

Cancer occurrence in Danish diabetes patients: Duration and insulin effects

Data processing and statistical analysis programs.

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Contents

1	Data processing	1
1.1	Merging registers: <code>DMCA</code>	1
1.2	Acquiring mortality information: <code>DMmort</code>	26
2	Statistical analysis with R	39
2.1	Read all datasets and convert to <code>.Rdata</code>	39
2.2	Create basic table and histogram for the paper	46
2.3	Analysis disregarding duration	54
2.4	Analysis incorporating duration	67
2.5	Analysis of mortality and cumulative mortality	77

Chapter 1

Data processing

This chapter gives a detailed overview of the data acquisition and statistical analyses. The first part is a description and printout of an SAS-program used for tabulation. The second is a description and printout of the R-programs that do all analyses of data and produce all graphs (and a couple more).

Data is collected from 1) The national Diabetes Register 2) The Danish Cancer Register (individual records with dates of birth, diagnosis and death) and 3) Statistics Denmark (tabulated data of risk time and deaths).

1.1 Merging registers: DMCA

```
1 "Program: DMCA.sas" 13:55 Thursday, March 31, 2011
```

```
NOTE: Copyright (c) 2002-2008 by SAS Institute Inc., Cary, NC, USA.
NOTE: SAS (r) Proprietary Software 9.2 (TS2M0)
      Licensed to NNIT -BASIC PACKAGE AND ADDITIONAL PACKAGE, Site 50800704.
NOTE: This session is executing on the XP_PRO platform.
NOTE: SAS initialization used:
      real time      1.34 seconds
      cpu time       0.53 seconds
```

```
NOTE: AUTOEXEC processing beginning; file is c:\stat\sas\autoexec.sas.
```

```
-----
C:\Bendix\Steno\DM-register\NDR\projects\Cancer\sas\DMCA.sas
-----
```

```
NOTE: Libref HER was successfully assigned as follows:
      Engine: V9
      Physical Name: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\sas
NOTE: Libref DATA was successfully assigned as follows:
      Engine: V9
      Physical Name: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\data
```

```
NOTE: AUTOEXEC processing completed.
```

```
1 *****
2 NOTE: This version of the program also splits follow-up by
3     DM-duration and Ins-duration
4     Datasets are produced for the entire available follow-up
5     too, NOT classified by the duration variables the names of
6     these are preceded with "x" (for eXtended).
7
8     This particular version subdivides the state DM/Ins>=1995 by
9     diabetes type, that is whether age at diagnosis is before 30
10    and date of insulin is within 3 months of diagnosis.
11    ***** ;
12
13    * The date from which we trust the inclusion date to be the first ;
14    %let validdate = '01JAN1995'd ;
15    * Set the entry and exit dates for the entire follow-up endeavour ;
16    %let truncdate = '01JAN1995'd ;
17    %let censdate = '31DEC2009'd ;
18    * Where do we break the duration of DM and Ins - note we start at 1 month (1/12=0.08333);
19    %let durbreaks = %str(0, 0.08333, 0.25 to 2 by 0.25, 2.5 to 5 by 0.5, 6, 7 to 19 by 2) ;
20    * Define the ranges for period-tabulation ;
```

```

21      data _null_ ;
22      call symput( 'Plo'      , year( &truncdate. ) - 1 ) ; * Last year before FU ;
23      call symput( 'Phi'      , year( &censdate. ) + 1 ) ; * First year after FU ;
24      call symput( 'Pfirst'    , year( &truncdate. ) - 1900 ) ; * 1st tab break ;
25      call symput( 'Plast'     , year( &censdate. ) - 1900 + 1 ) ; * last tab break ;
26      run ;

```

NOTE: Numeric values have been converted to character values at the places given by: (Line):(Column).

22:45 23:45 24:45 25:52

NOTE: DATA statement used (Total process time):

real time 0.07 seconds
cpu time 0.00 seconds

```

27      * Just to check it all went well ;
28      %put validdate = &validdate.
29      truncdate = &truncdate.
30      censdate = &censdate. ;
validdate = '01JAN1995'd truncdate = '01JAN1995'd censdate = '31DEC2009'd
31      %put Plo = &Plo.
32      Phi = &Phi.
33      Pfirst = &Pfirst.
34      Plast = &Plast. ;
Plo = 1994 Phi = 2010 Pfirst = 95 Plast = 110
35      %put durbreaks = &durbreaks ;
durbreaks = 0, 0.08333, 0.25 to 2 by 0.25, 2.5 to 5 by 0.5, 6, 7 to 19 by 2
36      * Set the selector of subgroups to analyse ;
37      %let dgrp = 21,22,241,242,243,249,251,26,28,
38      33,
39      51,
40      70,
41      82,83,84,
42      91,92,
43      101,103,
44      113,
45      121,
46      131,132,133,139 ;
47      %let diagselect = diag in (&dgrp.) ;
48      * Variable names for tabulation purposes, note DX and D259 here ;
49      %let dvars = D0 D999
50      D21 D22 D241 D242 D243 D249 D251 D259 D26 D28
51      D33
52      D51
53      D70
54      D82 D83 D84
55      D91 D92
56      D101 D103
57      D113
58      D121
59      D131 D132 D133 D139 ;
60
61      * Get the formats and the Lexis macro ;
62      options nosource2 ;
63      %inc "CRG-fmts.sas" ;
NOTE: Format SEX has been output.
NOTE: Format DIAG has been output.

```

NOTE: PROCEDURE FORMAT used (Total process time):

real time 0.14 seconds
cpu time 0.00 seconds

```

148     %inc "C:\stat\sas\macro\Lexis.sas" ;
1306
1307     -----;
1308     * Preprocessing of the cancer register to first primary tumours ;
1309
1310     * First take the cancer registry, remove all non-cancers ;
1311     data cancer ;
1312     set data.cancer ;
1313     * Remove 'not counted as cancer' and non-melanoma skin cancer ;
1314     if ( diag in (52,150) ) then delete ;
1315     * Recode the leukaemias to one group (139 is a not used value in formats) ;
1316     if diag in (134,135,136,137) then diag = 139 ;
1317     * Recode the colon cancers to the three separate subsites and the rest ;
1318     * 24.1 Ascending colon C18.0, C18.1, C18.2
1319     * 24.2 Transverse colon C18.3, C18.4, C18.5
1320     * 24.3 Descending and sigmoid colon C18.6, C18.7, C19, C19.9
1321     * 24.9 Other colon (unspec. or multiple)
1322     * 25.1 Rectum (excl. anus) C20, C209
1323     * This means that colorectal cancers are to be taken as the sum of these
1324     * 5 groups, but also that the group 24.9 is NOT of interest per se ;
1325     if( diag eq 24 ) then diag = 249 ;
1326     if( icdpyrs in ("C180","C181","C182") ) then diag = 241 ;
1327     if( icdpyrs in ("C183","C184","C185") ) then diag = 242 ;
1328     if( icdpyrs in ("C186","C187","C19","C199") ) then diag = 243 ;
1329     if( icdpyrs in ("C20","C209") ) then diag = 251 ;
1330     * Finally make a single code for the sites not among those analysed ;
1331     if not ( diag in ( &dgrp. ) ) then diag = 999 ;

```

```
332      run ;
```

```
NOTE: There were 1748815 observations read from the data set DATA.CANCER.
NOTE: The data set WORK.CANCER has 1286419 observations and 31 variables.
NOTE: DATA statement used (Total process time):
      real time           12.81 seconds
      cpu time             1.25 seconds
```

```
333
334      * Sort by id and date of diagnosis ;
335      proc sort data = cancer ;
336          by id d_diagnosedato ;
337      run ;
```

```
NOTE: There were 1286419 observations read from the data set WORK.CANCER.
NOTE: The data set WORK.CANCER has 1286419 observations and 31 variables.
NOTE: PROCEDURE SORT used (Total process time):
      real time           19.81 seconds
      cpu time             2.71 seconds
```

```
338
339      * Select only the first real tumor ;
340      data cancer ;
341          set cancer ;
342          by id ;
343          if first.id ;
344      run ;
```

```
NOTE: There were 1286419 observations read from the data set WORK.CANCER.
NOTE: The data set WORK.CANCER has 1195147 observations and 31 variables.
NOTE: DATA statement used (Total process time):
      real time           11.01 seconds
      cpu time             0.98 seconds
```

```
345
346      * Check the total number of first primary cancers ;
347      title "All cancers diagnosed 1995 ff." ;
348      &tab. cancer ;
349      where ( D_diagnosedato ge &truncdate. ) ;
350      class diag D_diagnosedato ;
351      table all diag = "Diag",
352            D_diagnosedato * f = comma6.
353            all * f = comma10.
354            / rts = 6 ;
355      format D_diagnosedato year4. ;
356      keylabel n = " " ;
357      run ;
```

```
NOTE: There were 382049 observations read from the data set WORK.CANCER.
WHERE D_diagnosedato>='01JAN1995'D;
NOTE: The PROCEDURE TABULATE printed pages 1-2.
NOTE: PROCEDURE TABULATE used (Total process time):
      real time           1.01 seconds
      cpu time             0.62 seconds
```

```
358
359      * Then merge with the diabetes register ;
360      data data.candi;
361          merge cancer
362            data.diabetes ;
363          by id ;
364          keep sex diag diaggrp DMtype
365            doBT doDM doI doCA doX doDD ;
366          format sex sex.
367            doBT doDM doI doCA doX doDD ddmmyy10. ;
368      * Demographic dates collected from CRG and NDR ;
369      doBT = min( D_foddto , D_fdsdato ) ;
370      doDD = min( D_statdato, D_dodsdto ) ;
371      doX = min( D_statdato, D_dodsdto, &censdate. ) ;
372      * Event-dates ;
373      doDM = D_inkldto ;
374      doI = D_ins ;
375      doCA = D_diagnosedato ;
376      * If DM-duration can be trusted set DMtype to 2 otherwise 0, missing if no DM ;
377      DMtype = ( doDM ge &validdate. ) * 2 + doDM - doDM ;
378      * Change to a value 1 for those considered to be T1D ;
379      if (      DMtype > 0      and /* Diagnosed after 1.1.1995 */
380          (DoDM-doBT) < 35*365.25 and /* Diagnosed before age 35, */
381          doI > .z      and /* on insulin */
382          (doI-doDM) < 60 )      /* within 2 months of incl. */
383          then DMtype = 1 ;
384      run ;
```

```
NOTE: Missing values were generated as a result of performing an operation on missing values.
Each place is given by: (Number of times) at (Line):(Column).
```

```

449181 at 370:10    1119643 at 377:40
NOTE: There were 1195147 observations read from the data set WORK.CANCER.
NOTE: There were 437593 observations read from the data set DATA.DIABETES.
NOTE: The data set DATA.CANDI has 1557236 observations and 10 variables.
NOTE: DATA statement used (Total process time):
      real time           5.43 seconds
      cpu time            1.71 seconds

385
386      * The dataset data.candi now has a record for each person who has either a
387      * first primary cancer diagnosis or a diabetes diagnosis ;
388
389      *-----;
390      * Compute the person-years to be removed from the Well state ;
391
392      data Well ;
393          set data.candi ;
394          * Anyone dead before period of interest is excluded ;
395          if ( .z < doDD < &truncdate.) then delete ;
396          * The Lexis variables ;
397          entry = min( doDM, doCA ) ;
398          exit  = doX ;
399          fail  = 0 ;
400      run ;

NOTE: There were 1557236 observations read from the data set DATA.CANDI.
NOTE: The data set WORK.WELL has 862016 observations and 13 variables.
NOTE: DATA statement used (Total process time):
      real time           2.98 seconds
      cpu time            0.59 seconds

401
402      * Split by calendar time ;
403      %Lexis( data = Well,
404             out = WellP,
405             breaks = &Pfirst. to &Plast. by 1,
406             origin = '01Jan1900'd,
407             scale = 365.25,
408             left = P,
409             risk = Yx )

NOTE: There were 862016 observations read from the data set WORK.WELL.
NOTE: The data set WORK.DISCRD has 0 observations and 16 variables.
NOTE: The data set WORK.WELLP has 5497068 observations and 16 variables.
NOTE: DATA statement used (Total process time):
      real time           18.82 seconds
      cpu time            4.14 seconds

410      * Split by age ;
411      %Lexis( data = WellP,
412             out = WellAP,
413             breaks = 0 to 100 by 1,
414             origin = doBT,
415             scale = 365.25,
416             left = A,
417             risk = Yx )

NOTE: There were 5497068 observations read from the data set WORK.WELLP.
NOTE: The data set WORK.DISCRD has 0 observations and 17 variables.
NOTE: The data set WORK.WELLAP has 10462327 observations and 17 variables.
NOTE: DATA statement used (Total process time):
      real time           51.01 seconds
      cpu time            45.14 seconds

418
419      * Establish the correct calendar time and birth date variables ;
420      data WellAP ;
421          set WellAP ;
422          P = P + 1900 ;
423          C = min( max( year( doBT ), P-A-1 ), P-A ) ;
424      run ;

NOTE: There were 10462327 observations read from the data set WORK.WELLAP.
NOTE: The data set WORK.WELLAP has 10462327 observations and 18 variables.
NOTE: DATA statement used (Total process time):
      real time           1:19.12
      cpu time            11.14 seconds

425
426      proc summary data = WellAP nway ;
427          class sex A P C ;
428          var Yx ;
429          output out = WellYx ( keep = sex A P C Yx )
430          sum = Yx ;

```

```
431      run ;
```

```
NOTE: There were 10462327 observations read from the data set WORK.WELLAP.
NOTE: The data set WORK.WELLYX has 6000 observations and 5 variables.
NOTE: PROCEDURE SUMMARY used (Total process time):
      real time      8.21 seconds
      cpu time       8.40 seconds
```

```
432
433      * The dataset WellYx now has the Person-years lived in Other Ca
434      and DM together, in the variable Yx, classified by sex, A, P, C ;
435
436      *-----;
437      * Get the population data and subtract the risk time in other states ;
438
439      libname demo 'c:\Bendix\demodb\data' ;
NOTE: Directory for library DEMO contains files of mixed engine types.
NOTE: Libref DEMO was successfully assigned as follows:
      Engine:      V9
      Physical Name: c:\Bendix\demodb\data
440
441      data demo ;
442      set demo.ydk1971ff ( rename = ( agr = A
443      per = P
444      coh = C
445      risk = Ytot ) ) ;
446      keep sex A P C Ytot upper ;
447      if ( &Plo. < P < &Phi. and A < 100 ) ;
448      run ;
```

```
NOTE: There were 15600 observations read from the data set DEMO.YDK1971FF.
NOTE: The data set WORK.DEMO has 6000 observations and 6 variables.
NOTE: DATA statement used (Total process time):
      real time      0.14 seconds
      cpu time       0.04 seconds
```

```
449
450      proc sort data=demo ;
451      by sex A P C ;
452      run ;
```

```
NOTE: There were 6000 observations read from the data set WORK.DEMO.
NOTE: The data set WORK.DEMO has 6000 observations and 6 variables.
NOTE: PROCEDURE SORT used (Total process time):
      real time      0.10 seconds
      cpu time       0.03 seconds
```

```
453
454      * Merge with the risk time dataset and compute the correct Ys ;
455      data WellY ;
456      merge WellYx
457      demo ( in = pop ) ;
458      by sex A P C ;
459      keep sex A P C Y ;
460      if pop ;
461      if Yx le .z then Yx = 0 ;
462      Y = Ytot - Yx ;
463      run ;
```

```
NOTE: There were 6000 observations read from the data set WORK.WELLYX.
NOTE: There were 6000 observations read from the data set WORK.DEMO.
NOTE: The data set WORK.WELLY has 6000 observations and 5 variables.
NOTE: DATA statement used (Total process time):
      real time      0.01 seconds
      cpu time       0.01 seconds
```

```
464
465      * The dataset WellY now has the risk time in the "Well" state classified
466      by sex, A, P and C. This dataset will since be amended by events of
467      the cancers in question ;
468
469      *-----;
470      * Extract the events in the transition Well -> Ca ;
471
472      data WellCa ;
473      set data.candi ;
474      * Only cancer diagnoses prior to DM or in persons without DM ;
475      if ( '31DEC1994'd < doCA < doDM ) or
476      ( '31DEC1994'd < doCA and doDM le .z ) ;
477      A = floor( ( doCA - doBT ) / 365.25 ) ;
478      * Remove persons with date of birth > date of Ca diagnosis ;
479      if ( A ge 0 ) ;
480      P = year( doCa ) ;
481      * Make sure that the date of birth fits with A and P ;
482      C = min( max( year( doBT ), P-A-1 ), P-A ) ;
```

```
483      run ;
```

```
NOTE: There were 1557236 observations read from the data set DATA.CANDI.
NOTE: The data set WORK.WELLCA has 346198 observations and 13 variables.
NOTE: DATA statement used (Total process time):
      real time      8.21 seconds
      cpu time       0.53 seconds
```

```
484
485      * Cancers subdivided into the relevant subgroups ;
486      proc summary data = WellCa ;
487          class sex A P C diag ; * Note that 2^5=32 ;
488          output out = WellCaD ( rename = ( _freq_ = D )
489                                  keep = diag sex A P C _freq_ _type_
490                                  where = ( _type_ in (30,31) ) ) ;
491      run ;
```

```
NOTE: There were 346198 observations read from the data set WORK.WELLCA.
NOTE: The data set WORK.WELLCAD has 72601 observations and 7 variables.
NOTE: PROCEDURE SUMMARY used (Total process time):
      real time      0.70 seconds
      cpu time       0.78 seconds
```

```
492
493      data Well ;
494          set WellCaD ;
495          keep diag sex A P C D ;
496          if A < 100 and &Plo. < P < &Phi. ;
497          if diag le .z then diag = 0 ; * Corresponds to the sum over all diagnoses ;
498          if D le .z then D = 0 ;
499      run ;
```

```
NOTE: There were 72601 observations read from the data set WORK.WELLCAD.
NOTE: The data set WORK.WELL has 72490 observations and 6 variables.
NOTE: DATA statement used (Total process time):
      real time      0.17 seconds
      cpu time       0.04 seconds
```

```
500
501      proc sort data = Well ;
502          by sex A P C diag ;
503      run ;
```

```
NOTE: There were 72490 observations read from the data set WORK.WELL.
NOTE: The data set WORK.WELL has 72490 observations and 6 variables.
NOTE: PROCEDURE SORT used (Total process time):
      real time      0.25 seconds
      cpu time       0.10 seconds
```

```
504
505      * Transpose the dataset to have one column per diag ;
506      proc transpose data = Well
507          out = WellD ( drop = _NAME_ )
508          prefix = D ;
509          by sex A P C ;
510          id diag ;
511          format diag ;
512          var D ;
513      run ;
```

```
NOTE: There were 72490 observations read from the data set WORK.WELL.
NOTE: The data set WORK.WELLD has 5844 observations and 31 variables.
NOTE: PROCEDURE TRANSPOSE used (Total process time):
      real time      0.54 seconds
      cpu time       0.32 seconds
```

```
514
515      * Dataset WellD now have all the cancer transitions out of Well,
516      * each type in a separate variable, data classified by sex A P C,
517      * instances with no cancers are missing and other cancers coded 999 ;
518
519      *-----;
520      * Merge the events in Well with the person-years in Well ;
521
522      data WellCa ;
523          merge WellY
524              WellD ;
525          by sex A P C ;
526      * This is the non-Diabetic state ;
527          state = "Well " ;
528          DMtype = 0 ;
529      run ;
```

```
NOTE: There were 6000 observations read from the data set WORK.WELLY.
```


NOTE: There were 5844 observations read from the data set WORK.WELLD.
 NOTE: The data set WORK.WELLCA has 6000 observations and 34 variables.
 NOTE: DATA statement used (Total process time):
 real time 0.03 seconds
 cpu time 0.03 seconds

```
530
531           proc contents data = WellCa                   ; run ;
```

NOTE: PROCEDURE CONTENTS used (Total process time):
 real time 0.34 seconds
 cpu time 0.03 seconds

NOTE: The PROCEDURE CONTENTS printed page 3.

```
532           proc print data = WellCa ( obs=20 ) ; run ;
```

NOTE: There were 20 observations read from the data set WORK.WELLCA.
 NOTE: The PROCEDURE PRINT printed page 4.
 NOTE: PROCEDURE PRINT used (Total process time):
 real time 0.06 seconds
 cpu time 0.00 seconds

```
533
534           * The dataset WellCa now has the person-years in Well and the transitions to
535           the different Cancers out of that state ;
536
537           *-----;
538           * The person-years and total cancers for the transition DM -> (DM+Ca),
539           but before the DM -> DM/Ins transition ;
540
541           data DM ;
542           set data.candi ;
543           * NOTE: Only include persons with cancer at least 30 days after DM or no cancer
544           *       and of course only persons with a DM diagnosis after 1.1.1995;
545           if ( doDM gt .z ) and
546            ( doDM lt (doCA+31) or doCa le .z ) ;
547           * The Lexis variables defining the follow-up ;
548           entry = doDM ;
549           exit  = min( doCA, doI, doX ) ;
550           fail  = max( 0, diag ) * ( abs(doCA-exit)<0.5 ) ; * Set to 0 if no cancer diagnosis ;
551           run ;
```

NOTE: Missing values were generated as a result of performing an operation on missing values.
 Each place is given by: (Number of times) at (Line):(Column).
 362089 at 546:21 362089 at 550:30 362089 at 550:38

NOTE: There were 1557236 observations read from the data set DATA.CANDI.
 NOTE: The data set WORK.DM has 403959 observations and 13 variables.
 NOTE: DATA statement used (Total process time):
 real time 0.75 seconds
 cpu time 0.46 seconds

```
552
553           * split by calendar time ;
554           %Lexis( data = DM,
555                    out = DMP,
556                    breaks = &Pfirst. to &Plast. by 1,
557                    origin = '01Jan1900'd,
558                    scale = 365.25,
559                    left = P ) ;
```

NOTE: There were 403959 observations read from the data set WORK.DM.
 NOTE: The data set WORK.DISCRD has 0 observations and 16 variables.
 NOTE: The data set WORK.DMP has 1951044 observations and 16 variables.
 NOTE: DATA statement used (Total process time):
 real time 9.96 seconds
 cpu time 1.57 seconds

```
560           * Split by age ;
561           %Lexis( data = DMP,
562                    out = DMAP,
563                    breaks = 0 to 100 by 1,
564                    origin = doBT,
565                    scale = 365.25,
566                    left = A ) ;
```

NOTE: There were 1951044 observations read from the data set WORK.DMP.
 NOTE: The data set WORK.DISCRD has 0 observations and 17 variables.
 NOTE: The data set WORK.DMAP has 3676132 observations and 17 variables.
 NOTE: DATA statement used (Total process time):
 real time 15.85 seconds
 cpu time 15.07 seconds

```
567           * Fix the period and cohort variables ;
```

```

568     data DMAP ;
569         set DMAP ;
570         P = P + 1900 ;
571         C = min( max( year( doBT ), P-A-1 ), P-A ) ;
572     run ;

```

NOTE: There were 3676132 observations read from the data set WORK.DMAP.
NOTE: The data set WORK.DMAP has 3676132 observations and 18 variables.
NOTE: DATA statement used (Total process time):
real time 12.48 seconds
cpu time 3.06 seconds

```

573     * Split by diabetes duration ;
574     %Lexis( data = DMAP,
575             out = DMAPD,
576             breaks = &durbreaks.,
577             origin = doDM,
578             scale = 365.25,
579             left = DMdur ) ;

```

NOTE: There were 3676132 observations read from the data set WORK.DMAP.
NOTE: The data set WORK.DISCARD has 0 observations and 19 variables.
NOTE: The data set WORK.DMAPD has 7331956 observations and 19 variables.
NOTE: DATA statement used (Total process time):
real time 30.57 seconds
cpu time 10.90 seconds

```

580
581     *-----;
582     * Summarizing the split data ;
583
584     * Tabulation of risktime ;
585     proc summary data = DMAPD nway ;
586         where DMtype > 0 ;
587         class sex A P C DMdur DMtype ;
588         var risk ;
589         output out = DMY ( rename = ( risk = Y )
590                             keep = sex A P C DMdur DMtype risk )
591         sum = ;
592     run ;

```

NOTE: There were 5951846 observations read from the data set WORK.DMAPD.
WHERE DMtype>0;
NOTE: The data set WORK.DMY has 89019 observations and 7 variables.
NOTE: PROCEDURE SUMMARY used (Total process time):
real time 2.76 seconds
cpu time 7.95 seconds

```

593
594     * Tabulation of cases by classification variables and cancer type ;
595     proc summary data = DMAPD ;
596         where DMtype > 0 and fail > 0 ;
597         class sex A P C DMdur DMtype fail ; * OBS: 2^7=128 ;
598         output out = DMD1 ( rename = ( _freq_ = D
599                                     fail = diag )
600                             keep = sex A P C DMdur DMtype fail _freq_ _type_
601                             where = ( _type_ in (126,127) ) ) ;
602     run ;

```

NOTE: There were 20872 observations read from the data set WORK.DMAPD.
WHERE (DMtype>0) and (fail>0);
NOTE: The data set WORK.DMD1 has 34691 observations and 9 variables.
NOTE: PROCEDURE SUMMARY used (Total process time):
real time 2.12 seconds
cpu time 2.06 seconds

```

603
604     data DMD1 ;
605         set DMD1 ;
606         if diag le .z then diag=0 ;
607     run ;

```

NOTE: There were 34691 observations read from the data set WORK.DMD1.
NOTE: The data set WORK.DMD1 has 34691 observations and 9 variables.
NOTE: DATA statement used (Total process time):
real time 0.06 seconds
cpu time 0.01 seconds

```

608
609     proc sort data = DMD1 ;
610         by sex A P C DMdur DMtype diag ;
611     run ;

```

NOTE: There were 34691 observations read from the data set WORK.DMD1.

NOTE: The data set WORK.DMDL has 34691 observations and 9 variables.
 NOTE: PROCEDURE SORT used (Total process time):
 real time 0.09 seconds
 cpu time 0.07 seconds

```
612
613      * Transpose the dataset to have one column per diag ;
614      proc transpose data = DMD1
615          out = DMD
616          prefix = D ;
617      by sex A P C DMdur DMtype ;
618      id diag ;
619      format diag ;
620      var D ;
621      run ;
```

NOTE: There were 34691 observations read from the data set WORK.DMDL.
 NOTE: The data set WORK.DMD has 14746 observations and 34 variables.
 NOTE: PROCEDURE TRANSPOSE used (Total process time):
 real time 0.21 seconds
 cpu time 0.22 seconds

```
622
623      data DMCA ;
624      merge DMD DMY ;
625      by sex A P C DMdur DMtype ;
626      state = "DM " ;
627      run ;
```

NOTE: There were 14746 observations read from the data set WORK.DMD.
 NOTE: There were 89019 observations read from the data set WORK.DMY.
 NOTE: The data set WORK.DMCA has 89019 observations and 36 variables.
 NOTE: DATA statement used (Total process time):
 real time 0.70 seconds
 cpu time 0.17 seconds

```
628
629      * The dataset DMCAa now has the Person-years and different cancers from
630      state DM, subdivided by the factors of interest including duration ;
631
632      proc contents data = DMCA          ; run ;
```

NOTE: PROCEDURE CONTENTS used (Total process time):
 real time 0.03 seconds
 cpu time 0.01 seconds

NOTE: The PROCEDURE CONTENTS printed page 5.

```
633      proc print data = DMCA ( obs=20 ) ; run ;
```

NOTE: There were 20 observations read from the data set WORK.DMCA.
 NOTE: The PROCEDURE PRINT printed page 6.
 NOTE: PROCEDURE PRINT used (Total process time):
 real time 0.00 seconds
 cpu time 0.00 seconds

```
634
635      *-----;
636      * The person-years and total cancers for the transition
637      * DM/ins -> (DM/ins+Ca) ;
638
639      data Ins ;
640      set data.candi ;
641      if ( doI gt .z ) and
642          ( doI lt doCA or doCa le .z ) ;
643      * The Lexis variables ;
644      entry = doI ;
645      exit = min( doCA, doX ) ;
646      fail = max( 0, diag ) * ( abs(doCA-exit)<0.5 ) ; * Set to 0 if no cancer diagnosis ;
647      run ;
```

NOTE: Missing values were generated as a result of performing an operation on missing values.
 Each place is given by: (Number of times) at (Line):(Column).
 91991 at 646:30 91991 at 646:38

NOTE: There were 1557236 observations read from the data set DATA.CANDI.
 NOTE: The data set WORK.INS has 99674 observations and 13 variables.
 NOTE: DATA statement used (Total process time):
 real time 20.87 seconds
 cpu time 0.43 seconds

```
648
649      * Split by calendar time ;
650      %Lexis( data = Ins,
651          out = InsP,
```

```

652         breaks = &Pfirst. to &Plast. by 1,
653         origin = '01Jan1900'd,
654         scale = 365.25,
655         left = P )

```

```

NOTE: There were 99674 observations read from the data set WORK.INS.
NOTE: The data set WORK.DISCRD has 0 observations and 16 variables.
NOTE: The data set WORK.INSAP has 741361 observations and 16 variables.
NOTE: DATA statement used (Total process time):
      real time           3.57 seconds
      cpu time            0.42 seconds

```

```

656     * Split by age ;
657     %Lexis( data = InsP,
658           out = InsAP,
659           breaks = 0 to 100 by 1,
660           origin = doBT,
661           scale = 365.25,
662           left = A )

```

```

NOTE: There were 741361 observations read from the data set WORK.INSAP.
NOTE: The data set WORK.DISCRD has 0 observations and 17 variables.
NOTE: The data set WORK.INSAP has 1430192 observations and 17 variables.
NOTE: DATA statement used (Total process time):
      real time           6.40 seconds
      cpu time            5.93 seconds

```

```

663     * Fix the period and cohort variables ;
664     data InsAP ;
665     set InsAP ;
666     P = P + 1900 ;
667     C = min( max( year( doBT ), P-A-1 ), P-A ) ;
668     run ;

```

```

NOTE: There were 1430192 observations read from the data set WORK.INSAP.
NOTE: The data set WORK.DISCRD has 0 observations and 18 variables.
NOTE: DATA statement used (Total process time):
      real time           5.28 seconds
      cpu time            1.04 seconds

```

```

669     * Split by DM duration ;
670     %Lexis( data = InsAP,
671           out = InsAPD,
672           breaks = &durbreaks.,
673           origin = doDM,
674           scale = 365.25,
675           left = DMdur )

```

```

NOTE: There were 1430192 observations read from the data set WORK.INSAP.
NOTE: The data set WORK.DISCRD has 0 observations and 19 variables.
NOTE: The data set WORK.INSAPD has 2152911 observations and 19 variables.
NOTE: DATA statement used (Total process time):
      real time           9.21 seconds
      cpu time            4.03 seconds

```

```

676     * Split by Insulin duration ;
677     %Lexis( data = InsAPD,
678           out = InsAPDI,
679           breaks = &durbreaks.,
680           origin = doI,
681           scale = 365.25,
682           left = Insdur )

```

```

NOTE: There were 2152911 observations read from the data set WORK.INSAPD.
NOTE: The data set WORK.DISCRD has 0 observations and 20 variables.
NOTE: The data set WORK.INSAPDI has 3336990 observations and 20 variables.
NOTE: DATA statement used (Total process time):
      real time          12.59 seconds
      cpu time           6.48 seconds

```

```

683
684     *-----;
685     * Summarizing the split data for DM/Ins diagnosed after 1995 ;
686
687     * Tabulation of risktime ;
688     proc summary data = InsAPDI nway ;
689       where DMtype > 0 ;
690       class sex A P C DMdur Insdur DMtype ;
691       var risk ;
692       output out = InsY ( rename = ( risk = Y )
693                        keep = sex A P C DMdur Insdur DMtype risk )
694       sum = ;
695     run ;

```

NOTE: There were 1453822 observations read from the data set WORK.INSAPDI.
WHERE DMtype>0;

NOTE: The data set WORK.INSY has 456261 observations and 8 variables.

NOTE: PROCEDURE SUMMARY used (Total process time):

real time 2.20 seconds
cpu time 3.57 seconds

696

697 * Tabulation of cases by classification variables and cancer type ;

698 proc summary data = InsAPDI ;

699 where DMtype > 0 and fail > 0 ;

700 class sex A P C DMdur Insdur DMtype fail ; * OBS: 2^8=256 ;

701 output out = Insl (rename = (_freq_ = D

702 fail = diag)

703 keep = sex A P C DMdur Insdur DMtype fail _freq_ _type_

704 where = (_type_ in (254,255))) ;

705 run ;

NOTE: There were 2974 observations read from the data set WORK.INSAPDI.

WHERE (DMtype>0) and (fail>0);

NOTE: The data set WORK.INSL has 5912 observations and 10 variables.

NOTE: PROCEDURE SUMMARY used (Total process time):

real time 1.12 seconds
cpu time 1.10 seconds

706

707 data Insl ;

708 set Insl ;

709 if diag le .z then diag=0 ;

710

run ;

NOTE: There were 5912 observations read from the data set WORK.INSL.

NOTE: The data set WORK.INSL has 5912 observations and 10 variables.

NOTE: DATA statement used (Total process time):

real time 0.04 seconds
cpu time 0.01 seconds

711

712 proc sort data = Insl ;

713 by sex A P C DMdur Insdur DMtype diag ;

714

run ;

NOTE: There were 5912 observations read from the data set WORK.INSL.

NOTE: The data set WORK.INSL has 5912 observations and 10 variables.

NOTE: PROCEDURE SORT used (Total process time):

real time 0.01 seconds
cpu time 0.01 seconds

715

716 * Transpose the dataset to have one column per diag ;

717 proc transpose data = Insl

718 out = InsD

719 prefix = D ;

720 by sex A P C DMdur Insdur DMtype ;

721 id diag ;

722 format diag ;

723 var D ;

724

run ;

NOTE: There were 5912 observations read from the data set WORK.INSL.

NOTE: The data set WORK.INSL has 2943 observations and 35 variables.

NOTE: PROCEDURE TRANSPOSE used (Total process time):

real time 0.04 seconds
cpu time 0.04 seconds

725

726 data InsCa ;

727 merge InsD InsY ;

728 by sex A P C DMdur Insdur DMtype ;

729 state = "DM/Ins" ;

730 * Because of date uncertainty we do not count the first month on

731 insulin in the insulin group --- to avoid insulin treatment after

732 diagnosis of cancer being clsiddied as insulin exposure prior to cancer ;

733 if(Insdur eq 0) then state="DM " ;

734

run ;

NOTE: There were 2943 observations read from the data set WORK.INSL.

NOTE: There were 456261 observations read from the data set WORK.INSY.

NOTE: The data set WORK.INSY has 456261 observations and 37 variables.

NOTE: DATA statement used (Total process time):

real time 2.84 seconds
cpu time 0.87 seconds

```

735
736 * The dataset InsCa now has the Person-years and different cancers from
737 state DM/Ins, subdivided by the factors of interest including durations ;
738
739 proc contents data = InsCa ; run ;

NOTE: PROCEDURE CONTENTS used (Total process time):
      real time      0.03 seconds
      cpu time       0.01 seconds

NOTE: The PROCEDURE CONTENTS printed page 7.

740 proc print data = InsCa ( obs=20 ) ; run ;

NOTE: There were 20 observations read from the data set WORK.INSKA.
NOTE: The PROCEDURE PRINT printed page 8.
NOTE: PROCEDURE PRINT used (Total process time):
      real time      0.00 seconds
      cpu time       0.00 seconds

741
742 *-----;
743 * Combine the three datasets to the final one - the duration case ;
744
745 data data.DMCA ;
746 set WellCa
747     DMCA ( in = DM )
748     InsCa ( in = Ins ) ;
749 drop upper _name_ i ;
750 label A = "Agr"
751     P = "Pgr"
752     C = "Cgr"
753     Ax = "Age"
754     Px = "Per"
755     Cx = "Coh"
756     state = "State"
757     DMtype = "DM type"
758     DMdur = "Time since DoDM (inclusion)"
759     Insdur = "Time since DoI (1st insulin)"
760     Y = "Person-years"
761     D0 = "All malignant neoplasms"
762     D21 = "Oesophagus"
763     D22 = "Stomach"
764     D24 = "Colon"
765     D241 = "Ascending colon"
766     D242 = "Transverse colon"
767     D243 = "Descending colon"
768     D249 = "Other colon"
769     D251 = "Rectum"
770     D259 = "Colorectal"
771     D26 = "Liver"
772     D28 = "Pancreas"
773     D33 = "Lung"
774     D51 = "Melanoma"
775     D70 = "Breast"
776     D82 = "Cervix"
777     D83 = "Uterus"
778     D84 = "Ovary"
779     D91 = "Prostate"
780     D92 = "Testis"
781     D101 = "Kidney"
782     D103 = "Bladder"
783     D113 = "Brain"
784     D121 = "Thyroid"
785     D131 = "Hodgkin's lymphoma"
786     D132 = "Non-Hodgkin lymphoma"
787     D133 = "Multiple myeloma"
788     D139 = "Leukaemia"
789     D999 = "Other" ;
790 * Correct triangle means in a Lexis diagram ;
791 upper = P-A-C ;
792 Ax = A + (1+upper)/3 ;
793 Px = P + (2+upper)/3 ;
794 Cx = Px - Ax ;
795 * Anchor the two duration scales in 0 ;
796 if DMdur le .z then DMdur = 0 ;
797 if Insdur le .z then Insdur = 0 ;
798 * Stick a 0 in for all the missing values where no cancers were observed ;
799 array allnum{*} _numeric_ ;
800 do i = 1 to dim(allnum) ;
801     allnum{i} = max( allnum{i}, 0 ) ;
802 end ;
803 * Define colon and colorectal cancers excl. anus ;
804 D24 = D241 + D242 + D243 + D249 ;
805 D259 = D241 + D242 + D243 + D249 + D251 ;
806 run ;

NOTE: There were 6000 observations read from the data set WORK.WELLCA.

```

NOTE: There were 89019 observations read from the data set WORK.DMCA.
 NOTE: There were 456261 observations read from the data set WORK.INSCA.
 NOTE: The data set DATA.DMCAD has 551280 observations and 41 variables.
 NOTE: DATA statement used (Total process time):
 real time 5.42 seconds
 cpu time 2.46 seconds

```
807
808     title 'Dataset with duration variables (only doDM > 31.12.1994)';
809     proc contents data = data.DMCaD ;
810     run ;
```

NOTE: PROCEDURE CONTENTS used (Total process time):
 real time 0.06 seconds
 cpu time 0.04 seconds

NOTE: The PROCEDURE CONTENTS printed page 9.

```
811
812     proc tabulate data=data.DMCaD order=data missing
813                 noseps formchar="          ";
814     class state P DMtype ;
815     var Y &dvars. ;
816     table all
817           state*DMtype
818           state*DMtype*P,
819           ( Y * f=comma13.1
820             (n="No. cells" D0 D259 D33 D70 D91 D999) * f=comma10.0 )
821           / rts = 25 ;
822     table Y * f=comma10.0
823           ( &dvars. ) * f=comma10.0 ,
824           sum=" " * ( all state )
825           / rts = 14 ;
826     keylabel sum=" "
827           n=" " ;
828     run ;
```

NOTE: There were 551280 observations read from the data set DATA.DMCAD.
 NOTE: The PROCEDURE TABULATE printed pages 10-11.
 NOTE: PROCEDURE TABULATE used (Total process time):
 real time 0.45 seconds
 cpu time 0.73 seconds

```
829
830     *-----;
831     * Tabulate witout duration using the DMSP and InsAP datasets ;
832
833     *-----;
834     * First the DM state ;
835
836     * Tabulation of risktime ;
837     proc summary data = DMAPD nway ;
838     class sex A P C DMtype ;
839     var risk ;
840     output out = DMY ( rename = ( risk = Y )
841                       keep = sex A P C DMtype risk )
842     sum = ;
843     run ;
```

NOTE: There were 7331956 observations read from the data set WORK.DMAPD.
 NOTE: The data set WORK.DMY has 13030 observations and 6 variables.
 NOTE: PROCEDURE SUMMARY used (Total process time):
 real time 7.84 seconds
 cpu time 6.68 seconds

```
844
845     * Tabulation of cases by classification variables and cancer type ;
846     proc summary data = DMAPD ;
847     where fail > 0 ;
848     class sex A P C DMtype fail ; * OBS: 2^6=64 ;
849     output out = DMD1 ( rename = ( _freq_ = D
850                                   fail = diag )
851                           keep = sex A P C DMtype fail _freq_ _type_
852                           where = ( _type_ in (62,63) ) ) ;
853     run ;
```

NOTE: There were 27809 observations read from the data set WORK.DMAPD.
 WHERE fail>0;
 NOTE: The data set WORK.DMDL has 23695 observations and 8 variables.
 NOTE: PROCEDURE SUMMARY used (Total process time):
 real time 20.43 seconds
 cpu time 1.71 seconds

```
854
855     data DMD1 ;
```

```

856         set DMD1 ;
857         if diag le .z then diag=0 ;
858         run ;

```

NOTE: There were 23695 observations read from the data set WORK.DMDL.
NOTE: The data set WORK.DMDL has 23695 observations and 8 variables.
NOTE: DATA statement used (Total process time):
real time 0.03 seconds
cpu time 0.01 seconds

```

859
860         proc sort data = DMD1 ;
861             by sex A P C DMtype diag ;
862         run ;

```

NOTE: There were 23695 observations read from the data set WORK.DMDL.
NOTE: The data set WORK.DMDL has 23695 observations and 8 variables.
NOTE: PROCEDURE SORT used (Total process time):
real time 0.04 seconds
cpu time 0.04 seconds

```

863
864         * Transpose the dataset to have one column per diag ;
865         proc transpose data = DMD1
866             out = DMD
867             prefix = D ;
868             by sex A P C DMtype ;
869             id diag ;
870             format diag ;
871             var D ;
872         run ;

```

NOTE: There were 23695 observations read from the data set WORK.DMDL.
NOTE: The data set WORK.DMD has 4907 observations and 33 variables.
NOTE: PROCEDURE TRANSPOSE used (Total process time):
real time 0.12 seconds
cpu time 0.12 seconds

```

873
874         data DMCA ;
875         merge DMD DMY ;
876         by sex A P C DMtype ;
877         state = "DM " ;
878         run ;

```

NOTE: There were 4907 observations read from the data set WORK.DMD.
NOTE: There were 13030 observations read from the data set WORK.DMY.
NOTE: The data set WORK.DMCA has 13030 observations and 35 variables.
NOTE: DATA statement used (Total process time):
real time 0.07 seconds
cpu time 0.03 seconds

```

879
880         * The dataset DMCA now has the Person-years and different cancers from
881         state DM, subdivided by the factors of interest ;
882
883         *-----;
884         * Then the DM/Ins state ;
885
886         * Tabulation of risktime ;
887         proc summary data = InsAPDI nway ;
888             class sex A P C DMtype ;
889             var risk ;
890             output out = InsY ( rename = ( risk = Y )
891                 keep = sex A P C DMtype risk )
892             sum = ;
893         run ;

```

NOTE: There were 3336990 observations read from the data set WORK.INSAPDI.
NOTE: The data set WORK.INSY has 13538 observations and 6 variables.
NOTE: PROCEDURE SUMMARY used (Total process time):
real time 0.87 seconds
cpu time 2.86 seconds

```

894
895         * Tabulation of cases by classification variables and cancer type ;
896         proc summary data = InsAPDI ;
897             where fail > 0 ;
898             class sex A P C DMtype fail ; * OBS: 2^6=64 ;
899             output out = Ins1 ( rename = ( _freq_ = D
900                 fail = diag )
901                 keep = sex A P C DMtype fail _freq_ _type_
902                 where = ( _type_ in (62,63) ) ) ;
903         run ;

```


NOTE: There were 7424 observations read from the data set WORK.INSAPDI.
WHERE fail>0;

NOTE: The data set WORK.INSL has 10207 observations and 8 variables.

NOTE: PROCEDURE SUMMARY used (Total process time):

real time 0.57 seconds
cpu time 0.56 seconds

```
904
905     data Insl ;
906     set Insl ;
907     if diag le .z then diag=0 ;
908     run ;
```

NOTE: There were 10207 observations read from the data set WORK.INSL.

NOTE: The data set WORK.INSL has 10207 observations and 8 variables.

NOTE: DATA statement used (Total process time):

real time 0.03 seconds
cpu time 0.01 seconds

```
909
910     proc sort data = Insl ;
911         by sex A P C DMtype diag ;
912     run ;
```

NOTE: There were 10207 observations read from the data set WORK.INSL.

NOTE: The data set WORK.INSL has 10207 observations and 8 variables.

NOTE: PROCEDURE SORT used (Total process time):

real time 0.04 seconds
cpu time 0.01 seconds

```
913
914     * Transpose the dataset to have one column per diag ;
915     proc transpose data = Insl
916         out = InSD
917         prefix = D ;
918         by sex A P C DMtype ;
919         id diag ;
920         format diag ;
921         var D ;
922     run ;
```

NOTE: There were 10207 observations read from the data set WORK.INSL.

NOTE: The data set WORK.INSD has 3499 observations and 33 variables.

NOTE: PROCEDURE TRANSPOSE used (Total process time):

real time 0.06 seconds
cpu time 0.06 seconds

```
923
924     data InSCa ;
925     merge InSD InSY ;
926     by sex A P C DMtype ;
927     state = "DM/Ins" ;
928     run ;
```

NOTE: There were 3499 observations read from the data set WORK.INSD.

NOTE: There were 13538 observations read from the data set WORK.INSY.

NOTE: The data set WORK.INSCA has 13538 observations and 35 variables.

NOTE: DATA statement used (Total process time):

real time 0.03 seconds
cpu time 0.03 seconds

```
929
930     * The dataset InSCa now has the Person-years and different cancers from
931     state DM/Ins, subdivided by the factors of interest ;
932
933     *-----;
934     * Combine the three datasets to the final one - the duration case ;
935
936     data data.DMCA ;
937     set WellCa
938         DMCA ( in = DM )
939         InSCa ( in = InS ) ;
940     drop upper _name_ i ;
941     label A = "Agr"
942           P = "Pgr"
943           C = "Cgr"
944           Ax = "Age"
945           Px = "Per"
946           Cx = "Coh"
947           state = "State"
948           DMtype = "DM type"
949           Y = "Person-years"
950           DO = "All malignant neoplasms"
```

```

951         D21 = "Oesophagus"
952         D22 = "Stomach"
953         D24 = "Colon"
954         D241 = "Ascending colon"
955         D242 = "Transverse colon"
956         D243 = "Descending colon"
957         D249 = "Other colon"
958         D251 = "Rectum"
959         D259 = "Colorectal"
960         D26 = "Liver"
961         D28 = "Pancreas"
962         D33 = "Lung"
963         D51 = "Melanoma"
964         D70 = "Breast"
965         D82 = "Cervix"
966         D83 = "Uterus"
967         D84 = "Ovary"
968         D91 = "Prostate"
969         D92 = "Testis"
970         D101 = "Kidney"
971         D103 = "Bladder"
972         D113 = "Brain"
973         D121 = "Thyroid"
974         D131 = "Hodgkin's lymphoma"
975         D132 = "Non-Hodgkin lymphoma"
976         D133 = "Multiple myeloma"
977         D139 = "Leukaemia"
978         D999 = "Other" ;
979     * Correct triangle means in a Lexis diagram ;
980     upper = P-A-C ;
981     Ax = A + (1+upper)/3 ;
982     Px = P + (2-upper)/3 ;
983     Cx = Px - Ax ;
984     * Stick a 0 in for all the missing values where no cancers were observed ;
985     array allnum{*} _numeric_ ;
986     do i = 1 to dim(allnum) ;
987         allnum{i} = max( allnum{i}, 0 ) ;
988     end ;
989     * Define colon and colorectal cancers excl. anus ;
990     D24 = D241 + D242 + D243 + D249 ;
991     D259 = D241 + D242 + D243 + D249 + D251 ;
992     run ;

```

NOTE: There were 6000 observations read from the data set WORK.WELLCA.
NOTE: There were 13030 observations read from the data set WORK.DMCA.
NOTE: There were 13538 observations read from the data set WORK.INSCA.
NOTE: The data set DATA.DMCAA has 32568 observations and 39 variables.
NOTE: DATA statement used (Total process time):
real time 0.40 seconds
cpu time 0.14 seconds

```

993
994     title 'Dataset without duration variables' ;
995     proc contents data = data.DMCA ;
996     run ;

```

NOTE: PROCEDURE CONTENTS used (Total process time):
real time 0.03 seconds
cpu time 0.01 seconds

NOTE: The PROCEDURE CONTENTS printed page 12.

```

997
998     proc tabulate data=data.DMCA order=data missing
999         noseps formchar=" ";
1000     class state P DMtype ;
1001     var Y &dvars. ;
1002     table all
1003         state*DMtype
1004         state*DMtype*P,
1005         ( Y * f=comma13.1
1006         (n="No. cells" D0 D259 D33 D70 D91 D999) * f=comma10.0 )
1007         / rts = 25 ;
1008     table Y * f=comma10.0
1009         ( &dvars. ) * f=comma10.0 ,
1010         sum=" " * ( all state )
1011         / rts = 14 ;
1012     keylabel sum=" "
1013         n=" " ;
1014     run ;

```

NOTE: There were 32568 observations read from the data set DATA.DMCAA.
NOTE: The PROCEDURE TABULATE printed pages 13-15.
NOTE: PROCEDURE TABULATE used (Total process time):
real time 0.09 seconds
cpu time 0.09 seconds

```

1015
1016      * Finally export the relevant data for analysis in XPT format ;
1017      libname xptA xport './data/DMCaA.xpt';
NOTE: Libref XPTA was successfully assigned as follows:
      Engine:          XPORT
      Physical Name: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\data\DMCaA.xpt
1018      libname xptD xport './data/DMCaD.xpt';
NOTE: Libref XPTD was successfully assigned as follows:
      Engine:          XPORT
      Physical Name: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\data\DMCaD.xpt
1019      proc copy in=data out=xptA memtype=data; select DMCaA ; run;

NOTE: Copying DATA.DMCAA to XPTA.DMCAA (memtype=DATA).
NOTE: There were 32568 observations read from the data set DATA.DMCAA.
NOTE: The data set XPTA.DMCAA has 32568 observations and 39 variables.
NOTE: PROCEDURE COPY used (Total process time):
      real time          0.68 seconds
      cpu time           0.15 seconds
    
```

```

1020      proc copy in=data out=xptD memtype=data; select DMCaD ; run;

NOTE: Copying DATA.DMCAD to XPTD.DMCAD (memtype=DATA).
NOTE: There were 551280 observations read from the data set DATA.DMCAD.
NOTE: The data set XPTD.DMCAD has 551280 observations and 41 variables.
NOTE: PROCEDURE COPY used (Total process time):
      real time          3.95 seconds
      cpu time           1.64 seconds
    
```

```

NOTE: SAS Institute Inc., SAS Campus Drive, Cary, NC USA 27513-2414
NOTE: The SAS System used:
      real time          6:46.68
      cpu time           2:42.42
    
```

All cancers diagnosed 1995 ff.

13:55 Thursday, March 31, 2011 1

	Diagnosedat0														
	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009
All	22,430	22,654	23,009	23,649	24,018	24,121	24,408	24,912	25,332	26,128	26,850	27,810	28,049	28,887	29,792
Diag															
21	282	325	331	311	315	327	362	370	349	375	344	358	338	354	369
22	524	507	481	493	491	412	469	450	486	473	482	511	491	503	482
26	247	218	223	241	270	258	258	283	266	252	219	244	247	272	269
28	551	548	624	668	665	674	703	684	708	743	732	733	821	771	834
33	3,100	3,013	3,164	3,040	3,222	3,305	3,324	3,412	3,291	3,504	3,491	3,591	3,738	3,584	3,597
51	965	853	861	839	966	1,037	983	1,002	1,171	1,051	1,228	1,320	1,389	1,439	1,692
70	3,093	3,308	3,272	3,403	3,471	3,545	3,658	3,857	3,735	3,688	3,727	3,851	3,866	4,473	5,317
82	491	476	415	421	423	380	402	356	401	366	395	367	346	341	361
83	601	574	570	575	579	578	630	581	615	613	604	619	594	673	683
84	560	517	551	563	572	565	562	560	526	471	530	498	492	477	491
91	1,285	1,431	1,496	1,641	1,736	1,823	1,905	2,108	2,286	2,673	3,092	3,192	3,502	3,684	3,587
92	293	287	294	287	296	268	243	274	276	308	278	303	312	286	321
101	413	453	421	490	452	491	482	430	464	509	500	550	526	552	589
103	1,354	1,389	1,460	1,498	1,490	1,429	1,429	1,449	1,559	1,505	1,533	1,495	1,496	1,448	1,428
113	627	621	616	703	649	675	623	629	625	655	652	657	688	753	725
121	118	138	115	139	134	163	130	128	149	187	148	151	166	173	186
131	110	114	123	125	110	107	119	131	137	102	114	142	137	114	122
132	682	682	708	695	697	706	694	701	770	734	766	802	842	757	748
133	297	299	282	274	283	310	311	283	301	313	338	392	378	355	368
139	621	611	639	677	713	679	666	710	673	756	757	778	769	697	613
241	600	574	631	632	612	578	681	598	664	693	701	771	728	763	739
242	232	262	268	294	304	275	311	285	309	330	315	298	337	347	374
243	1,000	979	1,010	1,031	1,027	1,036	1,025	1,094	1,034	986	1,107	1,127	1,010	1,027	1,001
249	152	168	152	162	164	175	168	151	187	202	190	207	203	201	194
251	958	972	1,058	996	999	1,021	1,060	1,090	1,085	1,205	1,147	1,316	1,222	1,291	1,278
999	3,274	3,335	3,244	3,451	3,378	3,304	3,210	3,296	3,265	3,434	3,460	3,537	3,411	3,552	3,424

(Continued)

All cancers diagnosed 1995 ff.

13:55 Thursday, March 31, 2011 2

All	
All	382,049
Diag	
21	5,110
22	7,255
26	3,767
28	10,459
33	50,376
51	16,796
70	56,264
82	5,941
83	9,089

```

84      7,935
91     35,441
92     4,326
101    7,322
103    21,962
113    9,898
121    2,225
131    1,807
132    10,984
133    4,784
139    10,359
241    9,965
242    4,541
243    15,494
249    2,676
251    16,698
999    50,575

```

All cancers diagnosed 1995 ff.

13:55 Thursday, March 31, 2011 3

The CONTENTS Procedure

Data Set Name	WORK.WELLCA	Observations	6000
Member Type	DATA	Variables	34
Engine	V9	Indexes	0
Created	31 Mar 2011 Thu 13:58:55 o'clock	Observation Length	272
Last Modified	31 Mar 2011 Thu 13:58:55 o'clock	Deleted Observations	0
Protection		Compressed	NO
Data Set Type		Sorted	NO
Label			
Data Representation	WINDOWS_32		
Encoding	wlatin1 Western (Windows)		

Engine/Host Dependent Information

Data Set Page Size	16384
Number of Data Set Pages	101
First Data Page	1
Max Obs per Page	60
Obs in First Data Page	44
Number of Data Set Repairs	0
Filename	C:\DOCUME~1\bxc\LOCALS~1\Temp\SAS Temporary Files_TD1532\wellca.sas7bdat
Release Created	9.0202MO
Host Created	XP_PRO

Alphabetic List of Variables and Attributes

#	Variable	Type	Len	Format	Label
2	A	Num	8		Left endpoint of interval (transformed scale)
4	C	Num	8		Cohort
6	D0	Num	8		
25	D21	Num	8		
22	D22	Num	8		
12	D26	Num	8		
26	D28	Num	8		
17	D33	Num	8		
18	D51	Num	8		
28	D70	Num	8		
32	D82	Num	8		
31	D83	Num	8		
30	D84	Num	8		
13	D91	Num	8		
10	D92	Num	8		
7	D101	Num	8		
16	D103	Num	8		
8	D113	Num	8		
20	D121	Num	8		
15	D131	Num	8		
14	D132	Num	8		
27	D133	Num	8		
11	D139	Num	8		
21	D241	Num	8		
19	D242	Num	8		
24	D243	Num	8		
29	D249	Num	8		
23	D251	Num	8		
9	D999	Num	8		
34	DMtype	Num	8		
3	P	Num	8		Left endpoint of interval (transformed scale)
5	Y	Num	8		
1	sex	Num	8	SEX.	Sex
33	state	Char	6		

All cancers diagnosed 1995 ff.

13:55 Thursday, March 31, 2011 4

D
s M

```

      D D D   D   D D D   D D D   D D   D   D   t   t
0      s      1 1 9 D 1 D D 1 1 1 D D 2 1 2 D 2 2 D D 1 D 2 D D D a y
b      e      D 0 1 9 9 3 2 9 3 3 0 3 5 4 2 4 2 5 4 2 2 3 7 4 8 8 8 t p
s      x   A   P   C       Y   0 1 3 9 2 9 6 1 2 1 3 3 1 2 1 1 2 1 3 1 8 3 0 9 4 3 2 e e

 1 Males 0 1995 1994 17870.42 2 1 1 . . . . . Well 0
 2 Males 0 1995 1995 18024.75 4 1 1 2 . . . . . Well 0
 3 Males 0 1996 1995 18060.71 2 . 1 . 1 . . . . . Well 0
 4 Males 0 1996 1996 17425.55 2 1 1 . . . . . Well 0
 5 Males 0 1997 1996 17447.70 3 1 . . . 2 . . . . . Well 0
 6 Males 0 1997 1997 17385.87 1 . . 1 . . . . . Well 0
 7 Males 0 1998 1997 17407.82 4 . . 4 . . . . . Well 0
 8 Males 0 1998 1998 17034.24 4 . . 4 . . . . . Well 0
 9 Males 0 1999 1998 17062.80 2 1 . 1 . . . . . Well 0
10 Males 0 1999 1999 16950.96 4 . 3 1 . . . . . Well 0
11 Males 0 2000 1999 16977.87 6 1 1 3 . . 1 . . . . . Well 0
12 Males 0 2000 2000 17208.51 1 . . 1 . . . . . Well 0
13 Males 0 2001 2000 17234.46 5 . 1 2 . 2 . . . . . Well 0
14 Males 0 2001 2001 16739.01 2 . 1 1 . . . . . Well 0
15 Males 0 2002 2001 16766.37 2 . . 2 . . . . . Well 0
16 Males 0 2002 2002 16493.67 5 . 2 3 . . . . . Well 0
17 Males 0 2003 2002 16518.45 2 1 . 1 . . . . . Well 0
18 Males 0 2003 2003 16674.90 2 . . 1 . 1 . . . . . Well 0
19 Males 0 2004 2003 16669.08 3 . . 2 . 1 . . . . . Well 0
20 Males 0 2004 2004 16568.33 5 1 . 3 1 . . . . . Well 0
All cancers diagnosed 1995 ff.                                     13:55 Thursday, March 31, 2011 5

```

The CONTENTS Procedure

```

Data Set Name      WORK.DMCA      Observations      89019
Member Type       DATA          Variables          36
Engine            V9              Indexes            0
Created           31 Mar 2011 Thu 14:00:10 o'clock Observation Length 288
Last Modified     31 Mar 2011 Thu 14:00:10 o'clock Deleted Observations 0
Protection                               Compressed        NO
Data Set Type                               Sorted            NO
Label
Data Representation WINDOWS_32
Encoding          wlatin1 Western (Windows)

```

Engine/Host Dependent Information

```

Data Set Page Size      16384
Number of Data Set Pages 1590
First Data Page         1
Max Obs per Page        56
Obs in First Data Page  41
Number of Data Set Repairs 0
Filename                C:\DOCUME~1\bx\LOCALS~1\Temp\SAS Temporary Files\_TD1532\dmca.sas7bdat
Release Created         9.0202MO
Host Created            XP_PRO

```

Alphabetic List of Variables and Attributes

#	Variable	Type	Len	Format	Label
2	A	Num	8		Left endpoint of interval (transformed scale)
4	C	Num	8		
8	D0	Num	8		
21	D21	Num	8		
26	D22	Num	8		
13	D26	Num	8		
23	D28	Num	8		
16	D33	Num	8		
14	D51	Num	8		
31	D70	Num	8		
33	D82	Num	8		
32	D83	Num	8		
34	D84	Num	8		
30	D91	Num	8		
9	D92	Num	8		
19	D101	Num	8		
22	D103	Num	8		
11	D113	Num	8		
18	D121	Num	8		
12	D131	Num	8		
15	D132	Num	8		
25	D133	Num	8		
20	D139	Num	8		
28	D241	Num	8		
29	D242	Num	8		
24	D243	Num	8		
17	D249	Num	8		
27	D251	Num	8		
10	D999	Num	8		
5	DMdur	Num	8		Left endpoint of interval (transformed scale)
6	DMtype	Num	8		

```

3  P          Num      8          Left endpoint of interval (transformed scale)
35 Y          Num      8          Risktime in interval
7  _NAME_     Char      8          NAME OF FORMER VARIABLE
1  sex        Num      8          SEX.
36 state     Char      6
All cancers diagnosed 1995 ff.

```

13:55 Thursday, March 31, 2011 6

		D																											
		M									N																		
		t A									t A																		
		y M									y M																		
		D 9 1 1 D D 1 D 2 1 1 1 D 1 D 2 1 D 2 2 2 2 D D D D									D 9 1 1 D D 1 D 2 1 1 1 D 1 D 2 1 D 2 2 2 2 D D D D																		
		e - 0 2 9 3 1 6 1 2 3 9 1 1 9 1 3 8 3 3 2 1 1 1 2 1 0 3 2 4									e - 0 2 9 3 1 6 1 2 3 9 1 1 9 1 3 8 3 3 2 1 1 1 2 1 0 3 2 4									Y e									
1	Males 0 1995 1995 0.00000 2																											0.08333 DM
2	Males 0 1995 1995 0.08333 2																											0.16667 DM
3	Males 0 1995 1995 0.25000 2																											0.25000 DM
4	Males 0 1995 1995 0.50000 2																											0.25000 DM
5	Males 0 1995 1995 0.75000 2																											0.05767 DM
6	Males 0 1996 1995 0.75000 2																											0.03901 DM
7	Males 0 1997 1996 0.00000 1																											0.07118 DM
8	Males 0 1997 1997 0.00000 2																											0.08333 DM
9	Males 0 1997 1997 0.08333 2																											0.16667 DM
10	Males 0 1997 1997 0.25000 2																											0.20859 DM
11	Males 0 1998 1997 0.00000 2																											0.08333 DM
12	Males 0 1998 1997 0.08333 2																											0.10627 DM
13	Males 0 1998 1997 0.25000 2																											0.04141 DM
14	Males 0 1998 1997 0.50000 2																											0.25000 DM
15	Males 0 1998 1997 0.75000 2																											0.23357 DM
16	Males 0 1998 1998 0.00000 1																											0.01574 DM
17	Males 0 1998 1998 0.00000 2																											0.08333 DM
18	Males 0 1998 1998 0.08333 2																											0.16667 DM
19	Males 0 1998 1998 0.25000 2																											0.25000 DM
20	Males 0 1998 1998 0.50000 2																											0.25000 DM

13:55 Thursday, March 31, 2011 7

The CONTENTS Procedure

```

Data Set Name       WORK.INSCA             Observations      456261
Member Type        DATA                 Variables         37
Engine             V9                       Indexes           0
Created            31 Mar 2011 Thu 14:01:12 o'clock Observation Length 296
Last Modified      31 Mar 2011 Thu 14:01:12 o'clock Deleted Observations 0
Protection                                                Compressed        NO
Data Set Type                                            Sorted           NO
Label
Data Representation WINDOWS_32
Encoding           wlatin1  Western (Windows)

```

Engine/Host Dependent Information

```

Data Set Page Size      16384
Number of Data Set Pages 8296
First Data Page         1
Max Obs per Page       55
Obs in First Data Page 39
Number of Data Set Repairs 0
Filename                C:\DOCUME~1\bx\LOCALS~1\Temp\SAS Temporary Files\_TD1532\insca.sas7bdat
Release Created         9.0202MO
Host Created            XP_PRO

```

Alphabetic List of Variables and Attributes

#	Variable	Type	Len	Format	Label
2	A	Num	8		Left endpoint of interval (transformed scale)
4	C	Num	8		
9	DO	Num	8		
18	D21	Num	8		
29	D22	Num	8		
24	D26	Num	8		
17	D28	Num	8		
15	D33	Num	8		
13	D51	Num	8		
31	D70	Num	8		
33	D82	Num	8		
34	D83	Num	8		
35	D84	Num	8		
28	D91	Num	8		
11	D92	Num	8		
19	D101	Num	8		
27	D103	Num	8		
14	D113	Num	8		
26	D121	Num	8		
10	D131	Num	8		
22	D132	Num	8		
21	D133	Num	8		

28	D70	Num	8	Breast
32	D82	Num	8	Cervix
31	D83	Num	8	Uterus
30	D84	Num	8	Ovary
13	D91	Num	8	Prostate
10	D92	Num	8	Testis
7	D101	Num	8	Kidney
16	D103	Num	8	Bladder
8	D113	Num	8	Brain
20	D121	Num	8	Thyroid
15	D131	Num	8	Hodgkin's lymphoma
14	D132	Num	8	Non-Hodgkin lymphoma
27	D133	Num	8	Multiple myeloma
11	D139	Num	8	Leukaemia
21	D241	Num	8	Ascending colon
19	D242	Num	8	Transverse colon
24	D243	Num	8	Descending colon
29	D249	Num	8	Other colon
23	D251	Num	8	Rectum
41	D259	Num	8	Colorectal
9	D999	Num	8	Other
35	DMdur	Num	8	Time since DoDM (inclusion)
34	DMtype	Num	8	DM type
36	Insdur	Num	8	Time since DoI (1st insulin)
3	P	Num	8	Pgr
38	Px	Num	8	Per
5	Y	Num	8	Person-years
1	sex	Num	8	SEX.
33	state	Char	6	State

Dataset with duration variables (only doDM > 31.12.1994)

13:55 Thursday, March 31, 2011 10

		All malignant neoplasms								
		Person-years	No. cells	Colorectal	Lung	Breast	Prostate	Other		
All		77,183,679.2	551,280	369,984	47,497	48,917	54,925	34,377	48,785	
State	DM type									
Well	0	75,637,670.4	6,000	346,138	44,079	45,585	52,488	31,713	45,606	
DM	2	1,305,668.9	117,114	21,050	3,098	2,933	2,185	2,437	2,804	
	1	823.4	6,456	2	0	0	0	0	0	
DM/Ins	2	195,089.4	366,155	2,767	318	398	249	226	372	
	1	44,427.0	55,555	27	2	1	3	1	3	
State	DM type	Pgr								
Well	0	1995	4,997,400.3	400	21,127	2,748	2,933	2,974	1,192	3,074
		1996	5,017,439.1	400	21,264	2,742	2,847	3,140	1,322	3,102
		1997	5,028,556.3	400	21,549	2,884	2,981	3,110	1,376	3,031
		1998	5,036,218.0	400	22,042	2,896	2,872	3,244	1,508	3,176
		1999	5,041,088.8	400	22,244	2,818	3,000	3,283	1,580	3,128
		2000	5,045,750.8	400	22,197	2,828	3,015	3,337	1,640	3,004
		2001	5,051,178.6	400	22,283	2,929	3,042	3,424	1,714	2,906
		2002	5,052,995.1	400	22,800	2,908	3,129	3,639	1,906	2,975
		2003	5,050,427.1	400	22,963	2,928	2,967	3,505	2,077	2,936
		2004	5,047,109.5	400	23,339	2,998	3,110	3,411	2,381	3,054
		2005	5,043,837.3	400	23,936	3,051	3,136	3,462	2,728	3,062
		2006	5,043,879.0	400	24,590	3,213	3,137	3,527	2,847	3,100
		2007	5,049,649.2	400	24,703	2,986	3,263	3,545	3,064	3,029
		2008	5,061,199.4	400	25,235	3,107	3,115	4,073	3,246	3,069
		2009	5,070,942.0	400	25,866	3,043	3,038	4,814	3,132	2,960
DM	2	1995	6,428.0	2,365	141	19	23	7	8	14
		1996	18,019.1	4,286	288	38	34	33	27	47
		1997	29,262.1	5,040	469	69	62	38	36	77
		1998	40,254.0	5,894	609	89	57	55	60	98
		1999	51,778.4	6,798	790	122	102	79	63	122
		2000	62,924.8	7,532	999	140	149	93	93	160
		2001	74,310.6	8,075	1,167	168	172	137	113	147
		2002	86,249.1	8,590	1,328	195	172	123	128	208
		2003	99,405.6	8,906	1,370	212	184	141	136	180
		2004	112,366.8	9,511	1,797	272	263	170	207	241
		2005	123,715.7	9,531	2,045	292	258	181	273	274
		2006	133,648.5	9,869	2,206	343	330	226	257	305
		2007	144,034.3	10,070	2,329	353	359	218	341	253
		2008	156,027.2	10,267	2,633	390	348	306	330	332
		2009	167,244.8	10,380	2,879	396	420	378	365	346
	1	1995	36.9	260	0	0	0	0	0	0
		1996	49.8	425	0	0	0	0	0	0
		1997	52.8	429	0	0	0	0	0	0
		1998	54.4	436	0	0	0	0	0	0
		1999	53.5	441	0	0	0	0	0	0
		2000	53.9	441	0	0	0	0	0	0
		2001	54.4	436	0	0	0	0	0	0
		2002	55.0	452	0	0	0	0	0	0
		2003	53.8	441	1	0	0	0	0	0
		2004	56.7	429	0	0	0	0	0	0
		2005	54.2	442	0	0	0	0	0	0
		2006	61.8	456	1	0	0	0	0	0
		2007	58.1	440	0	0	0	0	0	0
		2008	63.9	460	0	0	0	0	0	0
		2009	64.3	468	0	0	0	0	0	0

DM/Ins	2	1995	339.2	1,378	5	1	1	0	0	1
		1996	1,471.0	5,383	12	1	0	1	1	2
		1997	2,646.2	9,489	25	3	5	0	1	3
		1998	3,862.6	12,525	43	6	7	4	3	9
		1999	5,305.8	16,550	68	5	7	5	4	14
		2000	6,971.2	20,369	84	8	13	11	3	15
		2001	8,843.6	23,538	109	12	17	8	10	15
		2002	10,971.5	27,267	128	14	20	10	7	17
		2003	13,277.9	28,794	161	18	29	14	11	22
		2004	16,169.3	32,185	242	27	34	22	20	25
		2005	19,119.4	33,560	279	32	37	27	25	43
		2006	22,145.6	36,424	316	39	39	24	29	41
		2007	25,238.5	37,677	407	53	60	30	38	51
		2008	28,027.3	40,159	423	47	60	43	32	65
		2009	30,700.4	40,857	465	52	69	50	42	49
	1	1995	142.9	466	0	0	0	0	0	0
		1996	511.1	1,350	0	0	0	0	0	0
		1997	917.7	2,145	0	0	0	0	0	0
		1998	1,331.8	2,755	0	0	0	0	0	0
		1999	1,743.6	3,312	0	0	0	0	0	0
		2000	2,150.4	3,736	1	0	0	0	0	0
		2001	2,562.5	4,021	2	0	0	0	0	0
		2002	2,958.7	4,268	2	0	0	1	0	0
		2003	3,348.7	4,362	2	0	0	0	0	0
		2004	3,749.5	4,519	0	0	0	0	0	0
		2005	4,141.5	4,604	1	0	0	0	0	0
		2006	4,581.7	4,806	3	0	1	0	0	2
		2007	4,982.1	4,914	4	0	0	1	0	0
		2008	5,437.1	5,104	4	0	0	1	0	1
		2009	5,867.7	5,193	8	2	0	0	1	0

Dataset with duration variables (only doDM > 31.12.1994)

13:55 Thursday, March 31, 2011 11

State				
	All	Well	DM	DM/Ins
Person-years	77,183,679	75,637,670	1,306,492	239,516
All malignant neoplasms				
Other	369,984	346,138	21,052	2,794
Oesophagus	48,785	45,606	2,804	375
Stomach	4,931	4,586	307	38
Ascending colon	6,964	6,460	445	59
Transverse colon	9,551	8,762	724	65
Descending colon	4,361	3,991	326	44
Other colon	14,886	13,893	900	93
Rectum	2,561	2,343	201	17
Colorectal	16,138	15,090	947	101
Liver	47,497	44,079	3,098	320
Pancreas	3,418	2,879	420	119
Lung	9,917	8,466	1,122	329
Melanoma	48,917	45,585	2,933	399
Breast	16,479	15,881	530	68
Cervix	54,925	52,488	2,185	252
Uterus	5,848	5,691	132	25
Ovary	8,691	8,057	571	63
Prostate	7,751	7,400	314	37
Testis	34,377	31,713	2,437	227
Kidney	4,301	4,257	37	7
Bladder	7,017	6,410	512	95
Brain	21,204	19,687	1,373	144
Thyroid	9,677	9,232	388	57
Hodgkin's lymphoma	2,188	2,104	66	18
Non-Hodgkin lymphoma	1,784	1,713	61	10
Multiple myeloma	10,653	10,036	551	66
Leukaemia	4,630	4,335	269	26
	10,030	9,473	497	60

Dataset without duration variables

13:55 Thursday, March 31, 2011 12

The CONTENTS Procedure

Data Set Name	DATA.DMCAA	Observations	32568
Member Type	DATA	Variables	39
Engine	V9	Indexes	0
Created	31 Mar 2011 Thu 14:01:52 o'clock	Observation Length	312
Last Modified	31 Mar 2011 Thu 14:01:52 o'clock	Deleted Observations	0
Protection		Compressed	NO
Data Set Type		Sorted	NO
Label			
Data Representation	WINDOWS_32		

Encoding wlatin1 Western (Windows)

Engine/Host Dependent Information

Data Set Page Size 16384
 Number of Data Set Pages 627
 First Data Page 1
 Max Obs per Page 52
 Obs in First Data Page 36
 Number of Data Set Repairs 0
 Filename C:\Bendix\Steno\DM-register\NDR\projects\Cancer\data\dmcaa.sas7bdat
 Release Created 9.0202MO
 Host Created XP_PRO

Alphabetic List of Variables and Attributes

#	Variable	Type	Len	Format	Label
2	A	Num	8		Agr
35	Ax	Num	8		Age
4	C	Num	8		Cgr
37	Cx	Num	8		Coh
6	D0	Num	8		All malignant neoplasms
25	D21	Num	8		Oesophagus
22	D22	Num	8		Stomach
38	D24	Num	8		Colon
12	D26	Num	8		Liver
26	D28	Num	8		Pancreas
17	D33	Num	8		Lung
18	D51	Num	8		Melanoma
28	D70	Num	8		Breast
32	D82	Num	8		Cervix
31	D83	Num	8		Uterus
30	D84	Num	8		Ovary
13	D91	Num	8		Prostate
10	D92	Num	8		Testis
7	D101	Num	8		Kidney
16	D103	Num	8		Bladder
8	D113	Num	8		Brain
20	D121	Num	8		Thyroid
15	D131	Num	8		Hodgkin's lymphoma
14	D132	Num	8		Non-Hodgkin lymphoma
27	D133	Num	8		Multiple myeloma
11	D139	Num	8		Leukaemia
21	D241	Num	8		Ascending colon
19	D242	Num	8		Transverse colon
24	D243	Num	8		Descending colon
29	D249	Num	8		Other colon
23	D251	Num	8		Rectum
39	D259	Num	8		Colorectal
9	D999	Num	8		Other
34	DMtype	Num	8		DM type
3	P	Num	8		Pgr
36	Px	Num	8		Per
5	Y	Num	8		Person-years
1	sex	Num	8	SEX.	Sex
33	state	Char	6		State

Dataset without duration variables

13:55 Thursday, March 31, 2011 13

		Person-years	No. cells	All malignant neoplasms	Colorectal	Lung	Breast	Prostate	Other	
All		78,046,684.3	32,568	381,371	49,248	50,301	56,201	35,410	50,488	
State	DM type									
Well	0	75,637,670.4	6,000	346,138	44,079	45,585	52,488	31,713	45,606	
DM	0	425,407.0	5,215	6,937	1,130	796	780	674	1,045	
	2	1,302,136.6	5,948	20,870	3,085	2,895	2,176	2,425	2,780	
	1	300.3	1,867	2	0	0	0	0	0	
DM/Ins	0	437,598.1	5,426	4,450	621	588	496	359	658	
	2	198,621.7	5,666	2,947	331	436	258	238	396	
	1	44,950.1	2,446	27	2	1	3	1	3	
State	DM type	Pgr								
Well	0	1995	4,997,400.3	400	21,127	2,748	2,933	2,974	1,192	3,074
		1996	5,017,439.1	400	21,264	2,742	2,847	3,140	1,322	3,102
		1997	5,028,556.3	400	21,549	2,884	2,981	3,110	1,376	3,031
		1998	5,036,218.0	400	22,042	2,896	2,872	3,244	1,508	3,176
		1999	5,041,088.8	400	22,244	2,818	3,000	3,283	1,580	3,128
		2000	5,045,750.8	400	22,197	2,828	3,015	3,337	1,640	3,004
		2001	5,051,178.6	400	22,283	2,929	3,042	3,424	1,714	2,906
		2002	5,052,995.1	400	22,800	2,908	3,129	3,639	1,906	2,975
		2003	5,050,427.1	400	22,963	2,928	2,967	3,505	2,077	2,936
		2004	5,047,109.5	400	23,339	2,998	3,110	3,411	2,381	3,054
		2005	5,043,837.3	400	23,936	3,051	3,136	3,462	2,728	3,062
		2006	5,043,879.0	400	24,590	3,213	3,137	3,527	2,847	3,100
		2007	5,049,649.2	400	24,703	2,986	3,263	3,545	3,064	3,029

		2008	5,061,199.4	400	25,235	3,107	3,115	4,073	3,246	3,069
		2009	5,070,942.0	400	25,866	3,043	3,038	4,814	3,132	2,960
DM	0	1995	59,424.4	396	899	132	104	94	85	142
		1996	52,372.8	392	797	134	97	102	66	135
		1997	46,530.7	381	752	130	91	91	62	106
		1998	41,527.9	365	643	90	66	68	50	109
		1999	36,566.0	357	642	117	74	68	71	77
		2000	32,143.7	352	537	85	79	62	59	85
		2001	28,275.1	347	510	82	51	58	52	80
		2002	24,901.0	344	382	62	53	44	39	50
		2003	21,750.9	340	351	54	44	31	32	59
		2004	18,859.4	336	340	62	37	39	36	58
		2005	16,439.8	332	256	41	20	22	33	34
		2006	14,314.4	328	280	49	33	40	26	37
		2007	12,468.0	322	204	36	14	24	24	26
		2008	10,994.9	315	190	28	19	19	26	28
		2009	8,838.2	308	154	28	14	18	13	19
	2	1995	6,353.0	390	138	19	23	5	8	14
		1996	17,910.9	393	282	38	34	33	27	46
		1997	29,156.3	395	465	69	62	38	36	76
		1998	40,126.8	396	607	89	57	55	60	98
		1999	51,627.9	398	785	122	100	79	63	120
		2000	62,746.2	400	991	139	148	93	92	160
		2001	74,107.1	399	1,156	167	170	135	112	146
		2002	86,021.0	398	1,322	194	171	123	128	205
		2003	99,126.1	398	1,358	212	180	141	136	179
		2004	112,042.9	396	1,782	270	259	170	206	236
		2005	123,383.1	395	2,032	291	255	180	272	273
		2006	133,304.8	396	2,183	342	323	226	254	303
		2007	143,663.2	398	2,304	350	354	216	340	250
		2008	155,680.4	398	2,613	389	347	305	328	330
		2009	166,886.8	398	2,852	394	412	377	363	344
	1	1995	10.3	82	0	0	0	0	0	0
		1996	16.2	128	0	0	0	0	0	0
		1997	17.8	126	0	0	0	0	0	0
		1998	19.3	125	0	0	0	0	0	0
		1999	18.9	132	0	0	0	0	0	0
		2000	19.5	123	0	0	0	0	0	0
		2001	20.6	125	0	0	0	0	0	0
		2002	21.4	128	0	0	0	0	0	0
		2003	21.4	125	1	0	0	0	0	0
		2004	21.5	127	0	0	0	0	0	0
		2005	20.2	128	0	0	0	0	0	0
		2006	24.2	131	1	0	0	0	0	0
		2007	22.5	125	0	0	0	0	0	0
		2008	23.8	131	0	0	0	0	0	0
		2009	22.8	131	0	0	0	0	0	0
DM/Ins	0	1995	28,787.2	375	256	39	37	23	7	43
		1996	29,825.2	383	272	44	36	31	15	35
		1997	30,385.0	378	232	36	21	31	13	39
		1998	30,580.6	377	295	34	43	29	26	49
		1999	30,867.6	373	298	39	46	41	18	38
		2000	31,034.5	371	316	36	42	38	29	45
		2001	30,972.5	367	302	49	41	34	14	52
		2002	30,689.6	365	290	45	39	34	27	48
		2003	30,326.4	358	300	33	45	31	20	44
		2004	30,046.4	355	343	42	52	38	29	49
		2005	29,548.3	351	283	37	37	30	28	40
		2006	28,866.3	347	338	63	41	27	31	43
		2007	27,992.5	346	336	57	35	41	34	51
		2008	26,629.0	342	323	38	38	26	44	47
		2009	21,047.0	338	266	29	35	42	24	35
	2	1995	414.2	266	8	1	1	2	0	1
		1996	1,579.2	365	18	1	0	1	1	3
		1997	2,751.9	374	29	3	5	0	1	4
		1998	3,989.8	380	45	6	7	4	3	9
		1999	5,456.2	387	73	5	9	5	4	16
		2000	7,149.9	386	92	9	14	11	4	15
		2001	9,047.1	386	120	13	19	10	11	16

(Continued)

Dataset without duration variables

13:55 Thursday, March 31, 2011 14

State	DM type	Pgr	Person-years	No. cells	All malignant neoplasms					
					Colorectal	Lung	Breast	Prostate	Other	
DM/Ins	2	2002	11,199.5	389	134	15	21	10	7	20
		2003	13,557.4	392	173	18	33	14	11	23
		2004	16,493.2	395	257	29	38	22	21	30
		2005	19,452.1	391	292	33	40	28	26	44
		2006	22,489.3	387	339	40	46	24	32	43
		2007	25,609.6	386	432	56	65	32	39	54
		2008	28,374.1	391	443	48	61	44	34	67
		2009	31,058.4	391	492	54	77	51	44	51
	1	1995	169.6	86	0	0	0	0	0	0

1996	544.7	137	0	0	0	0	0	0	0
1997	952.7	148	0	0	0	0	0	0	0
1998	1,366.8	150	0	0	0	0	0	0	0
1999	1,778.1	154	0	0	0	0	0	0	0
2000	2,184.8	159	1	0	0	0	0	0	0
2001	2,596.3	163	2	0	0	0	0	0	0
2002	2,992.3	166	2	0	0	1	0	0	0
2003	3,381.1	170	2	0	0	0	0	0	0
2004	3,784.6	176	0	0	0	0	0	0	0
2005	4,175.6	179	1	0	0	0	0	0	0
2006	4,619.3	184	3	0	1	0	0	0	2
2007	5,017.7	187	4	0	0	1	0	0	0
2008	5,477.2	192	4	0	0	1	0	1	1
2009	5,909.2	195	8	2	0	0	1	0	0

Dataset without duration variables

13:55 Thursday, March 31, 2011 15

	State			
	All	Well	DM	DM/Ins
Person-years	78,046,684	75,637,670	1,727,844	681,170
All				
malignant				
neoplasms	381,371	346,138	27,809	7,424
Other	50,488	45,606	3,825	1,057
Oesophagus	5,105	4,586	407	112
Stomach	7,244	6,460	619	165
Ascending				
colon	9,933	8,762	972	199
Transverse				
colon	4,535	3,991	437	107
Descending				
colon	15,452	13,893	1,260	299
Other colon	2,665	2,343	265	57
Rectum	16,663	15,090	1,281	292
Colorectal	49,248	44,079	4,215	954
Liver	3,755	2,879	631	245
Pancreas	10,371	8,466	1,309	596
Lung	50,301	45,585	3,691	1,025
Melanoma	16,774	15,881	702	191
Breast	56,201	52,488	2,956	757
Cervix	5,939	5,691	181	67
Uterus	9,065	8,057	792	216
Ovary	7,923	7,400	421	102
Prostate	35,410	31,713	3,099	598
Testis	4,326	4,257	42	27
Kidney	7,306	6,410	686	210
Bladder	21,936	19,687	1,825	424
Brain	9,871	9,232	481	158
Thyroid	2,224	2,104	88	32
Hodgkin's				
lymphoma	1,806	1,713	72	21
Non-Hodgkin				
lymphoma	10,963	10,036	734	193
Multiple				
myeloma	4,773	4,335	349	89
Leukaemia	10,342	9,473	684	185

1.2 Acquiring mortality information: DMmort

1 "Program: DMmort.sas" 21:40 Monday, March 21, 2011

NOTE: Copyright (c) 2002-2008 by SAS Institute Inc., Cary, NC, USA.
 NOTE: SAS (r) Proprietary Software 9.2 (TS2M0)
 Licensed to NNIT -BASIC PACKAGE AND ADDITIONAL PACKAGE, Site 50800704.
 NOTE: This session is executing on the XP_PRO platform.
 NOTE: SAS initialization used:
 real time 2.42 seconds
 cpu time 0.49 seconds

NOTE: AUTOEXEC processing beginning; file is c:\stat\sas\autoexec.sas.

C:\Bendix\Steno\DM-register\NDR\projects\Cancer\sas\DMmort.sas

NOTE: Libref HER was successfully assigned as follows:
 Engine: V9
 Physical Name: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\sas
 NOTE: Libref DATA was successfully assigned as follows:
 Engine: V9
 Physical Name: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\data

NOTE: AUTOEXEC processing completed.

```

1      libname demodb "C:\Bendix\Demodb\data" ;
NOTE: Directory for library DEMODB contains files of mixed engine types.
NOTE: Libref DEMODB was successfully assigned as follows:
      Engine:          V9
      Physical Name: C:\Bendix\Demodb\data
1      !
2      libname data    "..\data"              ; * The total no deaths in the population ;
NOTE: Libref DATA was successfully assigned as follows:
      Engine:          V9
      Physical Name: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\data
2      !
3
4
5      *****
6      NOTE: This program enumerates deaths among diabetes patients
7      in order to provide the data background for a mortality
8      analysis which is necessary for calculation of cumulative
9      risks.
10     ***** ;
11     * The date from which we trust the inclusion date to be the first ;
12     %let validdate = '01JAN1995'd ;
13     * Set the entry and exit dates for the entire follow-up endeavour ;
14     %let truncdate = '01JAN1995'd ;
15     %let censdate = '31DEC2009'd ;
16     * Set the breaks for the tabulation of deaths by duration ;
17     %let durbreaks = %str(0 to 2 by 0.25, 2.5 to 5 by 0.5, 6, 7 to 19 by 2) ;
18
19     * Define the ranges for period-tabulation ;
20     data _null_ ;
21     call symput( 'Plo'   , year( &truncdate. ) - 1 ) ; * Last year before FU ;
22     call symput( 'Phi'   , year( &censdate. ) + 1 ) ; * First year after FU ;
23     call symput( 'Pfirst', year( &truncdate. ) - 1900 ) ; * 1st tab break ;
24     call symput( 'Plast' , year( &censdate. ) - 1900 + 1 ) ; * last tab break ;
25     run ;

NOTE: Numeric values have been converted to character values at the places given by: (Line):(Column).
21:45 22:45 23:45 24:52
NOTE: DATA statement used (Total process time):
      real time          0.04 seconds
      cpu time           0.00 seconds

26
27     proc format ;
28     value sex
29         1="Males"
30         2="Females" ;
NOTE: Format SEX has been output.
31     run ;

NOTE: PROCEDURE FORMAT used (Total process time):
      real time          0.10 seconds
      cpu time           0.03 seconds

32
33     *-----;
34     * Preprocessing of the cancer register to first primary tumours ;
35
36     * First take the cancer registry, remove all non-first primary cancers ;
37     data cancer ;
38     set data.cancer ;
39     * Diagnoses not counted as cancer and non-Mel skin cancer excluded ;
40     if ( diag in (52,150) ) then delete ;
41     run ;

NOTE: There were 1748815 observations read from the data set DATA.CANCER.
NOTE: The data set WORK.CANCER has 1286419 observations and 31 variables.
NOTE: DATA statement used (Total process time):
      real time          14.50 seconds
      cpu time           1.23 seconds

42
43     * Sort by id and tumornumber ;
44     proc sort data = cancer ;
45     by id d_diagnosedato ;
46     run ;

NOTE: There were 1286419 observations read from the data set WORK.CANCER.
NOTE: The data set WORK.CANCER has 1286419 observations and 31 variables.
NOTE: PROCEDURE SORT used (Total process time):
      real time          13.17 seconds
      cpu time           2.73 seconds

```

```

47
48     * Select only the first real tumor ;
49     data cancer ;
50     set cancer ;
51     by id ;
52     if first.id ;
53     run ;

```

NOTE: There were 1286419 observations read from the data set WORK.CANCER.
NOTE: The data set WORK.CANCER has 1195147 observations and 31 variables.
NOTE: DATA statement used (Total process time):
real time 4.64 seconds
cpu time 1.07 seconds

```

54
55     * Then merge with the diabetes register ;
56     data candi;
57     merge cancer
58         data.diabetes ;
59     by id ;
60     keep sex diag diaggrp DMtype
61         doBT doDM doI doCA doX doDD ;
62     format sex sex.
63         doBT doDM doI doCA doX doDD ddmmyy10. ;
64     * Demographic dates collected from CRG and NDR ;
65     doBT = min( D_foddto , D_fdsdato ) ;
66     doDD = min( D_statdato, D_dodsdto ) ;
67     doX = min( D_statdato, D_dodsdto, &censdate. ) ;
68     * Event-dates ;
69     doDM = D_inkldto ;
70     doI = D_ins ;
71     doCA = D_diagnosedato ;
72     * Characteristics for diabetes patients --- missing if no DM ;
73     * If DM-duration can be trusted (and DMtype defined) then 2 ;
74     DMtype = ( doDM ge &valldate. ) * 2 + doDM - doDM ;
75     * Change to a value 1 for those considered to be T1D ;
76     if ( DMtype > 0 and
77         (doDM-doBT) < 35*365.25 and
78         doI > .z and
79         (doI-doDM) < 90 ) then DMtype = 1 ;
80     run ;

```

NOTE: Missing values were generated as a result of performing an operation on missing values.
Each place is given by: (Number of times) at (Line):(Column).
449181 at 66:10 1119643 at 74:40

NOTE: There were 1195147 observations read from the data set WORK.CANCER.
NOTE: There were 437593 observations read from the data set DATA.DIABETES.
NOTE: The data set WORK.CANDI has 1557236 observations and 10 variables.
NOTE: DATA statement used (Total process time):
real time 8.82 seconds
cpu time 1.46 seconds

```

81
82     *****
83     NOTE: The dataset candi now has a record for each person who has
84         either a first primary cancer diagnosis or a diabetes diagnosis
85
86         We will then need to select the deaths by the state in which it
87         occurs, that is Cancer, DM or DM/ins. The sum of these
88         must be subtracted from the total poulation deaths to get the
89         deaths in the non-cancer, non-DM population. Only the deaths
90         from the states DM and DM/ins will be subject to analysis
91         and included in the dataset along with the cancer incidence
92         data, deaths in the cancer state will not be counted, regardless
93         of wheter DM has occurred previously or not
94     *****
95
96     data dead ;
97     set candi ( where = ( doDD ge &valldate. and
98                         doDD le &censdate. and
99                         doDD ge doDM and
100                        doDD ge doCA ) ) ;
101     length state $ 10 ;
102     state = "Well" ; * Hopefully no one will be left in this state ;
103     if ( doDM gt .z and
104         doDM lt doDD and
105         doCA le .z )
106     then if ( doI gt .z )
107         then state = "DM/Ins" ;
108         else state = "DM" ;
109     if ( doCA gt .z )
110     then state = "Cancer" ;
111     * Note that the state Cancer here is ANY of the three cancer states,
112     including those subsequent to diabetes diagnosis. The deaths
113     occurring here are not going to be analysed in the round ;
114     * Compute timescales and birth cohort ;
115     A = floor( ( doDD - doBT ) / 365.25 ) ;

```

```

116     P = year( doDD ) ;
117     C = year( doBT ) ;
118     * Duration in prespecified intervals ;
119     do br = &durbreaks. ;
120         if (doDD-doDM)/365.25 > br then DMdur = br ;
121         if (doDD-doI)/365.25 > br then Insdur = br ;
122     end ;
123     * Restrict to the relevant age range
124     (population deaths are coded 99 for 99+ ages) ;
125     if A < 99 ;
126     run ;

```

NOTE: Missing values were generated as a result of performing an operation on missing values.
Each place is given by: (Number of times) at (Line):(Column).

5985198 at 120:15 5985198 at 120:21 8250238 at 121:15 8250238 at 121:21

NOTE: There were 396406 observations read from the data set WORK.CANDI.
WHERE (doDD>='01JAN1995'D and doDD<='31DEC2009'D) and (doDD>=doCA);

NOTE: The data set WORK.DEAD has 395024 observations and 17 variables.

NOTE: DATA statement used (Total process time):

real time 8.10 seconds
cpu time 2.31 seconds

```

127
128     title "All deaths in the union of the Cancer register and the Diabetes register" ;
129     proc tabulate data = dead noseps missing formchar = " " ;
130         class A P DMdur Insdur state DMtype ;
131         table all P DMdur Insdur,
132             all * f=comma8.
133             state * DMtype * f=comma7.
134             / rts=8 ;
135         table all A="Age",
136             P * f=comma6.
137             / rts = 5 ;
138         keylabel n = ' ' ;
139     run ;

```

NOTE: There were 395024 observations read from the data set WORK.DEAD.

NOTE: The PROCEDURE TABULATE printed pages 1-3.

NOTE: PROCEDURE TABULATE used (Total process time):

real time 0.98 seconds
cpu time 0.67 seconds

```

140
141     * Collapse deaths over the duration variables ;
142     proc summary data = dead nway ;
143         class sex A P ;
144         output out = tdead ( keep = sex A P _freq_
145                             rename = ( _freq_ = DD ) ) ;
146     run ;

```

NOTE: There were 395024 observations read from the data set WORK.DEAD.

NOTE: The data set WORK.TDEAD has 2774 observations and 4 variables.

NOTE: PROCEDURE SUMMARY used (Total process time):

real time 0.23 seconds
cpu time 0.25 seconds

```

147
148     * Get the population mortality data (i.e. deaths), restrict to the relevant period ;
149     data mort ;
150     set demodb.mdk1974ff ( rename = ( agr = A
151                                     per = P
152                                     D = DAll ) ) ;
153     if ( &Plo. < P < &Phi. and
154         -0.1 < A < 99 ) ;
155     run ;

```

NOTE: There were 7200 observations read from the data set DEMODB.MDK1974FF.

NOTE: The data set WORK.MORT has 2970 observations and 6 variables.

NOTE: DATA statement used (Total process time):

real time 0.03 seconds
cpu time 0.00 seconds

```

156
157     proc sort data = mort ;
158         by sex A P ;
159     run ;

```

NOTE: There were 2970 observations read from the data set WORK.MORT.

NOTE: The data set WORK.MORT has 2970 observations and 6 variables.

NOTE: PROCEDURE SORT used (Total process time):

real time 0.03 seconds
cpu time 0.03 seconds

160

```

161     title "Deaths in the total Danish population" ;
162     proc tabulate data = mort noseps missing formchar="          " ;
163         var Dall ;
164         class sex A P ;
165         table all A="Age",
166             P * Dall=" " * f=comma6.
167             / rts = 5 ;
168         keylabel sum = ' ' ;
169     run ;

```

NOTE: There were 2970 observations read from the data set WORK.MORT.

NOTE: The PROCEDURE TABULATE printed pages 4-5.

NOTE: PROCEDURE TABULATE used (Total process time):

```

real time      0.04 seconds
cpu time       0.04 seconds

```

```

170
171     * Merge the population deaths with the deaths among DM and cancer patients,
172     in order to subtract the latter from the former to get the deaths from state Well ;
173
174     data mortwell ;
175         merge mort tdead ;
176         by sex A P ;
177         keep state sex A P DD ;
178         length state $ 10 ;
179         if DD le .z then DD = 0 ;
180         state = "Well" ;
181         DD = DALL - DD ;
182     run ;

```

NOTE: There were 2970 observations read from the data set WORK.MORT.

NOTE: There were 2774 observations read from the data set WORK.TDEAD.

NOTE: The data set WORK.MORTWELL has 2970 observations and 5 variables.

NOTE: DATA statement used (Total process time):

```

real time      0.01 seconds
cpu time       0.01 seconds

```

```

183
184     title "Dead in state Well" ;
185     proc tabulate data = mortwell noseps missing formchar="          " ;
186         var DD ;
187         class sex A P ;
188         table all A="Age",
189             all * DD=" " * f=comma7.
190             P * DD=" " * f=comma6.
191             / rts = 5 ;
192         keylabel sum = ' ' ;
193     run ;

```

NOTE: There were 2970 observations read from the data set WORK.MORTWELL.

NOTE: The PROCEDURE TABULATE printed pages 6-7.

NOTE: PROCEDURE TABULATE used (Total process time):

```

real time      0.04 seconds
cpu time       0.04 seconds

```

```

194
195     title "Deaths among all non-cancer DM-patients" ;
196     proc summary data = dead nway missing ;
197         where substr(state,1,2) eq "DM" ;
198         class DMtype sex A P DMdur Insdur state ;
199         output out = tdeadd ( keep = DMtype state sex A P DMdur Insdur _freq_
200                             rename = ( _freq_ = DD ) ) ;
201     run ;

```

NOTE: There were 93422 observations read from the data set WORK.DEAD.

WHERE SUBSTR(state, 1, 2)='DM';

NOTE: The data set WORK.TDEADD has 42590 observations and 8 variables.

NOTE: PROCEDURE SUMMARY used (Total process time):

```

real time      0.34 seconds
cpu time       0.39 seconds

```

```

202
203     proc tabulate data = tdeadd noseps formchar="          " missing ;
204         class DMtype state sex A P DMdur Insdur ;
205         var DD ;
206         table all DMdur Insdur,
207             state * DMtype * DD=" " * f=comma7.
208             / rts=8 ;
209         keylabel sum = ' ' ;
210     run ;

```

NOTE: There were 42590 observations read from the data set WORK.TDEADD.

NOTE: The PROCEDURE TABULATE printed page 8.

NOTE: PROCEDURE TABULATE used (Total process time):

```

real time      0.07 seconds

```



```

cpu time          0.12 seconds

211
212 ***** ;
213 * Stack data and clean out the two inaccurate negative death counts ;
214 data data.DMmortD ;
215     set mortwell
216     tdeadd ;
217     DD = max( DD, 0 ) ;
218 run ;

NOTE: There were 2970 observations read from the data set WORK.MORTWELL.
NOTE: There were 42590 observations read from the data set WORK.TDEADD.
NOTE: The data set DATA.DMMORTD has 45560 observations and 8 variables.
NOTE: DATA statement used (Total process time):
      real time          0.15 seconds
      cpu time           0.01 seconds

219
220 proc tabulate data = data.DMmortD missing noseps formchar="          " ;
221     class DMtype state sex A P DMdur Insdur ;
222     var DD ;
223     table all P DMdur Insdur,
224           ( all sex state*DMtype ) * DD=" " * f=comma7.
225           / rts=8 ;
226     keylabel sum = ' ' ;
227 run ;

NOTE: There were 45560 observations read from the data set DATA.DMMORTD.
NOTE: The PROCEDURE TABULATE printed page 9.
NOTE: PROCEDURE TABULATE used (Total process time):
      real time          0.07 seconds
      cpu time           0.12 seconds

228
229 proc contents data = data.DMmortD ;
230 run ;

NOTE: PROCEDURE CONTENTS used (Total process time):
      real time          0.54 seconds
      cpu time           0.00 seconds

NOTE: The PROCEDURE CONTENTS printed page 10.

231
232 * Finally export the relevant data for analysis in XPT format ;
233 libname xptD xport './data/DMmortD.xpt';
NOTE: Libref XPTD was successfully assigned as follows:
Engine:          XPORT
Physical Name: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\data\DMmortD.xpt
234 proc copy in=data out=xptD memtype=data; select DMmortD ; run;

NOTE: Copying DATA.DMMORTD to XPTD.DMMORTD (memtype=DATA).
NOTE: There were 45560 observations read from the data set DATA.DMMORTD.
NOTE: The data set XPTD.DMMORTD has 45560 observations and 8 variables.
NOTE: PROCEDURE COPY used (Total process time):
      real time          0.20 seconds
      cpu time           0.03 seconds

NOTE: SAS Institute Inc., SAS Campus Drive, Cary, NC USA 27513-2414
NOTE: The SAS System used:
      real time          55.46 seconds
      cpu time           11.24 seconds

```

All deaths in the union of the Cancer register and the Diabetes register 21:40 Monday, March 21, 2011 1

	state											
	Cancer			DM			DM/Ins			Well		
	All	.	0	1	2	0	2	0	1	2	2	
All	395,024	259,392	15,132	12	26,953	25,513	41,681	18,754	104	7,370	113	
P												
1995	25,444	18,062	1,619	1	206	3,753	432	1,337	1	26	7	
1996	24,791	17,604	1,385	.	468	3,120	845	1,303	1	58	7	
1997	25,097	17,750	1,334	1	660	2,753	1,180	1,337	.	73	9	
1998	24,816	17,349	1,231	.	830	2,352	1,594	1,313	3	137	7	
1999	25,648	17,568	1,240	1	1,108	2,231	1,968	1,317	2	200	13	
2000	25,884	17,599	1,103	.	1,343	1,903	2,297	1,345	6	277	11	
2001	26,039	17,532	1,009	2	1,568	1,649	2,643	1,290	2	337	7	
2002	26,564	17,454	941	1	1,827	1,508	3,003	1,378	7	436	9	

2003	26,847	17,306	972	.	2,062	1,253	3,341	1,330	9	565	9
2004	26,484	16,920	855	1	2,238	1,102	3,522	1,237	7	596	6
2005	26,653	16,676	794	.	2,471	977	3,807	1,159	13	749	7
2006	27,552	17,223	740	1	2,724	909	3,942	1,160	9	839	5
2007	27,620	17,007	677	.	2,966	732	4,143	1,135	10	942	8
2008	27,659	16,898	621	3	3,119	641	4,283	1,034	13	1,042	5
2009	27,926	16,444	611	1	3,363	630	4,681	1,079	21	1,093	3
DMdur											
.	259,532	259,392	.	.	27	113
0	7,103	.	11	.	2,955	23	3,957	1	4	152	.
0.25	4,022	.	33	1	1,773	76	1,994	10	2	133	.
0.5	3,468	.	40	.	1,397	102	1,743	9	4	173	.
0.75	3,222	.	79	2	1,160	149	1,670	23	4	135	.
1	3,090	.	99	.	1,033	230	1,544	33	1	150	.
1.25	2,848	.	107	.	962	208	1,391	28	1	151	.
1.5	2,792	.	109	1	860	297	1,345	43	4	133	.
1.75	2,803	.	132	1	823	288	1,377	35	3	144	.
2	5,401	.	272	1	1,541	627	2,506	122	3	329	.
2.5	5,203	.	285	.	1,404	710	2,357	153	1	293	.
3	5,300	.	354	1	1,272	803	2,350	214	2	304	.
3.5	5,233	.	412	1	1,193	912	2,152	255	3	305	.
4	5,408	.	495	1	1,127	1,138	1,937	370	5	335	.
4.5	5,897	.	609	.	1,058	1,423	1,927	528	5	347	.
5	11,574	.	1,341	.	1,941	2,899	3,360	1,350	10	673	.
6	9,961	.	1,214	1	1,535	2,475	2,698	1,414	6	618	.
7	16,636	.	2,361	.	2,431	4,075	3,745	2,805	18	1,201	.
9	12,664	.	2,080	2	1,482	3,135	2,235	2,764	16	950	.
11	9,408	.	1,784	.	747	2,451	1,085	2,704	11	626	.
13	6,432	.	1,499	.	232	1,786	308	2,388	1	218	.
15	4,122	.	1,049	.	.	1,134	.	1,939	.	.	.
17	2,357	.	608	.	.	511	.	1,238	.	.	.
19	548	.	159	.	.	61	.	328	.	.	.
Insdur											
.	357,418	259,392	8,937	.	21,766	25,513	41,681	9	.	7	113
0	3,186	.	395	.	1,264	.	.	716	4	807	.
0.25	1,725	.	214	1	619	.	.	448	2	441	.
0.5	1,484	.	200	.	430	.	.	461	5	388	.
0.75	1,459	.	232	2	328	.	.	551	4	342	.
1	1,317	.	180	.	239	.	.	587	1	310	.
1.25	1,175	.	187	.	165	.	.	528	1	294	.
1.5	1,200	.	177	1	166	.	.	576	4	276	.
1.75	1,147	.	170	1	158	.	.	541	2	275	.
2	2,151	.	335	1	260	.	.	993	3	559	.
2.5	1,962	.	295	.	246	.	.	973	2	446	.
3	1,791	.	290	1	174	.	.	924	1	401	.
3.5	1,678	.	263	1	151	.	.	876	3	384	.
4	1,601	.	265	1	145	.	.	848	6	336	.
4.5	1,467	.	233	.	146	.	.	776	5	307	.
5	2,554	.	411	1	180	.	.	1,442	9	511	.
6	2,165	.	433	.	156	.	.	1,194	6	376	.
7	3,607	.	630	.	215	.	.	2,238	19	505	.
9	2,488	.	489	2	97	.	.	1,620	15	265	.
11	1,807	.	404	.	34	.	.	1,239	11	119	.
13	1,290	.	318	.	14	.	.	936	1	21	.
15	352	.	74	278	.	.	.

All deaths in the union of the Cancer register and the Diabetes register

21:40 Monday, March 21, 2011 2

P

	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009
All	25,444	24,791	25,097	24,816	25,648	25,884	26,039	26,564	26,847	26,484	26,653	27,552	27,620	27,659	27,926
Age															
0	5	2	5	2	2	1	2	.	4	2	1	4	5	2	2
1	2	4	1	3	2	2	2	4	3	4	3	1	.	2	2
2	1	1	3	4	3	.	8	3	6	.	2	1	4	1	2
3	5	3	3	3	3	2	2	2	1	4	.	1	2	1	2
4	3	1	3	4	3	2	3	3	3	5	3	.	2	.	3
5	5	2	3	4	2	4	3	2	3	1	2	4	1	1	.
6	1	6	2	.	2	1	3	1	1	2	3	1	2	.	4
7	2	1	1	2	2	1	11	2	.	2	2	2	3	3	3
8	1	4	3	3	1	1	1	1	1	1	2	2	.	3	3
9	2	2	4	3	3	1	6	4	2	6	2
10	4	3	3	2	.	3	1	3	2	.	.	1	2	2	1
11	4	2	4	3	4	1	2	2	2	2	.	2	1	3	3
12	2	3	.	2	3	3	3	2	2	5	2	2	.	1	3
13	2	2	5	1	2	5	7	2	1	2	1	1	2	3	2
14	5	1	2	2	1	1	5	2	2	2	3	.	2	4	1
15	4	4	3	1	1	.	.	3	4	4	3	3	5	.	2
16	.	1	4	5	2	7	.	3	.	6	1	5	3	4	4
17	7	1	2	2	1	6	1	1	5	1	4	6	2	2	1
18	5	4	1	5	6	4	3	5	1	2	6	4	7	5	6
19	2	3	8	.	6	5	3	3	4	2	4	2	1	4	4
20	6	6	3	5	2	8	2	3	1	4	3	2	1	1	3
21	6	2	4	4	4	5	3	4	4	10	3	3	1	5	5
22	9	3	9	2	4	.	1	9	7	2	2	4	6	4	5
23	4	.	7	3	5	6	4	7	5	2	7	4	3	7	11

51	2,484	178	205	181	181	168	185	145	157	164	172	173	150	145	146	134
52	2,738	201	202	224	214	194	167	175	153	176	164	165	205	186	157	155
53	2,749	172	215	180	202	205	166	185	175	175	166	198	177	185	176	172
54	3,054	185	209	234	214	221	220	215	230	192	204	172	209	205	174	170
55	3,111	197	231	223	196	205	237	239	217	205	210	192	171	186	178	224
56	3,157	199	199	214	243	212	213	255	228	219	215	189	202	194	187	188
57	3,291	275	229	212	203	229	215	239	238	258	222	181	213	200	191	186
58	3,565	263	255	215	218	248	250	255	262	274	233	220	236	213	215	208
59	3,661	274	275	212	247	224	257	234	249	254	242	255	273	232	221	212
60	3,982	329	297	274	294	271	214	248	261	229	265	263	275	261	256	245
61	4,122	326	309	255	280	263	258	259	244	255	258	264	320	328	236	267
62	4,372	352	341	316	304	300	281	224	267	275	262	266	304	288	315	277
63	4,594	382	365	332	348	304	265	287	267	295	255	279	258	314	308	335
64	4,762	407	362	317	392	314	322	307	287	287	288	245	312	277	298	347
65	5,051	449	464	393	390	361	349	313	295	326	284	232	264	302	301	328
66	5,346	477	450	424	442	389	383	349	348	293	309	271	322	294	318	277
67	5,783	533	531	502	469	445	374	374	396	370	329	322	253	258	307	320
68	6,089	567	543	489	463	461	432	419	398	371	355	341	305	326	332	287
69	6,742	677	587	583	531	512	479	458	407	413	388	360	327	354	345	321
70	7,095	720	600	631	553	578	503	477	458	416	377	361	386	357	336	342
71	7,722	718	712	633	593	533	586	538	523	470	457	398	417	414	380	350
72	8,288	839	750	702	677	606	585	574	503	514	497	422	405	419	423	372
73	9,184	915	821	774	711	735	616	647	625	525	517	500	484	448	418	448
74	9,731	976	842	833	805	735	695	639	636	602	548	536	516	473	426	469
75	10,650	1,013	998	863	883	776	774	710	723	640	604	572	574	527	485	508
76	11,169	907	1,069	999	916	859	783	764	781	683	649	597	592	550	533	487
77	12,126	1,064	981	982	944	932	903	865	881	777	717	644	656	582	617	581
78	12,883	1,015	1,067	970	1,010	986	994	973	888	881	760	704	666	717	617	635
79	13,731	1,210	1,065	1,039	1,003	1,054	1,001	1,021	989	871	832	799	779	695	679	694
80	14,487	1,180	1,119	1,092	1,060	1,041	1,097	1,077	1,008	960	919	869	766	811	747	741
81	15,250	1,313	1,209	1,072	1,074	1,095	974	1,096	1,125	1,031	971	926	900	890	793	781
82	16,111	1,323	1,330	1,191	1,162	1,128	1,069	1,066	1,178	1,112	1,012	950	925	932	846	887
83	16,667	1,343	1,311	1,251	1,164	1,184	1,050	1,142	1,098	1,186	1,100	1,036	956	983	920	943
84	16,766	1,328	1,299	1,402	1,164	1,202	1,119	1,099	1,092	1,017	1,111	1,094	990	984	904	961
85	17,075	1,349	1,300	1,276	1,266	1,281	1,155	1,106	1,090	1,125	971	1,111	1,054	1,061	967	963
86	17,040	1,379	1,235	1,273	1,231	1,227	1,186	1,134	1,154	1,030	983	996	1,103	1,086	994	1,029
87	17,106	1,309	1,275	1,237	1,145	1,188	1,259	1,209	1,192	1,094	1,046	1,006	931	1,143	1,038	1,034
88	16,629	1,222	1,138	1,241	1,181	1,179	1,109	1,158	1,187	1,058	1,040	1,005	968	1,017	1,004	1,122
89	15,740	1,064	1,079	1,078	1,037	1,147	1,088	1,153	1,103	1,099	1,003	980	992	984	927	1,006

(Continued)
Dead in state Well

21:40 Monday, March 21, 2011 7

Age	Period															
	All	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009
90	14,853	977	1,033	966	986	1,065	967	1,073	1,099	1,099	980	970	869	896	952	921
91	13,538	938	918	899	900	899	910	954	917	974	900	870	881	866	878	834
92	12,164	839	725	754	776	801	761	877	926	861	844	817	825	810	795	753
93	10,237	648	632	644	636	652	676	714	715	712	696	744	683	700	677	708
94	8,938	577	588	527	538	579	525	599	644	601	606	608	643	592	662	649
95	7,086	436	411	440	410	494	446	479	472	464	470	518	490	534	511	511
96	5,614	315	333	350	318	351	363	353	387	360	411	424	398	398	421	432
97	4,177	250	232	269	221	272	279	268	289	279	273	300	325	276	319	325
98	3,050	179	175	166	160	194	203	197	218	206	207	207	205	227	250	256

Deaths among all non-cancer DM-patients

21:40 Monday, March 21, 2011 8

All DMdur	state				
	DM		DM/Ins		
	DMtype		DMtype		
	0	2	0	1	2
All	25,513	41,681	18,754	104	7,370
0	23	3,957	1	4	152
0.25	76	1,994	10	2	133
0.5	102	1,743	9	4	173
0.75	149	1,670	23	4	135
1	230	1,544	33	1	150
1.25	208	1,391	28	1	151
1.5	297	1,345	43	4	133
1.75	288	1,377	35	3	144
2	627	2,506	122	3	329
2.5	710	2,357	153	1	293
3	803	2,350	214	2	304
3.5	912	2,152	255	3	305
4	1,138	1,937	370	5	335
4.5	1,423	1,927	528	5	347
5	2,899	3,360	1,350	10	673
6	2,475	2,698	1,414	6	618

7	4,075	3,745	2,805	18	1,201
9	3,135	2,235	2,764	16	950
11	2,451	1,085	2,704	11	626
13	1,786	308	2,388	1	218
15	1,134	.	1,939	.	.
17	511	.	1,238	.	.
19	61	.	328	.	.
Insdur					
.	25,513	41,681	9	.	7
0	.	.	716	4	807
0.25	.	.	448	2	441
0.5	.	.	461	5	388
0.75	.	.	551	4	342
1	.	.	587	1	310
1.25	.	.	528	1	294
1.5	.	.	576	4	276
1.75	.	.	541	2	275
2	.	.	993	3	559
2.5	.	.	973	2	446
3	.	.	924	1	401
3.5	.	.	876	3	384
4	.	.	848	6	336
4.5	.	.	776	5	307
5	.	.	1,442	9	511
6	.	.	1,194	6	376
7	.	.	2,238	19	505
9	.	.	1,620	15	265
11	.	.	1,239	11	119
13	.	.	936	1	21
15	.	.	278	.	.

Deaths among all non-cancer DM-patients

21:40 Monday, March 21, 2011 9

Period	state								
	Sex			DM		DM/Ins		Well	
	All	Males	Females	DMtype 0	DMtype 2	DMtype 0	DMtype 1	DMtype 2	DMtype .
All	556,920	274,133	282,787	25,513	41,681	18,754	104	7,370	463,498
1995	42,835	21,359	21,476	3,753	432	1,337	1	26	37,286
1996	41,191	20,668	20,523	3,120	845	1,303	1	58	35,864
1997	39,798	19,777	20,021	2,753	1,180	1,337	.	73	34,455
1998	38,689	19,355	19,334	2,352	1,594	1,313	3	137	33,290
1999	38,844	19,004	19,840	2,231	1,968	1,317	2	200	33,126
2000	37,519	18,333	19,186	1,903	2,297	1,345	6	277	31,691
2001	37,805	18,406	19,399	1,649	2,643	1,290	2	337	31,884
2002	37,910	18,374	19,536	1,508	3,003	1,378	7	436	31,578
2003	36,732	17,993	18,739	1,253	3,341	1,330	9	565	30,234
2004	35,302	17,332	17,970	1,102	3,522	1,237	7	596	28,838
2005	34,489	16,906	17,583	977	3,807	1,159	13	749	27,784
2006	34,224	16,697	17,527	909	3,942	1,160	9	839	27,365
2007	34,380	16,846	17,534	732	4,143	1,135	10	942	27,418
2008	33,369	16,504	16,865	641	4,283	1,034	13	1,042	26,356
2009	33,833	16,579	17,254	630	4,681	1,079	21	1,093	26,329
DMdur									
.	463,498	225,684	237,814	463,498
0	4,137	2,202	1,935	23	3,957	1	4	152	.
0.25	2,215	1,167	1,048	76	1,994	10	2	133	.
0.5	2,031	1,132	899	102	1,743	9	4	173	.
0.75	1,981	1,036	945	149	1,670	23	4	135	.
1	1,958	1,022	936	230	1,544	33	1	150	.
1.25	1,779	983	796	208	1,391	28	1	151	.
1.5	1,822	966	856	297	1,345	43	4	133	.
1.75	1,847	996	851	288	1,377	35	3	144	.
2	3,587	1,971	1,616	627	2,506	122	3	329	.
2.5	3,514	1,887	1,627	710	2,357	153	1	293	.
3	3,673	1,995	1,678	803	2,350	214	2	304	.
3.5	3,627	1,913	1,714	912	2,152	255	3	305	.
4	3,785	2,032	1,753	1,138	1,937	370	5	335	.
4.5	4,230	2,220	2,010	1,423	1,927	528	5	347	.
5	8,292	4,235	4,057	2,899	3,360	1,350	10	673	.
6	7,211	3,674	3,537	2,475	2,698	1,414	6	618	.
7	11,844	6,016	5,828	4,075	3,745	2,805	18	1,201	.
9	9,100	4,604	4,496	3,135	2,235	2,764	16	950	.
11	6,877	3,508	3,369	2,451	1,085	2,704	11	626	.
13	4,701	2,341	2,360	1,786	308	2,388	1	218	.
15	3,073	1,507	1,566	1,134	.	1,939	.	.	.
17	1,749	841	908	511	.	1,238	.	.	.
19	389	201	188	61	.	328	.	.	.
Insdur									
.	530,708	259,922	270,786	25,513	41,681	9	.	7	463,498
0	1,527	808	719	.	.	716	4	807	.
0.25	891	475	416	.	.	448	2	441	.
0.5	854	462	392	.	.	461	5	388	.

0.75	897	475	422	.	.	551	4	342	.
1	898	492	406	.	.	587	1	310	.
1.25	823	445	378	.	.	528	1	294	.
1.5	856	462	394	.	.	576	4	276	.
1.75	818	428	390	.	.	541	2	275	.
2	1,555	802	753	.	.	993	3	559	.
2.5	1,421	765	656	.	.	973	2	446	.
3	1,326	750	576	.	.	924	1	401	.
3.5	1,263	676	587	.	.	876	3	384	.
4	1,190	666	524	.	.	848	6	336	.
4.5	1,088	587	501	.	.	776	5	307	.
5	1,962	1,086	876	.	.	1,442	9	511	.
6	1,576	845	731	.	.	1,194	6	376	.
7	2,762	1,495	1,267	.	.	2,238	19	505	.
9	1,900	1,039	861	.	.	1,620	15	265	.
11	1,369	737	632	.	.	1,239	11	119	.
13	958	550	408	.	.	936	1	21	.
15	278	166	112	.	.	278	.	.	.

Deaths among all non-cancer DM-patients

21:40 Monday, March 21, 2011 10

The CONTENTS Procedure

Data Set Name	DATA.DMMORTD	Observations	45560
Member Type	DATA	Variables	8
Engine	V9	Indexes	0
Created	21 March 2011 Monday 21:41:06 o'clock	Observation Length	72
Last Modified	21 March 2011 Monday 21:41:06 o'clock	Deleted Observations	0
Protection		Compressed	NO
Data Set Type		Sorted	NO
Label			
Data Representation	WINDOWS_32		
Encoding	wlatin1 Western (Windows)		

Engine/Host Dependent Information

Data Set Page Size	8192
Number of Data Set Pages	404
First Data Page	1
Max Obs per Page	113
Obs in First Data Page	88
Number of Data Set Repairs	0
Filename	C:\Bendix\Steno\DM-register\NDR\projects\Cancer\data\dmmortd.sas7bdat
Release Created	9.0202MO
Host Created	XP_PRO

Alphabetic List of Variables and Attributes

#	Variable	Type	Len	Format	Label
1	A	Num	8		Age (99 ~ 99+)
4	DD	Num	8		
7	DMdur	Num	8		
6	DMtype	Num	8		
8	Insdur	Num	8		
3	P	Num	8		Period
2	sex	Num	8	SEX.	Sex
5	state	Char	10		

Chapter 2

Statistical analysis with R

The statistical analyses is split across a number of separate programs in order to facilitate debugging and maintenance of the programs.

2.1 Read all datasets and convert to .Rdata

```
R 2.12.1
-----
Program: readDM.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Started: torsdag 31. marts 2011, 17:29:09
-----
> library( Epi )

Attaching package: 'Epi'

The following object(s) are masked from 'package:base':

    merge.data.frame

> library( foreign )
>
> # First, get the names of the diagnosis groups
> dxnam <- read.table( "../data/diagnames.txt", header=T, as.is=T )
>
> # Read the data sets from SAS and store in R format for analysis
>
> # The dataset classified by state, sex, A, P and C only; all patients
> dmca <- read.xport( "../data/dmcaA.xpt" )
> names(dmca) <- tolower(names(dmca))
> names(dmca)[grep("dmtype",names(dmca))] <- "DMtype"
> names(dmca)
 [1] "sex"      "a"        "p"        "c"        "y"        "d0"       "d101"    "d113"
 [9] "d999"    "d92"     "d139"    "d26"     "d91"     "d132"    "d131"    "d103"
[17] "d33"     "d51"     "d242"    "d121"    "d241"    "d22"     "d251"    "d243"
[25] "d21"     "d28"     "d133"    "d70"     "d249"    "d84"     "d83"     "d82"
[33] "state"   "DMtype"  "ax"      "px"      "cx"      "d24"     "d259"
> dmca <- transform( dmca, state = Relevel(dmca$state,3),
+                   State = Relevel(dmca$state,list(3,1;2)),
+                   sex = factor(sex,labels=c("M","F")) )
> addmargins( with( dmca, tapply(y ,list(p,state),sum,na.rm=T) ) )
      Well      DM      DM/Ins      Sum
1995 4997400  65787.74 29371.06 5092559
1996 5017439  70299.86 31949.12 5119688
1997 5028556  75704.82 34089.55 5138351
1998 5036218  81673.93 35937.20 5153829
1999 5041089  88212.86 38101.93 5167404
2000 5045751  94909.44 40369.14 5181029
2001 5051179 102402.67 42615.91 5196197
2002 5052995 110943.45 44881.40 5208820
2003 5050427 120898.38 47264.85 5218590
2004 5047109 130923.80 50324.23 5228358
2005 5043837 139843.07 53175.93 5236856
2006 5043879 147643.33 55974.86 5247497
2007 5049649 156153.72 58619.75 5264423
2008 5061199 166699.02 60480.40 5288379
2009 5070942 175747.84 58014.59 5304704
Sum 75637670 1727843.93 681169.91 78046684
> addmargins( with( dmca, tapply(d0,list(p,state),sum,na.rm=T) ) )
      Well      DM      DM/Ins      Sum
1995 21127 1037 264 22428
```

```

1996 21264 1079 290 22633
1997 21549 1217 261 23027
1998 22042 1250 340 23632
1999 22244 1427 371 24042
2000 22197 1528 409 24134
2001 22283 1666 424 24373
2002 22800 1704 426 24930
2003 22963 1710 475 25148
2004 23339 2122 600 26061
2005 23936 2288 576 26800
2006 24590 2464 680 27734
2007 24703 2508 772 27983
2008 25235 2803 770 28808
2009 25866 3006 766 29638
Sum 346138 27809 7424 381371
> addmargins( with( dmca, table(p,state) ) )
state
p Well DM DM/Ins Sum
1995 400 868 727 1995
1996 400 913 885 2198
1997 400 902 900 2202
1998 400 886 907 2193
1999 400 887 914 2201
2000 400 875 916 2191
2001 400 871 916 2187
2002 400 870 920 2190
2003 400 863 920 2183
2004 400 859 926 2185
2005 400 855 921 2176
2006 400 855 918 2173
2007 400 845 919 2164
2008 400 844 925 2169
2009 400 837 924 2161
Sum 6000 13030 13538 32568
> # Reorder the columns sensibly
> d.col <- grep("d",names(dmca))
> d.num <- as.numeric(gsub( "d", "", names(dmca)[d.col] ))
> d.col <- d.col[!is.na(d.num)]
> code <- d.num[!is.na(d.num)]
> d.num <- code/(1+9*(500>code & code>200))
> ov <- order(d.num)
> c.col <- match( c("state","State","DMtype","sex",
+ "a","p","c","ax","px","cx","y"),
+ names(dmca) )
> dmca <- dmca[,c(c.col,d.col[ov])]
> str( dmca )
'data.frame': 32568 obs. of 40 variables:
 $ state : Factor w/ 3 levels "Well","DM","DM/Ins": 1 1 1 1 1 1 1 1 1 1 ...
 $ State : Factor w/ 2 levels "Well","DM+DM/Ins": 1 1 1 1 1 1 1 1 1 1 ...
 $ DMtype: num 0 0 0 0 0 0 0 0 0 0 ...
 $ sex : Factor w/ 2 levels "M","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ a : num 0 0 0 0 0 0 0 0 0 0 ...
 $ p : num 1995 1995 1996 1996 1997 ...
 $ c : num 1994 1995 1995 1996 1996 ...
 $ ax : num 0.667 0.333 0.667 0.333 0.667 ...
 $ px : num 1995 1996 1996 1997 1997 ...
 $ cx : num 1995 1995 1996 1996 1997 ...
 $ y : num 17870 18025 18061 17426 17448 ...
 $ d0 : num 2 4 2 2 3 1 4 4 2 4 ...
 $ d21 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d22 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d24 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d241 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d242 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d243 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d249 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d251 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d259 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d26 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d28 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d33 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d51 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d70 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d82 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d83 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d84 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d91 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d92 : num 0 0 1 0 0 0 0 0 0 0 ...
 $ d101 : num 1 1 0 1 1 0 0 0 1 0 ...
 $ d103 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d113 : num 1 1 1 1 0 0 0 0 0 3 ...
 $ d121 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d131 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d132 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d133 : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d139 : num 0 0 0 0 2 0 0 0 0 0 ...
 $ d999 : num 0 2 0 0 0 1 4 4 1 1 ...
>
> # Now get the diagnosis-names for these columns and their column numbers

```

```

> # to have a reference object for the analyses
> d.col <- length(c.col)+(1:length(d.col))
> d.nam <- dxnam$name[match(code[ov],dxnam$code)]
> ( dxnam <- data.frame( col = names(dmca)[d.col],
+                       d.col = d.col,
+                       code = code[ov],
+                       d.num = d.num[ov],
+                       d.nam ) )
  col d.col code d.num d.nam
1  d0    12    0   0.0 All malignant neoplasms
2  d21   13   21  21.0 Oesophagus
3  d22   14   22  22.0 Stomach
4  d24   15   24  24.0 Colon incl. rectosigmoideum
5  d241  16  241  24.1 Ascending colon
6  d242  17  242  24.2 Transverse colon
7  d243  18  243  24.3 Descending and sigmoid colon
8  d249  19  249  24.9 Other colon (unspec. or multiple)
9  d251  20  251  25.1 Rectum (excl. anus)
10 d259  21  259  25.9 Colorectal cancer (excl. anus)
11 d26   22   26  26.0 Liver
12 d28   23   28  28.0 Pancreas
13 d33   24   33  33.0 Lung, bronchus and pleura
14 d51   25   51  51.0 Melanoma of skin
15 d70   26   70  70.0 Breast
16 d82   27   82  82.0 Cervix uteri
17 d83   28   83  83.0 Corpus uteri
18 d84   29   84  84.0 Ovary, fallopian tube etc.
19 d91   30   91  91.0 Prostate
20 d92   31   92  92.0 Testis
21 d101  32  101 101.0 Kidney
22 d103  33  103 103.0 Urinary bladder
23 d113  34  113 113.0 Brain
24 d121  35  121 121.0 Thyroid
25 d131  36  131 131.0 Hodgkin's lymphoma
26 d132  37  132 132.0 Non-Hodgkin lymphoma
27 d133  38  133 133.0 Multiple myeloma
28 d139  39  139 139.0 Leukaemia
29 d999  40  999 999.0 Other
>
> # Save both objects
> save( dmca, dxnam, file = "../data/dmcaA.Rdata" )
>
> # Only patients diagnosed after 1.1.1995,
> # classified by sex, A, P, C and the two durations
> dmca <- read.xport( "../data/dmcaD.xpt" )
> names(dmca) <- tolower(names(dmca))
> names(dmca)[grep("dmtype",names(dmca))] <- "DMtype"
> names(dmca)[grep( "dmdur",names(dmca))] <- "DMDur"
> names(dmca)[grep("insdur",names(dmca))] <- "InsDur"
> system.time( dmca <- transform( dmca, state = relevel( dmca$state, 3 ),
+                               sex = factor(sex,labels=c("M","F")) ) )
  user system elapsed
  3.44  0.36   3.80
> addmargins( with( dmca, tapply(y ,list(p,state),sum,na.rm=T) ) )
  Well DM DM/Ins Sum
1995 4997400 6464.926 482.1881 5004347
1996 5017439 18068.922 1982.1235 5037490
1997 5028556 29314.834 3563.8722 5061435
1998 5036218 40308.328 5194.3360 5081721
1999 5041089 51831.841 7049.3769 5099970
2000 5045751 62978.707 9121.6431 5117851
2001 5051179 74364.965 11406.0354 5136950
2002 5052995 86304.047 13930.1957 5153229
2003 5050427 99459.383 16626.6338 5166513
2004 5047109 112423.413 19918.7508 5179452
2005 5043837 123769.920 23260.9720 5190868
2006 5043879 133710.327 26727.2484 5204317
2007 5049649 144092.451 30220.5727 5223962
2008 5061199 156091.194 33464.3244 5250755
2009 5070942 167309.119 36568.0685 5274819
Sum 75637670 1306492.379 239516.3416 77183679
> addmargins( with( dmca, tapply(d0,list(p,state),sum,na.rm=T) ) )
  Well DM DM/Ins Sum
1995 21127 141 5 21273
1996 21264 288 12 21564
1997 21549 469 25 22043
1998 22042 609 43 22694
1999 22244 790 68 23102
2000 22197 999 85 23281
2001 22283 1167 111 23561
2002 22800 1328 130 24258
2003 22963 1371 163 24497
2004 23339 1797 242 25378
2005 23936 2045 280 26261
2006 24590 2207 319 27116
2007 24703 2329 411 27443
2008 25235 2633 427 28295
2009 25866 2879 473 29218
Sum 346138 21052 2794 369984

```

```

> addmargins( with( dmca, table(p,state) ) )
      state
p      Well      DM DM/Ins      Sum
1995   400   2625   1844   4869
1996   400   4711   6733  11844
1997   400   5469  11634  17503
1998   400   6330  15280  22010
1999   400   7239  19862  27501
2000   400   7973  24105  32478
2001   400   8511  27559  36470
2002   400   9042  31535  40977
2003   400   9347  33156  42903
2004   400   9940  36704  47044
2005   400   9973  38164  48537
2006   400  10325  41230  51955
2007   400  10510  42591  53501
2008   400  10727  45263  56390
2009   400  10848  46050  57298
Sum    6000 123570 421710 551280
>
> # Reorder the columns sensibly
> d.col <- grep("d",names(dmca))
> d.num <- as.numeric(gsub( "d", "", names(dmca)[d.col] ))
> d.col <- d.col[!is.na(d.num)]
> code <- d.num[!is.na(d.num)]
> d.num <- code/(1+9*(500>code & code>200))
> ov <- order(d.num)
> # Columns with the relevant covariates
> c.col <- match( c("state","DMtype","sex","a","p","c","ax","px","cx",
+                 "DMDur","InsDur","y"),
+               names(dmca) )
> dmca <- dmca[,c(c.col,d.col[ov])]
> str( dmca )
'data.frame': 551280 obs. of  41 variables:
 $ state : Factor w/ 3 levels "Well","DM","DM/Ins": 1 1 1 1 1 1 1 1 1 1 ...
 $ DMtype: num  0 0 0 0 0 0 0 0 0 0 ...
 $ sex   : Factor w/ 2 levels "M","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ a     : num  0 0 0 0 0 0 0 0 0 0 ...
 $ p     : num  1995 1995 1996 1996 1997 ...
 $ c     : num  1994 1995 1995 1996 1996 ...
 $ ax    : num  0.667 0.333 0.667 0.333 0.667 ...
 $ px    : num  1995 1996 1996 1997 1997 ...
 $ cx    : num  1995 1995 1996 1996 1997 ...
 $ DMDur : num  0 0 0 0 0 0 0 0 0 0 ...
 $ InsDur: num  0 0 0 0 0 0 0 0 0 0 ...
 $ y     : num  17870 18025 18061 17426 17448 ...
 $ d0    : num  2 4 2 2 3 1 4 4 2 4 ...
 $ d21   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d22   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d24   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d241  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d242  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d243  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d249  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d251  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d259  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d26   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d28   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d33   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d51   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d70   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d82   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d83   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d84   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d91   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d92   : num  0 0 1 0 0 0 0 0 0 0 ...
 $ d101  : num  1 1 0 1 1 0 0 0 1 0 ...
 $ d103  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d113  : num  1 1 1 1 0 0 0 0 0 3 ...
 $ d121  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d131  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d132  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d133  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ d139  : num  0 0 0 0 2 0 0 0 0 0 ...
 $ d999  : num  0 2 0 0 0 1 4 4 1 1 ...
>
> # Now get the diagnosis-names for these columns and their column numbers
> # to have a reference object for the analyses
>
> dxnam$d.col <- length(c.col)+(1:length(d.col))
> dxnam
  col d.col code d.num          d.nam
1   d0    13     0   0.0 All malignant neoplasms
2  d21    14     21  21.0      Oesophagus
3  d22    15     22  22.0          Stomach
4  d24    16     24  24.0 Colon incl. rectosigmoideum
5 d241    17    241  24.1      Ascending colon
6 d242    18    242  24.2      Transverse colon
7 d243    19    243  24.3 Descending and sigmoid colon

```

```

8 d249 20 249 24.9 Other colon (unspec. or multiple)
9 d251 21 251 25.1 Rectum (excl. anus)
10 d259 22 259 25.9 Colorectal cancer (excl. anus)
11 d26 23 26 26.0 Liver
12 d28 24 28 28.0 Pancreas
13 d33 25 33 33.0 Lung, bronchus and pleura
14 d51 26 51 51.0 Melanoma of skin
15 d70 27 70 70.0 Breast
16 d82 28 82 82.0 Cervix uteri
17 d83 29 83 83.0 Corpus uteri
18 d84 30 84 84.0 Ovary, fallopian tube etc.
19 d91 31 91 91.0 Prostate
20 d92 32 92 92.0 Testis
21 d101 33 101 101.0 Kidney
22 d103 34 103 103.0 Urinary bladder
23 d113 35 113 113.0 Brain
24 d121 36 121 121.0 Thyroid
25 d131 37 131 131.0 Hodgkin's lymphoma
26 d132 38 132 132.0 Non-Hodgkin lymphoma
27 d133 39 133 133.0 Multiple myeloma
28 d139 40 139 139.0 Leukaemia
29 d999 41 999 999.0 Other
>
> # Fix the two duration variables
> # First the left endpoints
> ileft <- sort( unique( dmca$DMDur ) )
> # Then half of the lengths, the last repeated twice
> ilength <- diff(ileft)
> nd <- length(ilength)
> ilength <- ilength[c(1:nd,nd)]
> dmca$DMDur <- dmca$DMDur + (as.integer(dmca$state)>1)*ilength[match(dmca$DMDur ,ileft)]/2
> dmca$InsDur <- dmca$InsDur + (as.integer(dmca$state)>2)*ilength[match(dmca$InsDur,ileft)]/2
> # ... and control it
> with( dmca, cbind(table( DMDur,state),
+ table(InsDur,state)) )
Error in cbind(table(DMDur, state), table(InsDur, state)) :
number of rows of matrices must match (see arg 2)
Calls: with -> with.default -> eval -> eval -> cbind
Execution halted

```

R 2.12.1

```

-----
Program: readmort.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Started: torsdag 31. marts 2011, 17:30:00
-----

```

```
> library(Epi)
```

```
Attaching package: 'Epi'
```

```
The following object(s) are masked from 'package:base':
```

```
merge.data.frame
```

```
> library(foreign)
```

```

> # Get the data classified by duration
> ddd <- read.xport("../data/DMmortD.xpt" )
> names(ddd) <- tolower( names(ddd) )
> ddd$dmttype <- addNA( ddd$dmttype )
> summary(ddd)

```

a	sex	p	dd	state
Min. : 0.0	Min. :1.000	Min. :1995	Min. : 0.00	DM :21925
1st Qu.:63.0	1st Qu.:1.000	1st Qu.:1999	1st Qu.: 1.00	DM/Ins:20665
Median :75.0	Median :1.000	Median :2003	Median : 1.00	Well : 2970
Mean :71.8	Mean :1.462	Mean :2003	Mean : 12.22	
3rd Qu.:84.0	3rd Qu.:2.000	3rd Qu.:2006	3rd Qu.: 3.00	
Max. :98.0	Max. :2.000	Max. :2009	Max. :862.00	

dmttype	dmdur	insdur
0 :19740	Min. : 0.000	Min. : 0.000
1 : 101	1st Qu.: 2.000	1st Qu.: 1.250
2 :22749	Median : 5.000	Median : 3.000
NA: 2970	Mean : 6.027	Mean : 3.999
	3rd Qu.: 9.000	3rd Qu.: 6.000
	Max. : 19.000	Max. : 15.000
	NA's :2970.000	NA's :24911.000

```
> ddd <- subset( ddd, as.integer(dmttype)>1 )
```

```
> summary(ddd)
```

a	sex	p	dd	state
Min. : 0.00	Min. :1.000	Min. :1995	Min. : 0.00	DM :15759
1st Qu.:61.00	1st Qu.:1.000	1st Qu.:2001	1st Qu.: 1.00	DM/Ins: 7091
Median :74.00	Median :1.000	Median :2004	Median : 1.00	Well : 2970
Mean :70.63	Mean :1.458	Mean :2004	Mean : 19.85	
3rd Qu.:84.00	3rd Qu.:2.000	3rd Qu.:2007	3rd Qu.: 3.00	
Max. :98.00	Max. :2.000	Max. :2009	Max. :862.00	

dmttype	dmdur	insdur
0 : 0	Min. : 0.000	Min. : 0.000

```

1 : 101 1st Qu.: 1.250 1st Qu.: 0.750
2 :22749 Median : 3.000 Median : 2.000
NA: 2970 Mean : 3.674 Mean : 2.921
      3rd Qu.: 6.000 3rd Qu.: 4.500
      Max. : 13.000 Max. : 13.000
      NA's :2970.000 NA's :18736.000
> with( ddd, table(state,dmtype) )
      dmtype
state  0    1    2 <NA>
DM     0    0 15759    0
DM/Ins 0   101 6990    0
Well   0    0    0 2970
> ddd$dmdur[is.na(ddd$dmdur)] <- 0
> ddd$insdur[is.na(ddd$insdur)] <- 0
> ddd <- with( ddd,
+             aggregate( dd, list(state=state,
+                               sex=sex,
+                               a=a,
+                               p=p,
+                               DMDur= dmdur,
+                               InsDur=insdur), sum, na.rm=T ) )
> names(ddd)[match("x",names(ddd))] <- "dd"
> ddd <- transform( ddd,
+                  state = relevel(state,3),
+                  sex = factor(sex,labels=c("M","F")) )
> str( ddd )
'data.frame': 25818 obs. of 7 variables:
 $ state : Factor w/ 3 levels "Well","DM","DM/Ins": 1 1 1 1 1 1 1 1 1 1 ...
 $ sex   : Factor w/ 2 levels "M","F": 1 2 1 2 1 2 1 2 1 2 ...
 $ a     : num 0 0 1 1 2 2 3 3 4 4 ...
 $ p     : num 1995 1995 1995 1995 1995 ...
 $ DMDur : num 0 0 0 0 0 0 0 0 0 0 ...
 $ InsDur: num 0 0 0 0 0 0 0 0 0 0 ...
 $ dd    : num 196 152 19 15 9 7 7 4 12 1 ...
> head( ddd )
  state sex a  p DMDur InsDur dd
1 Well  M 0 1995 0 0 196
2 Well  F 0 1995 0 0 152
3 Well  M 1 1995 0 0 19
4 Well  F 1 1995 0 0 15
5 Well  M 2 1995 0 0 9
6 Well  F 2 1995 0 0 7
> summary( ddd )
      state      sex      a      p      DMDur
Well : 2970  M:14002  Min. : 0.00  Min. :1995  Min. : 0.000
DM : 15759  F:11816  1st Qu.:61.00  1st Qu.:2001  1st Qu.: 0.500
DM/Ins: 7089      Median :74.00  Median :2004  Median : 2.500
      Mean :70.63  Mean :2004  Mean : 3.251
      3rd Qu.:84.00  3rd Qu.:2007  3rd Qu.: 5.000
      Max. :98.00  Max. :2009  Max. :13.000

      InsDur      dd
Min. : 0.0000  Min. : 0.00
1st Qu.: 0.0000  1st Qu.: 1.00
Median : 0.0000  Median : 1.00
Mean : 0.8006  Mean : 19.86
3rd Qu.: 0.0000  3rd Qu.: 3.00
Max. :13.0000  Max. :862.00
> rbind(
+ addmargins(with(ddd,tapply(dd,list( state ,sex),sum))),
+ addmargins(with(ddd,tapply(dd,list(Relevel(state,list(1,2:3)),sex),sum)))[2,,drop=F])[c(1:3,5,4),]
      M      F      Sum
Well  225684 237814 463498
DM    21846 19835 41681
DM/Ins 4319 3155 7474
DM+DM/Ins 26165 22990 49155
Sum    251849 260804 512653
>
> # Fix the two duration variables
> # First the left endpoints
> ileft <- sort( unique( ddd$DMDur ) )
> # Then half of the lengths, the last repeated twice
> ilength <- diff(ileft)
> nd <- length(ilength)
> ilength <- ilength[c(1:nd,nd)]
> ddd$DMDur <- ddd$DMDur + (as.integer(ddd$state)>1)*ilength[match(ddd$DMDur ,ileft)]/2
> ddd$InsDur <- ddd$InsDur + (as.integer(ddd$state)>2)*ilength[match(ddd$InsDur,ileft)]/2
> # ... and control it
> with( ddd, cbind(table( DMDur,state),
+                 table(InsDur,state)) )
      Well  DM DM/Ins Well  DM DM/Ins
0      2970  0 0 2970 15759 0
0.125  0 1305 145 0 0 787
0.375  0 987 131 0 0 434
0.625  0 909 174 0 0 385
0.875  0 897 137 0 0 337
1.125  0 847 146 0 0 307
1.375  0 815 150 0 0 291
1.625  0 775 135 0 0 271
1.875  0 789 144 0 0 269

```

```

2.25  0 984  324  0  0  543
2.75  0 938  287  0  0  423
3.25  0 925  301  0  0  388
3.75  0 855  305  0  0  371
4.25  0 774  336  0  0  336
4.75  0 777  343  0  0  302
5.5   0 854  645  0  0  468
6.5   0 731  605  0  0  355
8     0 703  1118 0  0  453
10    0 497  884  0  0  239
12    0 286  581  0  0  111
14    0 111  198  0  0  19
>
>
> # Get the cancer incidence data, but only tabulate the
> # person-years by state, sex, duration etc.
> load( "../data/dmcaD.Rdata" )
> yy <- with( dmca,
+             aggregate( y, list(state=state,
+                               sex=sex,
+                               a=a,
+                               p=p,
+                               DMDur=DMDur,
+                               InsDur=InsDur), sum, na.rm=T ) )
> names(yy)[match("x",names(yy))] <- "y"
> str( yy )
'data.frame': 284374 obs. of 7 variables:
 $ state : Factor w/ 3 levels "Well","DM","DM/Ins": 1 1 1 1 1 1 1 1 1 1 ...
 $ sex   : Factor w/ 2 levels "M","F": 1 2 1 2 1 2 1 2 1 2 ...
 $ a     : num 0 0 1 1 2 2 3 3 4 4 ...
 $ p     : num 1995 1995 1995 1995 1995 ...
 $ DMDur : num 0 0 0 0 0 0 0 0 0 0 ...
 $ InsDur: num 0 0 0 0 0 0 0 0 0 0 ...
 $ y     : num 35895 34122 35329 33666 35008 ...
> levels(ddd$state) <- levels(dmca$state)
> DMm <- merge( ddd, yy, all=T )
> with( DMm, table(is.na(y),!is.na(dd)) )

      FALSE  TRUE
FALSE 260650 23724
TRUE   0     2094
> # A lille bit of cleaning
> DMm$dd[is.na(DMm$dd)] <- 0
> DMm$y[is.na(DMm$y)] <- 0
> DMm <- subset( DMm, y>0 )
> str(DMm)
'data.frame': 284374 obs. of 8 variables:
 $ state : Factor w/ 3 levels "Well","DM","DM/Ins": 1 1 1 1 1 1 1 1 1 1 ...
 $ sex   : Factor w/ 2 levels "M","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ a     : num 0 0 0 0 0 0 0 0 0 0 ...
 $ p     : num 1995 1996 1997 1998 1999 ...
 $ DMDur : num 0 0 0 0 0 0 0 0 0 0 ...
 $ InsDur: num 0 0 0 0 0 0 0 0 0 0 ...
 $ dd    : num 196 219 187 160 169 208 163 159 164 153 ...
 $ y     : num 35895 35486 34834 34442 34014 ...
> summary(DMm)
      state      sex      a      p      DMDur
Well : 3000  M:139777  Min. : 0.00  Min. :1995  Min. : 0.000
DM   : 42276  F:144597  1st Qu.:37.00  1st Qu.:2001  1st Qu.: 1.625
DM/Ins:239098      Mean :53.45  Mean :2004  Mean : 4.114
      3rd Qu.:72.00  3rd Qu.:2007  3rd Qu.: 5.500
      Max. :99.00  Max. :2009  Max. :14.000

      InsDur      dd      y
Min. : 0.000  Min. : 0.000  Min. :9.770e-15
1st Qu.: 0.375  1st Qu.: 0.000  1st Qu.:2.158e-01
Median : 1.125  Median : 0.000  Median :5.515e-01
Mean : 1.678  Mean : 1.786  Mean :2.713e+02
3rd Qu.: 2.250  3rd Qu.: 0.000  3rd Qu.:1.680e+00
Max. :14.000  Max. :862.000  Max. :4.482e+04
>
> with( DMm,
+       cbind(
+         rbind( addmargins( tapply( dd, list( state, sex ), sum ) ),
+         addmargins( tapply( dd, list( Relevel(state,list(1,2:3)), sex ), sum ) ) [2,,drop=F] ) [c(1:3,5,4)],
+         round(
+         rbind( addmargins( tapply( y, list( state, sex ), sum ) ),
+         addmargins( tapply( y, list( Relevel(state,list(1,2:3)), sex ), sum ) ) [2,,drop=F] ) [c(1:3,5,4)]/1000, 1 )
+       )
Well  225684 237814 463498 37646.2 37991.5 75637.7
DM    19737 17987 37724 652.4 627.1 1279.5
DM/Ins 3872 2782 6654 137.0 102.5 239.5
DM+DM/Ins 23609 20769 44378 789.4 729.6 1519.0
Sum    249293 258583 507876 38435.6 38721.1 77156.7
>
> # Save the mortality data
> save( DMm, file="../data/DMmD.Rdata" )
>
>

```

```
-----
Program: readmort.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Ended: torsdag 31. marts 2011, 17:30:54
Elapsed: 00:00:53
-----
```

```
> proc.time()
  user system elapsed
52.04   0.85  54.36
```

2.2 Create basic table and histogram for the paper

R 2.12.1

```
-----
Program: table1.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Started: torsdag 31. marts 2011, 17:30:55
-----
```

```
> # A few numbers for the description of the diabetes register
>
> # Read in the diabetes register
> dr <- read.ssd( "../data", "diabetes" )
```

```
C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r>call "C:\Program Files\SAS\SASFoundation\9.2\sas.exe" -sysin C:\DOCUME~1\
```

```
> str( dr )
'data.frame': 437593 obs. of 14 variables:
 $ D_FODDTP: num -21914 14610 14610 -21549 15341 ...
 $ C_SEX : Factor w/ 2 levels "K","M": 1 1 1 1 2 2 2 2 1 1 ...
 $ D_INKLDT: num 10981 16700 17757 12227 16713 ...
 $ C_INKLAA: Factor w/ 6 levels "blod2i5","blod5i1",...: 3 5 5 3 5 5 5 5 3 ...
 $ D_DODSDT: num 11499 NA NA 12460 NA ...
 $ D_LPR : num 11436 16700 17757 NA 16713 ...
 $ D_FODT : num 10981 NA NA 12227 NA ...
 $ D_BLOD2I: num NA NA NA NA NA NA NA NA NA ...
 $ D_BLOD5I: num NA NA NA NA NA ...
 $ D_OAD : num NA NA NA NA NA ...
 $ D_INS : num NA 16719 17784 NA 16758 ...
 $ V_PID : Factor w/ 434329 levels "\f","\f\001ÿÿ\00330ï",...: 111980 213805 101004 303857 379238 203896 26265 323344 1579
 $ ID : num 1256431 1256457 1256458 1256474 1256543 ...
 $ SEX : num 2 2 2 2 1 1 1 1 2 2 ...
> for( i in c(1,3,5:11) ) dr[,i] <- dr[,i]/365.25+1960
> dr <- dr[,1:11]
> names( dr ) <- c("foddto","sex","inkltdto","inkl","dodsdto","lpr","fodt","blod2i5","blod5i1","oad","ins")
> str( dr )
'data.frame': 437593 obs. of 11 variables:
 $ foddto : num 1900 2000 2000 1901 2002 ...
 $ sex : Factor w/ 2 levels "K","M": 1 1 1 1 2 2 2 2 1 1 ...
 $ inkltdto: num 1990 2006 2009 1993 2006 ...
 $ inkl : Factor w/ 6 levels "blod2i5","blod5i1",...: 3 5 5 3 5 5 5 5 3 ...
 $ dodsdto: num 1991 NA NA 1994 NA ...
 $ lpr : num 1991 2006 2009 NA 2006 ...
 $ fodt : num 1990 NA NA 1993 NA ...
 $ blod2i5: num NA NA NA NA NA NA NA NA NA ...
 $ blod5i1: num NA NA NA NA NA ...
 $ oad : num NA NA NA NA NA ...
 $ ins : num NA 2006 2009 NA 2006 ...
>
> # How many records at end of 2009
> tt <- with( dr, table(ind=inkltdto<2010,exclude=NULL) )
> addmargins( tt )
ind
TRUE <NA> Sum
437593 0 437593
> tt[2]
<NA>
0
>
> # Prevalent diabetes at 1995
> tt <- with( dr, table("ind<95"=inkltdto<1995,"dod<95"=dodsdto<1995,exclude=NULL) )
> addmargins(tt)
dod<95
ind<95 FALSE TRUE <NA> Sum
FALSE 76586 25 235353 311964
TRUE 59599 27017 39013 125629
<NA> 0 0 0 0
Sum 136185 27042 274366 437593
> addmargins(tt[,-2])
dod<95
ind<95 FALSE <NA> Sum
FALSE 76586 235353 311939
TRUE 59599 39013 98612
<NA> 0 0 0
Sum 136185 274366 410551
>
```



```

> # Prevalent diabetes at 2010
> tt <- with( dr, table("ind<2010"=inkldto<2010,"dod<2010"=dodsdto<2010,exclude=NULL) )
> addmargins(tt)
      dod<2010
ind<2010  TRUE  <NA>   Sum
      TRUE 163227 274366 437593
      <NA>    0      0      0
      Sum 163227 274366 437593
>
> # Incident cases 1995-2009 inkl
> tt <- with( dr, table("ind>94"=inkldto>1994,"ind>10"=inkldto>2010,exclude=NULL) )
> addmargins(tt)
      ind>10
ind>94  FALSE  <NA>   Sum
      FALSE 102930  0 102930
      TRUE  334663  0 334663
      <NA>    0      0      0
      Sum  437593  0 437593
> tt[2,1]
[1] 334663
>
> # Construct table 1
> load( file = "../data/dmcaD.Rdata" )
> dnam <- as.character( dxnam$d.nam )
> vnam <- as.character( dxnam$col )
> # Create the table
> dims <- list( diag = c( "PYRS", dnam, "Deaths" ),
+             outer(c("M","F"),c("Well","DM","DM+Ins"),paste) )
> ttca <-
+ ttr <- array( NA, dim=sapply(dims,length), dimnames=dims )
> dims <- list( diag = c( "PYRS", dnam, "Deaths" ),
+             outer(c("M","F"),c("Ins=DM","DM=Pop"),paste) )
> ttst <- array( NA, dim=sapply(dims,length), dimnames=dims )
>
> # First cases
> for( i in 1:length(vnam) )
+ ttca[dnam[i],] <- tapply( dmca[,vnam[i]], list( dmca$sex, dmca$state ), sum )
> # Then the person-years
> ttca[ "PYRS",] <- tapply( dmca[, "y" ], list( dmca$sex, dmca$state ), sum )
> # And finally the deaths
> load( file="../data/DMmD.Rdata" )
> str(DMm)
'data.frame': 284374 obs. of  8 variables:
 $ state : Factor w/ 3 levels "Well","DM","DM/Ins": 1 1 1 1 1 1 1 1 1 1 ...
 $ sex   : Factor w/ 2 levels "M","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ a     : num  0 0 0 0 0 0 0 0 0 0 ...
 $ p     : num 1995 1996 1997 1998 1999 ...
 $ DMDur : num  0 0 0 0 0 0 0 0 0 0 ...
 $ InsDur: num  0 0 0 0 0 0 0 0 0 0 ...
 $ dd    : num 196 219 187 160 169 208 163 159 164 153 ...
 $ y     : num 35895 35486 34834 34442 34014 ...
> ttca["Deaths",] <- as.vector( with( DMm, tapply( dd, list( sex, state ), sum ) ) )
>
> ( cases <-
+ rbind(
+ formatC( ttca[1,drop=F]/1000, digits=1, big.mark=",", width=7, format="f" ),
+ formatC( ttca[-1,], digits=0, big.mark=",", width=7, format="f" ) ) )
      M Well  F Well  M DM  F DM
PYRS      "37,646.2" "37,991.5" " 652.4" " 627.1"
All malignant neoplasms "167,394" "178,744" " 11,378" " 8,654"
Oesophagus      " 3,282" " 1,304" " 235" " 64"
Stomach         " 4,171" " 2,289" " 287" " 132"
Colon incl. rectosigmoideum "13,853" "15,136" " 1,118" " 938"
Ascending colon " 3,636" " 5,126" " 311" " 385"
Transverse colon " 1,819" " 2,172" " 168" " 145"
Descending and sigmoid colon " 7,292" " 6,601" " 539" " 322"
Other colon (unspec. or multiple) " 1,106" " 1,237" " 100" " 86"
Rectum (excl. anus) " 8,876" " 6,214" " 607" " 309"
Colorectal cancer (excl. anus) "22,729" "21,350" " 1,725" " 1,247"
Liver           " 1,776" " 1,103" " 325" " 77"
Pancreas       " 4,041" " 4,425" " 525" " 446"
Lung, bronchus and pleura "25,302" "20,283" " 1,673" " 1,068"
Melanoma of skin " 7,008" " 8,873" " 311" " 208"
Breast         " 298" " 52,190" " 13" " 2,118"
Cervix uteri   " 0" " 5,691" " 0" " 127"
Corpus uteri   " 0" " 8,057" " 0" " 538"
Ovary, fallopian tube etc. " 0" " 7,400" " 0" " 297"
Prostate       "31,713" " 0" " 2,355" " 0"
Testis        " 4,257" " 0" " 36" " 0"
Kidney        " 3,976" " 2,434" " 306" " 181"
Urinary bladder "14,781" " 4,906" " 1,071" " 250"
Brain         " 4,922" " 4,310" " 205" " 156"
Thyroid       " 593" " 1,511" " 24" " 39"
Hodgkin's lymphoma " 990" " 723" " 35" " 22"
Non-Hodgkin lymphoma " 5,434" " 4,602" " 313" " 219"
Multiple myeloma " 2,452" " 1,883" " 157" " 100"
Leukaemia     " 5,423" " 4,050" " 280" " 197"
Other         "24,246" "21,360" " 1,502" " 1,168"
Deaths       "225,684" "237,814" " 19,737" " 17,987"

```

```

M DM+Ins F DM+Ins
PYRS " 137.0" " 102.5"
All malignant neoplasms " 1,609" " 1,185"
Oesophagus " 30" " 8"
Stomach " 41" " 18"
Colon incl. rectosigmoideum " 135" " 84"
Ascending colon " 36" " 29"
Transverse colon " 27" " 17"
Descending and sigmoid colon " 64" " 29"
Other colon (unspec. or multiple) " 8" " 9"
Rectum (excl. anus) " 71" " 30"
Colorectal cancer (excl. anus) " 206" " 114"
Liver " 100" " 19"
Pancreas " 182" " 147"
Lung, bronchus and pleura " 248" " 151"
Melanoma of skin " 37" " 31"
Breast " 4" " 248"
Cervix uteri " 0" " 25"
Corpus uteri " 0" " 63"
Ovary, fallopian tube etc. " 0" " 37"
Prostate " 227" " 0"
Testis " 7" " 0"
Kidney " 55" " 40"
Urinary bladder " 115" " 29"
Brain " 30" " 27"
Thyroid " 6" " 12"
Hodgkin's lymphoma " 8" " 2"
Non-Hodgkin lymphoma " 37" " 29"
Multiple myeloma " 18" " 8"
Leukaemia " 37" " 23"
Other " 221" " 154"
Deaths " 3,872" " 2,782"
>
> load( file="../data/prcan.Rdata" )
> str( p.can )
num [1:29, 1:2, 1:3, 1:3, 1:2] 0.13048 0.00272 0.00323 0.0108 0.00265 ...
- attr(*, "dimnames")=List of 6
..$ diag : chr [1:29] "All malignant neoplasms" "Oesophagus" "Stomach" "Colon incl. rectosigmoideum" ...
..$ sex : chr [1:2] "M" "F"
..$ model : chr [1:2] "Main" "Interact"
..$ state : chr [1:3] "Well" "DM" "DM/ins"
..$ age.in: chr [1:3] "60" "65" "70"
..$ dur.in: chr [1:2] "0" "2"
> ttcrc[-c(1,30),] <- ftable( p.can[,,"Main",,"65",,"0"], col.vars=3:2 )
> ( risks <-
+ formatC( ttcrc*100, digits=1, width=4, format="f" ) )

diag M Well F Well M DM F DM M DM+Ins
PYRS " NA" " NA" " NA" " NA" " NA"
All malignant neoplasms "17.3" "13.6" "17.9" "14.3" "17.8"
Oesophagus " 0.3" " 0.1" " 0.4" " 0.1" " 0.4"
Stomach " 0.4" " 0.2" " 0.4" " 0.2" " 0.5"
Colon incl. rectosigmoideum " 1.5" " 1.3" " 1.8" " 1.4" " 1.6"
Ascending colon " 0.4" " 0.4" " 0.5" " 0.5" " 0.4"
Transverse colon " 0.2" " 0.2" " 0.3" " 0.2" " 0.3"
Descending and sigmoid colon " 0.8" " 0.6" " 0.9" " 0.5" " 0.8"
Other colon (unspec. or multiple) " 0.1" " 0.1" " 0.2" " 0.1" " 0.1"
Rectum (excl. anus) " 1.0" " 0.5" " 1.0" " 0.5" " 0.8"
Colorectal cancer (excl. anus) " 2.5" " 1.8" " 2.8" " 1.9" " 2.3"
Liver " 0.2" " 0.1" " 0.6" " 0.1" " 1.1"
Pancreas " 0.4" " 0.4" " 0.7" " 0.6" " 3.1"
Lung, bronchus and pleura " 3.2" " 2.3" " 3.1" " 2.3" " 3.6"
Melanoma of skin " 0.5" " 0.4" " 0.4" " 0.3" " 0.3"
Breast " 0.0" " 3.4" " 0.0" " 3.3" " 0.0"
Cervix uteri " NA" " 0.2" " NA" " 0.2" " NA"
Corpus uteri " NA" " 0.7" " NA" " 1.1" " NA"
Ovary, fallopian tube etc. " NA" " 0.6" " NA" " 0.6" " NA"
Prostate " 4.0" " NA" " 3.4" " NA" " 2.2"
Testis " 0.0" " NA" " 0.0" " NA" " 0.0"
Kidney " 0.4" " 0.2" " 0.5" " 0.3" " 0.6"
Urinary bladder " 1.7" " 0.5" " 1.8" " 0.4" " 1.5"
Brain " 0.3" " 0.2" " 0.3" " 0.2" " 0.3"
Thyroid " 0.0" " 0.0" " 0.0" " 0.0" " 0.0"
Hodgkin's lymphoma " 0.0" " 0.0" " 0.1" " 0.0" " 0.1"
Non-Hodgkin lymphoma " 0.4" " 0.4" " 0.5" " 0.4" " 0.3"
Multiple myeloma " 0.3" " 0.2" " 0.3" " 0.2" " 0.2"
Leukaemia " 0.5" " 0.3" " 0.4" " 0.3" " 0.4"
Other " NA" " NA" " NA" " NA" " NA"
Deaths "13.7" " 9.1" "24.2" "16.4" "38.3"

diag F DM+Ins
PYRS " NA"
All malignant neoplasms "16.1"
Oesophagus " 0.1"
Stomach " 0.3"
Colon incl. rectosigmoideum " 1.1"
Ascending colon " 0.4"
Transverse colon " 0.2"
Descending and sigmoid colon " 0.4"

```

```

Other colon (unspec. or multiple) " 0.1"
Rectum (excl. anus) " 0.4"
Colorectal cancer (excl. anus) " 1.5"
Liver " 0.3"
Pancreas " 3.1"
Lung, bronchus and pleura " 2.8"
Melanoma of skin " 0.3"
Breast " 2.9"
Cervix uteri " 0.2"
Corpus uteri " 1.0"
Ovary, fallopian tube etc. " 0.6"
Prostate " NA"
Testis " NA"
Kidney " 0.6"
Urinary bladder " 0.6"
Brain " 0.3"
Thyroid " 0.1"
Hodgkin's lymphoma " 0.0"
Non-Hodgkin lymphoma " 0.4"
Multiple myeloma " 0.1"
Leukaemia " 0.3"
Other " NA"
Deaths "27.9"

```

```

>
> # Tests for effects
> load( file="./data/ana3dx.Rdata" )
> ttst[-c(1,30,31),] <- ftable( ttst[,1:2], col.vars=3:2 )
> ( tests <-
+ formatC( ttst, digits=3, width=5, format="f" ) )

```

```

diag      M Ins=DM F Ins=DM M DM=Pop F DM=Pop
PYRS      " NA"  " NA"  " NA"  " NA"
All malignant neoplasms "0.000" "0.000" "0.000" "0.000"
Oesophagus "0.113" "0.599" "0.005" "0.435"
Stomach   "0.605" "0.047" "0.005" "0.015"
Colon incl. rectosigmoideum "0.607" "0.515" "0.000" "0.000"
Ascending colon "0.776" "0.766" "0.000" "0.000"
Transverse colon "0.222" "0.571" "0.000" "0.054"
Descending and sigmoid colon "0.516" "0.547" "0.000" "0.738"
Other colon (unspec. or multiple) "0.725" "0.895" "0.000" "0.032"
Rectum (excl. anus) "0.312" "0.512" "0.058" "0.996"
Colorectal cancer (excl. anus) "0.394" "0.242" "0.000" "0.000"
Liver     "0.000" "0.000" "0.000" "0.000"
Pancreas  "0.000" "0.000" "0.000" "0.000"
Lung, bronchus and pleura "0.003" "0.007" "0.000" "0.000"
Melanoma of skin "0.340" "0.893" "0.824" "0.003"
Breast    "0.491" "0.944" "0.055" "0.388"
Cervix uteri " NA"  "0.512" " NA"  "0.261"
Corpus uteri " NA"  "0.720" " NA"  "0.000"
Ovary, fallopian tube etc. " NA"  "0.598" " NA"  "0.823"
Prostate  "0.013" " NA"  "0.000" " NA"
Testis    "0.361" " NA"  "0.446" " NA"
Kidney    "0.002" "0.000" "0.000" "0.000"
Urinary bladder "0.632" "0.334" "0.000" "0.186"
Brain     "0.352" "0.039" "0.000" "0.001"
Thyroid   "0.495" "0.012" "0.596" "0.073"
Hodgkin's lymphoma "0.530" "0.918" "0.000" "0.006"
Non-Hodgkin lymphoma "0.587" "0.165" "0.003" "0.282"
Multiple myeloma "0.959" "0.680" "0.490" "0.423"
Leukaemia "0.444" "0.656" "0.061" "0.171"
Other     " NA"  " NA"  " NA"  " NA"
Deaths    " NA"  " NA"  " NA"  " NA"

```

```

>
> table1 <-
+ cbind( cases, risks, tests )
>
> options( width=200 )
> ( rownames(table1) <- gsub( "\\(excl. anus\\)", "", rownames(table1) ) )
[1] "PYRS" "All malignant neoplasms" "Oesophagus" "Stomach"
[6] "Ascending colon" "Transverse colon" "Descending and sigmoid colon" "Other col
[11] "Colorectal cancer" "Liver" "Pancreas" "Lung, bro
[16] "Breast" "Cervix uteri" "Corpus uteri" "Ovary, fa
[21] "Testis" "Kidney" "Urinary bladder" "Brain"
[26] "Hodgkin's lymphoma" "Non-Hodgkin lymphoma" "Multiple myeloma" "Leukaemia
[31] "Deaths"
> wh <- c(1:4,11,6:8,10,12:31)
> table1[wh,]

```

```

PYRS      M Well      F Well      M DM      F DM      M DM+Ins F DM+Ins M Well F Well M DM      F DM      M DM
"37,646.2" "37,991.5" " 652.4" " 627.1" " 137.0" " 102.5" " NA" " NA" " NA" " NA" " NA" " NA" " NA" " NA"
All malignant neoplasms "167,394" "178,744" " 11,378" " 8,654" " 1,609" " 1,185" "17.3" "13.6" "17.9" "14.3" "17.
Oesophagus " 3,282" " 1,304" " 235" " 64" " 30" " 8" " 0.3" " 0.1" " 0.4" " 0.1" " 0.
Stomach    " 4,171" " 2,289" " 287" " 132" " 41" " 18" " 0.4" " 0.2" " 0.4" " 0.2" " 0.
Colorectal cancer " 22,729" " 21,350" " 1,725" " 1,247" " 206" " 114" " 2.5" " 1.8" " 2.8" " 1.9" " 2.
Ascending colon " 3,636" " 5,126" " 311" " 385" " 36" " 29" " 0.4" " 0.4" " 0.5" " 0.5" " 0.
Transverse colon " 1,819" " 2,172" " 168" " 145" " 27" " 17" " 0.2" " 0.2" " 0.3" " 0.2" " 0.
Descending and sigmoid colon " 7,292" " 6,601" " 539" " 322" " 64" " 29" " 0.8" " 0.6" " 0.9" " 0.5" " 0.
Rectum     " 8,876" " 6,214" " 607" " 309" " 71" " 30" " 1.0" " 0.5" " 1.0" " 0.5" " 0.
Liver      " 1,776" " 1,103" " 325" " 77" " 100" " 19" " 0.2" " 0.1" " 0.6" " 0.1" " 1.
Pancreas   " 4,041" " 4,425" " 525" " 446" " 182" " 147" " 0.4" " 0.4" " 0.7" " 0.6" " 3.

```

```

Lung, bronchus and pleura " 25,302" " 20,283" " 1,673" " 1,068" " 248" " 151" " 3.2" " 2.3" " 3.1" " 2.3" " 3.
Melanoma of skin " 7,008" " 8,873" " 311" " 208" " 37" " 31" " 0.5" " 0.4" " 0.4" " 0.3" " 0.
Breast " 298" " 52,190" " 13" " 2,118" " 4" " 248" " 0.0" " 3.4" " 0.0" " 3.3" " 0.
Cervix uteri " 0" " 5,691" " 0" " 127" " 0" " 25" " NA" " 0.2" " NA" " 0.2" " N
Corpus uteri " 0" " 8,057" " 0" " 538" " 0" " 63" " NA" " 0.7" " NA" " 1.1" " N
Ovary, fallopian tube etc. " 0" " 7,400" " 0" " 297" " 0" " 37" " NA" " 0.6" " NA" " 0.6" " N
Prostate " 31,713" " 0" " 2,355" " 0" " 227" " 0" " 4.0" " NA" " 3.4" " NA" " 2.
Testis " 4,257" " 0" " 36" " 0" " 7" " 0" " 0.0" " NA" " 0.0" " NA" " 0.
Kidney " 3,976" " 2,434" " 306" " 181" " 55" " 40" " 0.4" " 0.2" " 0.5" " 0.3" " 0.
Urinary bladder " 14,781" " 4,906" " 1,071" " 250" " 115" " 29" " 1.7" " 0.5" " 1.8" " 0.4" " 1.
Brain " 4,922" " 4,310" " 205" " 156" " 30" " 27" " 0.3" " 0.2" " 0.3" " 0.2" " 0.
Thyroid " 593" " 1,511" " 24" " 39" " 6" " 12" " 0.0" " 0.0" " 0.0" " 0.0" " 0.
Hodgkin's lymphoma " 990" " 723" " 35" " 22" " 8" " 2" " 0.0" " 0.0" " 0.1" " 0.0" " 0.
Non-Hodgkin lymphoma " 5,434" " 4,602" " 313" " 219" " 37" " 29" " 0.4" " 0.4" " 0.5" " 0.4" " 0.
Multiple myeloma " 2,452" " 1,883" " 157" " 100" " 18" " 8" " 0.3" " 0.2" " 0.3" " 0.2" " 0.
Leukaemia " 5,423" " 4,050" " 280" " 197" " 37" " 23" " 0.5" " 0.3" " 0.4" " 0.3" " 0.
Other " 24,246" " 21,360" " 1,502" " 1,168" " 221" " 154" " NA" " NA" " NA" " NA" " N
Deaths "225,684" "237,814" " 19,737" " 17,987" " 3,872" " 2,782" "13.7" " 9.1" "24.2" "16.4" "38.

```

```

>
> library( Hmisc )
Loading required package: survival
Loading required package: splines

Attaching package: 'Hmisc'

The following object(s) are masked from 'package:survival':

  untangle.specials

The following object(s) are masked from 'package:base':

  format.pval, round.POSIXt, trunc.POSIXt, units

> zz <- latex( table1[wh,], file="..table1.tex", booktabs=TRUE )
>

```

```

-----
Program: table1.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Ended: torsdag 31. marts 2011, 17:31:55
Elapsed: 00:01:00
-----

```

```

> proc.time()
  user system elapsed
48.28  2.26  61.54

```

```
R 2.12.1
```

```

-----
Program: dur-hist.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Started: torsdag 31. marts 2011, 17:31:56
-----

```

```
> library( Epi )
```

```
Attaching package: 'Epi'
```

```
The following object(s) are masked from 'package:base':
```

```
merge.data.frame
```

```

> # A handy function for starting plot devices
> source( "c:/stat/r/bxc/library.sources/useful/r/plr.r" )
>
> #####
> # Show the differences between the diagnosis dated for those who have
> # both by reading the join of the diabetes register and the CR
> candi <- read.xport( "../data/candi.xpt" )
> names(candi) <- tolower(names(candi))
> for( i in 4:9 ) candi[,i] <- candi[,i]/365.25 + 1960
> head(candi)
  diag diaggrp sex      dobt dodm doi      doca      dox      dodd dmtype
1  70         70  2 1900.003  NA  NA 1970.497 1979.433 1979.433      NA
2  242        20  2 1900.003  NA  NA 1983.162 1992.580 1992.580      NA
3   22         20  1 1900.003  NA  NA 1970.582 1972.939 1972.939      NA
4  249         20  1 1900.003  NA  NA 1964.498 1976.110 1976.110      NA
5   91         90  1 1900.003  NA  NA 1978.001 1980.747 1980.747      NA
6   51         50  2 1900.003  NA  NA 1961.834 1980.257 1980.257      NA
> summary(candi)
      diag      diaggrp      sex      dobt
Min.   : 21.0   Min.   : 10.00   Min.   :1.000   Min.   :1846
1st Qu.: 51.0   1st Qu.: 20.00   1st Qu.:1.000   1st Qu.:1907
Median : 91.0   Median : 70.00   Median :2.000   Median :1923
Mean   : 239.1   Mean   : 62.95   Mean   :1.507   Mean   :1923
3rd Qu.: 242.0   3rd Qu.: 90.00   3rd Qu.:2.000   3rd Qu.:1940
Max.   : 999.0   Max.   : 140.00   Max.   :2.000   Max.   :2010
NA's   :362089.0 NA's   :362089.000
      dodm      doi      doca      dox
Min.   : 1942   Min.   : 1994   Min.   : 1943   Min.   :1921
1st Qu.: 1994   1st Qu.: 1995   1st Qu.: 1969   1st Qu.:1979

```

```

Median : 2001   Median : 2001   Median : 1985   Median :1998
Mean : 2000    Mean : 2001    Mean : 1983    Mean :1992
3rd Qu.: 2006   3rd Qu.: 2006   3rd Qu.: 1999   3rd Qu.:2010
Max. : 2010    Max. : 2010    Max. : 2010    Max. :2010
NA's :1119643  NA's :1447828  NA's :362089
dodd      dmttype
Min. : 1921    Min. :0.000e+00
1st Qu.: 1972  1st Qu.:0.000e+00
Median : 1989  Median :2.000e+00
Mean : 1985    Mean :1.411e+00
3rd Qu.: 2000  3rd Qu.:2.000e+00
Max. : 2011    Max. :2.000e+00
NA's :449181  NA's :1.120e+06
>
> plt( "diag-diff", height=10, width=10 )
> par( mfrow=c(2,2), mgp=c(3,1,0)/1.6, mar=c(3,3,0,0) )
> ymax <- 1400
>
> # Cancer - Diabetes
> with( subset( candi, abs(doca-dodm)<2 & dodm>1995 ),
+ hist( doca-dodm, breaks=seq(-2,2,1/12),
+ col=gray(0.4), border=gray(0.49), las=1,
+ xlim=c(-2,2), xlab="",#Date of Cancer - date of DM (years)",
+ ylim=c(0,ymax), ylab="", main="" ) )
> abline( v=0, col="red" )
> mtext( "Cancer after DM", at= 0.5, adj=0, line=-2, cex=0.7 )
> mtext( "Cancer before DM", at=-0.5, adj=1, line=-2, cex=0.7 )
>
> # Cancer - Insulin
> with( subset( candi, abs(doca-doi)<2 & doi>1995 ),
+ hist( doca-doi, breaks=seq(-2,2,1/12),
+ col=gray(0.4), border=gray(0.49), las=1,
+ xlim=c(-2,2), xlab="",#Date of Cancer - date of Insulin (years)",
+ yaxt="n", ylim=c(0,ymax), ylab="", main="" ) )
> abline( v=0, col="red" )
> mtext( "Cancer after Insulin", at= 0.5, adj=0, line=-2, cex=0.7 )
> mtext( "Cancer before Insulin", at=-0.5, adj=1, line=-2, cex=0.7 )
>
> if(TRUE){
+ # Transform the dates of diagnosis of cancer by adding a uniform over
+ # a month
+ candr <- transform( candi, doca = doca+runif(length(doca),0,1/12)*(doca<2005) )
+
+ # Cancer - Diabetes
+ with( subset( candr, abs(doca-dodm)<2 & dodm>1995 ),
+ hist( doca-dodm, breaks=seq(-2,2,1/12),
+ col=gray(0.4), border=gray(0.49), las=1,
+ xlim=c(-2,2), xlab="Date of Cancer - date of DM (years)",
+ ylim=c(0,ymax), ylab="", main="" ) )
+ abline( v=0, col="red" )
+ #mtext( "DM before Cancer", at= 0.5, adj=0, line=-2, cex=0.7 )
+ #mtext( "Cancer before DM", at=-0.5, adj=1, line=-2, cex=0.7 )
+
+ # Cancer - Insulin
+ with( subset( candr, abs(doca-doi)<2 & doi>1995 ),
+ hist( doca-doi, breaks=seq(-2,2,1/12),
+ col=gray(0.4), border=gray(0.49), las=1,
+ xlim=c(-2,2), xlab="Date of Cancer - date of Insulin (years)",
+ yaxt="n", ylim=c(0,ymax), ylab="", main="" ) )
+ abline( v=0, col="red" )
+ #mtext( "Insulin before Cancer", at= 0.5, adj=0, line=-2, cex=0.7 )
+ #mtext( "Cancer before Insulin", at=-0.5, adj=1, line=-2, cex=0.7 )
+
+ # Transform the dates of diagnosis of cancer by adding a uniform
+ candr <- transform( candr, doca = doca+runif(length(doca),-1/12,1/12),
+ dodm = dodm+runif(length(dodm),-1/12,1/12),
+ doi = doi +runif(length(doi ),-1/12,1/12) )
+ }
>
> if(FALSE){
+ # Cancer - Diabetes
+ with( subset( candr, abs(doca-dodm)<2 & dodm>1995 ),
+ hist( doca-dodm, breaks=seq(-2,2,1/12),
+ col=gray(0.4), border=gray(0.49), las=1,
+ xlim=c(-2,2), xlab="Date of Cancer - date of DM (years)",
+ ylim=c(0,ymax), ylab="", main="" ) )
+ abline( v=0, col="red" )
+ #mtext( "DM before Cancer", at= 0.5, adj=0, line=-2, cex=0.7 )
+ #mtext( "Cancer before DM", at=-0.5, adj=1, line=-2, cex=0.7 )
+
+ # Cancer - Insulin
+ with( subset( candr, abs(doca-doi)<2 & doi>1995 ),
+ hist( doca-doi, breaks=seq(-2,2,1/12),
+ col=gray(0.4), border=gray(0.49), las=1,
+ xlim=c(-2,2), xlab="Date of Cancer - date of Insulin (years)",
+ yaxt="n", ylim=c(0,ymax), ylab="", main="" ) )
+ abline( v=0, col="red" )
+ #mtext( "Insulin before Cancer", at= 0.5, adj=0, line=-2, cex=0.7 )
+ #mtext( "Cancer before Insulin", at=-0.5, adj=1, line=-2, cex=0.7 )
}

```

```

+ }
>
> dev.off()
null device
  1
>
> #####
> # Get the data file ;
> load( file = "../data/dmcaD.Rdata" )
> str( dmca )
'data.frame':  508062 obs. of  41 variables:
 $ state : Factor w/  3 levels "Well","DM","DM/Ins":  1  1  1  1  1  1  1  1  1  1 ...
 $ DMtype: num  0  0  0  0  0  0  0  0  0  0 ...
 $ sex   : Factor w/  2 levels "M","F":  1  1  1  1  1  1  1  1  1  1 ...
 $ a     : num  0  0  0  0  0  0  0  0  0  0 ...
 $ p     : num  1995 1995 1996 1996 1997 ...
 $ c     : num  1994 1995 1995 1996 1996 ...
 $ ax    : num  0.667 0.333 0.667 0.333 0.667 ...
 $ px    : num  1995 1996 1996 1997 1997 ...
 $ cx    : num  1995 1995 1996 1996 1997 ...
 $ DMDur: num  0  0  0  0  0  0  0  0  0 ...
 $ InsDur: num  0  0  0  0  0  0  0  0  0 ...
 $ y     : num  17870 18025 18061 17426 17448 ...
 $ d0    : num  2  4  2  2  3  1  4  4  2  4 ...
 $ d21   : num  0  0  0  0  0  0  0  0  0 ...
 $ d22   : num  0  0  0  0  0  0  0  0  0 ...
 $ d24   : num  0  0  0  0  0  0  0  0  0 ...
 $ d241  : num  0  0  0  0  0  0  0  0  0 ...
 $ d242  : num  0  0  0  0  0  0  0  0  0 ...
 $ d243  : num  0  0  0  0  0  0  0  0  0 ...
 $ d249  : num  0  0  0  0  0  0  0  0  0 ...
 $ d251  : num  0  0  0  0  0  0  0  0  0 ...
 $ d259  : num  0  0  0  0  0  0  0  0  0 ...
 $ d26   : num  0  0  0  0  0  0  0  0  0 ...
 $ d28   : num  0  0  0  0  0  0  0  0  0 ...
 $ d33   : num  0  0  0  0  0  0  0  0  0 ...
 $ d51   : num  0  0  0  0  0  0  0  0  0 ...
 $ d70   : num  0  0  0  0  0  0  0  0  0 ...
 $ d82   : num  0  0  0  0  0  0  0  0  0 ...
 $ d83   : num  0  0  0  0  0  0  0  0  0 ...
 $ d84   : num  0  0  0  0  0  0  0  0  0 ...
 $ d91   : num  0  0  0  0  0  0  0  0  0 ...
 $ d92   : num  0  0  1  0  0  0  0  0  0 ...
 $ d101  : num  1  1  0  1  1  0  0  0  1  0 ...
 $ d103  : num  0  0  0  0  0  0  0  0  0 ...
 $ d113  : num  1  1  1  1  0  0  0  0  0  3 ...
 $ d121  : num  0  0  0  0  0  0  0  0  0 ...
 $ d131  : num  0  0  0  0  0  0  0  0  0 ...
 $ d132  : num  0  0  0  0  0  0  0  0  0 ...
 $ d133  : num  0  0  0  0  0  0  0  0  0 ...
 $ d139  : num  0  0  0  0  2  0  0  0  0 ...
 $ d999  : num  0  2  0  0  0  1  4  4  1  1 ...
>
> # Where are the cancers in terms of duration
> dd <- with( dmca, cbind(tapply(d0,list( DMDur,state),sum),
+                          tapply(d0,list(InsDur,state),sum)) )
> dd[is.na(dd)] <- 0
> addmargins( dd, 1 )

```

	Well	DM	DM/Ins	Well	DM	DM/Ins
0	346138	0	0	346138	20032	0
0.166665	0	1044	38	0	0	198
0.375	0	1084	65	0	0	205
0.625	0	969	59	0	0	162
0.875	0	866	48	0	0	146
1.125	0	799	59	0	0	119
1.375	0	770	46	0	0	123
1.625	0	765	46	0	0	117
1.875	0	706	49	0	0	126
2.25	0	1309	110	0	0	198
2.75	0	1301	117	0	0	182
3.25	0	1107	127	0	0	156
3.75	0	1045	123	0	0	139
4.25	0	1037	108	0	0	122
4.75	0	931	117	0	0	108
5.5	0	1610	238	0	0	165
6.5	0	1278	232	0	0	166
8	0	1775	468	0	0	196
10	0	1046	388	0	0	96
12	0	467	269	0	0	50
14	0	123	87	0	0	20
Sum	346138	20032	2794	346138	20032	2794

```

> # Cumulative numbers from the bottom
> apply( dd[nrow(dd):1,], 2, cumsum )[nrow(dd):1,]

```

	Well	DM	DM/Ins	Well	DM	DM/Ins
0	346138	20032	2794	346138	20032	2794
0.166665	0	20032	2794	0	0	2794
0.375	0	18988	2756	0	0	2596
0.625	0	17904	2691	0	0	2391
0.875	0	16935	2632	0	0	2229

```

1.125      0 16069 2584      0      0 2083
1.375      0 15270 2525      0      0 1964
1.625      0 14500 2479      0      0 1841
1.875      0 13735 2433      0      0 1724
2.25       0 13029 2384      0      0 1598
2.75       0 11720 2274      0      0 1400
3.25       0 10419 2157      0      0 1218
3.75       0  9312 2030      0      0 1062
4.25       0  8267 1907      0      0  923
4.75       0  7230 1799      0      0  801
5.5        0  6299 1682      0      0  693
6.5        0  4689 1444      0      0  528
8          0  3411 1212      0      0  362
10         0  1636  744      0      0  166
12         0   590  356      0      0   70
14         0   123   87      0      0   20
>
> # Where are the PYRS in terms of duration
> yy <- with( dmca, cbind(tapply(y,list( DMDur,state),sum),
+ tapply(y,list(InsDur,state),sum)) )/1000
> yy[is.na(yy)] <- 0
> round(addmargins( yy, 1 ),1)
      Well      DM DM/Ins      Well      DM DM/Ins
0      75637.7  0.0  0.0 75637.7 1279.5  0.0
0.166665  0.0 43.6  1.8  0.0  0.0  7.9
0.375     0.0 62.4  4.5  0.0  0.0 11.5
0.625     0.0 60.0  4.9  0.0  0.0 11.1
0.875     0.0 57.6  5.1  0.0  0.0 10.6
1.125     0.0 55.4  5.2  0.0  0.0 10.2
1.375     0.0 53.4  5.2  0.0  0.0  9.8
1.625     0.0 51.3  5.3  0.0  0.0  9.5
1.875     0.0 49.3  5.3  0.0  0.0  9.1
2.25      0.0 92.8 10.8  0.0  0.0 17.2
2.75      0.0 85.6 10.9  0.0  0.0 15.8
3.25      0.0 78.7 11.0  0.0  0.0 14.4
3.75      0.0 72.4 11.1  0.0  0.0 13.2
4.25      0.0 66.2 11.1  0.0  0.0 11.9
4.75      0.0 60.4 11.0  0.0  0.0 10.9
5.5       0.0 103.3 21.8  0.0  0.0 18.6
6.5       0.0  81.8 21.1  0.0  0.0 14.9
8         0.0 110.6 38.3  0.0  0.0 21.4
10        0.0  60.3 29.9  0.0  0.0 12.9
12        0.0  27.5 18.7  0.0  0.0  6.8
14        0.0   7.0  6.5  0.0  0.0  2.0
Sum      75637.7 1279.5 239.5 75637.7 1279.5 239.5
> # Cumulative numbers from the bottom
> round(apply( yy[nrow(yy):1,], 2, cumsum ) [nrow(yy):1,],1)
      Well      DM DM/Ins      Well      DM DM/Ins
0      75637.7 1279.5 239.5 75637.7 1279.5 239.5
0.166665  0.0 1279.5 239.5  0.0  0.0 239.5
0.375     0.0 1235.9 237.7  0.0  0.0 231.6
0.625     0.0 1173.5 233.3  0.0  0.0 220.1
0.875     0.0 1113.6 228.3  0.0  0.0 209.1
1.125     0.0 1055.9 223.3  0.0  0.0 198.5
1.375     0.0 1000.5 218.1  0.0  0.0 188.3
1.625     0.0  947.1 212.8  0.0  0.0 178.4
1.875     0.0  895.8 207.5  0.0  0.0 169.0
2.25      0.0  846.5 202.2  0.0  0.0 159.9
2.75      0.0  753.8 191.4  0.0  0.0 142.7
3.25      0.0  668.2 180.5  0.0  0.0 127.0
3.75      0.0  589.4 169.5  0.0  0.0 112.6
4.25      0.0  517.1 158.4  0.0  0.0  99.4
4.75      0.0  450.9 147.4  0.0  0.0  87.4
5.5       0.0  390.5 136.3  0.0  0.0  76.5
6.5       0.0  287.2 114.5  0.0  0.0  57.9
8         0.0  205.4  93.3  0.0  0.0  43.1
10        0.0   94.8  55.0  0.0  0.0  21.7
12        0.0   34.5  25.1  0.0  0.0   8.8
14        0.0    7.0   6.5  0.0  0.0   2.0
>
> #####
> # Distribution of cases by duration
> #####
> ph <- 6 # Height in inches of upper barplots
> fr <- 1/6 # Fraction of this for the lower barplots
> mai <- c(2.5,2.6,1,0.5)/4 # Single plot margins in inches
> mh <- mai[1]+mai[3] # Vertical margin space
> th <- ph*(1+fr)+2*mh # Total height of the entire graph
>
> plt( "dur-hist", height=th, width=th )
> layout( matrix(1:4,2,2), height=rep(c(ph+mh,ph*fr+mh),2))
> par( mai=mai, mgp=c(3,1,0.4)/1.5, las=1 )
> barplot(height=t(dd[,3:2]/ilength), width=ilength,
+ space=0, xaxt="n", yaxs="i", col=gray(c(3,7)/10),
+ xlim=c(0,15), ylim=c(0,6800),
+ xlab="Diabetes duration" )
> axis(side=1,at=seq(0,15,3),labels=seq(0,15,3))
> axis(side=1,at=seq(0,15,1),labels=rep("",16))
> mtext( side=3, line=0, "Cancer cases per year", adj=0.1 )

```

```

>
> barplot(t(dd[,6]/ilength), width=ilength,
+         space=0,xaxt="n",yaxt="n",
+         yaxs="i",col=gray(3/10),
+         xlim=c(0,15),ylim=c(0,6800*fr),xlab="Insulin duration" )
> axis(side=1,at=seq(0,15,3),labels=seq(0,15,3))
> axis(side=1,at=seq(0,15,1),labels=rep("",16))
> axis(side=2,at=0:2*500)
> # axis(side=2,at=0:15*100,labels=rep("",16) )
>
> barplot(t(yy[,3:2]/ilength), width=ilength,
+         space=0,xaxt="n",yaxs="i",col=gray(c(3,7)/10),
+         xlim=c(0,15), ylim=c(0,300),xlab="Diabetes duration" )
> axis(side=1,at=seq(0,15,3),labels=seq(0,15,3))
> axis(side=1,at=seq(0,15,1),labels=rep("",16))
> mtext( side=3, line=0, "Average no. at risk (1000s)", adj=0.1 )
>
> barplot(t(yy[,6]/ilength), width=ilength,
+         space=0, xaxt="n", yaxt="n",
+         yaxs="i",col=gray(3/10),
+         xlim=c(0,15),ylim=c(0,300*fr),xlab="Insulin duration")
> axis(side=1,at=seq(0,15,3),labels=seq(0,15,3))
> axis(side=1,at=seq(0,15,1),labels=rep("",16))
> axis(side=2,at=0:2*20)
> # axis(side=2,at=0:6*10,labels=rep("",7) )
> dev.off()
null device
      1
>

```

```

-----
Program: dur-hist.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Ended: torsdag 31. marts 2011, 17:32:41
Elapsed: 00:00:44
-----

```

```

> proc.time()
  user system elapsed
32.42   6.06  45.87

```

2.3 Analysis disregarding duration

These programs use the suffix “a” for those including prevalent cases and suffix “i” for those only including incident cases.

```
R 2.12.1
```

```

-----
Program: anai1.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Started: torsdag 31. marts 2011, 17:32:42
-----

```

```

> # Same analysis as in anai1.r, except persons diagnosed with diabetes
> # prior to 1995 are included here
>
> library( Epi )

```

```
Attaching package: 'Epi'
```

```
The following object(s) are masked from 'package:base':
```

```

  merge.data.frame
> library( splines )
> # A wrapper for ns() where boundary knots are taken as the
> # smallest of the knots= argument
> source( "C:/Bendix/Steno/DM-register/NDR/R/Ns.r" )
> Ns
function (x, df = NULL, knots = NULL, intercept = FALSE, Boundary.knots = NULL)
{
  if (is.null(Boundary.knots)) {
    if (!is.null(knots)) {
      knots <- sort(unique(knots))
      ok <- c(1, length(knots))
      Boundary.knots <- knots[ok]
      knots <- knots[-ok]
    }
  }
  ns(x, df = df, knots = knots, intercept = intercept, Boundary.knots = Boundary.knots)
}
>
> # Get the data file:
> load( file = "../data/dmcaA.Rdata" )
> stat.table( list(state,DMtype), list( sum(y/1000), sum(d0), count() ),
+            data=dmca, margins=T )

```



```
-----DMtype-----
state      0      1      2      Total
Well      75637.67    NA    NA    75637.67
          346138.00    NA    NA    346138.00
          6000         0         0         6000

DM         425.41    0.30 1302.14   1727.84
          6937.00    2.00 20870.00  27809.00
          5215    1867    5948    13030

DM/Ins     437.60   44.95  198.62    681.17
          4450.00   27.00 2947.00   7424.00
          5426    2446    5666    13538

Total     76500.68  45.25 1500.76  78046.68
          357525.00  29.00 23817.00 381371.00
          16641    4313   11614   32568
-----
```

```
> stat.table( list(state,DMtype), list( sum(y), sum(d0), count() ), data=dmca )
```

```
-----DMtype-----
state      0      1      2
Well      75637670.45    NA    NA
          346138.00    NA    NA
          6000         0         0

DM         425406.99   300.32 1302136.62
          6937.00    2.00  20870.00
          5215    1867    5948

DM/Ins     437598.13 44950.07 198621.70
          4450.00   27.00  2947.00
          5426    2446    5666
-----
```

```
> str( dmca )
'data.frame': 32568 obs. of 40 variables:
 $ state : Factor w/ 3 levels "Well","DM","DM/Ins": 1 1 1 1 1 1 1 1 1 1 ...
 $ State : Factor w/ 2 levels "Well","DM+DM/Ins": 1 1 1 1 1 1 1 1 1 1 ...
 $ DMtype: num 0 0 0 0 0 0 0 0 0 0 ...
 $ sex   : Factor w/ 2 levels "M","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ a     : num 0 0 0 0 0 0 0 0 0 0 ...
 $ p     : num 1995 1995 1996 1996 1997 ...
 $ c     : num 1994 1995 1995 1996 1996 ...
 $ ax    : num 0.667 0.333 0.667 0.333 0.667 ...
 $ px    : num 1995 1996 1996 1997 1997 ...
 $ cx    : num 1995 1995 1996 1996 1997 ...
 $ y     : num 17870 18025 18061 17426 17448 ...
 $ d0    : num 2 4 2 2 3 1 4 4 2 4 ...
 $ d21   : num 0 0 0 0 0 0 0 0 0 ...
 $ d22   : num 0 0 0 0 0 0 0 0 0 ...
 $ d24   : num 0 0 0 0 0 0 0 0 0 ...
 $ d241  : num 0 0 0 0 0 0 0 0 0 ...
 $ d242  : num 0 0 0 0 0 0 0 0 0 ...
 $ d243  : num 0 0 0 0 0 0 0 0 0 ...
 $ d249  : num 0 0 0 0 0 0 0 0 0 ...
 $ d251  : num 0 0 0 0 0 0 0 0 0 ...
 $ d259  : num 0 0 0 0 0 0 0 0 0 ...
 $ d26   : num 0 0 0 0 0 0 0 0 0 ...
 $ d28   : num 0 0 0 0 0 0 0 0 0 ...
 $ d33   : num 0 0 0 0 0 0 0 0 0 ...
 $ d51   : num 0 0 0 0 0 0 0 0 0 ...
 $ d70   : num 0 0 0 0 0 0 0 0 0 ...
 $ d82   : num 0 0 0 0 0 0 0 0 0 ...
 $ d83   : num 0 0 0 0 0 0 0 0 0 ...
 $ d84   : num 0 0 0 0 0 0 0 0 0 ...
 $ d91   : num 0 0 0 0 0 0 0 0 0 ...
 $ d92   : num 0 0 1 0 0 0 0 0 0 ...
 $ d101  : num 1 1 0 1 1 0 0 0 1 0 ...
 $ d103  : num 0 0 0 0 0 0 0 0 0 ...
 $ d113  : num 1 1 1 1 0 0 0 0 3 ...
 $ d121  : num 0 0 0 0 0 0 0 0 0 ...
 $ d131  : num 0 0 0 0 0 0 0 0 0 ...
 $ d132  : num 0 0 0 0 0 0 0 0 0 ...
 $ d133  : num 0 0 0 0 0 0 0 0 0 ...
 $ d139  : num 0 0 0 0 2 0 0 0 0 ...
 $ d999  : num 0 2 0 0 0 1 4 4 1 1 ...
> d.col <- dxnam$d.col
> c.col <- 1:(d.col[1]-1)
>
> # Construct an array to hold the results
> dnam <- list( diag = dxnam$d.nam,
+             sex = c("M","F"),
+             type = c("DM/noIns","DM/Ins","Ins vs. noIns", "DM"),
+             est = c("Est","lo","hi") )
> res <- array( NA, dim=sapply(dnam,length), dimnames=dnam )
```

```

> # Construct an array to hold the no. cancer cases analysed
> dnam <- list( diag = c(as.character(dxn$dxnam),"PYRS","Deaths"),
+             sex = c("M","F"),
+             type = c("Well","DM/noIns","DM/Ins","DM") )
> nca <- array( NA, dim=sapply(dnam,length), dimnames=dnam )
>
> Nres <- dim( res )[1]
>
> # Knots for the natural splines
> a.kn <- seq( 10, 100,,9)
> p.kn <- seq(1995,2009,,5)
> c.kn <- seq(1900,2005,,9)
> # Contrast matrix to extract each of the RRs and also their ratio
> CM <- rbind( c( 1, 0),
+             c( 0, 1),
+             c(-1, 1) )
> rownames(CM) <- c("DM/noIns","DM/Ins","Ins vs. noIns")
>
> # Analysis for all sites
> for( i in 1:Nres )
+ {
+ data <- dmca[,c(c.col,d.col[i])]
+ names(data)[ncol(data)] <- "D"
+ m1 <- glm( D ~ Ns(ax,knots=a.kn) +
+           Ns(px,knots=p.kn) +
+           Ns(cx,knots=c.kn) +
+           state + offset( log(y) ),
+           family = poisson,
+           data = subset(data,sex=="M") )
+ f1 <- glm( D ~ Ns(ax,knots=a.kn) +
+           Ns(px,knots=p.kn) +
+           Ns(cx,knots=c.kn) +
+           state + offset( log(y) ),
+           family = poisson,
+           data = subset(data,sex=="F") )
+ # Collapse the DM and DM/ins levels and repeat all
+ m2 <- update( m1, ~ . - state + State )
+ f2 <- update( f1, ~ . - state + State )
+ # The RR estimates
+ res[i,"M",1:3,] <- ci.lin( m1, subset="state", ctr.mat=CM, E=T )[5:7]
+ res[i,"F",1:3,] <- ci.lin( f1, subset="state", ctr.mat=CM, E=T )[5:7]
+ res[i,"M", 4,] <- ci.lin( m2, subset="State", E=T )[5:7]
+ res[i,"F", 4,] <- ci.lin( f2, subset="State", E=T )[5:7]
+ # The total number of cases
+ nca[i,1:3] <- with(data,tapply( D, list(sex,state), sum, na.rm=T ))
+ }
There were 50 or more warnings (use warnings() to see the first 50)
> # The rows of person years
> nca["PYRS" ,1:3] <- with(dmca,tapply( y/1000, list(sex,state), sum, na.rm=T ))
> # Get the right number of cases for the analysis of DM as one state
> nca[,4] <- nca[,2] + nca[,3]
> # Get rid of the male/females in the wrong places
> no.M <- c( grep("uteri",dimnames(res)[["diag"]]),
+          grep("Ovary",dimnames(res)[["diag"]]) )
> no.F <- c( grep("Prost",dimnames(res)[["diag"]]),
+          grep("Testi",dimnames(res)[["diag"]]) )
> res[no.M,"M",,] <- NA
> res[no.F,"F",,] <- NA
> round( ftable( res, row.vars=1:2 ), 2 )

```

diag	sex	type DM/noIns			DM/Ins			Ins vs. noIns			DM		
		est	Est	lo hi	Est	lo hi	Est	lo hi	Est	lo hi	Est	lo hi	
All malignant neoplasms	M	1.16	1.15	1.18	1.15	1.12	1.19	0.99	0.96	1.03	1.16	1.15	1.18
	F	1.15	1.13	1.17	1.19	1.15	1.24	1.04	1.00	1.08	1.16	1.14	1.18
Oesophagus	M	1.25	1.11	1.40	1.31	1.07	1.61	1.05	0.83	1.33	1.26	1.14	1.40
	F	0.90	0.72	1.12	0.89	0.57	1.39	0.99	0.61	1.61	0.90	0.74	1.10
Stomach	M	1.26	1.13	1.39	1.26	1.04	1.52	1.00	0.81	1.24	1.26	1.15	1.38
	F	1.28	1.11	1.49	1.45	1.11	1.90	1.13	0.84	1.52	1.32	1.16	1.50
Colon incl. rectosigmoideum	M	1.31	1.24	1.38	1.18	1.06	1.31	0.90	0.80	1.01	1.28	1.22	1.35
	F	1.17	1.11	1.24	1.12	1.00	1.26	0.96	0.84	1.09	1.17	1.11	1.23
Ascending colon	M	1.40	1.26	1.54	1.29	1.06	1.57	0.92	0.75	1.14	1.37	1.25	1.51
	F	1.30	1.19	1.42	1.03	0.84	1.26	0.79	0.64	0.99	1.25	1.15	1.36
Transverse colon	M	1.45	1.26	1.66	1.38	1.06	1.80	0.96	0.71	1.28	1.44	1.27	1.63
	F	1.16	1.00	1.34	1.27	0.96	1.68	1.10	0.80	1.49	1.18	1.03	1.34
Descending and sigmoid colon	M	1.20	1.11	1.30	1.07	0.92	1.24	0.89	0.75	1.05	1.17	1.10	1.26
	F	1.06	0.96	1.16	1.13	0.95	1.35	1.07	0.88	1.30	1.07	0.99	1.16
Other colon (unspec. or multiple)	M	1.50	1.26	1.79	1.23	0.85	1.77	0.82	0.55	1.22	1.44	1.23	1.70
	F	1.25	1.03	1.50	1.22	0.83	1.78	0.98	0.64	1.48	1.24	1.04	1.47
Rectum (excl. anus)	M	1.10	1.02	1.18	1.01	0.88	1.16	0.92	0.78	1.07	1.08	1.01	1.15
	F	1.02	0.92	1.12	0.86	0.70	1.06	0.85	0.68	1.06	0.99	0.90	1.08
Colorectal cancer (excl. anus)	M	1.23	1.18	1.28	1.11	1.02	1.21	0.91	0.83	0.99	1.20	1.16	1.25
	F	1.13	1.08	1.19	1.05	0.95	1.16	0.93	0.83	1.04	1.12	1.07	1.17
Liver	M	3.63	3.28	4.02	5.35	4.62	6.20	1.47	1.25	1.74	4.01	3.66	4.38
	F	1.78	1.48	2.14	2.56	1.90	3.45	1.44	1.03	2.02	1.93	1.64	2.27
Pancreas	M	2.08	1.92	2.26	3.72	3.32	4.17	1.79	1.57	2.04	2.43	2.27	2.61
	F	1.90	1.75	2.07	3.47	3.07	3.93	1.83	1.58	2.11	2.20	2.05	2.37
Lung, bronchus and pleura	M	1.07	1.03	1.12	1.18	1.09	1.27	1.10	1.01	1.20	1.09	1.05	1.14
	F	1.03	0.97	1.08	1.04	0.93	1.15	1.01	0.90	1.14	1.03	0.98	1.08
Melanoma of skin	M	0.97	0.87	1.07	0.79	0.65	0.96	0.82	0.66	1.02	0.93	0.85	1.01

Breast	F	0.81	0.72	0.91	0.80	0.64	0.98	0.99	0.78	1.26	0.80	0.72	0.89
	M	0.87	0.56	1.36	1.12	0.53	2.38	1.28	0.55	3.02	0.92	0.63	1.37
	F	1.07	1.03	1.11	0.98	0.91	1.05	0.92	0.84	0.99	1.05	1.01	1.08
Cervix uteri	M	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	F	1.00	0.86	1.16	1.10	0.86	1.40	1.11	0.84	1.46	1.02	0.90	1.16
Corpus uteri	M	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	F	1.59	1.48	1.71	1.67	1.45	1.91	1.05	0.90	1.22	1.61	1.50	1.72
Ovary, fallopian tube etc.	M	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
	F	1.03	0.94	1.14	0.92	0.76	1.12	0.89	0.72	1.11	1.01	0.92	1.10
Prostate	M	0.96	0.93	1.00	0.73	0.68	0.80	0.76	0.70	0.83	0.91	0.88	0.95
	F	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Testis	M	0.81	0.59	1.10	0.71	0.49	1.04	0.88	0.54	1.43	0.77	0.60	0.98
	F	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
Kidney	M	1.49	1.34	1.64	1.58	1.33	1.88	1.06	0.88	1.30	1.51	1.38	1.65
	F	1.62	1.42	1.85	2.03	1.62	2.53	1.25	0.97	1.61	1.70	1.52	1.91
Urinary bladder	M	1.15	1.09	1.21	1.05	0.94	1.17	0.91	0.81	1.03	1.13	1.08	1.19
	F	0.98	0.88	1.10	0.96	0.78	1.20	0.98	0.77	1.25	0.98	0.89	1.08
Brain	M	1.08	0.96	1.23	1.04	0.84	1.29	0.96	0.75	1.23	1.07	0.96	1.20
	F	1.12	0.98	1.30	1.42	1.13	1.79	1.26	0.97	1.65	1.19	1.05	1.35
Thyroid	M	1.21	0.84	1.73	1.21	0.66	2.19	1.00	0.50	1.99	1.21	0.88	1.65
	F	1.12	0.86	1.47	1.27	0.82	1.95	1.13	0.68	1.86	1.16	0.92	1.46
Hodgkin's lymphoma	M	1.58	1.15	2.16	1.32	0.79	2.20	0.84	0.46	1.50	1.50	1.14	1.97
	F	1.65	1.12	2.44	0.97	0.43	2.16	0.59	0.24	1.42	1.46	1.02	2.08
Non-Hodgkin lymphoma	M	1.15	1.04	1.28	0.93	0.76	1.14	0.81	0.65	1.01	1.10	1.01	1.21
	F	1.12	1.00	1.26	1.33	1.09	1.63	1.19	0.95	1.50	1.16	1.05	1.29
Multiple myeloma	M	1.00	0.86	1.15	0.95	0.72	1.25	0.95	0.70	1.29	0.99	0.87	1.12
	F	1.03	0.87	1.23	1.13	0.81	1.56	1.09	0.76	1.57	1.05	0.90	1.23
Leukaemia	M	1.05	0.95	1.17	1.15	0.96	1.38	1.10	0.89	1.34	1.07	0.98	1.18
	F	1.11	0.98	1.25	1.09	0.86	1.39	0.99	0.76	1.29	1.10	0.99	1.23
Other	M	1.25	1.20	1.31	1.25	1.16	1.36	1.00	0.91	1.09	1.25	1.20	1.31
	F	1.27	1.21	1.33	1.39	1.27	1.53	1.10	0.99	1.22	1.29	1.24	1.35

> round(ftable(nca, col.vars=3:2), 0)

diag	type	Well	DM/noIns		DM/Ins		DM	F	
sex	M	F	M	F	M	F	M	F	F
All malignant neoplasms		167394	178744	15626	12183	4143	3281	19769	15464
Oesophagus		3282	1304	322	85	92	20	414	105
Stomach		4171	2289	416	203	111	54	527	257
Colon incl. rectosigmoideum		13853	15136	1583	1351	364	298	1947	1649
Ascending colon		3636	5126	442	530	104	95	546	625
Transverse colon		1819	2172	234	203	57	50	291	253
Descending and sigmoid colon		7292	6601	764	496	173	126	937	622
Other colon (unspec. or multiple)		1106	1237	143	122	30	27	173	149
Rectum (excl. anus)		8876	6214	832	449	201	91	1033	540
Colorectal cancer (excl. anus)		22729	21350	2415	1800	565	389	2980	2189
Liver		1776	1103	500	131	200	45	700	176
Pancreas		4041	4425	687	622	329	267	1016	889
Lung, bronchus and pleura		25302	20283	2294	1397	664	361	2958	1758
Melanoma of skin		7008	8873	410	292	104	87	514	379
Breast		298	52190	21	2935	7	750	28	3685
Cervix uteri		0	5691	0	181	0	67	0	248
Corpus uteri		0	8057	0	792	0	216	0	1008
Ovary, fallopian tube etc.		0	7400	0	421	0	102	0	523
Prostate		31713	0	3099	0	598	0	3697	0
Testis		4257	0	42	0	27	0	69	0
Kidney		3976	2434	430	256	130	80	560	336
Urinary bladder		14781	4906	1475	350	342	82	1817	432
Brain		4922	4310	273	208	83	75	356	283
Thyroid		593	1511	32	56	11	21	43	77
Hodgkin's lymphoma		990	723	44	28	15	6	59	34
Non-Hodgkin lymphoma		5434	4602	422	312	98	95	520	407
Multiple myeloma		2452	1883	208	141	52	37	260	178
Leukaemia		5423	4050	407	277	119	66	526	343
Other		24246	21360	2129	1696	596	461	2725	2157
PYRS		37646	37991	871	857	372	309	1243	1166
Deaths		NA	NA	NA	NA	NA	NA	NA	NA

> save(res, nca, file="../data/anala.Rdata")

>

```
-----
Program: anala.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Ended: torsdag 31. marts 2011, 17:35:53
Elapsed: 00:03:10
-----
```

```
> proc.time()
user system elapsed
185.07 5.23 191.51
```

R 2.12.1

```
-----
Program: anali.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Started: torsdag 31. marts 2011, 17:35:54
-----
```

```
> # Same analysis as in anala.r, except persons diagnosed with diabetes
> # prior to 1995 are excluded
```

>

```

> library( Epi )
Attaching package: 'Epi'

The following object(s) are masked from 'package:base':

  merge.data.frame

> library( splines )
> # A wrapper for ns() where boundary knots are taken as the
> # smallest of the knots= argument
> source( "C:/Bendix/Steno/DM-register/NDR/R/Ns.r" )
> Ns
function (x, df = NULL, knots = NULL, intercept = FALSE, Boundary.knots = NULL)
{
  if (is.null(Boundary.knots)) {
    if (!is.null(knots)) {
      knots <- sort(unique(knots))
      ok <- c(1, length(knots))
      Boundary.knots <- knots[ok]
      knots <- knots[-ok]
    }
  }
  ns(x, df = df, knots = knots, intercept = intercept, Boundary.knots = Boundary.knots)
}
>
> # Get the data file:
> load( file = "../data/dmcaA.Rdata" )
> stat.table( list(state,DMtype), list( sum(y/1000), sum(d0), count() ),
+           data=dmca, margins=T )
-----
state      0      1      2      Total
-----
Well      75637.67    NA     NA    75637.67
          346138.00    NA     NA   346138.00
          6000         0         0     6000

DM         425.41    0.30 1302.14  1727.84
          6937.00    2.00 20870.00 27809.00
          5215     1867    5948    13030

DM/Ins     437.60   44.95  198.62   681.17
          4450.00   27.00 2947.00  7424.00
          5426     2446    5666   13538

Total      76500.68   45.25 1500.76  78046.68
          357525.00  29.00 23817.00 381371.00
          16641     4313   11614   32568
-----

> dmca <- subset( dmca, state %in% "Well" | DMtype > 0 )
> stat.table( list(state,DMtype), list( sum(y), sum(d0), count() ), data=dmca )
-----
state      0      1      2
-----
Well      75637670.45    NA     NA
          346138.00    NA     NA
          6000         0         0

DM         NA    300.32 1302136.62
          NA     2.00  20870.00
          0     1867    5948

DM/Ins     NA 44950.07 198621.70
          NA   27.00  2947.00
          0   2446    5666
-----

> str( dmca )
'data.frame': 21927 obs. of 40 variables:
 $ state : Factor w/ 3 levels "Well","DM","DM/Ins": 1 1 1 1 1 1 1 1 1 1 ...
 $ State : Factor w/ 2 levels "Well","DM+DM/Ins": 1 1 1 1 1 1 1 1 1 1 ...
 $ DMtype: num 0 0 0 0 0 0 0 0 0 0 ...
 $ sex   : Factor w/ 2 levels "M","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ a     : num 0 0 0 0 0 0 0 0 0 0 ...
 $ p     : num 1995 1995 1996 1996 1997 ...
 $ c     : num 1994 1995 1995 1996 1996 ...
 $ ax    : num 0.667 0.333 0.667 0.333 0.667 ...
 $ px    : num 1995 1996 1996 1997 1997 ...
 $ cx    : num 1995 1995 1996 1996 1997 ...
 $ y     : num 17870 18025 18061 17426 17448 ...
 $ d0    : num 2 4 2 2 3 1 4 4 2 4 ...
 $ d21   : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d22   : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d24   : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d241  : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d242  : num 0 0 0 0 0 0 0 0 0 0 ...
 $ d243  : num 0 0 0 0 0 0 0 0 0 0 ...

```

```

$ d249 : num 0 0 0 0 0 0 0 0 0 0 ...
$ d251 : num 0 0 0 0 0 0 0 0 0 0 ...
$ d259 : num 0 0 0 0 0 0 0 0 0 0 ...
$ d26 : num 0 0 0 0 0 0 0 0 0 0 ...
$ d28 : num 0 0 0 0 0 0 0 0 0 0 ...
$ d33 : num 0 0 0 0 0 0 0 0 0 0 ...
$ d51 : num 0 0 0 0 0 0 0 0 0 0 ...
$ d70 : num 0 0 0 0 0 0 0 0 0 0 ...
$ d82 : num 0 0 0 0 0 0 0 0 0 0 ...
$ d83 : num 0 0 0 0 0 0 0 0 0 0 ...
$ d84 : num 0 0 0 0 0 0 0 0 0 0 ...
$ d91 : num 0 0 0 0 0 0 0 0 0 0 ...
$ d92 : num 0 0 1 0 0 0 0 0 0 0 ...
$ d101 : num 1 1 0 1 1 0 0 0 1 0 ...
$ d103 : num 0 0 0 0 0 0 0 0 0 0 ...
$ d113 : num 1 1 1 1 0 0 0 0 0 3 ...
$ d121 : num 0 0 0 0 0 0 0 0 0 0 ...
$ d131 : num 0 0 0 0 0 0 0 0 0 0 ...
$ d132 : num 0 0 0 0 0 0 0 0 0 0 ...
$ d133 : num 0 0 0 0 0 0 0 0 0 0 ...
$ d139 : num 0 0 0 0 2 0 0 0 0 0 ...
$ d999 : num 0 2 0 0 0 1 4 4 1 1 ...
> d.col <- dxnam$d.col
> c.col <- 1:(d.col[1]-1)
>
> # Construct an array to hold the results
> dnam <- list( diag = dxnam$d.nam,
+             sex = c("M","F"),
+             type = c("DM/noIns","DM/Ins","Ins vs. noIns", "DM"),
+             est = c("Est","lo","hi") )
> res <- array( NA, dim=sapply(dnam,length), dimnames=dnam )
> # Construct an array to hold the no. cancer cases analysed
> dnam <- list( diag = c(as.character(dxnam$d.nam),"PYRS","Deaths"),
+             sex = c("M","F"),
+             type = c("Well","DM/noIns","DM/Ins","DM") )
> nca <- array( NA, dim=sapply(dnam,length), dimnames=dnam )
>
> Nres <- dim( res )[1]
>
> # Knots for the natural splines
> a.kn <- seq( 10, 100,,9)
> p.kn <- seq(1995,2009,,5)
> c.kn <- seq(1900,2005,,9)
> # Contrast matrix to extract each of the RRs and also their ratio
> CM <- rbind( c( 1, 0),
+             c( 0, 1),
+             c(-1, 1) )
> rownames(CM) <- c("DM/noIns","DM/Ins","Ins vs. noIns")
>
> # Analysis for all sites
> for( i in 1:Nres )
+ {
+ data <- dmca[,c(c.col,d.col[i])]
+ names(data)[ncol(data)] <- "D"
+ m1 <- glm( D ~ Ns(ax,knots=a.kn) +
+           Ns(px,knots=p.kn) +
+           Ns(cx,knots=c.kn) +
+           state + offset( log(y) ),
+           family = poisson,
+           data = subset(data,sex=="M") )
+ f1 <- glm( D ~ Ns(ax,knots=a.kn) +
+           Ns(px,knots=p.kn) +
+           Ns(cx,knots=c.kn) +
+           state + offset( log(y) ),
+           family = poisson,
+           data = subset(data,sex=="F") )
+ # Collapse the DM and DM/ins levels and repeat all
+ m2 <- update( m1, ~ . - state + State )
+ f2 <- update( f1, ~ . - state + State )
+ # The RR estimates
+ res[i,"M",1:3,] <- ci.lin( m1, subset="state", ctr.mat=CM, E=T )[,5:7]
+ res[i,"F",1:3,] <- ci.lin( f1, subset="state", ctr.mat=CM, E=T )[,5:7]
+ res[i,"M", 4,] <- ci.lin( m2, subset="State", E=T )[,5:7]
+ res[i,"F", 4,] <- ci.lin( f2, subset="State", E=T )[,5:7]
+ # The total number of cases
+ nca[i,1:3] <- with(data,tapply( D, list(sex,state), sum, na.rm=T ) )
+ }
There were 50 or more warnings (use warnings() to see the first 50)
> # The rows of person years
> nca["PYRS" ,,1:3] <- with(dmca,tapply( y/1000, list(sex,state), sum, na.rm=T ) )
> # Get the right number of cases for the analysis of DM as one state
> nca[,4] <- nca[,2] + nca[,3]
> # Get rid of the male/females in the wrong places
> no.M <- c( grep("uteri",dimnames(res)[["diag"]]),
+           grep("Ovary",dimnames(res)[["diag"]]) )
> no.F <- c( grep("Prost",dimnames(res)[["diag"]]),
+           grep("Testi",dimnames(res)[["diag"]]) )
> res[no.M,"M",,] <- NA
> res[no.F,"F",,] <- NA

```

```

> round( ftable( res, row.vars=1:2 ), 2 )
      type DM/noIns      DM/Ins      Ins vs. noIns      DM
      est  Est  lo  hi  Est  lo  hi  Est  lo  hi  Est  lo  hi
diag      sex
All malignant neoplasms M      1.19 1.17 1.21  1.35 1.29 1.42  1.14 1.08 1.20  1.21 1.19 1.23
                        F      1.17 1.15 1.20  1.44 1.37 1.53  1.23 1.16 1.30  1.20 1.18 1.23
Oesophagus      M      1.27 1.11 1.45  1.24 0.87 1.79  0.98 0.67 1.43  1.27 1.12 1.44
                        F      0.96 0.75 1.24  1.15 0.57 2.30  1.19 0.57 2.49  0.98 0.77 1.24
Stomach      M      1.25 1.11 1.41  1.53 1.15 2.05  1.23 0.90 1.68  1.28 1.15 1.43
                        F      1.29 1.09 1.54  1.85 1.19 2.87  1.43 0.89 2.28  1.34 1.14 1.58
Colon incl. rectosigmoideum M      1.32 1.24 1.40  1.32 1.11 1.56  1.00 0.84 1.19  1.32 1.24 1.40
                        F      1.22 1.14 1.30  1.10 0.89 1.35  0.90 0.73 1.12  1.20 1.13 1.28
Ascending colon M      1.40 1.24 1.57  1.33 0.96 1.84  0.95 0.68 1.34  1.39 1.24 1.55
                        F      1.38 1.25 1.54  1.02 0.71 1.47  0.74 0.51 1.08  1.35 1.22 1.50
Transverse colon M      1.46 1.24 1.71  1.88 1.29 2.76  1.29 0.86 1.94  1.50 1.29 1.74
                        F      1.22 1.03 1.44  1.48 0.93 2.36  1.22 0.75 1.99  1.24 1.06 1.45
Descending and sigmoid colon M      1.20 1.10 1.31  1.21 0.95 1.55  1.01 0.78 1.30  1.20 1.11 1.31
                        F      1.05 0.94 1.18  0.95 0.66 1.35  0.90 0.62 1.30  1.04 0.94 1.16
Other colon (unspec. or multiple) M      1.60 1.31 1.95  0.98 0.49 1.96  0.61 0.30 1.25  1.53 1.26 1.86
                        F      1.28 1.03 1.59  1.43 0.77 2.67  1.12 0.58 2.15  1.29 1.05 1.59
Rectum (excl. anus) M      1.11 1.02 1.21  1.09 0.87 1.36  0.98 0.77 1.24  1.11 1.03 1.20
                        F      1.00 0.90 1.13  0.91 0.64 1.31  0.91 0.62 1.32  1.00 0.89 1.11
Colorectal cancer (excl. anus) M      1.24 1.18 1.30  1.22 1.07 1.40  0.99 0.86 1.14  1.24 1.18 1.30
                        F      1.16 1.09 1.22  1.04 0.87 1.25  0.90 0.75 1.09  1.15 1.08 1.21
Liver      M      3.37 2.99 3.80  8.12 6.63 9.93  2.41 1.93 3.00  3.90 3.50 4.35
                        F      1.55 1.23 1.96  4.01 2.57 6.26  2.59 1.58 4.23  1.77 1.43 2.19
Pancreas      M      2.36 2.16 2.58  6.89 5.98 7.94  2.92 2.49 3.42  2.86 2.64 3.10
                        F      2.19 1.99 2.40  7.21 6.17 8.42  3.30 2.77 3.93  2.65 2.43 2.88
Lung, bronchus and pleura M      1.14 1.08 1.19  1.45 1.29 1.64  1.28 1.13 1.45  1.17 1.12 1.23
                        F      1.10 1.04 1.17  1.44 1.23 1.68  1.31 1.11 1.54  1.14 1.07 1.20
Melanoma of skin M      0.95 0.85 1.06  0.76 0.55 1.05  0.80 0.57 1.12  0.92 0.83 1.03
                        F      0.77 0.68 0.89  0.85 0.60 1.21  1.10 0.76 1.60  0.78 0.69 0.89
Breast      M      0.76 0.43 1.33  1.97 0.73 5.30  2.59 0.84 7.94  0.89 0.54 1.46
                        F      1.05 1.00 1.10  1.01 0.89 1.14  0.96 0.84 1.09  1.04 1.00 1.09
Cervix uteri M      NA  NA  NA  NA  NA  NA  NA  NA  NA  NA  NA  NA  NA
                        F      1.03 0.86 1.23  1.41 0.95 2.09  1.37 0.89 2.09  1.08 0.92 1.27
Corpus uteri M      NA  NA  NA  NA  NA  NA  NA  NA  NA  NA  NA  NA
                        F      1.57 1.44 1.71  1.65 1.30 2.10  1.05 0.82 1.36  1.58 1.45 1.71
Ovary, fallopian tube etc. M      NA  NA  NA  NA  NA  NA  NA  NA  NA  NA  NA  NA
                        F      1.07 0.96 1.20  1.15 0.83 1.58  1.07 0.76 1.50  1.08 0.97 1.20
Prostate      M      0.97 0.93 1.01  0.76 0.67 0.86  0.79 0.69 0.90  0.94 0.91 0.98
                        F      NA  NA  NA  NA  NA  NA  NA  NA  NA  NA  NA  NA
Testis      M      0.88 0.63 1.22  0.50 0.24 1.05  0.57 0.25 1.28  0.78 0.58 1.06
                        F      NA  NA  NA  NA  NA  NA  NA  NA  NA  NA  NA  NA
Kidney      M      1.47 1.30 1.65  2.04 1.58 2.63  1.39 1.06 1.83  1.53 1.38 1.71
                        F      1.66 1.43 1.93  3.38 2.48 4.62  2.04 1.45 2.86  1.83 1.59 2.10
Urinary bladder M      1.21 1.14 1.29  1.10 0.92 1.32  0.91 0.75 1.10  1.20 1.13 1.27
                        F      1.02 0.90 1.16  1.15 0.80 1.65  1.13 0.77 1.64  1.03 0.91 1.16
Brain      M      1.15 1.01 1.33  1.15 0.82 1.63  1.00 0.69 1.44  1.15 1.01 1.31
                        F      1.20 1.02 1.41  1.77 1.23 2.54  1.47 1.00 2.18  1.26 1.09 1.47
Thyroid      M      1.31 0.88 1.96  1.80 0.80 4.04  1.38 0.57 3.35  1.38 0.96 1.99
                        F      1.08 0.78 1.48  2.20 1.25 3.89  2.05 1.07 3.90  1.22 0.92 1.62
Hodgkin's lymphoma M      1.84 1.31 2.58  1.96 0.98 3.95  1.07 0.50 2.29  1.86 1.37 2.53
                        F      1.81 1.18 2.79  0.95 0.24 3.81  0.52 0.12 2.22  1.69 1.12 2.55
Non-Hodgkin lymphoma M      1.18 1.05 1.32  1.00 0.72 1.38  0.85 0.60 1.19  1.16 1.04 1.29
                        F      1.14 1.00 1.30  1.35 0.94 1.93  1.18 0.81 1.73  1.16 1.02 1.32
Multiple myeloma M      1.07 0.91 1.25  0.99 0.63 1.55  0.92 0.57 1.49  1.06 0.91 1.23
                        F      1.04 0.85 1.27  0.77 0.38 1.54  0.74 0.36 1.52  1.02 0.84 1.23
Leukaemia      M      1.03 0.92 1.16  1.05 0.76 1.45  1.01 0.72 1.43  1.03 0.92 1.16
                        F      1.16 1.01 1.34  1.25 0.83 1.89  1.08 0.70 1.66  1.17 1.02 1.34
Other      M      1.26 1.20 1.33  1.44 1.26 1.64  1.14 0.99 1.31  1.28 1.22 1.35
                        F      1.30 1.23 1.38  1.65 1.41 1.92  1.26 1.07 1.48  1.34 1.27 1.41
>
> # For completeness, insert the deaths in the last line
> load( file="./data/DMmD.Rdata" )
> nca["Deaths",,1:3] <- with( DMm, tapply( dd, list(sex,state), sum ) )
> nca["Deaths",,4] <- nca["Deaths",,2]+nca["Deaths",,3]
>
> round( ftable( nca, col.vars=3:2 ) )
      type Well      DM/noIns      DM/Ins      DM
      sex  M      F      M      F      M      F      M      F
diag
All malignant neoplasms 167394 178744  11837 9035 1716 1258 13553 10293
Oesophagus      3282  1304  242  65  30  8  272  73
Stomach      4171  2289  299  139  46  20  345  159
Colon incl. rectosigmoideum 13853 15136  1163 981 138 88 1301 1069
Ascending colon  3636  5126  324  399  37  29  361  428
Transverse colon 1819  2172  174  151  27  18  201  169
Descending and sigmoid colon 7292  6601  554  342  66  31  620  373
Other colon (unspec. or multiple) 1106  1237  111  89  8  10  119  99
Rectum (excl. anus) 8876  6214  625  316  77  30  702  346
Colorectal cancer (excl. anus) 22729 21350  1788 1297  215 118 2003 1415
Liver      1776  1103  338  78  103  20  441  98
Pancreas      4041  4425  570  504  208 169  778  673
Lung, bronchus and pleura 25302 20283  1766 1129  274 163 2040 1292
Melanoma of skin  7008  8873  314  214  38  32  352  246
Breast      298  52190  13  2163  4  257  17  2420
Cervix uteri  0  5691  0  132  0  25  0  157
Corpus uteri  0  8057  0  567  0  67  0  634

```

```

Ovary, fallopian tube etc.      0 7400      0 313      0 38      0 351
Prostate                       31713 0      2425 0      239 0      2664 0
Testis                         4257 0      37 0      7 0      44 0
Kidney                         3976 2434      319 187      60 41      379 228
Urinary bladder                14781 4906      1110 259      118 30      1228 289
Brain                          4922 4310      219 163      33 30      252 193
Thyroid                        593 1511      26 40      6 12      32 52
Hodgkin's lymphoma             990 723      38 23      8 2      46 25
Non-Hodgkin lymphoma           5434 4602      321 229      37 30      358 259
Multiple myeloma                2452 1883      165 103      19 8      184 111
Leukaemia                      5423 4050      292 205      37 23      329 228
Other                          24246 21360      1555 1225      234 165      1789 1390
PYRS                           37646 37991      664 638      139 104      804 742
Deaths                         225684 237814      19737 17987      3872 2782      23609 20769
> round( apply( nca, c(1,3), sum ) )

```

diag	Well	DM/noIns	DM/Ins	DM
All malignant neoplasms	346138	20872	2974	23846
Oesophagus	4586	307	38	345
Stomach	6460	438	66	504
Colon incl. rectosigmoideum	28989	2144	226	2370
Ascending colon	8762	723	66	789
Transverse colon	3991	325	45	370
Descending and sigmoid colon	13893	896	97	993
Other colon (unspec. or multiple)	2343	200	18	218
Rectum (excl. anus)	15090	941	107	1048
Colorectal cancer (excl. anus)	44079	3085	333	3418
Liver	2879	416	123	539
Pancreas	8466	1074	377	1451
Lung, bronchus and pleura	45585	2895	437	3332
Melanoma of skin	15881	528	70	598
Breast	52488	2176	261	2437
Cervix uteri	5691	132	25	157
Corpus uteri	8057	567	67	634
Ovary, fallopian tube etc.	7400	313	38	351
Prostate	31713	2425	239	2664
Testis	4257	37	7	44
Kidney	6410	506	101	607
Urinary bladder	19687	1369	148	1517
Brain	9232	382	63	445
Thyroid	2104	66	18	84
Hodgkin's lymphoma	1713	61	10	71
Non-Hodgkin lymphoma	10036	550	67	617
Multiple myeloma	4335	268	27	295
Leukaemia	9473	497	60	557
Other	45606	2780	399	3179
PYRS	75638	1302	244	1546
Deaths	463498	37724	6654	44378

```

> save( res, nca, file="./data/anali.Rdata" )
>
-----
Program: anali.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Ended: torsdag 31. marts 2011, 17:38:07
Elapsed: 00:02:13
-----
> proc.time()
  user system elapsed
128.90   3.79  134.10

R 2.12.1
-----
Program: plotia.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Started: torsdag 31. marts 2011, 17:38:08
-----
> library( Epi )

Attaching package: 'Epi'

The following object(s) are masked from 'package:base':

  merge.data.frame

> source( "c:/stat/r/bxc/library.sources/useful/r/plt.r" )
> source( "c:/stat/r/bxc/library.sources/useful/r/cnr.r" )
> load( file="./data/anala.Rdata" )
> str( res )
num [1:29, 1:2, 1:4, 1:3] 1.16 1.25 1.26 1.31 1.4 ...
- attr(*, "dimnames")=List of 4
..$ diag: chr [1:29] "All malignant neoplasms" "Oesophagus" "Stomach" "Colon incl. rectosigmoideum" ...
..$ sex : chr [1:2] "M" "F"
..$ type: chr [1:4] "DM/noIns" "DM/Ins" "Ins vs. noIns" "DM"
..$ est : chr [1:3] "Est" "lo" "hi"
> dimnames(res)[[1]] <- gsub( "\\(excl\\. anus)", "", dimnames(res)[[1]] )
> res["Breast", "M", ,] <- NA
> Nres <- dim(res)[1]

```

```

>
> # Check that sites comprising all cancers are properly selected
> xsites <- c(1,4,10,29:31)
> dimnames(nca)[[1]][ xsites]
[1] "All malignant neoplasms"      "Colon incl. rectosigmoideum"
[3] "Colorectal cancer (excl. anus)" "Other"
[5] "PYRS"                          "Deaths"
> dimnames(nca)[[1]][-xsites]
[1] "Oesophagus"          "Stomach"
[3] "Ascending colon"     "Transverse colon"
[5] "Descending and sigmoid colon" "Other colon (unspec. or multiple)"
[7] "Rectum (excl. anus)" "Liver"
[9] "Pancreas"           "Lung, bronchus and pleura"
[11] "Melanoma of skin"   "Breast"
[13] "Cervix uteri"       "Corpus uteri"
[15] "Ovary, fallopian tube etc." "Prostate"
[17] "Testis"             "Kidney"
[19] "Urinary bladder"    "Brain"
[21] "Thyroid"            "Hodgkin's lymphoma"
[23] "Non-Hodgkin lymphoma" "Multiple myeloma"
[25] "Leukaemia"
> nca[ 1,,] -
+ apply( nca[-xsites,,], 2:3, sum )
  type
sex Well DM/noIns DM/Ins  DM
M 24246 2129 596 2725
F 21360 1696 461 2157
> nca["Other",,]
  type
sex Well DM/noIns DM/Ins  DM
M 24246 2129 596 2725
F 21360 1696 461 2157
>
> round( ftable( nca[ 30,,drop=F], col.vars=3:2 ), 1 )
  type Well DM/noIns DM/Ins  DM
sex M F M F M F M F M F
diag
PYRS 37646.2 37991.5 870.7 857.2 372.5 308.7 1243.1 1165.9
> ftable( nca[-30,,], col.vars=3:2 )
  type Well DM/noIns DM/Ins  DM
sex M F M F M F M F M F
diag
All malignant neoplasms 167394 178744 15626 12183 4143 3281 19769 15464
Oesophagus 3282 1304 322 85 92 20 414 105
Stomach 4171 2289 416 203 111 54 527 257
Colon incl. rectosigmoideum 13853 15136 1583 1351 364 298 1947 1649
Ascending colon 3636 5126 442 530 104 95 546 625
Transverse colon 1819 2172 234 203 57 50 291 253
Descending and sigmoid colon 7292 6601 764 496 173 126 937 622
Other colon (unspec. or multiple) 1106 1237 143 122 30 27 173 149
Rectum (excl. anus) 8876 6214 832 449 201 91 1033 540
Colorectal cancer (excl. anus) 22729 21350 2415 1800 565 389 2980 2189
Liver 1776 1103 500 131 200 45 700 176
Pancreas 4041 4425 687 622 329 267 1016 889
Lung, bronchus and pleura 25302 20283 2294 1397 664 361 2958 1758
Melanoma of skin 7008 8873 410 292 104 87 514 379
Breast 298 52190 21 2935 7 750 28 3685
Cervix uteri 0 5691 0 181 0 67 0 248
Corpus uteri 0 8057 0 792 0 216 0 1008
Ovary, fallopian tube etc. 0 7400 0 421 0 102 0 523
Prostate 31713 0 3099 0 598 0 3697 0
Testis 4257 0 42 0 27 0 69 0
Kidney 3976 2434 430 256 130 80 560 336
Urinary bladder 14781 4906 1475 350 342 82 1817 432
Brain 4922 4310 273 208 83 75 356 283
Thyroid 593 1511 32 56 11 21 43 77
Hodgkin's lymphoma 990 723 44 28 15 6 59 34
Non-Hodgkin lymphoma 5434 4602 422 312 98 95 520 407
Multiple myeloma 2452 1883 208 141 52 37 260 178
Leukaemia 5423 4050 407 277 119 66 526 343
Other 24246 21360 2129 1696 596 461 2725 2157
Deaths NA NA NA NA NA NA NA NA
> # What fraction does the analysed sites comprise:
> ftable( round( 100 - 100 * nca["Other",,drop=F] / nca[1,,drop=F], 1 ),
+ col.vars=3:2 )
  type Well DM/noIns DM/Ins  DM
sex M F M F M F M F M F
diag
Other 85.5 88.0 86.4 86.1 85.6 85.9 86.2 86.1
>
> sub <- c(1:3,10,5:7,9,11:28)
> dimnames(res)[[1]][-sub]
[1] "Colon incl. rectosigmoideum" "Other colon (unspec. or multiple)"
[3] "Other"
> dimnames(res)[[1]][sub]
[1] "All malignant neoplasms" "Oesophagus"
[3] "Stomach" "Colorectal cancer"
[5] "Ascending colon" "Transverse colon"
[7] "Descending and sigmoid colon" "Rectum"

```



```

[9] "Liver" "Pancreas"
[11] "Lung, bronchus and pleura" "Melanoma of skin"
[13] "Breast" "Cervix uteri"
[15] "Corpus uteri" "Ovary, fallopian tube etc."
[17] "Prostate" "Testis"
[19] "Kidney" "Urinary bladder"
[21] "Brain" "Thyroid"
[23] "Hodgkin's lymphoma" "Non-Hodgkin lymphoma"
[25] "Multiple myeloma" "Leukaemia"
> plt( "RRa-raw0-N", width=11, height=8 )
> par( mar=c(3,1,1,1), mgp=c(3,1,0)/1.6 )
> Nres <- dim( res[sub,,] ) [1]
> plotEst( res[sub,"M","DM",], txtpos=Nres:1, y=Nres:1+0.15, col="#0000FF",
+ xlog=T, xlim=c(0.5,5), grid=c(6:19/10,4:10/2), vref=1, ylim=c(1,Nres),
+ xtic=c(0.5,0.7,1,1.5,2,5), xlab="RR, DM vs. non-DM" )
> linesEst( res[sub,"F","DM",], y=Nres:1-0.15, col="#FF0000" )
> text( cnr(0.99,0.95), "M", adj=c(1,1), col="#0000FF", font=2 )
> text( cnr(0.99,0.92), "F", adj=c(1,1), col="#FF0000", font=2 )
> text( rep(0.52,Nres), Nres:1+0.05, nca[sub,"M","DM"], col="blue", adj=c(1,0), cex=0.7 )
> text( rep(0.52,Nres), Nres:1-0.05, nca[sub,"F","DM"], col="red", adj=c(1,1), cex=0.7 )
> dev.off()
null device
1
>
> plt( "RRa-ins1", width=11, height=8 )
> par( mar=c(3,1,1,1), mgp=c(3,1,0)/1.6 )
> Nres <- dim( res[sub,,] ) [1]
> plotEst( res[sub,"M","DM/noIns",], txtpos=Nres:1, y=Nres:1+0.3, col="#0000FF",
+ xlog=T, xlim=c(0.5,5), grid=c(5:15/10,4:10/2), vref=1, ylim=c(1,Nres),
+ xtic=c(0.5,0.7,1,1.5,2,3,4,5), xlab="RR, DM / DM+ins vs. non-DM" )
> linesEst( res[sub,"M","DM/Ins",], y=Nres:1+0.1, col="#9999FF" )
> linesEst( res[sub,"F","DM/noIns",], y=Nres:1-0.1, col="#FF0000" )
> linesEst( res[sub,"F","DM/Ins",], y=Nres:1-0.3, col="#FF9999" )
> text( cnr(0.99,0.99), "Light color: on insulin",
+ adj=c(1,1), col="#999999", font=1 )
> text( cnr(0.99,0.95), "M", adj=c(1,1), col="#0000FF", font=2 )
> text( cnr(0.99,0.92), "F", adj=c(1,1), col="#FF0000", font=2 )
> dev.off()
null device
1
>
> plt( "RRa-insRR", width=11, height=8 )
> par( mar=c(3,1,1,1), mgp=c(3,1,0)/1.6 )
> plotEst( res[sub,"M","Ins vs. noIns",], txtpos=Nres:1, y=Nres:1+0.15, col="#0000FF",
+ xlog=T, xlim=c(0.2,10), grid=c(2:19/10,4:20/2), vref=1, ylim=c(1,Nres),
+ xtic=c(0.2,0.4,0.6,0.8,1,1.5,2:10), xlab="RR, DM/Insulin: Yes vs. No" )
> linesEst( res[sub,"F","Ins vs. noIns",], y=Nres:1-0.15, col="#FF0000" )
> text( cnr(0.99,0.95), "M", adj=c(1,1), col="#0000FF", font=2 )
> text( cnr(0.99,0.92), "F", adj=c(1,1), col="#FF0000", font=2 )
> dev.off()
null device
1
>
> sub <- c( grep("Oesop",dimnames(res)[["diag"]]),
+ grep("Stoma",dimnames(res)[["diag"]]),
+ grep("Color",dimnames(res)[["diag"]]),
+ grep("Liver",dimnames(res)[["diag"]]),
+ grep("Pancr",dimnames(res)[["diag"]]),
+ grep("Melan",dimnames(res)[["diag"]]),
+ grep("Corpu",dimnames(res)[["diag"]]),
+ grep("Prost",dimnames(res)[["diag"]]),
+ grep("Testi",dimnames(res)[["diag"]]),
+ grep("Kidne",dimnames(res)[["diag"]]),
+ grep("Brain",dimnames(res)[["diag"]]),
+ grep("Non-H",dimnames(res)[["diag"]]) )
> Nres <- length( sub )
>
> plt( "RRa-sub", width=5.5, height=4 )
> par( mar=c(3,1,1,1), mgp=c(3,1,0)/1.6 )
> plotEst( res[sub,"M","DM",], txtpos=Nres:1, y=Nres:1+0.15, ylim=c(0.5,Nres+0.5),
+ col="#0000FF",
+ xlog=T, xlim=c(0.5,5), grid=c(5:15/10,4:10/2), vref=1,
+ xtic=c(0.5,0.7,1,1.5,2,3,4,5), xlab="RR, DM vs. non-DM" )
> linesEst( res[sub,"F","DM",], y=Nres:1-0.15, col="#FF0000" )
> text( cnr(0.99,0.97), "M", adj=c(1,1), col="#0000FF", font=2 )
> text( cnr(0.99,0.92), "F", adj=c(1,1), col="#FF0000", font=2 )
> dev.off()
null device
1
>
> plt( "RRa-ins-sub", width=5.5, height=4 )
> par( mar=c(3,1,1,1), mgp=c(3,1,0)/1.6 )
> plotEst( res[sub,"M","DM/noIns",], txtpos=Nres:1, y=Nres:1+0.3, col="#0000FF",
+ xlog=T, xlim=c(0.5,5), grid=c(5:15/10,4:10/2), vref=1, ylim=c(0.5,Nres+0.5),
+ xtic=c(0.5,0.7,1,1.5,2,3,4,5), xlab="RR, DM / DM+ins vs. non-DM" )
> linesEst( res[sub,"M","DM/Ins",], y=Nres:1+0.1, col="#9999FF" )
> linesEst( res[sub,"F","DM/noIns",], y=Nres:1-0.1, col="#FF0000" )
> linesEst( res[sub,"F","DM/Ins",], y=Nres:1-0.3, col="#FF9999" )
> text( cnr(0.99,0.97), "M", adj=c(1,1), col="#0000FF", font=2 )

```

```

> text( cnr(0.99,0.92), "F", adj=c(1,1), col="#FF0000", font=2 )
> dev.off()
null device
  1
>

-----
Program: plot1a.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Ended: torsdag 31. marts 2011, 17:38:09
Elapsed: 00:00:00
-----
> proc.time()
  user system elapsed
  0.89   0.14   1.50

R 2.12.1

-----
Program: plot1i.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Started: fredag 01. april 2011, 00:21:37
-----
> library( Epi )

Attaching package: 'Epi'

The following object(s) are masked from 'package:base':

  merge.data.frame

> source( "c:/stat/r/bxc/library.sources/useful/r/plr.r" )
> source( "c:/stat/r/bxc/library.sources/useful/r/cnr.r" )
> load( file="./data/anali.Rdata" )
> str( res )
 num [1:29, 1:2, 1:4, 1:3] 1.19 1.27 1.25 1.32 1.4 ...
- attr(*, "dimnames")=List of 4
 ..$ diag: chr [1:29] "All malignant neoplasms" "Oesophagus" "Stomach" "Colon incl. rectosigmoideum" ...
 ..$ sex : chr [1:2] "M" "F"
 ..$ type: chr [1:4] "DM/noIns" "DM/Ins" "Ins vs. noIns" "DM"
 ..$ est : chr [1:3] "Est" "lo" "hi"
> dimnames(res)[[1]] <- gsub(" \\(excl\\. anus)", "", dimnames(res)[[1]])
> res["Breast", "M", ,] <- NA
> Nres <- dim(res)[1]
>
> # Check that sites comprising all cancers are properly selected
> xsites <- c(1,4,10,29:31)
> dimnames(nca)[[1]][ xsites]
[1] "All malignant neoplasms" "Colon incl. rectosigmoideum"
[3] "Colorectal cancer (excl. anus)" "Other"
[5] "PYRS" "Deaths"
> dimnames(nca)[[1]][-xsites]
[1] "Oesophagus" "Stomach"
[3] "Ascending colon" "Transverse colon"
[5] "Descending and sigmoid colon" "Other colon (unspec. or multiple)"
[7] "Rectum (excl. anus)" "Liver"
[9] "Pancreas" "Lung, bronchus and pleura"
[11] "Melanoma of skin" "Breast"
[13] "Cervix uteri" "Corpus uteri"
[15] "Ovary, fallopian tube etc." "Prostate"
[17] "Testis" "Kidney"
[19] "Urinary bladder" "Brain"
[21] "Thyroid" "Hodgkin's lymphoma"
[23] "Non-Hodgkin lymphoma" "Multiple myeloma"
[25] "Leukaemia"
> nca[ 1,,] -
+ apply( nca[-xsites,,], 2:3, sum )
 type
sex Well DM/noIns DM/Ins DM
M 24246 1555 234 1789
F 21360 1225 165 1390
> nca["Other",,]
 type
sex Well DM/noIns DM/Ins DM
M 24246 1555 234 1789
F 21360 1225 165 1390
>
> round( ftable( nca[ 30,,drop=F], col.vars=3:2 ), 1 )
 type Well DM/noIns DM/Ins DM
sex M F M F M F M F
diag
PYRS 37646.2 37991.5 664.5 638.0 139.4 104.2 803.8 742.2
> ftable( nca[-30,,
 type Well DM/noIns DM/Ins
sex M F M F M F M F
diag
All malignant neoplasms 167394 178744 11837 9035 1716 1258 13553 10293
Oesophagus 3282 1304 242 65 30 8 272 73
Stomach 4171 2289 299 139 46 20 345 159
Colon incl. rectosigmoideum 13853 15136 1163 981 138 88 1301 1069

```

Ascending colon	3636	5126	324	399	37	29	361	428
Transverse colon	1819	2172	174	151	27	18	201	169
Descending and sigmoid colon	7292	6601	554	342	66	31	620	373
Other colon (unspec. or multiple)	1106	1237	111	89	8	10	119	99
Rectum (excl. anus)	8876	6214	625	316	77	30	702	346
Colorectal cancer (excl. anus)	22729	21350	1788	1297	215	118	2003	1415
Liver	1776	1103	338	78	103	20	441	98
Pancreas	4041	4425	570	504	208	169	778	673
Lung, bronchus and pleura	25302	20283	1766	1129	274	163	2040	1292
Melanoma of skin	7008	8873	314	214	38	32	352	246
Breast	298	52190	13	2163	4	257	17	2420
Cervix uteri	0	5691	0	132	0	25	0	157
Corpus uteri	0	8057	0	567	0	67	0	634
Ovary, fallopian tube etc.	0	7400	0	313	0	38	0	351
Prostate	31713	0	2425	0	239	0	2664	0
Testis	4257	0	37	0	7	0	44	0
Kidney	3976	2434	319	187	60	41	379	228
Urinary bladder	14781	4906	1110	259	118	30	1228	289
Brain	4922	4310	219	163	33	30	252	193
Thyroid	593	1511	26	40	6	12	32	52
Hodgkin's lymphoma	990	723	38	23	8	2	46	25
Non-Hodgkin lymphoma	5434	4602	321	229	37	30	358	259
Multiple myeloma	2452	1883	165	103	19	8	184	111
Leukaemia	5423	4050	292	205	37	23	329	228
Other	24246	21360	1555	1225	234	165	1789	1390
Deaths	225684	237814	19737	17987	3872	2782	23609	20769

```

> # What fraction does the analysed sites comprise:
> ftable( round( 100 - 100 * nca["Other",,,drop=F] / nca[1,,drop=F], 1 ),
+        col.vars=3:2 )
      type Well      DM/noIns      DM/Ins      DM
sex      M      F      M      F      M      F      M      F
diag
Other    85.5 88.0    86.9 86.4    86.4 86.9 86.8 86.5
>
> sub <- c(1:3,10,5:7,9,11:28)
> dimnames(res)[[1]][-sub]
[1] "Colon incl. rectosigmoideum"      "Other colon (unspec. or multiple)"
[3] "Other"
> dimnames(res)[[1]][sub]
[1] "All malignant neoplasms"      "Oesophagus"
[3] "Stomach"                       "Colorectal cancer"
[5] "Ascending colon"              "Transverse colon"
[7] "Descending and sigmoid colon"  "Rectum"
[9] "Liver"                         "Pancreas"
[11] "Lung, bronchus and pleura"     "Melanoma of skin"
[13] "Breast"                       "Cervix uteri"
[15] "Corpus uteri"                 "Ovary, fallopian tube etc."
[17] "Prostate"                    "Testis"
[19] "Kidney"                      "Urinary bladder"
[21] "Brain"                       "Thyroid"
[23] "Hodgkin's lymphoma"          "Non-Hodgkin lymphoma"
[25] "Multiple myeloma"            "Leukaemia"
>
> plt( "RRi-raw0-N", width=11, height=8 )
> par( mar=c(3,1,1,1), mgp=c(3,1,0)/1.6 )
> Nres <- dim( res[sub,,] ) [1]
> plotEst( res[sub,"M","DM",], txtpos=Nres:1, y=Nres:1+0.15, col="#0000FF",
+         xlog=T, xlim=c(0.5,5), grid=c(6:19/10,4:10/2), vref=1, ylim=c(1,Nres),
+         xtic=c(0.5,0.7,1,1.5,2:5), xlab="RR, DM vs. non-DM" )
> linesEst( res[sub,"F","DM",], y=Nres:1-0.15, col="#FF0000" )
> text( cnr(0.99,0.95), "M", adj=c(1,1), col="#0000FF", font=2 )
> text( cnr(0.99,0.92), "F", adj=c(1,1), col="#FF0000", font=2 )
> text( rep(0.52,Nres), Nres:1+0.05, nca[sub,"M","DM"], col="blue", adj=c(1,0), cex=0.7 )
> text( rep(0.52,Nres), Nres:1-0.05, nca[sub,"F","DM"], col="red", adj=c(1,1), cex=0.7 )
> dev.off()
null device
1
>
> plt( "RRi-ins0", width=11, height=8 )
> par( mar=c(3,1,1,1), mgp=c(3,1,0)/1.6 )
> Nres <- dim( res[sub,,] ) [1]
> plotEst( res[sub,"M","DM/noIns",], txtpos=Nres:1, y=Nres:1+0.3, col="#0000FF",
+         xlog=T, xlim=c(0.5,5), grid=c(5:15/10,4:10/2), vref=1, ylim=c(1,Nres),
+         xtic=c(0.5,0.7,1,1.5,2:3,4,5), xlab="RR, DM / DM+ins vs. non-DM" )
> linesEst( res[sub,"M","DM/Ins",], y=Nres:1+0.1, col="#9999FF" )
> linesEst( res[sub,"F","DM/noIns",], y=Nres:1-0.1, col="#FF0000" )
> linesEst( res[sub,"F","DM/Ins",], y=Nres:1-0.3, col="#FF9999" )
> text( cnr(0.99,0.99), "Light color: on insulin",
+       adj=c(1,1), col="#999999", font=1 )
> text( cnr(0.99,0.95), "M", adj=c(1,1), col="#0000FF", font=2 )
> text( cnr(0.99,0.92), "F", adj=c(1,1), col="#FF0000", font=2 )
> dev.off()
null device
1
>
> plt( "RRi-ins1", width=9, height=10 )
> par( mar=c(3,1,1,1), mgp=c(3,1,0)/1.6 )
> delta <- 0.08
> Nres <- dim( res[sub,,] ) [1]

```

```

> plotEst( res[sub,"M","DM/noIns",], txtpos=Nres:1, y=Nres:1+3*delta, col="#0000FF",
+         xlog=T, xlim=c(0.5,5), grid=c(5:15/10,4:10/2), vref=1, ylim=c(1,Nres),
+         xtic=c(0.5,0.7,1,1.5,2,3,4,5), xlab="RR, DM / DM+ins vs. non-DM" )
> linesEst( res[sub,"M","DM/Ins" ,], y=Nres:1+1*delta, col="AAAAFF" )
> linesEst( res[sub,"F","DM/noIns",], y=Nres:1-1*delta, col="FF0000" )
> linesEst( res[sub,"F","DM/Ins" ,], y=Nres:1-3*delta, col="FFAAAA" )
> text( cnr(0.99,0.99), "Light color: insulin users",
+       adj=c(1,1), col="AAAAAA", font=1 )
> text( cnr(0.99,0.95), "M", adj=c(1,1), col="#0000FF", font=2 )
> text( cnr(0.99,0.92), "F", adj=c(1,1), col="FF0000", font=2 )
> dev.off()
null device
1
>
> plt( "RRi-ins1w", width=11, height=8 )
> par( mar=c(3,1,1,1), mgp=c(3,1,0)/1.6 )
> Nres <- dim( res[sub,,] )[1]
> plotEst( res[sub,"M","DM/noIns",], txtpos=Nres:1, y=Nres:1+0.3, col="#0000FF",
+         xlog=T, xlim=c(0.5,5), grid=c(5:15/10,4:10/2), vref=1, ylim=c(1,Nres),
+         xtic=c(0.5,0.7,1,1.5,2,3,4,5), xlab="RR, DM / DM+ins vs. non-DM" )
> linesEst( res[sub,"M","DM/Ins" ,], y=Nres:1+0.1, col="#9999FF" )
> linesEst( res[sub,"F","DM/noIns",], y=Nres:1-0.1, col="FF0000" )
> linesEst( res[sub,"F","DM/Ins" ,], y=Nres:1-0.3, col="FF9999" )
> text( cnr(0.99,0.99), "Light color: on insulin",
+       adj=c(1,1), col="#999999", font=1 )
> text( cnr(0.99,0.95), "M", adj=c(1,1), col="#0000FF", font=2 )
> text( cnr(0.99,0.92), "F", adj=c(1,1), col="FF0000", font=2 )
> dev.off()
null device
1
>
> plt( "RRi-insRR", width=9, height=10 )
> par( mar=c(3,1,1,1), mgp=c(3,1,0)/1.6 )
> plotEst( res[sub,"M","Ins vs. noIns",], txtpos=Nres:1, y=Nres:1+0.15, col="#0000FF",
+         xlog=T, xlim=c(0.5,5), grid=c(5:15/10,4:10/2), vref=1, ylim=c(1,Nres),
+         xtic=c(0.5,0.7,1,1.5,2,3,4,5), xlab="RR, DM+ins vs. DM" )
> linesEst( res[sub,"F","Ins vs. noIns",], y=Nres:1-0.15, col="FF0000" )
> text( cnr(0.99,0.95), "M", adj=c(1,1), col="#0000FF", font=2 )
> text( cnr(0.99,0.92), "F", adj=c(1,1), col="FF0000", font=2 )
> dev.off()
null device
1
>
> sub <- c( grep("Oesop",dimnames(res)[["diag"]]),
+         grep("Stoma",dimnames(res)[["diag"]]),
+         grep("Color",dimnames(res)[["diag"]]),
+         grep("Liver",dimnames(res)[["diag"]]),
+         grep("Pancr",dimnames(res)[["diag"]]),
+         grep("Melan",dimnames(res)[["diag"]]),
+         grep("Corpu",dimnames(res)[["diag"]]),
+         grep("Prost",dimnames(res)[["diag"]]),
+         grep("Testi",dimnames(res)[["diag"]]),
+         grep("Kidne",dimnames(res)[["diag"]]),
+         grep("Brain",dimnames(res)[["diag"]]),
+         grep("Non-H",dimnames(res)[["diag"]]) )
> Nres <- length( sub )
>
> plt( "RRi-sub", width=5.5, height=4 )
> par( mar=c(3,1,1,1), mgp=c(3,1,0)/1.6 )
> plotEst( res[sub,"M","DM",], txtpos=Nres:1, y=Nres:1+0.15, ylim=c(0.5,Nres+0.5),
+         col="#0000FF",
+         xlog=T, xlim=c(0.5,5), grid=c(5:15/10,4:10/2), vref=1,
+         xtic=c(0.5,0.7,1,1.5,2,3,4,5), xlab="RR, DM vs. non-DM" )
> linesEst( res[sub,"F","DM",], y=Nres:1-0.15, col="FF0000" )
> text( cnr(0.99,0.97), "M", adj=c(1,1), col="#0000FF", font=2 )
> text( cnr(0.99,0.92), "F", adj=c(1,1), col="FF0000", font=2 )
> dev.off()
null device
1
>
> plt( "RRi-ins-sub", width=5.5, height=4 )
> par( mar=c(3,1,1,1), mgp=c(3,1,0)/1.6 )
> plotEst( res[sub,"M","DM/noIns",], txtpos=Nres:1, y=Nres:1+0.3, col="#0000FF",
+         xlog=T, xlim=c(0.5,5), grid=c(5:15/10,4:10/2), vref=1, ylim=c(0.5,Nres+0.5),
+         xtic=c(0.5,0.7,1,1.5,2,3,4,5), xlab="RR, DM / DM+ins vs. non-DM" )
> linesEst( res[sub,"M","DM/Ins" ,], y=Nres:1+0.1, col="#9999FF" )
> linesEst( res[sub,"F","DM/noIns",], y=Nres:1-0.1, col="FF0000" )
> linesEst( res[sub,"F","DM/Ins" ,], y=Nres:1-0.3, col="FF9999" )
> text( cnr(0.99,0.97), "M", adj=c(1,1), col="#0000FF", font=2 )
> text( cnr(0.99,0.92), "F", adj=c(1,1), col="FF0000", font=2 )
> dev.off()
null device
1
>

```

```

-----
Program: plot1i.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Ended: fredag 01. april 2011, 00:21:38

```

Elapsed: 00:00:00

```
-----
> proc.time()
  user  system elapsed
  0.85   0.14   1.39
```

2.4 Analysis incorporating duration

R 2.13.0

```
-----
Program: ana3dx.R
Folder:  C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Started: tirsdag 21. juni 2011, 13:55:35
-----
```

```
> options( width=135 )
> library( Epi )
```

Attaching package: 'Epi'

The following object(s) are masked from 'package:base':

merge.data.frame

```
> library( splines )
> source( "c:/stat/r/bxc/library.sources/Epi/pkg/r/Wald.R" )
> Wald
function (obj, H0 = 0, ...)
{
  rl <- ci.lin(obj, ..., vcov = TRUE)
  beta <- rl$est
  vcov <- rl$vcov
  if (missing(H0))
    H0 <- beta * 0
  if (length(H0) != length(beta))
    stop("H0 has length ", length(H0), " but the set of selected parameters has length ",
         length(beta), ":\n", paste(round(beta, options()[["digits"]]),
                                     collapse = " "))
  chi <- t(beta - H0) %*% solve(vcov, beta - H0)
  df <- length(beta)
  p <- 1 - pchisq(chi, df)
  c(Chisq = chi, d.f. = df, P = p)
}
>
> #####
> # A wrapper for ns() where boundary knots are taken as the
> # smallest and largest of the knots= argument
> source( "C:/Bendix/Steno/DM-register/NDR/R/Ns.r" )
> Ns
function (x, df = NULL, knots = NULL, intercept = FALSE, Boundary.knots = NULL)
{
  if (is.null(Boundary.knots)) {
    if (!is.null(knots)) {
      knots <- sort(unique(knots))
      ok <- c(1, length(knots))
      Boundary.knots <- knots[ok]
      knots <- knots[-ok]
    }
  }
  ns(x, df = df, knots = knots, intercept = intercept, Boundary.knots = Boundary.knots)
}
>
> #####
> # Get the data file ;
> load( file = "../data/dmcaD.Rdata" )
> dim( dmca )
[1] 508062 41
> names( dmca )
[1] "state" "DMtype" "sex" "a" "p" "c" "ax" "px" "cx" "DMDur" "InsDur" "y" "d0" "
[15] "d22" "d24" "d241" "d242" "d243" "d249" "d251" "d259" "d26" "d28" "d33" "d51" "d70" "
[29] "d83" "d84" "d91" "d92" "d101" "d103" "d113" "d121" "d131" "d132" "d133" "d139" "d999" "
> # Collapse to a two-level ( DM / non-DM ) factor
> dmca$State <- Relevel( dmca$state, list(1,2:3) )
>
> #####
> # Compute the quantiles of the durations just for inspection
> durDM <- with( subset( dmca, DMDur>0 ), rep( DMDur,d0 ) )
> durIns <- with( subset( dmca, InsDur>0 ), rep( InsDur,d0 ) )
> wh.dmi <- as.integer(factor(durDM))
> wh.ins <- as.integer(factor(durIns))
> durDM <- durDM + runif( length(durDM), -ilength[wh.dmi]/2, ilength[wh.dmi]/2 )
> durIns <- durIns + runif( length(durIns), -ilength[wh.ins]/2, ilength[wh.ins]/2 )
> print( round( cbind( quantile( durDM , probs=(0:20)/20 ),
+                   quantile( durIns, probs=(0:20)/20 ) ), 1 ) )
      [,1] [,2]
0%    0.1 0.1
```

```

5%      0.3 0.2
10%     0.5 0.4
15%     0.8 0.5
20%     1.1 0.7
25%     1.5 1.0
30%     1.8 1.3
35%     2.2 1.6
40%     2.6 1.8
45%     3.0 2.2
50%     3.5 2.5
55%     4.0 2.9
60%     4.5 3.3
65%     5.0 3.8
70%     5.6 4.3
75%     6.3 5.0
80%     7.5 5.7
85%     8.0 6.6
90%     9.2 7.9
95%    10.7 9.4
100%   15.0 15.0
>
> #####
> # Subset to avoid fitting problems
> dmca <- subset( dmca, y>0 )
>
> # Compute the relevant column numbers in the data frame
> diagnames <- as.character(dxn$dxnam)
> d.col <- dxn$d.col
> diagnames <- diagnames[-length(d.col)]
> d.col <- d.col[-length(d.col)]
> cbind( d.col, diagnames )
  d.col diagnames
[1,] "13" "All malignant neoplasms"
[2,] "14" "Oesophagus"
[3,] "15" "Stomach"
[4,] "16" "Colon incl. rectosigmoideum"
[5,] "17" "Ascending colon"
[6,] "18" "Transverse colon"
[7,] "19" "Descending and sigmoid colon"
[8,] "20" "Other colon (unspec. or multiple)"
[9,] "21" "Rectum (excl. anus)"
[10,] "22" "Colorectal cancer (excl. anus)"
[11,] "23" "Liver"
[12,] "24" "Pancreas"
[13,] "25" "Lung, bronchus and pleura"
[14,] "26" "Melanoma of skin"
[15,] "27" "Breast"
[16,] "28" "Cervix uteri"
[17,] "29" "Corpus uteri"
[18,] "30" "Ovary, fallopian tube etc."
[19,] "31" "Prostate"
[20,] "32" "Testis"
[21,] "33" "Kidney"
[22,] "34" "Urinary bladder"
[23,] "35" "Brain"
[24,] "36" "Thyroid"
[25,] "37" "Hodgkin's lymphoma"
[26,] "38" "Non-Hodgkin lymphoma"
[27,] "39" "Multiple myeloma"
[28,] "40" "Leukaemia"
> c.col <- (1:ncol(dmca))[-d.col]
> Nres <- length(d.col)
>
> #####
> # Knots for the natural splines
> a.kn <- seq( 10, 100,,9)
> p.kn <- seq(1995,2009,,5)
> c.kn <- seq(1900,2005,,9)
> # Duration points
> d.pt <- seq(0,14,0.2)
> # Subsets of the duration vector
> d2 <- (d.pt>=2)
> d5 <- (d.pt>=5)
>
> #####
> # Construct structures to hold the results
>
> # An array for the estimated RRs
> dnam <- list( diag = diagnames,
+             sex = c("M","F"),
+             type = c("DMDur", "InsDur-0", "InsDur-2", "InsDur-5",
+                   "Ins-RR-0", "Ins-RR-2", "Ins-RR-5",
+                   "DMDuri", "InsDuri-0", "InsDuri-2", "InsDuri-5",
+                   "Ins-RRi-0", "Ins-RRi-2", "Ins-RRi-5"),
+             dur = c(d.pt),
+             est = c("RR","lo","hi") )
> res <- array( NA, dim=sapply(dnam,length), dimnames=dnam )
>
> # An array to hold the tests for Main effects, and specific interaction terms

```

```

> dnam <- list( diag = diagnames,
+             sex = c("M","F"),
+             type = c("Ins-eff", "DM-eff", "DM-all", "DM0", "Ins0", "DMdur-at-Ins", "DMdur*Insdur", "Interact-2") )
> tst <- array( NA, dim=sapply(dnam,length), dimnames=dnam )
>
> # A list to hold the duration knots
> knots <- list()
>
> # Input to a prediction frame for the rates to use for computing
> # cumulative risk - used both for the array and the prediction frame
> pr.int <- 0.05 # Length of interval between incidence predictions
> pr.lng <- 10 # Length of period (in years)
> pr.dur <- seq( 0, pr.lng-pr.int, pr.int )
> per.in <- 1998 # The starting year for prediction
>
> # An array to hold the predicted incidence rates (from which we later
> # shall compute the cumulative risks (probabilities of specific
> # cancers).
> dnam <- list( diag = c(diagnames, "Death"),
+             sex = c("M","F"),
+             model = c("Main", "Interact"),
+             pr.dur = pr.dur,
+             state = levels( dmca$state ),
+             age.in = c(60,65,70),
+             dur.in = c(0,2) )
> prr <- array( NA, dim=sapply(dnam,length), dimnames=dnam )
>
> # Make a prediction data frame, based on the array prr - this way we
> # are sure that the prediction frame has the same structure and
> # sequence as the array:
> pr.frame <- as.data.frame( as.table( prr[1,1,1,,] ) )
> # Convert the three numeric classifications to proper numeric vectors
> for( i in c(1,3,4) ) pr.frame[,i] <-
+ as.numeric( as.character( pr.frame[,i] ) )
> pr.frame <- transform( pr.frame,
+                       ax = age.in + pr.dur,
+                       px = per.in + pr.dur,
+                       DMDur = ( dur.in + pr.dur ) * (state!="Well"),
+                       InsDur = ( dur.in + pr.dur ) * (state=="DM/Ins"),
+                       y = 0.05 ) [c("ax", "px", "DMDur", "InsDur", "state", "y")]
> str( pr.frame )
'data.frame': 3600 obs. of 6 variables:
 $ ax : num 60 60 60.1 60.1 60.2 ...
 $ px : num 1998 1998 1998 1998 1998 ...
 $ DMDur : num 0 0 0 0 0 0 0 0 0 ...
 $ InsDur : num 0 0 0 0 0 0 0 0 0 ...
 $ state : Factor w/ 3 levels "Well","DM","DM/Ins": 1 1 1 1 1 1 1 1 1 ...
 $ y : num 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.05 ...
>
> #####
> # The analysis loops over knots, sites and sexes
>
> # Knots and contrast matrices for diabetes duration and insulin duration
>
> # Sites loop
> for( i in 1:dim(res)[1] )
+ {
+ # i <- 4
+ # Copy the relevant set of cases to the column "D"
+ data <- dmca[,c(c.col,d.col[i])]
+ names(data)[ncol(data)] <- "D"
+
+ # Define number of knots depending on site
+ nd <- ifelse( i==1, 5, 4 )
+ ni <- nd - 1
+
+ # Sex loop
+ for( sx in dimnames(res)$sex )
+ {
+ # sx <- "F"
+ # Skip if there are no cancers - the knots calculation will crash
+ if( sum( data$D[data$sex==sx] ) == 0 ) next
+
+ # Define knots for DM and for insulin duration using the quantiles of
+ # the durations for cases, note the effect beyond the last is linear
+ durDM <- with( subset( data, DMDur>0 & sex==sx ), rep( DMDur,D ) )
+ durIns <- with( subset( data, InsDur>0 & sex==sx ), rep( InsDur,D ) )
+ wh.dmi <- as.integer(factor(durDM))
+ wh.ins <- as.integer(factor(durIns))
+ durDM <- durDM + runif( length(durDM ), -ilength[wh.dmi]/2, ilength[wh.dmi]/2 )
+ durIns <- durIns + runif( length(durIns), -ilength[wh.ins]/2, ilength[wh.ins]/2 )
+
+ # We choose the last knot so that the thast 1/nd cases are in the
+ # linear domain of the duration effect
+ d.kn <- quantile( durDM , probs=0:(nd-1)/nd )
+ i.kn <- quantile( durIns, probs=0:(ni-1)/ni )
+
+ # Define the corresponding contrast matrices
+ CD <- Ns(d.pt,knots=d.kn)

```

```

+ CI <- Ns(d.pt,knots=i.kn)
+ CL <- cbind(1,d.pt)
+
+ # Report when and where we are
+ cat( format( Sys.time(), "%H:%M:%S" ),
+      ", sex=", sx,
+      ", site=", i,
+      ", dimnames(res)$diag[i],
+      "\n", sep="" )
+ flush.console()
+
+ # Fit the model - remember to make it identifiable, otherwise the
+ # prediction will go wrong.
+ m1 <- glm( D ~ Ns( ax,knots=a.kn) +
+           detrend( Ns(px ,knots=p.kn), px ) +
+           Ns(px-ax,knots=c.kn) + state +
+           Ns( DMDur,knots=d.kn) +
+           Ns(InsDur,knots=i.kn) +
+           offset( log(y) ),
+           family = poisson,
+           data = subset(data,sex==sx) )
+ mi <- update( m1, . ~ . + I((DMDur-InsDur)*(state=="DM/Ins"))
+             + I( DMDur*InsDur) )
+
+ # For illustration, show the parameters that we extract:
+ if( i == 1 & sx=="M" )
+ {
+   cat( "\nParameters extracted for construction of curves from main effects model:\n", i, sx )
+   print( round( ci.lin( m1, subset=c("state","DMDur","InsDur") ), 2 ) )
+   cat( "\nParameters extracted for construction of curves from interaction model:\n", i, sx )
+   print( round( ci.lin( mi, subset=c("stateDM","Dur") ), 2 ) )
+ }
+
+ # The predicted log-incidence rates saved in the array
+ prr[i,sx,"Main" ,,,] <- predict( m1, newdata=pr.frame )
+ prr[i,sx,"Interact" ,,,] <- predict( mi, newdata=pr.frame )
+
+ # Duration effects from the main effects model
+ res[i,sx, "DMDur" ,,] <- ci.lin( m1, subset=c("state","DMDur"),
+                                ctr.mat=cbind(1,0,CD), E=T )[,5:7]
+ res[i,sx,"InsDur-0",,] <- ci.lin( m1, subset=c("state","DMDur","InsDur"),
+                                ctr.mat=cbind(0,1,CD,CI), E=T )[,5:7]
+ res[i,sx,"InsDur-2",1:sum(d2),] <- ci.lin( m1, subset=c("state","DMDur","InsDur"),
+                                ctr.mat=cbind(0,1,CD[d2,],CI[1:sum(d2),]), E=T )[,5:7]
+ res[i,sx,"InsDur-5",1:sum(d5),] <- ci.lin( m1, subset=c("state","DMDur","InsDur"),
+                                ctr.mat=cbind(0,1,CD[d5,],CI[1:sum(d5),]), E=T )[,5:7]
+
+ # Rate-ratios relative to non-insulin treated from main-effects model
+ res[i,sx,"Ins-RR-0",,] <- ci.lin( m1, subset=c("state","DMDur","InsDur"),
+                                ctr.mat=cbind(-1,1,CD-CD,CI), E=T )[,5:7]
+ res[i,sx,"Ins-RR-2",1:sum(d2),] <- ci.lin( m1, subset=c("state","DMDur","InsDur"),
+                                ctr.mat=cbind(-1,1,CD[d2,]-CD[d2,],CI[1:sum(d2),]), E=T )[,5:7]
+ res[i,sx,"Ins-RR-5",1:sum(d5),] <- ci.lin( m1, subset=c("state","DMDur","InsDur"),
+                                ctr.mat=cbind(-1,1,CD[d5,]-CD[d5,],CI[1:sum(d5),]), E=T )[,5:7]
+
+ # Duration effects from the interaction model.
+ res[i,sx, "DMDuri" ,,] <- ci.lin( mi, subset=c("stateDM","Dur"),
+                                ctr.mat=cbind(1,0,CD,CI-CI,0,0), E=T )[,5:7]
+ res[i,sx,"InsDuri-0",,] <- ci.lin( mi, subset=c("stateDM","Dur"),
+                                ctr.mat=cbind(0,1,CD,CI,0,d.pt^2), E=T )[,5:7]
+ res[i,sx,"InsDuri-2",1:sum(d2),] <- ci.lin( mi, subset=c("stateDM","Dur"),
+                                ctr.mat=cbind(0,1,CD[d2,],CI[1:sum(d2),],2,d.pt[d2]*d.pt[1:sum(d2)]), E=T )[,5:7]
+ res[i,sx,"InsDuri-5",1:sum(d5),] <- ci.lin( mi, subset=c("stateDM","Dur"),
+                                ctr.mat=cbind(0,1,CD[d5,],CI[1:sum(d5),],5,d.pt[d5]*d.pt[1:sum(d5)]), E=T )[,5:7]
+
+ # Rate-ratios relative to non-insulin treated from interaction model
+ res[i,sx,"Ins-RRi-0",,] <- ci.lin( mi, subset=c("stateDM","Dur"),
+                                ctr.mat=cbind(-1,1,CD-CD,CI,0,d.pt*d.pt), E=T )[,5:7]
+ res[i,sx,"Ins-RRi-2",1:sum(d2),] <- ci.lin( mi, subset=c("stateDM","Dur"),
+                                ctr.mat=cbind(-1,1,CD[d2,]-CD[d2,],2,d.pt[d2]*d.pt[1:sum(d2)]), E=T )[,5:7]
+ res[i,sx,"Ins-RRi-5",1:sum(d5),] <- ci.lin( mi, subset=c("stateDM","Dur"),
+                                ctr.mat=cbind(-1,1,CD[d5,]-CD[d5,],5,d.pt[d5]*d.pt[1:sum(d5)]), E=T )[,5:7]
+
+ # Test for insulin effect, diabetes effect and duration interactions etc.
+ # A Contrast matrix is needed in order to test whether the difference
+ # between the two intercepts are 0 simultaneously with the insulin
+ # duration being 0
+ IC <- diag(ni+1)[-2,]
+ IC[1,2] <- -1
+ Ins.test <- Wald( m1, subset=c("stateDM","InsDur"), ctr.mat=IC )
+ All.test <- Wald( m1, subset=c("stateDM","InsDur","DMDur") )
+ DM.test <- c( "Chisq"=All.test[1]-Ins.test[1],
+              "d.f."=All.test[2]-Ins.test[2],
+              "P"=1-pchisq(All.test[1]-Ins.test[1],All.test[2]-Ins.test[2]) )
+
+ tst[i,sx,] <- c(Ins.test[3], DM.test[3], All.test[3],
+               ci.lin(mi,subset=c("stateDM","I\\("))[,4],
+               1-pchisq( m1$deviance-mi$deviance, m1$df.residual-mi$df.residual ) )
+ knots <- c( knots, list( list(d.kn=d.kn,i.kn=i.kn) ) )

```



```

+ names( knots )[length(knots)] <- dimnames(res)[[1]][i]
+ } # end of sex loop
+ } # end of sites loop
13:55:45, sex=M, site=1, All malignant neoplasms

Parameters extracted for construction of curves from main effects model:
  1 M              Estimate StdErr      z P 2.5% 97.5%
stateDM           0.65   0.04 17.16 0 0.58 0.73
stateDM/Ins       1.42   0.10 14.82 0 1.23 1.60
Ns(DMDur, knots = d.kn)1 -0.43 0.04 -10.12 0 -0.51 -0.34
Ns(DMDur, knots = d.kn)2 -0.30 0.03 -9.65 0 -0.36 -0.24
Ns(DMDur, knots = d.kn)3 -1.03 0.09 -12.04 0 -1.19 -0.86
Ns(DMDur, knots = d.kn)4 -0.19 0.02 -8.47 0 -0.24 -0.15
Ns(InsDur, knots = i.kn)1 -0.39 0.08 -5.10 0 -0.55 -0.24
Ns(InsDur, knots = i.kn)2 -1.14 0.18 -6.35 0 -1.49 -0.79
Ns(InsDur, knots = i.kn)3 -0.30 0.07 -4.68 0 -0.43 -0.18

Parameters extracted for construction of curves from interaction model:
  1 M              Estimate StdErr      z P 2.5% 97.5%
stateDM           0.65   0.04 16.89 0.00 0.57 0.72
stateDM/Ins       1.55   0.10 14.98 0.00 1.35 1.76
Ns(DMDur, knots = d.kn)1 -0.43 0.04 -10.11 0.00 -0.51 -0.34
Ns(DMDur, knots = d.kn)2 -0.29 0.03 -9.14 0.00 -0.35 -0.23
Ns(DMDur, knots = d.kn)3 -1.01 0.09 -11.80 0.00 -1.18 -0.84
Ns(DMDur, knots = d.kn)4 -0.18 0.02 -7.56 0.00 -0.22 -0.13
Ns(InsDur, knots = i.kn)1 -0.45 0.08 -5.58 0.00 -0.61 -0.29
Ns(InsDur, knots = i.kn)2 -1.40 0.22 -6.37 0.00 -1.83 -0.97
Ns(InsDur, knots = i.kn)3 -0.58 0.14 -4.03 0.00 -0.87 -0.30
I((DMDur - InsDur) * (state == "DM/Ins")) -0.04 0.01 -3.16 0.00 -0.06 -0.01
I(DMDur * InsDur) 0.01 0.00 1.89 0.06 0.00 0.01
13:56:47, sex=F, site=1, All malignant neoplasms
13:57:45, sex=M, site=2, Oesophagus
13:59:36, sex=F, site=2, Oesophagus
14:01:35, sex=M, site=3, Stomach
14:03:05, sex=F, site=3, Stomach
14:04:29, sex=M, site=4, Colon incl. rectosigmoideum
14:05:50, sex=F, site=4, Colon incl. rectosigmoideum
14:07:08, sex=M, site=5, Ascending colon
14:08:26, sex=F, site=5, Ascending colon
14:09:46, sex=M, site=6, Transverse colon
14:11:13, sex=F, site=6, Transverse colon
14:12:56, sex=M, site=7, Descending and sigmoid colon
14:14:30, sex=F, site=7, Descending and sigmoid colon
14:15:53, sex=M, site=8, Other colon (unspec. or multiple)
14:17:33, sex=F, site=8, Other colon (unspec. or multiple)
14:19:08, sex=M, site=9, Rectum (excl. anus)
14:20:39, sex=F, site=9, Rectum (excl. anus)
14:22:08, sex=M, site=10, Colorectal cancer (excl. anus)
14:23:28, sex=F, site=10, Colorectal cancer (excl. anus)
14:24:46, sex=M, site=11, Liver
14:25:58, sex=F, site=11, Liver
14:27:15, sex=M, site=12, Pancreas
14:28:43, sex=F, site=12, Pancreas
14:29:59, sex=M, site=13, Lung, bronchus and pleura
14:31:20, sex=F, site=13, Lung, bronchus and pleura
14:32:43, sex=M, site=14, Melanoma of skin
14:33:55, sex=F, site=14, Melanoma of skin
14:35:08, sex=M, site=15, Breast
14:37:11, sex=F, site=15, Breast
14:38:31, sex=F, site=16, Cervix uteri
14:39:54, sex=F, site=17, Corpus uteri
14:41:09, sex=F, site=18, Ovary, fallopian tube etc.
14:42:20, sex=M, site=19, Prostate
14:43:56, sex=M, site=20, Testis
14:45:12, sex=M, site=21, Kidney
14:46:22, sex=F, site=21, Kidney
14:47:34, sex=M, site=22, Urinary bladder
14:48:55, sex=F, site=22, Urinary bladder
14:50:07, sex=M, site=23, Brain
14:51:18, sex=F, site=23, Brain
14:52:27, sex=M, site=24, Thyroid
14:53:46, sex=F, site=24, Thyroid
14:55:00, sex=M, site=25, Hodgkin's lymphoma
14:56:17, sex=F, site=25, Hodgkin's lymphoma
14:57:40, sex=M, site=26, Non-Hodgkin lymphoma
14:58:51, sex=F, site=26, Non-Hodgkin lymphoma
15:00:03, sex=M, site=27, Multiple myeloma
15:01:43, sex=F, site=27, Multiple myeloma
15:03:42, sex=M, site=28, Leukaemia
15:04:55, sex=F, site=28, Leukaemia
There were 50 or more warnings (use warnings() to see the first 50)
>
> # Get rid of the male/females in the wrong places
> no.M <- c( grep("uteri",dimnames(res)[["diag"]]),
+          grep("Ovary",dimnames(res)[["diag"]]) )
> no.F <- c( grep("Prost",dimnames(res)[["diag"]]),
+          grep("Testi",dimnames(res)[["diag"]]) )
> res[no.M,"M",,] <- NA
> res[no.F,"F",,] <- NA

```

```

>
> save( res, prr, pr.frame, tst, knots, file="../data/ana3dx.Rdata" )
>
-----
Program: ana3dx.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Ended: tirsdag 21. juni 2011, 15:06:10
Elapsed: 01:10:34
-----
> proc.time()
  user system elapsed
3782.25  450.98 4236.15

R 2.13.0
-----
Program: plot3dx.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Started: torsdag 23. juni 2011, 17:22:53
-----
> library( Epi )

Attaching package: 'Epi'

The following object(s) are masked from 'package:base':

  merge.data.frame

> # library( Useful )
> source( "c:/stat/r/bxc/library.sources/useful/r/plt.r" )
> source( "c:/stat/r/bxc/library.sources/useful/r/cnr.r" )
>
> # Functions used to plot the duration effects
> #####
> # A function to do one site for one sex
> plot.one <-
+ function( i, sex, clr=c("blue","red")[(sex=="F")+1], what=c("dm","i0","i2","i5"),
+           xax=FALSE, yax=FALSE, yl=c(1/2,5), anno=TRUE, raw=TRUE, int=FALSE,
+           lt=1, ci=TRUE, knpl=FALSE, ... )
+ {
+   if( int %in% c("mr","ir") ) what <- "i0"
+   # clr <- c(clr,clr)[1:2]
+   plot( NA, xlim=c(0,14)+c(-1,0)/2, ylim=yl, log="y",
+         xaxt="n", yaxt="n", xlab="", ylab="", yaxs="i", ... )
+   if( xax )
+     {
+       axis( side=1, at=seq(0,12,3), las=1 )
+       axis( side=1, at=seq(0,14,1), labels=rep("",15) )
+       # mtext( side=1, line=2, at=6, "DM duration" )
+     }
+   if( yax ) axis( side=2, las=1 )
+   abline( v=0:25,
+           h=c(c(5:20,seq(25,50,5))/100,
+               c(5:20,seq(25,50,5))/10,
+               c(5:20,seq(25,50,5)),
+               c(5:20,seq(25,50,5))*10,
+               c(5:20,seq(25,50,5))*100),
+           col=gray(0.9) )
+   abline(h=1)
+   if( "dm" %in% what )
+     matlines( d.pt, dur[i,sex,switch( int, "mc"="DMDur",
+                                         "mr"="Ins-RR-0",
+                                         "ic"="DMDuri",
+                                         "ir"="Ins-RRi-0" )],,],
+              type="l", lty=1, lwd=if(ci) c(3,1,1) else c(3,NA,NA),col=clr )
+   if( "i0" %in% what )
+     matlines( d.pt, dur[i,sex,switch( int, "mc"="InsDur-0",
+                                         "mr"="Ins-RR-0",
+                                         "ic"="InsDuri-0",
+                                         "ir"="Ins-RRi-0" )],,],
+              type="l",lty=c("21","42","42"), lwd=if(ci) c(3,1,1) else c(2,NA,NA),col=clr )
+   if( "i2" %in% what )
+     matlines( d.pt+2, dur[i,sex,switch( int, "mc"="InsDur-2",
+                                         "mr"="Ins-RR-2",
+                                         "ic"="InsDuri-2",
+                                         "ir"="Ins-RRi-2" )],,],
+              type="l",lty=c("21","42","42"), lwd=if(ci) c(3,1,1) else c(2,NA,NA),col=clr )
+   if( "i5" %in% what )
+     matlines( d.pt+5, dur[i,sex,switch( int, "mc"="InsDur-5",
+                                         "mr"="Ins-RR-5",
+                                         "ic"="InsDuri-5",
+                                         "ir"="Ins-RRi-5" )],,],
+              type="l",lty=c("21","42","42"),lwd=if(ci) c(3,1,1) else c(2,NA,NA),col=clr )
+   if( anno )
+     {
+     dnam <- paste( diagnames[i], " ", " ", sex, sep="" )
+     wd <- strwidth( dnam, font=2, cex=1.2 )
+     rect( -1, 10^(par("usr")[4])*0.9, ceiling(wd), 10^(par("usr")[4]),
+           col="white", border=gray(0.9) )
+     }

```

```

+ text( -0.5, 10^(par("usr")[4])*0.95, dnam, adj=c(0,0.5), font=2, cex=1.2 )
+ }
+ box()
+ if( raw )
+ {
+   if( int %in% c("mc","ic") )
+   {
+     e.pt <- 1:2/3-1
+     points( e.pt, c(res[i,sex,"DM/noIns","Est"],
+                   res[i,sex,"DM/Ins","Est"]),
+           col=if(clr=="blue") c("#0000FF","#AAAAFF")
+           else c("#FF0000","#FFAAAA"), pch=16 )
+     segments( e.pt, c(res[i,sex,"DM/noIns","lo"],
+                     res[i,sex,"DM/Ins","lo"]),
+             e.pt, c(res[i,sex,"DM/noIns","hi"],
+                   res[i,sex,"DM/Ins","hi"]),
+             col=if(clr=="blue") c("#0000FF","#AAAAFF")
+             else c("#FF0000","#FFAAAA"), lwd=2 )
+   }
+   else
+   {
+     e.pt <- -0.5
+     points( e.pt, res[i,sex,"Ins vs. noIns","Est"],
+           col=clr, pch=16 )
+     segments( e.pt, res[i,sex,"Ins vs. noIns","lo"],
+             e.pt, res[i,sex,"Ins vs. noIns","hi"],
+             col=clr, lwd=2 )
+   }
+ }
+ if( knpl )
+ {
+   kl <- knots[grep(substr(diagnames[i],1,8),names(knots))]
+   if( length(kl)==2 ) kl <- kl[(sex=="F")+1]
+   if( "dm" %in% what ) rug( kl[[1]][[1]], side=1, col=clr, lwd=2 )
+   if( "i0" %in% what ) rug( kl[[1]][[2]], side=3, col=clr, lwd=2 )
+ }
+ } # End of function
>
> # The category 'unspecified colon has crept in, it is deleted as is "others"
> load( file="./data/ana3dx.Rdata" )
> dur <- res[-c(8,29),,,]
> load( file="./data/anali.Rdata" )
> res <- res[-c(8,29),,,]
> # The naming of the cancers is a bit unfortunate
> dimnames(res)[[1]] <- gsub( "\\(excl. anus\\)", "", dimnames(res)[[1]] )
> dimnames(dur)[[1]] <- gsub( "\\(excl. anus\\)", "", dimnames(dur)[[1]] )
> cbind( dimnames(res)[[1]],
+       dimnames(dur)[[1]] )
+
+   [,1]                [,2]
[1,] "All malignant neoplasms" "All malignant neoplasms"
[2,] "Oesophagus" "Oesophagus"
[3,] "Stomach" "Stomach"
[4,] "Colon incl. rectosigmoideum" "Colon incl. rectosigmoideum"
[5,] "Ascending colon" "Ascending colon"
[6,] "Transverse colon" "Transverse colon"
[7,] "Descending and sigmoid colon" "Descending and sigmoid colon"
[8,] "Rectum" "Rectum"
[9,] "Colorectal cancer" "Colorectal cancer"
[10,] "Liver" "Liver"
[11,] "Pancreas" "Pancreas"
[12,] "Lung, bronchus and pleura" "Lung, bronchus and pleura"
[13,] "Melanoma of skin" "Melanoma of skin"
[14,] "Breast" "Breast"
[15,] "Cervix uteri" "Cervix uteri"
[16,] "Corpus uteri" "Corpus uteri"
[17,] "Ovary, fallopian tube etc." "Ovary, fallopian tube etc."
[18,] "Prostate" "Prostate"
[19,] "Testis" "Testis"
[20,] "Kidney" "Kidney"
[21,] "Urinary bladder" "Urinary bladder"
[22,] "Brain" "Brain"
[23,] "Thyroid" "Thyroid"
[24,] "Hodgkin's lymphoma" "Hodgkin's lymphoma"
[25,] "Non-Hodgkin lymphoma" "Non-Hodgkin lymphoma"
[26,] "Multiple myeloma" "Multiple myeloma"
[27,] "Leukaemia" "Leukaemia"
> str( dur )
num [1:27, 1:2, 1:14, 1:71, 1:3] 2.05 1.04 1.57 2.31 2.33 ...
- attr(*, "dimnames")=List of 5
..$ diag: chr [1:27] "All malignant neoplasms" "Oesophagus" "Stomach" "Colon incl. rectosigmoideum" ...
..$ sex: chr [1:2] "M" "F"
..$ type: chr [1:14] "DMDur" "InsDur-0" "InsDur-2" "InsDur-5" ...
..$ dur: chr [1:71] "0" "0.2" "0.4" "0.6" ...
..$ est: chr [1:3] "RR" "lo" "hi"
> str( res )
num [1:27, 1:2, 1:4, 1:3] 1.19 1.27 1.25 1.32 1.4 ...
- attr(*, "dimnames")=List of 4
..$ diag: chr [1:27] "All malignant neoplasms" "Oesophagus" "Stomach" "Colon incl. rectosigmoideum" ...
..$ sex: chr [1:2] "M" "F"

```

```

..$ type: chr [1:4] "DM/noIns" "DM/Ins" "Ins vs. noIns" "DM"
..$ est : chr [1:3] "Est" "lo" "hi"
>
> # Get the number of sites and the duration points for the estimates
> Nres <- dim( dur )[1]
> d.pt <- as.numeric(dimnames(dur)$dur)
> diagnames <- dimnames(dur)$diag
>
> #####
> # Loop over marginal / interaction model ("m","i") and comparisons ("c","r")
> for( tp in c("mc","mr","ic","ir") )
+ # tp <- "mc"
+ {
+   if( tp %in% c("mc","ic") )
+   {
+     rrtxt <- "Rate ratio: DM/no-Ins, DM/Ins vs. non-DM"
+     durtxt <- "Diabetes duration (years)"
+   }
+   else
+   {
+     rrtxt <- "Rate ratio: DM/Ins vs. DM/no-Ins"
+     durtxt <- "Insulin duration (years)"
+   }
+
+ # Single organs
+ for( i in 1:(dim(dur)[1]) )
+ {
+   # i <- 1
+   # tp <- "mr"
+   plt( paste( substr(gsub(" ", "", dimnames(dur)[[1]][i]), 1, 4), tp, sep="-" ),
+         height=5+6/8, width=6+5/8, pointsize=10 )
+   par( mfrow=c(1,2), mar=c(0,0,0,0), omi=c(4,4,2,1)/8, mgp=c(3,1,0)/1.6 )
+   plot.one( i, "M", xax=TRUE, yax=TRUE, anno=FALSE, yl=c(0.5,5),
+             raw=TRUE, int=tp, knpl=TRUE )
+   text( cnr(95,97), "M", font=1, cex=1.5, adj=c(1,1) )
+   plot.one( i, "F", xax=TRUE, yax=FALSE, anno=FALSE, yl=c(0.5,5),
+             raw=TRUE, int=tp, knpl=TRUE )
+   text( cnr(95,97), "F", font=1, cex=1.5, adj=c(1,1) )
+   mtext( side=1, line=2, durtxt, outer=T )
+   mtext( side=2, line=2, rrtxt, outer=T )
+   mtext( side=3, line=0.1, diagnames[i], outer=T, adj=0, cex=1.5 )
+   dev.off()
+ }
+
+ # Prostate & breast in one display
+ plt( paste("PrBr", tp, sep="-" ),
+       height=5+6/8, width=6+5/8, pointsize=10 )
+ par( mfrow=c(1,2), mar=c(0,0,0,0), omi=c(4,4,2,1)/8, mgp=c(3,1,0)/1.6 )
+ plot.one( 18, "M", xax=TRUE, yax=TRUE, anno=FALSE, yl=c(0.2,2),
+           raw=TRUE, int=tp, knpl=TRUE )
+ plot.one( 14, "F", xax=TRUE, yax=FALSE, anno=FALSE, yl=c(0.5,5),
+           raw=TRUE, int=tp, knpl=TRUE )
+ text( cnr(95,97), "F", font=1, cex=1.5, adj=c(1,1) )
+ mtext( side=1, line=2, durtxt, outer=T )
+ mtext( side=2, line=2, rrtxt, outer=T )
+ mtext( side=3, line=0.1, diagnames[18], outer=T, adj=0, cex=1.5 )
+ mtext( side=3, line=0.1, diagnames[14], outer=T, adj=0, cex=1.5, at=0.5 )
+ dev.off()
+
+ # Testis and ovary in one display
+ plt( paste("TeOv", tp, sep="-" ),
+       height=5+6/8, width=6+5/8, pointsize=10 )
+ par( mfrow=c(1,2), mar=c(0,0,0,0), omi=c(4,4,2,1)/8, mgp=c(3,1,0)/1.6 )
+ plot.one( 19, "M", xax=TRUE, yax=TRUE, anno=FALSE, yl=c(0.5,5),
+           raw=TRUE, int=tp, knpl=TRUE )
+ plot.one( 17, "F", xax=TRUE, yax=FALSE, anno=FALSE, yl=c(0.5,5),
+           raw=TRUE, int=tp, knpl=TRUE )
+ mtext( side=1, line=2, durtxt, outer=T )
+ mtext( side=2, line=2, rrtxt, outer=T )
+ mtext( side=3, line=0.1, diagnames[19], outer=T, adj=0, cex=1.5 )
+ mtext( side=3, line=0.1, diagnames[17], outer=T, adj=0, cex=1.5, at=0.5 )
+ dev.off()
+
+ # Cervix and corpus uteri in one display
+ plt( paste("Uter", tp, sep="-" ),
+       height=5+6/8, width=6+5/8, pointsize=10 )
+ par( mfrow=c(1,2), mar=c(0,0,0,0), omi=c(4,4,2,1)/8, mgp=c(3,1,0)/1.6 )
+ plot.one( 16, "F", xax=TRUE, yax=TRUE, anno=FALSE, yl=c(0.5,5),
+           raw=TRUE, int=tp, knpl=TRUE )
+ plot.one( 17, "F", xax=TRUE, yax=FALSE, anno=FALSE, yl=c(0.5,5),
+           raw=TRUE, int=tp, knpl=TRUE )
+ text( cnr(95,97), "F", font=1, cex=1.5, adj=c(1,1) )
+ mtext( side=1, line=2, durtxt, outer=T )
+ mtext( side=2, line=2, rrtxt, outer=T )
+ mtext( side=3, line=0.1, diagnames[16], outer=T, adj=0, cex=1.5 )
+ mtext( side=3, line=0.1, diagnames[17], outer=T, adj=0, cex=1.5, at=0.5 )
+ dev.off()
+
+ # Ovary and corpus uteri in one display

```

```

+ plt( paste("0vCo", tp, sep="-" ),
+       height=5+6/8, width=6+5/8, pointsize=10 )
+ par( mfrow=c(1,2), mar=c(0,0,0,0), omi=c(4,4,2,1)/8, mgp=c(3,1,0)/1.6 )
+ plot.one( 17, "F", xax=TRUE, yax=TRUE, anno=FALSE, yl=c(0.5,5),
+          raw=TRUE, int=tp, knpl=TRUE )
+ plot.one( 16, "F", xax=TRUE, yax=FALSE, anno=FALSE, yl=c(0.5,5),
+          raw=TRUE, int=tp, knpl=TRUE )
+ text( cnr(95,97), "F", font=1, cex=1.5, adj=c(1,1) )
+ mtext( side=1, line=2, durtxt, outer=T )
+ mtext( side=2, line=2, rrtxt, outer=T )
+ mtext( side=3, line=0.1, diagnames[17], outer=T, adj=0, cex=1.5 )
+ mtext( side=3, line=0.1, diagnames[16], outer=T, adj=0, cex=1.5, at=0.5 )
+ dev.off()
+
+ # Redo liver and pancreas
+ for( i in 10:11 )
+ {
+ fl <- 1.6
+ plt( paste( substr(gsub(" ", "", dimnames(dur)[[1]][i]), 1, 4), tp, sep="-" ),
+       height=5*fl+5/8, width=6+5/8, pointsize=10 )
+ par( mfrow=c(1,2), mar=c(0,0,0,0), omi=c(4,4,2,1)/8, mgp=c(3,1,0)/1.6 )
+ plot.one( i, "M", xax=TRUE, yax=TRUE, anno=FALSE, yl=c(0.5,0.5*10^fl),
+          raw=TRUE, int=tp, knpl=TRUE )
+ text( cnr(95,98), "M", font=1, cex=1.5, adj=c(1,1) )
+ plot.one( i, "F", xax=TRUE, yax=FALSE, anno=FALSE, yl=c(0.5,0.5*10^fl),
+          raw=TRUE, int=tp, knpl=TRUE )
+ text( cnr(95,98), "F", font=1, cex=1.5, adj=c(1,1) )
+ mtext( side=1, line=2, durtxt, outer=T )
+ mtext( side=2, line=2, rrtxt, outer=T )
+ mtext( side=3, line=0.1, diagnames[i], outer=T, adj=0, cex=1.5 )
+ dev.off()
+ }
+ } # end of loop over c("mc","mr","ic","ir")
There were 50 or more warnings (use warnings() to see the first 50)
>
> #####
> # Graphs for the paper
> zz <- strsplit(diagnames, "")
> dnsp <- sapply( lapply( zz, FUN=function(x,p) grep(p,x), " " ), FUN = function(x) x[1] ) - 1
> cbind( diagnames, dnsp )
  diagnames          dnsp
[1,] "All malignant neoplasms"      "3"
[2,] "Oesophagus"                   NA
[3,] "Stomach"                       NA
[4,] "Colon incl. rectosigmoideum"   "5"
[5,] "Ascending colon"              "9"
[6,] "Transverse colon"             "10"
[7,] "Descending and sigmoid colon"  "10"
[8,] "Rectum"                       NA
[9,] "Colorectal cancer"            "10"
[10,] "Liver"                       NA
[11,] "Pancreas"                    NA
[12,] "Lung, bronchus and pleura"    "5"
[13,] "Melanoma of skin"            "8"
[14,] "Breast"                      NA
[15,] "Cervix uteri"               "6"
[16,] "Corpus uteri"               "6"
[17,] "Ovary, fallopian tube etc."   "6"
[18,] "Prostate"                   NA
[19,] "Testis"                     NA
[20,] "Kidney"                     NA
[21,] "Urinary bladder"            "7"
[22,] "Brain"                      NA
[23,] "Thyroid"                    NA
[24,] "Hodgkin's lymphoma"         "9"
[25,] "Non-Hodgkin lymphoma"       "11"
[26,] "Multiple myeloma"           "8"
[27,] "Leukaemia"                  NA
> dnshort <- substring( diagnames, 1, pmin(dnsp, nchar(diagnames), na.rm=T) )
> dnshort <- gsub(" ", "", dnshort )
>
> # First one:
> lomat <- rbind( c(18,1,2,13,3,4),
+               rep(16,6),
+               c(19,5,6,14,7,8),
+               rep(17,6),
+               c(20,9,10,15,11,12),
+               rep(21,6) )
> rw <- c(10,35,35,10,35,35)
> rh <- c(60,5,60,5,60,10)
> tp <- "mc"
>
> plt( "sub6", height=10.2,width=8)
> layout( lomat, widths=rw, heights=rh )
> par( mai=c(0,0,0.2,0), mgp=c(3,1,0)/1.6 )
> for( i in c(3,9,12,13) )
+ {
+ plot.one( i, "M", xax=TRUE, yax=TRUE, anno=FALSE, yl=c(0.5,5),

```

```

+       raw=TRUE, int=tp, knpl=TRUE )
+ text( cnr(95,97), "M", font=1, cex=1.2, adj=c(1,1) )
+ mtext( dnshort[i], font=1, cex=0.8, adj=0, side=3, line=0.1 )
+ plot.one( i, "F", xax=TRUE, yax=FALSE, anno=FALSE, yl=c(0.5,5),
+       raw=TRUE, int=tp, knpl=TRUE )
+ text( cnr(95,97), "F", font=1, cex=1.2, adj=c(1,1) )
+ }
> # Prostate and breast
> plot.one( 18, "M", xax=TRUE, yax=TRUE, anno=FALSE, yl=c(0.2,2),
+       raw=TRUE, int=tp, knpl=TRUE )
> text( cnr(95,97), "M", font=1, cex=1.2, adj=c(1,1) )
> mtext( dnshort[18], font=1, cex=0.8, adj=0, side=3, line=0.1 )
> plot.one( 14, "F", xax=TRUE, yax=FALSE, anno=FALSE, yl=c(0.5,5),
+       raw=TRUE, int=tp, knpl=TRUE )
> text( cnr(95,97), "F", font=1, cex=1.2, adj=c(1,1) )
> mtext( dnshort[14], font=1, cex=0.8, adj=0, side=3, line=0.1 )
> # Ovary and Corpus uteri
> plot.one( 17, "F", xax=TRUE, yax=TRUE, anno=FALSE, yl=c(0.5,5),
+       raw=TRUE, int=tp, knpl=TRUE )
> text( cnr(95,97), "F", font=1, cex=1.2, adj=c(1,1) )
> mtext( dnshort[17], font=1, cex=0.8, adj=0, side=3, line=0.1 )
> plot.one( 16, "F", xax=TRUE, yax=FALSE, anno=FALSE, yl=c(0.5,5),
+       raw=TRUE, int=tp, knpl=TRUE )
> text( cnr(95,97), "F", font=1, cex=1.2, adj=c(1,1) )
> mtext( diagnames[16], font=1, cex=0.8, adj=0, side=3, line=0.1 )
> mtext( "Diabetes duration (years)", side=1, line=-1, cex=0.8, outer=T )
> mtext( "Rate ratio versus the non-diabetic population", side=2,
+       line=-1, cex=0.8, outer=T )
> dev.off()
null device
  1
>
> lommat <- rbind( c(11,1,2,9,3,4),
+       rep(12,6),
+       c(14,5,6,10,7,8),
+       rep(13,6) )
> fl <- 1.6
> rw <- c(10,35,35,10,35,35)
> rh <- c(60*fl,5,60,10)
> tp <- "mc"
>
> plt( "sub4", height=10*((75+60*fl)/200)+0.2,width=8)
> layout( lommat, widths=rw, heights=rh )
> par( mai=c(0,0,0.2,0), mgp=c(3,1,0)/1.6 )
> for( i in c(10:11,20:21) )
+ {
+ fl <- ifelse( i<15, fl, 1 )
+ plot.one( i, "M", xax=TRUE, yax=TRUE, anno=FALSE, yl=c(0.5,0.5*10^fl),
+       raw=TRUE, int=tp, knpl=TRUE )
+ text( cnr(95,98), "M", font=1, cex=1.5, adj=c(1,1) )
+ mtext( diagnames[i], font=1, cex=0.8, adj=0, side=3, line=0.1 )
+ plot.one( i, "F", xax=TRUE, yax=FALSE, anno=FALSE, yl=c(0.5,0.5*10^fl),
+       raw=TRUE, int=tp, knpl=TRUE )
+ text( cnr(95,98), "F", font=1, cex=1.5, adj=c(1,1) )
+ }
> mtext( "Diabetes duration (years)", side=1, line=-1, cex=0.8, outer=T )
> mtext( "Rate ratio versus the non-diabetic population", side=2,
+       line=-1, cex=0.8, outer=T )
> dev.off()
null device
  1
>
> #####
> # Graphs for explanation of the curves
> i <- 1
>
> plt( "Allm-exp1",
+       height=5+6/8, width=6+5/8, pointsize=10 )
> par( mfrow=c(1,2), mar=c(0,0,0,0), omi=c(4,4,2,1)/8, mgp=c(3,1,0)/1.6 )
> plot( NA, axes=F, xlab="", ylab="", xlim=0:1, ylim=0:1 )
> plot.one( i, "F", xax=TRUE, yax=FALSE, anno=FALSE, yl=c(0.5,5),
+       clr=c("blue","red"), raw=TRUE, int="mc", knpl=FALSE, what="dm" )
Warning messages:
1: In if (clr == "blue") c("#0000FF", "#AAAAFF") else c("#FF0000", :
  the condition has length > 1 and only the first element will be used
2: In if (clr == "blue") c("#0000FF", "#AAAAFF") else c("#FF0000", :
  the condition has length > 1 and only the first element will be used
> mtext( side=1, line=2, durtxt, outer=T )
> mtext( side=2, line=2, "Rate ratio", outer=F )
> dev.off()
null device
  1
>
> plt( "Allm-exp2",
+       height=5+6/8, width=6+5/8, pointsize=10 )
> par( mfrow=c(1,2), mar=c(0,0,0,0), omi=c(4,4,2,1)/8, mgp=c(3,1,0)/1.6 )
> plot( NA, axes=F, xlab="", ylab="", xlim=0:1, ylim=0:1 )
> plot.one( i, "F", xax=TRUE, yax=FALSE, anno=FALSE, yl=c(0.5,5),
+       clr=c("blue","red"), raw=TRUE, int="mc", knpl=FALSE, what=c("dm","i0") )

```

```

Warning messages:
1: In if (clr == "blue") c("#0000FF", "#AAAAFF") else c("#FF0000", :
  the condition has length > 1 and only the first element will be used
2: In if (clr == "blue") c("#0000FF", "#AAAAFF") else c("#FF0000", :
  the condition has length > 1 and only the first element will be used
> mtext( side=1, line=2, durtxt, outer=T )
> mtext( side=2, line=2, "Rate ratio", outer=F )
> dev.off()
null device
1

>
> plt( "Allm-exp3",
+   height=5+6/8, width=6+5/8, pointsize=10 )
> par( mfrow=c(1,2), mar=c(0,0,0,0), omi=c(4,4,2,1)/8, mgp=c(3,1,0)/1.6 )
> plot( NA, axes=F, xlab="", ylab="", xlim=0:1, ylim=0:1 )
> plot.one( i, "F", xax=TRUE, yax=FALSE, anno=FALSE, yl=c(0.5,5),
+   clr=c("blue","red"), raw=TRUE, int="mc", knpl=FALSE, what=c("dm","i2") )
Warning messages:
1: In if (clr == "blue") c("#0000FF", "#AAAAFF") else c("#FF0000", :
  the condition has length > 1 and only the first element will be used
2: In if (clr == "blue") c("#0000FF", "#AAAAFF") else c("#FF0000", :
  the condition has length > 1 and only the first element will be used
> mtext( side=1, line=2, durtxt, outer=T )
> mtext( side=2, line=2, "Rate ratio", outer=F )
> dev.off()
null device
1

>
> plt( "Allm-exp4",
+   height=5+6/8, width=6+5/8, pointsize=10 )
> par( mfrow=c(1,2), mar=c(0,0,0,0), omi=c(4,4,2,1)/8, mgp=c(3,1,0)/1.6 )
> plot( NA, axes=F, xlab="", ylab="", xlim=0:1, ylim=0:1 )
> plot.one( i, "F", xax=TRUE, yax=FALSE, anno=FALSE, yl=c(0.5,5),
+   clr=c("blue","red"), raw=TRUE, int="mc", knpl=FALSE, what=c("dm","i5") )
Warning messages:
1: In if (clr == "blue") c("#0000FF", "#AAAAFF") else c("#FF0000", :
  the condition has length > 1 and only the first element will be used
2: In if (clr == "blue") c("#0000FF", "#AAAAFF") else c("#FF0000", :
  the condition has length > 1 and only the first element will be used
> mtext( side=1, line=2, durtxt, outer=T )
> mtext( side=2, line=2, "Rate ratio", outer=F )
> dev.off()
null device
1

>
> plt( "Allm-exp5",
+   height=5+6/8, width=6+5/8, pointsize=10 )
> par( mfrow=c(1,2), mar=c(0,0,0,0), omi=c(4,4,2,1)/8, mgp=c(3,1,0)/1.6 )
> plot( NA, axes=F, xlab="", ylab="", xlim=0:1, ylim=0:1 )
> plot.one( i, "F", xax=TRUE, yax=FALSE, anno=FALSE, yl=c(0.5,5),
+   clr=c("blue","red"), raw=TRUE, int="mc", knpl=FALSE, what=c("dm","i0","i2","i5") )
Warning messages:
1: In if (clr == "blue") c("#0000FF", "#AAAAFF") else c("#FF0000", :
  the condition has length > 1 and only the first element will be used
2: In if (clr == "blue") c("#0000FF", "#AAAAFF") else c("#FF0000", :
  the condition has length > 1 and only the first element will be used
> mtext( side=1, line=2, durtxt, outer=T )
> mtext( side=2, line=2, "Rate ratio", outer=F )
> dev.off()
null device
1

>
>
-----
Program: plot3dx.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Ended: torsdag 23. juni 2011, 17:22:59
Elapsed: 00:00:05
-----
> proc.time()
  user system elapsed
  4.18   0.34   5.82

```

2.5 Analysis of mortality and cumulative mortality

R 2.13.0

```

-----
Program: anam.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Started: tirsdag 21. juni 2011, 20:57:59
-----

```

```
> library( Epi )
```

```
Attaching package: 'Epi'
```

The following object(s) are masked from 'package:base':

```

merge.data.frame

> library( splines )
>
> #####
> # Includes a temporary fix for a bug that crashed apc.fit with only
> # two parameters in one of the effects (a drop=FALSE was missing)
> source( "C:/stat/R/BxC/library.sources/Epi/pkg/R/apc.fit.r" )
>
> #####
> # A wrapper for ns() where boundary knots are taken as the
> # smallest and largest of the knots= argument
> source( "C:/Bendix/Steno/DM-register/NDR/R/Ns.r" )
> Ns
function (x, df = NULL, knots = NULL, intercept = FALSE, Boundary.knots = NULL)
{
  if (is.null(Boundary.knots)) {
    if (!is.null(knots)) {
      knots <- sort(unique(knots))
      ok <- c(1, length(knots))
      Boundary.knots <- knots[ok]
      knots <- knots[-ok]
    }
  }
  ns(x, df = df, knots = knots, intercept = intercept, Boundary.knots = Boundary.knots)
}
> source("c:/stat/r/bxc/library.sources/useful/R/cnr.r")
>
> # Utility for deriving the RR from two independent set of rates with ci
> mkRR <-
+ function( A, B )
+ {
+   erf <- exp( 1.96 * sqrt( (log(A[,3]/A[,1])/1.96)^2 +
+                           (log(B[,3]/B[,1])/1.96)^2 ) )
+   RR <- cbind( A[,1]/B[,1],
+               A[,1]/B[,1]/erf,
+               A[,1]/B[,1]*erf )
+   RR
+ }
>
> load( file="../data/DMmD.Rdata" )
> str(DMm)
'data.frame': 284374 obs. of  8 variables:
 $ state : Factor w/ 3 levels "Well","DM","DM/Ins": 1 1 1 1 1 1 1 1 1 1 ...
 $ sex   : Factor w/ 2 levels "M","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ a     : num  0 0 0 0 0 0 0 0 0 0 ...
 $ p     : num 1995 1996 1997 1998 1999 ...
 $ DMDur : num  0 0 0 0 0 0 0 0 0 0 ...
 $ InsDur: num  0 0 0 0 0 0 0 0 0 0 ...
 $ dd    : num 196 219 187 160 169 208 163 159 164 153 ...
 $ y     : num 35895 35486 34834 34442 34014 ...
> names( DMm )[match( c("a", "p" ), names(DMm) )] <-
+ c("ax", "px")
>
> # First fit APC-models, disregarding duration:
> str( DMm )
'data.frame': 284374 obs. of  8 variables:
 $ state : Factor w/ 3 levels "Well","DM","DM/Ins": 1 1 1 1 1 1 1 1 1 1 ...
 $ sex   : Factor w/ 2 levels "M","F": 1 1 1 1 1 1 1 1 1 1 ...
 $ ax    : num  0 0 0 0 0 0 0 0 0 0 ...
 $ px    : num 1995 1996 1997 1998 1999 ...
 $ DMDur : num  0 0 0 0 0 0 0 0 0 0 ...
 $ InsDur: num  0 0 0 0 0 0 0 0 0 0 ...
 $ dd    : num 196 219 187 160 169 208 163 159 164 153 ...
 $ y     : num 35895 35486 34834 34442 34014 ...
> DMmA <- aggregate( DMm[,c("dd", "y")],
+                   by = DMm[,c("ax", "px", "sex", "state")],
+                   FUN = sum )
> names( DMmA )
[1] "ax" "px" "sex" "state" "dd" "y"
> names( DMmA )[match( c("ax", "px", "dd", "y"), names(DMmA) )] <- c("A", "P", "D", "Y")
> names( DMmA )
[1] "A" "P" "sex" "state" "D" "Y"
>
> # Separate APC-models for each sex and state, with slightly different sets of knots
> # for the three states
> Wpar <- list( A=seq(0,100,,10),
+             P=seq(1995,2009,,4),
+             C=seq(1895,2007,,7) )
> Dpar <-
+ Ipar <- list( A=seq(0,100,,7),
+             P=seq(1995,2009,,4),
+             C=seq(1895,2007,,6) )
> apc.WMp <- apc.fit( subset( DMmA, state=="Well" & sex=="M"), parm="APC", scale=1000, npar=Wpar, ref.p=2005 )
[1] "ML of APC-model Poisson with log(Y) offset : ( APC ):\n"

```


Analysis of deviance for Age-Period-Cohort model

	Resid.	Df	Resid. Dev	Df	Deviance	P(> Chi)
Age	1490		11837.5			
Age-drift	1489		8073.0	1	3764.5	< 2.2e-16
Age-Cohort	1484		7509.2	5	563.8	< 2.2e-16
Age-Period-Cohort	1482		7451.2	2	58.0	2.554e-13
Age-Period	1487		8050.3	-5	-599.1	< 2.2e-16
Age-drift	1489		8073.0	-2	-22.6	1.217e-05

```
> apc.WMc <- apc.fit( subset( DMmA, state=="Well" & sex=="M"), parm="ACP", scale=1000, npar=Wpar, ref.c=1940 )
[1] "ML of APC-model Poisson with log(Y) offset : ( ACP ): \n"
```

Analysis of deviance for Age-Period-Cohort model

	Resid.	Df	Resid. Dev	Df	Deviance	P(> Chi)
Age	1490		11837.5			
Age-drift	1489		8073.0	1	3764.5	< 2.2e-16
Age-Cohort	1484		7509.2	5	563.8	< 2.2e-16
Age-Period-Cohort	1482		7451.2	2	58.0	2.554e-13
Age-Period	1487		8050.3	-5	-599.1	< 2.2e-16
Age-drift	1489		8073.0	-2	-22.6	1.217e-05

```
> apc.WFp <- apc.fit( subset( DMmA, state=="Well" & sex=="F"), parm="APC", scale=1000, npar=Wpar, ref.p=2005 )
[1] "ML of APC-model Poisson with log(Y) offset : ( APC ): \n"
```

Analysis of deviance for Age-Period-Cohort model

	Resid.	Df	Resid. Dev	Df	Deviance	P(> Chi)
Age	1490		14184			
Age-drift	1489		12205	1	1979.40	< 2.2e-16
Age-Cohort	1484		11590	5	614.70	< 2.2e-16
Age-Period-Cohort	1482		11576	2	14.13	0.000853
Age-Period	1487		12204	-5	-628.06	< 2.2e-16
Age-drift	1489		12205	-2	-0.77	0.679170

```
> apc.WFc <- apc.fit( subset( DMmA, state=="Well" & sex=="F"), parm="ACP", scale=1000, npar=Wpar, ref.c=1940 )
[1] "ML of APC-model Poisson with log(Y) offset : ( ACP ): \n"
```

Analysis of deviance for Age-Period-Cohort model

	Resid.	Df	Resid. Dev	Df	Deviance	P(> Chi)
Age	1490		14184			
Age-drift	1489		12205	1	1979.40	< 2.2e-16
Age-Cohort	1484		11590	5	614.70	< 2.2e-16
Age-Period-Cohort	1482		11576	2	14.13	0.000853
Age-Period	1487		12204	-5	-628.06	< 2.2e-16
Age-drift	1489		12205	-2	-0.77	0.679170

```
> apc.DMp <- apc.fit( subset( DMmA, state=="DM" & sex=="M"), parm="APC", scale=1000, npar=Dpar, ref.p=2005 )
[1] "ML of APC-model Poisson with log(Y) offset : ( APC ): \n"
```

Analysis of deviance for Age-Period-Cohort model

	Resid.	Df	Resid. Dev	Df	Deviance	P(> Chi)
Age	1488		1560.9			
Age-drift	1487		1200.7	1	360.24	< 2e-16
Age-Cohort	1483		1102.4	4	98.24	< 2e-16
Age-Period-Cohort	1481		1094.7	2	7.72	0.02109
Age-Period	1485		1192.7	-4	-98.01	< 2e-16
Age-drift	1487		1200.7	-2	-7.95	0.01881

```
> apc.DMc <- apc.fit( subset( DMmA, state=="DM" & sex=="M"), parm="ACP", scale=1000, npar=Dpar, ref.c=1940 )
[1] "ML of APC-model Poisson with log(Y) offset : ( ACP ): \n"
```

Analysis of deviance for Age-Period-Cohort model

	Resid.	Df	Resid. Dev	Df	Deviance	P(> Chi)
Age	1488		1560.9			
Age-drift	1487		1200.7	1	360.24	< 2e-16
Age-Cohort	1483		1102.4	4	98.24	< 2e-16
Age-Period-Cohort	1481		1094.7	2	7.72	0.02109
Age-Period	1485		1192.7	-4	-98.01	< 2e-16
Age-drift	1487		1200.7	-2	-7.95	0.01881

```
> apc.DFp <- apc.fit( subset( DMmA, state=="DM" & sex=="F"), parm="APC", scale=1000, npar=Dpar, ref.p=2005 )
[1] "ML of APC-model Poisson with log(Y) offset : ( APC ): \n"
```

Analysis of deviance for Age-Period-Cohort model

	Resid.	Df	Resid. Dev	Df	Deviance	P(> Chi)
Age	1489		1410.9			
Age-drift	1488		1230.1	1	180.802	< 2.2e-16
Age-Cohort	1484		1157.1	4	73.012	5.244e-15
Age-Period-Cohort	1482		1156.3	2	0.797	0.6712
Age-Period	1486		1229.0	-4	-72.663	6.216e-15
Age-drift	1488		1230.1	-2	-1.147	0.5636

```
> apc.DFc <- apc.fit( subset( DMmA, state=="DM" & sex=="F"), parm="ACP", scale=1000, npar=Dpar, ref.c=1940 )
[1] "ML of APC-model Poisson with log(Y) offset : ( ACP ): \n"
```

Analysis of deviance for Age-Period-Cohort model

	Resid.	Df	Resid. Dev	Df	Deviance	P(> Chi)
Age	1489		1410.9			
Age-drift	1488		1230.1	1	180.802	< 2.2e-16

```

Age-Cohort          1484    1157.1  4   73.012  5.244e-15
Age-Period-Cohort  1482    1156.3  2    0.797  0.6712
Age-Period          1486    1229.0 -4  -72.663  6.216e-15
Age-drift           1488    1230.1 -2   -1.147  0.5636
> apc.IMp <- apc.fit( subset( DMmA, state=="DM/Ins" & sex=="M"), parm="APC", scale=1000, npar=Ipar, ref.p=2005 )
[1] "ML of APC-model Poisson with log(Y) offset : ( APC ):\n"

```

Analysis of deviance for Age-Period-Cohort model

```

                Resid. Df Resid. Dev Df Deviance P(>|Chi|)
Age              1453      1187.1
Age-drift        1452      1135.8  1   51.346  7.746e-13
Age-Cohort       1448      1124.7  4   11.111  0.025341
Age-Period-Cohort 1446      1116.5  2    8.229  0.016334
Age-Period       1450      1126.2 -4   -9.690  0.045987
Age-drift        1452      1135.8 -2   -9.650  0.008025
> apc.IMc <- apc.fit( subset( DMmA, state=="DM/Ins" & sex=="M"), parm="ACP", scale=1000, npar=Ipar, ref.c=1940 )
[1] "ML of APC-model Poisson with log(Y) offset : ( ACP ):\n"

```

Analysis of deviance for Age-Period-Cohort model

```

                Resid. Df Resid. Dev Df Deviance P(>|Chi|)
Age              1453      1187.1
Age-drift        1452      1135.8  1   51.346  7.746e-13
Age-Cohort       1448      1124.7  4   11.111  0.025341
Age-Period-Cohort 1446      1116.5  2    8.229  0.016334
Age-Period       1450      1126.2 -4   -9.690  0.045987
Age-drift        1452      1135.8 -2   -9.650  0.008025
> apc.IFp <- apc.fit( subset( DMmA, state=="DM/Ins" & sex=="F"), parm="APC", scale=1000, npar=Ipar, ref.p=2005 )
[1] "ML of APC-model Poisson with log(Y) offset : ( APC ):\n"

```

Analysis of deviance for Age-Period-Cohort model

```

                Resid. Df Resid. Dev Df Deviance P(>|Chi|)
Age              1459      1117.6
Age-drift        1458      1108.8  1    8.8381  0.00295
Age-Cohort       1454      1104.5  4    4.2849  0.36882
Age-Period-Cohort 1452      1103.3  2    1.1281  0.56891
Age-Period       1456      1107.3 -4   -3.9439  0.41365
Age-drift        1458      1108.8 -2   -1.4691  0.47973
> apc.IFc <- apc.fit( subset( DMmA, state=="DM/Ins" & sex=="F"), parm="ACP", scale=1000, npar=Ipar, ref.c=1940 )
[1] "ML of APC-model Poisson with log(Y) offset : ( ACP ):\n"

```

Analysis of deviance for Age-Period-Cohort model

```

                Resid. Df Resid. Dev Df Deviance P(>|Chi|)
Age              1459      1117.6
Age-drift        1458      1108.8  1    8.8381  0.00295
Age-Cohort       1454      1104.5  4    4.2849  0.36882
Age-Period-Cohort 1452      1103.3  2    1.1281  0.56891
Age-Period       1456      1107.3 -4   -3.9439  0.41365
Age-drift        1458      1108.8 -2   -1.4691  0.47973
>
> # Plot the estimates from the period-major parmaetrizations
> # and save the estimates at the same time
> pdf( "../graph/APC.pdf", width=10 )
> par( mar=c(3,4,1,4), mgp=c(3,1,0)/1.6, las=1 )
> apc.frame( a.lab=seq(0,100,20), a.tic=seq(0,100,10),
+           cp.lab=seq(1920,2010,20), cp.tic=seq(1900,2010,10),
+           r.lab=outer(c(1,2,5),10^(-2:2)), gap=7,
+           r.tic=outer(1:9,10^(-2:2)),
+           r.txt="Mortality rate per 1000 PY" )
> WMP <- apc.lines( apc.WMp, col="blue", lwd=1 )
> WFP <- apc.lines( apc.WFp, col="red", lwd=1 )
> DMP <- apc.lines( apc.DMp, col="blue", lwd=2 )
> DFP <- apc.lines( apc.DFp, col="red", lwd=2 )
> IMP <- apc.lines( apc.IMp, col="blue", lwd=3 )
> IFP <- apc.lines( apc.IFp, col="red", lwd=3 )
> dev.off()
null device
1
>
> # Plot the estimates from the cohort-major parmaetrizations
> pdf( "../graph/ACP.pdf", width=10 )
> par( mar=c(3,4,1,4), mgp=c(3,1,0)/1.6, las=1 )
> apc.frame( a.lab=seq(0,90,20), a.tic=seq(0,90,10),
+           cp.lab=seq(1920,2000,20), cp.tic=seq(1900,2010,10),
+           r.lab=outer(c(1,2,5),10^(-2:2)),
+           r.tic=outer(1:9,10^(-2:2)), gap=7,
+           r.txt="Mortality rate per 1000 PY" )
> apc.lines( apc.WMc, col="blue", lwd=1 )
> apc.lines( apc.WFc, col="red", lwd=1 )
> apc.lines( apc.DMc, col="blue", lwd=2 )
> apc.lines( apc.DFc, col="red", lwd=2 )
> apc.lines( apc.IMc, col="blue", lwd=3 )
> apc.lines( apc.IFc, col="red", lwd=3 )
> dev.off()
null device
1

```

```

>
> # Plot the RRs from the period-major parametrizations
> pdf( "../graph/APC-RR.pdf", width=10 )
> par( mar=c(3,4,1,4), mgp=c(3,1,0)/1.6, las=1 )
> apc.frame( a.lab=seq(0,90,20), a.tic=seq(0,90,10),
+           cp.lab=seq(1920,2000,20), cp.tic=seq(1900,2010,10),
+           r.lab=outer(c(1,2,5),10^(-2:2)),
+           r.tic=outer(1:9,10^(-2:2)),
+           r.txt="Mortality rate ratio" )
> matlines( WMP$A[,1], mkRR(DMP$A[,-1],WMP$A[,-1]), lty=1, col="blue", lwd=c(3,1,1) )
> pc.matlines( WMP$P[,1], mkRR(DMP$P[,-1],WMP$P[,-1]), lty=1, col="blue", lwd=c(3,1,1) )
> pc.matlines( WMP$C[,1], mkRR(DMP$C[,-1],WMP$C[,-1]), lty=1, col="blue", lwd=c(3,1,1) )
Warning messages:
1: In (log(A[, 3]/A[, 1])/1.96)^2 + (log(B[, 3]/B[, 1])/1.96)^2 :
longer object length is not a multiple of shorter object length
2: In A[, 1]/B[, 1] :
longer object length is not a multiple of shorter object length
3: In A[, 1]/B[, 1] :
longer object length is not a multiple of shorter object length
4: In A[, 1]/B[, 1] :
longer object length is not a multiple of shorter object length
> mia <- match( IMP$A[,1], WMP$A[,1] )
> mip <- match( IMP$P[,1], WMP$P[,1] )
> mic <- match( IMP$C[,1], WMP$C[,1] )
> matlines( IMP$A[,1], mkRR(IMP$A[,-1],WMP$A[mia,-1]), lty=1, col="red", lwd=c(3,1,1) )
> pc.matlines( IMP$P[,1], mkRR(IMP$P[,-1],WMP$P[mip,-1]), lty=1, col="red", lwd=c(3,1,1) )
> pc.matlines( IMP$C[,1], mkRR(IMP$C[,-1],WMP$C[mic,-1]), lty=1, col="red", lwd=c(3,1,1) )
>
> matlines( WFP$A[,1], mkRR(DFP$A[,-1],WFP$A[,-1]), lty=3, col="blue", lwd=c(3,1,1) )
> pc.matlines( WFP$P[,1], mkRR(DFP$P[,-1],WFP$P[,-1]), lty=3, col="blue", lwd=c(3,1,1) )
> pc.matlines( WFP$C[,1], mkRR(DFP$C[,-1],WFP$C[,-1]), lty=3, col="blue", lwd=c(3,1,1) )
Warning messages:
1: In (log(A[, 3]/A[, 1])/1.96)^2 + (log(B[, 3]/B[, 1])/1.96)^2 :
longer object length is not a multiple of shorter object length
2: In A[, 1]/B[, 1] :
longer object length is not a multiple of shorter object length
3: In A[, 1]/B[, 1] :
longer object length is not a multiple of shorter object length
4: In A[, 1]/B[, 1] :
longer object length is not a multiple of shorter object length
> mia <- match( IFP$A[,1], WFP$A[,1] )
> mip <- match( IFP$P[,1], WFP$P[,1] )
> mic <- match( IFP$C[,1], WFP$C[,1] )
> matlines( IFP$A[,1], mkRR(IFP$A[,-1],WFP$A[mia,-1]), lty=3, col="red", lwd=c(3,1,1) )
> pc.matlines( IFP$P[,1], mkRR(IFP$P[,-1],WFP$P[mip,-1]), lty=3, col="red", lwd=c(3,1,1) )
> pc.matlines( IFP$C[,1], mkRR(IFP$C[,-1],WFP$C[mic,-1]), lty=3, col="red", lwd=c(3,1,1) )
> dev.off()
null device
1

>
> # Knots for the natural splines in the model for mortality
> a.kn <- seq( 10, 100, ,9)
> p.kn <- seq(1995,2009, ,5)
> c.kn <- seq(1900,2005, ,9)
> # Duration points
> d.pt <- seq(0,14,0.2)
> # Knots for diabetes duration and insulin duration
> d.kn <- c(0,1,3,5,10)
> i.kn <- c(0,1, 4 ,10)
>
> load( file="../data/ana3dx.Rdata" )
> # Check the prediction frame supplied from ana3dx.r
> str( pr.frame )
'data.frame': 3600 obs. of 6 variables:
 $ ax : num 60 60 60.1 60.1 60.2 ...
 $ px : num 1998 1998 1998 1998 1998 ...
 $ DMDur : num 0 0 0 0 0 0 0 0 0 0 ...
 $ InsDur: num 0 0 0 0 0 0 0 0 0 0 ...
 $ state : Factor w/ 3 levels "Well","DM","DM/Ins": 1 1 1 1 1 1 1 1 1 1 ...
 $ y : num 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.05 ...
>
> sx <- levels(DMm$sex)[1]
> for( sx in levels(DMm$sex) )
+ {
+ # We allow for different age-period and cohort effects between
+ # the three states (as opposed to what we did for incidence rates),
+ # but since we are using predict to
+ # Fit the model separately for diabetics and non-diabetics
+ mp <- glm( dd ~ -1 +
+           ( Ns( ax,knots=a.kn,i=T) +
+             detrend( Ns(px ,knots=p.kn ), px ) +
+             Ns(px-ax,knots=c.kn ) ):state +
+             Ns( DMDur,knots=d.kn) +
+             Ns(InsDur,knots=i.kn) +
+             offset( log(y) ),
+             family = poisson,
+             data = subset(DMm,sex==sx) )
+ mi <- update( mp, . ~ . + I((DMDur-InsDur)*(state=="DM/Ins"))
+             + I( DMDur*InsDur) )
+ }

```

```

+ # The predicted log-incidence rates saved in the array
+ # Note this depends critically on the order of rows in the
+ # prediction frame and the definition of the last two dimensions in
+ # the array prr:
+ prr["Death",sx,"Main",,,] <- predict( mp, newdata=pr.frame )
+ prr["Death",sx,"Interact",,,] <- predict( mi, newdata=pr.frame )
+ }
Warning messages:
1: glm.fit: fitted rates numerically 0 occurred
2: glm.fit: fitted rates numerically 0 occurred
> # End of sex loop
> str( pr.frame )
'data.frame': 3600 obs. of 6 variables:
 $ ax      : num  60 60 60.1 60.1 60.2 ...
 $ px      : num  1998 1998 1998 1998 1998 ...
 $ DMdur   : num  0 0 0 0 0 0 0 0 0 0 ...
 $ InsDur  : num  0 0 0 0 0 0 0 0 0 0 ...
 $ state   : Factor w/ 3 levels "Well","DM","DM/Ins": 1 1 1 1 1 1 1 1 1 1 ...
 $ y       : num  0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.05 0.05 ...
> str( prr )
num [1:29, 1:2, 1:2, 1:200, 1:3, 1:3, 1:2] -7.76 -11.49 -11.24 -10.23 -11.61 ...
- attr(*, "dimnames")=List of 7
..$ diag   : chr [1:29] "All malignant neoplasms" "Oesophagus" "Stomach" "Colon incl. rectosigmoideum" ...
..$ sex    : chr [1:2] "M" "F"
..$ model  : chr [1:2] "Main" "Interact"
..$ pr.dur : chr [1:200] "0" "0.05" "0.1" "0.15" ...
..$ state  : chr [1:3] "Well" "DM" "DM/Ins"
..$ age.in : chr [1:3] "60" "65" "70"
..$ dur.in : chr [1:2] "0" "2"
>
> save( res, prr, tst, file="../data/ana3dm.Rdata" )
>

-----
Program: anam.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Ended: tirsdag 21. juni 2011, 21:00:44
Elapsed: 00:02:44
-----
> proc.time()
  user system elapsed
150.04   8.93  165.73

R 2.13.0
-----
Program: prob3dx.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Started: torsdag 23. juni 2011, 17:39:48
-----
> library( Epi )

Attaching package: 'Epi'

The following object(s) are masked from 'package:base':

  merge.data.frame

> library( splines )
>
> load( file="../data/ana3dm.Rdata" )
> str( prr )
num [1:29, 1:2, 1:2, 1:200, 1:3, 1:3, 1:2] -7.76 -11.49 -11.24 -10.23 -11.61 ...
- attr(*, "dimnames")=List of 7
..$ diag   : chr [1:29] "All malignant neoplasms" "Oesophagus" "Stomach" "Colon incl. rectosigmoideum" ...
..$ sex    : chr [1:2] "M" "F"
..$ model  : chr [1:2] "Main" "Interact"
..$ pr.dur : chr [1:200] "0" "0.05" "0.1" "0.15" ...
..$ state  : chr [1:3] "Well" "DM" "DM/Ins"
..$ age.in : chr [1:3] "60" "65" "70"
..$ dur.in : chr [1:2] "0" "2"
>
> # The array prr contains the predicted log-rates from two different
> # models for 29 different events, computed for 200 timepoints starting
> # at 3 different ages and two different durations and 3 different states
> dnam <- dimnames( prr )
> s.can <- array( NA, dimnames =dnam,
+               dim=sapply(dnam,length) )
> p.can <- array( NA, dimnames =dnam[-4],
+               dim=sapply(dnam[-4],length) )
>
> # Just teh firt of each for use in debugging
> # dg <- dimnames(p.can)[["diag"]][1]
> # sx <- dimnames(p.can)[["sex"]][1]
> # mo <- dimnames(p.can)[["model"]][1]
> # st <- dimnames(p.can)[["state"]][1]
> # ai <- dimnames(p.can)[["age.in"]][1]
> # di <- dimnames(p.can)[["dur.in"]][1]
>
> for( sx in dimnames(p.can)[["sex"]] )

```


	0.22	0.12	0.65	0.18	1.51	0.35	0.22	0.12	0.72	0.19	1.35	0.37
Liver	0.22	0.12	0.65	0.18	1.51	0.35	0.22	0.12	0.72	0.19	1.35	0.37
Pancreas	0.47	0.48	0.85	0.75	4.02	3.68	0.47	0.48	0.61	0.49	0.86	0.85
Lung, bronchus and pleura	3.81	2.45	3.65	2.38	4.12	3.18	3.81	2.45	3.43	2.27	4.22	3.05
Melanoma of skin	0.45	0.37	0.38	0.26	0.22	0.19	0.45	0.37	0.38	0.26	0.23	0.20
Breast	0.04	3.00	0.02	2.90	0.07	2.50	0.04	3.00	0.03	2.87	0.11	2.55
Cervix uteri	NA	0.22	NA	0.21	NA	0.27	NA	0.22	NA	0.23	NA	0.30
Corpus uteri	NA	0.77	NA	1.10	NA	0.92	NA	0.77	NA	1.11	NA	1.00
Ovary, fallopian tube etc.	NA	0.63	NA	0.61	NA	0.57	NA	0.63	NA	0.61	NA	0.55
Prostate	4.70	NA	3.91	NA	2.48	NA	4.70	NA	3.76	NA	2.21	NA
Testis	0.02	NA	0.02	NA	0.01	NA	0.02	NA	0.01	NA	0.01	NA
Kidney	0.41	0.26	0.51	0.39	0.63	0.58	0.41	0.26	0.45	0.37	0.48	0.51
Urinary bladder	2.19	0.57	2.27	0.51	1.71	0.76	2.19	0.57	2.17	0.46	1.85	0.75
Brain	0.31	0.24	0.30	0.27	0.29	0.28	0.31	0.24	0.27	0.26	0.17	0.16
Thyroid	0.03	0.05	0.03	0.04	0.03	0.05	0.03	0.05	0.03	0.03	0.03	0.03
Hodgkin's lymphoma	0.03	0.02	0.04	0.03	0.03	0.02	0.03	0.02	0.04	0.03	0.01	0.02
Non-Hodgkin lymphoma	0.49	0.39	0.52	0.39	0.37	0.33	0.49	0.39	0.51	0.37	0.34	0.31
Multiple myeloma	0.31	0.21	0.29	0.20	0.16	0.20	0.31	0.21	0.27	0.18	0.16	0.20
Leukaemia	0.59	0.37	0.53	0.38	0.33	0.40	0.59	0.37	0.52	0.36	0.34	0.35
Death	23.52	16.36	35.72	26.05	49.75	39.67	23.52	16.36	37.64	26.97	51.39	39.63


```

> round( ftable( p.can[,,"Interact",,]*100, col.vars=c(5,3,2), row.vars=c(4,1) ), 1)
dur.in 0
state Well DM DM/Ins Well DM DM/Ins
sex M F M F M F M F M F M F
age.in diag
60 All malignant neoplasms 13.0 11.5 13.7 12.3 13.9 13.9 13.0 11.5 13.2 11.9 12.2 12.6
Oesophagus 0.3 0.1 0.3 0.1 0.4 0.1 0.3 0.1 0.3 0.1 0.4 0.2
Stomach 0.3 0.1 0.4 0.2 0.3 0.2 0.3 0.1 0.3 0.2 0.4 0.3
Colon incl. rectosigmoideum 1.1 0.9 1.3 1.0 1.1 0.7 1.1 0.9 1.2 1.0 1.0 0.6
Ascending colon 0.3 0.3 0.3 0.4 0.4 0.3 0.3 0.3 0.3 0.4 0.3 0.3
Transverse colon 0.1 0.1 0.2 0.1 0.2 0.1 0.1 0.1 0.2 0.2 0.2 0.1
Descending and sigmoid colon 0.6 0.4 0.6 0.4 0.5 0.2 0.6 0.4 0.6 0.4 0.5 0.2
Other colon (unspec. or multiple) 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.0 0.1
Rectum (excl. anus) 0.8 0.4 0.8 0.4 0.6 0.4 0.8 0.4 0.8 0.4 0.5 0.3
Colorectal cancer (excl. anus) 1.8 1.3 2.1 1.4 1.7 1.0 1.8 1.3 2.0 1.4 1.6 0.9
Liver 0.1 0.1 0.5 0.1 1.1 0.2 0.1 0.1 0.5 0.1 1.0 0.2
Pancreas 0.3 0.3 0.6 0.4 2.4 2.0 0.3 0.3 0.5 0.3 0.6 0.5
Lung, bronchus and pleura 2.2 1.7 2.2 1.7 2.7 2.4 2.2 1.7 2.1 1.7 2.8 2.3
Melanoma of skin 0.5 0.4 0.4 0.3 0.3 0.2 0.5 0.4 0.4 0.3 0.3 0.2
Breast 0.0 3.6 0.0 3.5 0.1 3.2 0.0 3.6 0.0 3.5 0.1 3.2
Cervix uteri NA 0.2 NA 0.2 NA 0.2 NA 0.2 NA 0.2 NA 0.3
Corpus uteri NA 0.6 NA 0.9 NA 0.8 NA 0.6 NA 1.0 NA 0.9
Ovary, fallopian tube etc. NA 0.5 NA 0.5 NA 0.5 NA 0.5 NA 0.5 NA 0.5
Prostate 2.9 NA 2.5 NA 1.5 NA 2.9 NA 2.4 NA 1.4 NA
Testis 0.0 NA 0.0 NA 0.0 NA 0.0 NA 0.0 NA 0.0 NA
Kidney 0.3 0.2 0.4 0.2 0.5 0.4 0.3 0.2 0.3 0.2 0.4 0.3
Urinary bladder 1.1 0.4 1.2 0.3 1.0 0.5 1.1 0.4 1.2 0.3 1.1 0.5
Brain 0.3 0.2 0.3 0.2 0.2 0.2 0.3 0.2 0.2 0.2 0.1 0.1
Thyroid 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
Hodgkin's lymphoma 0.0 0.0 0.1 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
Non-Hodgkin lymphoma 0.4 0.3 0.4 0.3 0.3 0.3 0.4 0.3 0.4 0.3 0.3 0.2
Multiple myeloma 0.2 0.1 0.2 0.1 0.1 0.1 0.2 0.1 0.2 0.1 0.1 0.1
Leukaemia 0.4 0.2 0.3 0.2 0.2 0.2 0.4 0.2 0.3 0.2 0.2 0.2
Death 8.3 5.1 17.1 10.6 29.3 21.2 8.3 5.1 18.1 11.1 29.5 20.9
65 All malignant neoplasms 17.3 13.6 17.9 14.3 18.0 16.1 17.3 13.6 17.2 13.8 15.5 14.5
Oesophagus 0.3 0.1 0.4 0.1 0.4 0.2 0.3 0.1 0.4 0.1 0.5 0.2
Stomach 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.2 0.4 0.4
Colon incl. rectosigmoideum 1.5 1.3 1.8 1.4 1.5 0.9 1.5 1.3 1.7 1.4 1.4 0.8
Ascending colon 0.4 0.4 0.5 0.5 0.5 0.4 0.4 0.4 0.5 0.5 0.4 0.4
Transverse colon 0.2 0.2 0.3 0.2 0.3 0.1 0.2 0.2 0.3 0.2 0.3 0.1
Descending and sigmoid colon 0.8 0.6 0.9 0.5 0.7 0.2 0.8 0.6 0.9 0.5 0.6 0.2
Other colon (unspec. or multiple) 0.1 0.1 0.2 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1 0.1
Rectum (excl. anus) 1.0 0.5 1.0 0.5 0.7 0.5 1.0 0.5 1.0 0.5 0.6 0.4
Colorectal cancer (excl. anus) 2.5 1.8 2.8 1.9 2.2 1.4 2.5 1.8 2.7 1.9 2.0 1.2
Liver 0.2 0.1 0.6 0.1 1.3 0.3 0.2 0.1 0.7 0.1 1.3 0.3
Pancreas 0.4 0.4 0.7 0.6 3.2 2.8 0.4 0.4 0.6 0.4 0.8 0.7
Lung, bronchus and pleura 3.2 2.3 3.1 2.3 3.7 3.1 3.2 2.3 2.9 2.2 3.8 3.0
Melanoma of skin 0.5 0.4 0.4 0.3 0.2 0.2 0.5 0.4 0.4 0.3 0.2 0.2
Breast 0.0 3.4 0.0 3.3 0.1 3.0 0.0 3.4 0.0 3.3 0.1 3.0
Cervix uteri NA 0.2 NA 0.2 NA 0.3 NA 0.2 NA 0.2 NA 0.3
Corpus uteri NA 0.7 NA 1.1 NA 0.9 NA 0.7 NA 1.1 NA 1.0
Ovary, fallopian tube etc. NA 0.6 NA 0.6 NA 0.6 NA 0.6 NA 0.6 NA 0.5
Prostate 4.0 NA 3.4 NA 2.1 NA 4.0 NA 3.3 NA 1.9 NA
Testis 0.0 NA 0.0 NA 0.0 NA 0.0 NA 0.0 NA 0.0 NA
Kidney 0.4 0.2 0.5 0.3 0.6 0.5 0.4 0.2 0.4 0.3 0.5 0.4
Urinary bladder 1.7 0.5 1.8 0.5 1.4 0.7 1.7 0.5 1.7 0.4 1.6 0.7
Brain 0.3 0.2 0.3 0.2 0.3 0.2 0.3 0.2 0.3 0.2 0.2 0.2
Thyroid 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
Hodgkin's lymphoma 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0
Non-Hodgkin lymphoma 0.4 0.4 0.5 0.4 0.3 0.3 0.4 0.4 0.5 0.3 0.3 0.3
Multiple myeloma 0.3 0.2 0.3 0.2 0.1 0.2 0.3 0.2 0.2 0.1 0.1 0.2
Leukaemia 0.5 0.3 0.4 0.3 0.3 0.3 0.5 0.3 0.4 0.3 0.3 0.3
Death 13.7 9.1 24.4 16.5 38.7 28.6 13.7 9.1 25.8 17.1 39.4 28.4
70 All malignant neoplasms 20.3 14.7 20.7 15.3 20.7 16.9 20.3 14.7 19.6 14.6 17.3 15.1
Oesophagus 0.4 0.1 0.4 0.1 0.4 0.2 0.4 0.1 0.4 0.1 0.5 0.2
Stomach 0.5 0.2 0.5 0.3 0.4 0.3 0.5 0.2 0.5 0.2 0.5 0.4
Colon incl. rectosigmoideum 1.9 1.7 2.2 1.8 1.8 1.2 1.9 1.7 2.1 1.8 1.7 1.1
Ascending colon 0.5 0.6 0.6 0.7 0.6 0.6 0.5 0.6 0.6 0.7 0.5 0.5
Transverse colon 0.3 0.3 0.3 0.3 0.4 0.2 0.3 0.3 0.3 0.3 0.3 0.2
Descending and sigmoid colon 1.0 0.7 1.1 0.7 0.8 0.3 1.0 0.7 1.0 0.7 0.8 0.3

```

Other colon (unspec. or multiple)	0.1	0.1	0.2	0.2	0.1	0.2	0.1	0.1	0.2	0.1	0.1	0.2
Rectum (excl. anus)	1.1	0.6	1.1	0.6	0.8	0.5	1.1	0.6	1.1	0.6	0.7	0.5
Colorectal cancer (excl. anus)	3.1	2.4	3.3	2.4	2.6	1.7	3.1	2.4	3.2	2.4	2.4	1.5
Liver	0.2	0.1	0.7	0.2	1.5	0.3	0.2	0.1	0.7	0.2	1.4	0.4
Pancreas	0.5	0.5	0.8	0.7	4.0	3.7	0.5	0.5	0.6	0.5	0.9	0.8
Lung, bronchus and pleura	3.8	2.5	3.7	2.4	4.1	3.2	3.8	2.5	3.4	2.3	4.2	3.1
Melanoma of skin	0.5	0.4	0.4	0.3	0.2	0.2	0.5	0.4	0.4	0.3	0.2	0.2
Breast	0.0	3.0	0.0	2.9	0.1	2.5	0.0	3.0	0.0	2.9	0.1	2.6
Cervix uteri	NA	0.2	NA	0.2	NA	0.3	NA	0.2	NA	0.2	NA	0.3
Corpus uteri	NA	0.8	NA	1.1	NA	0.9	NA	0.8	NA	1.1	NA	1.0
Ovary, fallopian tube etc.	NA	0.6	NA	0.6	NA	0.6	NA	0.6	NA	0.6	NA	0.5
Prostate	4.7	NA	3.9	NA	2.5	NA	4.7	NA	3.8	NA	2.2	NA
Testis	0.0	NA	0.0	NA	0.0	NA	0.0	NA	0.0	NA	0.0	NA
Kidney	0.4	0.3	0.5	0.4	0.6	0.6	0.4	0.3	0.4	0.4	0.5	0.5
Urinary bladder	2.2	0.6	2.3	0.5	1.7	0.8	2.2	0.6	2.2	0.5	1.9	0.7
Brain	0.3	0.2	0.3	0.3	0.3	0.3	0.3	0.2	0.3	0.3	0.2	0.2
Thyroid	0.0	0.1	0.0	0.0	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.0
Hodgkin's lymphoma	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Non-Hodgkin lymphoma	0.5	0.4	0.5	0.4	0.4	0.3	0.5	0.4	0.5	0.4	0.3	0.3
Multiple myeloma	0.3	0.2	0.3	0.2	0.2	0.2	0.3	0.2	0.3	0.2	0.2	0.2
Leukaemia	0.6	0.4	0.5	0.4	0.3	0.4	0.6	0.4	0.5	0.4	0.3	0.4
Death	23.5	16.4	35.7	26.0	49.7	39.7	23.5	16.4	37.6	27.0	51.4	39.6

```
>
> save( p.can, file="../data/prcan.Rdata" )
> load( file="../data/prcan.Rdata" )
> round( ftable( (p.can[,,,1]/p.can[,,,2]-1)*100, col.vars=c(5,3,2), row.vars=c(4,1) ), 1 )
```

state	diag	age.in model sex	60			65			70				
			sex	M	F	Interact	M	F	Interact	M	F	Interact	M
Well	All malignant neoplasms		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Oesophagus		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Stomach		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Colon incl. rectosigmoideum		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Ascending colon		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Transverse colon		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Descending and sigmoid colon		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Other colon (unspec. or multiple)		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Rectum (excl. anus)		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Colorectal cancer (excl. anus)		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Liver		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Pancreas		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Lung, bronchus and pleura		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Melanoma of skin		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Breast		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Cervix uteri		NA	0.0	NA	0.0	NA	0.0	NA	0.0	NA	0.0	NA
	Corpus uteri		NA	0.0	NA	0.0	NA	0.0	NA	0.0	NA	0.0	NA
	Ovary, fallopian tube etc.		NA	0.0	NA	0.0	NA	0.0	NA	0.0	NA	0.0	NA
	Prostate		0.0	NA	0.0	NA	0.0	NA	0.0	NA	0.0	NA	0.0
	Testis		0.0	NA	0.0	NA	0.0	NA	0.0	NA	0.0	NA	0.0
	Kidney		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Urinary bladder		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	Brain		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Thyroid		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
Hodgkin's lymphoma		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
Non-Hodgkin lymphoma		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
Multiple myeloma		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
Leukaemia		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
Death		0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	
DM	All malignant neoplasms		4.0	3.5	3.6	3.5	4.6	4.0	4.2	4.0	5.5	4.5	5.3
	Oesophagus		4.7	9.0	5.9	11.1	4.2	9.1	5.3	11.2	3.6	9.1	4.8
	Stomach		2.4	1.4	3.5	5.6	2.8	1.5	3.9	5.3	3.5	1.5	4.5
	Colon incl. rectosigmoideum		2.8	1.0	3.3	1.7	3.4	1.3	3.9	2.1	4.3	2.0	5.0
	Ascending colon		-1.3	1.9	-2.6	0.4	-0.8	3.5	-1.9	2.0	0.8	5.6	0.1
	Transverse colon		0.5	-8.3	-0.8	-6.5	1.5	-8.0	0.5	-6.3	2.9	-7.5	2.3
	Descending and sigmoid colon		4.1	-1.3	6.1	2.2	4.1	-1.3	5.9	2.3	4.3	-1.0	6.1
	Other colon (unspec. or multiple)		15.3	19.3	15.3	15.7	15.8	19.2	15.7	15.6	16.6	18.7	16.3
	Rectum (excl. anus)		1.2	-0.5	1.4	-1.8	1.1	-0.6	1.3	-1.8	1.0	-0.6	1.3
	Colorectal cancer (excl. anus)		2.2	0.6	2.6	0.9	2.6	1.0	3.0	1.3	3.2	1.6	3.7
	Liver		-6.0	-2.1	-10.5	-1.3	-6.1	-2.2	-10.2	-1.2	-5.6	-2.4	-9.3
	Pancreas		35.1	35.5	31.6	42.6	38.0	39.7	34.4	46.9	42.7	45.6	38.8
	Lung, bronchus and pleura		4.6	4.2	4.5	3.1	5.3	4.7	5.3	3.7	6.5	5.4	6.6
	Melanoma of skin		-1.2	-1.5	-0.3	1.1	-1.1	-1.7	-0.2	0.8	-0.8	-1.8	0.1
	Breast		-18.4	1.0	-29.7	0.9	-12.0	1.0	-21.9	0.9	-6.6	1.1	-15.2
	Cervix uteri		NA	-4.6	NA	-5.9	NA	-4.8	NA	-6.1	NA	-5.0	NA
	Corpus uteri		NA	-2.4	NA	-1.5	NA	-2.2	NA	-1.3	NA	-2.0	NA
	Ovary, fallopian tube etc.		NA	0.4	NA	0.6	NA	0.4	NA	0.6	NA	0.5	NA
	Prostate		3.8	NA	3.7	NA	3.8	NA	3.7	NA	4.0	NA	4.1
	Testis		10.3	NA	14.6	NA	10.8	NA	15.2	NA	11.9	NA	16.2
	Kidney		9.1	0.3	10.0	3.5	10.1	1.1	11.1	4.2	11.6	2.6	12.7
	Urinary bladder		2.5	12.8	3.4	10.5	3.0	12.7	3.8	10.6	3.7	12.7	4.5
	Brain		14.2	2.4	13.6	4.1	14.3	2.8	13.7	4.2	14.6	3.2	14.0
Thyroid		5.8	16.8	14.9	40.5	5.4	16.0	14.2	40.2	5.0	17.8	13.4	
Hodgkin's lymphoma		5.4	11.8	13.1	8.9	8.0	14.5	14.2	11.7	11.4	19.0	16.7	
Non-Hodgkin lymphoma		1.5	4.2	1.1	6.3	1.6	4.4	1.3	6.4	1.9	4.9	1.7	
Multiple myeloma		3.9	13.5	7.0	11.5	4.2	12.9	7.2	11.1	4.8	12.5	7.5	
Leukaemia		-1.6	6.7	1.6	6.3	-0.7	6.5	2.3	6.1	0.7	6.3	3.5	
Death		-4.2	-2.4	-5.5	-3.7	-4.3	-2.5	-5.4	-3.7	-4.1	-2.3	-5.1	
DM/Ins	All malignant neoplasms		13.0	10.6	14.1	10.1	15.1	11.8	16.2	11.1	18.4	13.6	19.4

```

Oesophagus -16.2 -13.2 -20.0 -14.0 -17.7 -13.9 -22.4 -16.2 -19.4 -15.1 -25.3
Stomach 2.1 -25.8 -0.2 -33.3 1.1 -26.5 -1.4 -34.2 -0.1 -27.1 -2.8
Colon incl. rectosigmoideum 11.8 9.3 8.4 11.3 12.2 9.0 7.3 11.7 12.9 8.8 6.3
Ascending colon 13.8 3.8 12.7 10.2 15.1 5.8 10.0 13.0 18.0 8.7 5.7
Transverse colon 19.8 18.0 18.2 12.4 23.2 15.8 16.6 10.2 27.8 13.7 15.8
Descending and sigmoid colon 11.2 4.7 5.6 -0.4 9.1 4.3 3.6 -0.9 7.0 3.4 1.3
Other colon (unspec. or multiple) -8.4 17.5 56.6 32.7 -7.4 16.8 63.1 33.7 -5.6 15.6 71.5
Rectum (excl. anus) 8.9 12.5 9.7 15.7 10.2 9.5 11.7 12.9 12.3 7.2 15.0
Colorectal cancer (excl. anus) 11.0 10.3 8.7 12.5 11.7 9.5 8.7 12.6 12.9 8.9 9.1
Liver -2.9 -8.3 3.3 -7.8 0.1 -9.4 6.6 -9.2 4.9 -7.0 11.6
Pancreas 267.0 281.0 293.5 281.0 291.4 302.5 323.9 302.8 325.1 333.2 365.5
Lung, bronchus and pleura 0.5 5.3 -1.5 5.4 1.4 6.1 -2.0 4.7 2.9 7.8 -2.3
Melanoma of skin -0.4 3.1 -1.8 -4.3 -1.4 2.8 -3.0 -5.0 -3.0 2.7 -4.4
Breast -44.7 -0.6 -39.2 -1.1 -39.9 -0.7 -36.1 -1.5 -35.3 -0.7 -33.3
Cervix uteri NA -9.2 NA -8.0 NA -9.0 NA -8.2 NA -8.1 NA
Corpus uteri NA 1.7 NA -3.4 NA 0.4 NA -5.9 NA -0.9 NA
Ovary, fallopian tube etc. NA 7.6 NA 7.1 NA 6.4 NA 5.7 NA 5.1 NA
Prostate 11.3 NA 9.0 NA 11.4 NA 10.6 NA 11.9 NA 12.5
Testis 0.1 NA -14.5 NA 6.0 NA -11.4 NA 18.3 NA -3.9
Kidney 26.6 12.1 20.6 7.6 32.6 14.4 24.1 10.0 41.1 19.1 29.5
Urinary bladder -4.3 3.7 -8.0 6.6 -3.1 2.3 -7.9 4.3 -1.2 0.6 -7.4
Brain 47.1 23.0 63.3 52.6 48.2 26.1 66.2 62.2 50.2 29.6 71.8
Thyroid 23.4 52.8 2.5 55.9 26.4 52.6 -2.6 55.3 30.5 52.7 -7.6
Hodgkin's lymphoma 63.7 -5.4 107.0 0.5 66.1 -4.2 123.5 1.2 69.9 -1.9 136.2
Non-Hodgkin lymphoma 14.8 8.3 14.2 9.1 13.6 6.4 12.0 8.4 12.0 4.0 9.2
Multiple myeloma 4.3 -13.4 -1.5 -3.7 3.6 -12.9 -1.6 -2.1 2.6 -11.9 -1.0
Leukaemia 5.0 17.5 -1.4 17.6 3.1 16.4 -2.8 16.1 1.0 15.1 -4.5
Death -4.9 -3.7 -0.7 1.4 -5.4 -3.9 -1.9 0.7 -5.9 -4.0 -3.2
>
> # To prevent barplot from doing silly things.
> dimnames(p.can)[["state"]] <- rep("",3)
> ages <- as.numeric( dimnames(s.can)[["ages"]] )
>
> # Color scheme for cancer/dead/alive
> # clr <- c("lawngreen","blue","red")
> clr <- gray(c(5,1,9)/10)
>
> # Show the state occupancy functions
> # Put the probabilities together
> ff <- cbind( p.can[ 1,"F",1,3:1,2,"2"],
+ p.can["Death","F",1,3:1,2,"2"] )
> ff <- cbind( ff, 1-apply(ff,1,sum) )
> mm <- cbind( p.can[ 1,"M",1,3:1,2,"2"],
+ p.can["Death","M",1,3:1,2,"2"] )
> mm <- cbind( mm, 1-apply(mm,1,sum) )
> ff <- rbind( mm, ff)[c(3,6,2,5,1,4),]
> rownames(ff) <- rep(c("M","F"),3)
>
> pdf( "../graph/state-stack.pdf", height=9 )
> cex.all <- 1.2
> par( mar=c(3,3,3.5*cex.all,1), mgp=c(3,1,0)/1.5,
+ las=1, cex.axis=cex.all )
> barplot( t(ff), col=clr, space=c(0,1,4,1,4,1)/10,
+ yaxt="n", xaxt="n" )
> axis( side=2, at=0:5/5, labels=0:5*20 )
> mtext( c("Well","DM","DM / Ins"), font=2, cex=cex.all,
+ at=c(1,3,5,6), side=1, line=1.5 )
> mtext( rep(c("M","F"),3), font=2, cex=cex.all,
+ at=c(0.5,1.5,3,4,5,5,6,5), side=1, line=0.25 )
> mtext( "Cancer (alive or dead)", cex=cex.all,
+ col=clr[1], font=2, at=0, adj=0, side=3, line=0.5 )
> mtext( "Dead without cancer", cex=cex.all,
+ col=clr[2], font=2, at=0, adj=0, side=3, line=0.5+cex.all )
> mtext( "Alive without cancer", cex=cex.all,
+ col=clr[3], font=2, at=0, adj=0, side=3, line=0.5+cex.all*2 )
> mtext( "Born 1933,", cex=cex.all,
+ at=7, adj=1, side=3, line=0.5+cex.all*2 )
> mtext( "followed 1.1.1998-1.1.2007,", cex=cex.all,
+ at=7, adj=1, side=3, line=0.5+cex.all )
> mtext( "in ages 65-75", cex=cex.all,
+ at=7, adj=1, side=3, line=0.5 )
> abline( h=1:9/10, lty="19", col="white" )
> dev.off()
null device
1
>
> pdf( "../graph/state-stack-w.pdf", width=9 )
> cex.all <- 1.2
> par( mar=c(3,3,3.5*cex.all,1), mgp=c(3,1,0)/1.5,
+ las=1, cex.axis=cex.all )
> barplot( t(ff), col=clr, space=c(0,1,4,1,4,1)/10,
+ yaxt="n", xaxt="n" )
> axis( side=2, at=0:5/5, labels=0:5*20 )
> mtext( c("Well","DM","DM / Ins"), font=2, cex=cex.all,
+ at=c(1,3,5,6), side=1, line=1.5 )
> mtext( rep(c("M","F"),3), font=2, cex=cex.all,
+ at=c(0.5,1.5,3,4,5,5,6,5), side=1, line=0.25 )
> mtext( "Cancer (alive or dead)", cex=cex.all,
+ col=clr[1], font=2, at=0, adj=0, side=3, line=0.5 )

```



```

> mtext( "Dead without cancer", cex=cex.all,
+       col=clr[2], font=2, at=0, adj=0, side=3, line=0.5+cex.all )
> mtext( "Alive without cancer", cex=cex.all,
+       col=clr[3], font=2, at=0, adj=0, side=3, line=0.5+cex.all*2 )
> mtext( "Born 1933", cex=cex.all,
+       at=7, adj=1, side=3, line=0.5+cex.all*2 )
> mtext( "followed 1.1.1998-1.1.2007", cex=cex.all,
+       at=7, adj=1, side=3, line=0.5+cex.all )
> mtext( "in ages 65-75", cex=cex.all,
+       at=7, adj=1, side=3, line=0.5 )
> abline( h=1:9/10, lty="19", col="white" )
> dev.off()
null device
  1
>
> mclr <- c("#9999FF", "#0000DD", "#DDDDFF")
> fclr <- c("#FF9999", "#DD0000", "#FFDDDD")
> bclr <- c("transparent", "transparent", "transparent")
>
> pdf( "../graph/state-stack-2-3.pdf", height=8 )
> par( mfcol=c(2,3), mar=c(1,2,0,0), mgp=c(3,1,0)/1.5,
+     oma=c(3,3,2.5,1.5), las=1 )
> for( ai in dimnames(p.can)[["age.in"]] )
+ for( di in dimnames(p.can)[["dur.in"]] )
+ {
+ # Put the probabilities together
+ ff <- cbind( p.can[ 1,"F",1,3:1,ai,di],
+             p.can["Death","F",1,3:1,ai,di] )
+ ff <- cbind( ff, 1-apply(ff,1,sum) )
+ mm <- cbind( p.can[ 1,"M",1,3:1,ai,di],
+             p.can["Death","M",1,3:1,ai,di] )
+ mm <- cbind( mm, 1-apply(mm,1,sum) )
+ ff <- rbind( mm, ff)[c(3,6,2,5,1,4),]
+ rownames(ff) <- rep(c("M","F"),3)
+
+ barplot( t(ff), col=mclr, border=bclr, space=c(0,1,4,1,4,1)/10, width=1,
+         yaxt="n", xaxt="n", lwd=5 )
+ par( new=TRUE )
+ zz <- ff
+ zz[c(1,3,5),] <- 0
+ barplot( t(zz), col=fclr, border=bclr, space=c(0,1,4,1,4,1)/10, width=1,
+         yaxt="n", xaxt="n", lwd=5 )
+
+ abline( h=1:9/10, lty="14", col="white" )
+
+ if( ai==dimnames(p.can)[["age.in"]][1] )
+   axis( side=2, at=0:5/5, labels=0:5*20 )
+
+ if( di==dimnames(p.can)[["dur.in"]][2] )
+   {
+   mtext( "Duration 1 year", at=50, line=1, side=2 )
+   mtext( c("No DM","DM","DM / Ins"), font=1,
+         at=c(1,3.5,6), side=1, line=1.5 )
+   mtext( rep(c("M","F"),3), font=1,
+         at=c(0.5,1.5,3,4,5.5,6.5), side=1, line=0.25 )
+   }
+ mtext( paste("Duration at start:",dimnames(p.can)[["dur.in"]][1]), side=2, at=3/4, outer=T, las=0, line=0.5 )
+ mtext( paste("Duration at start:",dimnames(p.can)[["dur.in"]][2]), side=2, at=1/4, outer=T, las=0, line=0.5 )
+ mtext( paste("Age at start:",dimnames(p.can)[["age.in"]][1]), side=3, at=1/6, outer=T, line=0.5 )
+ mtext( paste("Age at start:",dimnames(p.can)[["age.in"]][2]), side=3, at=3/6, outer=T, line=0.5 )
+ mtext( paste("Age at start:",dimnames(p.can)[["age.in"]][3]), side=3, at=5/6, outer=T, line=0.5 )
+ }
>
> dev.off()
null device
  1
>
> pdf( "../graph/state-stack-3-2.pdf", height=8 )
> par( mfcol=c(3,2), mar=c(1,2,0,0), mgp=c(3,1,0)/1.5,
+     oma=c(3,3,2.5,1.5), las=1 )
> for( di in dimnames(p.can)[["dur.in"]] )
+ for( ai in dimnames(p.can)[["age.in"]] )
+ {
+ # Put the probabilities together
+ ff <- cbind( p.can[ 1,"F",1,3:1,ai,di],
+             p.can["Death","F",1,3:1,ai,di] )
+ ff <- cbind( ff, 1-apply(ff,1,sum) )
+ mm <- cbind( p.can[ 1,"M",1,3:1,ai,di],
+             p.can["Death","M",1,3:1,ai,di] )
+ mm <- cbind( mm, 1-apply(mm,1,sum) )
+ ff <- rbind( mm, ff)[c(3,6,2,5,1,4),]
+ rownames(ff) <- rep(c("M","F"),3)
+
+ barplot( t(ff), col=mclr, border=bclr, space=c(0,1,4,1,4,1)/10, width=1,
+         yaxt="n", xaxt="n", lwd=5 )
+ par( new=TRUE )
+ zz <- ff
+ zz[c(1,3,5),] <- 0
+ barplot( t(zz), col=fclr, border=bclr, space=c(0,1,4,1,4,1)/10, width=1,

```

```

+       yaxt="n", xaxt="n", lwd=5 )
+
+ abline( h=1:9/10, lty="14", col="white" )
+
+ if( ai==dimnames(p.can)[["age.in"]][1] )
+   axis( side=2, at=0:5/5, labels=0:5*20 )
+
+ if( di==dimnames(p.can)[["dur.in"]][2] )
+   {
+   mtext( "Duration 1 year", at=50, line=1, side=2 )
+   mtext( c("No DM","DM","DM / Ins"), font=1,
+         at=c(1,3.5,6), side=1, line=1.5 )
+   mtext( rep(c("M","F"),3), font=1,
+         at=c(0.5,1.5,3,4,5.5,6.5), side=1, line=0.25 )
+   }
+ mtext( paste("Duration at start:",dimnames(p.can)[["dur.in"]][1]), side=3, at=1/4, outer=T, line=0.5 )
+ mtext( paste("Duration at start:",dimnames(p.can)[["dur.in"]][2]), side=3, at=3/4, outer=T, line=0.5 )
+ mtext( paste("Age at start:",dimnames(p.can)[["age.in"]][3]), side=2, at=1/6, las=0, outer=T, line=0.5 )
+ mtext( paste("Age at start:",dimnames(p.can)[["age.in"]][2]), side=2, at=3/6, las=0, outer=T, line=0.5 )
+ mtext( paste("Age at start:",dimnames(p.can)[["age.in"]][1]), side=2, at=5/6, las=0, outer=T, line=0.5 )
+ }
+
>
> dev.off()
null device
  1
>
> if(FALSE){
+ pdf( "../graph/state-stack-3-2.pdf", width=9 )
+ par( mfcol=c(3,2), mar=c(1,2,0,0), mgp=c(3,1,0)/1.5,
+     oma=c(3,3,2.5,1.5), las=1 )
+ for( di in dimnames(p.can)[["dur.in"]] )
+ for( ai in dimnames(p.can)[["age.in"]] )
+ {
+ # Put the probabilities together
+ ff <- cbind( p.can[ 1,"F",1,3:1,ai,di],
+             p.can["Death","F",1,3:1,ai,di] )
+ ff <- cbind( ff, 1-apply(ff,1,sum) )
+ mm <- cbind( p.can[ 1,"M",1,3:1,ai,di],
+             p.can["Death","M",1,3:1,ai,di] )
+ mm <- cbind( mm, 1-apply(mm,1,sum) )
+ ff <- rbind( mm, ff)[c(3,6,2,5,1,4),]
+ rownames(ff) <- rep(c("M","F"),3)
+
+ barplot( t(ff), col=clr, border=clr, space=c(0,1,4,1,4,1)/10,
+         yaxt="n", xaxt="n" )
+ abline( h=1:9/10, lty="14", col="white" )
+
+ if( di==dimnames(p.can)[["dur.in"]][1] )
+   axis( side=2, at=0:5/5, labels=0:5*20 )
+
+ if( ai==dimnames(p.can)[["age.in"]][3] )
+   {
+   mtext( "Duration 1 year", at=50, line=1, side=2 )
+   mtext( c("Well","DM","DM / Ins"), font=1,
+         at=c(1,3.5,6), side=1, line=1.5 )
+   mtext( rep(c("M","F"),3), font=1,
+         at=c(0.5,1.5,3,4,5.5,6.5), side=1, line=0.25 )
+   }
+ mtext( paste("Duration at start:",dimnames(p.can)[["dur.in"]][1]), side=3, at=1/4, outer=T, line=0.5 )
+ mtext( paste("Duration at start:",dimnames(p.can)[["dur.in"]][2]), side=3, at=3/4, outer=T, line=0.5 )
+ mtext( paste("Age at start:",dimnames(p.can)[["age.in"]][3]), side=2, at=1/6, las=0, outer=T, line=0.5 )
+ mtext( paste("Age at start:",dimnames(p.can)[["age.in"]][2]), side=2, at=3/6, las=0, outer=T, line=0.5 )
+ mtext( paste("Age at start:",dimnames(p.can)[["age.in"]][1]), side=2, at=5/6, las=0, outer=T, line=0.5 )
+ }
+ dev.off()
+ }
>
-----
Program: prob3dx.R
Folder: C:\Bendix\Steno\DM-register\NDR\projects\Cancer\r
Ended: torsdag 23. juni 2011, 17:39:49
Elapsed: 00:00:01
-----
> proc.time()
  user system elapsed
  1.50   0.23   1.95

```