPP4	0	1	2	3	4	5	Sum
0	0	12165	1261	137	12	1	13576
1	14460	1826	228	29	2	1	16546
2	443	62	6	0	0	0	511
3	12	1	1	0	0	0	14
Sum	14915	14054	1496	166	14	2	30647

The best overview is created if we list the tables for the matched and un-matched next to each other. However we first check that that have the same sets of rows:

```
> identical( rownames(dt.tab), rownames(dm.tab) )
[1] TRUE
> identical( rownames(ct.tab), rownames(cm.tab) )
[1] TRUE
> identical( rownames(mt.tab), rownames(mm.tab) )
[1] TRUE
```

```
> cbind( dt.tab, dm.tab )
```

	SGLT2	Other	SGLT2	Other	SGLT2	Other	SGLT2	Other
Sex M	10822.0	132244.0	61.2	58.3	10777.0	10801.0	61.2	61.3
F	6856.0	94740.0	38.8	41.7	6833.0	6809.0	38.8	38.7
Index = First Line	157.0	70185.0	0.9	30.9	157.0	146.0	0.9	0.8
Index not FL: Mean / SD	8.9	8.4	5.2	5.7	8.9	8.9	5.2	5.6
Age at index <40	630.0	11106.0	3.6	4.9	627.0	1023.0	3.6	5.8
40	2379.0	27582.0	13.5	12.2	2371.0	2600.0	13.5	14.8
50	5310.0	50352.0	30.0	22.2	5279.0	4704.0	30.0	26.7
60	5838.0	63988.0	33.0	28.2	5817.0	5160.0	33.0	29.3
70	3028.0	50123.0	17.1	22.1	3023.0	3153.0	17.2	17.9
80+	493.0	23833.0	2.8	10.5	493.0	970.0	2.8	5.5
Age: Mean / SD	60.4	63.2	11.0	13.6	60.4	60.4	11.0	12.7
Index date 2012	20.0	4468.0	0.1	2.0	20.0	109.0	0.1	0.6
2013	1929.0	53123.0	10.9	23.4	1929.0	1875.0	11.0	10.6
2014	3038.0	52261.0	17.2	23.0	3038.0	2881.0	17.3	16.4
2015	4761.0	56853.0	26.9	25.0	4747.0	4940.0	27.0	28.1
2016	7930.0	60279.0	44.9	26.6	7876.0	7805.0	44.7	44.3
Date of first line 1995	739.0	10675.0	4.2	4.7	736.0	965.0	4.2	5.5
1996	294.0	3164.0	1.7	1.4	293.0	330.0	1.7	1.9
1997	306.0	3145.0	1.7	1.4	306.0	308.0	1.7	1.7
1998	415.0	4008.0	2.3	1.8	412.0	433.0	2.3	2.5
1999	525.0	4604.0	3.0	2.0	525.0	508.0	3.0	2.9
2000	564.0	4963.0	3.2	2.2	562.0	595.0	3.2	3.4
2001	652.0	5527.0	3.7	2.4	649.0	657.0	3.7	3.7
2002	753.0	5860.0	4.3	2.6	750.0	695.0	4.3	3.9
2003	919.0	7273.0	5.2	3.2	912.0	870.0	5.2	4.9
2004	953.0	7504.0	5.4	3.3	945.0	893.0	5.4	5.1
2005	1048.0	8005.0	5.9	3.5	1044.0	943.0	5.9	5.4
2006	1173.0	8560.0	6.6	3.8	1171.0	1022.0	6.6	5.8
2007	1242.0	9342.0	7.0	4.1	1235.0	1096.0	7.0	6.2
2008	1288.0	10100.0	7.3	4.4	1284.0	1238.0	7.3	7.0
2009	1315.0	10342.0	7.4	4.6	1307.0	1190.0	7.4	6.8
2010	1301.0	11079.0	7.4	4.9	1299.0	1219.0	7.4	6.9
2011	1158.0	11679.0	6.6	5.1	1155.0	1191.0	6.6	6.8
2012	900.0	11901.0	5.1	5.2	895.0	1060.0	5.1	6.0
2013	725.0	25332.0	4.1	11.2	724.0	805.0	4.1	4.6
2014	593.0	21549.0	3.4	9.5	591.0	664.0	3.4	3.8
2015	481.0	21609.0	2.7	9.5	481.0	563.0	2.7	3.2
2016	334.0	20763.0	1.9	9.1	334.0	365.0	1.9	2.1
Frailty 0	11663.0	145101.0	66.0	63.9	11622.0	11660.0	66.0	66.2
1	6015.0	81883.0	34.0	36.1	5988.0	5950.0	34.0	33.8

```
> cbind( ct.tab, cm.tab )
```

	SGLT2	Other	SGLT2	Other	SGLT2	Other	SGLT2	Other
prv.FL	17521	156799	99.1	69.1	17453	17464	99.1	99.2
prv.TIA	480	7881	2.7	3.5	479	434	2.7	2.5
prv.Angina	2348	29626	13.3	13.1	2336	2371	13.3	13.5
prv.Bleed	737	13032	4.2	5.7	731	692	4.2	3.9
prv.COPD	584	12222	3.3	5.4	584	566	3.3	3.2
prv.PAD	861	15553	4.9	6.9	861	839	4.9	4.8
prv.HF	702	13182	4.0	5.8	701	737	4.0	4.2
prv.Cancer	862	20305	4.9	8.9	861	906	4.9	5.1
prv.DMcompl	3297	27477	18.7	12.1	3274	3272	18.6	18.6
prv.Neuro	1032	9309	5.8	4.1	1027	998	5.8	5.7
prv.DKD	671	8484	3.8	3.7	670	710	3.8	4.0
prv.DiaEye	2204	20020	12.5	8.8	2191	2271	12.4	12.9
prv.Hypo	613	8993	3.5	4.0	613	594	3.5	3.4
prv.AtrFib	1042	18499	5.9	8.1	1039	991	5.9	5.6
prv.MI	1412	19911	8.0	8.8	1406	1399	8.0	7.9
prv.UnstAng	653	8459	3.7	3.7	647	628	3.7	3.6
prv.HmStr	144	2642	0.8	1.2	144	147	0.8	0.8
prv.DiaFoot	156	2295	0.9	1.0	156	135	0.9	0.8
prv.Other	814	11625	4.6	5.1	811	773	4.6	4.4
prv.PeriAng	902	10607	5.1	4.7	898	894	5.1	5.1
prv.IscStr	828	15774	4.7	6.9	824	825	4.7	4.7
prv.Amp	17	543	0.1	0.2	17	12	0.1	0.1
prv.CKD	101	6537	0.6	2.9	101	81	0.6	0.5
prv.PCIsten	156	2317	0.9	1.0	156	167	0.9	0.9
prv.CABG	477	6534	2.7	2.9	475	464	2.7	2.6
prv.Keto	95	2156	0.5	0.9	95	102	0.5	0.6
prv.Dial	1	80	0.0	0.0	1	0	0.0	0.0
pre.CVD	5268	76805	29.8	33.8	5248	5195	29.8	29.5
pre.Str	1263	22710	7.1	10.0	1258	1251	7.1	7.1
pre.FPA	1001	12080	5.7	5.3	997	975	5.7	5.5
pre.Mic	6021	53275	34.1	23.5	5988	5899	34.0	33.5

```
> cbind( mt.tab, mm.tab )
```

	SGLT2	Other	SGLT2	Other	SGLT2	Other	SGLT2	Other
had.ACE	6830	72133	38.6	31.8	6802	6962	38.6	39.5
had.Sta	13263	126144	75.0	55.6	13204	13336	75.0	75.7
had.BB1	4771	63033	27.0	27.8	4755	4740	27.0	26.9
had.ARB	6104	56367	34.5	24.8	6072	6075	34.5	34.5
had.A1A	883	14102	5.0	6.2	883	898	5.0	5.1
had.DHP	5354	59189	30.3	26.1	5337	5354	30.3	30.4
had.WtL	120	1029	0.7	0.5	120	129	0.7	0.7
had.RPA	1134	16626	6.4	7.3	1131	1165	6.4	6.6
had.Wrf	721	14724	4.1	6.5	719	687	4.1	3.9
had.Asp	6226	68351	35.2	30.1	6205	6309	35.2	35.8
had.HCD	2330	44177	13.2	19.5	2321	2313	13.2	13.1
had.THZ	2697	33724	15.3	14.9	2684	2717	15.2	15.4
had.Ccs	925	21060	5.2	9.3	925	923	5.3	5.2
had.DXI	288	4525	1.6	2.0	287	274	1.6	1.6
had.Dgo	434	10410	2.5	4.6	433	424	2.5	2.4
had.AP1	175	3882	1.0	1.7	174	182	1.0	1.0
had.Ami	39	1328	0.2	0.6	39	36	0.2	0.2
had.DTI	218	3451	1.2	1.5	216	213	1.2	1.2
had.NHP	297	3665	1.7	1.6	292	269	1.7	1.5
had.Fla	15	200	0.1	0.1	15	13	0.1	0.1
had.Metformin	11391	80273	64.4	35.4	11333	11345	64.4	64.4
had.GLP1	4470	13314	25.3	5.9	4419	4296	25.1	24.4
had.MetxSGLT2	0	215	0.0	0.1	0	0	0.0	0.0

```

had.MetxDPP4    3192    8967    18.1    4.0    3149    3174    17.9    18.0
had.SGLT2         0    5432     0.0    2.4         0         1     0.0     0.0
had.longIns     2375   11834    13.4    5.2   2351   2315    13.4    13.1
had.mixIns       984   11555     5.6    5.1    984   1023     5.6     5.8
had.DPP4        3085   14701    17.5    6.5   3060   3115    17.4    17.7
had.SU          4095   30627    23.2   13.5   4074   4116    23.1    23.4
had.intIns       932   13647     5.3    6.0    928    939     5.3     5.3
had.fastIns     1034    7846     5.8    3.5   1027   1008     5.8     5.7
had.TZD          58     224     0.3    0.1     56     58     0.3     0.3
had.Acarbose     32     229     0.2    0.1     32     35     0.2     0.2
had.TZDxDPP4      1         1     0.0    0.0         1         0     0.0     0.0
got.Ins         4067   36359    23.0   16.0   4042   4241    23.0    24.1
got.Hyp        13819  152904    78.2   67.4  13759  13641    78.1    77.5
got.CVD        16183  176968    91.5   78.0  16016  15743    90.9    89.4

```

```

> save( dt.tab, dm.tab,
+       ct.tab, cm.tab,
+       mt.tab, mm.tab, file="btabSGoth.Rda" )

```

3.7 Survival analysis datasets: Lexis objects

In this section we take the original and the matched data and set up Lexis-objects for the survival analyses; we make separate objects for Death, heart failure (HF) and combined outcomes.

First get the relevant data:

```

> library( Epi )
> library( survival )
> print( sessionInfo(), l=F )
R version 3.5.0 (2018-04-23)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows Server 2012 R2 x64 (build 9600)

```

Matrix products: default

attached base packages:

```
[1] stats      graphics  grDevices  utils      datasets  methods    base
```

other attached packages:

```
[1] survival_2.41-3 Epi_2.30
```

loaded via a namespace (and not attached):

```

[1] cmprsk_2.2-7      zoo_1.8-1          MASS_7.3-49        compiler_3.5.0
[5] Matrix_1.2-14     plyr_1.8.4         parallel_3.5.0     tools_3.5.0
[9] etm_0.6-2         Rcpp_0.12.16       splines_3.5.0      grid_3.5.0
[13] numDeriv_2016.8-1 lattice_0.20-35

```

```

> clear()
> load( file = "adatSGoth.Rda" )
> lls()

```

	name	mode	class	dim	size(Kb)
1	mset	list	data.frame	35220 171	53,136.6
2	oset	list	data.frame	244662 171	355,719.3
3	pscore	numeric	table	96 2	7.8
4	psmatch	numeric	table	94 2	7.7

```

...now input from ../rep/anaSGoth.tex
> cbind( table( apply( table(mset$pnr,mset$Ixdr), 1, paste, collapse="-") ) )
      [,1]
0-1 12165
0-2  1261
0-3   137
0-4    12
0-5     1
1-0 14460
1-1  1826
1-2   228
1-3    29
1-4     2
1-5     1
2-0   443
2-1    62
2-2     6
3-0    12
3-1     1
3-2     1

```

We will follow persons in episodes from date of new use, `doIx`, till either date of event.

For later use we define both the time since index (`tfi`) and current date (period — `per`) and current age (`cua`) as timescales. The latter not to be confused with age at index date, `age`.

3.8 Collecting analysis results and key data

We want to collect analysis results and background data for the analyses. The latter are classified by index drug and PY/events, the former by adjusted/non-adjusted analysis and HR/c.i./s.e. In addition both are classified by endpoint, data, and subset:

```

> lst <- list( endp = c("HF", "ACD", "ACD+HF", "CVDD", "MI", "Str", "IscStr",
+                      "CVDD+MI+Str", "ACD+MI+Str", "DKD"),
+             data = c("OnDr", "Total"),
+             sub = c("AllPtt", "preCVD", "noCVD") )
> dat <- NArray( c( lst, list( ix = c("SGLT2", "Other"),
+                               dat = c("N", "PY", "Event") ) ) )
> res <- NArray( c( lst, list( adj = c("Raw", "Adj"),
+                               res = c("HR", "lo", "up", "se") ) ) )
> length( dat ) ; str( dat )
[1] 360
logi [1:10, 1:2, 1:3, 1:2, 1:3] NA NA NA NA NA NA ...
- attr(*, "dimnames")=List of 5
..$ endp: chr [1:10] "HF" "ACD" "ACD+HF" "CVDD" ...
..$ data: chr [1:2] "OnDr" "Total"
..$ sub : chr [1:3] "AllPtt" "preCVD" "noCVD"
..$ ix : chr [1:2] "SGLT2" "Other"
..$ dat : chr [1:3] "N" "PY" "Event"
> length( res ) ; str( res )
[1] 480
logi [1:10, 1:2, 1:3, 1:2, 1:4] NA NA NA NA NA NA ...
- attr(*, "dimnames")=List of 5
..$ endp: chr [1:10] "HF" "ACD" "ACD+HF" "CVDD" ...

```

```

..$ data: chr [1:2] "OnDr" "Total"
..$ sub : chr [1:3] "AllPtt" "preCVD" "noCVD"
..$ adj : chr [1:2] "Raw" "Adj"
..$ res : chr [1:4] "HR" "lo" "up" "se"

```

3.9 Survival dataset: Lexis objects

Here is a definition of a function that produces a Lexis object with follow-up till `mset$doX` for the event D:

```

> mkLex <-
+ function( )
+ {
+   Lx <- Lexis( entry = list( per = doIx,
+                             cua = doIx-doBth,
+                             tfi = 0 ),
+               exit = list( per = doX ),
+               exit.status = factor( D, labels=c("OnDr","Event") ),
+               data = subset( mset, is.na(doDth) | doIx < doDth ) )
+   Lx <- cutLexis( Lx, cut = Lx$doTm,
+                  new.state = "OffDr",
+                  pre = "OnDr" )
+   Lx
+ }
> mset$D <- with( mset, !is.na(deHF) & deHF<2017 )
> mset$doX <- with( mset, pmin( doDth, deHF, 2017, na.rm=TRUE ) )
> lxHF <- mkLex( )

```

NOTE: entry.status has been set to "OnDr" for all.

```
> summary( lxHF )
```

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	25766	9054	400	35220	9454	38479.17	35220
OffDr	0	8947	107	9054	107	10025.73	9054
Sum	25766	18001	507	44274	9561	48504.90	35220

```
> summary( lxHF, by="Ixdr" )
```

\$SGLT2

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	12572	4887	151	17610	5038	18851.19	17610
OffDr	0	4819	68	4887	68	5592.04	4887
Sum	12572	9706	219	22497	5106	24443.23	17610

\$Other

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	13194	4167	249	17610	4416	19627.99	17610
OffDr	0	4128	39	4167	39	4433.69	4167
Sum	13194	8295	288	21777	4455	24061.68	17610

3.9.1 Follow-up data and events

First we devise a function to extract the person-years and events from the Lexis object:

```
> fill.dat <-
+ function( LexDat, outc )
+ {
+   whc <- c(" Persons:", "Risk time:", "Event")
+   cat( outc, ":\n" )
+   print( sm <- summary( LexDat, by="IxdR" ) )
+   s2 <- summary( LexDat, by=c("IxdR", "pre.CVD" ) )
+   for( ix in c("Other", "SGLT2" ) )
+     {
+       dat[outc, "AllPtt", ix,] <- sm[[ix]][[1]][c(1,3), whc]
+       dat[outc, "noCVD", ix,] <- s2[[paste(ix, 0, sep=".")]][[1]][c(1,3), whc]
+       dat[outc, "preCVD", ix,] <- s2[[paste(ix, 1, sep=".")]][[1]][c(1,3), whc]
+     }
+   invisible(NULL)
+ }
> fill.dat( lxHF, "HF" )
```

HF :

\$SGLT2

Transitions:

From	To	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	OnDr	12572	4887	151	17610	5038	18851.19	17610
OffDr	OffDr	0	4819	68	4887	68	5592.04	4887
Sum	Sum	12572	9706	219	22497	5106	24443.23	17610

\$Other

Transitions:

From	To	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	OnDr	13194	4167	249	17610	4416	19627.99	17610
OffDr	OffDr	0	4128	39	4167	39	4433.69	4167
Sum	Sum	13194	8295	288	21777	4455	24061.68	17610

```
> round( ftable( dat[1:2,,,], col.vars=c(4,5) ), 1 )
```

			ix	SGLT2	Other				
			dat	N	PY	Event	N	PY	Event
endp	data	sub							
HF	OnDr	AllPtt		17610.0	18851.2	151.0	17610.0	19628.0	249.0
		preCVD		5248.0	5334.9	124.0	5195.0	5350.6	189.0
		noCVD		12362.0	13516.3	27.0	12415.0	14277.4	60.0
	Total	AllPtt		17610.0	24443.2	219.0	17610.0	24061.7	288.0
		preCVD		5248.0	6964.6	173.0	5195.0	6598.4	214.0
		noCVD		12362.0	17478.6	46.0	12415.0	17463.3	74.0
ACD	OnDr	AllPtt		NA	NA	NA	NA	NA	NA
		preCVD		NA	NA	NA	NA	NA	NA
		noCVD		NA	NA	NA	NA	NA	NA
	Total	AllPtt		NA	NA	NA	NA	NA	NA
		preCVD		NA	NA	NA	NA	NA	NA
		noCVD		NA	NA	NA	NA	NA	NA

3.9.2 Analysis

Follow-up is now analysed by Cox-models adjusted and non-adjusted, total or on drug and separately for all persons and persons with and without prior CVD. These are named with an *m.* and combination of *r/a* (raw/adjusted), *t/d* (total/on drug) and *p/n/y* (patients/no CVD/yes CVD):

```
> m.tpr <- coxph( Surv( tfi, tfi+lex.dur, lex.Xst=="Event" ) ~
+               I(Ixdr=="SGLT2") + cluster(pnr),
+               data = lxHF )
> m.tpa <- update( m.tpr, . ~ . + I(doIx-doBth) + sex + I(doIx-doDM)
+               + prv.MI + prv.HF + prv.AtrFib + frail
+               + had.BBl + had.NHP + had.Ala + had.ACE )
> m.dpr <- update( m.tpr, data = subset( lxHF, lex.Cst=="OnDr" ) )
> m.dpa <- update( m.tpa, data = subset( lxHF, lex.Cst=="OnDr" ) )
> m.tnr <- update( m.tpr, data = subset( lxHF, pre.CVD==1 ) )
> m.tna <- update( m.tpa, data = subset( lxHF, pre.CVD==1 ) )
> m.dnr <- update( m.dpr, data = subset( lxHF, pre.CVD==1 & lex.Cst=="OnDr" ) )
> m.dna <- update( m.dpa, data = subset( lxHF, pre.CVD==1 & lex.Cst=="OnDr" ) )
> m.tyr <- update( m.tpr, data = subset( lxHF, pre.CVD==0 ) )
> m.tya <- update( m.tpa, data = subset( lxHF, pre.CVD==0 ) )
> m.dyr <- update( m.dpr, data = subset( lxHF, pre.CVD==0 & lex.Cst=="OnDr" ) )
> m.dya <- update( m.dpa, data = subset( lxHF, pre.CVD==0 & lex.Cst=="OnDr" ) )
```

With these models fitted we can now extract the HRs etc. and put into the right slots of *res*:

```
> get4 <- function( m ) ci.lin( m, subset="SGLT2", Exp=TRUE )[,c(5:7,2)]
> res["HF","Total","AllPtt","Raw",] <- get4( m.tpr )
> res["HF","Total","AllPtt","Adj",] <- get4( m.tpa )
> res["HF","OnDr","AllPtt","Raw",] <- get4( m.dpr )
> res["HF","OnDr","AllPtt","Adj",] <- get4( m.dpa )
> res["HF","Total","preCVD","Raw",] <- get4( m.tnr )
> res["HF","Total","preCVD","Adj",] <- get4( m.tna )
> res["HF","OnDr","preCVD","Raw",] <- get4( m.dnr )
> res["HF","OnDr","preCVD","Adj",] <- get4( m.dna )
> res["HF","Total","noCVD","Raw",] <- get4( m.tyr )
> res["HF","Total","noCVD","Adj",] <- get4( m.tya )
> res["HF","OnDr","noCVD","Raw",] <- get4( m.dyr )
> res["HF","OnDr","noCVD","Adj",] <- get4( m.dya )
```

This can now be packed into a function that does this for a given type of event:

```
> fill.res <- function( LexDat, outc )
+ {
+   m.tpr <- coxph( Surv( tfi, tfi+lex.dur, lex.Xst=="Event" ) ~
+               I(Ixdr=="SGLT2") + cluster(pnr),
+               data = LexDat )
+   m.tpa <- update( m.tpr, . ~ . + I(doIx-doBth) + sex + I(doIx-doDM)
+               + prv.MI + prv.HF + prv.AtrFib + frail
+               + had.BBl + had.NHP + had.Ala + had.ACE )
+   m.dpr <- update( m.tpr, data = subset( LexDat, lex.Cst=="OnDr" ) )
+   m.dpa <- update( m.tpa, data = subset( LexDat, lex.Cst=="OnDr" ) )
+   m.tnr <- update( m.tpr, data = subset( LexDat, pre.CVD==1 ) )
+   m.tna <- update( m.tpa, data = subset( LexDat, pre.CVD==1 ) )
+   m.dnr <- update( m.dpr, data = subset( LexDat, pre.CVD==1 & lex.Cst=="OnDr" ) )
+   m.dna <- update( m.dpa, data = subset( LexDat, pre.CVD==1 & lex.Cst=="OnDr" ) )
+ }
```

```

+
+ m.tyr <- update( m.tpr, data = subset( LexDat, pre.CVD==0 ) )
+ m.tya <- update( m.tpa, data = subset( LexDat, pre.CVD==0 ) )
+ m.dyr <- update( m.dpr, data = subset( LexDat, pre.CVD==0 & lex.Cst=="OnDr" ) )
+ m.dya <- update( m.dpa, data = subset( LexDat, pre.CVD==0 & lex.Cst=="OnDr" ) )
+
+ res[outc,"Total","AllPtt","Raw",] <- get4( m.tpr )
+ res[outc,"Total","AllPtt","Adj",] <- get4( m.tpa )
+ res[outc,"OnDr","AllPtt","Raw",] <- get4( m.dpr )
+ res[outc,"OnDr","AllPtt","Adj",] <- get4( m.dpa )
+
+ res[outc,"Total","preCVD","Raw",] <- get4( m.tnr )
+ res[outc,"Total","preCVD","Adj",] <- get4( m.tna )
+ res[outc,"OnDr","preCVD","Raw",] <- get4( m.dnr )
+ res[outc,"OnDr","preCVD","Adj",] <- get4( m.dna )
+
+ res[outc,"Total","noCVD","Raw",] <- get4( m.tyr )
+ res[outc,"Total","noCVD","Adj",] <- get4( m.tya )
+ res[outc,"OnDr","noCVD","Raw",] <- get4( m.dyr )
+ res[outc,"OnDr","noCVD","Adj",] <- get4( m.dya )
+ invisible( NULL )
+ }

```

So combining this with the function that constructs the *Lexis* object we get:

```

> mset$D <- with( mset, !is.na(deHF) & deHF<2017 )
> mset$doX <- with( mset, pmin( doDth, deHF, 2017, na.rm=TRUE ) )
> lxHF <- mkLex()

```

NOTE: entry.status has been set to "OnDr" for all.

```

> fill.res( lxHF, "HF" )
> round( ftable( res[1:2,,,], col.vars=c(2,5) ), 3 )

```

			data	OnDr			Total				
			res	HR	lo	up	se	HR	lo	up	se
endp	sub	adj									
HF	AllPtt	Raw		0.621	0.508	0.759	0.102	0.750	0.628	0.894	0.090
		Adj		0.614	0.502	0.752	0.103	0.739	0.617	0.884	0.092
	preCVD	Raw		0.653	0.521	0.818	0.115	0.773	0.633	0.942	0.101
		Adj		0.655	0.522	0.822	0.116	0.772	0.631	0.945	0.103
	noCVD	Raw		0.469	0.297	0.740	0.233	0.619	0.424	0.903	0.193
		Adj		0.469	0.297	0.741	0.233	0.616	0.421	0.900	0.194
ACD	AllPtt	Raw		NA	NA	NA	NA	NA	NA	NA	NA
		Adj		NA	NA	NA	NA	NA	NA	NA	NA
	preCVD	Raw		NA	NA	NA	NA	NA	NA	NA	NA
		Adj		NA	NA	NA	NA	NA	NA	NA	NA
	noCVD	Raw		NA	NA	NA	NA	NA	NA	NA	NA
		Adj		NA	NA	NA	NA	NA	NA	NA	NA

So we just repeat this for all types of outcome:

```

> mset$D <- with( mset, !is.na(doDth) & doDth<2017 )
> mset$doX <- with( mset, pmin( doDth, 2017, na.rm=TRUE ) )
> lxACD <- mkLex()

```

NOTE: entry.status has been set to "OnDr" for all.

```

> fill.res( lxACD, "ACD" )
> fill.dat( lxACD, "ACD" )

```

```
ACD :
$SGLT2
```

```
Transitions:
  To
```

From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	12492	4942	176	17610	5118	18960.02	17610
OffDr	0	4818	124	4942	124	5704.68	4942
Sum	12492	9760	300	22552	5242	24664.70	17610

```
$Other
```

```
Transitions:
  To
```

From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	12857	4235	518	17610	4753	19839.60	17610
OffDr	0	4096	139	4235	139	4523.57	4235
Sum	12857	8331	657	21845	4892	24363.18	17610

```
> mset$D <- with( mset, ( !is.na(deHF) | !is.na(doDth) ) &
+                  ( deHF<2017 | doDth<2017 ) )
> mset$doX <- with( mset, pmin( doDth, deHF, 2017, na.rm=TRUE ) )
> lxACDHF <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxACDHF, "ACD+HF" )
> fill.dat( lxACDHF, "ACD+HF" )
```

```
ACD+HF :
$SGLT2
```

```
Transitions:
  To
```

From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	12399	4887	324	17610	5211	18851.19	17610
OffDr	0	4703	184	4887	184	5592.04	4887
Sum	12399	9590	508	22497	5395	24443.23	17610

```
$Other
```

```
Transitions:
  To
```

From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	12719	4167	724	17610	4891	19627.99	17610
OffDr	0	4002	165	4167	165	4433.69	4167
Sum	12719	8169	889	21777	5056	24061.68	17610

```
> mset$D <- with( mset, !is.na(deCVDD) & deCVDD<2017 )
> mset$doX <- with( mset, pmin( doDth, deCVDD, 2017, na.rm=TRUE ) )
> lxCVDD <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxCVDD, "CVDD" )
> fill.dat( lxCVDD, "CVDD" )
```

```
CVDD :
$SGLT2
```

```
Transitions:
  To
```

From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	12640	4942	28	17610	4970	18960.02	17610
OffDr	0	4919	23	4942	23	5704.68	4942
Sum	12640	9861	51	22552	4993	24664.70	17610

\$Other

Transitions:

To

From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	13281	4235	94	17610	4329	19839.60	17610
OffDr	0	4209	26	4235	26	4523.57	4235
Sum	13281	8444	120	21845	4355	24363.18	17610

```
> mset$D <- with( mset, !is.na(deMI) & deMI<2017 )
> mset$doX <- with( mset, pmin( doDth, deMI, 2017, na.rm=TRUE ) )
> lxMI <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxMI, "MI" )
> fill.dat( lxMI, "MI" )
```

MI :

\$SGLT2

Transitions:

To

From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	12594	4912	104	17610	5016	18884.71	17610
OffDr	0	4877	35	4912	35	5645.23	4912
Sum	12594	9789	139	22522	5051	24529.94	17610

\$Other

Transitions:

To

From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	13273	4203	134	17610	4337	19726.99	17610
OffDr	0	4172	31	4203	31	4467.15	4203
Sum	13273	8375	165	21813	4368	24194.14	17610

```
> mset$D <- with( mset, !is.na(deStr) & deStr<2017 )
> mset$doX <- with( mset, pmin( doDth, deStr, 2017, na.rm=TRUE ) )
> lxStr <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxStr, "Str" )
> fill.dat( lxStr, "Str" )
```

Str :

\$SGLT2

Transitions:

To

From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	12594	4905	111	17610	5016	18876.26	17610
OffDr	0	4870	35	4905	35	5638.26	4905
Sum	12594	9775	146	22515	5051	24514.52	17610

\$Other

Transitions:

From	To	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	OnDr	13264	4200	146	17610	4346	19731.68	17610
OffDr	OffDr	0	4166	34	4200	34	4460.67	4200
Sum	Sum	13264	8366	180	21810	4380	24192.34	17610

```
> mset$D <- with( mset, !is.na(deIscStr) & deIscStr<2017 )
> mset$doX <- with( mset, pmin( doDth, deIscStr, 2017, na.rm=TRUE ) )
> lxIcStr <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxIcStr, "IscStr" )
> fill.dat( lxIcStr, "IscStr" )
```

IscStr :
\$SGLT2

Transitions:

From	To	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	OnDr	12598	4909	103	17610	5012	18880.17	17610
OffDr	OffDr	0	4881	28	4909	28	5645.92	4909
Sum	Sum	12598	9790	131	22519	5040	24526.08	17610

\$Other

Transitions:

From	To	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	OnDr	13275	4206	129	17610	4335	19743.20	17610
OffDr	OffDr	0	4174	32	4206	32	4468.83	4206
Sum	Sum	13275	8380	161	21816	4367	24212.03	17610

```
> mset$D <- with( mset, ( ( !is.na(deCVDD) & deCVDD < 2017 ) |
+ ( !is.na(deMI) & deMI < 2017 ) |
+ ( !is.na(deStr) & deStr < 2017 ) ) )
> mset$doX <- with( mset, pmin( doDth, deCVDD, deMI, deStr, 2017, na.rm=TRUE ) )
> lxCVDDx <- mkLex()
```

NOTE: entry.status has been set to "OnDr" for all.

```
> fill.res( lxCVDDx, "CVDD+MI+Str" )
> fill.dat( lxCVDDx, "CVDD+MI+Str" )
```

CVDD+MI+Str :
\$SGLT2

Transitions:

From	To	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	OnDr	12499	4876	235	17610	5111	18802.67	17610
OffDr	OffDr	0	4793	83	4876	83	5581.85	4876
Sum	Sum	12499	9669	318	22486	5194	24384.52	17610

\$Other

Transitions:

From	To	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	OnDr	12499	4876	235	17610	5111	18802.67	17610
OffDr	OffDr	0	4793	83	4876	83	5581.85	4876
Sum	Sum	12499	9669	318	22486	5194	24384.52	17610

```

OnDr 13094 4168 348 17610 4516 19621.37 17610
OffDr 0 4084 84 4168 84 4404.24 4168
Sum 13094 8252 432 21778 4600 24025.62 17610
> mset$D <- with( mset, ( ( !is.na(doDth) & doDth < 2017 ) |
+ ( !is.na(deMI) & deMI < 2017 ) |
+ ( !is.na(deStr) & deStr < 2017 ) ) )
> mset$doX <- with( mset, pmin( doDth, deMI, deStr, 2017, na.rm=TRUE ) )
> lxACDx <- mkLex()

```

NOTE: entry.status has been set to "OnDr" for all.

```

> fill.res( lxACDx, "ACD+MI+Str" )
> fill.dat( lxACDx, "ACD+MI+Str" )

```

ACD+MI+Str :
\$SGLT2

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	12356	4876	378	17610	5254	18802.67	17610
OffDr	0	4699	177	4876	177	5581.85	4876
Sum	12356	9575	555	22486	5431	24384.52	17610

\$Other

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	12684	4168	758	17610	4926	19621.37	17610
OffDr	0	3976	192	4168	192	4404.24	4168
Sum	12684	8144	950	21778	5118	24025.62	17610

```

> mset$D <- with( mset, !is.na(deDKD) & deDKD<2017 )
> mset$doX <- with( mset, pmin( doDth, deDKD, 2017, na.rm=TRUE ) )
> lxKid <- mkLex()

```

NOTE: entry.status has been set to "OnDr" for all.

```

> fill.res( lxKid, "DKD" )
> fill.dat( lxKid, "DKD" )

```

DKD :
\$SGLT2

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	12583	4890	137	17610	5027	18845.32	17610
OffDr	0	4845	45	4890	45	5610.39	4890
Sum	12583	9735	182	22500	5072	24455.71	17610

\$Other

Transitions:

	To						
From	OnDr	OffDr	Event	Records:	Events:	Risk time:	Persons:
OnDr	13207	4163	240	17610	4403	19610.92	17610
OffDr	0	4113	50	4163	50	4415.55	4163
Sum	13207	8276	290	21773	4453	24026.47	17610

So we can summarize results:

```
> round( ftable( dat, col.vars=c(2,4,5) ), 0 )
```

		data			OnDr			Total			Other		
		ix	SGLT2					SGLT2					
		dat	N	PY	Event	N	PY	Event	N	PY	Event	N	PY
endp	sub												
HF	AllPtt		17610	18851	151	17610	19628	249	17610	24443	219	17610	24062
	preCVD		5248	5335	124	5195	5351	189	5248	6965	173	5195	6598
	noCVD		12362	13516	27	12415	14277	60	12362	17479	46	12415	17463
ACD	AllPtt		17610	18960	176	17610	19840	518	17610	24665	300	17610	24363
	preCVD		5248	5426	83	5195	5500	261	5248	7138	149	5195	6813
	noCVD		12362	13534	93	12415	14340	257	12362	17527	151	12415	17550
ACD+HF	AllPtt		17610	18851	324	17610	19628	724	17610	24443	508	17610	24062
	preCVD		5248	5335	204	5195	5351	415	5248	6965	312	5195	6598
	noCVD		12362	13516	120	12415	14277	309	12362	17479	196	12415	17463
CVDD	AllPtt		17610	18960	28	17610	19840	94	17610	24665	51	17610	24363
	preCVD		5248	5426	22	5195	5500	64	5248	7138	34	5195	6813
	noCVD		12362	13534	6	12415	14340	30	12362	17527	17	12415	17550
MI	AllPtt		17610	18885	104	17610	19727	134	17610	24530	139	17610	24194
	preCVD		5248	5389	56	5195	5445	70	5248	7062	80	5195	6730
	noCVD		12362	13496	48	12415	14282	64	12362	17468	59	12415	17464
Str	AllPtt		17610	18876	111	17610	19732	146	17610	24515	146	17610	24192
	preCVD		5248	5391	57	5195	5442	84	5248	7060	79	5195	6715
	noCVD		12362	13485	54	12415	14289	62	12362	17455	67	12415	17477
IscStr	AllPtt		17610	18880	103	17610	19743	129	17610	24526	131	17610	24212
	preCVD		5248	5394	52	5195	5450	73	5248	7069	68	5195	6729
	noCVD		12362	13486	51	12415	14293	56	12362	17457	63	12415	17483
CVDD+MI+Str	AllPtt		17610	18803	235	17610	19621	348	17610	24385	318	17610	24026
	preCVD		5248	5354	130	5195	5388	207	5248	6987	182	5195	6633
	noCVD		12362	13448	105	12415	14233	141	12362	17397	136	12415	17393
ACD+MI+Str	AllPtt		17610	18803	378	17610	19621	758	17610	24385	555	17610	24026
	preCVD		5248	5354	188	5195	5388	393	5248	6987	290	5195	6633
	noCVD		12362	13448	190	12415	14233	365	12362	17397	265	12415	17393
DKD	AllPtt		17610	18845	137	17610	19611	240	17610	24456	182	17610	24026
	preCVD		5248	5390	50	5195	5408	98	5248	7062	68	5195	6677
	noCVD		12362	13455	87	12415	14203	142	12362	17393	114	12415	17350

```
> round( ftable( res, col.vars=c(2,5) ), 3 )
```

			data			OnDr			Total		
			res	HR	lo	up	se	HR	lo	up	se
endp	sub	adj									
HF	AllPtt	Raw	0.621	0.508	0.759	0.102	0.750	0.628	0.894	0.090	
		Adj	0.614	0.502	0.752	0.103	0.739	0.617	0.884	0.092	
	preCVD	Raw	0.653	0.521	0.818	0.115	0.773	0.633	0.942	0.101	
		Adj	0.655	0.522	0.822	0.116	0.772	0.631	0.945	0.103	
	noCVD	Raw	0.469	0.297	0.740	0.233	0.619	0.424	0.903	0.193	
		Adj	0.469	0.297	0.741	0.233	0.616	0.421	0.900	0.194	
ACD	AllPtt	Raw	0.351	0.296	0.417	0.087	0.451	0.394	0.518	0.070	
		Adj	0.417	0.350	0.496	0.088	0.511	0.445	0.586	0.070	
	preCVD	Raw	0.321	0.251	0.410	0.125	0.436	0.360	0.529	0.098	
		Adj	0.397	0.310	0.508	0.126	0.527	0.435	0.639	0.098	
	noCVD	Raw	0.377	0.297	0.479	0.122	0.458	0.377	0.555	0.099	
		Adj	0.427	0.334	0.545	0.125	0.490	0.403	0.595	0.099	
ACD+HF	AllPtt	Raw	0.460	0.404	0.524	0.067	0.563	0.505	0.629	0.056	
		Adj	0.510	0.447	0.582	0.067	0.609	0.545	0.680	0.056	
	preCVD	Raw	0.490	0.415	0.579	0.085	0.599	0.520	0.689	0.072	
		Adj	0.541	0.458	0.639	0.085	0.659	0.572	0.760	0.073	
	noCVD	Raw	0.404	0.327	0.500	0.108	0.499	0.419	0.593	0.088	
		Adj	0.441	0.356	0.548	0.110	0.521	0.438	0.620	0.089	

CVDD	AllPtt	Raw	0.311	0.204	0.474	0.214	0.424	0.306	0.588	0.167
		Adj	0.373	0.241	0.578	0.223	0.490	0.351	0.684	0.170
	preCVD	Raw	0.350	0.217	0.567	0.245	0.417	0.280	0.619	0.202
		Adj	0.434	0.264	0.715	0.254	0.529	0.353	0.792	0.206
	noCVD	Raw	0.210	0.087	0.506	0.449	0.420	0.236	0.748	0.294
		Adj	0.237	0.094	0.593	0.469	0.436	0.246	0.773	0.292
MI	AllPtt	Raw	0.807	0.624	1.045	0.132	0.831	0.665	1.040	0.114
		Adj	0.829	0.640	1.074	0.132	0.843	0.674	1.055	0.114
	preCVD	Raw	0.804	0.565	1.142	0.179	0.908	0.671	1.228	0.154
		Adj	0.866	0.608	1.234	0.181	0.959	0.709	1.297	0.154
	noCVD	Raw	0.798	0.546	1.169	0.194	0.731	0.524	1.021	0.170
		Adj	0.799	0.546	1.168	0.194	0.729	0.523	1.017	0.170
Str	AllPtt	Raw	0.785	0.611	1.009	0.128	0.799	0.638	1.001	0.115
		Adj	0.819	0.636	1.055	0.129	0.819	0.653	1.027	0.116
	preCVD	Raw	0.681	0.484	0.958	0.174	0.732	0.542	0.989	0.153
		Adj	0.719	0.506	1.020	0.179	0.765	0.564	1.039	0.156
	noCVD	Raw	0.914	0.630	1.326	0.190	0.869	0.618	1.222	0.174
		Adj	0.940	0.648	1.365	0.190	0.876	0.623	1.231	0.174
IscStr	AllPtt	Raw	0.823	0.630	1.074	0.136	0.802	0.630	1.019	0.122
		Adj	0.862	0.660	1.126	0.136	0.822	0.646	1.045	0.123
	preCVD	Raw	0.715	0.496	1.030	0.186	0.722	0.522	0.999	0.165
		Adj	0.754	0.519	1.094	0.190	0.754	0.543	1.048	0.168
	noCVD	Raw	0.953	0.644	1.409	0.200	0.887	0.621	1.267	0.182
		Adj	0.986	0.667	1.459	0.200	0.896	0.627	1.279	0.182
CVDD+MI+Str	AllPtt	Raw	0.700	0.593	0.827	0.085	0.727	0.628	0.842	0.075
		Adj	0.738	0.624	0.872	0.086	0.750	0.647	0.868	0.075
	preCVD	Raw	0.631	0.507	0.787	0.112	0.698	0.576	0.846	0.098
		Adj	0.693	0.554	0.867	0.114	0.752	0.620	0.912	0.099
	noCVD	Raw	0.784	0.607	1.013	0.131	0.746	0.595	0.935	0.115
		Adj	0.799	0.618	1.033	0.131	0.747	0.596	0.936	0.115
ACD+MI+Str	AllPtt	Raw	0.516	0.456	0.584	0.063	0.576	0.518	0.640	0.054
		Adj	0.570	0.503	0.645	0.064	0.616	0.554	0.684	0.054
	preCVD	Raw	0.480	0.404	0.571	0.088	0.572	0.495	0.661	0.074
		Adj	0.549	0.461	0.653	0.089	0.639	0.552	0.740	0.074
	noCVD	Raw	0.545	0.456	0.651	0.091	0.567	0.487	0.661	0.078
		Adj	0.581	0.486	0.694	0.091	0.582	0.500	0.678	0.077
DKD	AllPtt	Raw	0.585	0.474	0.721	0.107	0.615	0.509	0.743	0.096
		Adj	0.589	0.477	0.727	0.107	0.618	0.512	0.747	0.097
	preCVD	Raw	0.508	0.361	0.714	0.174	0.549	0.405	0.745	0.156
		Adj	0.533	0.377	0.753	0.177	0.576	0.423	0.785	0.158
	noCVD	Raw	0.634	0.485	0.830	0.137	0.655	0.514	0.834	0.123
		Adj	0.630	0.481	0.825	0.138	0.652	0.511	0.830	0.124

3.10 Exposure tables by drug

We can then produce an overview of the number of persons, risk time and events by index medication; to this end we define functions that uses the `by` argument of the `summary.Lexis` to classify events and follow-up by index drug in various groupings:

```
> odr <- c("Met","SU","GLP1","DPP4","TZD","Aca","fIns","iIns","lIns","mIns")
> tabFU <- ZArray( list( Ix = c("Other",odr,
+                               "SGLT2","Dapa","Empa","Cana"),
+                               wh = c("nPers","FU","meanfu","sdFU","maxFU") ) )
> str( tabFU )
```

```

num [1:15, 1:5] 0 0 0 0 0 0 0 0 0 0 0 ...
- attr(*, "dimnames")=List of 2
 ..$ Ix: chr [1:15] "Other" "Met" "SU" "GLP1" ...
 ..$ wh: chr [1:5] "nPers" "FU" "meanfu" "sdFU" ...

> getFU <-
+ function( lx ) c( length( unique( lx$lex.id ) ),
+                   sum( lx$lex.dur ),
+                   mean( lx$lex.dur ),
+                   sd( lx$lex.dur ),
+                   max( lx$lex.dur ) )
> mset$doX <- with( mset, pmin( doDth, 2017, na.rm=TRUE ) )
> Lx <- Lexis( entry = list( per = doIx,
+                           cua = doIx-doBth,
+                           tfi = 0 ),
+             exit = list( per = doX ),
+             data = subset( mset, is.na(doDth) | doIx < doDth ) )
> summary( Lx, by="Ixdr", simplify=FALSE )

$SGLT2

Transitions:
  To
From    0 Records: Events: Risk time: Persons:
  0 17610    17610      0    24664.7    17610

$Other

Transitions:
  To
From    0 Records: Events: Risk time: Persons:
  0 17610    17610      0    24363.18    17610

> tabFU["Other",] <- getFU( subset( Lx, Ixdr=="Other" ) )
> for( oo in odr ) tabFU[oo,] <- getFU( subset( Lx, Epdr==oo ) )
> tabFU["SGLT2",] <- getFU( subset( Lx, Ixdr=="SGLT2" ) )
> tabFU["Dapa",] <- getFU( subset( Lx, Ixatc %in% c("A10BD15","A10BK01") ) )
> tabFU["Cana",] <- getFU( subset( Lx, Ixatc %in% c("A10BD16","A10BK02") ) )
> tabFU["Empa",] <- getFU( subset( Lx, Ixatc %in% c("A10BD20","A10BK03") ) )
> round( tabFU, 2 )

      wh
Ix      nPers    FU meanfu sdFU maxFU
Other 17610 24363.18   1.38 1.07  4.08
Met    1938  2547.93   1.31 1.02  4.07
SU     2086  3125.47   1.50 1.10  4.07
GLP1   2606  3609.82   1.39 1.07  4.08
DPP4   3653  4898.94   1.34 1.04  4.08
TZD     25    47.80   1.91 1.35  3.98
Aca     11    16.75   1.52 0.72  3.07
fIns   1939  2435.78   1.26 1.05  4.08
iIns   1235  2084.12   1.69 1.13  4.08
lIns   3488  4452.67   1.28 1.02  4.07
mIns    629  1143.88   1.82 1.12  4.07
SGLT2 17610 24664.70   1.40 1.05  4.05
Dapa  11064 19701.73   1.78 1.09  4.05
Empa   6070  4308.64   0.71 0.52  2.35
Cana    477   654.52   1.37 0.65  2.59

```

3.11 Saving it all

Fially we save all results:

```
> save( res, dat, tabFU, file = "resSGoth.Rda" )
```

3.12 Reformatting

The results are here reformatted to Excel-format, `xlsx`, by the `xlsx` package of R, so we load that concomitantly with the data.

```
> library( Epi )
> library( xlsx )
> clear()
> load( "btabSGoth.Rda" )
> load( "resSGoth.Rda" )
> lls()
  name    mode    class  dim          size(Kb)
1 cm.tab numeric matrix 31 4             3.4
2 ct.tab numeric matrix 31 4             3.4
3 dat     numeric array 10 2 3 2 3         5.5
4 dm.tab numeric matrix 40 4             3.9
5 dt.tab numeric matrix 40 4             3.9
6 mm.tab numeric matrix 37 4             3.8
7 mt.tab numeric matrix 37 4             3.8
8 res     numeric array 10 2 3 2 4         6.4
9 tabFU   numeric matrix 15 5             2.6
```

With this in place we can now construct the tables wanted for the sheet in th desided order.

3.12.1 Baseline tables

In order to check that we get the rows correct we read the rownames from the supplied spreadsheet, in order to put these in as a column in the new sheet for control:

```
> cat("Sample size
+ Age, years
+ Women
+ CV-history
+ Myocardial infarction
+ Unstable angina
+ Heart failure
+ Atrial fibrillation
+ Stroke
+ PAD
+ Microvascular disease
+ CKD
+ Frailty (yes)
+ Metformin
+ SU
+ TZD
+ GLP1
+ DPP4
+ Insulin
```

```

...now input from ../rep/2xlSGoth.tex
+ Anti hypertensive therapy
+ LOOP diuretics
+ Low ceiling diuretics
+ ACE Inhibitors
+ ARBs
+ Statin therapy
+ Beta blockers
+ Aldosterone antagonists
+ Index year
+ 2012
+ 2013
+ 2014
+ 2015
+ 2016
+ 2017
+ ", file='ol.txt' )
> ol <- read.table('ol.txt',header=FALSE,sep='\t',as.is=TRUE)

```

Baseline pre-matching

We can now construct the pre-matching table

```

> bt <- rbind( "Sample size"= dt.tab[1,2:1]+dt.tab[2,2:1],
+             "Age" = NA,
+             dt.tab["F",2:1,drop=FALSE],
+             ct.tab["pre.CVD",2:1,drop=FALSE],
+             ct.tab["prv.MI",2:1,drop=FALSE],
+             ct.tab["prv.UnstAng",2:1,drop=FALSE],
+             ct.tab["prv.HF",2:1,drop=FALSE],
+             ct.tab["prv.AtrFib",2:1,drop=FALSE],
+             ct.tab["pre.Str",2:1,drop=FALSE],
+             ct.tab["prv.PAD",2:1,drop=FALSE],
+             ct.tab["pre.Mic",2:1,drop=FALSE],
+             ct.tab["prv.CKD",2:1,drop=FALSE],
+             "Frail"=dt.tab["1",2:1],
+             mt.tab["had.Metformin",2:1,drop=FALSE],
+             mt.tab["had.SU",2:1,drop=FALSE],
+             mt.tab["had.TZD",2:1,drop=FALSE],
+             mt.tab["had.GLP1",2:1,drop=FALSE],
+             mt.tab["had.DPP4",2:1,drop=FALSE],
+             mt.tab["got.Ins",2:1,drop=FALSE],
+             mt.tab["got.Hyp",2:1,drop=FALSE],
+             mt.tab["had.HCD",2:1,drop=FALSE],
+             mt.tab["had.THZ",2:1,drop=FALSE],
+             mt.tab["had.ACE",2:1,drop=FALSE],
+             mt.tab["had.ARB",2:1,drop=FALSE],
+             mt.tab["had.Sta",2:1,drop=FALSE],
+             mt.tab["had.BB1",2:1,drop=FALSE],
+             mt.tab["had.A1A",2:1,drop=FALSE],
+             "Index year"=NA,
+             dt.tab["Index date 2012",2:1,drop=FALSE],
+             dt.tab["2013",2:1,drop=FALSE],
+             dt.tab["2014",2:1,drop=FALSE],
+             dt.tab["2015",2:1,drop=FALSE],
+             dt.tab["2016",2:1,drop=FALSE],

```

```

+           '2017'=NA)
> str(ol)
'data.frame':      34 obs. of  1 variable:
 $ V1: chr  "Sample size" "Age, years" "Women" "CV-history" ...
> bt <- cbind(bt[,2],NA,NA,bt[,1],NA,NA)
> bt["Age",c(2,3,5,6)] <- dt.tab["Age: Mean / SD",c(1,3,2,4)]
> colnames( bt ) <- c("SGLT-2","mean","sd","Other","mean","sd")
> cbind( ol, bt )

```

	V1	SGLT-2	mean	sd	Other	mean	sd
Sample size	Sample size	17678	NA	NA	226984	NA	NA
Age	Age, years	NA	60.4	11	NA	63.2	13.6
F	Women	6856	NA	NA	94740	NA	NA
pre.CVD	CV-history	5268	NA	NA	76805	NA	NA
prv.MI	Myocardial infarction	1412	NA	NA	19911	NA	NA
prv.UnstAng	Unstable angina	653	NA	NA	8459	NA	NA
prv.HF	Heart failure	702	NA	NA	13182	NA	NA
prv.AtrFib	Atrial fibrillation	1042	NA	NA	18499	NA	NA
pre.Str	Stroke	1263	NA	NA	22710	NA	NA
prv.PAD	PAD	861	NA	NA	15553	NA	NA
pre.Mic	Microvascular disease	6021	NA	NA	53275	NA	NA
prv.CKD	CKD	101	NA	NA	6537	NA	NA
Frail	Frailty (yes)	6015	NA	NA	81883	NA	NA
had.Metformin	Metformin	11391	NA	NA	80273	NA	NA
had.SU	SU	4095	NA	NA	30627	NA	NA
had.TZD	TZD	58	NA	NA	224	NA	NA
had.GLP1	GLP1	4470	NA	NA	13314	NA	NA
had.DPP4	DPP4	3085	NA	NA	14701	NA	NA
got.Ins	Insulin	4067	NA	NA	36359	NA	NA
got.Hyp	Anti hypertensive therapy	13819	NA	NA	152904	NA	NA
had.HCD	LOOP diuretics	2330	NA	NA	44177	NA	NA
had.THZ	Low ceiling diuretics	2697	NA	NA	33724	NA	NA
had.ACE	ACE Inhibitors	6830	NA	NA	72133	NA	NA
had.ARB	ARBs	6104	NA	NA	56367	NA	NA
had.Sta	Statin therapy	13263	NA	NA	126144	NA	NA
had.BB1	Beta blockers	4771	NA	NA	63033	NA	NA
had.Ala	Aldosterone antagonists	883	NA	NA	14102	NA	NA
Index year	Index year	NA	NA	NA	NA	NA	NA
Index date 2012	2012	20	NA	NA	4468	NA	NA
2013	2013	1929	NA	NA	53123	NA	NA
2014	2014	3038	NA	NA	52261	NA	NA
2015	2015	4761	NA	NA	56853	NA	NA
2016	2016	7930	NA	NA	60279	NA	NA
2017	2017	NA	NA	NA	NA	NA	NA

```

> write.xlsx( cbind( 'Org. labs'=ol, bt ),
+             "SGoth.xlsx",
+             sheetName = "Baseline pre-matching",
+             append = FALSE,
+             showNA = FALSE )

```

Baseline after matching

The data for post matching have exactly the same structure; the tables are just called 'm.tab' instead of 't.tab':

```

> bm <- rbind( "Sample size"= dm.tab[1,2:1]+dm.tab[2,2:1],
+             "Age" = NA,
+             dm.tab["F",2:1,drop=FALSE],
+             cm.tab["pre.CVD",2:1,drop=FALSE],
+             cm.tab["prv.MI",2:1,drop=FALSE],
+             cm.tab["prv.UnstAng",2:1,drop=FALSE],
+             cm.tab["prv.HF",2:1,drop=FALSE],
+             cm.tab["prv.AtrFib",2:1,drop=FALSE],
+             cm.tab["pre.Str",2:1,drop=FALSE],
+             cm.tab["prv.PAD",2:1,drop=FALSE],
+             cm.tab["pre.Mic",2:1,drop=FALSE],
+             cm.tab["prv.CKD",2:1,drop=FALSE],
+             "Frail"=dm.tab["1",2:1],
+             mm.tab["had.Metformin",2:1,drop=FALSE],
+             mm.tab["had.SU",2:1,drop=FALSE],
+             mm.tab["had.TZD",2:1,drop=FALSE],
+             mm.tab["had.GLP1",2:1,drop=FALSE],
+             mm.tab["had.DPP4",2:1,drop=FALSE],
+             mm.tab["got.Ins",2:1,drop=FALSE],
+             mm.tab["got.Hyp",2:1,drop=FALSE],
+             mm.tab["had.HCD",2:1,drop=FALSE],
+             mm.tab["had.THZ",2:1,drop=FALSE],
+             mm.tab["had.ACE",2:1,drop=FALSE],
+             mm.tab["had.ARB",2:1,drop=FALSE],
+             mm.tab["had.Sta",2:1,drop=FALSE],
+             mm.tab["had.BB1",2:1,drop=FALSE],
+             mm.tab["had.A1A",2:1,drop=FALSE],
+             "Index year"=NA,
+             dm.tab["Index date 2012",2:1,drop=FALSE],
+             dm.tab["2013",2:1,drop=FALSE],
+             dm.tab["2014",2:1,drop=FALSE],
+             dm.tab["2015",2:1,drop=FALSE],
+             dm.tab["2016",2:1,drop=FALSE],
+             '2017'=NA)
> str(ol)
'data.frame':      34 obs. of  1 variable:
 $ V1: chr  "Sample size" "Age, years" "Women" "CV-history" ...
> bm <- cbind(bm[,2],NA,NA,bm[,1],NA,NA)
> bm["Age",c(2,3,5,6)] <- dm.tab["Age: Mean / SD",c(1,3,2,4)]
> colnames( bm ) <- c("SGLT-2","mean","sd","Other","mean","sd")
> cbind( ol, bm )

```

	V1	SGLT-2	mean	sd	Other	mean	sd
Sample size	Sample size	17610	NA	NA	17610	NA	NA
Age	Age, years	NA	60.4	11	NA	60.4	12.7
F	Women	6833	NA	NA	6809	NA	NA
pre.CVD	CV-history	5248	NA	NA	5195	NA	NA
prv.MI	Myocardial infarction	1406	NA	NA	1399	NA	NA
prv.UnstAng	Unstable angina	647	NA	NA	628	NA	NA
prv.HF	Heart failure	701	NA	NA	737	NA	NA
prv.AtrFib	Atrial fibrillation	1039	NA	NA	991	NA	NA
pre.Str	Stroke	1258	NA	NA	1251	NA	NA
prv.PAD	PAD	861	NA	NA	839	NA	NA
pre.Mic	Microvascular disease	5988	NA	NA	5899	NA	NA
prv.CKD	CKD	101	NA	NA	81	NA	NA
Frail	Frailty (yes)	5988	NA	NA	5950	NA	NA
had.Metformin	Metformin	11333	NA	NA	11345	NA	NA
had.SU	SU	4074	NA	NA	4116	NA	NA

had.TZD	TZD	56	NA	NA	58	NA	NA
had.GLP1	GLP1	4419	NA	NA	4296	NA	NA
had.DPP4	DPP4	3060	NA	NA	3115	NA	NA
got.Ins	Insulin	4042	NA	NA	4241	NA	NA
got.Hyp	Anti hypertensive therapy	13759	NA	NA	13641	NA	NA
had.HCD	LOOP diuretics	2321	NA	NA	2313	NA	NA
had.THZ	Low ceiling diuretics	2684	NA	NA	2717	NA	NA
had.ACE	ACE Inhibitors	6802	NA	NA	6962	NA	NA
had.ARB	ARBs	6072	NA	NA	6075	NA	NA
had.Sta	Statin therapy	13204	NA	NA	13336	NA	NA
had.BBl	Beta blockers	4755	NA	NA	4740	NA	NA
had.Ala	Aldosterone antagonists	883	NA	NA	898	NA	NA
Index year	Index year	NA	NA	NA	NA	NA	NA
Index date 2012	2012	20	NA	NA	109	NA	NA
2013	2013	1929	NA	NA	1875	NA	NA
2014	2014	3038	NA	NA	2881	NA	NA
2015	2015	4747	NA	NA	4940	NA	NA
2016	2016	7876	NA	NA	7805	NA	NA
2017	2017	NA	NA	NA	NA	NA	NA

```

> write.xlsx( cbind( 'Org. labs'=ol, bm ),
+             "SGoth.xlsx",
+ sheetName = "Baseline after matching",
+   append = TRUE,
+   showNA = FALSE )

```

3.12.2 Treatment distribution

```

> drnam <- c(
+ 'SGLT-2',
+ ' Dapagliflozin',
+ ' Empagliflozin',
+ ' Canagliflozin',
+ ' Ipragliflozin',
+ ' Luseogliflozin',
+ ' Tofugliflozin',
+ '-',
+ 'Other',
+ ' Metformin',
+ ' SU',
+ ' DPP-4',
+ ' TZD ',
+ ' GLP-1',
+ ' All insulin',
+ ' fast-acting Insulin',
+ ' intermediate-acting Insulin',
+ ' long-acting Insulin',
+ ' mix Insulin',
+ ' Acarbose',
+ ' Amylin alog',
+ ' Metiglinides' )
> FUtab <- tabFU[c(12:15,rep(NA,4),1,2,3,5,6,4,NA,8:11,7,NA,NA),]
> cbind( drnam, rownames(FUtab) )

      drnam
[1,] "SGLT-2"          "SGLT2"

```

```

[2,] " Dapagliflozin"      "Dapa"
[3,] " Empagliflozin"     "Empa"
[4,] " Canagliflozin"     "Cana"
[5,] " Ipragliflozin"     NA
[6,] " Luseogliflozin"    NA
[7,] " Tofugliflozin"     NA
[8,] "- "                 NA
[9,] "Other"              "Other"
[10,] " Metformin"        "Met"
[11,] " SU"               "SU"
[12,] " DPP-4"            "DPP4"
[13,] " TZD "             "TZD"
[14,] " GLP-1"            "GLP1"
[15,] " All insulin"      NA
[16,] " fast-acting Insulin" "fIns"
[17,] " intermediate-acting Insulin" "iIns"
[18,] " long-acting Insulin" "lIns"
[19,] " mix Insulin"       "mIns"
[20,] " Acarbose"         "Aca"
[21,] " Amylin alog"      NA
[22,] " Metiglinides"     NA

> FUtab[15,] <- apply( FUtab[16:19,], 2, sum )
> rownames(FUtab) <- drnam
> colnames(FUtab) <- c(
+ 'Number of patients',
+ 'Total follow-up time',
+ 'Mean follow-up time',
+ 'Sd follow-up time',
+ 'maximum follow-up time')
> FUtab

```

	wh		
Ix	Number of patients	Total follow-up time	Mean follow-up time
SGLT-2	17610	24664.69678	1.4006074
Dapagliflozin	11064	19701.72553	1.7807055
Empagliflozin	6070	4308.63518	0.7098246
Canagliflozin	477	654.51882	1.3721569
Ipragliflozin	NA	NA	NA
Luseogliflozin	NA	NA	NA
Tofugliflozin	NA	NA	NA
-	NA	NA	NA
Other	17610	24363.17522	1.3834852
Metformin	1938	2547.93361	1.3147232
SU	2086	3125.47023	1.4983079
DPP-4	3653	4898.94251	1.3410738
TZD	25	47.80287	1.9121150
GLP-1	2606	3609.82341	1.3851970
All insulin	7291	10116.45175	6.0388915
fast-acting Insulin	1939	2435.78303	1.2562058
intermediate-acting Insulin	1235	2084.11841	1.6875453
long-acting Insulin	3488	4452.66804	1.2765677
mix Insulin	629	1143.88227	1.8185728
Acarbose	11	16.75086	1.5228051
Amylin alog	NA	NA	NA
Metiglinides	NA	NA	NA

	wh		
Ix	Sd follow-up time	maximum follow-up time	
SGLT-2	1.0487551	4.051335	

Dapagliflozin	1.0865149	4.051335
Empagliflozin	0.5157299	2.348392
Canagliflozin	0.6478901	2.589322
Ipragliflozin	NA	NA
Luseogliflozin	NA	NA
Tofugliflozin	NA	NA
-	NA	NA
Other	1.0653458	4.078713
Metformin	1.0169789	4.073238
SU	1.0963919	4.070500
DPP-4	1.0394548	4.078713
TZD	1.3529273	3.982888
GLP-1	1.0650624	4.075975
All insulin	4.3263044	16.303901
fast-acting Insulin	1.0514882	4.078713
intermediate-acting Insulin	1.1338177	4.078713
long-acting Insulin	1.0243434	4.073238
mix Insulin	1.1166552	4.073238
Acarbose	0.7169525	3.068446
Amylin alog	NA	NA
Metiglinides	NA	NA

```

> write.xlsx( FUt看,
+             "SGoth.xlsx",
+ sheetName = "Treatment distribution",
+   append = TRUE,
+   showNA = FALSE )

```

3.12.3 Events

```

> cat(
+ 'Number of patients
+ Total follow-up time - on treatment
+ Number of patients with event - on treatment
+ Total follow-up time - ITT
+ Number of patients with event - ITT
+ ', file='oc' )
> ( oc <- read.table('oc',header=FALSE,sep='\t',as.is=TRUE)[,1] )

[1] "Number of patients" "Total follow-up time - on treatment"
[3] "Number of patients with event - on treatment" "Total follow-up time - ITT"
[5] "Number of patients with event - ITT"

> cat(
+ 'HHF
+ All-cause death
+ All-cause death or HHF
+ Cardiavascular death
+ Myocardial infarction
+ Stroke
+ Ischemic stroke
+ MACE (cardivascular death, MI or stroke)
+ modified MACE (All-cause death, MI or stroke)
+ Kidney disease
+ ', file='ol' )
> ( ol <- read.table('ol',header=FALSE,sep='\t',as.is=TRUE)[,1] )

```

```

[1] "HHF" "All-cause death"
[3] "All-cause death or HHF" "Cardiavascular death"
[5] "Myocardial infarction" "Stroke"
[7] "Ischemic stroke" "MACE (cardivascular death, MI or stroke)"
[9] "modified MACE (All-cause death, MI or stroke)" "Kidney disease"

```

The data for this is in the `dat` object:

```

> str( dat )
num [1:10, 1:2, 1:3, 1:2, 1:3] 17610 17610 17610 17610 17610 ...
- attr(*, "dimnames")=List of 5
 ..$ endp: chr [1:10] "HF" "ACD" "ACD+HF" "CVDD" ...
 ..$ data: chr [1:2] "OnDr" "Total"
 ..$ sub : chr [1:3] "AllPtt" "preCVD" "noCVD"
 ..$ ix  : chr [1:2] "SGLT2" "Other"
 ..$ dat : chr [1:3] "N" "PY" "Event"

> cbind( ol, dimnames(dat)[[1]] )
      ol
[1,] "HHF" "HF"
[2,] "All-cause death" "ACD"
[3,] "All-cause death or HHF" "ACD+HF"
[4,] "Cardiavascular death" "CVDD"
[5,] "Myocardial infarction" "MI"
[6,] "Stroke" "Str"
[7,] "Ischemic stroke" "IscStr"
[8,] "MACE (cardivascular death, MI or stroke)" "CVDD+MI+Str"
[9,] "modified MACE (All-cause death, MI or stroke)" "ACD+MI+Str"
[10,] "Kidney disease" "DKD"

> ft <- ftable( dat[,1,1:2,,drop=FALSE], col.vars=c(4,2,5) )
> round( ft, 1 )

```

		ix data dat	SGLT2 OnDr N	PY	Event	Total N	PY	Event	Other OnDr N	PY	Event
endp	sub										
HF	AllPtt	17610.0	18851.2	151.0	17610.0	24443.2	219.0	17610.0	19628.0	249.0	17610.0
ACD	AllPtt	17610.0	18960.0	176.0	17610.0	24664.7	300.0	17610.0	19839.6	518.0	17610.0
ACD+HF	AllPtt	17610.0	18851.2	324.0	17610.0	24443.2	508.0	17610.0	19628.0	724.0	17610.0
CVDD	AllPtt	17610.0	18960.0	28.0	17610.0	24664.7	51.0	17610.0	19839.6	94.0	17610.0
MI	AllPtt	17610.0	18884.7	104.0	17610.0	24529.9	139.0	17610.0	19727.0	134.0	17610.0
Str	AllPtt	17610.0	18876.3	111.0	17610.0	24514.5	146.0	17610.0	19731.7	146.0	17610.0
IscStr	AllPtt	17610.0	18880.2	103.0	17610.0	24526.1	131.0	17610.0	19743.2	129.0	17610.0
CVDD+MI+Str	AllPtt	17610.0	18802.7	235.0	17610.0	24384.5	318.0	17610.0	19621.4	348.0	17610.0
ACD+MI+Str	AllPtt	17610.0	18802.7	378.0	17610.0	24384.5	555.0	17610.0	19621.4	758.0	17610.0
DKD	AllPtt	17610.0	18845.3	137.0	17610.0	24455.7	182.0	17610.0	19610.9	240.0	17610.0

This is the table needed (except for the column on persons, which should not be repeated):

```

> py <- data.frame( as.matrix(ft) )[-c(4,10)]
> py

```

	SGLT2_OnDr_N	SGLT2_OnDr_PY	SGLT2_OnDr_Event	SGLT2_Total_PY	SGLT2_Total_Event
HF_AllPtt	17610	18851.19	151	24443.23	219
ACD_AllPtt	17610	18960.02	176	24664.70	300
ACD+HF_AllPtt	17610	18851.19	324	24443.23	508
CVDD_AllPtt	17610	18960.02	28	24664.70	51
MI_AllPtt	17610	18884.71	104	24529.94	139
Str_AllPtt	17610	18876.26	111	24514.52	146

IscStr_AllPtt	17610	18880.17	103	24526.08	13
CVDD+MI+Str_AllPtt	17610	18802.67	235	24384.52	31
ACD+MI+Str_AllPtt	17610	18802.67	378	24384.52	55
DKD_AllPtt	17610	18845.32	137	24455.71	18
	Other_OnDr_N	Other_OnDr_PY	Other_OnDr_Event	Other_Total_PY	Other_Total_Event
HF_AllPtt	17610	19627.99	249	24061.68	28
ACD_AllPtt	17610	19839.60	518	24363.18	65
ACD+HF_AllPtt	17610	19627.99	724	24061.68	88
CVDD_AllPtt	17610	19839.60	94	24363.18	12
MI_AllPtt	17610	19726.99	134	24194.14	16
Str_AllPtt	17610	19731.68	146	24192.34	18
IscStr_AllPtt	17610	19743.20	129	24212.03	16
CVDD+MI+Str_AllPtt	17610	19621.37	348	24025.62	43
ACD+MI+Str_AllPtt	17610	19621.37	758	24025.62	95
DKD_AllPtt	17610	19610.92	240	24026.47	29

```
> colnames( py )
[1] "SGLT2_OnDr_N"      "SGLT2_OnDr_PY"      "SGLT2_OnDr_Event"   "SGLT2_Total_PY"
[5] "SGLT2_Total_Event" "Other_OnDr_N"        "Other_OnDr_PY"       "Other_OnDr_Event"
[9] "Other_Total_PY"    "Other_Total_Event"

> colnames(py) <- c(oc,oc[-1])
> rownames(py) <- ol
```

With this in order we can now write it to the excel sheet:

```
> write.xlsx( py,
+             "SGoth.xlsx",
+             sheetName = "Events",
+             append = TRUE,
+             showNA = FALSE )
```

3.12.4 Hazard ratios

```
> ft <- ftable((dat[c(1:3,9,5,6),1:2,1,"SGLT2",,drop=FALSE]+
+              dat[c(1:3,9,5,6),1:2,1,"Other",,drop=FALSE])[,,,c(1,1),],row.vars=c(1,2,3))
> YD <- data.frame(as.matrix(ft))
> HR <- data.frame(as.matrix(ftable(res[c(1:3,9,5,6),1:2,1,1:2,c(1,4)],row.vars=c(1,2,3))))
> Endpoint <- sapply( strsplit( rownames(HR), "_" ), FUN=function(x) x[1] )
> Adjusted <- sapply( strsplit( rownames(HR), "_" ), FUN=function(x) x[3] )
> Analysis <- sapply( strsplit( rownames(HR), "_" ), FUN=function(x) x[2] )
> ( HR <- cbind(Endpoint,Adjusted,Analysis,HR,YD)[,c(1:3,6:8,4:5)] )
```

	Endpoint	Adjusted	Analysis	N	PY	Event	HR	se
HF_OnDr_Raw	HF	Raw	OnDr	35220	38479.17	400	0.6211633	0.10232191
HF_OnDr_Adj	HF	Adj	OnDr	35220	38479.17	400	0.6140398	0.10315404
HF_Total_Raw	HF	Raw	Total	35220	48504.90	507	0.7497195	0.09005768
HF_Total_Adj	HF	Adj	Total	35220	48504.90	507	0.7389602	0.09162821
ACD_OnDr_Raw	ACD	Raw	OnDr	35220	38799.62	694	0.3514844	0.08720105
ACD_OnDr_Adj	ACD	Adj	OnDr	35220	38799.62	694	0.4167922	0.08842890
ACD_Total_Raw	ACD	Raw	Total	35220	49027.87	957	0.4513379	0.06982434
ACD_Total_Adj	ACD	Adj	Total	35220	49027.87	957	0.5107222	0.07007331
ACD+HF_OnDr_Raw	ACD+HF	Raw	OnDr	35220	38479.17	1048	0.4598323	0.06662555
ACD+HF_OnDr_Adj	ACD+HF	Adj	OnDr	35220	38479.17	1048	0.5097771	0.06748081
ACD+HF_Total_Raw	ACD+HF	Raw	Total	35220	48504.90	1397	0.5633668	0.05585373
ACD+HF_Total_Adj	ACD+HF	Adj	Total	35220	48504.90	1397	0.6091078	0.05644259
ACD+MI+Str_OnDr_Raw	ACD+MI+Str	Raw	OnDr	35220	38424.05	1136	0.5155899	0.06314070

ACD+MI+Str_OnDr_Adj	ACD+MI+Str	Adj	OnDr	35220	38424.05	1136	0.5697949	0.06352040
ACD+MI+Str_Total_Raw	ACD+MI+Str	Raw	Total	35220	48410.14	1505	0.5760104	0.05374049
ACD+MI+Str_Total_Adj	ACD+MI+Str	Adj	Total	35220	48410.14	1505	0.6156372	0.05376023
MI_OnDr_Raw	MI	Raw	OnDr	35220	38611.70	238	0.8074113	0.13157527
MI_OnDr_Adj	MI	Adj	OnDr	35220	38611.70	238	0.8292776	0.13214032
MI_Total_Raw	MI	Raw	Total	35220	48724.08	304	0.8313953	0.11404383
MI_Total_Adj	MI	Adj	Total	35220	48724.08	304	0.8431956	0.11420636
Str_OnDr_Raw	Str	Raw	OnDr	35220	38607.93	257	0.7849597	0.12799201
Str_OnDr_Adj	Str	Adj	OnDr	35220	38607.93	257	0.8192622	0.12890886
Str_Total_Raw	Str	Raw	Total	35220	48706.87	326	0.7991662	0.11512132
Str_Total_Adj	Str	Adj	Total	35220	48706.87	326	0.8185580	0.11551996

```
> write.xlsx( HR,
+           "SGoth.xlsx",
+ sheetName = "Hazard ratios",
+   append = TRUE,
+   showNA = FALSE )
```

3.12.5 Subgroup OT

This is same as above, except the we restrict to “OnDr”, and subclassify by previous CVD:

```
> str(dat)
num [1:10, 1:2, 1:3, 1:2, 1:3] 17610 17610 17610 17610 17610 ...
- attr(*, "dimnames")=List of 5
..$ endp: chr [1:10] "HF" "ACD" "ACD+HF" "CVDD" ...
..$ data: chr [1:2] "OnDr" "Total"
..$ sub : chr [1:3] "AllPtt" "preCVD" "noCVD"
..$ ix : chr [1:2] "SGLT2" "Other"
..$ dat : chr [1:3] "N" "PY" "Event"

> YD <-
+   data.frame(as.matrix(ftable(dat[c(1:3,9,5,6),"OnDr",,"SGLT2",] +
+                               dat[c(1:3,9,5,6),"OnDr",,"Other" ],row.vars=c(1,2))))
> str( YD )

'data.frame':      18 obs. of  3 variables:
 $ N      : num  35220 10443 24777 35220 10443 ...
 $ PY     : num  38479 10686 27794 38800 10926 ...
 $ Event: num  400 313 87 694 344 ...

> HR <-
+   data.frame(as.matrix(ftable(res[c(1:3,9,5,6),"OnDr",,"Adj",c(1,4)],row.vars=c(1,2))))
```

With this fixed we can now write the table:

```
> write.xlsx( cbind(YD,HR),
+           "SGoth.xlsx",
+ sheetName = "Subgroups OT",
+   append = TRUE,
+   showNA = FALSE )
```

3.12.6 Subgroup ITT

This is same as above, except the we restrict to “Total”, and subclassify by previous CVD:

```
> YD <-  
+   data.frame(as.matrix(ftable(dat[c(1:3,9,5,6),"Total",,"SGLT2",] +  
+                               dat[c(1:3,9,5,6),"Total",,"Other" ],row.vars=c(1,2))))  
> HR <-  
+   data.frame(as.matrix(ftable(res[c(1:3,9,5,6),"Total",,"Adj",c(1,4)],row.vars=c(1,2))))
```

With this fixed we can now write the table:

```
> write.xlsx( cbind(YD,HR),  
+             "SGoth.xlsx",  
+ sheetName = "Subgroups ITT",  
+   append = TRUE,  
+   showNA = FALSE )
```

Chapter 4

SAS programs

4.1 Rationale and overview

On the server of Statistics Denmark we constructed a comprehensive Danish Diabetes register, also encompassing persons that are not on drug treatment for their disease. The register is based on existing Danish registers, and crucially contains a classification of patients as T1 / T2, which is most reliable for persons alive after 2005 and increasingly uncertain for patients as the distance from date of death to 2005 increases.

In the process we also constructed a diabetes *drug* register where only drug treated patients were included, with a debut date equal to the first date of drug dispense.

The type 2 patients from this register constitute the base for the current analyses.

The following documented programs sequentially construct analysis data sets, using both register data used for the construction of the diabetes register

All created data will be in the data folder as SAS-data sets.

We have used the following SAS-programs:

01a-npr Uses the national patient register (NPR) to generate two data sets:

- **compl** one record per date and complication for all complications of relevant types recorded in the NPR (11.2 mio), not restricted to diabetes patients.
- **wcompl** a dataset with one record per person (not only diabetes patients either) with dates of the *first* complication of each type. Naturally, some of these will be missing if the patients never saw the type of complication, but at least one will be non-missing.

04d-rmps Generates two data sets:

- **disp** all dispensations to T2 patients in the period of the Register of Medicine Products Statistics (**rmps**) (1995–2016).
- **xdisp** all dispensed drugs to T2 patients in the period of the Register of Medicine Products Statistics (**rmps**) (1995–2016). This dataset contains separate records for each drug dispensed in combination pills.

07-newuse Uses the drug register data to define new user episodes of drugs; that is first use of any drug after a period of at least 180 days. Drug, date of initiation and date of cessation (180 days after last dispense) are recorded.

4.2 Program documentation

The following is a listing of the SAS-programs (that is the .log and .lst files) used to generate the base datasets. Each is preceded by a very brief description; main technical points are included as comments in the program code, found in the .log files.

4.2.1 optslibs.sas

This is common set of declarative commands that defines a couple of options, the location of the raw and the derived data sets and some global macro variables holding the follow-up period. It is included as autoexec file in all runs.

```
* This is the autoexec file used throughout ;
* options used throughout ;
options nocenter nonotes nomprint nosource2
      ps = 10000 /* 105 */
      ls = 90    /* 160 */
      obs = max
      formchar = ' '
/* format libraries we use */
fmtsearch = ( dsfmt.times_personstatistik
              dsfmt.brancher
              dsfmt.uddannelser
              dsfmt.geokoder
              dsfmt.sundhed
              DMfmt.drugfmt
              ttfmt.ttformat00
              ttfmt.ttformat10
              ttfmt.ttformat20 ) ;

* data libraries ;
libname ekstn 'E:\rawdata\705093\Opdatering_2018\Eksterne data\' ;
libname grund 'E:\rawdata\705093\Opdatering_2018\Grunddata\' ;
libname popul 'E:\rawdata\705093\Opdatering_2018\Population\' ;
libname dmdat 'E:\workdata\705093\BxC\demoDM\DATA\' ;
libname dafdat 'E:\workdata\705093\BxC\daffodil\DATA\' ;

* format libraries ;
libname ttfmt 'E:\workdata\705093\QSN_MLiJ\' ;
libname daffmt 'E:\workdata\705093\BxC\daffodil\data\' ;
libname DMfmt 'E:\workdata\705093\BxC\demoDM\data\' ;
libname dsfmt 'E:\Formater\SAS formater i Danmarks Statistik\FORMATKATALOG';

* useful constants ;
%let yrf = 1995 ; /* Range of years of population data */
%let yrl = 2017 ;
%let ini = '01JAN1996'd ; /* formerly primo and cutdate */
%let end = '01JAN2017'd ; * we have data including 2016 ;
%let tload = 15 ; * Age limit for OAD to define T1 ;
%let tlin = 30 ; * Age limit for Insulin to define T1 ;
%let pcoslo = 20 ; * Age interval for pcos (years) ;
%let pcoshi = 40 ;
%let gdmint = 200 ; * distance between GDM dates to constitute 2 GDM events (days) ;

* macro to exclude observations with dates in GDM grace period (days) ;
%macro xgdm( xdate,
            gdmpr = 30,
            gdmwin = 365 ) ;
/* this loop should produce a warning to be sure all instances of GDM are covered */

../sas/sasdata.tex
```

```
%do n = 1 %to 12 ;
    if ( doGDM&n. - &gdmpr. ) < &xdate. < ( doGDM&n. + &gdmwin. ) then delete ;
%end ;
%mend ;

* page ;
options notes ;
```

4.3 01a-npr

Reads NPR-records and defines dates of complications or the types relevant for propensity score matching (data set compl), as well as a wide-data set with the date of first complication of each type (data set wcompl).

1 "Program: 01a-npr.sas" 11:46 Saturday, May 5, 2018

NOTE: AUTOEXEC processing completed.

```
1      * all complaications diagnoses ;
2      %macro mold ;
3      data compl1977_93 ;
4          set %do i = 1977 %to 1993 ;
5              grund.lpradm&i. ( keep = pnr recnum c_adiag d_inddto )
6          %end ; ;
7          compl = put( c_adiag, $icd8gr. ) ;
8          if compl ne 'Other' ;
9      run ;
10     %mend ;
11     %mold ;
```

```
NOTE: There were 536233 observations read from the data set GRUND.LPRADM1977.
NOTE: There were 576420 observations read from the data set GRUND.LPRADM1978.
NOTE: There were 593268 observations read from the data set GRUND.LPRADM1979.
NOTE: There were 603108 observations read from the data set GRUND.LPRADM1980.
NOTE: There were 602085 observations read from the data set GRUND.LPRADM1981.
NOTE: There were 625460 observations read from the data set GRUND.LPRADM1982.
NOTE: There were 651402 observations read from the data set GRUND.LPRADM1983.
NOTE: There were 669845 observations read from the data set GRUND.LPRADM1984.
NOTE: There were 694325 observations read from the data set GRUND.LPRADM1985.
NOTE: There were 727293 observations read from the data set GRUND.LPRADM1986.
NOTE: There were 754517 observations read from the data set GRUND.LPRADM1987.
NOTE: There were 792697 observations read from the data set GRUND.LPRADM1988.
NOTE: There were 821266 observations read from the data set GRUND.LPRADM1989.
NOTE: There were 852356 observations read from the data set GRUND.LPRADM1990.
NOTE: There were 874072 observations read from the data set GRUND.LPRADM1991.
NOTE: There were 922353 observations read from the data set GRUND.LPRADM1992.
NOTE: There were 989327 observations read from the data set GRUND.LPRADM1993.
NOTE: The data set WORK.COMPL1977_93 has 1108835 observations and 5 variables.
NOTE: DATA statement used (Total process time):
      real time          11.40 seconds
      cpu time           2.09 seconds
```

```

13      %macro mnew ;
14      data compl1994_16
15          all94 ( keep = pnr recnum d_inddto v_sengdage c_adiag compl ) ;
16          * the last is for recnum link and hospitalizatiand cancer compl ;
17          set %do i = 1994 %to 2016 ;
18              grund.lpradm&i.          ( keep = pnr recnum d_inddto v_sengdage c_adiag )
19              %end ;
20              grund.lpradm_uafamb16 ( keep = pnr recnum d_inddto v_sengdage c_adiag )
21              ;
22          * sometimes only 3 characters (or none) are given,
23          so we remove trailing blanks and add 0s ;
24          dpad = trim(c_adiag) || '00000' ;
25          compl = put( substr( dpad, 2, 4 ), $icd10gr. ) ;
26          if compl ne 'Other' then output compl1994_16 ;
27          output all94 ;
28      run ;
29      %mend ;
30      %mnew ;

```

WARNING: Multiple lengths were specified for the variable C_ADIAG by input data set(s).
This can cause truncation of data.

```

NOTE: There were 2258243 observations read from the data set GRUND.LPRADM1994.
NOTE: There were 3099173 observations read from the data set GRUND.LPRADM1995.
NOTE: There were 3291605 observations read from the data set GRUND.LPRADM1996.
NOTE: There were 3381335 observations read from the data set GRUND.LPRADM1997.
NOTE: There were 3465118 observations read from the data set GRUND.LPRADM1998.
NOTE: There were 3573088 observations read from the data set GRUND.LPRADM1999.
NOTE: There were 3617722 observations read from the data set GRUND.LPRADM2000.
NOTE: There were 3907990 observations read from the data set GRUND.LPRADM2001.
NOTE: There were 4593801 observations read from the data set GRUND.LPRADM2002.
NOTE: There were 4630558 observations read from the data set GRUND.LPRADM2003.
NOTE: There were 4771082 observations read from the data set GRUND.LPRADM2004.
NOTE: There were 4971541 observations read from the data set GRUND.LPRADM2005.
NOTE: There were 5148309 observations read from the data set GRUND.LPRADM2006.
NOTE: There were 5177044 observations read from the data set GRUND.LPRADM2007.
NOTE: There were 5468126 observations read from the data set GRUND.LPRADM2008.
NOTE: There were 5892938 observations read from the data set GRUND.LPRADM2009.
NOTE: There were 5906084 observations read from the data set GRUND.LPRADM2010.
NOTE: There were 6204182 observations read from the data set GRUND.LPRADM2011.
NOTE: There were 6120611 observations read from the data set GRUND.LPRADM2012.
NOTE: There were 6305317 observations read from the data set GRUND.LPRADM2013.
NOTE: There were 6468603 observations read from the data set GRUND.LPRADM2014.
NOTE: There were 6878652 observations read from the data set GRUND.LPRADM2015.
NOTE: There were 6732177 observations read from the data set GRUND.LPRADM2016.
NOTE: There were 1952252 observations read from the data set GRUND.LPRADM_UAFAMB16.
NOTE: The data set WORK.COMPL1994_16 has 9721906 observations and 7 variables.
NOTE: The data set WORK.ALL94 has 113815551 observations and 6 variables.
NOTE: DATA statement used (Total process time):
      real time           1:48.17
      cpu time            32.34 seconds

```

```

31
32      data compl ( keep = pnr d_inddto recnum c_adiag compl ) ;
33      set compl1977_93
34          compl1994_16 ;
35      run ;

```

WARNING: Multiple lengths were specified for the variable C_ADIAG by input data set(s).
This can cause truncation of data.

```

NOTE: There were 1108835 observations read from the data set WORK.COMPL1977_93.
NOTE: There were 9721906 observations read from the data set WORK.COMPL1994_16.

```

NOTE: The data set WORK.COMPL has 10830741 observations and 5 variables.

NOTE: DATA statement used (Total process time):

```
real time      1.32 seconds
cpu time       1.32 seconds
```

```
36
37      * permanent dataset for hospital stays in the last year
38                and cancer in the last 5 years ;
39      data dafdat.hosp ;
40          set all94 ;
41          if d_inddto ge '01dec2011'd or
42             ( d_inddto ge '01dec2007'd and compl eq 'Cancer' ) ;
43      run ;
```

NOTE: There were 113815551 observations read from the data set WORK.ALL94.

NOTE: The data set DAFDAT.HOSP has 34324010 observations and 6 variables.

NOTE: DATA statement used (Total process time):

```
real time      17.62 seconds
cpu time       10.20 seconds
```

```
44
45      * operations and procedures
46      - incomplete, dialysis is in a different table yet to be requested
47      - Bari and PCIsten, CABG not requested (yet) ;
48      %macro mnew ;
49      data opr ( keep = recnum compl c_opr d_odto ) ;
50          set %do i = 1996 %to 2016 ;
51              grund.lprskso%&i.
52          %end ;
53          grund.lprskso_uafamb16
54          ;
55          if c_oprart eq '+' then delete ;
56                      compl = put( substr(c_opr,2,5), $icd5opr. ) ;
57          if compl eq 'Other' then compl = put( substr(c_opr,2,4), $icd4opr. ) ;
58          if compl eq 'Other' then compl = put( substr(c_opr,2,3), $icd3opr. ) ;
59          if compl eq 'Other' or substr(c_opr,2,6) in ('BJFD00','BJFD01')
60              then delete ;
61      run ;
62      %mend ;
63      %mnew ;
```

NOTE: There were 26253 observations read from the data set GRUND.LPRSKSOP1996.

NOTE: There were 29149 observations read from the data set GRUND.LPRSKSOP1997.

NOTE: There were 36035 observations read from the data set GRUND.LPRSKSOP1998.

NOTE: There were 40427 observations read from the data set GRUND.LPRSKSOP1999.

NOTE: There were 40704 observations read from the data set GRUND.LPRSKSOP2000.

NOTE: There were 47885 observations read from the data set GRUND.LPRSKSOP2001.

NOTE: There were 55872 observations read from the data set GRUND.LPRSKSOP2002.

NOTE: There were 61537 observations read from the data set GRUND.LPRSKSOP2003.

NOTE: There were 68480 observations read from the data set GRUND.LPRSKSOP2004.

NOTE: There were 64246 observations read from the data set GRUND.LPRSKSOP2005.

NOTE: There were 67259 observations read from the data set GRUND.LPRSKSOP2006.

NOTE: There were 72370 observations read from the data set GRUND.LPRSKSOP2007.

NOTE: There were 92049 observations read from the data set GRUND.LPRSKSOP2008.

NOTE: There were 95820 observations read from the data set GRUND.LPRSKSOP2009.

NOTE: There were 89075 observations read from the data set GRUND.LPRSKSOP2010.

NOTE: There were 132453 observations read from the data set GRUND.LPRSKSOP2011.

NOTE: There were 99757 observations read from the data set GRUND.LPRSKSOP2012.

NOTE: There were 130556 observations read from the data set GRUND.LPRSKSOP2013.

NOTE: There were 128032 observations read from the data set GRUND.LPRSKSOP2014.

NOTE: There were 319846 observations read from the data set GRUND.LPRSKSOP2015.
 NOTE: There were 176484 observations read from the data set GRUND.LPRSKSOP2016.
 NOTE: There were 397906 observations read from the data set GRUND.LPRSKSOP_UAFAMB16.
 NOTE: The data set WORK.OPR has 373450 observations and 4 variables.
 NOTE: DATA statement used (Total process time):
 real time 4.84 seconds
 cpu time 0.48 seconds

```
64
65      * attach person numbers and dates using recnum ;
66      proc sort data = opr    ; by recnum ; run ;
```

NOTE: There were 373450 observations read from the data set WORK.OPR.
 NOTE: The data set WORK.OPR has 373450 observations and 4 variables.
 NOTE: PROCEDURE SORT used (Total process time):
 real time 0.07 seconds
 cpu time 0.15 seconds

```
67      proc sort data = all94 ; by recnum ; run ;
```

NOTE: There were 113815551 observations read from the data set WORK.ALL94.
 NOTE: The data set WORK.ALL94 has 113815551 observations and 6 variables.
 NOTE: PROCEDURE SORT used (Total process time):
 real time 55.79 seconds
 cpu time 1:46.48

```
68      data opr ;
69      merge opr ( in = op )
70      all94 ;
71      by recnum ;
72      if op ;
73      run ;
```

NOTE: There were 373450 observations read from the data set WORK.OPR.
 NOTE: There were 113815551 observations read from the data set WORK.ALL94.
 NOTE: The data set WORK.OPR has 373450 observations and 8 variables.
 NOTE: DATA statement used (Total process time):
 real time 19.34 seconds
 cpu time 19.34 seconds

```
74
75      * combine with the other complications ;
76      data dafdat.compl ;
77      set compl ( rename = ( d_inddto = doCompl ) )
78      opr ( rename = ( d_odto   = doCompl ) ) ;
79      run ;
```

WARNING: Multiple lengths were specified for the variable C_ADIAG by input data set(s).
 This can cause truncation of data.
 NOTE: There were 10830741 observations read from the data set WORK.COMPL.
 NOTE: There were 373450 observations read from the data set WORK.OPR.
 NOTE: The data set DAFDAT.COMPL has 11204191 observations and 8 variables.
 NOTE: DATA statement used (Total process time):
 real time 3.07 seconds
 cpu time 1.54 seconds

```
80
```

```

81      title1 'All recorded complications / diagnoses' ;
82      proc tabulate data = dafdat.compl missing noseps ;
83          where ( doCompl ge '01jan1977'd and
84                  doCompl lt '01jan2016'd ) ;
85          class compl doCompl ;
86          table compl,
87              ( all doCompl="Date" ) * f = comma9.
88              / rts = 9 condense ;
89          format doCompl year4. ;
90          keylabel n = ' ' ;
91      run ;

```

NOTE: There were 10665972 observations read from the data set DAFDAT.COMPL.
WHERE (doCompl>='01JAN1977'D and doCompl<'01JAN2016'D);

NOTE: The PROCEDURE TABULATE printed page 1.

NOTE: PROCEDURE TABULATE used (Total process time):

real time	3.93 seconds
cpu time	5.18 seconds

```

92      title1 ;
93
94      proc sort data = dafdat.compl ;
95          by pnr compl doCompl ;
96      run ;

```

NOTE: There were 11204191 observations read from the data set DAFDAT.COMPL.

NOTE: The data set DAFDAT.COMPL has 11204191 observations and 8 variables.

NOTE: PROCEDURE SORT used (Total process time):

real time	6.59 seconds
cpu time	6.06 seconds

```

97
98      * restrict to first complication of each type ;
99      data compl ;
100         set dafdat.compl ;
101         by pnr compl doCompl ;
102         if first.compl ;
103     run ;

```

NOTE: There were 11204191 observations read from the data set DAFDAT.COMPL.

NOTE: The data set WORK.COMPL has 3670846 observations and 8 variables.

NOTE: DATA statement used (Total process time):

real time	4.48 seconds
cpu time	2.01 seconds

```

104
105      proc transpose data = compl
106                      out = dafdat.wcompl ( drop = _NAME_ _LABEL_ )
107                      prefix = do ;
108          by pnr ;
109          var doCompl ;
110          id compl ;
111      run ;

```

NOTE: There were 3670846 observations read from the data set WORK.COMPL.

NOTE: The data set DAFDAT.WCOMPL has 1997992 observations and 28 variables.

NOTE: PROCEDURE TRANSPOSE used (Total process time):

real time	6.14 seconds
cpu time	4.70 seconds

```

112
113      title1 'First complication dates for each patient' ;
114      proc contents data = dafdat.wcompl varnum ; run ;

```

NOTE: PROCEDURE CONTENTS used (Total process time):

```

      real time      0.01 seconds
      cpu time       0.00 seconds

```

NOTE: The PROCEDURE CONTENTS printed page 2.

NOTE: SAS Institute Inc., SAS Campus Drive, Cary, NC USA 27513-2414

NOTE: The SAS System used:

```

      real time      4:03.11
      cpu time       3:12.04

```

4.3.1 01a-npr.lst

All recorded complications / diagnoses

11:46 Saturday, May 5, 2018 1

	Date							
	All	1977	1978	1979	1980	1981	1982	1983
compl								
Amp	3,616	.	.	.	.	.	.	.
Angina	778,839	727	984	1,191	1,544	1,765	2,231	2,503
AtrFib	752,964	342	367	440	504	591	647	752
Bari	14	.	.	.	.	.	.	.
Bleed	396,063	298	274	318	309	371	308	326
CABG	44,125	.	.	.	.	.	.	.
CKD	218,502	398	381	334	395	434	410	429
COPD	750,894	816	1,019	1,026	1,196	1,180	1,268	1,341
Cancer	4,079,961	6,552	8,725	9,689	10,745	11,613	13,190	15,189
DKD	41,429	46	50	53	57	66	82	69
DMcompl	155,493	4	6	6	6	5	10	11
DiaEye	229,465	1,833	2,035	2,423	2,727	3,552	4,319	4,814
DiaFoot	34,012	.	.	.	.	.	.	.
Dial	15,397	.	.	.	.	.	.	.
HF	432,557	500	632	701	795	897	1,006	1,237
HmStr	126,008	598	719	738	772	946	1,031	1,112
Hypo	97,435	331	363	433	513	440	471	537
IscStr	516,149	768	932	1,120	1,131	1,316	1,671	1,740
Keto	26,118	.	.	.	.	.	.	.
MI	583,196	2,634	3,094	3,064	3,439	3,650	4,290	4,568
Neuro	62,660	1,016	1,105	1,246	1,340	1,456	1,544	1,670
Other	108,373	.	.	.	.	.	.	.
PAD	667,245	511	688	836	930	1,029	1,227	1,544
PCIsten	20,738	.	.	.	.	.	.	.
PeriAng	190,503	7,448	8,641	9,278	9,444	9,637	9,937	9,758
TIA	207,302	558	686	694	788	906	1,091	1,211
UnstAng	126,914	.	.	.	.	.	.	.

(Continued)

	Date							
	1984	1985	1986	1987	1988	1989	1990	1991
compl								
Amp	.	.	.	.	.	.	.	.
Angina	2,900	3,694	4,427	5,426	6,815	8,111	8,902	11,267
AtrFib	847	1,065	1,272	1,613	1,925	2,479	3,021	3,721
Bari	.	.	.	.	.	.	.	.
Bleed	330	332	369	354	420	395	502	526
CABG	.	.	.	.	.	.	.	.
CKD	523	720	652	464	474	491	463	624
COPD	1,610	1,884	2,040	2,240	2,544	3,065	3,825	4,724
Cancer	15,990	17,703	19,903	22,738	25,813	28,629	35,127	40,342
DKD	70	80	103	96	120	207	171	193
DMcompl	11	20	39	28	119	91	204	321
DiaEye	5,119	5,647	6,662	7,152	8,561	9,349	9,251	8,733
DiaFoot	.	.	*	*	.	.	*	4
Dial	.	.	.	*	.	.	.	9
HF	1,335	1,685	1,859	2,320	2,902	3,677	4,936	6,034
HmStr	1,205	1,256	1,343	1,445	1,468	1,632	1,795	2,101
Hypo	596	642	663	737	738	818	872	960
IscStr	1,999	2,101	2,069	2,117	2,207	2,372	2,684	3,085
Keto	.	.	*	*	*	*	.	*
MI	5,003	5,813	6,396	7,073	7,547	7,821	8,437	9,564
Neuro	1,720	1,817	2,062	2,108	2,343	2,291	2,176	2,340
Other	.	.	.	.	.	.	.	.
PAD	1,780	1,844	2,043	2,193	2,518	2,753	3,442	4,424
PCIsten	.	.	.	.	.	.	.	.
PeriAng	9,989	10,521	11,033	5,431	4,805	4,592	4,497	4,630
TIA	1,309	1,533	1,710	1,809	2,063	2,324	2,640	3,173
UnstAng	.	.	.	.	.	*	*	6

(Continued)

	Date							
	1992	1993	1994	1995	1996	1997	1998	1999
compl								
Amp	.	.	.	.	159	143	138	146
Angina	14,179	17,303	23,955	29,454	35,132	39,128	41,720	37,796
AtrFib	5,099	7,002	11,097	14,221	16,955	19,554	22,436	26,325
Bari	.	.	.	.	.	.	.	.
Bleed	617	957	11,698	13,738	13,951	14,152	15,096	15,373
CABG	.	.	.	.	2,056	2,356	2,662	3,005
CKD	882	864	2,728	2,187	2,340	2,187	2,265	3,303
COPD	6,438	10,415	15,188	20,620	23,621	27,418	30,499	33,229
Cancer	51,739	88,044	142,598	144,761	145,634	150,686	147,842	149,616
DKD	229	525	1,253	1,097	1,309	1,250	1,368	1,546
DMcompl	386	3,112	4,588	5,190	5,055	5,836	6,346	7,430
DiaEye	9,127	10,215	2,689	3,198	3,544	4,091	5,128	5,552
DiaFoot	8	94	663	771	841	1,184	1,598	1,875
Dial	17	86	923	2,170	2,044	2,555	2,865	2,519
HF	7,812	10,528	13,690	15,350	15,454	14,983	16,378	16,904
HmStr	2,345	2,727	4,065	4,442	4,660	4,712	5,109	5,017
Hypo	1,098	1,195	2,037	3,288	3,465	3,646	3,552	4,144
IscStr	3,494	5,111	17,156	20,605	21,323	22,431	24,264	26,631
Keto	*	46	739	760	766	812	846	804

MI	10,339	11,685	16,787	19,303	17,709	17,089	16,819	16,935
Neuro	1,946	2,431	986	944	1,131	1,122	1,334	1,422
Other	.	.	.	.	2,558	2,626	2,916	4,750
PAD	5,379	7,541	23,861	25,570	28,048	26,885	27,251	27,482
PCIsten	.	.	.	.	134	243	422	1,397
PeriAng	4,177	4,406	1,586	1,499	2,047	2,016	2,055	2,298
TIA	3,502	4,129	5,591	7,200	7,168	7,325	7,746	7,193
UnstAng	11	90	2,835	3,545	4,052	4,505	4,993	6,009

(Continued)

	Date							
	2000	2001	2002	2003	2004	2005	2006	2007
compl								
Amp	134	176	168	200	193	207	192	172
Angina	36,037	35,094	35,706	33,888	32,354	32,772	31,498	27,318
AtrFib	28,983	31,385	29,121	27,057	27,030	28,084	30,463	32,232
Bari	.	.	.	.	.	.	*	*
Bleed	16,845	17,287	18,080	18,233	18,677	18,219	18,499	18,408
CABG	2,880	2,774	3,169	2,781	2,329	2,113	2,021	1,970
CKD	4,129	5,614	7,128	7,765	8,600	9,260	10,339	12,022
COPD	33,099	35,554	33,565	32,806	32,158	32,299	33,025	31,879
Cancer	139,347	145,119	150,414	149,286	149,968	151,431	160,431	166,977
DKD	1,584	1,714	1,590	1,791	1,780	1,809	2,117	1,484
DMcompl	6,838	7,023	7,435	7,740	7,383	9,317	6,916	5,862
DiaEye	5,167	5,300	5,097	7,290	7,729	8,849	7,172	7,051
DiaFoot	1,901	1,594	1,580	1,509	1,392	1,188	1,411	1,407
Dial	2,103	.	.	8	9	4	16	18
HF	16,944	16,909	17,364	16,982	16,780	16,517	17,375	15,639
HmStr	4,874	4,836	4,821	5,061	5,113	4,880	4,582	4,590
Hypo	3,903	4,262	4,543	4,971	4,708	4,573	4,438	4,148
IscStr	25,880	25,275	25,248	24,518	23,791	22,325	21,924	19,909
Keto	830	803	953	1,069	1,070	987	1,084	1,221
MI	18,325	20,356	23,944	25,263	25,187	24,546	23,264	23,629
Neuro	1,963	1,806	1,745	1,700	1,319	1,546	1,224	1,057
Other	5,114	5,076	5,074	5,489	5,865	5,453	5,597	6,057
PAD	26,249	26,307	27,707	27,599	27,118	28,212	27,879	28,195
PCIsten	709	831	1,291	1,480	1,715	1,903	1,739	1,723
PeriAng	2,381	2,575	2,828	2,931	2,992	3,013	3,118	2,621
TIA	6,863	7,053	7,216	7,226	7,247	7,695	7,882	7,811
UnstAng	8,030	7,527	8,192	7,572	6,677	6,827	6,802	5,849

(Continued)

	Date							
	2008	2009	2010	2011	2012	2013	2014	2015
compl								
Amp	173	206	225	179	173	218	206	208
Angina	25,096	28,760	28,972	28,254	27,069	27,519	24,401	22,947
AtrFib	35,398	40,019	41,170	44,999	48,707	54,362	54,392	57,287
Bari	*	.	.	.	4	*	4	*
Bleed	17,734	18,421	19,085	19,021	19,986	21,242	23,286	22,026

CABG	1,674	1,810	1,770	1,785	1,627	1,728	1,814	1,801
CKD	12,621	13,771	14,307	15,910	17,505	19,172	17,529	18,882
COPD	33,010	34,114	33,751	35,447	35,978	37,977	38,029	40,997
Cancer	190,242	191,686	189,552	198,961	191,358	199,012	196,123	207,186
DKD	1,972	1,978	1,491	1,693	1,925	3,342	1,896	3,223
DMcompl	8,511	7,781	5,657	6,218	6,622	9,581	5,004	8,781
DiaEye	7,951	6,602	5,427	6,386	6,445	6,269	4,256	6,753
DiaFoot	1,534	1,679	1,847	1,898	1,766	2,026	2,045	2,194
Dial	16	8	5	*	*	6	10	*
HF	16,719	18,154	18,186	19,096	19,544	21,405	20,913	22,415
HmStr	4,521	4,446	4,484	4,227	4,436	4,586	4,600	4,713
Hypo	4,349	4,256	4,084	3,698	3,456	3,689	3,490	3,328
IscStr	19,952	19,835	19,562	18,944	20,031	19,944	20,469	20,215
Keto	1,351	1,427	1,397	1,478	1,727	1,904	1,992	2,044
MI	22,956	23,192	23,870	23,151	22,854	23,943	24,890	24,767
Neuro	1,741	1,398	1,351	1,422	1,579	1,802	1,399	2,058
Other	5,175	5,980	5,647	6,880	6,864	6,967	6,910	7,375
PAD	29,546	30,073	30,617	31,186	31,666	32,898	30,575	31,639
PCIsten	1,470	1,734	793	605	672	604	543	730
PeriAng	3,002	2,803	2,857	2,985	3,163	4,377	4,118	5,014
TIA	8,056	8,484	9,165	9,196	9,896	10,310	10,289	10,564
UnstAng	6,095	5,547	5,399	5,475	5,451	5,321	5,414	4,685

First complication dates for each patient

11:46 Saturday, May 5, 2018 2

The CONTENTS Procedure

Data Set Name	DAFDAT.WCOMPL	Observations	1997992
Member Type	DATA	Variables	28
Engine	V9	Indexes	0
Created	05/05/2018 11:50:02	Observation Length	232
Last Modified	05/05/2018 11:50:02	Deleted Observations	0
Protection		Compressed	NO
Data Set Type		Sorted	NO
Label			
Data Representation	WINDOWS_64		
Encoding	wlatin1 Western (Windows)		

Engine/Host Dependent Information

Data Set Page Size	65536
Number of Data Set Pages	7086
First Data Page	*
Max Obs per Page	282
Obs in First Data Page	265
Number of Data Set Repairs	0
ExtendObsCounter	YES
Filename	E:\workdata\705093\BxC\daffodil\DATA\wcompl.sas7bdat
Release Created	9.0401M3
Host Created	X64_SRV12

Variables in Creation Order

#	Variable	Type	Len	Format	Informat	Label
*	pnr	Char	12	\$12.	\$10.	Personnummer
*	doTIA	Num	8	DATE9.		
*	doAngina	Num	8	DATE9.		
4	doBleed	Num	8	DATE9.		

5	doCOPD	Num	8	DATE9.
6	doPAD	Num	8	DATE9.
7	doHF	Num	8	DATE9.
8	doCancer	Num	8	DATE9.
9	doDMcompl	Num	8	DATE9.
10	doNeuro	Num	8	DATE9.
11	doDKD	Num	8	DATE9.
12	doDiaEye	Num	8	DATE9.
13	doHypo	Num	8	DATE9.
14	doAtrFib	Num	8	DATE9.
15	doMI	Num	8	DATE9.
16	doUnstAng	Num	8	DATE9.
17	doHmStr	Num	8	DATE9.
18	doDiaFoot	Num	8	DATE9.
19	doOther	Num	8	DATE9.
20	doPeriAng	Num	8	DATE9.
21	doIscStr	Num	8	DATE9.
22	doAmp	Num	8	DATE9.
23	doCKD	Num	8	DATE9.
24	doPCIsten	Num	8	DATE9.
25	doCABG	Num	8	DATE9.
26	doKeto	Num	8	DATE9.
27	doDial	Num	8	DATE9.
28	doBari	Num	8	DATE9.

4.4 04a-rmps

Reads all non-DM medication and produces a dataset `wmed` with date of first purchase of a range of medications.

1 "Program: 04a-rmps.sas" 12:25 Friday, May 4, 2018

NOTE: AUTOEXEC processing completed.

```

1      %macro med ;
2      data med ;
3          set %do i = 1995 %to 2017 ;
4              grund.lmdb&i. ( keep = pnr atc eksd
5                          where = ( substr(atc,1,3) in
6                              ('A08','B01','C01','C03','C07','C08','C09','C10','H02') ) )
7              %end ; ;
8      * Grouping of non-DM medicines ;
9          medgr = put( substr(atc,1,3), $med3oth. ) ;
10         if ( medgr eq "Other" ) then medgr = put( substr(atc,1,4), $med4oth. ) ;
11         if ( medgr eq "Other" ) then medgr = put( substr(atc,1,5), $med5oth. ) ;
12         if ( medgr eq "Other" ) then medgr = put( substr(atc,1,7), $med7oth. ) ;
13         if ( medgr eq "Other" ) then delete ;
14         if ( atc eq "C09DX04" ) then delete ;
15     run ;
16     %mend ;
17     %med ;

```

NOTE: There were 1569620 observations read from the data set GRUND.LMDB1995.
 WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',

```

'H02');
NOTE: There were 1699112 observations read from the data set GRUND.LMDB1996.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 1805191 observations read from the data set GRUND.LMDB1997.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 1936488 observations read from the data set GRUND.LMDB1998.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 2085940 observations read from the data set GRUND.LMDB1999.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 2227335 observations read from the data set GRUND.LMDB2000.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 2441676 observations read from the data set GRUND.LMDB2001.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 2732372 observations read from the data set GRUND.LMDB2002.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 3083882 observations read from the data set GRUND.LMDB2003.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 3468769 observations read from the data set GRUND.LMDB2004.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 3767302 observations read from the data set GRUND.LMDB2005.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 4089355 observations read from the data set GRUND.LMDB2006.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 4384245 observations read from the data set GRUND.LMDB2007.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 4709751 observations read from the data set GRUND.LMDB2008.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 4826535 observations read from the data set GRUND.LMDB2009.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 4925490 observations read from the data set GRUND.LMDB2010.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 4987124 observations read from the data set GRUND.LMDB2011.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 5023355 observations read from the data set GRUND.LMDB2012.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 4915248 observations read from the data set GRUND.LMDB2013.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 4762917 observations read from the data set GRUND.LMDB2014.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 4553864 observations read from the data set GRUND.LMDB2015.
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
NOTE: There were 4327744 observations read from the data set GRUND.LMDB2016.

```

```
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
```

NOTE: There were 2090999 observations read from the data set GRUND.LMDB2017.

```
WHERE SUBSTR(atc, 1, 3) in ('A08', 'B01', 'C01', 'C03', 'C07', 'C08', 'C09', 'C10',
'H02');
```

NOTE: The data set WORK.MED has 75682297 observations and 4 variables.

NOTE: DATA statement used (Total process time):

```
real time          1:26.07
```

```
cpu time           1:25.78
```

18

```
19      proc sort  data = med ;
```

```
20          by pnr medgr eksd ;
```

```
21      run ;
```

NOTE: There were 75682297 observations read from the data set WORK.MED.

NOTE: The data set WORK.MED has 75682297 observations and 4 variables.

NOTE: PROCEDURE SORT used (Total process time):

```
real time          17.40 seconds
```

```
cpu time           41.34 seconds
```

22

```
23      * late prescriptions for use with SGLT2 ;
```

24

```
25      data dafdat.lmed ;
```

```
26          set med ;
```

```
27          if eksd ge '01dec2011'd ;
```

```
28      run ;
```

NOTE: There were 75682297 observations read from the data set WORK.MED.

NOTE: The data set DAFDAT.LMED has 25061393 observations and 4 variables.

NOTE: DATA statement used (Total process time):

```
real time          8.93 seconds
```

```
cpu time           5.84 seconds
```

29

```
30      data med ( keep = pnr eksd medgr ) ;
```

```
31          set med ;
```

```
32          by pnr medgr ;
```

```
33          if first.medgr ;
```

```
34      run ;
```

NOTE: There were 75682297 observations read from the data set WORK.MED.

NOTE: The data set WORK.MED has 2916253 observations and 3 variables.

NOTE: DATA statement used (Total process time):

```
real time          7.25 seconds
```

```
cpu time           7.24 seconds
```

35

```
36      title1 'All first prescriptions - entire population' ;
```

```
37      proc tabulate data = med missing noseps ;
```

```
38          class medgr ;
```

```
39          table medgr, n * f=comma12. / rts=60 ;
```

```
40          format medgr $lmedgr. ;
```

```
41      run ;
```

NOTE: There were 2916253 observations read from the data set WORK.MED.

NOTE: The PROCEDURE TABULATE printed page 1.

NOTE: PROCEDURE TABULATE used (Total process time):
 real time 0.50 seconds
 cpu time 0.34 seconds

```

42      title1 ;
43
44      proc transpose data = med
45                  out = dafdat.wmed
46                  prefix = do ;
47      by pnr ;
48      var eksd ;
49      id medgr ;
50      run ;

```

NOTE: There were 2916253 observations read from the data set WORK.MED.
 NOTE: The data set DAFDAT.WMED has 549969 observations and 23 variables.
 NOTE: PROCEDURE TRANSPOSE used (Total process time):
 real time 3.14 seconds
 cpu time 2.18 seconds

```

51
52      %let medddates =
53      doACE doAP1 doARB doAlA doAmi doAsp doBB1 doCcs doDHP doDTI
54      doDXI doDgo doFla doHCD doNHP doRPA doSta doTHZ doWrf doWtL ;
55
56      title1 'All medications for persons in DK after 1 dec 2011' ;
57      proc contents data = dafdat.wmed ;
58      run ;

```

NOTE: PROCEDURE CONTENTS used (Total process time):
 real time 0.01 seconds
 cpu time 0.01 seconds

NOTE: The PROCEDURE CONTENTS printed page 2.

```

59
60      title1 'First (other) medication dates for persons in DK' ;
61      proc contents data = dafdat.wmed ;
62      run ;

```

NOTE: PROCEDURE CONTENTS used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

NOTE: The PROCEDURE CONTENTS printed page 3.

```

63
64      proc tabulate data = dafdat.wmed missing noseps ;
65      class &medddates. ;
66      table all &medddates. ,
67          n * f=comma12.
68          / rts = 15 ;
69      format &medddates. year4. ;
70      keylabel n = ' ' ;
71      run ;

```

NOTE: There were 549969 observations read from the data set DAFDAT.WMED.
 NOTE: The PROCEDURE TABULATE printed page 4.
 NOTE: PROCEDURE TABULATE used (Total process time):
 real time 0.40 seconds

cpu time 1.51 seconds

72 title1 ;

NOTE: SAS Institute Inc., SAS Campus Drive, Cary, NC USA 27513-2414

NOTE: The SAS System used:

real time 2:04.07

cpu time 2:24.42

4.4.1 04a-rmps.lst

All first prescriptions - entire population

12:25 Friday, May 4, 2018 1

	N
medgr	
ACE: ACE inhibitors	319,467
AP1: Other antiplatelets	34,601
ARB: ARB	187,722
ALA: Aldosterone antagonists	87,902
Ami: Amiodarone	13,626
Asp: Low dose aspirin	300,987
BBl: Beta blockers	254,657
Ccs: Corticosteroids	223,780
DHP: Dihydropyridines (calcium channel blockers)	236,240
DTI: Direct thrombin inhibitor	11,465
DXI: Direct factor Xa inhibitors	22,135
Dgo: Digoxin	76,966
Fla: Flekanide	1,929
HCD: High ceiling diuretics (loop-diuretics)	248,131
NHP: Non-hydropyridines (calcium channel blockers)	54,401
RPA: Receptor P2Y12 antagonists	80,047
Sta: Statins	340,655
THZ: Low ceiling diuretics (thiazides)	260,951
Wrf: Warfarin	72,389
WtL: Weight loss drugs	88,202

All medications for persons in DK after * dec 2011

12:25 Friday, May 4, 2018 2

The CONTENTS Procedure

Data Set Name	DAFDAT.WMED	Observations	549969
Member Type	DATA	Variables	23
Engine	V9	Indexes	0
Created	04/05/2018 12:27:15	Observation Length	140
Last Modified	04/05/2018 12:27:15	Deleted Observations	0
Protection		Compressed	NO
Data Set Type		Sorted	NO
Label			
Data Representation	WINDOWS_64		
Encoding	wlatin1 Western (Windows)		

Engine/Host Dependent Information

Data Set Page Size	65536
Number of Data Set Pages	1178

```

First Data Page          *
Max Obs per Page        467
Obs in First Data Page   443
Number of Data Set Repairs 0
ExtendObsCounter        YES
Filename                 E:\workdata\705093\BxC\daffodil\DATA\wmed.sas7bdat
Release Created          9.0401M3
Host Created             X64_SRV12

```

Alphabetic List of Variables and Attributes

#	Variable	Type	Len	Format	Label
*	_LABEL_	Char	40		LABEL OF FORMER VARIABLE
*	_NAME_	Char	8		NAME OF FORMER VARIABLE
4	doACE	Num	4	YYMMDDN8.	
21	doAPL	Num	4	YYMMDDN8.	
7	doARB	Num	4	YYMMDDN8.	
14	doALA	Num	4	YYMMDDN8.	
15	doAmi	Num	4	YYMMDDN8.	
8	doAsp	Num	4	YYMMDDN8.	
6	doBBl	Num	4	YYMMDDN8.	
9	doCcs	Num	4	YYMMDDN8.	
10	doDHP	Num	4	YYMMDDN8.	
22	doDTI	Num	4	YYMMDDN8.	
18	doDXI	Num	4	YYMMDDN8.	
16	doDgo	Num	4	YYMMDDN8.	
23	doFla	Num	4	YYMMDDN8.	
11	doHCD	Num	4	YYMMDDN8.	
20	doNHP	Num	4	YYMMDDN8.	
19	doRPA	Num	4	YYMMDDN8.	
5	doSta	Num	4	YYMMDDN8.	
12	doTHZ	Num	4	YYMMDDN8.	
17	doWrf	Num	4	YYMMDDN8.	
13	doWtL	Num	4	YYMMDDN8.	
*	pnr	Char	12	\$12.	

First (other) medication dates for persons in DK

12:25 Friday, May 4, 2018 3

The CONTENTS Procedure

Data Set Name	DAFDAT.WMED	Observations	549969
Member Type	DATA	Variables	23
Engine	V9	Indexes	0
Created	04/05/2018 12:27:15	Observation Length	140
Last Modified	04/05/2018 12:27:15	Deleted Observations	0
Protection		Compressed	NO
Data Set Type		Sorted	NO
Label			
Data Representation	WINDOWS_64		
Encoding	wlatin1 Western (Windows)		

Engine/Host Dependent Information

```

Data Set Page Size      65536
Number of Data Set Pages 1178
First Data Page         *
Max Obs per Page        467
Obs in First Data Page   443
Number of Data Set Repairs 0

```

```

ExtendObsCounter      YES
Filename              E:\workdata\705093\BxC\daffodil\DATA\wmed.sas7bdat
Release Created       9.0401M3
Host Created          X64_SRV12

```

Alphabetic List of Variables and Attributes

#	Variable	Type	Len	Format	Label
*	_LABEL_	Char	40		LABEL OF FORMER VARIABLE
*	_NAME_	Char	8		NAME OF FORMER VARIABLE
4	doACE	Num	4	YYMMDDN8.	
21	doAP1	Num	4	YYMMDDN8.	
7	doARB	Num	4	YYMMDDN8.	
14	doAlA	Num	4	YYMMDDN8.	
15	doAmi	Num	4	YYMMDDN8.	
8	doAsp	Num	4	YYMMDDN8.	
6	doBB1	Num	4	YYMMDDN8.	
9	doCcs	Num	4	YYMMDDN8.	
10	doDHP	Num	4	YYMMDDN8.	
22	doDTI	Num	4	YYMMDDN8.	
18	doDXI	Num	4	YYMMDDN8.	
16	doDgo	Num	4	YYMMDDN8.	
23	doFla	Num	4	YYMMDDN8.	
11	doHCD	Num	4	YYMMDDN8.	
20	doNHP	Num	4	YYMMDDN8.	
19	doRPA	Num	4	YYMMDDN8.	
5	doSta	Num	4	YYMMDDN8.	
12	doTHZ	Num	4	YYMMDDN8.	
17	doWrf	Num	4	YYMMDDN8.	
13	doWtL	Num	4	YYMMDDN8.	
*	pnr	Char	12	\$12.	

First (other) medication dates for persons in DK

12:25 Friday, May 4, 2018 4

All	549,969
doACE	
.	230,502
1995	40,622
1996	10,823
1997	10,341
1998	9,575
1999	10,275
2000	12,099
2001	13,904
2002	14,840
2003	16,752
2004	18,505
2005	18,467
2006	18,256
2007	18,186
2008	17,908
2009	27,156
2010	15,717
2011	11,634
2012	9,044
2013	7,484
2014	5,911
2015	5,193
2016	4,845

2017	1,930
doAP1	
.	515,368
1995	169
1996	126
1997	397
1998	1,422
1999	2,735
2000	2,888
2001	2,969
2002	3,166
2003	2,184
2004	1,980
2005	2,154
2006	2,100
2007	2,115
2008	2,448
2009	2,456
2010	2,053
2011	1,328
2012	854
2013	552
2014	287
2015	109
2016	74
2017	35
doARB	
.	362,247
1995	4,189
1996	3,450
1997	5,003
1998	8,096
1999	7,839
2000	6,177
2001	8,137
2002	11,769
2003	11,259
2004	10,249
2005	10,258
2006	10,191
2007	11,193
2008	9,958
2009	6,820
2010	10,204
2011	11,567
2012	9,332
2013	8,279
2014	7,377
2015	6,912
2016	6,501
2017	2,962
doA1A	
.	462,067
1995	6,839
1996	2,083
1997	1,896
1998	1,955
1999	3,186
2000	4,859
2001	4,628
2002	4,383
2003	4,100

2004	4,188
2005	4,418
2006	4,197
2007	4,035
2008	4,017
2009	4,035
2010	3,922
2011	4,233
2012	4,133
2013	4,206
2014	3,762
2015	3,640
2016	3,488
2017	1,699
doAmi	
.	536,343
1995	448
1996	222
1997	251
1998	296
1999	344
2000	490
2001	605
2002	591
2003	672
2004	619
2005	717
2006	766
2007	755
2008	766
2009	735
2010	700
2011	709
2012	707
2013	735
2014	738
2015	709
2016	702
2017	349
doAsp	
.	248,982
1995	45,554
1996	13,159
1997	12,084
1998	12,098
1999	12,332
2000	13,620
2001	16,633
2002	18,556
2003	18,255
2004	17,032
2005	15,286
2006	15,869
2007	15,117
2008	15,698
2009	12,161
2010	9,980
2011	8,666
2012	6,991
2013	5,704
2014	5,120
2015	4,761

2016	4,334
2017	1,977
doBB1	
.	295,312
1995	41,834
1996	10,354
1997	10,251
1998	10,583
1999	11,352
2000	12,903
2001	13,377
2002	14,818
2003	13,663
2004	13,533
2005	12,237
2006	10,603
2007	10,172
2008	9,306
2009	8,934
2010	8,509
2011	8,208
2012	7,654
2013	6,717
2014	6,088
2015	5,766
2016	5,285
2017	2,510
doCcs	
.	326,189
1995	28,829
1996	15,454
1997	13,270
1998	12,334
1999	11,269
2000	11,014
2001	10,219
2002	9,675
2003	8,967
2004	8,903
2005	8,959
2006	8,676
2007	8,407
2008	8,224
2009	8,187
2010	7,985
2011	7,741
2012	7,124
2013	6,899
2014	6,438
2015	6,229
2016	5,993
2017	2,984
doDHP	
.	313,729
1995	28,361
1996	8,566
1997	8,536
1998	8,803
1999	8,287
2000	8,028
2001	8,699
2002	8,672

2003	8,466
2004	9,750
2005	11,611
2006	12,420
2007	14,051
2008	13,504
2009	13,750
2010	12,950
2011	11,674
2012	9,564
2013	8,069
2014	6,836
2015	6,549
2016	6,187
2017	2,907
doDTI	
.	538,504
2008	48
2009	241
2010	423
2011	1,770
2012	3,052
2013	2,607
2014	1,891
2015	737
2016	515
2017	181
doDXI	
.	527,834
2009	236
2010	419
2011	420
2012	758
2013	2,598
2014	3,651
2015	4,823
2016	5,749
2017	3,481
doDgo	
.	473,003
1995	22,199
1996	4,090
1997	3,572
1998	3,750
1999	3,526
2000	3,222
2001	3,142
2002	2,836
2003	2,820
2004	2,624
2005	2,494
2006	2,306
2007	2,262
2008	2,193
2009	2,162
2010	2,125
2011	2,128
2012	2,032
2013	1,948
2014	1,773
2015	1,602
2016	1,482

2017	678
doFla	
.	548,040
1995	352
1996	100
1997	99
1998	102
1999	113
2000	113
2001	102
2002	71
2003	52
2004	49
2005	51
2006	59
2007	65
2008	50
2009	62
2010	51
2011	92
2012	75
2013	74
2014	62
2015	53
2016	56
2017	26
doHCD	
.	301,838
1995	48,541
1996	12,361
1997	10,790
1998	10,244
1999	10,065
2000	9,536
2001	9,803
2002	9,618
2003	9,426
2004	9,381
2005	9,702
2006	9,599
2007	9,438
2008	9,169
2009	9,371
2010	9,506
2011	9,239
2012	8,472
2013	8,065
2014	7,793
2015	7,360
2016	7,254
2017	3,398
doNHP	
.	495,568
1995	20,915
1996	3,758
1997	3,157
1998	3,080
1999	2,772
2000	2,503
2001	2,341
2002	1,992
2003	1,916

2004	1,880
2005	1,543
2006	1,454
2007	1,269
2008	1,066
2009	917
2010	771
2011	669
2012	592
2013	480
2014	460
2015	377
2016	320
2017	169
doRPA	
.	469,922
1998	10
1999	554
2000	1,519
2001	1,939
2002	3,061
2003	3,736
2004	3,816
2005	3,957
2006	3,813
2007	3,824
2008	3,860
2009	3,877
2010	4,917
2011	6,671
2012	6,527
2013	6,321
2014	6,594
2015	6,379
2016	5,926
2017	2,746
doSta	
.	209,314
1995	6,291
1996	3,558
1997	3,974
1998	5,617
1999	7,947
2000	8,494
2001	10,861
2002	17,678
2003	26,305
2004	29,372
2005	26,444
2006	28,397
2007	27,031
2008	26,612
2009	20,882
2010	18,586
2011	16,812
2012	14,103
2013	11,402
2014	9,831
2015	8,908
2016	8,225
2017	3,325
doTHZ	

.	289,018
1995	47,202
1996	13,633
1997	12,955
1998	13,284
1999	12,888
2000	13,223
2001	13,316
2002	12,932
2003	15,429
2004	14,965
2005	14,620
2006	12,038
2007	10,573
2008	9,679
2009	8,692
2010	7,637
2011	6,665
2012	5,342
2013	4,360
2014	3,813
2015	3,326
2016	2,973
2017	1,406
doWrf	
.	477,580
1995	2,849
1996	1,484
1997	1,826
1998	2,474
1999	3,238
2000	3,344
2001	3,565
2002	3,719
2003	4,013
2004	4,108
2005	4,314
2006	4,283
2007	4,113
2008	3,795
2009	3,715
2010	3,761
2011	3,972
2012	3,328
2013	3,175
2014	2,769
2015	2,310
2016	1,666
2017	568
doWtL	
.	461,767
1995	31,629
1996	14,997
1997	10,068
1998	7,434
1999	6,598
2000	4,432
2001	3,483
2002	2,179
2003	473
2004	415
2005	501

2006	698
2007	1,342
2008	972
2009	1,009
2010	493
2011	354
2012	288
2013	258
2014	188
2015	165
2016	148
2017	78

4.5 04d-rmps

Reads and restricts the register-created dataset `prmps` to the type 2 patients.

Processes the records of anti-diabetic medicine from the RMPS and creates three files; one with one record per T2 patient (`pRMPS`) with dates of first purchase of each group of diabetes drugs. There are separate first purchase dates for any type of a given drug which also includes combination pills, and first purchase date for single drug pills.

The other data sets created, (`disp`) has one record per anti-diabetic prescription, respectively one record per drug-type dispensation (`xdisp`). The latter means that combination pills contribute one record per drug in the pill.

1 "Program: 04d-rmps.sas" 19:40 Tuesday, May 8, 2018

NOTE: AUTOEXEC processing completed.

```

1      * Base population of persons that we use ( DMdreg ) ;
2      * including the first dates of mono drug (donlXX) or any (danyXX) ;
3      data dafdat.pRMPS ;
4          merge DMdat.prmps ( in = drug )
5                  DMdat.DMdreg ( in = t2dm
6                                where = ( DMtp eq "T2" ) ) ;
7          by pnr ;
8          if drug and t2dm ;
9      run ;
```

NOTE: There were 426299 observations read from the data set DMDAT.PRMPs.

NOTE: There were 383033 observations read from the data set DMDAT.DMDREG.
WHERE DMtp='T2';

NOTE: The data set DAFDAT.PRMPs has 383033 observations and 30 variables.

NOTE: DATA statement used (Total process time):

```

real time      2.34 seconds
cpu time       0.21 seconds
```

```

10
11      %let drdates = donlMet    danyMet
12                      donlSU     danySU
13                      donlTZD    danyTZD
```

```

14          donlDPP4  danyDPP4
15                  danyGLP1
16          donlSGLT2 danySGLT2
17          donlAca   danyAca
18                  danyMeg
19          dofIns doiIns domIns dolIns ;
20
21          title1 "T2 patients from the RPMS" ;
22          proc tabulate data = dafdat.pRMPs missing noseps ;
23              class &drdates. doOAD doRMPs ;
24              table all &drdates. doOAD doRMPs,
25                  n * f=comma10.
26                  / rts = 15 ;
27              format &drdates. doOAD doRMPs year4. ;
28              keylabel n = ' ' ;
29          run ;

```

NOTE: There were 383033 observations read from the data set DAFDAT.PRMPs.

NOTE: The PROCEDURE TABULATE printed page 1.

NOTE: PROCEDURE TABULATE used (Total process time):

real time 0.39 seconds

cpu time 1.03 seconds

```

30          title1 ;
31
32          * Read the entire drug register files (again) and match dispensations to
32          ! persons;
33          %macro med ;
34          data rmps ;
35              length druggr $ 7 ;
36              set %do i = 1995 %to 2017 ;
37                  grund.lmdb&i. ( keep = pnr ATC eksd apk volume packsize doso
38                      where = ( substr(atc,1,3) eq 'A10' ) )
39              %end ; ;
40          * Grouping of drugs as a character ;
41                  druggr = put(          atc          , $atc5grp. ) ;
42          if ( druggr eq "Other" ) then druggr = put( substr(atc,1,5), $atc4grp. ) ;
43          run ;
44          %mend ;
45          %med ;

```

NOTE: There were 561710 observations read from the data set GRUND.LMDB1995.
WHERE SUBSTR(atc, 1, 3)='A10';

NOTE: There were 626242 observations read from the data set GRUND.LMDB1996.
WHERE SUBSTR(atc, 1, 3)='A10';

NOTE: There were 670823 observations read from the data set GRUND.LMDB1997.
WHERE SUBSTR(atc, 1, 3)='A10';

NOTE: There were 732412 observations read from the data set GRUND.LMDB1998.
WHERE SUBSTR(atc, 1, 3)='A10';

NOTE: There were 795111 observations read from the data set GRUND.LMDB1999.
WHERE SUBSTR(atc, 1, 3)='A10';

NOTE: There were 826954 observations read from the data set GRUND.LMDB2000.
WHERE SUBSTR(atc, 1, 3)='A10';

NOTE: There were 906834 observations read from the data set GRUND.LMDB2001.
WHERE SUBSTR(atc, 1, 3)='A10';

NOTE: There were 985199 observations read from the data set GRUND.LMDB2002.
WHERE SUBSTR(atc, 1, 3)='A10';

NOTE: There were 1067000 observations read from the data set GRUND.LMDB2003.
WHERE SUBSTR(atc, 1, 3)='A10';

NOTE: There were 1179974 observations read from the data set GRUND.LMDB2004.
WHERE SUBSTR(atc, 1, 3)='A10';

NOTE: There were 1290910 observations read from the data set GRUND.LMDB2005.
 WHERE SUBSTR(atc, 1, 3)='A10';
 NOTE: There were 1407903 observations read from the data set GRUND.LMDB2006.
 WHERE SUBSTR(atc, 1, 3)='A10';
 NOTE: There were 1519940 observations read from the data set GRUND.LMDB2007.
 WHERE SUBSTR(atc, 1, 3)='A10';
 NOTE: There were 1659418 observations read from the data set GRUND.LMDB2008.
 WHERE SUBSTR(atc, 1, 3)='A10';
 NOTE: There were 1751050 observations read from the data set GRUND.LMDB2009.
 WHERE SUBSTR(atc, 1, 3)='A10';
 NOTE: There were 1875341 observations read from the data set GRUND.LMDB2010.
 WHERE SUBSTR(atc, 1, 3)='A10';
 NOTE: There were 2003132 observations read from the data set GRUND.LMDB2011.
 WHERE SUBSTR(atc, 1, 3)='A10';
 NOTE: There were 2101706 observations read from the data set GRUND.LMDB2012.
 WHERE SUBSTR(atc, 1, 3)='A10';
 NOTE: There were 2130959 observations read from the data set GRUND.LMDB2013.
 WHERE SUBSTR(atc, 1, 3)='A10';
 NOTE: There were 2152197 observations read from the data set GRUND.LMDB2014.
 WHERE SUBSTR(atc, 1, 3)='A10';
 NOTE: There were 2164328 observations read from the data set GRUND.LMDB2015.
 WHERE SUBSTR(atc, 1, 3)='A10';
 NOTE: There were 2252557 observations read from the data set GRUND.LMDB2016.
 WHERE SUBSTR(atc, 1, 3)='A10';
 NOTE: There were 1130278 observations read from the data set GRUND.LMDB2017.
 WHERE SUBSTR(atc, 1, 3)='A10';
 NOTE: The data set WORK.RMPS has 31791978 observations and 8 variables.
 NOTE: DATA statement used (Total process time):
 real time 8:17.41
 cpu time 50.09 seconds

```

46
47      proc sort  data = rmps ;
48          by pnr druggr eksd ;
49      run ;

```

NOTE: There were 31791978 observations read from the data set WORK.RMPS.
 NOTE: The data set WORK.RMPS has 31791978 observations and 8 variables.
 NOTE: PROCEDURE SORT used (Total process time):
 real time 7.85 seconds
 cpu time 18.76 seconds

```

50
51      * file of dispensations in the T2 drug-treated pateints ;
52      data dafdat.disp ;
53          merge rmps
54              dafdat.pRMPS ( keep = pnr doDM
55                          in = ok ) ;
56          by pnr ;
57          if ok ;
58      run ;

```

NOTE: There were 31791978 observations read from the data set WORK.RMPS.
 NOTE: There were 383033 observations read from the data set DAFDAT.PRMPs.
 NOTE: The data set DAFDAT.DISP has 26205558 observations and 9 variables.
 NOTE: DATA statement used (Total process time):
 real time 10.75 seconds
 cpu time 6.96 seconds

```

59
60      * dataset where combination pills are sorted to components ;
61      data dafdat.xdisp ;
62          set dafdat.disp ;
63          if druggr eq '212' then do ;
64              druggr = '11' ; output ;
65              druggr = '12' ; output ;
66          end ; else
67          if druggr eq '213' then do ;
68              druggr = '11' ; output ;
69              druggr = '13' ; output ;
70          end ; else
71          if druggr eq '214' then do ;
72              druggr = '11' ; output ;
73              druggr = '14' ; output ;
74          end ; else
75          if druggr eq '216' then do ;
76              druggr = '11' ; output ;
77              druggr = '16' ; output ;
78          end ; else
79          if druggr eq '218' then do ;
80              druggr = '11' ; output ;
81              druggr = '18' ; output ;
82          end ; else
83          if druggr eq '223' then do ;
84              druggr = '12' ; output ;
85              druggr = '13' ; output ;
86          end ; else
87          if druggr eq '234' then do ;
88              druggr = '13' ; output ;
89              druggr = '14' ; output ;
90          end ; else
91          if druggr eq '246' then do ;
92              druggr = '14' ; output ;
93              druggr = '16' ; output ;
94          end ; else
95              output ;
96      run ;

```

NOTE: There were 26205558 observations read from the data set DAFDAT.DISP.

NOTE: The data set DAFDAT.XDISP has 26878885 observations and 9 variables.

NOTE: DATA statement used (Total process time):

real time	21.59 seconds
cpu time	5.03 seconds

```

97
98      title1 "Dispensations on T2 from the RPMS" ;
99      proc tabulate data = dafdat.disp missing noseps ;
100          class eksd druggr atc ;
101          table all eksd = "Date",
102              ( all druggr ) * f=comma12.
103              / rts = 6 condense ;
104          table druggr * atc,
105              n * f=comma10.
106              / indent=2 rts = 53 ;
107          keylabel n = ' ' ;
108          format eksd year4.
109              druggr $druggr.
110              atc $atc_L1L1_kt. ;
111      run ;

```

NOTE: There were 26205558 observations read from the data set DAFDAT.DISP.

NOTE: The PROCEDURE TABULATE printed pages 2-3.

NOTE: PROCEDURE TABULATE used (Total process time):

```
real time      6.68 seconds
cpu time       10.15 seconds
```

```
112
113     title1 "Dispensed *drugs* to T2 ptt. from the RPMS" ;
114     proc tabulate data = dafdat.xdisp missing noseps ;
115         class eksd druggr ;
116         table all eksd = "Date",
117             ( all druggr ) * f=comma12.
118             / rts = 6  condense ;
119         format eksd year4.
120         druggr $druggr. ;
121     run ;
```

NOTE: There were 26878885 observations read from the data set DAFDAT.XDISP.

NOTE: The PROCEDURE TABULATE printed page 4.

NOTE: PROCEDURE TABULATE used (Total process time):

```
real time      25.32 seconds
cpu time       8.51 seconds
```

```
122     title1 ;
123
124     proc contents data = dafdat.pRMPS ; run ;
```

NOTE: PROCEDURE CONTENTS used (Total process time):

```
real time      0.10 seconds
cpu time       0.01 seconds
```

NOTE: The PROCEDURE CONTENTS printed page 5.

```
125     proc contents data = dafdat.disp ; run ;
```

NOTE: PROCEDURE CONTENTS used (Total process time):

```
real time      0.10 seconds
cpu time       0.00 seconds
```

NOTE: The PROCEDURE CONTENTS printed page 6.

```
126     proc contents data = dafdat.xdisp ; run ;
```

NOTE: PROCEDURE CONTENTS used (Total process time):

```
real time      0.00 seconds
cpu time       0.00 seconds
```

NOTE: The PROCEDURE CONTENTS printed page 7.

NOTE: SAS Institute Inc., SAS Campus Drive, Cary, NC USA 27513-2414

NOTE: The SAS System used:

```
real time      9:32.83
cpu time       1:40.92
```

4.5.1 04d-rmps.lst

T2 patients from the RPMS

19:40 Tuesday, May 8, 2018 1

All	383,033
donlMet	
.	78,235
1995	11,973
1996	4,138
1997	3,867
1998	4,750
1999	6,524
2000	8,577
2001	9,114
2002	9,674
2003	11,451
2004	13,032
2005	13,052
2006	14,161
2007	16,496
2008	19,000
2009	20,802
2010	22,635
2011	26,920
2012	23,094
2013	16,548
2014	15,044
2015	16,507
2016	17,439
danyMet	
.	77,135
1995	11,973
1996	4,138
1997	3,867
1998	4,750
1999	6,524
2000	8,577
2001	9,114
2002	9,674
2003	11,451
2004	13,090
2005	13,111
2006	14,307
2007	16,622
2008	19,106
2009	20,931
2010	22,751
2011	26,960
2012	23,160
2013	16,616
2014	15,088
2015	16,580
2016	17,508
donlSU	
.	194,558
1995	40,775
1996	9,707
1997	9,155
1998	9,975
1999	9,731
2000	8,765
2001	9,086
2002	8,470
2003	9,750
2004	9,349

2005	8,913
2006	8,109
2007	8,009
2008	7,101
2009	5,931
2010	5,846
2011	4,591
2012	3,579
2013	3,206
2014	2,888
2015	2,940
2016	2,599
danySU	
.	194,557
1995	40,775
1996	9,707
1997	9,155
1998	9,975
1999	9,731
2000	8,765
2001	9,086
2002	8,470
2003	9,750
2004	9,349
2005	8,913
2006	8,109
2007	8,010
2008	7,102
2009	5,932
2010	5,845
2011	4,590
2012	3,579
2013	3,206
2014	2,888
2015	2,940
2016	2,599
donlTZD	
.	378,464
2000	89
2001	625
2002	405
2003	326
2004	414
2005	458
2006	563
2007	566
2008	382
2009	303
2010	177
2011	91
2012	51
2013	38
2014	36
2015	25
2016	20
danyTZD	
.	373,107
2000	89
2001	625
2002	405
2003	327
2004	1,092

2005	1,397
2006	2,080
2007	1,826
2008	938
2009	615
2010	311
2011	57
2012	42
2013	35
2014	37
2015	25
2016	25
donlDPP4	
.	337,192
2007	2,258
2008	4,403
2009	3,198
2010	4,372
2011	4,617
2012	4,432
2013	5,016
2014	5,379
2015	6,029
2016	6,137
danyDPP4	
.	314,315
2007	2,258
2008	5,094
2009	5,403
2010	7,462
2011	7,688
2012	7,387
2013	7,767
2014	8,057
2015	8,683
2016	8,919
danyGLP1	
.	346,850
2007	171
2008	1,015
2009	2,179
2010	7,125
2011	6,379
2012	5,124
2013	3,492
2014	2,890
2015	3,576
2016	4,232
donlSGLT2	
.	366,795
2012	20
2013	1,928
2014	2,922
2015	4,459
2016	6,909
danySGLT2	
.	365,916
2012	20
2013	1,928
2014	3,003
2015	4,615
2016	7,551

```

donlAca
.          375,997
1995          620
1996        1,147
1997        1,071
1998        1,096
1999          671
2000          436
2001          400
2002          237
2003          210
2004          186
2005          163
2006          132
2007          112
2008          108
2009           70
2010           96
2011           56
2012           75
2013           55
2014           42
2015           38
2016           15
danyAca
.          375,997
1995          620
1996        1,147
1997        1,071
1998        1,096
1999          671
2000          436
2001          400
2002          237
2003          210
2004          186
2005          163
2006          132
2007          112
2008          108
2009           70
2010           96
2011           56
2012           75
2013           55
2014           42
2015           38
2016           15
danyMeg
.          383,033
dofIns
.          337,947
1995         4,177
1996         1,114
1997          978
1998         1,060
1999         1,115
2000         1,179
2001         1,192
2002         1,268
2003         1,412
2004         1,532

```

2005	1,653
2006	1,743
2007	1,825
2008	1,983
2009	2,213
2010	2,330
2011	2,468
2012	2,683
2013	2,965
2014	3,182
2015	3,416
2016	3,598
doiIns	
.	314,553
1995	10,500
1996	2,388
1997	2,272
1998	2,531
1999	2,959
2000	3,205
2001	3,113
2002	3,411
2003	3,952
2004	3,839
2005	3,555
2006	3,312
2007	3,289
2008	2,436
2009	2,138
2010	2,206
2011	2,204
2012	2,208
2013	2,727
2014	2,449
2015	2,160
2016	1,626
domIns	
.	336,762
1995	3,740
1996	1,236
1997	1,239
1998	1,628
1999	1,803
2000	1,846
2001	1,915
2002	1,943
2003	2,682
2004	3,288
2005	3,328
2006	3,700
2007	3,913
2008	2,845
2009	2,357
2010	1,784
2011	1,621
2012	1,434
2013	1,330
2014	1,134
2015	924
2016	581
dolIns	
.	340,944

1997	*
1998	*
1999	*
2000	*
2004	494
2005	926
2006	598
2007	738
2008	3,510
2009	4,289
2010	3,666
2011	3,754
2012	3,894
2013	3,595
2014	4,209
2015	5,209
2016	7,202
doOAD	
.	19,528
1995	43,675
1996	10,343
1997	9,642
1998	10,670
1999	10,990
2000	11,113
2001	11,847
2002	11,718
2003	13,935
2004	14,412
2005	14,319
2006	14,844
2007	16,285
2008	18,011
2009	18,975
2010	21,135
2011	24,885
2012	21,739
2013	15,851
2014	14,669
2015	16,527
2016	17,920
doRMPS	
1995	54,189
1996	10,785
1997	10,032
1998	11,056
1999	11,365
2000	11,552
2001	12,226
2002	12,089
2003	14,392
2004	14,969
2005	14,814
2006	15,394
2007	16,751
2008	18,495
2009	19,347
2010	21,475
2011	25,159
2012	22,024
2013	16,368
2014	15,164

2015	16,966
2016	18,421

Dispensations on T2 from the RPMS

19:40 Tuesday, May 8, 2018 2

	druggr					
	All	Metformin	SU	TZD	DPP4	GLP1
All	26,205,558	11,743,209	6,010,980	62,122	605,015	1,050,971
Date						
1995	364,856	68,573	209,175	.	.	.
1996	420,944	82,128	236,688	.	.	.
1997	454,555	91,503	250,638	.	.	.
1998	504,996	104,375	271,182	.	.	.
1999	563,147	127,803	290,980	.	.	.
2000	608,447	164,539	293,860	115	.	.
2001	679,074	205,400	303,689	2,734	.	.
2002	748,965	252,127	307,795	3,725	.	.
2003	834,071	303,458	321,128	4,286	.	.
2004	943,171	368,259	334,014	5,064	.	.
2005	1,039,651	425,324	339,883	5,835	.	.
2006	1,148,795	497,333	341,096	7,207	.	.
2007	1,256,261	565,912	340,288	8,394	5,375	371
2008	1,390,371	657,116	336,426	7,677	27,297	5,169
2009	1,484,065	729,019	315,244	7,236	33,489	14,312
2010	1,604,634	809,837	291,733	4,928	40,926	58,850
2011	1,736,175	909,317	265,320	1,469	49,903	108,984
2012	1,832,221	981,406	231,891	1,192	57,354	137,962
2013	1,861,340	993,609	200,590	950	66,300	150,395
2014	1,881,166	988,958	175,371	525	79,009	151,692
2015	1,890,045	956,713	155,239	355	90,592	160,477
2016	1,971,181	982,643	137,500	276	101,147	172,492
2017	987,427	477,857	61,250	154	53,623	90,267

(Continued)

	druggr					
	SGLT2	Acarbose	MetxTZD	MetxDPP4	MetxSGLT2	SUxTZD
All	144,566	109,318	115,942	547,406	9,605	271
Date						
1995	.	1,870	.	.	.	.
1996	.	6,338	.	.	.	.
1997	.	9,438	.	.	.	.
1998	.	11,337	.	.	.	.
1999	.	11,262	.	.	.	.
2000	.	10,017	.	.	.	.
2001	.	8,997	.	.	.	.
2002	.	7,373	.	.	.	.
2003	.	6,358	*	.	.	.
2004	.	5,555	3,392	.	.	.
2005	.	5,067	9,671	.	.	.
2006	.	4,674	18,141	.	.	.
2007	.	4,201	25,239	.	.	49
2008	.	3,820	23,459	2,026	.	65

2009	.	3,044	20,612	16,103	.	87
2010	.	2,473	15,339	30,713	.	70
2011	.	2,125	88	48,139	.	.
2012	20	1,810	.	59,664	.	.
2013	6,241	1,566	.	70,564	.	.
2014	16,046	916	.	80,636	272	.
2015	30,592	794	.	89,795	937	.
2016	53,389	283	.	98,277	4,475	.
2017	38,278	.	.	51,489	3,921	.

(Continued)

druggr						
	TZDxDPP4	DPP4xSGLT2	InsxGLP1	fastIns	intIns	longIns
All	69	34	949	903,942	1,985,315	1,120,783
Date						
1995	.	.	.	20,240	45,899	.
1996	.	.	.	21,779	51,880	.
1997	.	.	.	23,266	55,421	*
1998	.	.	.	25,897	61,848	*
1999	.	.	.	27,767	68,147	*
2000	.	.	.	28,140	71,326	5
2001	.	.	.	30,282	80,327	.
2002	.	.	.	32,445	90,277	.
2003	.	.	.	33,232	100,890	.
2004	.	.	.	35,361	110,421	1,082
2005	.	.	.	38,201	114,485	6,460
2006	.	.	.	40,639	117,892	10,788
2007	.	.	.	43,728	119,922	14,098
2008	.	.	.	46,131	115,391	29,668
2009	.	.	.	48,781	105,192	57,097
2010	.	.	.	49,646	99,622	74,583
2011	.	.	.	49,042	93,930	90,485
2012	.	.	.	51,083	91,204	107,918
2013	.	.	.	52,557	92,183	120,825
2014	14	.	.	55,105	92,755	139,137
2015	11	.	.	58,240	90,264	162,097
2016	26	.	.	61,273	81,286	196,948
2017	18	34	949	31,107	34,753	109,589

(Continued)

druggr	
mixIns	
All	1,795,061
Date	
1995	19,099
1996	22,131
1997	24,288
1998	30,356
1999	37,187
2000	40,445

2001	47,645
2002	55,223
2003	64,718
2004	80,023
2005	94,725
2006	111,025
2007	128,684
2008	136,126
2009	133,849
2010	125,914
2011	117,373
2012	110,717
2013	105,560
2014	100,730
2015	93,939
2016	81,166
2017	34,138

Dispensations on T2 from the RPMS

19:40 Tuesday, May 8, 2018 3

Metformin		
A10BA02	metformin	11,743,209
SU		
A10BB01	glibenclamid	1,257,899
A10BB03	tolbutamid	417,734
A10BB04	glibornurid	98
A10BB07	glipizid	656,429
A10BB09	gliclazid	564,254
A10BB12	glimepirid	2,892,080
A10BX02	repaglinid	222,391
A10BX03	nateglinid	95
TZD		
A10BG02	rosiglitazon	41,362
A10BG03	pioglitazon	20,760
DPP4		
A10BH01	sitagliptin	405,232
A10BH02	vildagliptin	76,189
A10BH03	saxagliptin	38,701
A10BH04	alogliptin	6,665
A10BH05	linagliptin	78,228
GLP1		
A10BJ01	exenatid	43,375
A10BJ02	liraglutid	996,743
A10BJ03	lixisenatid	2,662
A10BJ05	dulaglutid	8,191
SGLT2		
A10BK01	dapagliflozin	94,670
A10BK02	canagliflozin	5,478
A10BK03	empagliflozin	44,418
Acarbose		
A10BF01	acarbose	109,318
MetxTZD		
A10BD03	metformin og rosiglitazon	115,942
MetxDPP4		
A10BD07	metformin og sitagliptin	267,209
A10BD08	metformin og vildagliptin	270,674
A10BD10	metformin og saxagliptin	274
A10BD11	metformin og linagliptin	1,882
A10BD13	metformin og alogliptin	7,367
MetxSGLT2		

A10BD15	metformin og dapagliflozin	4,283
A10BD16	metformin og canagliflozin	225
A10BD20	metformin og empagliflozin	5,097
SUxTZD		
A10BD04	glimepirid og rosiglitazon	271
TZDxDPP4		
A10BD09	pioglitazon og alogliptin	69
DPP4xSGLT2		
A10BD21	saxagliptin og dapagliflozin	34
InsxGLP1		
A10AE56	insulin degludec og liraglutid	949
fastIns		
A10AB01	insulin (human)	461,700
A10AB04	insulin lispro	22,989
A10AB05	insulin aspart	408,159
A10AB06	insulin glulisin	11,094
intIns		
A10AC01	insulin (human)	1,985,315
longIns		
A10AE01	insulin (human)	8
A10AE04	insulin glargin	633,768
A10AE05	insulin detemir	434,416
A10AE06	insulin degludec	52,591
mixIns		
A10AD01	insulin (human)	650,168
A10AD04	insulin lispro	14,676
A10AD05	insulin aspart	1,130,076
A10AD06	insulin degludec og insulin aspart	141

Dispensed *drugs* to T2 ptt. from the RPMS

19:40 Tuesday, May 8, 2018 4

	druggr					
	All	Metformin	SU	TZD	DPP4	GLP1
	N	N	N	N	N	N
All	26,878,885	12,416,162	6,011,251	178,404	1,152,524	1,050,971
Date						
1995	364,856	68,573	209,175	.	.	.
1996	420,944	82,128	236,688	.	.	.
1997	454,555	91,503	250,638	.	.	.
1998	504,996	104,375	271,182	.	.	.
1999	563,147	127,803	290,980	.	.	.
2000	608,447	164,539	293,860	115	.	.
2001	679,074	205,400	303,689	2,734	.	.
2002	748,965	252,127	307,795	3,725	.	.
2003	834,072	303,459	321,128	4,287	.	.
2004	946,563	371,651	334,014	8,456	.	.
2005	1,049,322	434,995	339,883	15,506	.	.
2006	1,166,936	515,474	341,096	25,348	.	.
2007	1,281,549	591,151	340,337	33,682	5,375	371
2008	1,415,921	682,601	336,491	31,201	29,323	5,169
2009	1,520,867	765,734	315,331	27,935	49,592	14,312
2010	1,650,756	855,889	291,803	20,337	71,639	58,850
2011	1,784,402	957,544	265,320	1,557	98,042	108,984
2012	1,891,885	1,041,070	231,891	1,192	117,018	137,962
2013	1,931,904	1,064,173	200,590	950	136,864	150,395
2014	1,962,088	1,069,866	175,371	539	159,659	151,692
2015	1,980,788	1,047,445	155,239	366	180,398	160,477

2016	2,073,959	1,085,395	137,500	302	199,450	172,492
2017	1,042,889	533,267	61,250	172	105,164	90,267

(Continued)

	druggr					
	SGLT2	Acarbose	InsxGLP1	fastIns	intIns	longIns
	N	N	N	N	N	N
All	154,205	109,318	949	903,942	1,985,315	1,120,783
Date						
1995	.	1,870	.	20,240	45,899	.
1996	.	6,338	.	21,779	51,880	.
1997	.	9,438	.	23,266	55,421	*
1998	.	11,337	.	25,897	61,848	*
1999	.	11,262	.	27,767	68,147	*
2000	.	10,017	.	28,140	71,326	5
2001	.	8,997	.	30,282	80,327	.
2002	.	7,373	.	32,445	90,277	.
2003	.	6,358	.	33,232	100,890	.
2004	.	5,555	.	35,361	110,421	1,082
2005	.	5,067	.	38,201	114,485	6,460
2006	.	4,674	.	40,639	117,892	10,788
2007	.	4,201	.	43,728	119,922	14,098
2008	.	3,820	.	46,131	115,391	29,668
2009	.	3,044	.	48,781	105,192	57,097
2010	.	2,473	.	49,646	99,622	74,583
2011	.	2,125	.	49,042	93,930	90,485
2012	20	1,810	.	51,083	91,204	107,918
2013	6,241	1,566	.	52,557	92,183	120,825
2014	16,318	916	.	55,105	92,755	139,137
2015	31,529	794	.	58,240	90,264	162,097
2016	57,864	283	.	61,273	81,286	196,948
2017	42,233	.	949	31,107	34,753	109,589

(Continued)

	druggr	
	mixIns	
	N	
All	1,795,061	
Date		
1995	19,099	
1996	22,131	
1997	24,288	
1998	30,356	
1999	37,187	
2000	40,445	
2001	47,645	
2002	55,223	
2003	64,718	

2004	80,023
2005	94,725
2006	111,025
2007	128,684
2008	136,126
2009	133,849
2010	125,914
2011	117,373
2012	110,717
2013	105,560
2014	100,730
2015	93,939
2016	81,166
2017	34,138

19:40 Tuesday, May 8, 2018 5

The CONTENTS Procedure

Data Set Name	DAFDAT.PRMP5	Observations	383033
Member Type	DATA	Variables	30
Engine	V9	Indexes	0
Created	08/05/2018 19:40:12	Observation Length	232
Last Modified	08/05/2018 19:40:12	Deleted Observations	0
Protection		Compressed	NO
Data Set Type		Sorted	NO
Label			
Data Representation	WINDOWS_64		
Encoding	wlatin1 Western (Windows)		

Engine/Host Dependent Information

Data Set Page Size	65536
Number of Data Set Pages	1359
First Data Page	*
Max Obs per Page	282
Obs in First Data Page	265
Number of Data Set Repairs	0
ExtendObsCounter	YES
Filename	E:\workdata\705093\BxC\daffodil\DATA\prmps.sas7bdat
Release Created	9.0401M3
Host Created	X64_SRV12

Alphabetic List of Variables and Attributes

#	Variable	Type	Len	Format	Informat	Label
28	DMtp	Char	*			Type of DM
14	danyAca	Num	8			
9	danyDPP4	Num	8			
10	danyGLP1	Num	8			
15	danyMeg	Num	8			
*	danyMet	Num	8			
12	danySGLT2	Num	8			
5	danySU	Num	8			
7	danyTZD	Num	8			
26	doBth	Num	8	DDMMYY10.		
29	doDM	Num	8	DDMMYY10.		
27	doDth	Num	8	DDMMYY10.		

22	doIns	Num	8	DDMMYY10.			
24	doIns2	Num	4	YYMMDDN8.			
21	doOAD	Num	8	DDMMYY10.			
23	doOAD2	Num	4	YYMMDDN8.			
20	doRMPS	Num	8				
16	dofIns	Num	8				
17	doiIns	Num	8				
19	dolIns	Num	8				
18	domIns	Num	8				
13	donlAca	Num	8				
8	donlDPP4	Num	8				
*	donlMet	Num	8				
11	donlSGLT2	Num	8				
4	donlSU	Num	8				
6	donlTZD	Num	8				
30	inCr	Char	4				
*	pnr	Char	12	\$12.	\$10.	Personnummer	
25	sex	Num	8				

19:40 Tuesday, May 8, 2018 6

The CONTENTS Procedure

Data Set Name	DAFDAT.DISP	Observations	26205558
Member Type	DATA	Variables	9
Engine	V9	Indexes	0
Created	08/05/2018 19:48:40	Observation Length	72
Last Modified	08/05/2018 19:48:40	Deleted Observations	0
Protection		Compressed	NO
Data Set Type		Sorted	NO
Label			
Data Representation	WINDOWS_64		
Encoding	wlatin1 Western (Windows)		

Engine/Host Dependent Information

Data Set Page Size	65536
Number of Data Set Pages	28861
First Data Page	*
Max Obs per Page	908
Obs in First Data Page	880
Number of Data Set Repairs	0
ExtendObsCounter	YES
Filename	E:\workdata\705093\BxC\daffodil\DATA\disp.sas7bdat
Release Created	9.0401M3
Host Created	X64_SRV12

Alphabetic List of Variables and Attributes

#	Variable	Type	Len	Format	Informat	Label
6	ATC	Char	8	\$8.	\$16.	ATC-kode detaljeret (s)
8	PACKSIZE	Num	8	13.3	13.3	Numerisk pakningsstrrelse (s)
7	Volume	Num	8	13.3	13.3	Mype
4	apk	Num	8	BEST12.		Antal pakninger
9	doDM	Num	8	DDMMYY10.		
5	doso	Char	7	\$7.		Doseringskode
1	druggr	Char	7			
3	eksd	Num	4	YYMMDDN8.		Ekspeditionsdato
2	pnr	Char	12	\$12.	\$10.	Personnummer

19:40 Tuesday, May 8, 2018 7

The CONTENTS Procedure

Data Set Name	DAFDAT.XDISP	Observations	26878885
Member Type	DATA	Variables	9
Engine	V9	Indexes	0
Created	08/05/2018 19:48:50	Observation Length	72
Last Modified	08/05/2018 19:48:50	Deleted Observations	0
Protection		Compressed	NO
Data Set Type		Sorted	NO
Label			
Data Representation	WINDOWS_64		
Encoding	wlatin1 Western (Windows)		

Engine/Host Dependent Information

Data Set Page Size	65536
Number of Data Set Pages	29603
First Data Page	*
Max Obs per Page	908
Obs in First Data Page	880
Number of Data Set Repairs	0
ExtendObsCounter	YES
Filename	E:\workdata\705093\BxC\daffodil\DATA\xdisp.sas7bdat
Release Created	9.0401M3
Host Created	X64_SRV12

Alphabetic List of Variables and Attributes

#	Variable	Type	Len	Format	Informat	Label
6	ATC	Char	8	\$8.	\$16.	ATC-kode detaljeret (s)
8	PACKSIZE	Num	8	13.3	13.3	Numerisk pakningsstrrelse (s)
7	Volume	Num	8	13.3	13.3	Mype
4	apk	Num	8	BEST12.		Antal pakninger
9	doDM	Num	8	DDMMYY10.		
5	doso	Char	7	\$7.		Doseringskode
1	druggr	Char	7			
3	eksd	Num	4	YYMMDDN8.		Ekspeditionsdato
2	pnr	Char	12	\$12.	\$10.	Personnummer

4.6 07-newuse

Extracts the new user dates of various drugs and defines the index dates (doIx) and index drugs (Ixdr) for each episode. There may be several episodes for each person, even episodes that start the same day, if more than one drug is first dispensed the same day.

Adds counts of pre and post index HF events and date of the first of the post-index ones. Also adds indicators of use of drugs during the last year before index.

1 "Program: 07-newuse.sas" 16:43 Wednesday, May 9, 2018

NOTE: AUTOEXEC processing completed.

```

1      * Enumerate the new user epidsodes after 2012 with date and drug,
2      based on the dispensation data ;
3
4      * maximal allowed gap allowed before we call it a stop (days) ;
5      %let mgap = 180 ;
6      * windows of evaluation from index date and back ;
7      %let mwin = 365.25 ; * medication ;
8      %let hwin = 365.25 ; * hospitalization ;
9      %let cwin = 365.25*5 ; * cancer diagnosis ;
10     * date of SGLT2 intro on market ;
11     %let s2i = '01dec2012'd ;
12
13     * note we use the dataset with single drugs,
14     so some dispensations yield 2 different episodes ;
15     proc sort data = dafdat.xdisp ( where = ( eksd lt &end. ) )
16         out = sxdisp ;
17         by pnr druggr eksd ;
18     run ;

```

NOTE: There were 25835996 observations read from the data set DAFDAT.XDISP.
WHERE eksd<'01JAN2017'D;

NOTE: The data set WORK.SXDISP has 25835996 observations and 9 variables.

NOTE: PROCEDURE SORT used (Total process time):

real time	25.78 seconds
cpu time	13.07 seconds

```

19
20     * dataset with starting dates for episodes ;
21     * newepi has one record per episode ;
22     * newrec has a record per dispensation in episodes ;
23     data newepi
24         newrec ;
25         set sxdisp ( keep = pnr druggr atc eksd doDM ) ;
26         by pnr druggr ;
27         if first.pnr then epiN = 0 ;
28         retain doIx Ixdr Ixatc ;
29         if ( first.druggr ) then do ; Ixdr = put( druggr, $druggr. ) ;
30                                     Ixatc = atc ; end ;
31         if ( ( first.druggr ) or
32             ( ~first.druggr and dif( eksd ) gt &mwin. ) ) and
33             ( eksd gt &s2i. )
34             then do ;
35                 doIx = eksd ;
36                 epiN + 1 ;
37                 output newepi ;
38             end ;
39         if epiN gt 0 then output newrec ;
40     run ;

```

NOTE: There were 25835996 observations read from the data set WORK.SXDISP.

NOTE: The data set WORK.NEWEPI has 244715 observations and 9 variables.

NOTE: The data set WORK.NEWREC has 4450151 observations and 9 variables.

NOTE: DATA statement used (Total process time):

real time	5.96 seconds
cpu time	3.81 seconds

```

41
42      * Now find the last dispensation in each episode ;
43      data epiX ( keep = pnr druggr eksd epiN
44                  rename = ( eksd = lastpr ) ) ;
45          set newrec ;
46          by pnr druggr epiN ;
47          if last.epiN ;
48      run ;

```

NOTE: There were 4450151 observations read from the data set WORK.NEWREC.

NOTE: The data set WORK.EPIX has 307602 observations and 4 variables.

NOTE: DATA statement used (Total process time):

```

      real time      0.78 seconds
      cpu time       0.56 seconds

```

```

49
50      * Merge last dispensation in each episode with the episodes and
51        compute date of termination (if before end of study) ;
52      data newu ;
53          merge newepi ( in = ok )
54                      epiX ;
55          by pnr druggr epiN ;
56          if ok ;
57          doTm = lastpr + &mgap. ;
58          if doTm gt &end. then doTm = . ;
59      run ;

```

NOTE: There were 244715 observations read from the data set WORK.NEWEPI.

NOTE: There were 307602 observations read from the data set WORK.EPIX.

NOTE: The data set WORK.NEWU has 244715 observations and 11 variables.

NOTE: DATA statement used (Total process time):

```

      real time      0.14 seconds
      cpu time       0.12 seconds

```

```

60
61      * epiN is not chronological so make it;
62      proc sort  data = newu ; by pnr doIx lxdx ; run ;

```

NOTE: There were 244715 observations read from the data set WORK.NEWU.

NOTE: The data set WORK.NEWU has 244715 observations and 11 variables.

NOTE: PROCEDURE SORT used (Total process time):

```

      real time      0.07 seconds
      cpu time       0.14 seconds

```

```

63      data newu ;
64          set newu ;
65          by pnr ;
66          if first.pnr then epN = 0 ;
67          epN+1 ;
68          epiN = epN ;
69          drop epN ;
70      run ;

```

NOTE: There were 244715 observations read from the data set WORK.NEWU.

NOTE: The data set WORK.NEWU has 244715 observations and 11 variables.

NOTE: DATA statement used (Total process time):

```

      real time      0.09 seconds
      cpu time       0.07 seconds

```

```

71
72      * newu now has one record per new-use episode
73      - some persons have more episodes, some overlapping,
74      - and even with identical index dates ;
75      title1 'All new start episodes (some persons with > 1) in T2 after dec 2012' ;
76      proc tabulate data = newu missing noseps ;
77          class lxdx doIx doTm epiN;
78          table all lxdx,
79              ( all doIx doTm ) * f = comma7.
80              / rts = 15 condense ;
81          table all epiN,
82              ( all lxdx ) * f=comma7.
83              / rts = 8 indent = 2 ;
84          format doIx doTm yyqs6.
85              lxdx $druggr. ;
86      run ;

```

NOTE: There were 244715 observations read from the data set WORK.NEWU.

NOTE: The PROCEDURE TABULATE printed pages 1-3.

NOTE: PROCEDURE TABULATE used (Total process time):

```

real time      0.10 seconds
cpu time       0.31 seconds

```

```

87      title1 ;
88
89      * Sort all diabetes dispensations by pnr and date ;
90      proc sort data = dafdat.disp out = disp ;
91          by pnr eksd ;
92      run ;

```

NOTE: There were 26205558 observations read from the data set DAFDAT.DISP.

NOTE: The data set WORK.DISP has 26205558 observations and 9 variables.

NOTE: PROCEDURE SORT used (Total process time):

```

real time      23.18 seconds
cpu time       11.06 seconds

```

```

93
94      * Restrict NPR records to persons in data ;
95      proc sort data = newu (keep=pnr) out = pers nodupkey ; by pnr ; run ;

```

NOTE: There were 244715 observations read from the data set WORK.NEWU.

NOTE: 88533 observations with duplicate key values were deleted.

NOTE: The data set WORK.PERS has 156182 observations and 1 variables.

NOTE: PROCEDURE SORT used (Total process time):

```

real time      0.06 seconds
cpu time       0.09 seconds

```

```

96      data phosp ;
97          merge dafdat.hosp pers ( in = ok ) ;
98          by pnr ;
99          if ok ;
100      run ;

```

NOTE: There were 34324010 observations read from the data set DAFDAT.HOSP.

NOTE: There were 156182 observations read from the data set WORK.PERS.

NOTE: The data set WORK.PHOSP has 1889909 observations and 6 variables.

NOTE: DATA statement used (Total process time):

```

real time      26.14 seconds

```

cpu time 4.73 seconds

```

101
102      * Find date and type of first line dispensation (FL) for each person ;
103      data FL ( keep = pnr doFL FLdr FLatc ) ;
104          set disp ;
105          by pnr eksd ;
106          if first.pnr then do ;
107              doFL      = eksd ;
108              FLdr      = druggr ;
109              FLatc     = atc ;
110              output ;
111          end ;
112          format doFl ddmmyy10. ;
113      run ;

```

NOTE: There were 26205558 observations read from the data set WORK.DISP.

NOTE: The data set WORK.FL has 383033 observations and 4 variables.

NOTE: DATA statement used (Total process time):

real time 5.17 seconds
 cpu time 3.74 seconds

```

114
115      * Things to merge onto the >episodes<, which are classified by pnr,
116      doIx and lxdx. The characteristics we append to the episodes comes
117      from datasets with multiple records per pnr. Hence we must merge with
118      subsets of the episodes datasets where only one intancen of each pnr
119      is present ;
120
121      * datasets to collect covariate information across episodes within persons ;
122      data hosp ; * hospitalizations and cancer in the last 5 years ;
123      run ;

```

NOTE: The data set WORK.HOSP has 1 observations and 0 variables.

NOTE: DATA statement used (Total process time):

real time 0.00 seconds
 cpu time 0.00 seconds

```

124      data ldrug ; * DM drugs in last year before doIx ;
125      run ;

```

NOTE: The data set WORK.LDRUG has 1 observations and 0 variables.

NOTE: DATA statement used (Total process time):

real time 0.00 seconds
 cpu time 0.00 seconds

```

126      data lmed ; * Other drugs in last year before doIx ;
127      run ;

```

NOTE: The data set WORK.LMED has 1 observations and 0 variables.

NOTE: DATA statement used (Total process time):

real time 0.01 seconds
 cpu time 0.01 seconds

```

128
129      options nomprint ;
130

```

```

131      %macro colcov ;
132
133      * This macro COLlects COVariates for the episodes ;
134
135      %do ne = 1 %to 11 ;
136
137      ***** start of looping with &ne. ***** ;
138
139      data hosp&ne. ( keep = pnr epiN doIx maxH frail doCancer ) ;
140          merge newu ( in = nu
141                      where = (epiN eq &ne.) )
142                      phosp ;
143          by pnr ;
144          retain maxH doCancer ;
145          label maxH = 'Longest hospital stay in last year before doIx'
146                frail = 'More than 3 consecutive hospital days last yr' ;
147          if nu ;
148          if first.pnr then do ;
149              maxH = 0 ;
150              doCancer = . ;
151          end ;
152          * The latest cancer during the last cwin days before doIx ;
153          if (doIx - &cwin.) < d_inddto < doIx and compl eq 'Cancer'
154              then doCancer = max( doCancer, d_inddto ) ;
155          * Maximum bed-days in the last hwin days before doIx ;
156          if (doIx - &hwin.) < d_inddto < doIx
157              then maxH = max( maxH, v_sengdage ) ;
158          if last.pnr then do ;
159              frail = ( maxH ge 4 ) ;
160              output ;
161          end ;
162      run ;
163
164      data hosp ; set hosp hosp&ne. ; run ;
165
166      * derive other DM dispensations in the last year before doIx ;
167      data ldrug&ne. ;
168          merge newu ( in = nu
169                      where = (epiN eq &ne.) )
170                      dafdat.disp ( where = (eksd ge (&s2i.-366)) ) ;
171          by pnr ;
172          if nu ;
173          if ( ( doIx - &mwin. ) < eksd <= doIx ) and ( druggr ne lxr ) ;
174          drgr = put( druggr, $drugr. ) ;
175      run ;
176
177      proc sort data = ldrug&ne. ;
178          by pnr drgr eksd ;
179      run ;
180
181      * last dispense before index in the last year ;
182      data ldrug&ne. ;
183          set ldrug&ne. ;
184          by pnr drgr eksd ;
185          if last.drgr ;
186          format eksd ddmmyy10. ;
187      run ;
188
189      * transpose to be able to merge to analysis dataset ;
190      proc transpose data = ldrug&ne.
191          out = ldrug&ne. ( drop = _LABEL_ _NAME_ )
192          prefix = dol ;

```

```

193         by pnr epiN ;
194         var eksd ;
195         id drgr ;
196     run ;
197
198     data ldrug ; set ldrug ldrug&ne. ; run ;
199
200     * other types of dispensations taken out during last year before doIx ;
201     data lmed&ne. ;
202         merge newu ( in = nu
203                     where = (epiN eq &ne.) )
204         dafdat.lmed ;
205         by pnr ;
206         if nu ;
207         if ( ( doIx - &mwin. ) < eksd < doIx ) ;
208     run ;
209
210     proc sort data = lmed&ne. ;
211         by pnr medgr eksd ;
212     run ;
213
214     * last dispense before index in the last year ;
215     data lmed&ne. ;
216         set lmed&ne. ;
217         by pnr medgr eksd ;
218         if last.medgr ;
219         format eksd ddmmyy10. ;
220     run ;
221
222     * turn it on side to merge to analysis dataset ;
223     proc transpose data = lmed&ne.
224         out = lmed&ne. ( drop = _LABEL_ _NAME_ )
225         prefix = dol ;
226         by pnr epiN ;
227         var eksd ;
228         id medgr ;
229     run ;
230
231     data lmed ; set lmed lmed&ne. ; run ;
232
233     %end ;
234
235     %mend colcov ;
236
237     %colcov ;

```

NOTE: There were 156182 observations read from the data set WORK.NEWU.
WHERE epiN=1;

NOTE: There were 1889909 observations read from the data set WORK.PHOSP.

NOTE: The data set WORK.HOSP1 has 156182 observations and 6 variables.

NOTE: DATA statement used (Total process time):

real time	0.46 seconds
cpu time	0.35 seconds

NOTE: There were 1 observations read from the data set WORK.HOSP.

NOTE: There were 156182 observations read from the data set WORK.HOSP1.

NOTE: The data set WORK.HOSP has 156183 observations and 6 variables.

NOTE: DATA statement used (Total process time):

real time	0.03 seconds
cpu time	0.01 seconds

NOTE: There were 156182 observations read from the data set WORK.NEWU.
WHERE epiN=1;
NOTE: There were 10576531 observations read from the data set DAFDAT.DISP.
WHERE eksd>='01DEC2011'D;
NOTE: The data set WORK.LDRUG1 has 924554 observations and 16 variables.
NOTE: DATA statement used (Total process time):
real time 20.59 seconds
cpu time 3.48 seconds

NOTE: There were 924554 observations read from the data set WORK.LDRUG1.
NOTE: The data set WORK.LDRUG1 has 924554 observations and 16 variables.
NOTE: PROCEDURE SORT used (Total process time):
real time 0.40 seconds
cpu time 0.50 seconds

NOTE: There were 924554 observations read from the data set WORK.LDRUG1.
NOTE: The data set WORK.LDRUG1 has 251732 observations and 16 variables.
NOTE: DATA statement used (Total process time):
real time 0.32 seconds
cpu time 0.14 seconds

NOTE: There were 251732 observations read from the data set WORK.LDRUG1.
NOTE: The data set WORK.LDRUG1 has 152371 observations and 16 variables.
NOTE: PROCEDURE TRANSPOSE used (Total process time):
real time 0.37 seconds
cpu time 0.29 seconds

NOTE: There were 1 observations read from the data set WORK.LDRUG.
NOTE: There were 152371 observations read from the data set WORK.LDRUG1.
NOTE: The data set WORK.LDRUG has 152372 observations and 16 variables.
NOTE: DATA statement used (Total process time):
real time 0.04 seconds
cpu time 0.03 seconds

NOTE: There were 156182 observations read from the data set WORK.NEWU.
WHERE epiN=1;
NOTE: There were 25061393 observations read from the data set DAFDAT.LMED.
NOTE: The data set WORK.LMED1 has 1824109 observations and 12 variables.
NOTE: DATA statement used (Total process time):
real time 14.70 seconds
cpu time 3.15 seconds

NOTE: There were 1824109 observations read from the data set WORK.LMED1.
NOTE: The data set WORK.LMED1 has 1824109 observations and 12 variables.
NOTE: PROCEDURE SORT used (Total process time):
real time 0.62 seconds
cpu time 0.92 seconds

NOTE: There were 1824109 observations read from the data set WORK.LMED1.
NOTE: The data set WORK.LMED1 has 416530 observations and 12 variables.
NOTE: DATA statement used (Total process time):
 real time 0.56 seconds
 cpu time 0.35 seconds

NOTE: There were 416530 observations read from the data set WORK.LMED1.
NOTE: The data set WORK.LMED1 has 124862 observations and 22 variables.
NOTE: PROCEDURE TRANSPOSE used (Total process time):
 real time 0.45 seconds
 cpu time 0.37 seconds

NOTE: There were 1 observations read from the data set WORK.LMED.
NOTE: There were 124862 observations read from the data set WORK.LMED1.
NOTE: The data set WORK.LMED has 124863 observations and 22 variables.
NOTE: DATA statement used (Total process time):
 real time 0.04 seconds
 cpu time 0.03 seconds

NOTE: There were 57025 observations read from the data set WORK.NEWU.
 WHERE epiN=2;
NOTE: There were 1889909 observations read from the data set WORK.PHOSP.
NOTE: The data set WORK.HOSP2 has 57025 observations and 6 variables.
NOTE: DATA statement used (Total process time):
 real time 0.42 seconds
 cpu time 0.26 seconds

NOTE: There were 156183 observations read from the data set WORK.HOSP.
NOTE: There were 57025 observations read from the data set WORK.HOSP2.
NOTE: The data set WORK.HOSP has 213208 observations and 6 variables.
NOTE: DATA statement used (Total process time):
 real time 0.04 seconds
 cpu time 0.04 seconds

NOTE: There were 57025 observations read from the data set WORK.NEWU.
 WHERE epiN=2;
NOTE: There were 10576531 observations read from the data set DAFDAT.DISP.
 WHERE eksd>='01DEC2011'D;
NOTE: The data set WORK.LDRUG2 has 513113 observations and 16 variables.
NOTE: DATA statement used (Total process time):
 real time 22.59 seconds
 cpu time 3.23 seconds

NOTE: There were 513113 observations read from the data set WORK.LDRUG2.
NOTE: The data set WORK.LDRUG2 has 513113 observations and 16 variables.
NOTE: PROCEDURE SORT used (Total process time):
 real time 0.15 seconds

cpu time 0.34 seconds

NOTE: There were 513113 observations read from the data set WORK.LDRUG2.

NOTE: The data set WORK.LDRUG2 has 130759 observations and 16 variables.

NOTE: DATA statement used (Total process time):

real time 0.13 seconds

cpu time 0.14 seconds

NOTE: There were 130759 observations read from the data set WORK.LDRUG2.

NOTE: The data set WORK.LDRUG2 has 56686 observations and 16 variables.

NOTE: PROCEDURE TRANSPOSE used (Total process time):

real time 0.15 seconds

cpu time 0.15 seconds

NOTE: There were 152372 observations read from the data set WORK.LDRUG.

NOTE: There were 56686 observations read from the data set WORK.LDRUG2.

NOTE: The data set WORK.LDRUG has 209058 observations and 16 variables.

NOTE: DATA statement used (Total process time):

real time 0.03 seconds

cpu time 0.03 seconds

NOTE: There were 57025 observations read from the data set WORK.NEWU.

WHERE epiN=2;

NOTE: There were 25061393 observations read from the data set DAFDAT.LMED.

NOTE: The data set WORK.LMED2 has 705486 observations and 12 variables.

NOTE: DATA statement used (Total process time):

real time 13.29 seconds

cpu time 2.96 seconds

NOTE: There were 705486 observations read from the data set WORK.LMED2.

NOTE: The data set WORK.LMED2 has 705486 observations and 12 variables.

NOTE: PROCEDURE SORT used (Total process time):

real time 0.17 seconds

cpu time 0.37 seconds

NOTE: There were 705486 observations read from the data set WORK.LMED2.

NOTE: The data set WORK.LMED2 has 163287 observations and 12 variables.

NOTE: DATA statement used (Total process time):

real time 0.17 seconds

cpu time 0.17 seconds

NOTE: There were 163287 observations read from the data set WORK.LMED2.

NOTE: The data set WORK.LMED2 has 48093 observations and 22 variables.

NOTE: PROCEDURE TRANSPOSE used (Total process time):

real time 0.15 seconds

cpu time 0.15 seconds

NOTE: There were 124863 observations read from the data set WORK.LMED.

NOTE: There were 48093 observations read from the data set WORK.LMED2.

NOTE: The data set WORK.LMED has 172956 observations and 22 variables.

NOTE: DATA statement used (Total process time):

real time 0.04 seconds

cpu time 0.04 seconds

NOTE: There were 20996 observations read from the data set WORK.NEWU.

WHERE epiN=3;

NOTE: There were 1889909 observations read from the data set WORK.PHOSP.

NOTE: The data set WORK.HOSP3 has 20996 observations and 6 variables.

NOTE: DATA statement used (Total process time):

real time 0.31 seconds

cpu time 0.31 seconds

NOTE: There were 213208 observations read from the data set WORK.HOSP.

NOTE: There were 20996 observations read from the data set WORK.HOSP3.

NOTE: The data set WORK.HOSP has 234204 observations and 6 variables.

NOTE: DATA statement used (Total process time):

real time 0.04 seconds

cpu time 0.04 seconds

NOTE: There were 20996 observations read from the data set WORK.NEWU.

WHERE epiN=3;

NOTE: There were 10576531 observations read from the data set DAFDAT.DISP.

WHERE eksd>='01DEC2011'D;

NOTE: The data set WORK.LDRUG3 has 233601 observations and 16 variables.

NOTE: DATA statement used (Total process time):

real time 20.28 seconds

cpu time 3.20 seconds

NOTE: There were 233601 observations read from the data set WORK.LDRUG3.

NOTE: The data set WORK.LDRUG3 has 233601 observations and 16 variables.

NOTE: PROCEDURE SORT used (Total process time):

real time 0.07 seconds

cpu time 0.17 seconds

NOTE: There were 233601 observations read from the data set WORK.LDRUG3.

NOTE: The data set WORK.LDRUG3 has 58769 observations and 16 variables.

NOTE: DATA statement used (Total process time):

real time 0.07 seconds

cpu time 0.07 seconds

NOTE: There were 58769 observations read from the data set WORK.LDRUG3.

NOTE: The data set WORK.LDRUG3 has 20838 observations and 16 variables.

NOTE: PROCEDURE TRANSPOSE used (Total process time):

real time 0.06 seconds

cpu time 0.06 seconds

NOTE: There were 209058 observations read from the data set WORK.LDRUG.
NOTE: There were 20838 observations read from the data set WORK.LDRUG3.
NOTE: The data set WORK.LDRUG has 229896 observations and 16 variables.
NOTE: DATA statement used (Total process time):
 real time 0.04 seconds
 cpu time 0.04 seconds

NOTE: There were 20996 observations read from the data set WORK.NEWU.
 WHERE epiN=3;
NOTE: There were 25061393 observations read from the data set DAFDAT.LMED.
NOTE: The data set WORK.LMED3 has 261298 observations and 12 variables.
NOTE: DATA statement used (Total process time):
 real time 13.29 seconds
 cpu time 2.98 seconds

NOTE: There were 261298 observations read from the data set WORK.LMED3.
NOTE: The data set WORK.LMED3 has 261298 observations and 12 variables.
NOTE: PROCEDURE SORT used (Total process time):
 real time 0.07 seconds
 cpu time 0.14 seconds

NOTE: There were 261298 observations read from the data set WORK.LMED3.
NOTE: The data set WORK.LMED3 has 61549 observations and 12 variables.
NOTE: DATA statement used (Total process time):
 real time 0.06 seconds
 cpu time 0.06 seconds

NOTE: There were 61549 observations read from the data set WORK.LMED3.
NOTE: The data set WORK.LMED3 has 18097 observations and 22 variables.
NOTE: PROCEDURE TRANSPOSE used (Total process time):
 real time 0.06 seconds
 cpu time 0.06 seconds

NOTE: There were 172956 observations read from the data set WORK.LMED.
NOTE: There were 18097 observations read from the data set WORK.LMED3.
NOTE: The data set WORK.LMED has 191053 observations and 22 variables.
NOTE: DATA statement used (Total process time):
 real time 0.04 seconds
 cpu time 0.04 seconds

NOTE: There were 7284 observations read from the data set WORK.NEWU.
 WHERE epiN=4;
NOTE: There were 1889909 observations read from the data set WORK.PHOSP.
NOTE: The data set WORK.HOSP4 has 7284 observations and 6 variables.
NOTE: DATA statement used (Total process time):
 real time 0.31 seconds
 cpu time 0.31 seconds

NOTE: There were 234204 observations read from the data set WORK.HOSP.

NOTE: There were 7284 observations read from the data set WORK.HOSP4.

NOTE: The data set WORK.HOSP has 241488 observations and 6 variables.

NOTE: DATA statement used (Total process time):

real time 0.03 seconds

cpu time 0.03 seconds

NOTE: There were 7284 observations read from the data set WORK.NEWU.

WHERE epiN=4;

NOTE: There were 10576531 observations read from the data set DAFDAT.DISP.

WHERE eksd>='01DEC2011'D;

NOTE: The data set WORK.LDRUG4 has 92725 observations and 16 variables.

NOTE: DATA statement used (Total process time):

real time 18.45 seconds

cpu time 3.18 seconds

NOTE: There were 92725 observations read from the data set WORK.LDRUG4.

NOTE: The data set WORK.LDRUG4 has 92725 observations and 16 variables.

NOTE: PROCEDURE SORT used (Total process time):

real time 0.06 seconds

cpu time 0.03 seconds

NOTE: There were 92725 observations read from the data set WORK.LDRUG4.

NOTE: The data set WORK.LDRUG4 has 22943 observations and 16 variables.

NOTE: DATA statement used (Total process time):

real time 0.04 seconds

cpu time 0.04 seconds

NOTE: There were 22943 observations read from the data set WORK.LDRUG4.

NOTE: The data set WORK.LDRUG4 has 7250 observations and 16 variables.

NOTE: PROCEDURE TRANSPOSE used (Total process time):

real time 0.03 seconds

cpu time 0.03 seconds

NOTE: There were 229896 observations read from the data set WORK.LDRUG.

NOTE: There were 7250 observations read from the data set WORK.LDRUG4.

NOTE: The data set WORK.LDRUG has 237146 observations and 16 variables.

NOTE: DATA statement used (Total process time):

real time 0.06 seconds

cpu time 0.03 seconds

NOTE: There were 7284 observations read from the data set WORK.NEWU.

WHERE epiN=4;

NOTE: There were 25061393 observations read from the data set DAFDAT.LMED.

NOTE: The data set WORK.LMED4 has 89172 observations and 12 variables.

NOTE: DATA statement used (Total process time):

real time 12.68 seconds

cpu time 2.87 seconds

NOTE: There were 89172 observations read from the data set WORK.LMED4.
NOTE: The data set WORK.LMED4 has 89172 observations and 12 variables.
NOTE: PROCEDURE SORT used (Total process time):
 real time 0.03 seconds
 cpu time 0.03 seconds

NOTE: There were 89172 observations read from the data set WORK.LMED4.
NOTE: The data set WORK.LMED4 has 21153 observations and 12 variables.
NOTE: DATA statement used (Total process time):
 real time 0.03 seconds
 cpu time 0.03 seconds

NOTE: There were 21153 observations read from the data set WORK.LMED4.
NOTE: The data set WORK.LMED4 has 6254 observations and 22 variables.
NOTE: PROCEDURE TRANSPOSE used (Total process time):
 real time 0.01 seconds
 cpu time 0.01 seconds

NOTE: There were 191053 observations read from the data set WORK.LMED.
NOTE: There were 6254 observations read from the data set WORK.LMED4.
NOTE: The data set WORK.LMED has 197307 observations and 22 variables.
NOTE: DATA statement used (Total process time):
 real time 0.06 seconds
 cpu time 0.04 seconds

NOTE: There were 2267 observations read from the data set WORK.NEWU.
 WHERE epiN=5;
NOTE: There were 1889909 observations read from the data set WORK.PHOSP.
NOTE: The data set WORK.HOSP5 has 2267 observations and 6 variables.
NOTE: DATA statement used (Total process time):
 real time 0.38 seconds
 cpu time 0.23 seconds

NOTE: There were 241488 observations read from the data set WORK.HOSP.
NOTE: There were 2267 observations read from the data set WORK.HOSP5.
NOTE: The data set WORK.HOSP has 243755 observations and 6 variables.
NOTE: DATA statement used (Total process time):
 real time 0.06 seconds
 cpu time 0.04 seconds

NOTE: There were 2267 observations read from the data set WORK.NEWU.
 WHERE epiN=5;
NOTE: There were 10576531 observations read from the data set DAFDAT.DISP.
 WHERE eksd>='01DEC2011'D;
NOTE: The data set WORK.LDRUG5 has 30908 observations and 16 variables.
NOTE: DATA statement used (Total process time):
 real time 19.32 seconds

cpu time 3.18 seconds

NOTE: There were 30908 observations read from the data set WORK.LDRUG5.

NOTE: The data set WORK.LDRUG5 has 30908 observations and 16 variables.

NOTE: PROCEDURE SORT used (Total process time):

real time 0.01 seconds

cpu time 0.00 seconds

NOTE: There were 30908 observations read from the data set WORK.LDRUG5.

NOTE: The data set WORK.LDRUG5 has 7778 observations and 16 variables.

NOTE: DATA statement used (Total process time):

real time 0.01 seconds

cpu time 0.01 seconds

NOTE: There were 7778 observations read from the data set WORK.LDRUG5.

NOTE: The data set WORK.LDRUG5 has 2253 observations and 16 variables.

NOTE: PROCEDURE TRANSPOSE used (Total process time):

real time 0.01 seconds

cpu time 0.01 seconds

NOTE: There were 237146 observations read from the data set WORK.LDRUG.

NOTE: There were 2253 observations read from the data set WORK.LDRUG5.

NOTE: The data set WORK.LDRUG has 239399 observations and 16 variables.

NOTE: DATA statement used (Total process time):

real time 0.07 seconds

cpu time 0.07 seconds

NOTE: There were 2267 observations read from the data set WORK.NEWU.

WHERE epiN=5;

NOTE: There were 25061393 observations read from the data set DAFDAT.LMED.

NOTE: The data set WORK.LMED5 has 26004 observations and 12 variables.

NOTE: DATA statement used (Total process time):

real time 9.92 seconds

cpu time 2.95 seconds

NOTE: There were 26004 observations read from the data set WORK.LMED5.

NOTE: The data set WORK.LMED5 has 26004 observations and 12 variables.

NOTE: PROCEDURE SORT used (Total process time):

real time 0.01 seconds

cpu time 0.01 seconds

NOTE: There were 26004 observations read from the data set WORK.LMED5.

NOTE: The data set WORK.LMED5 has 6289 observations and 12 variables.

NOTE: DATA statement used (Total process time):

real time 0.01 seconds

cpu time 0.01 seconds

NOTE: There were 6289 observations read from the data set WORK.LMED5.
NOTE: The data set WORK.LMED5 has 1933 observations and 22 variables.
NOTE: PROCEDURE TRANSPOSE used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

NOTE: There were 197307 observations read from the data set WORK.LMED.
NOTE: There were 1933 observations read from the data set WORK.LMED5.
NOTE: The data set WORK.LMED has 199240 observations and 22 variables.
NOTE: DATA statement used (Total process time):
 real time 0.04 seconds
 cpu time 0.04 seconds

NOTE: There were 671 observations read from the data set WORK.NEWU.
 WHERE epiN=6;
NOTE: There were 1889909 observations read from the data set WORK.PHOSP.
NOTE: The data set WORK.HOSP6 has 671 observations and 6 variables.
NOTE: DATA statement used (Total process time):
 real time 0.37 seconds
 cpu time 0.31 seconds

NOTE: There were 243755 observations read from the data set WORK.HOSP.
NOTE: There were 671 observations read from the data set WORK.HOSP6.
NOTE: The data set WORK.HOSP has 244426 observations and 6 variables.
NOTE: DATA statement used (Total process time):
 real time 0.06 seconds
 cpu time 0.04 seconds

NOTE: There were 671 observations read from the data set WORK.NEWU.
 WHERE epiN=6;
NOTE: There were 10576531 observations read from the data set DAFDAT.DISP.
 WHERE eksd>='01DEC2011'D;
NOTE: The data set WORK.LDRUG6 has 9086 observations and 16 variables.
NOTE: DATA statement used (Total process time):
 real time 3.84 seconds
 cpu time 3.36 seconds

NOTE: There were 9086 observations read from the data set WORK.LDRUG6.
NOTE: The data set WORK.LDRUG6 has 9086 observations and 16 variables.
NOTE: PROCEDURE SORT used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

NOTE: There were 9086 observations read from the data set WORK.LDRUG6.
NOTE: The data set WORK.LDRUG6 has 2384 observations and 16 variables.
NOTE: DATA statement used (Total process time):
 real time 0.01 seconds
 cpu time 0.01 seconds

NOTE: There were 2384 observations read from the data set WORK.LDRUG6.

NOTE: The data set WORK.LDRUG6 has 666 observations and 16 variables.

NOTE: PROCEDURE TRANSPOSE used (Total process time):

real time 0.00 seconds

cpu time 0.00 seconds

NOTE: There were 239399 observations read from the data set WORK.LDRUG.

NOTE: There were 666 observations read from the data set WORK.LDRUG6.

NOTE: The data set WORK.LDRUG has 240065 observations and 16 variables.

NOTE: DATA statement used (Total process time):

real time 0.07 seconds

cpu time 0.04 seconds

NOTE: There were 671 observations read from the data set WORK.NEWU.

WHERE epiN=6;

NOTE: There were 25061393 observations read from the data set DAFDAT.LMED.

NOTE: The data set WORK.LMED6 has 6251 observations and 12 variables.

NOTE: DATA statement used (Total process time):

real time 3.01 seconds

cpu time 3.00 seconds

NOTE: There were 6251 observations read from the data set WORK.LMED6.

NOTE: The data set WORK.LMED6 has 6251 observations and 12 variables.

NOTE: PROCEDURE SORT used (Total process time):

real time 0.00 seconds

cpu time 0.00 seconds

NOTE: There were 6251 observations read from the data set WORK.LMED6.

NOTE: The data set WORK.LMED6 has 1668 observations and 12 variables.

NOTE: DATA statement used (Total process time):

real time 0.01 seconds

cpu time 0.01 seconds

NOTE: There were 1668 observations read from the data set WORK.LMED6.

NOTE: The data set WORK.LMED6 has 539 observations and 21 variables.

NOTE: PROCEDURE TRANSPOSE used (Total process time):

real time 0.00 seconds

cpu time 0.00 seconds

NOTE: There were 199240 observations read from the data set WORK.LMED.

NOTE: There were 539 observations read from the data set WORK.LMED6.

NOTE: The data set WORK.LMED has 199779 observations and 22 variables.

NOTE: DATA statement used (Total process time):

real time 0.07 seconds

cpu time 0.03 seconds

NOTE: There were 207 observations read from the data set WORK.NEWU.
WHERE epiN=7;

NOTE: There were 1889909 observations read from the data set WORK.PHOSP.

NOTE: The data set WORK.HOSP7 has 207 observations and 6 variables.

NOTE: DATA statement used (Total process time):

real time 0.37 seconds

cpu time 0.25 seconds

NOTE: There were 244426 observations read from the data set WORK.HOSP.

NOTE: There were 207 observations read from the data set WORK.HOSP7.

NOTE: The data set WORK.HOSP has 244633 observations and 6 variables.

NOTE: DATA statement used (Total process time):

real time 0.04 seconds

cpu time 0.00 seconds

NOTE: There were 207 observations read from the data set WORK.NEWU.

WHERE epiN=7;

NOTE: There were 10576531 observations read from the data set DAFDAT.DISP.

WHERE eksd>='01DEC2011'D;

NOTE: The data set WORK.LDRUG7 has 2840 observations and 16 variables.

NOTE: DATA statement used (Total process time):

real time 3.31 seconds

cpu time 3.31 seconds

NOTE: There were 2840 observations read from the data set WORK.LDRUG7.

NOTE: The data set WORK.LDRUG7 has 2840 observations and 16 variables.

NOTE: PROCEDURE SORT used (Total process time):

real time 0.01 seconds

cpu time 0.01 seconds

NOTE: There were 2840 observations read from the data set WORK.LDRUG7.

NOTE: The data set WORK.LDRUG7 has 749 observations and 16 variables.

NOTE: DATA statement used (Total process time):

real time 0.00 seconds

cpu time 0.00 seconds

NOTE: There were 749 observations read from the data set WORK.LDRUG7.

NOTE: The data set WORK.LDRUG7 has 207 observations and 15 variables.

NOTE: PROCEDURE TRANSPOSE used (Total process time):

real time 0.01 seconds

cpu time 0.01 seconds

NOTE: There were 240065 observations read from the data set WORK.LDRUG.

NOTE: There were 207 observations read from the data set WORK.LDRUG7.

NOTE: The data set WORK.LDRUG has 240272 observations and 16 variables.

NOTE: DATA statement used (Total process time):

real time 0.06 seconds

cpu time 0.03 seconds

NOTE: There were 207 observations read from the data set WORK.NEWU.
WHERE epiN=7;
NOTE: There were 25061393 observations read from the data set DAFDAT.LMED.
NOTE: The data set WORK.LMED7 has 1649 observations and 12 variables.
NOTE: DATA statement used (Total process time):
real time 2.98 seconds
cpu time 2.98 seconds

NOTE: There were 1649 observations read from the data set WORK.LMED7.
NOTE: The data set WORK.LMED7 has 1649 observations and 12 variables.
NOTE: PROCEDURE SORT used (Total process time):
real time 0.00 seconds
cpu time 0.00 seconds

NOTE: There were 1649 observations read from the data set WORK.LMED7.
NOTE: The data set WORK.LMED7 has 478 observations and 12 variables.
NOTE: DATA statement used (Total process time):
real time 0.00 seconds
cpu time 0.00 seconds

NOTE: There were 478 observations read from the data set WORK.LMED7.
NOTE: The data set WORK.LMED7 has 161 observations and 19 variables.
NOTE: PROCEDURE TRANSPOSE used (Total process time):
real time 0.01 seconds
cpu time 0.01 seconds

NOTE: There were 199779 observations read from the data set WORK.LMED.
NOTE: There were 161 observations read from the data set WORK.LMED7.
NOTE: The data set WORK.LMED has 199940 observations and 22 variables.
NOTE: DATA statement used (Total process time):
real time 0.07 seconds
cpu time 0.03 seconds

NOTE: There were 64 observations read from the data set WORK.NEWU.
WHERE epiN=8;
NOTE: There were 1889909 observations read from the data set WORK.PHOSP.
NOTE: The data set WORK.HOSP8 has 64 observations and 6 variables.
NOTE: DATA statement used (Total process time):
real time 0.37 seconds
cpu time 0.20 seconds

NOTE: There were 244633 observations read from the data set WORK.HOSP.
NOTE: There were 64 observations read from the data set WORK.HOSP8.
NOTE: The data set WORK.HOSP has 244697 observations and 6 variables.
NOTE: DATA statement used (Total process time):
real time 0.06 seconds
cpu time 0.06 seconds

NOTE: There were 64 observations read from the data set WORK.NEWU.
WHERE epiN=8;
NOTE: There were 10576531 observations read from the data set DAFDAT.DISP.
WHERE eksd>='01DEC2011'D;
NOTE: The data set WORK.LDRUG8 has 845 observations and 16 variables.
NOTE: DATA statement used (Total process time):
real time 3.31 seconds
cpu time 3.31 seconds

NOTE: There were 845 observations read from the data set WORK.LDRUG8.
NOTE: The data set WORK.LDRUG8 has 845 observations and 16 variables.
NOTE: PROCEDURE SORT used (Total process time):
real time 0.00 seconds
cpu time 0.00 seconds

NOTE: There were 845 observations read from the data set WORK.LDRUG8.
NOTE: The data set WORK.LDRUG8 has 241 observations and 16 variables.
NOTE: DATA statement used (Total process time):
real time 0.00 seconds
cpu time 0.00 seconds

NOTE: There were 241 observations read from the data set WORK.LDRUG8.
NOTE: The data set WORK.LDRUG8 has 64 observations and 14 variables.
NOTE: PROCEDURE TRANSPOSE used (Total process time):
real time 0.01 seconds
cpu time 0.01 seconds

NOTE: There were 240272 observations read from the data set WORK.LDRUG.
NOTE: There were 64 observations read from the data set WORK.LDRUG8.
NOTE: The data set WORK.LDRUG has 240336 observations and 16 variables.
NOTE: DATA statement used (Total process time):
real time 0.06 seconds
cpu time 0.04 seconds

NOTE: There were 64 observations read from the data set WORK.NEWU.
WHERE epiN=8;
NOTE: There were 25061393 observations read from the data set DAFDAT.LMED.
NOTE: The data set WORK.LMED8 has 457 observations and 12 variables.
NOTE: DATA statement used (Total process time):
real time 2.95 seconds
cpu time 2.93 seconds

NOTE: There were 457 observations read from the data set WORK.LMED8.
NOTE: The data set WORK.LMED8 has 457 observations and 12 variables.
NOTE: PROCEDURE SORT used (Total process time):
real time 0.00 seconds
cpu time 0.00 seconds

NOTE: There were 457 observations read from the data set WORK.LMED8.
NOTE: The data set WORK.LMED8 has 131 observations and 12 variables.
NOTE: DATA statement used (Total process time):
 real time 0.01 seconds
 cpu time 0.01 seconds

NOTE: There were 131 observations read from the data set WORK.LMED8.
NOTE: The data set WORK.LMED8 has 48 observations and 17 variables.
NOTE: PROCEDURE TRANSPOSE used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

NOTE: There were 199940 observations read from the data set WORK.LMED.
NOTE: There were 48 observations read from the data set WORK.LMED8.
NOTE: The data set WORK.LMED has 199988 observations and 22 variables.
NOTE: DATA statement used (Total process time):
 real time 0.06 seconds
 cpu time 0.03 seconds

NOTE: There were 15 observations read from the data set WORK.NEWU.
 WHERE epiN=9;
NOTE: There were 1889909 observations read from the data set WORK.PHOSP.
NOTE: The data set WORK.HOSP9 has 15 observations and 6 variables.
NOTE: DATA statement used (Total process time):
 real time 0.37 seconds
 cpu time 0.26 seconds

NOTE: There were 244697 observations read from the data set WORK.HOSP.
NOTE: There were 15 observations read from the data set WORK.HOSP9.
NOTE: The data set WORK.HOSP has 244712 observations and 6 variables.
NOTE: DATA statement used (Total process time):
 real time 0.06 seconds
 cpu time 0.03 seconds

NOTE: There were 15 observations read from the data set WORK.NEWU.
 WHERE epiN=9;
NOTE: There were 10576531 observations read from the data set DAFDAT.DISP.
 WHERE eksd>='01DEC2011'D;
NOTE: The data set WORK.LDRUG9 has 221 observations and 16 variables.
NOTE: DATA statement used (Total process time):
 real time 3.32 seconds
 cpu time 3.28 seconds

NOTE: There were 221 observations read from the data set WORK.LDRUG9.
NOTE: The data set WORK.LDRUG9 has 221 observations and 16 variables.
NOTE: PROCEDURE SORT used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

NOTE: There were 221 observations read from the data set WORK.LDRUG9.
NOTE: The data set WORK.LDRUG9 has 65 observations and 16 variables.
NOTE: DATA statement used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

NOTE: There were 65 observations read from the data set WORK.LDRUG9.
NOTE: The data set WORK.LDRUG9 has 15 observations and 13 variables.
NOTE: PROCEDURE TRANSPOSE used (Total process time):
 real time 0.01 seconds
 cpu time 0.01 seconds

NOTE: There were 240336 observations read from the data set WORK.LDRUG.
NOTE: There were 15 observations read from the data set WORK.LDRUG9.
NOTE: The data set WORK.LDRUG has 240351 observations and 16 variables.
NOTE: DATA statement used (Total process time):
 real time 0.06 seconds
 cpu time 0.06 seconds

NOTE: There were 15 observations read from the data set WORK.NEWU.
 WHERE epiN=9;
NOTE: There were 25061393 observations read from the data set DAFDAT.LMED.
NOTE: The data set WORK.LMED9 has 81 observations and 12 variables.
NOTE: DATA statement used (Total process time):
 real time 2.93 seconds
 cpu time 2.93 seconds

NOTE: There were 81 observations read from the data set WORK.LMED9.
NOTE: The data set WORK.LMED9 has 81 observations and 12 variables.
NOTE: PROCEDURE SORT used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

NOTE: There were 81 observations read from the data set WORK.LMED9.
NOTE: The data set WORK.LMED9 has 33 observations and 12 variables.
NOTE: DATA statement used (Total process time):
 real time 0.01 seconds
 cpu time 0.01 seconds

NOTE: There were 33 observations read from the data set WORK.LMED9.
NOTE: The data set WORK.LMED9 has 12 observations and 14 variables.
NOTE: PROCEDURE TRANSPOSE used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

NOTE: There were 199988 observations read from the data set WORK.LMED.

NOTE: There were 12 observations read from the data set WORK.LMED9.
NOTE: The data set WORK.LMED has 200000 observations and 22 variables.
NOTE: DATA statement used (Total process time):
 real time 0.07 seconds
 cpu time 0.06 seconds

NOTE: There were 3 observations read from the data set WORK.NEWU.
 WHERE epiN=10;
NOTE: There were 1889909 observations read from the data set WORK.PHOSP.
NOTE: The data set WORK.HOSP10 has 3 observations and 6 variables.
NOTE: DATA statement used (Total process time):
 real time 0.29 seconds
 cpu time 0.28 seconds

NOTE: There were 244712 observations read from the data set WORK.HOSP.
NOTE: There were 3 observations read from the data set WORK.HOSP10.
NOTE: The data set WORK.HOSP has 244715 observations and 6 variables.
NOTE: DATA statement used (Total process time):
 real time 0.04 seconds
 cpu time 0.04 seconds

NOTE: There were 3 observations read from the data set WORK.NEWU.
 WHERE epiN=10;
NOTE: There were 10576531 observations read from the data set DAFDAT.DISP.
 WHERE eksd>='01DEC2011'D;
NOTE: The data set WORK.LDRUG10 has 24 observations and 16 variables.
NOTE: DATA statement used (Total process time):
 real time 3.18 seconds
 cpu time 3.15 seconds

NOTE: There were 24 observations read from the data set WORK.LDRUG10.
NOTE: The data set WORK.LDRUG10 has 24 observations and 16 variables.
NOTE: PROCEDURE SORT used (Total process time):
 real time 0.01 seconds
 cpu time 0.01 seconds

NOTE: There were 24 observations read from the data set WORK.LDRUG10.
NOTE: The data set WORK.LDRUG10 has 11 observations and 16 variables.
NOTE: DATA statement used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

NOTE: There were 11 observations read from the data set WORK.LDRUG10.
NOTE: The data set WORK.LDRUG10 has 3 observations and 9 variables.
NOTE: PROCEDURE TRANSPOSE used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

NOTE: There were 240351 observations read from the data set WORK.LDRUG.
NOTE: There were 3 observations read from the data set WORK.LDRUG10.
NOTE: The data set WORK.LDRUG has 240354 observations and 16 variables.
NOTE: DATA statement used (Total process time):
 real time 0.07 seconds
 cpu time 0.04 seconds

NOTE: There were 3 observations read from the data set WORK.NEWU.
 WHERE epiN=10;
NOTE: There were 25061393 observations read from the data set DAFDAT.LMED.
NOTE: The data set WORK.LMED10 has 3 observations and 12 variables.
NOTE: DATA statement used (Total process time):
 real time 2.70 seconds
 cpu time 2.70 seconds

NOTE: There were 3 observations read from the data set WORK.LMED10.
NOTE: The data set WORK.LMED10 has 3 observations and 12 variables.
NOTE: PROCEDURE SORT used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

NOTE: There were 3 observations read from the data set WORK.LMED10.
NOTE: The data set WORK.LMED10 has 2 observations and 12 variables.
NOTE: DATA statement used (Total process time):
 real time 0.01 seconds
 cpu time 0.01 seconds

NOTE: There were 2 observations read from the data set WORK.LMED10.
NOTE: The data set WORK.LMED10 has 2 observations and 4 variables.
NOTE: PROCEDURE TRANSPOSE used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

NOTE: There were 200000 observations read from the data set WORK.LMED.
NOTE: There were 2 observations read from the data set WORK.LMED10.
NOTE: The data set WORK.LMED has 200002 observations and 22 variables.
NOTE: DATA statement used (Total process time):
 real time 0.07 seconds
 cpu time 0.04 seconds

NOTE: There were 1 observations read from the data set WORK.NEWU.
 WHERE epiN=11;
NOTE: There were 1889909 observations read from the data set WORK.PHOSP.
NOTE: The data set WORK.HOSP11 has 1 observations and 6 variables.
NOTE: DATA statement used (Total process time):
 real time 0.34 seconds
 cpu time 0.29 seconds

NOTE: There were 244715 observations read from the data set WORK.HOSP.
NOTE: There were 1 observations read from the data set WORK.HOSP11.
NOTE: The data set WORK.HOSP has 244716 observations and 6 variables.
NOTE: DATA statement used (Total process time):
 real time 0.06 seconds
 cpu time 0.04 seconds

NOTE: There were 1 observations read from the data set WORK.NEWU.
 WHERE epiN=11;
NOTE: There were 10576531 observations read from the data set DAFDAT.DISP.
 WHERE eksd>='01DEC2011'D;
NOTE: The data set WORK.LDRUG11 has 11 observations and 16 variables.
NOTE: DATA statement used (Total process time):
 real time 3.20 seconds
 cpu time 3.20 seconds

NOTE: There were 11 observations read from the data set WORK.LDRUG11.
NOTE: The data set WORK.LDRUG11 has 11 observations and 16 variables.
NOTE: PROCEDURE SORT used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

NOTE: There were 11 observations read from the data set WORK.LDRUG11.
NOTE: The data set WORK.LDRUG11 has 5 observations and 16 variables.
NOTE: DATA statement used (Total process time):
 real time 0.01 seconds
 cpu time 0.01 seconds

NOTE: There were 5 observations read from the data set WORK.LDRUG11.
NOTE: The data set WORK.LDRUG11 has 1 observations and 7 variables.
NOTE: PROCEDURE TRANSPOSE used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

NOTE: There were 240354 observations read from the data set WORK.LDRUG.
NOTE: There were 1 observations read from the data set WORK.LDRUG11.
NOTE: The data set WORK.LDRUG has 240355 observations and 16 variables.
NOTE: DATA statement used (Total process time):
 real time 0.07 seconds
 cpu time 0.06 seconds

NOTE: There were 1 observations read from the data set WORK.NEWU.
 WHERE epiN=11;
NOTE: There were 25061393 observations read from the data set DAFDAT.LMED.
NOTE: The data set WORK.LMED11 has 5 observations and 12 variables.
NOTE: DATA statement used (Total process time):
 real time 2.71 seconds
 cpu time 2.67 seconds

NOTE: There were 5 observations read from the data set WORK.LMED11.
 NOTE: The data set WORK.LMED11 has 5 observations and 12 variables.
 NOTE: PROCEDURE SORT used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

NOTE: There were 5 observations read from the data set WORK.LMED11.
 NOTE: The data set WORK.LMED11 has 4 observations and 12 variables.
 NOTE: DATA statement used (Total process time):
 real time 0.01 seconds
 cpu time 0.01 seconds

NOTE: There were 4 observations read from the data set WORK.LMED11.
 NOTE: The data set WORK.LMED11 has 1 observations and 6 variables.
 NOTE: PROCEDURE TRANSPOSE used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

NOTE: There were 200002 observations read from the data set WORK.LMED.
 NOTE: There were 1 observations read from the data set WORK.LMED11.
 NOTE: The data set WORK.LMED has 200003 observations and 22 variables.
 NOTE: DATA statement used (Total process time):
 real time 0.07 seconds
 cpu time 0.06 seconds

```

238
239      * Cause of death ;
240      data cod ( keep = pnr deCVDD coD ) ;
241          set grund.dodsaasg2016 ;
242          format deCVDD ddmmyy10. ;
243      * label coD = "Cause of (CVD) death"
244          deCVDD = "Date of CVD-death" ;
245          if ( substr( C_DODTILGRUNDL_ACME, 1, 1 ) eq "I" and
246              substr( C_DODTILGRUNDL_ACME, 1, 3 ) ne "I10" ) ;
247          deCVDD = D_DODSDATO ;
248          coD = C_DODTILGRUNDL_ACME ;
249          if deCVDD > '01DEC2012'd ;
250      run ;

```

NOTE: There were 811233 observations read from the data set GRUND.DODSAASG2016.
 NOTE: The data set WORK.COD has 39750 observations and 3 variables.
 NOTE: DATA statement used (Total process time):
 real time 0.76 seconds
 cpu time 0.07 seconds

```

251
252      proc sort  data = cod  nodupkey ; by pnr ; run ;

```

NOTE: There were 39750 observations read from the data set WORK.COD.
 NOTE: 0 observations with duplicate key values were deleted.
 NOTE: The data set WORK.COD has 39750 observations and 3 variables.
 NOTE: PROCEDURE SORT used (Total process time):
 real time 0.01 seconds

cpu time 0.01 seconds

```

253
254     title 'Causes of death counted as CVD' ;
255     proc tabulate data = cod missing noseps ;
256         class coD deCVDD ;
257         table all coD,
258             ( all deCVDD ) * f=comma7.
259             / rts = 6 ;
260         format deCVDD year4.
261             coD $ICD10_L1L1_KT. ;
262         keylabel n = ' ' ;
263     run ;

```

NOTE: There were 39750 observations read from the data set WORK.COD.

NOTE: The PROCEDURE TABULATE printed page 4.

NOTE: PROCEDURE TABULATE used (Total process time):

real time 0.50 seconds
 cpu time 0.03 seconds

```

264     title ;
265
266     * Merge in type and date of firstline treatment, date and cause of death,
267       dates of first complications and populaion information ;
268     data newu ;
269         merge newu ( in = nu )
270             FL
271             cod
272             dafdat.wcompl
273             DMdat.pop ;
274         by pnr ;
275         if nu ;
276     run ;

```

NOTE: There were 244715 observations read from the data set WORK.NEWU.

NOTE: There were 383033 observations read from the data set WORK.FL.

NOTE: There were 39750 observations read from the data set WORK.COD.

NOTE: There were 1997992 observations read from the data set DAFDAT.WCOMPL.

NOTE: There were 7411436 observations read from the data set DMDAT.POP.

NOTE: The data set WORK.NEWU has 244715 observations and 48 variables.

NOTE: DATA statement used (Total process time):

real time 9.62 seconds
 cpu time 3.56 seconds

```

277
278     * Then merge with the datasets classified by epiN too ;
279     proc sort data = newu ; by epiN pnr ; run ;

```

NOTE: There were 244715 observations read from the data set WORK.NEWU.

NOTE: The data set WORK.NEWU has 244715 observations and 48 variables.

NOTE: PROCEDURE SORT used (Total process time):

real time 0.32 seconds
 cpu time 0.28 seconds

```

280     data newu ;
281         merge newu ( in = nu )
282             lmed
283             ldrug

```

```

284         hosp ;
285     by epiN pnr ;
286     if nu ;
287     label doIx = 'Index date'
288           doTm = 'Index drug termination date'
289           doFL = 'Date of first line treatment'
290           FLdr = 'First line drug'
291           FLatc = 'First line drug (atc)'
292           Ixdr = 'Index drug'
293           Ixatc = 'Index drug (atc)'
294           epiN = 'Drug episode no since 2012-12-01' ;
295 run ;

```

NOTE: There were 244715 observations read from the data set WORK.NEWU.
 NOTE: There were 200003 observations read from the data set WORK.LMED.
 NOTE: There were 240355 observations read from the data set WORK.LDRUG.
 NOTE: There were 244716 observations read from the data set WORK.HOSP.
 NOTE: The data set WORK.NEWU has 244715 observations and 84 variables.
 NOTE: DATA statement used (Total process time):
 real time 0.53 seconds
 cpu time 0.28 seconds

```

296
297     * Adding complications AFTER index date ;
298     * As before this needs to be in a loop over the episode numbers ;
299     * Macro for defining >first< complications after doIx ;
300     %macro getcomp( nam, cl ) ;
301         retain de&nam. ;
302         format de&nam. ddmmyy10. ;
303         if first.pnr then de&nam. = . ;
304         if doCompl > doIx and
305             de&nam. le .z and
306             compl in ( &cl. ) then de&nam. = doCompl ;
307     %mend ;
308
309     data compl ; run ;

```

NOTE: The data set WORK.COMPL has 1 observations and 0 variables.
 NOTE: DATA statement used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

```

310
311     %macro colcomp ;
312     **** Loop over episode numbers **** ;
313     %do ne = 1 %to 11 ;
314
315     data compl&ne. ( drop = doCompl ) ;
316         merge newu ( in = nu
317                     where = (epiN eq &ne.) )
318         dafdat.compl ;
319         by pnr ;
320         if nu ;
321         %getcomp( HF , "HF" )
322         %getcomp( MACE, %str("MI","HmStr","IscStr") )
323         %getcomp( MI , "MI" )
324         %getcomp( Str , %str("HmStr","IscStr") )
325         %getcomp( IscStr, "IscStr" )
326         %getcomp( AF , "AtrFib" )
327         %getcomp( HH , "Hypo" )

```

```

328      %getcomp( DKD , "DKD" )
329      if last.pnr then output ;
330      run ;
331
332      data compl ; set compl compl&ne. ; run ;
333
334      %end ;
335      **** End of loop over episode numbers **** ;
336      %mend colcomp ;
337
338      %colcomp ;

```

NOTE: There were 156182 observations read from the data set WORK.NEWU.

WHERE epiN=1;

NOTE: There were 11204191 observations read from the data set DAFDAT.COMPL.

NOTE: The data set WORK.COMPL1 has 156182 observations and 98 variables.

NOTE: DATA statement used (Total process time):

real time 8.63 seconds

cpu time 2.10 seconds

NOTE: There were 1 observations read from the data set WORK.COMPL.

NOTE: There were 156182 observations read from the data set WORK.COMPL1.

NOTE: The data set WORK.COMPL has 156183 observations and 98 variables.

NOTE: DATA statement used (Total process time):

real time 0.21 seconds

cpu time 0.10 seconds

NOTE: There were 57025 observations read from the data set WORK.NEWU.

WHERE epiN=2;

NOTE: There were 11204191 observations read from the data set DAFDAT.COMPL.

NOTE: The data set WORK.COMPL2 has 57025 observations and 98 variables.

NOTE: DATA statement used (Total process time):

real time 2.12 seconds

cpu time 2.04 seconds

NOTE: There were 156183 observations read from the data set WORK.COMPL.

NOTE: There were 57025 observations read from the data set WORK.COMPL2.

NOTE: The data set WORK.COMPL has 213208 observations and 98 variables.

NOTE: DATA statement used (Total process time):

real time 0.35 seconds

cpu time 0.12 seconds

NOTE: There were 20996 observations read from the data set WORK.NEWU.

WHERE epiN=3;

NOTE: There were 11204191 observations read from the data set DAFDAT.COMPL.

NOTE: The data set WORK.COMPL3 has 20996 observations and 98 variables.

NOTE: DATA statement used (Total process time):

real time 2.00 seconds

cpu time 1.87 seconds

NOTE: There were 213208 observations read from the data set WORK.COMPL.

NOTE: There were 20996 observations read from the data set WORK.COMPL3.

NOTE: The data set WORK.COMPL has 234204 observations and 98 variables.

NOTE: DATA statement used (Total process time):

real time	0.39 seconds
cpu time	0.14 seconds

NOTE: There were 7284 observations read from the data set WORK.NEWU.

WHERE epiN=4;

NOTE: There were 11204191 observations read from the data set DAFDAT.COMPL.

NOTE: The data set WORK.COMPL4 has 7284 observations and 98 variables.

NOTE: DATA statement used (Total process time):

real time	1.96 seconds
cpu time	1.89 seconds

NOTE: There were 234204 observations read from the data set WORK.COMPL.

NOTE: There were 7284 observations read from the data set WORK.COMPL4.

NOTE: The data set WORK.COMPL has 241488 observations and 98 variables.

NOTE: DATA statement used (Total process time):

real time	0.40 seconds
cpu time	0.14 seconds

NOTE: There were 2267 observations read from the data set WORK.NEWU.

WHERE epiN=5;

NOTE: There were 11204191 observations read from the data set DAFDAT.COMPL.

NOTE: The data set WORK.COMPL5 has 2267 observations and 98 variables.

NOTE: DATA statement used (Total process time):

real time	1.93 seconds
cpu time	1.78 seconds

NOTE: There were 241488 observations read from the data set WORK.COMPL.

NOTE: There were 2267 observations read from the data set WORK.COMPL5.

NOTE: The data set WORK.COMPL has 243755 observations and 98 variables.

NOTE: DATA statement used (Total process time):

real time	0.40 seconds
cpu time	0.17 seconds

NOTE: There were 671 observations read from the data set WORK.NEWU.

WHERE epiN=6;

NOTE: There were 11204191 observations read from the data set DAFDAT.COMPL.

NOTE: The data set WORK.COMPL6 has 671 observations and 98 variables.

NOTE: DATA statement used (Total process time):

real time	1.92 seconds
cpu time	1.84 seconds

NOTE: There were 243755 observations read from the data set WORK.COMPL.

NOTE: There were 671 observations read from the data set WORK.COMPL6.

NOTE: The data set WORK.COMPL has 244426 observations and 98 variables.

NOTE: DATA statement used (Total process time):

real time	0.42 seconds
cpu time	0.11 seconds

NOTE: There were 207 observations read from the data set WORK.NEWU.
WHERE epiN=7;
NOTE: There were 11204191 observations read from the data set DAFDAT.COMPL.
NOTE: The data set WORK.COMPL7 has 207 observations and 98 variables.
NOTE: DATA statement used (Total process time):
real time 1.90 seconds
cpu time 1.78 seconds

NOTE: There were 244426 observations read from the data set WORK.COMPL.
NOTE: There were 207 observations read from the data set WORK.COMPL7.
NOTE: The data set WORK.COMPL has 244633 observations and 98 variables.
NOTE: DATA statement used (Total process time):
real time 0.42 seconds
cpu time 0.18 seconds

NOTE: There were 64 observations read from the data set WORK.NEWU.
WHERE epiN=8;
NOTE: There were 11204191 observations read from the data set DAFDAT.COMPL.
NOTE: The data set WORK.COMPL8 has 64 observations and 98 variables.
NOTE: DATA statement used (Total process time):
real time 1.89 seconds
cpu time 1.81 seconds

NOTE: There were 244633 observations read from the data set WORK.COMPL.
NOTE: There were 64 observations read from the data set WORK.COMPL8.
NOTE: The data set WORK.COMPL has 244697 observations and 98 variables.
NOTE: DATA statement used (Total process time):
real time 0.43 seconds
cpu time 0.09 seconds

NOTE: There were 15 observations read from the data set WORK.NEWU.
WHERE epiN=9;
NOTE: There were 11204191 observations read from the data set DAFDAT.COMPL.
NOTE: The data set WORK.COMPL9 has 15 observations and 98 variables.
NOTE: DATA statement used (Total process time):
real time 1.87 seconds
cpu time 1.76 seconds

NOTE: There were 244697 observations read from the data set WORK.COMPL.
NOTE: There were 15 observations read from the data set WORK.COMPL9.
NOTE: The data set WORK.COMPL has 244712 observations and 98 variables.
NOTE: DATA statement used (Total process time):
real time 0.42 seconds
cpu time 0.11 seconds

NOTE: There were 3 observations read from the data set WORK.NEWU.
WHERE epiN=10;
NOTE: There were 11204191 observations read from the data set DAFDAT.COMPL.

NOTE: The data set WORK.COMPL10 has 3 observations and 98 variables.

NOTE: DATA statement used (Total process time):

real time	1.79 seconds
cpu time	1.68 seconds

NOTE: There were 244712 observations read from the data set WORK.COMPL.

NOTE: There were 3 observations read from the data set WORK.COMPL10.

NOTE: The data set WORK.COMPL has 244715 observations and 98 variables.

NOTE: DATA statement used (Total process time):

real time	0.40 seconds
cpu time	0.09 seconds

NOTE: There were 1 observations read from the data set WORK.NEWU.

WHERE epiN=11;

NOTE: There were 11204191 observations read from the data set DAFDAT.COMPL.

NOTE: The data set WORK.COMPL11 has 1 observations and 98 variables.

NOTE: DATA statement used (Total process time):

real time	1.76 seconds
cpu time	1.65 seconds

NOTE: There were 244715 observations read from the data set WORK.COMPL.

NOTE: There were 1 observations read from the data set WORK.COMPL11.

NOTE: The data set WORK.COMPL has 244716 observations and 98 variables.

NOTE: DATA statement used (Total process time):

real time	0.42 seconds
cpu time	0.17 seconds

```

339
340     data dafdat.episodes ;
341         merge newu ( in = nu )
342             compl ;
343         by epiN pnr ;
344         if nu ;
345         format doFL doIx doTm doBth doDM doDth ddmmyy10. ;
346     run ;

```

NOTE: There were 244715 observations read from the data set WORK.NEWU.

NOTE: There were 244716 observations read from the data set WORK.COMPL.

NOTE: The data set DAFDAT.EPISODES has 244715 observations and 98 variables.

NOTE: DATA statement used (Total process time):

real time	0.89 seconds
cpu time	0.29 seconds

```

347
348     title1 'New episodes (1,2,3) after December 2012' ;
349     proc tabulate data = dafdat.episodes (where = (epiN le 3) ) missing noseps ;
350         class doIx deCVDD deHF deMACE deMI deStr deAF deHH epiN ;
351         table epiN = "Episode no:", all
352             deCVDD deHF deMACE deMI deStr deAF deHH,
353             ( all doIx ) * f=comma8.
354             / rts = 11 condense ;
355         format deCVDD deHF deMACE deMI deStr deAF deHH doIx year4.
356             Ixatc $atc_L1L1_kt. ;
357     run ;

```

NOTE: There were 234203 observations read from the data set DAFDAT.EPISODES.
WHERE epiN<=3;

NOTE: The PROCEDURE TABULATE printed page 5.

NOTE: PROCEDURE TABULATE used (Total process time):

real time 1.12 seconds
cpu time 0.20 seconds

```
358
359     title1 'All new episodes after December 2012' ;
360     proc tabulate data = dafdat.episodes missing noseps ;
361         class doIx deCVDD deHF deMACE deMI deStr deAF deHH epiN ;
362         table all
363             deCVDD deHF deMACE deMI deStr deAF deHH,
364             ( all doIx ) * f=comma8.
365             / rts = 11 condense ;
366         format deCVDD deHF deMACE deMI deStr deAF deHH doIx year4.
367             Ixatc $atc_L1L1_kt. ;
368     run ;
```

NOTE: There were 244715 observations read from the data set DAFDAT.EPISODES.

NOTE: The PROCEDURE TABULATE printed page 6.

NOTE: PROCEDURE TABULATE used (Total process time):

real time 0.10 seconds
cpu time 0.18 seconds

```
369
370     proc tabulate data = dafdat.episodes missing noseps ;
371         class doIx Ixdr Ixatc epiN ;
372         table Ixdr * (all Ixatc),
373             ( all doIx ) * f=comma7.
374             / rts = 40 indent=2 ;
375         table Ixdr * (all Ixatc),
376             ( all epiN ) * f=comma7.
377             / rts = 40 indent=2 ;
378         format doIx year4.
379             Ixatc $atc_L1L1_kt. ;
380         label Ixdr= Ixatc= ;
381     run ;
```

NOTE: There were 244715 observations read from the data set DAFDAT.EPISODES.

NOTE: The PROCEDURE TABULATE printed pages 7-9.

NOTE: PROCEDURE TABULATE used (Total process time):

real time 0.10 seconds
cpu time 0.20 seconds

```
382
383     proc sort      data = dafdat.episodes ; by pnr epiN ; run ;
```

NOTE: There were 244715 observations read from the data set DAFDAT.EPISODES.

NOTE: The data set DAFDAT.EPISODES has 244715 observations and 98 variables.

NOTE: PROCEDURE SORT used (Total process time):

real time 1.10 seconds
cpu time 0.48 seconds

```
384     proc contents data = dafdat.episodes varnum ; run ;
```

NOTE: PROCEDURE CONTENTS used (Total process time):

```

real time      0.00 seconds
cpu time       0.00 seconds

```

NOTE: The PROCEDURE CONTENTS printed page 10.

NOTE: SAS Institute Inc., SAS Campus Drive, Cary, NC USA 27513-2414

NOTE: The SAS System used:

```

real time      5:48.44
cpu time       2:22.87

```

4.6.1 07-newuse.lst

All new start episodes (some persons with > 1) in T2 after dec 2012 1
16:43 Wednesday, May 9, 2018

	doIx								
	All	2012/4	2013/1	2013/2	2013/3	2013/4	2014/1	2014/2	2014/3
	N	N	N	N	N	N	N	N	N
All	244,715	4,489	14,766	14,323	12,172	13,800	14,864	13,624	12,338
Ixdr									
Acarbose	179	9	24	16	11	9	13	12	9
DPP4	39,306	673	2,248	2,172	1,875	2,444	2,579	2,333	1,989
GLP1	17,370	383	1,275	1,034	788	821	956	818	823
Metformin	90,029	1,936	5,996	5,575	4,733	5,147	5,494	5,050	4,600
SGLT2	17,678	20	302	554	485	588	616	744	672
SU	19,099	412	1,427	1,354	1,137	1,242	1,348	1,201	1,061
TZD	156	4	13	12	11	12	20	10	8
fastIns	20,145	342	1,081	1,129	1,018	1,159	1,205	1,145	1,074
intIns	11,859	262	919	914	807	870	913	754	688
longIns	23,244	299	959	1,088	914	1,093	1,260	1,155	1,086
mixIns	5,650	149	522	475	393	415	460	402	328

(Continued)

	doIx								
	2014/4	2015/1	2015/2	2015/3	2015/4	2016/1	2016/2	2016/3	2016/4
	N	N	N	N	N	N	N	N	N
All	14,490	15,767	15,707	13,987	16,163	17,297	18,563	15,141	17,224
Ixdr									
Acarbose	18	11	13	9	9	9	7	.	.
DPP4	2,344	2,609	2,724	2,330	2,485	2,694	2,920	2,269	2,618
GLP1	952	1,047	1,199	1,038	1,143	1,149	1,353	1,194	1,397
Metformin	5,309	5,668	5,694	5,177	5,852	6,254	6,611	5,264	5,669
SGLT2	1,006	1,131	1,119	892	1,619	1,878	2,122	1,730	2,200
SU	1,119	1,244	1,202	1,100	1,111	1,080	1,175	868	1,018
TZD	5	8	7	4	15	8	5	5	9
fastIns	1,321	1,353	1,241	1,208	1,341	1,362	1,352	1,292	1,522
intIns	754	859	707	606	647	619	600	475	465
longIns	1,299	1,453	1,472	1,347	1,662	1,991	2,176	1,861	2,129
mixIns	363	384	329	276	279	253	242	183	197

(Continued)

	doTm								
	.	2013/2	2013/3	2013/4	2014/1	2014/2	2014/3	2014/4	2015/1
	N	N	N	N	N	N	N	N	N
All	156,920	801	3,138	3,820	3,942	4,671	5,482	5,359	5,381
Ixdr									
Acarbose	.	*	11	7	8	13	10	12	8
DPP4	25,382	104	432	531	551	709	889	849	800
GLP1	12,190	41	214	233	250	315	301	283	307
Metformin	63,905	251	925	1,139	1,181	1,317	1,629	1,572	1,643
SGLT2	12,581	4	61	136	162	221	216	244	263
SU	9,998	85	373	447	438	490	607	574	614
TZD	43	*	8	5	6	10	13	13	11
fastIns	6,891	183	619	696	649	775	854	891	805
intIns	5,449	49	240	294	334	409	456	420	412
longIns	17,774	49	142	181	206	249	264	294	317
mixIns	2,707	31	113	151	157	163	243	207	201

(Continued)

	doTm							
	2015/2	2015/3	2015/4	2016/1	2016/2	2016/3	2016/4	2017/1
	N	N	N	N	N	N	N	N
All	5,970	6,904	7,136	6,950	7,346	8,923	11,794	178
Ixdr								
Acarbose	10	11	24	5	14	12	31	.
DPP4	908	1,182	1,236	1,173	1,243	1,455	1,833	29
GLP1	324	335	385	420	471	597	689	15
Metformin	1,726	1,958	2,154	2,058	2,041	2,633	3,830	67
SGLT2	348	432	468	452	505	684	892	9
SU	627	744	709	711	765	826	1,077	14
TZD	6	4	6	6	7	9	8	.
fastIns	998	1,064	1,019	952	1,060	1,215	1,454	20
intIns	451	522	451	480	509	622	751	10
longIns	383	421	452	451	506	624	920	11
mixIns	189	231	232	242	225	246	309	*

All new start episodes (some persons with > 1) in T2 after dec 2012 2
 16:43 Wednesday, May 9, 2018

All	Ixdr								
	Acarbo-	DPP4	GLP1	Metfor-	SGLT2	SU	TZD	fastIns	intIns
	se								
N	N	N	N	N	N	N	N	N	N

All	244,715	179	39,306	17,370	90,029	17,678	19,099	156	20,145	11,859
*	156,182	135	24,604	8,786	79,030	6,909	10,298	67	9,628	5,351
*	57,025	33	11,378	4,993	7,764	6,165	6,622	52	5,902	4,264
*	20,996	7	2,463	2,380	2,123	3,018	1,621	22	2,851	1,564
4	7,284	*	616	858	748	1,091	385	9	1,191	505
5	2,267	*	179	254	253	336	117	*	403	125
6	671	.	44	77	74	109	40	*	114	35
7	207	.	17	18	25	36	10	.	38	13
8	64	.	*	*	10	10	4	.	15	*
9	15	.	*	*	*	*	*	.	*	.
10	*	.	.	.	.	*	.	.	.	.
11	*	.	.	.	.	.	.	.	*	.

(Continued)

All new start episodes (some persons with > 1) in T2 after dec 2012 3
 16:43 Wednesday, May 9, 2018

Ixdr		
longIns mixIns		
	N	N
All	23,244	5,650
*	8,700	2,674
*	8,114	1,738
*	4,119	828
4	1,593	285
5	513	83
6	147	28
7	39	11
8	16	*
9	*	.
10	*	*
11	.	.

Causes of death counted as CVD

16:43 Wednesday, May 9, 2018 4

deCVDD						
	All	2012	2013	2014	2015	2016
All	39,750	794	8,948	9,463	10,360	10,185
coD						
I009	*	.	.	*	.	.
I018	*	.	.	*	.	.
I019	10	.	*	*	*	*
I029	*	.	.	.	.	*
I050	*	.	*	*	.	.
I051	*	.	*	*	.	.
I052	*	.	.	.	*	.
I059	*	.	*	.	.	.
I060	7	.	4	*	*	*
I061	6	*	.	*	.	*
I062	206	*	38	56	53	58
I069	*	.	.	.	*	.

I082	*	.	.	.	*	.
I088	10	.	*	*	5	*
I089	4	.	*	*	.	*
I091	*	.	*	.	.	*
I092	*	.	*	.	.	.
I110	426	10	94	103	105	114
I119	68	*	20	17	15	13
I120	193	*	43	42	55	51
I129	*	.	*	.	.	*
I130	287	5	50	51	79	102
I131	34	.	5	7	10	12
I132	609	5	109	136	168	191
I139	33	.	6	7	6	14
I200	10	.	4	.	4	*
I201	*	.	.	*	*	.
I208	4	.	*	*	.	*
I209	76	*	16	25	21	13
I210	135	*	28	31	21	54
I211	56	*	16	9	14	14
I212	55	4	16	16	7	12
I213	351	9	79	81	82	100
I214	315	12	80	75	76	72
I219	4,081	99	1,061	1,014	1,019	888
I240	*	*	*	.	.	.
I241	*	.	.	.	.	*
I248	178	5	24	42	56	51
I249	1,236	28	228	242	366	372
I250	562	12	162	148	133	107
I251	1,786	32	431	440	447	436
I253	*	.	.	.	*	*
I255	382	6	81	82	111	102
I256	8	*	*	*	*	*
I258	377	6	86	83	105	97
I259	2,346	41	513	590	581	621
I260	70	.	18	18	21	13
I269	529	16	121	122	144	126
I270	69	.	18	14	18	19
I271	*	.	*	.	.	*
I272	16	.	*	*	4	9
I278	11	.	*	5	*	*
I279	94	*	18	29	22	22
I289	4	.	.	*	*	*
I300	7	.	.	*	*	*
I301	*	.	.	*	*	.
I309	*	.	.	*	.	.
I311	11	.	7	*	.	*
I312	4	.	*	*	*	.
I313	*	.	.	*	*	.
I318	*	.	*	.	.	.
I319	5	.	*	.	*	*
I330	91	*	28	20	20	22
I339	111	*	27	27	27	28
I340	148	6	29	36	40	37
I341	12	*	*	*	5	*
I342	11	.	*	*	5	*
I348	*	.	*	.	*	.
I349	18	*	4	5	4	4
I350	1,132	19	229	271	322	291
I351	112	*	30	28	27	25
I352	112	4	22	24	28	34
I358	*	.	.	*	.	*
I359	106	*	31	22	24	26

I361	8	.	4	*	*	*
I368	*	.	.	.	.	*
I369	*	.	*	.	.	.
I371	*	.	.	.	.	*
I38	11	.	*	*	*	*
I389	131	*	31	31	33	34
I400	7	.	*	.	4	*
I409	40	*	13	8	10	8
I420	195	4	32	56	54	49
I421	20	.	5	8	4	*
I422	20	.	5	7	6	*
I424	5	.	.	4	.	*
I425	5	.	.	*	.	*
I426	22	.	6	5	4	7
I427	*	.	.	.	*	*
I428	14	.	5	*	5	*
I429	179	*	36	41	53	47
I440	27	.	5	*	5	14
I441	21	.	4	5	6	6
I442	175	*	42	39	36	55
I443	26	*	8	5	7	5
I447	*	.	.	*	.	*
I452	*	.	*	.	.	*
I453	5	.	*	*	.	*
I455	21	.	7	*	6	5
I458	*	.	.	*	.	*
I459	10	.	4	*	*	*
I460	402	9	91	89	94	119
I461	221	*	26	62	63	69
I470	*	.	*	*	.	.
I471	9	.	*	*	5	*
I472	25	*	10	*	6	5
I479	12	.	*	4	*	*
I48	*	*	.	.	.	.
I489	2,578	50	584	562	656	726
I490	94	*	28	19	22	23
I494	*	.	*	.	.	.
I495	73	5	17	10	20	21
I498	16	.	*	6	5	*
I499	120	*	29	28	30	31
I500	136	6	34	39	25	32
I501	531	10	119	129	135	138
I509	2,388	53	512	551	626	646
I510	*	.	.	*	.	.
I511	*	.	.	.	*	.
I513	*	.	*	.	.	.
I514	19	*	*	9	*	4
I515	6	*	*	*	.	*
I516	63	*	12	18	24	7
I517	20	*	5	5	*	7
I518	120	*	20	34	32	31
I519	379	12	71	74	134	88
I600	23	*	5	8	*	7
I601	51	5	6	16	14	10
I602	48	.	13	18	7	10
I603	12	.	4	*	*	*
I604	28	.	9	11	*	6
I605	8	.	.	*	*	*
I606	112	.	21	26	26	39
I607	52	*	9	13	14	15
I608	58	.	18	12	19	9
I609	239	7	55	65	52	60

I610	86	*	23	23	25	14
I611	37	*	11	*	11	10
I612	362	4	88	78	104	88
I613	85	.	18	20	26	21
I614	60	*	14	13	10	22
I615	56	*	10	15	9	20
I616	67	*	11	13	18	23
I618	167	*	26	40	48	52
I619	1,372	26	294	319	386	347
I620	199	4	42	52	46	55
I621	*	.	*	*	*	.
I629	28	*	5	*	4	16
I630	21	.	4	6	8	*
I631	19	*	*	9	4	*
I632	25	.	*	8	7	7
I633	110	*	19	31	33	24
I634	67	*	13	12	19	22
I635	31	*	6	12	6	6
I636	4	.	*	*	.	*
I638	69	.	15	20	17	17
I639	1,311	23	304	333	356	295
I64	261	6	48	.	105	102
I649	6,469	113	1,438	1,596	1,701	1,621
I671	16	.	*	4	7	*
I672	86	*	29	20	19	15
I673	5	.	*	*	*	.
I674	*	.	.	.	.	*
I675	*	.	.	.	*	*
I676	4	.	.	*	*	*
I677	*	.	.	*	.	*
I678	10	.	*	4	*	*
I679	67	*	6	26	23	11
I693	*	.	.	.	.	*
I694	5	.	.	.	.	5
I700	16	.	*	5	6	4
I701	4	.	*	*	*	.
I702	395	7	84	98	102	104
I708	16	.	4	4	4	4
I709	560	13	130	142	129	146
I710	385	9	91	102	80	103
I711	56	*	16	15	12	12
I712	21	.	11	*	6	*
I713	632	7	164	152	166	143
I714	122	*	24	37	29	30
I715	331	10	76	73	79	93
I716	58	*	14	8	17	16
I718	56	*	20	14	13	7
I719	72	*	19	16	18	18
I720	5	.	*	*	*	.
I722	*	.	.	*	.	.
I723	11	.	*	*	*	4
I724	*	.	*	.	.	*
I728	20	.	*	4	9	4
I729	10	.	*	*	*	5
I738	*	.	*	*	*	.
I739	48	*	9	11	10	16
I740	14	.	*	5	6	*
I741	8	.	.	*	*	4
I743	37	.	11	8	8	10
I744	4	.	*	*	*	*
I745	8	.	4	*	*	*
I748	58	*	14	13	17	12

I749	69	.	21	14	26	8
I772	9	.	*	.	4	*
I775	4	.	*	*	.	.
I778	16	.	*	*	5	5
I779	4	.	*	*	*	*
I780	*	.	*	*	.	.
I800	*	.	*	*	.	.
I801	*	.	*	.	*	.
I802	9	.	*	5	*	.
I803	18	.	5	4	*	6
I808	*	.	.	.	*	.
I809	*	.	.	*	.	*
I819	18	.	7	4	5	*
I820	*	*	*	.	*	.
I822	*	.	*	.	*	*
I828	22	*	4	7	5	5
I829	30	.	9	5	10	6
I830	5	.	.	*	*	*
I839	*	.	.	*	*	.
I850	18	.	5	*	*	7
I864	4	.	*	*	.	*
I868	*	.	.	.	.	*
I871	*	.	.	*	.	.
I872	6	.	.	*	*	*
I890	*	.	.	*	.	.
I898	*	.	.	.	*	.
I950	19	*	*	*	10	4
I951	*	.	.	.	.	*
I952	*	.	*	.	*	.
I958	*	.	.	*	*	.
I959	10	.	*	*	4	*
I999	24	.	*	4	8	10

New episodes (1,2,3) after December 2012

16:43 Wednesday, May 9, 2018 5

Episode no: *

	Index date					
	All	2012	2013	2014	2015	2016
	N	N	N	N	N	N
All	156,182	4,286	45,714	37,193	35,139	33,850
deCVDD						
.	153,541	4,172	44,513	36,459	34,741	33,656
2012	5	4	*	.	.	.
2013	270	40	230	.	.	.
2014	533	21	324	188	.	.
2015	822	29	324	294	175	.
2016	1,011	20	322	252	223	194
deHF						
.	152,053	4,116	43,934	36,027	34,445	33,531
2012	5	5	.	.	.	.
2013	540	62	478	.	.	.
2014	971	45	545	381	.	.
2015	1,206	30	419	440	317	.
2016	1,407	28	338	345	377	319
deMACE						
.	150,979	4,051	43,358	35,779	34,289	33,502
2012	*	*	.	.	.	.

2013	545	82	463	.	.	.
2014	1,191	52	743	396	.	.
2015	1,577	51	588	575	363	.
2016	1,888	48	562	443	487	348
deMI						
.	153,766	4,173	44,590	36,528	34,772	33,703
2013	258	37	221	.	.	.
2014	551	28	341	182	.	.
2015	742	28	287	267	160	.
2016	865	20	275	216	207	147
deStr						
.	153,302	4,160	44,429	36,418	34,647	33,648
2012	*	*	.	.	.	.
2013	303	47	256	.	.	.
2014	658	25	414	219	.	.
2015	868	23	315	324	206	.
2016	1,049	29	300	232	286	202
deAF						
.	151,090	4,059	43,561	35,781	34,243	33,446
2012	5	5	.	.	.	.
2013	597	77	520	.	.	.
2014	1,147	62	648	437	.	.
2015	1,528	41	513	533	441	.
2016	1,815	42	472	442	455	404
deHH						
.	154,230	4,208	44,759	36,657	34,854	33,752
2012	*	*	.	.	.	.
2013	277	35	242	.	.	.
2014	462	17	282	163	.	.
2015	582	9	234	204	135	.
2016	629	15	197	169	150	98

Episode no: *

Index date						
	All	2012	2013	2014	2015	2016
	N	N	N	N	N	N
All	57,025	188	7,884	13,309	16,699	18,945
deCVDD						
.	56,178	177	7,666	13,005	16,478	18,852
2012	*	*	.	.	.	.
2013	57	*	54	.	.	.
2014	139	*	59	77	.	.
2015	245	*	46	112	86	.
2016	404	*	59	115	135	93
deHF						
.	55,600	181	7,514	12,839	16,308	18,758
2012	*	*	.	.	.	.
2013	99	*	97	.	.	.
2014	274	.	119	155	.	.
2015	454	*	87	167	198	.
2016	596	*	67	148	193	187
deMACE						
.	55,393	178	7,446	12,731	16,273	18,765
2013	101	*	98	.	.	.

2014	298	*	128	167	.	.
2015	503	*	103	223	175	.
2016	730	*	109	188	251	180
deMI						
.	56,289	182	7,680	13,044	16,518	18,865
2013	49	*	48	.	.	.
2014	125	*	59	64	.	.
2015	227	*	45	107	73	.
2016	335	*	52	94	108	80
deStr						
.	56,111	184	7,645	12,989	16,449	18,844
2013	54	*	52	.	.	.
2014	176	*	70	105	.	.
2015	284	.	60	121	103	.
2016	400	*	57	94	147	101
deAF						
.	55,564	184	7,542	12,826	16,262	18,750
2013	75	.	75	.	.	.
2014	250	*	109	140	.	.
2015	460	*	81	181	197	.
2016	676	*	77	162	240	195
deHH						
.	56,173	180	7,639	13,009	16,489	18,856
2013	64	5	59	.	.	.
2014	168	*	73	92	.	.
2015	269	.	55	117	97	.
2016	351	.	58	91	113	89

Episode no: *

Index date						
	All	2012	2013	2014	2015	2016
	N	N	N	N	N	N
All	20,996	15	1,268	3,682	6,682	9,349
deCVDD						
.	20,735	14	1,231	3,611	6,586	9,293
2013	13	*	12	.	.	.
2014	30	.	11	19	.	.
2015	52	.	5	21	26	.
2016	166	.	9	31	70	56
deHF						
.	20,533	15	1,218	3,556	6,495	9,249
2013	12	.	12	.	.	.
2014	63	.	21	42	.	.
2015	144	.	12	44	88	.
2016	244	.	5	40	99	100
deMACE						
.	20,533	15	1,204	3,535	6,529	9,250
2013	12	.	12	.	.	.
2014	61	.	18	43	.	.
2015	130	.	13	61	56	.
2016	260	.	21	43	97	99
deMI						
.	20,785	15	1,237	3,614	6,606	9,313
2013	5	.	5	.	.	.

2014	30	.	9	21	.	.
2015	57	.	6	28	23	.
2016	119	.	11	19	53	36
deStr						
.	20,742	15	1,235	3,603	6,603	9,286
2013	7	.	7	.	.	.
2014	31	.	9	22	.	.
2015	74	.	7	33	34	.
2016	142	.	10	24	45	63
deAF						
.	20,535	15	1,212	3,551	6,518	9,239
2013	8	.	8	.	.	.
2014	53	.	19	34	.	.
2015	146	.	16	52	78	.
2016	254	.	13	45	86	110
deHH						
.	20,694	13	1,225	3,587	6,582	9,287
2013	18	*	17	.	.	.
2014	39	*	11	27	.	.
2015	80	.	4	33	43	.
2016	165	.	11	35	57	62

All new episodes after December 2012

16:43 Wednesday, May 9, 2018 6

Index date						
	All	2012	2013	2014	2015	2016
	N	N	N	N	N	N
All	244,715	4,489	55,061	55,316	61,624	68,225
deCVDD						
.	240,879	4,363	53,596	54,188	60,880	67,852
2012	7	6	*	.	.	.
2013	342	44	298	.	.	.
2014	709	24	396	289	.	.
2015	1,142	30	378	434	300	.
2016	1,636	22	392	405	444	373
deHF						
.	238,512	4,312	52,852	53,527	60,263	67,558
2012	7	7	.	.	.	.
2013	653	64	589	.	.	.
2014	1,319	45	688	586	.	.
2015	1,852	32	521	663	636	.
2016	2,372	29	411	540	725	667
deMACE						
.	237,249	4,244	52,192	53,146	60,130	67,537
2012	*	*	.	.	.	.
2013	660	85	575	.	.	.
2014	1,562	55	892	615	.	.
2015	2,238	53	705	867	613	.
2016	3,004	50	697	688	881	688
deMI						
.	241,266	4,370	53,696	54,300	60,967	67,933
2013	313	38	275	.	.	.
2014	715	30	412	273	.	.
2015	1,037	30	338	405	264	.
2016	1,384	21	340	338	393	292
deStr						
.	240,585	4,359	53,499	54,129	60,771	67,827

2012	*	*	.	.	.	.
2013	365	49	316	.	.	.
2014	868	26	493	349	.	.
2015	1,243	23	383	483	354	.
2016	1,652	30	370	355	499	398
deAF						
.	237,526	4,258	52,503	53,258	60,056	67,451
2012	5	5	.	.	.	.
2013	680	77	603	.	.	.
2014	1,454	63	778	613	.	.
2015	2,178	42	614	779	743	.
2016	2,872	44	563	666	825	774
deHH						
.	241,488	4,401	53,815	54,362	60,978	67,932
2012	*	*	.	.	.	.
2013	360	41	319	.	.	.
2014	672	21	367	284	.	.
2015	954	9	293	361	291	.
2016	1,239	15	267	309	355	293

All new episodes after December 2012

16:43 Wednesday, May 9, 2018 7

		Index date					
		All	2012	2013	2014	2015	2016
		N	N	N	N	N	N
Acarbose							
All		179	9	60	52	42	16
A10BF01	acarbose	179	9	60	52	42	16
DPP4							
All		39,306	673	8,739	9,245	10,148	10,501
A10BD07	metformin og sitagliptin	7,521	106	1,518	1,749	1,988	2,160
A10BD08	metformin og vildagliptin	6,861	157	1,892	1,633	1,547	1,632
A10BD09	pioglitazon og alogliptin	5	.	.	*	*	.
A10BD10	metformin og saxagliptin	16	.	*	6	4	*
A10BD11	metformin og linagliptin	104	*	20	21	28	34
A10BD13	metformin og alogliptin	343	.	.	82	158	103
A10BH01	sitagliptin	14,764	265	3,237	3,436	3,797	4,029
A10BH02	vildagliptin	2,931	58	769	820	694	590
A10BH03	saxagliptin	908	35	300	210	207	156
A10BH04	alogliptin	727	.	*	172	312	240
A10BH05	linagliptin	5,126	51	997	1,113	1,411	1,554
GLP1							
All		17,370	383	3,918	3,549	4,427	5,093
A10BJ01	exenatid	502	14	122	111	156	99
A10BJ02	liraglutid	16,499	369	3,781	3,388	4,239	4,722
A10BJ03	lixisenatid	79	.	15	50	9	5
A10BJ05	dulaglutid	290	.	.	.	23	267
Metformin							
All		90,029	1,936	21,451	20,453	22,391	23,798
A10BA02	metformin	89,248	1,923	21,267	20,280	22,176	23,602
A10BD03	metformin og rosiglitazon	61	*	17	14	18	11
A10BD07	metformin og sitagliptin	379	5	89	70	114	101
A10BD08	metformin og vildagliptin	294	7	77	81	68	61
A10BD10	metformin og saxagliptin	6	.	*	*	*	*
A10BD11	metformin og linagliptin	4	.	.	*	*	*
A10BD13	metformin og alogliptin	10	.	.	*	6	*
A10BD15	metformin og dapagliflozin	12	.	.	*	*	7

A10BD16	metformin og canagliflozin	*	.	.	.	*	.
A10BD20	metformin og empagliflozin	14	.	.	.	*	11
SGLT2							
All		17,678	20	1,929	3,038	4,761	7,930
A10BD15	metformin og dapagliflozin	407	.	.	84	102	221
A10BD16	metformin og canagliflozin	13	.	.	.	7	6
A10BD20	metformin og empagliflozin	487	.	.	.	54	433
A10BK01	dapagliflozin	10,684	20	1,929	2,659	3,069	3,007
A10BK02	canagliflozin	465	.	.	99	232	134
A10BK03	empagliflozin	5,622	.	.	196	1,297	4,129
SU							
All		19,099	412	5,160	4,729	4,657	4,141
A10BB01	glibenclamid	1,088	23	337	277	262	189
A10BB03	tolbutamid	327	7	103	79	80	58
A10BB07	glipizid	821	19	238	209	187	168
A10BB09	gliclazid	1,916	42	501	522	442	409
A10BB12	glimepirid	14,571	315	3,875	3,550	3,589	3,242
A10BX02	repaglinid	375	6	106	91	97	75
A10BX03	nateglinid	*	.	.	*	.	.
TZD							
All		156	4	48	43	34	27
A10BD03	metformin og rosiglitazon	10	.	5	*	*	*
A10BD09	pioglitazon og alogliptin	10	.	.	*	*	6
A10BG02	rosiglitazon	15	*	4	4	4	*
A10BG03	pioglitazon	121	*	39	35	26	18
fastIns							
All		20,145	342	4,387	4,745	5,143	5,528
A10AB01	insulin (human)	7,146	126	1,630	1,736	1,837	1,817
A10AB04	insulin lispro	67	*	11	17	16	22
A10AB05	insulin aspart	12,599	211	2,669	2,916	3,196	3,607
A10AB06	insulin glulisin	333	4	77	76	94	82
intIns							
All		11,859	262	3,510	3,109	2,819	2,159
A10AC01	insulin (human)	11,859	262	3,510	3,109	2,819	2,159
longIns							
All		23,244	299	4,054	4,800	5,934	8,157
A10AE04	insulin glargin	15,610	168	2,554	3,321	4,549	5,018
A10AE05	insulin detemir	5,575	131	1,484	1,463	1,370	1,127
A10AE06	insulin degludec	2,059	.	16	16	15	2,012
mixIns							
All		5,650	149	1,805	1,553	1,268	875
A10AD01	insulin (human)	643	15	225	170	127	106
A10AD04	insulin lispro	22	.	6	5	8	*
A10AD05	insulin aspart	4,980	134	1,574	1,378	1,131	763
A10AD06	insulin degludec og insulin aspart	5	.	.	.	*	*

All new episodes after December 2012

16:43 Wednesday, May 9, 2018 8

Drug episode no since 2012-12-01							
All	*	*	*	4	5		
N	N	N	N	N	N		
Acarbose							
All	179	135	33	7	*	*	
A10BF01	acarbose	179	135	33	7	*	*
DPP4							
All	39,306	24,604	11,378	2,463	616	179	

A10BD07	metformin og sitagliptin	7,521	4,760	2,244	389	96	24
A10BD08	metformin og vildagliptin	6,861	4,619	1,774	346	76	36
A10BD09	pioglitazon og alogliptin	5	*	*	.	.	*
A10BD10	metformin og saxagliptin	16	11	4	*	.	.
A10BD11	metformin og linagliptin	104	61	38	5	.	.
A10BD13	metformin og alogliptin	343	177	135	24	6	.
A10BH01	sitagliptin	14,764	8,872	4,461	1,062	262	74
A10BH02	vildagliptin	2,931	1,848	863	161	46	10
A10BH03	saxagliptin	908	578	241	71	12	4
A10BH04	alogliptin	727	341	257	90	29	7
A10BH05	linagliptin	5,126	3,335	1,359	314	89	23
GLP1							
All		17,370	8,786	4,993	2,380	858	254
A10BJ01	exenatid	502	236	134	74	34	16
A10BJ02	liraglutid	16,499	8,461	4,730	2,210	786	223
A10BJ03	lixisenatid	79	39	23	12	4	*
A10BJ05	dulaglutid	290	50	106	84	34	14
Metformin							
All		90,029	79,030	7,764	2,123	748	253
A10BA02	metformin	89,248	78,908	7,182	2,081	724	245
A10BD03	metformin og rosiglitazon	61	32	18	7	*	*
A10BD07	metformin og sitagliptin	379	33	310	16	15	4
A10BD08	metformin og vildagliptin	294	33	235	17	6	*
A10BD10	metformin og saxagliptin	6	.	5	.	*	.
A10BD11	metformin og linagliptin	4	.	4	.	.	.
A10BD13	metformin og alogliptin	10	.	8	*	.	.
A10BD15	metformin og dapagliflozin	12	10	*	.	.	*
A10BD16	metformin og canagliflozin	*	*	.	.	.	.
A10BD20	metformin og empagliflozin	14	13	*	.	.	.
SGLT2							
All		17,678	6,909	6,165	3,018	1,091	336
A10BD15	metformin og dapagliflozin	407	160	165	62	12	4
A10BD16	metformin og canagliflozin	13	4	8	.	*	.
A10BD20	metformin og empagliflozin	487	151	192	92	36	14
A10BK01	dapagliflozin	10,684	4,762	3,565	1,593	515	164
A10BK02	canagliflozin	465	175	185	70	19	12
A10BK03	empagliflozin	5,622	1,657	2,050	1,201	508	142
SU							
All		19,099	10,298	6,622	1,621	385	117
A10BB01	glibenclamid	1,088	631	357	70	17	7
A10BB03	tolbutamid	327	207	81	29	9	*
A10BB07	glipizid	821	489	260	53	14	*
A10BB09	gliclazid	1,916	993	675	176	47	15
A10BB12	glimepirid	14,571	7,779	5,124	1,255	287	89
A10BX02	repaglinid	375	198	125	38	11	*
A10BX03	nateglinid	*	*	.	.	.	.
TZD							
All		156	67	52	22	9	*
A10BD03	metformin og rosiglitazon	10	4	6	.	.	.
A10BD09	pioglitazon og alogliptin	10	.	*	5	*	*
A10BG02	rosiglitazon	15	5	7	*	.	.
A10BG03	pioglitazon	121	58	38	14	7	*
fastIns							
All		20,145	9,628	5,902	2,851	1,191	403
A10AB01	insulin (human)	7,146	3,675	2,051	929	332	115
A10AB04	insulin lispro	67	37	12	13	*	*
A10AB05	insulin aspart	12,599	5,790	3,736	1,856	822	277
A10AB06	insulin glulisin	333	126	103	53	36	8
intIns							
All		11,859	5,351	4,264	1,564	505	125
A10AC01	insulin (human)	11,859	5,351	4,264	1,564	505	125
longIns							

All		23,244	8,700	8,114	4,119	1,593	513
A10AE04	insulin glargin	15,610	5,583	5,524	2,884	1,119	359
A10AE05	insulin detemir	5,575	2,512	1,941	759	248	76
A10AE06	insulin degludec	2,059	605	649	476	226	78
mixIns							
All		5,650	2,674	1,738	828	285	83
A10AD01	insulin (human)	643	334	175	78	39	9
A10AD04	insulin lispro	22	12	5	*	*	.
A10AD05	insulin aspart	4,980	2,328	1,557	745	242	74
A10AD06	insulin degludec og insulin aspart	5	.	*	*	*	.

(Continued)

All new episodes after December 2012

16:43 Wednesday, May 9, 2018 9

		Drug episode no since 2012-12-01					
		6	7	8	9	10	11
		N	N	N	N	N	N
Acarbose							
All		.	.	.	.	.	.
A10BF01	acarbose	.	.	.	.	.	.
DPP4							
All		44	17	*	*	.	.
A10BD07	metformin og sitagliptin	5	*	.	.	.	.
A10BD08	metformin og vildagliptin	6	*	.	*	.	.
A10BD09	pioglitazon og alogliptin	.	.	.	.	.	.
A10BD10	metformin og saxagliptin	.	.	.	.	.	.
A10BD11	metformin og linagliptin	.	.	.	.	.	.
A10BD13	metformin og alogliptin	*	.	.	.	.	.
A10BH01	sitagliptin	22	8	*	*	.	.
A10BH02	vildagliptin	*	*	.	.	.	.
A10BH03	saxagliptin	*	.	.	.	.	.
A10BH04	alogliptin	*	.	*	.	.	.
A10BH05	linagliptin	4	*	.	.	.	.
GLP1							
All		77	18	*	*	.	.
A10BJ01	exenatid	8	.	.	.	.	.
A10BJ02	liraglutid	67	18	*	*	.	.
A10BJ03	lixisenatid	.	.	.	.	.	.
A10BJ05	dulaglutid	*	.	.	.	.	.
Metformin							
All		74	25	10	*	.	.
A10BA02	metformin	71	25	10	*	.	.
A10BD03	metformin og rosiglitazon	*	.	.	.	.	.
A10BD07	metformin og sitagliptin	*	.	.	.	.	.
A10BD08	metformin og vildagliptin	*	.	.	.	.	.
A10BD10	metformin og saxagliptin	.	.	.	.	.	.
A10BD11	metformin og linagliptin	.	.	.	.	.	.
A10BD13	metformin og alogliptin	.	.	.	.	.	.
A10BD15	metformin og dapagliflozin	.	.	.	.	.	.
A10BD16	metformin og canagliflozin	.	.	.	.	.	.
A10BD20	metformin og empagliflozin	.	.	.	.	.	.
SGLT2							
All		109	36	10	*	*	.
A10BD15	metformin og dapagliflozin	*	*	.	.	.	.
A10BD16	metformin og canagliflozin	.	.	.	.	.	.

A10BD20	metformin og empagliflozin	*	*	.	.	.	.
A10BK01	dapagliflozin	57	20	6	*	.	.
A10BK02	canagliflozin	*	.	*	.	*	.
A10BK03	empagliflozin	46	14	*	*	.	.
SU							
All		40	10	4	*	.	.
A10BB01	glibenclamid	*	*	*	.	.	.
A10BB03	tolbutamid	.	.	.	.	.	.
A10BB07	glipizid	*	.	*	.	.	.
A10BB09	gliclazid	8	*	.	*	.	.
A10BB12	glimepirid	28	7	*	*	.	.
A10BX02	repaglinid	.	.	*	.	.	.
A10BX03	nateglinid	.	.	.	.	.	.
TZD							
All		*	.	.	.	.	.
A10BD03	metformin og rosiglitazon	.	.	.	.	.	.
A10BD09	pioglitazon og alogliptin	*	.	.	.	.	.
A10BG02	rosiglitazon	.	.	.	.	.	.
A10BG03	pioglitazon	*	.	.	.	.	.
fastIns							
All		114	38	15	*	.	*
A10AB01	insulin (human)	30	10	4	.	.	.
A10AB04	insulin lispro	*	.	.	.	.	.
A10AB05	insulin aspart	80	24	11	*	.	*
A10AB06	insulin glulisin	*	4	.	.	.	.
intIns							
All		35	13	*	.	.	.
A10AC01	insulin (human)	35	13	*	.	.	.
longIns							
All		147	39	16	*	*	.
A10AE04	insulin glargin	99	29	11	*	*	.
A10AE05	insulin detemir	29	5	4	*	.	.
A10AE06	insulin degludec	19	5	*	.	.	.
mixIns							
All		28	11	*	.	*	.
A10AD01	insulin (human)	5	*	*	.	.	.
A10AD04	insulin lispro	.	.	.	.	.	.
A10AD05	insulin aspart	23	9	*	.	*	.
A10AD06	insulin degludec og insulin aspart	.	.	.	.	.	.

All new episodes after December 2012

16:43 Wednesday, May 9, 2018 10

The CONTENTS Procedure

Data Set Name	DAFDAT.EPISODES	Observations	244715
Member Type	DATA	Variables	98
Engine	V9	Indexes	0
Created	09/05/2018 16:49:07	Observation Length	648
Last Modified	09/05/2018 16:49:07	Deleted Observations	0
Protection		Compressed	NO
Data Set Type		Sorted	YES
Label			
Data Representation	WINDOWS_64		
Encoding	wlatin1 Western (Windows)		

Engine/Host Dependent Information

Data Set Page Size	65536
Number of Data Set Pages	2424

```

First Data Page          *
Max Obs per Page        101
Obs in First Data Page   83
Number of Data Set Repairs 0
ExtendObsCounter         YES
Filename                 E:\workdata\705093\BxC\daffodil\DATA\episodes.sas7bdat
Release Created          9.0401M3
Host Created             X64_SRV12

```

Variables in Creation Order

#	Variable	Type	Len	Format	Informat	Label
*	druggr	Char	7			
*	pnr	Char	12	\$12.	\$10.	Personnummer
*	eksd	Num	4	YYMMDDN8.		Ekspeditionsdato
4	ATC	Char	8	\$8.	\$16.	ATC-kode detaljeret (s)
5	doDM	Num	8	DDMMYY10.		
6	epiN	Num	8			Drug episode no since 2012-12-01
7	doIx	Num	8	DDMMYY10.		Index date
8	Ixdr	Char	10			Index drug
9	Ixatc	Char	8			Index drug (atc)
10	lastpr	Num	4	YYMMDDN8.		Ekspeditionsdato
11	doTm	Num	8	DDMMYY10.		Index drug termination date
12	doFL	Num	8	DDMMYY10.		Date of first line treatment
13	FLdr	Char	7			First line drug
14	FLatc	Char	8			First line drug (atc)
15	deCVDD	Num	8	DDMMYY10.		
16	coD	Char	4			
17	doTIA	Num	8	DATE9.		
18	doAngina	Num	8	DATE9.		
19	doBleed	Num	8	DATE9.		
20	doCOPD	Num	8	DATE9.		
21	doPAD	Num	8	DATE9.		
22	doHF	Num	8	DATE9.		
23	doCancer	Num	8	DATE9.		
24	doDMcompl	Num	8	DATE9.		
25	doNeuro	Num	8	DATE9.		
26	doDKD	Num	8	DATE9.		
27	doDiaEye	Num	8	DATE9.		
28	doHypo	Num	8	DATE9.		
29	doAtrFib	Num	8	DATE9.		
30	doMI	Num	8	DATE9.		
31	doUnstAng	Num	8	DATE9.		
32	doHmStr	Num	8	DATE9.		
33	doDiaFoot	Num	8	DATE9.		
34	doOther	Num	8	DATE9.		
35	doPeriAng	Num	8	DATE9.		
36	doIscStr	Num	8	DATE9.		
37	doAmp	Num	8	DATE9.		
38	doCKD	Num	8	DATE9.		
39	doPCIsten	Num	8	DATE9.		
40	doCABG	Num	8	DATE9.		
41	doKeto	Num	8	DATE9.		
42	doDial	Num	8	DATE9.		
43	doBari	Num	8	DATE9.		
44	sex	Num	8			
45	doBth	Num	8	DDMMYY10.		
46	whBth	Char	*			
47	doDth	Num	8	DDMMYY10.		
48	dSrc	Char	5			

49	dolACE	Num	4	DDMMYY10.	
50	dolSta	Num	4	DDMMYY10.	
51	dolBB1	Num	4	DDMMYY10.	
52	dolARB	Num	4	DDMMYY10.	
53	dolAlA	Num	4	DDMMYY10.	
54	dolDHP	Num	4	DDMMYY10.	
55	dolWtL	Num	4	DDMMYY10.	
56	dolRPA	Num	4	DDMMYY10.	
57	dolWrf	Num	4	DDMMYY10.	
58	dolAsp	Num	4	DDMMYY10.	
59	dolHCD	Num	4	DDMMYY10.	
60	dolTHZ	Num	4	DDMMYY10.	
61	dolCcs	Num	4	DDMMYY10.	
62	dolDXI	Num	4	DDMMYY10.	
63	dolDgo	Num	4	DDMMYY10.	
64	dolAP1	Num	4	DDMMYY10.	
65	dolAmi	Num	4	DDMMYY10.	
66	dolDTI	Num	4	DDMMYY10.	
67	dolNHP	Num	4	DDMMYY10.	
68	dolFla	Num	4	DDMMYY10.	
69	dolMetformin	Num	4	DDMMYY10.	
70	dolGLP1	Num	4	DDMMYY10.	
71	dolMetxSGLT2	Num	4	DDMMYY10.	
72	dolMetxDPP4	Num	4	DDMMYY10.	
73	dolSGLT2	Num	4	DDMMYY10.	
74	dolLongIns	Num	4	DDMMYY10.	
75	dolmixIns	Num	4	DDMMYY10.	
76	dolDPP4	Num	4	DDMMYY10.	
77	dolSU	Num	4	DDMMYY10.	
78	dolIntIns	Num	4	DDMMYY10.	
79	dolFastIns	Num	4	DDMMYY10.	
80	dolTZD	Num	4	DDMMYY10.	
81	dolAcarbose	Num	4	DDMMYY10.	
82	dolTZDxDPP4	Num	4	DDMMYY10.	
83	maxH	Num	8		Longest hospital stay in last year before doIx
84	frail	Num	8		More than * consecutive hospital days last yr
85	recnum	Char	20	\$20.	LPR-identnummer
86	C_ADIAG	Char	6	\$6.	\$6. C_ADIAG
87	compl	Char	7		
88	C_OPR	Char	10	\$10.	\$10. C_OPR
89	D_INDDTO	Num	8	DATE9.	DATE9. D_INDDTO
90	V_SENGDAGE	Num	8	6.	6. V_SENGDAGE
91	deHF	Num	8	DDMMYY10.	
92	deMACE	Num	8	DDMMYY10.	
93	deMI	Num	8	DDMMYY10.	
94	deStr	Num	8	DDMMYY10.	
95	deIscStr	Num	8	DDMMYY10.	
96	deAF	Num	8	DDMMYY10.	
97	deHH	Num	8	DDMMYY10.	
98	deDKD	Num	8	DDMMYY10.	

Sort Information

Sortedby	pnr epiN
Validated	YES
Character Set	ANSI