

Analysis of follow-up data using the Lexis functions in Epi

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Introduction

0.1 Technicalities

First we set some graphics parameters and load the packages needed:

```
> options(width = 90,
+         SweaveHooks=list(fig=function()
+                           par(mar = c(3, 3, 1, 1),
+                               mgp = c(3, 1, 0) / 1.6,
+                               las = 1,
+                               lend = "butt",
+                               bty = "n")))
> library(Epi)
> library(popEpi)
> library(survival)
> clear()

> installed.packages()[c("Epi", "popEpi"),
+                      c("Version", "Built"), drop = FALSE]
      Version Built
Epi      "2.55"  "4.4.1"
popEpi   "0.4.12" "4.4.0"
```

0.2 About this vignette

This vignette is an introduction to the `Lexis` machinery in the `Epi` package, intended for representation and manipulation of follow-up data (“event history data”) from studies where exact dates of events are known. It accommodates follow-up through multiple states and on multiple time scales.

This vignette uses an example from the `Epi` package to illustrate the set-up of a simple `Lexis` object (a data frame of follow-up intervals), as well as the subdivision of follow-up intervals needed for multistate representation and analysis of transition rates by flexible parametric functions.

The first chapter is exclusively on manipulation of the follow-up representation, but it points to the subsequent chapter where analysis is based on a `Lexis` representation with very small follow-up intervals.

Chapter 2 uses analysis of mortality rates among Danish diabetes patients (available in the `Epi` package) currently on insulin treatment or not, to illustrate the use of `Lexis` object in the analysis of rates.

0.3 History

The **Lexis** machinery in the **Epi** package was first conceived by Martyn Plummer[3, 1], and since its first appearance in the **Epi** package in 2008 it has been expanded with a number of utilities. An overview of these can be found in the last chapter of this note, “**Lexis functions**”.

Chapter 1

Representation of follow-up data in the Epi package

In the Epi-package, follow-up data is represented by adding some extra variables and a few attributes to a data frame. Such a data frame is called a `Lexis` object. The tools for handling follow-up data then use the structure of this for special plots, tabulations and modeling.

Follow-up data basically consists of a time of entry, a time of exit and an indication of the status at exit (normally either “alive” or “dead”) for each person. Implicitly is also assumed a status *during* the follow-up (usually “alive”).

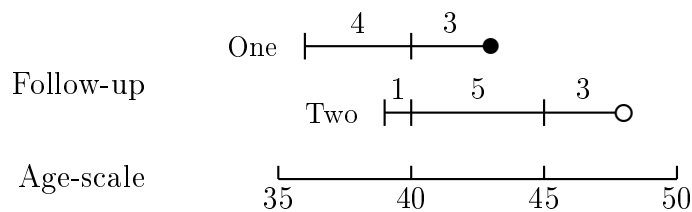


Figure 1.1: *Follow-up of two persons*

1.1 Time scales

A time scale is a variable that varies deterministically *within* each person during follow-up, *e.g.*:

- Age
- Calendar time
- Time since start of treatment
- Time since relapse

All time scales advance at the same pace, so the time followed is the same on all time scales. Therefore, it will suffice to use only the entry point on each of the time scales, for example:

- Age at entry

- Date of entry
- Time at treatment (*at* treatment this is 0)
- Time at relapse (*at* relapse this is 0)

In the `Epi` package, follow-up in a cohort is represented in a `Lexis` object. A `Lexis` object is a data frame with some extra structure to representing the follow-up. For the `DMlate` data — follow-up of diabetes patients in Denmark with recorded date of birth, date of diabetes, date of insulin use, date of first oral drug use, date of exit and date of death — we can construct a `Lexis` object by first including follow-up from entry to exit:

```
> data(DMlate)
> head(DMlate)
  sex  dobth  dodm  dodth  dooad doins  dox
50185 F 1940.256 1998.917      NA      NA  NA 2009.997
307563 M 1939.218 2003.309      NA 2007.446  NA 2009.997
294104 F 1918.301 2004.552      NA      NA  NA 2009.997
336439 F 1965.225 2009.261      NA      NA  NA 2009.997
245651 M 1932.877 2008.653      NA      NA  NA 2009.997
216824 F 1927.870 2007.886 2009.923      NA  NA 2009.923

> dmL <- Lexis(entry = list(per = dodm,
+                           age = dodm-dobth,
+                           tfD = 0),
+             exit = list(per = dox),
+             exit.status = factor(!is.na(dodth),
+                                 labels = c("DM", "Dead")),
+             data = DMlate)

NOTE: entry.status has been set to "DM" for all.
NOTE: Dropping 4 rows with duration of follow up < tol
> timeScales(dmL)
[1] "per" "age" "tfD"
```

(The excluded persons are persons with date of diabetes equal to date of death.)

The `entry` argument is a *named* list with the entry points on each of the time scales we want to use. It defines the names of the time scales and the entry points of the follow-up of each person. The `exit` argument gives the exit time on *one* of the time scales, so the name of the element in this list must match one of the names of the `entry` list. This is sufficient, because the follow-up time on all time scales is the same, in this case `dox-dodm`.

The `exit.status` is a categorical variable (a *factor*) that indicates the exit status — in this case whether the person (still) is in state `DM` or exits to `Dead` at the end of follow-up. In principle we should also indicate an `entry.status`, but the default is to assume that all persons enter in the *first* level of `exit.states` — in this case `DM`, because `FALSE < TRUE`.

Now take a look at the result:

```
> str(dmL)
Classes 'Lexis' and 'data.frame': 9996 obs. of 14 variables:
 $ per : num 1999 2003 2005 2009 2009 ...
 $ age : num 58.7 64.1 86.3 44 75.8 ...
 $ tfD : num 0 0 0 0 0 0 0 0 0 0 ...
 $ lex.dur: num 11.08 6.689 5.446 0.736 1.344 ...
 $ lex.Cst: Factor w/ 2 levels "DM","Dead": 1 1 1 1 1 1 1 1 1 1 ...
 $ lex.Xst: Factor w/ 2 levels "DM","Dead": 1 1 1 1 1 2 1 1 2 1 ...
```

```

$ lex.id : int  1 2 3 4 5 6 7 8 9 10 ...
$ sex    : Factor w/ 2 levels "M","F": 2 1 2 2 1 2 1 1 2 1 ...
$ dobth  : num  1940 1939 1918 1965 1933 ...
$ dodm   : num  1999 2003 2005 2009 2009 ...
$ dodth  : num  NA NA NA NA NA ...
$ dooad  : num  NA 2007 NA NA NA ...
$ doins  : num  NA NA NA NA NA NA NA NA NA NA ...
$ dox    : num  2010 2010 2010 2010 2010 ...
- attr(*, "time.scales")= chr [1:3] "per" "age" "tfD"
- attr(*, "time.since")= chr [1:3] "" "" ""
- attr(*, "breaks")=List of 3
..$ per: NULL
..$ age: NULL
..$ tfD: NULL

> head(dmL)[, 1:10]

lex.id    per    age tfD lex.dur lex.Cst lex.Xst sex    dobth    dodm
  1 1998.92 58.66  0  11.08    DM     DM    F 1940.256 1998.917
  2 2003.31 64.09  0   6.69    DM     DM    M 1939.218 2003.309
  3 2004.55 86.25  0   5.45    DM     DM    F 1918.301 2004.552
  4 2009.26 44.04  0   0.74    DM     DM    F 1965.225 2009.261
  5 2008.65 75.78  0   1.34    DM     DM    M 1932.877 2008.653
  6 2007.89 80.02  0   2.04    DM    Dead    F 1927.870 2007.886

```

The Lexis object `dmL` has a variable for each time scale, the value of which is the entry for each person on this time scale. The length of the follow-up time is in the variable `lex.dur` (duration). Note that the exit status is in the variable `lex.Xst` (eXit state). The variable `lex.Cst` is the state where the follow-up takes place (Current state), in this case DM (alive with diabetes) for all persons. This implies that observations *censored* in state Zst, say, are characterized by having `lex.Cst = lex.Xst = Zst`.

There is a `summary` function for Lexis objects that lists the number of transitions and records as well as the total amount of follow-up time; it also (optionally) prints information about the names of the variables that constitute the time scales:

```

> summary(dmL, timeScales = TRUE)
Transitions:
  To
From  DM Dead  Records:  Events: Risk time:  Persons:
  DM 7497 2499    9996    2499    54273.27    9996

Timescales:
per age tfD
"" "" ""

```

It is possible to get a visualization of the follow-up along the time scales chosen by using the `plot` method for Lexis objects. `dmL` is an object of *class* Lexis, so using the function `plot()` on it means that R will look for the function `plot.Lexis` and use this function.

```
> plot(dmL)
```

The function allows quite a bit of control over the output, and a `points.Lexis` function allows plotting of the endpoints of follow-up:

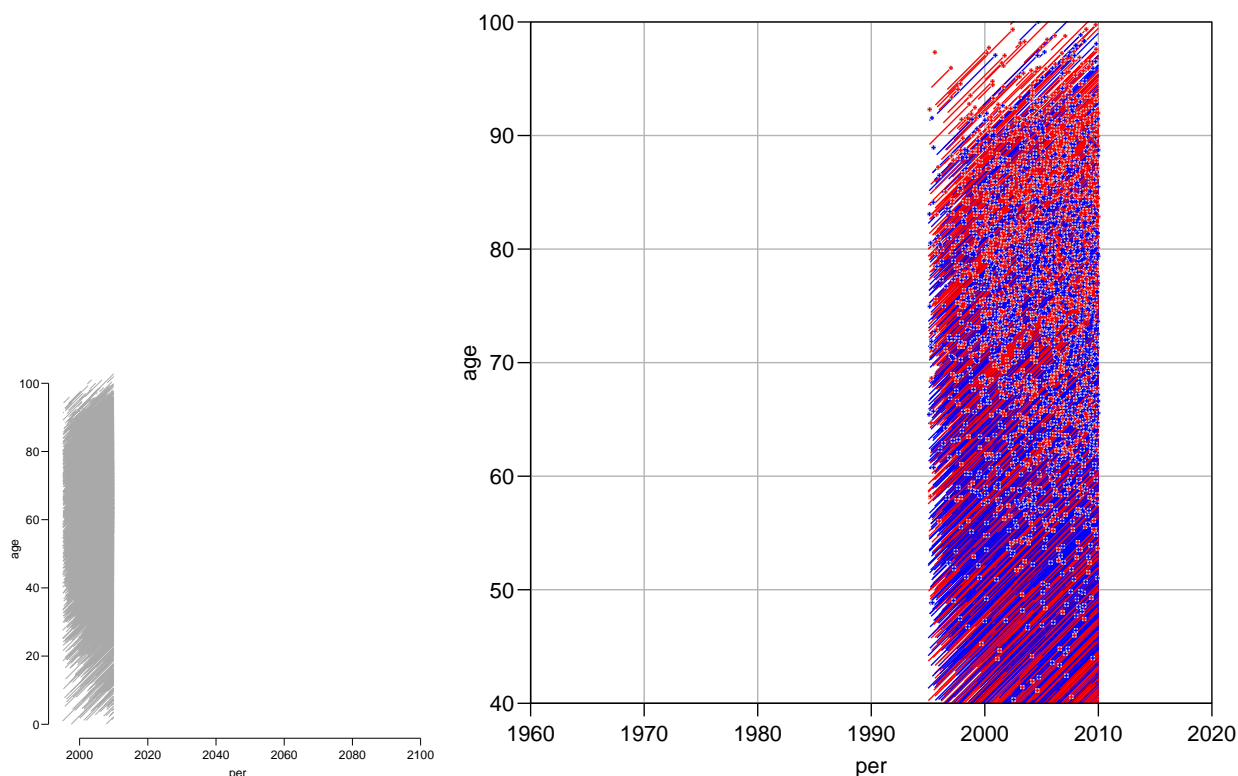


Figure 1.2: *Lexis diagram of the DMlate dataset; left panel is the default version, right panel is with some bells and whistles. The red lines are for women, blue for men, crosses indicate deaths.*

```
> par(mar = c(3, 3, 1, 1), mgp = c(3, 1, 0) / 1.6)
> plot(dmL, 1:2, lwd = 1, col = c("blue", "red")[dmL$sex],
+      grid = TRUE, lty.grid = 1, col.grid = gray(0.7),
+      xlim = 1960 + c(0, 60), xaxs = "i",
+      ylim = 40 + c(0, 60), yaxs = "i", las = 1)
> points(dmL, 1:2, pch = c(NA, 3)[dmL$lex.Xst],
+       col = "lightgray", lwd = 3, cex = 0.3)
> points(dmL, 1:2, pch = c(NA, 3)[dmL$lex.Xst],
+       col = c("blue", "red")[dmL$sex], lwd = 1, cex = 0.3)
> box(bty = 'o')
```

In the above code you will note that the values of the arguments `col` and `pch` are indexed by factors, using the convention in R that the index is taken as *number of the level* of the supplied factor. Thus `c("blue", "red")[dmL$sex]` is "blue" when `sex` is M (the first level of `sex`) and "red" when `sex` is F (the second level of `sex`).

The results of these two plotting commands are in figure 1.2, p. 6.

1.2 Splitting the follow-up time along a time scale

In next chapter we shall conduct statistical analysis of mortality rates, and a prerequisite for parametric analysis of rates is that follow-up time is subdivided in smaller intervals, where we can reasonably assume that rates are constant.

The follow-up time in a cohort can be subdivided (“split”) along a time scale, for example

current age. This is achieved by the `splitLexis` (note that it is *not* called `split.Lexis`). This requires that the time scale and the breakpoints on this time scale are supplied. Try:

```
> dmS1 <- splitLexis(dmL, "age", breaks = seq(0, 100, 5))
> summary(dmL)
```

Transitions:

	To						
From	DM	Dead	Records:	Events:	Risk time:	Persons:	
	DM	7497	2499	9996	2499	54273.27	9996

```
> summary(dmS1)
```

Transitions:

	To						
From	DM	Dead	Records:	Events:	Risk time:	Persons:	
	DM	18328	2499	20827	2499	54273.27	9996

We see that the number of persons and events and the amount of follow-up is the same in the two data sets; only the number of records differ — the extra records all have `lex.Cst = DM` and `lex.Xst = DM`.

To see how records are split for each individual, it is useful to list the results for a few individuals (whom we selected with a view to the illustrative usefulness):

```
> wh.id <- c(9, 27, 52, 484)
> subset(dmL, lex.id %in% wh.id)[, 1:10]
lex.id    per    age tfD lex.dur lex.Cst lex.Xst sex    dobth    dodm
  9 1998.96 61.87  0    9.51    DM    Dead  F 1937.083 1998.956
 27 2000.04 52.71  0    9.95    DM    DM    M 1947.331 2000.042
 52 1998.25 61.86  0   11.75    DM    DM    F 1936.393 1998.249
 484 1998.26 62.38  0   10.93    DM    Dead  F 1935.881 1998.260
```

```
> subset(dmS1, lex.id %in% wh.id)[, 1:10]
```

lex.id	per	age	tfD	lex.dur	lex.Cst	lex.Xst	sex	dobth	dodm
9	1998.96	61.87	0.00	3.13	DM	DM	F	1937.083	1998.956
9	2002.08	65.00	3.13	5.00	DM	DM	F	1937.083	1998.956
9	2007.08	70.00	8.13	1.38	DM	Dead	F	1937.083	1998.956
27	2000.04	52.71	0.00	2.29	DM	DM	M	1947.331	2000.042
27	2002.33	55.00	2.29	5.00	DM	DM	M	1947.331	2000.042
27	2007.33	60.00	7.29	2.67	DM	DM	M	1947.331	2000.042
52	1998.25	61.86	0.00	3.14	DM	DM	F	1936.393	1998.249
52	2001.39	65.00	3.14	5.00	DM	DM	F	1936.393	1998.249
52	2006.39	70.00	8.14	3.60	DM	DM	F	1936.393	1998.249
484	1998.26	62.38	0.00	2.62	DM	DM	F	1935.881	1998.260
484	2000.88	65.00	2.62	5.00	DM	DM	F	1935.881	1998.260
484	2005.88	70.00	7.62	3.31	DM	Dead	F	1935.881	1998.260

The resulting object, `dmS1`, is again a `Lexis` object, and the follow-up may be split further along another time scale, for example diabetes duration, `tfD`. Subsequently we list the results for the chosen individuals:

```
> dmS2 <- splitLexis(dmS1, "tfD", breaks = c(0, 1, 2, 5, 10, 20, 30, 40))
> subset(dmS2, lex.id %in% wh.id)[, 1:10]
```

lex.id	per	age	tfD	lex.dur	lex.Cst	lex.Xst	sex	dobth	dodm
9	1998.96	61.87	0.00	1.00	DM	DM	F	1937.083	1998.956
9	1999.96	62.87	1.00	1.00	DM	DM	F	1937.083	1998.956
9	2000.96	63.87	2.00	1.13	DM	DM	F	1937.083	1998.956
9	2002.08	65.00	3.13	1.87	DM	DM	F	1937.083	1998.956

9	2003.96	66.87	5.00	3.13	DM	DM	F	1937.083	1998.956
9	2007.08	70.00	8.13	1.38	DM	Dead	F	1937.083	1998.956
27	2000.04	52.71	0.00	1.00	DM	DM	M	1947.331	2000.042
27	2001.04	53.71	1.00	1.00	DM	DM	M	1947.331	2000.042
27	2002.04	54.71	2.00	0.29	DM	DM	M	1947.331	2000.042
27	2002.33	55.00	2.29	2.71	DM	DM	M	1947.331	2000.042
27	2005.04	57.71	5.00	2.29	DM	DM	M	1947.331	2000.042
27	2007.33	60.00	7.29	2.67	DM	DM	M	1947.331	2000.042
52	1998.25	61.86	0.00	1.00	DM	DM	F	1936.393	1998.249
52	1999.25	62.86	1.00	1.00	DM	DM	F	1936.393	1998.249
52	2000.25	63.86	2.00	1.14	DM	DM	F	1936.393	1998.249
52	2001.39	65.00	3.14	1.86	DM	DM	F	1936.393	1998.249
52	2003.25	66.86	5.00	3.14	DM	DM	F	1936.393	1998.249
52	2006.39	70.00	8.14	1.86	DM	DM	F	1936.393	1998.249
52	2008.25	71.86	10.00	1.75	DM	DM	F	1936.393	1998.249
484	1998.26	62.38	0.00	1.00	DM	DM	F	1935.881	1998.260
484	1999.26	63.38	1.00	1.00	DM	DM	F	1935.881	1998.260
484	2000.26	64.38	2.00	0.62	DM	DM	F	1935.881	1998.260
484	2000.88	65.00	2.62	2.38	DM	DM	F	1935.881	1998.260
484	2003.26	67.38	5.00	2.62	DM	DM	F	1935.881	1998.260
484	2005.88	70.00	7.62	2.38	DM	DM	F	1935.881	1998.260
484	2008.26	72.38	10.00	0.93	DM	Dead	F	1935.881	1998.260

A more efficient (and more intuitive) way of making this double split is to use the `splitMulti` function from the `popEpi` package:

```
> dmM <- splitMulti(dmL,
+                   age = seq(0, 100, 5),
+                   tfD = c(0, 1, 2, 5, 10, 20, 30, 40),
+                   drop = FALSE)
> summary(dmS2)
```

Transitions:

		To					
From	DM	Dead	Records:	Events:	Risk time:	Persons:	
	DM	40897	2499	43396	2499	54273.27	9996

```
> summary(dmM)
```

Transitions:

		To					
From	DM	Dead	Records:	Events:	Risk time:	Persons:	
	DM	40897	2499	43396	2499	54273.27	9996

Note we used the argument `drop = FALSE` which will retain follow-up also outside the window defined by the range of the breaks. Otherwise, the default for `splitMulti` would be to drop follow-up outside `age` $[0, 100]$ and `tfD` $[0, 40]$. This clipping behaviour is not available in `splitLexis`, nevertheless this may be exactly what we want in some situations.

The recommended way of splitting follow-up time is by `splitMulti`, because it is faster. But you should be aware that the result is a `data.table` object unless you set the option `"popEpi.datatable" = FALSE`. In some circumstances `data.tables` behaves slightly differently from `data.frames`. See the manual for `data.table`.

1.3 Cutting follow up time at dates of intermediate events

If we have a recording of the date of a specific event as for example recovery or relapse, we may classify follow-up time as being before or after this intermediate event, but it requires that follow-up records that straddle the event be cut in two and placed in separate records, one representing follow-up *before* the intermediate event, and another representing follow-up *after* the intermediate event. This is achieved with the function `cutLexis`, which takes three arguments: the time point of the intermediate event, the time scale that this point refers to, and the value of the (new) state following the date. Optionally, we may also define a new time scale with the argument `new.scale = .`

We are interested in the time before and after inception of insulin use, which occurs at the date `doins`:

```
> subset(dmL, lex.id %in% wh.id)
lex.id   per   age tfD lex.dur lex.Cst lex.Xst sex   dobth   dodm   dodth   dooad
   9 1998.96 61.87  0    9.51     DM   Dead  F 1937.083 1998.956 2008.464    NA
  27 2000.04 52.71  0    9.95     DM    DM  M 1947.331 2000.042    NA 2000.125
  52 1998.25 61.86  0   11.75     DM    DM  F 1936.393 1998.249    NA 2002.402
 484 1998.26 62.38  0   10.93     DM   Dead  F 1935.881 1998.260 2009.190 1998.260
doins     dox
  NA 2008.464
  NA 2009.997
2004.804 2009.997
2003.960 2009.190
> dmC <- cutLexis(data = dmL,
+                 cut = dmL$doins,
+                 timescale = "per",
+                 new.state = "Ins",
+                 new.scale = "tfI")
> subset(dmC, lex.id %in% wh.id)[, 1:10]
lex.id   per   age tfD tfI lex.dur lex.Cst lex.Xst sex   dobth
   9 1998.96 61.87 0.00 NA    9.51     DM   Dead  F 1937.083
  27 2000.04 52.71 0.00 NA    9.95     DM    DM  M 1947.331
  52 1998.25 61.86 0.00 NA    6.55     DM   Ins  F 1936.393
  52 2004.80 68.41 6.55  0    5.19     Ins  Ins  F 1936.393
 484 1998.26 62.38 0.00 NA    5.70     DM   Ins  F 1935.881
 484 2003.96 68.08 5.70  0    5.23     Ins  Dead  F 1935.881
```

Note that the process of cutting time is simplified by having all types of events referred to the calendar time scale. This is a generally applicable advice in handling follow-up data: Get all event times as *dates*, location of events and follow-up on other time scales can then easily be derived from this.

Note that individual 52 has had his follow-up cut at 6.55 years from diabetes diagnosis and individual 484 at 5.70 years from diabetes diagnosis. This dataset could then be split along the time scales as we did before with `dmL`.

The result of this can also be achieved by cutting the split dataset `dmS2` instead of `dmL`:

```
> dmS2C <- cutLexis(data = dmS2,
+                  cut = dmS2$doins,
+                  timescale = "per",
+                  new.state = "Ins",
+                  new.scale = "tfI")
> subset(dmS2C, lex.id %in% wh.id)
```



```
1998.260 2003.960 2009.190
```

Thus it does not matter in which order we use `splitLexis` and `cutLexis`. Mathematicians would say that `splitLexis` and `cutLexis` are commutative.

Note that for `lex.id = 484`, the follow-up subsequent to the event is classified as being in state `Ins`, but that the final transition to state `Dead` is preserved. This is the point of the `precursor.states=` argument, which defaults to `transient(dmS2)`—the transient states (states that a person can exit from). It names the states (in this case `DM`) that will be over-written by `new.state` (in this case `Ins`), while the state `Dead` should not be updated even if it is after the time where the persons moves to state `Ins`. In other words, only state `DM` is a precursor to state `Ins`, state `Dead` is always subsequent to state `Ins`.

Note that we defined a new time scale, `tfI`, using the argument `new.scale = tfI`. This has a special status relative to the other three time scales, it is defined as time since entry into a state, namely `Ins`, this is noted in the time scale part of the summary of `Lexis` object — the information sits in the attribute `time.since` of the `Lexis` object, which can be accessed by the function `timeSince()` or through the `summary()`:

```
> summary(dmS2C, timeScales = TRUE)
```

```
Transitions:
```

From	To	DM	Ins	Dead	Records:	Events:	Risk time:	Persons:
DM		35135	1694	2048	38877	3742	45885.49	9899
Ins		0	5762	451	6213	451	8387.77	1791
Sum		35135	7456	2499	45090	4193	54273.27	9996

```
Timescales:
```

per	age	tfD	tfI
""	""	""	"Ins"

Finally we can get a quick overview of the states and transitions by using `boxes` — `scale.R` scales transition rates to rates per 1000 PY:

```
> boxes(dmC, boxpos = TRUE, scale.R = 1000, show.BE = TRUE)
> legendbox(70, 95)
```

The explanatory box in the upper right corner was generated by `legendbox`.

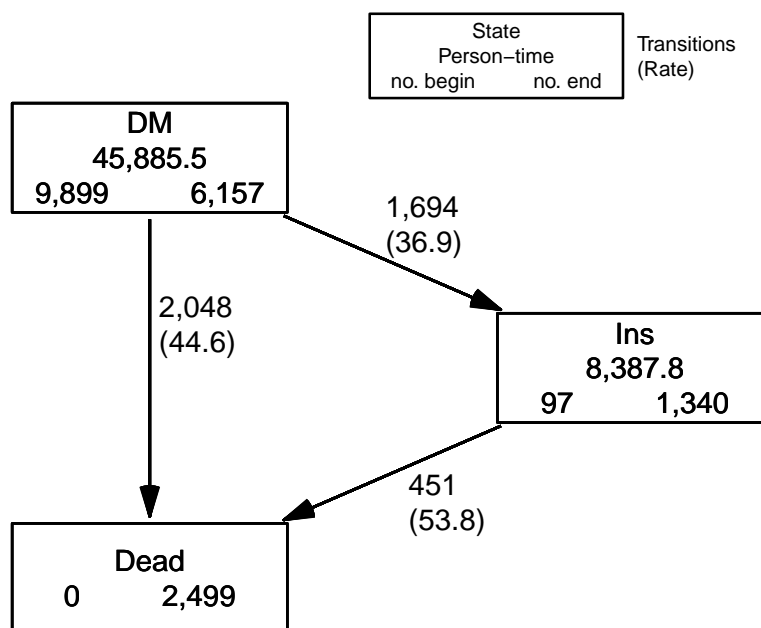


Figure 1.3: States, person years, transitions and rates in the cut dataset. The numbers in the boxes are person-years and the number of persons *Beginning*, resp. *Ending* their follow-up in each state (triggered by `show.BE = TRUE`). The numbers at the arrows are the number of transitions and transition rates per 1000 (triggered by `scale.R = 1000`). `./flup-box1`

Chapter 2

Modeling rates from Lexis objects

2.1 Covariates

In the dataset `dmS2C` there are three types of covariates that can be used to describe mortality rates:

1. time-dependent covariates
2. time scales
3. fixed covariates

There is only one time-dependent covariate here, namely `lex.Cst`, the current state of the person's follow up; it takes the values `DM` and `Ins` according to whether the person has ever purchased insulin at a given time of follow-up.

The time-scales are obvious candidates for explanatory variables for the rates, notably age and time from diagnosis (duration of diabetes) and insulin.

2.1.1 Time scales as covariates

If we want to model the effect of the time scale variables on occurrence rates, we will for each interval use either the value of the left endpoint in each interval or the middle. There is a function `timeBand` which returns either of these:

```
> timeBand(dmS2C, "age", "middle")[1:10]
[1] 57.5 57.5 62.5 62.5 62.5 67.5 67.5 62.5 67.5 67.5
> # For nice printing and column labelling we use the data.frame() function:
> data.frame(dmS2C[, c("per", "age", "tfD", "lex.dur")],
+           mid.age = timeBand(dmS2C, "age", "middle"),
+           mid.t = timeBand(dmS2C, "tfD", "middle"),
+           left.t = timeBand(dmS2C, "tfD", "left" ),
+           right.t = timeBand(dmS2C, "tfD", "right" ),
+           fact.t = timeBand(dmS2C, "tfD", "factor"))[1:15, ]
  per      age      tfD      lex.dur mid.age mid.t left.t right.t fact.t
1 1998.917 58.66119 0.0000000 1.00000000 57.5 0.5 0 1 (0,1]
2 1999.917 59.66119 1.0000000 0.33880903 57.5 1.5 1 2 (1,2]
3 2000.256 60.00000 1.3388090 0.66119097 62.5 1.5 1 2 (1,2]
4 2000.917 60.66119 2.0000000 3.00000000 62.5 3.5 2 5 (2,5]
5 2003.917 63.66119 5.0000000 1.33880903 62.5 7.5 5 10 (5,10]
```

6	2005.256	65.00000	6.3388090	3.66119097	67.5	7.5	5	10	(5,10]
7	2008.917	68.66119	10.0000000	1.08008214	67.5	15.0	10	20	(10,20]
8	2003.309	64.09035	0.0000000	0.90965092	62.5	0.5	0	1	(0,1]
9	2004.218	65.00000	0.9096509	0.09034908	67.5	0.5	0	1	(0,1]
10	2004.309	65.09035	1.0000000	1.00000000	67.5	1.5	1	2	(1,2]
11	2005.309	66.09035	2.0000000	3.00000000	67.5	3.5	2	5	(2,5]
12	2008.309	69.09035	5.0000000	0.90965092	67.5	7.5	5	10	(5,10]
13	2009.218	70.00000	5.9096509	0.77891855	72.5	7.5	5	10	(5,10]
14	2004.552	86.25051	0.0000000	1.00000000	87.5	0.5	0	1	(0,1]
15	2005.552	87.25051	1.0000000	1.00000000	87.5	1.5	1	2	(1,2]

Note that the values of these functions are characteristics of the intervals defined by `breaks =` , *not* the midpoints nor left or right endpoints of the *actual* follow-up intervals (which would be `tfD` and `tfD+lex.dur`, respectively).

These functions are intended for modeling time scale variables as factors (categorical variables) in which case the coding must be independent of the censoring and mortality pattern — it should only depend on the chosen grouping of the time scale. Modeling time scales as *quantitative* should not be based on these codings but directly on the values of the time-scale variables, i.e. the left endpoints of the intervals.

2.1.2 Differences between time scales

Apparently, the only fixed variable is `sex`, but formally the dates of birth (`dobth`), diagnosis (`dodm`) and first insulin purchase (`doins`) are fixed covariates too. They can be constructed as origins of time scales referred to the calendar time scale. Likewise, and possibly of greater interest, we can consider these origins on the age scale, calculated as the difference between age and another time scale.

These would then be age at birth (hardly relevant since it is the same for all persons), age at diabetes diagnosis and age at insulin treatment.

2.1.3 Keeping the relation between time scales

The midpoint (as well as the right interval endpoint) should be used with caution if the variable age at diagnosis `dodm-dobth` is modeled too; the age at diabetes is logically equal to the difference between current age (`age`) and time since diabetes diagnosis (`tfD`):

```
> summary((dmS2$age - dmS2$tfD) - (dmS2$dodm - dmS2$dobth))
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
    0         0         0         0         0         0
```

This calculation refers to the *start* of each interval — which are in the time scale variables in the Lexis object. But when using the middle of the intervals, this relationship is not preserved:

```
> summary(timeBand(dmS2, "age", "middle") -
+         timeBand(dmS2, "tfD", "middle") -
+         (dmS2$dodm - dmS2$dobth))
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
-7.4870 -2.0862 -0.3765    Inf  1.3641    Inf
```

If all three variables are to be included in a model, we must make sure that the *substantial* relationship between the variables be maintained. One way is to recompute age at diabetes

diagnosis from the two midpoint variables, but more straightforward would be to use the left endpoint of the intervals, that is the time scale variables in the `Lexis` object.

If we dissolve the relationship between the variables `age`, `tfD` and age at diagnosis by grouping we may obtain identifiability of the three separate effects, but it will be at the price of an arbitrary allocation of a linear trend between them.

For the sake of clarity, consider current age, a , duration of disease, d and age at diagnosis e , where

$$\text{current age} = \text{age at diagnosis} + \text{disease duration}, \quad \text{i.e.} \quad a = e + d \quad \Leftrightarrow \quad e + d - a = 0$$

If we model the effect of the quantitative variables a , e and d on the log-rates by three functions f , g and h : $\log(\lambda) = f(a) + g(d) + h(e)$ then for any κ :

$$\begin{aligned} \log(\lambda) &= f(a) + g(d) + h(e) + \kappa(e + d - a) \\ &= (f(a) - \kappa a) + (g(d) + \kappa d) + (h(e) + \kappa e) \\ &= \tilde{f}(a) + \tilde{g}(d) + \tilde{h}(e) \end{aligned}$$

In practical modeling this will turn up as a singular model matrix with one parameter aliased, corresponding to some arbitrarily chosen value of κ (depending on software conventions for singular models). This phenomenon is well known from age-period-cohort models.

Thus we see that we can move any slope around between the three terms, so if we achieve identifiability by using grouping of one of the variables we will in reality have settled for a particular value of κ , without known why we chose just that. The solution is to resort to predictions which are independent of the particular parametrization or choose a parametrization with explicit constraints.

2.2 Modeling of rates

As mentioned, the purpose of subdividing follow-up data in smaller intervals is to be able to model effects of time scale variables as parametric functions. When we split along a time scale we can get intervals that are as small as we want; if they are sufficiently small, an assumption of constant rates in each interval becomes reasonable.

In a model that assumes a constant occurrence rate in each of the intervals the likelihood contribution from each interval is the same as the likelihood contribution from a Poisson variate D , say, with mean $\lambda\ell$ where λ is the rate and ℓ is the interval length, and where the value of the variate D is 1 or 0 according to whether an event has occurred or not. Moreover, the likelihood contributions from all follow-up intervals from a single person are *conditionally* independent (conditional on having survived till the start of the interval in question). This implies that the total contribution to the likelihood from a single person is a product of terms, and hence the same as the likelihood of a number of independent Poisson terms, one from each interval.

Note that variables are neither Poisson distributed (*e.g.* they can only ever assume values 0 or 1) nor independent — it is only the likelihood for the follow-up data that happens to be the same as the likelihood from independent Poisson variates. Different models can have the same likelihood, a model cannot be inferred from the likelihood.

Parametric modeling of the rates is obtained by using the *values* of the time scales for each interval as *quantitative* explanatory variables, using for example splines. And of course also the values of the fixed covariates and the time-dependent variables for each interval. Thus the model will be one where the rate is assumed constant in each (small) interval, but where a parametric form of the *size* of the rate in each interval is imposed by the model, using the time scale as a quantitative covariate.

2.2.1 Interval length

In the first chapter we illustrated cutting and splitting by listing the results for a few individuals across a number of intervals. For illustrational purposes we used 5-year age bands to avoid excessive listings, but since the doubling time for mortality on the age scale is only slightly larger than 5 years, the assumption about constant rates in each interval would be pretty far fetched if we were to use 5 year intervals.

Thus, for modeling purposes we split the follow-up in 3 month intervals. When we use intervals of 3 months length it is superfluous to split along multiple time scales — the precise location of tightly spaced splits will be irrelevant from any practical point of view. `splitLexis` and `splitMulti` will allocate the actual split times for all of the time scale variables, so these can be used directly in modeling.

So we split the cut dataset in 3 months intervals along the age scale:

```
> dmCs <- splitLexis(dmC, time.scale = "age", breaks = seq(0, 110, 1/4))
> summary(dmCs, t = T)
```

Transitions:

From	To	DM	Ins	Dead	Records:	Events:	Risk time:	Persons:
DM	DM	189669	1694	2048	193411	3742	45885.49	9899
Ins	Ins	0	34886	451	35337	451	8387.77	1791
Sum	Sum	189669	36580	2499	228748	4193	54273.27	9996

Timescales:

per	age	tfD	tfI
""	""	""	"Ins"

We see that we now have 228,748 records and 9996 persons, so about 23 records per person. The total risk time is 54,275 years, a bit less than 3 months on average per record as expected.

2.2.2 Practicalities for splines

In this study we want to look at how mortality depend on age (`age`) and time since start of insulin use (`tfI`). If we want to use splines in the description we must allocate knots for anchoring the splines at each of the time scales, either by some *ad hoc* method or by using some sort of penalized splines as for example by `gam`; the latter will not be treated here; it belongs in the realm of the `mgcv` package.

Here we shall use the former approach and allocate 5 knots on each of the time-scales. We allocate knots so that we have the events evenly distributed between the knots. Since the insulin state starts at 0 for all individuals we include 0 as the first knot, such that any set of natural splines with these knots will have the value 0 at 0 on the time scale.

```
> (a.kn <- with(subset(dmCs, lex.Xst == "Dead"),
+               quantile(age+lex.dur, (1:5-0.5)/5)))
      10%      30%      50%      70%      90%
60.29350 71.31937 77.72758 82.72745 89.86393
> (i.kn <- c(0,
+           with(subset(dmCs, lex.Xst == "Dead" & lex.Cst == "Ins"),
+               quantile(tfI+lex.dur, (1:4)/5))))
      20%      40%      60%      80%
0.0000000 0.3093771 1.1307324 2.5489391 4.9117043
```

In the `Epi` package there is a convenience wrapper, `Ns`, for the natural spline generator `ns`, that takes the smallest and the largest of a set of supplied knots to be the boundary knots, so the explicit definition of the boundary knots becomes superfluous.

Note that it is a feature of the `Ns` (via the features of `ns`) that any generated spline function is 0 at the leftmost knot.

2.2.3 Poisson models

A model that describes mortality rates as only a function of age would then be:

```
> ma <- glm((lex.Xst == "Dead") ~ Ns(age, knots = a.kn),
+          family = poisson,
+          offset = log(lex.dur),
+          data = dmCs)
> summary(ma)
Call:
glm(formula = (lex.Xst == "Dead") ~ Ns(age, knots = a.kn), family = poisson,
    data = dmCs, offset = log(lex.dur))

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   -3.82830    0.03861  -99.16  <2e-16 ***
Ns(age, knots = a.kn)1  1.36254    0.08723   15.62  <2e-16 ***
Ns(age, knots = a.kn)2  1.49446    0.06845   21.83  <2e-16 ***
Ns(age, knots = a.kn)3  2.63557    0.07058   37.34  <2e-16 ***
Ns(age, knots = a.kn)4  1.94173    0.05769   33.66  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 27719  on 228747  degrees of freedom
Residual deviance: 25423  on 228743  degrees of freedom
AIC: 30431

Number of Fisher Scoring iterations: 8
```

The offset, $\log(\text{lex.dur})$ comes from the fact that the likelihood for the follow-up data during ℓ time is the same as that for independent Poisson variates with mean $\lambda\ell$, and that the default link function for the Poisson family is the log, so that we are using a linear model for the log-mean, $\log(\lambda) + \log(\ell)$. But when we want a model for the log-rate ($\log(\lambda)$), the term $\log(\ell)$ must still be included as a covariate, but with regression coefficient fixed to 1; a so-called *offset*. This is however a technicality; it just exploits that the likelihood of a particular Poisson model and that of the rates model is the same.

In the `Epi` package is a `glm` family, `poisreg` that has a more intuitive interface to the likelihood of rates, namely where the response is a 2-column matrix of events and person-time, respectively. This is in concert with the fact that the outcome variable in follow-up studies is bivariate: (event, risk time).

```
> Ma <- glm(cbind(lex.Xst == "Dead", lex.dur) ~ Ns(age, knots = a.kn),
+          family = poisreg,
+          data = dmCs)
> summary(Ma)
Call:
glm(formula = cbind(lex.Xst == "Dead", lex.dur) ~ Ns(age, knots = a.kn),
    family = poisreg, data = dmCs)
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-3.82830	0.03861	-99.15	<2e-16 ***
Ns(age, knots = a.kn)1	1.36254	0.08723	15.62	<2e-16 ***
Ns(age, knots = a.kn)2	1.49446	0.06845	21.83	<2e-16 ***
Ns(age, knots = a.kn)3	2.63557	0.07058	37.34	<2e-16 ***
Ns(age, knots = a.kn)4	1.94173	0.05769	33.66	<2e-16 ***

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

(Dispersion parameter for poisson family taken to be 1)

```
Null deviance: 27719  on 228747  degrees of freedom
Residual deviance: 25423  on 228743  degrees of freedom
AIC: 30431
```

Number of Fisher Scoring iterations: 7

Exploiting the multistate structure in the `Lexis` object there is a convenience wrapper for `glm` with the `poisreg` family, that just requires specification of the transitions in terms of from and to. Although it is called `glm.Lexis` it is *not* an S3 method for `Lexis` objects:

```
> Xa <- glm.Lexis(dmCs, from = "DM", to = "Dead",
+               formula = ~ Ns(age, knots = a.kn))
stats::glm Poisson analysis of Lexis object dmCs with log link:
Rates for the transition:
DM->Dead
```

The result is a `glm` object but with an extra attribute, `Lexis` with the name of the data, transition(s) modeled and model formula

```
> attr(Xa, "Lexis")
$data
[1] "dmCs"

$trans
[1] "DM->Dead"

$formula
~Ns(age, knots = a.kn)
<environment: 0x557c5de45388>

$scale
[1] 1
```

There are similar wrappers for `gam` and `coxph` models, `gam.Lexis` and `coxph.Lexis`, but these will not be elaborated in detail here.

The `from=` and `to=` can be omitted, in which case all possible transitions *into* any of the absorbing states is modeled:

```
> xa <- glm.Lexis(dmCs, formula = ~ Ns(age, knots = a.kn))
stats::glm Poisson analysis of Lexis object dmCs with log link:
Rates for transitions:
DM->Dead
Ins->Dead
```

We can check if the four models fitted are the same:

```
> c(deviance(ma), deviance(Ma), deviance(Xa), deviance(xa))
[1] 25422.92 25422.92 20902.31 25422.92
```

Oops! the model `Xa` is apparently not the same as the other three? This is because the explicit specification `from = "DM"`, `to = "Dead"`, omits modeling contributions from the `Ins → Dead` transition — the output actually said so — see also figure 1.3 on p. 12. The other three models all use both transitions — and assume that the two transition rates are the same, *i.e.* that start of insulin has no effect on mortality. We shall relax this assumption later.

The parameters from the model do not have any direct interpretation *per se*, but we can compute the estimated mortality rates for a range of ages using `ci.pred` with a suitably defined prediction data frame.

Note that if we use the `poisson` family of models, we must specify all covariates in the model, including the variable in the offset, `lex.dur` (remember that this was a covariate with coefficient fixed at 1). We set the latter to 1000, because we want the mortality rates per 1000 person-years. Using the `poisreg` family, the prediction will ignore any value of `lex.dur` specified in the prediction data frame, the returned rates will be per unit in which `lex.dur` is recorded.

```
> nd <- data.frame(age = 40:85, lex.dur = 1000)
> pr.0 <- ci.pred(ma, newdata = nd) # mortality per 100 PY
> pr.a <- ci.pred(Ma, newdata = nd)*1000 # mortality per 100 PY
> summary(pr.0/pr.a)

      Estimate      2.5%      97.5%
Min.   :1  Min.   :1  Min.   :1
1st Qu.:1  1st Qu.:1  1st Qu.:1
Median :1  Median :1  Median :1
Mean   :1  Mean   :1  Mean   :1
3rd Qu.:1  3rd Qu.:1  3rd Qu.:1
Max.   :1  Max.   :1  Max.   :1

> matshade(nd$age, pr.a, plot = TRUE,
+          type = "l", lty = 1,
+          log = "y", xlab = "Age (years)",
+          ylab = "DM mortality per 1000 PY")
```

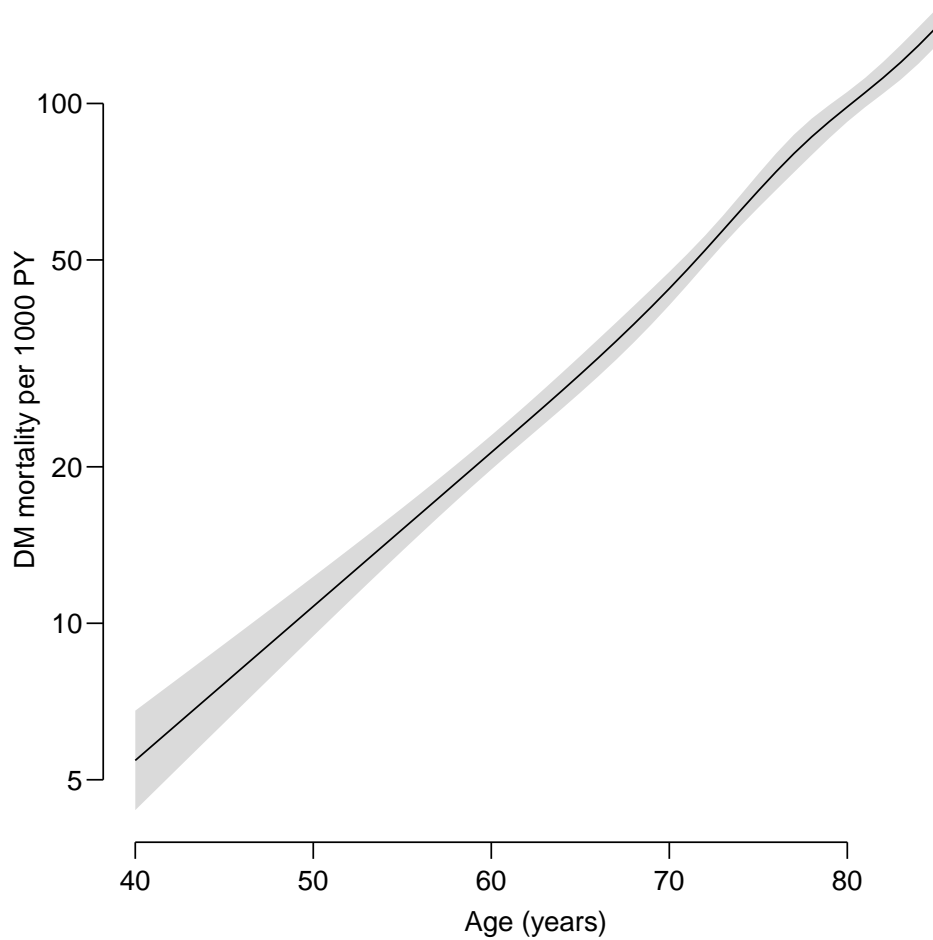


Figure 2.1: Mortality among Danish diabetes patients by age with 95% CI as shaded area. We see that the rates increase linearly on the log-scale, that is, exponentially by age../flup-pr-a

2.3 Time dependent covariate

A Poisson model approach to mortality by insulin status, would be to assume that the rate-ratio between patients on insulin and not on insulin is a fixed quantity, independent of time since start of insulin, independent of age. This is commonly termed a proportional hazards assumption, because the rates (hazards) in the two groups are proportional along the age (baseline time) scale.

```
> pm <- glm(cbind(lex.Xst == "Dead", lex.dur) ~ Ns(age, knots = a.kn)
+
+               family = poisreg,
+               data = dmCs)
> round(ci.exp(pm), 3)
```

	exp(Est.)	2.5%	97.5%
(Intercept)	0.022	0.021	0.024
Ns(age, knots = a.kn)1	4.248	3.581	5.040
Ns(age, knots = a.kn)2	5.008	4.376	5.731
Ns(age, knots = a.kn)3	16.832	14.624	19.373
Ns(age, knots = a.kn)4	7.994	7.126	8.968
lex.CstIns	1.985	1.791	2.200

```
sexF                0.668  0.617  0.724
```

Again we can simplify the code using `glm.Lexis`:

```
> pm <- glm.Lexis(dmCs, ~ Ns(age, knots = a.kn) + lex.Cst + sex)
stats::glm Poisson analysis of Lexis object dmCs with log link:
Rates for transitions:
DM->Dead
Ins->Dead
> round(ci.exp(pm), 3)

                exp(Est.)   2.5%  97.5%
(Intercept)          0.022  0.021  0.024
Ns(age, knots = a.kn)1  4.248  3.581  5.040
Ns(age, knots = a.kn)2  5.008  4.376  5.731
Ns(age, knots = a.kn)3 16.832 14.624 19.373
Ns(age, knots = a.kn)4  7.994  7.126  8.968
lex.CstIns            1.985  1.791  2.200
sexF                  0.668  0.617  0.724
```

So we see that persons on insulin have about twice the mortality of persons not on insulin and that women have 2/3 the mortality of men.

2.3.1 Time since insulin start

If we want to test whether the excess mortality depends on the time since start if insulin treatment, we can add a spline terms in `tfI`. But since `tfI` is a time scale defined as time since entry into a new state (`Ins`), the variable `tfI` will be missing for those in the `DM` state, so before modeling we must set the NAs to 0, which we do with `tsNA20` (acronym for timescale NAs to zero):

```
> pm <- glm(cbind(lex.Xst == "Dead", lex.dur) ~ Ns(age, knots = a.kn)
+                                             + Ns(tfI, knots = i.kn)
+                                             + lex.Cst + sex,
+      family = poisreg,
+      data = tsNA20(dmCs))
```

As noted before we could do this simpler with `glm.Lexis`, even without the `from=` and `to=` arguments, because we are modeling all transitions *into* the absorbing state (`Dead`):

```
> Pm <- glm.Lexis(tsNA20(dmCs),
+               form = ~ Ns(age, knots = a.kn)
+                       + Ns(tfI, knots = i.kn)
+                       + lex.Cst + sex)
stats::glm Poisson analysis of Lexis object tsNA20(dmCs) with log link:
Rates for transitions:
DM->Dead
Ins->Dead
> c(deviance(Pm), deviance(pm))
[1] 25096.33 25096.33
> identical(model.matrix(Pm), model.matrix(pm))
[1] TRUE
```

The coding of the effect of `tfI` is so that the value is 0 at 0, so the meaning of the estimate of the effect of `lex.Cst` is the RR between persons with and without insulin, immediately after start of insulin:

```
> round(ci.exp(Pm, subset = "ex"), 3)
      exp(Est.)  2.5% 97.5%
lex.CstIns    5.632 4.430  7.16
sexF          0.674 0.622  0.73
```

We see that the effect of `sex` is pretty much the same as before, but the effect of `lex.Cst` is much larger, it now refers to a different quantity, namely the RR at `tfI = 0`. If we want to see the effect of time since insulin, it is best viewed jointly with the effect of `age`:

```
> ndI <- data.frame(expand.grid(tfI = c(NA, seq(0, 15, 0.1)),
+                               ai = seq(40, 80, 10)),
+                 sex = "M",
+                 lex.Cst = "Ins")
> ndI <- transform(ndI, age = ai+tfI)
> head(ndI)
  tfI ai sex lex.Cst  age
1  NA 40  M     Ins   NA
2  0.0 40  M     Ins 40.0
3  0.1 40  M     Ins 40.1
4  0.2 40  M     Ins 40.2
5  0.3 40  M     Ins 40.3
6  0.4 40  M     Ins 40.4

> ndA <- data.frame(age = seq(40, 100, 0.1), tfI = 0, lex.Cst = "DM", sex = "M")
> pri <- ci.pred(Pm, ndI) * 1000
> pra <- ci.pred(Pm, ndA) * 1000
> matshade(ndI$age, pri, plot = TRUE, las = 1,
+          xlab = "Age (years)", ylab = "DM mortality per 1000 PY",
+          log = "y", lty = 1, col = "blue")
> matshade(ndA$age, pra)
```

In figure 2.2, p. 23, we see that mortality is high just after insulin start, but falls by almost a factor 3 during the first year. Also we see that there is a tendency that mortality in a given age is smallest for those with the longest duration of insulin use.

2.4 The Cox model

Note that in the implementation of Cox-model the `age` appears as response variable, slightly counter-intuitive as it really is a covariate. Hence the `age` part of the linear predictors is not in the model specification:

```
> cm <- coxph(Surv(age, age+lex.dur, lex.Xst == "Dead") ~
+            Ns(tfI, knots = i.kn) + lex.Cst + sex,
+            data = tsNA20(dmCs))
```

There is also a multistate wrapper for Cox models, requiring a l.h.s. side for the `formula` = argument:

```
> Cm <- coxph.Lexis(tsNA20(dmCs),
+                 form = age ~ Ns(tfI, knots = i.kn) + lex.Cst + sex)
```

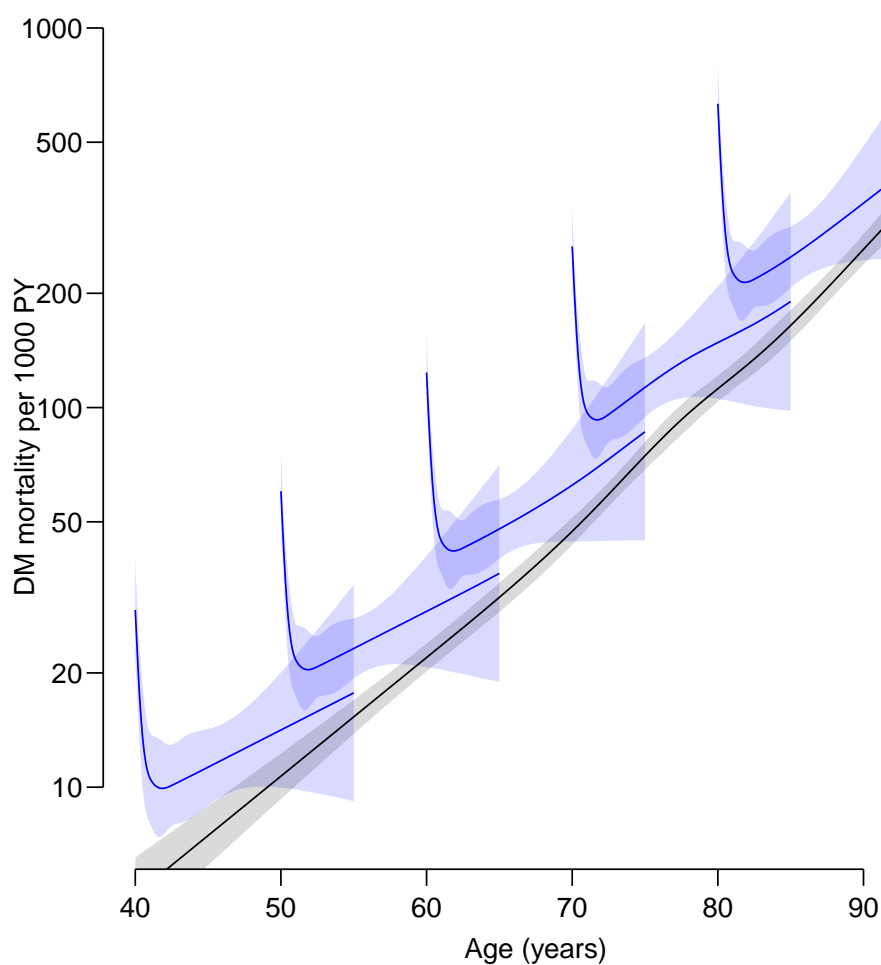



Figure 2.2: Mortality rates of persons on insulin, starting insulin at ages 40, 50, ..., 80 (blue), compared with persons not on insulin (black curve). Shaded areas are 95% CI.

`./flup-ins-time`

```
survival::coxph analysis of Lexis object tsNA20(dmCs):
```

```
Rates for transitions:
```

```
DM->Dead
```

```
Ins->Dead
```

```
Baseline timescale: age
```

```
> round(cbind(ci.exp(cm), ci.exp(Cm)), 4)
```

	exp(Est.)	2.5%	97.5%	exp(Est.)	2.5%	97.5%
Ns(tfI, knots = i.kn)1	0.2984	0.1942	0.4586	0.2984	0.1942	0.4586
Ns(tfI, knots = i.kn)2	0.3871	0.2901	0.5165	0.3871	0.2901	0.5165
Ns(tfI, knots = i.kn)3	0.1239	0.0629	0.2442	0.1239	0.0629	0.2442
Ns(tfI, knots = i.kn)4	0.4405	0.3484	0.5570	0.4405	0.3484	0.5570
lex.CstIns	5.6700	4.4501	7.2244	5.6700	4.4501	7.2244
lex.CstDead	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
sexF	0.6753	0.6232	0.7318	0.6753	0.6232	0.7318

Note that this is really a Cox model with two time scales: the baseline time scale `age` and the time since insulin, `tfi`. They are modeled differently, `age` non-parametrically and `tfi` with a smooth parametric spline. And only the spline effects is shown in the parameters.

We can compare the estimates from the Cox model with those from the Poisson model — we must add NAs because the Cox-model does not give the parameters for the baseline time scale (`age`), but also remove one of the parameters, because `coxph` parametrizes factors (in this case `lex.Cst`) by all defined levels and not only by the levels present in the dataset at hand (note the line of 1.0000000s in the print above):

```
> round(cbind(ci.exp(Pm),
+           rbind(matrix(NA, 5, 3),
+                 ci.exp(cm)[-6, ])), 3)
```

	exp(Est.)	2.5%	97.5%	exp(Est.)	2.5%	97.5%
(Intercept)	0.022	0.021	0.024	NA	NA	NA
Ns(age, knots = a.kn)1	4.208	3.546	4.993	NA	NA	NA
Ns(age, knots = a.kn)2	5.012	4.380	5.736	NA	NA	NA
Ns(age, knots = a.kn)3	16.560	14.386	19.063	NA	NA	NA
Ns(age, knots = a.kn)4	7.921	7.061	8.885	NA	NA	NA
Ns(tfI, knots = i.kn)1	0.298	0.194	0.458	0.298	0.194	0.459
Ns(tfI, knots = i.kn)2	0.385	0.289	0.514	0.387	0.290	0.517
Ns(tfI, knots = i.kn)3	0.125	0.064	0.246	0.124	0.063	0.244
Ns(tfI, knots = i.kn)4	0.438	0.346	0.553	0.441	0.348	0.557
lex.CstIns	5.632	4.430	7.160	5.670	4.450	7.224
sexF	0.674	0.622	0.730	0.675	0.623	0.732

Thus we see that the Poisson and Cox gives pretty much the same results. You may argue that Cox requires a smaller dataset, because there is no need to subdivide data in small intervals *before* insulin use. But certainly the time *after* insulin inception need to be if the effect of this time should be modeled.

The drawback of the Cox-modeling is that it is not possible to show the absolute rates as we did in figure 2.2 on 23.

2.5 Marginal effect of time since insulin

When we plot the marginal effect of `tfI` from the two models we get pretty much the same; here we plot the RR relative to `tfI = 2` years. Note that we are deriving the RR as the ratio of two sets of predictions, from the data frames `nd` and `nr`—variables assumed to have the same values in the two data frames need not be included in the prediction frames, but numerical variables omitted must be indicated in the `xvars=` argument. For further details, consult the help page for `ci.lin`, specifically the use of a list as the `ctr.mat` argument:

```
> nd <- data.frame(tfI = seq(0, 15, , 151), lex.Cst = "Ins", sex = "M")
> nr <- data.frame(tfI = 2, lex.Cst = "Ins", sex = "M")
> # We need to put in xvars="age" because age is in the model but not
> # in the prediction frames
> ppr <- ci.exp(pm, list(nd, nr), xvars = "age")
> cpr <- ci.exp(cm, list(nd, nr))
> par(mar = c(3, 3, 1, 1), mgp = c(3, 1, 0)/1.6, las = 1, bty = "n")
> matshade(nd$tfI, cbind(ppr, cpr), plot = T,
+         lty = c(1, 2), log = "y",
+         xlab = "Time since insulin (years)", ylab = "Mortality rate ratio")
> abline(h = 1, lty = 3)
```

In figure 2.3, p. 25, we see that the duration effect is exactly the same from the two modeling approaches (Cox and Poisson).

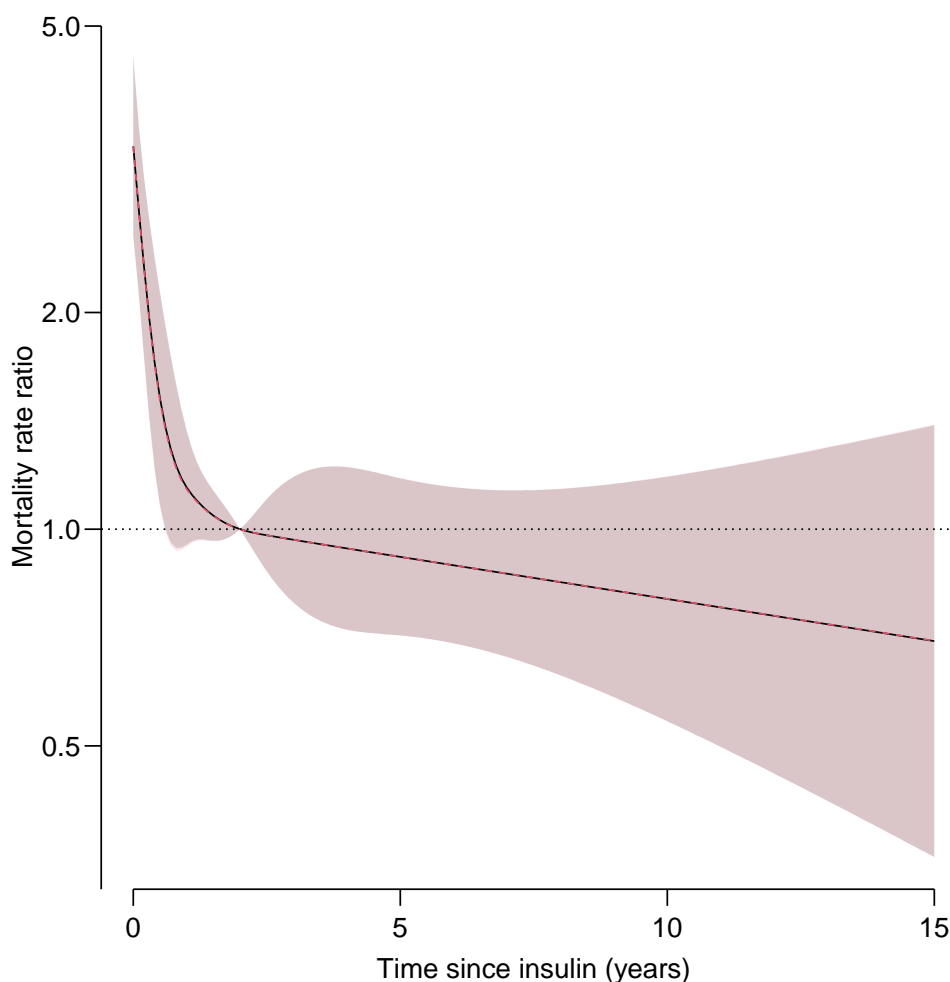


Figure 2.3: *The naked duration effects on mortality relative to 2 years of duration. Black from Poisson model, red from Cox model. The two sets of estimates are identical, and so are the standard errors, so the two shaded areas overlap almost perfectly.* `./flup-Ieff`

We will also want the RR relative to the non-insulin users — recall these are coded 0 on the `tfI` variable:

```
> nd <- data.frame(tfI = seq(0, 15, , 151), lex.Cst = "Ins", sex = "M")
> nr <- data.frame(tfI = 0, lex.Cst = "DM", sex = "M")
> ppr <- ci.exp(pm, list(nd, nr), xvars = "age")
> cpr <- ci.exp(cm, list(nd, nr))
> par(mar = c(3, 3, 1, 1), mgp = c(3, 1, 0)/1.6, las = 1, bty = "n")
> matshade(nd$tfI, cbind(ppr, cpr), lwd = 2,
+         xlab = "Time since insulin (years)",
+         ylab = "Rate ratio relative to non-Insulin",
+         lty = c(1, 2), log = "y", plot = T)
```

In figure 2.4, p. 26, we see the effect of increasing duration of insulin use *for a fixed age* which is a bit artificial, so we would like to see the *joint* effects of age and insulin duration. What we cannot see is how the duration affects mortality relative to **current** age (at the age attained at the same time as the attained `tfI`).

Another way of interpreting this curve is as the rate ratio relative to a person not on insulin, so we see that the RR (or hazard ratio, HR as some call it) is over 5 at the start of

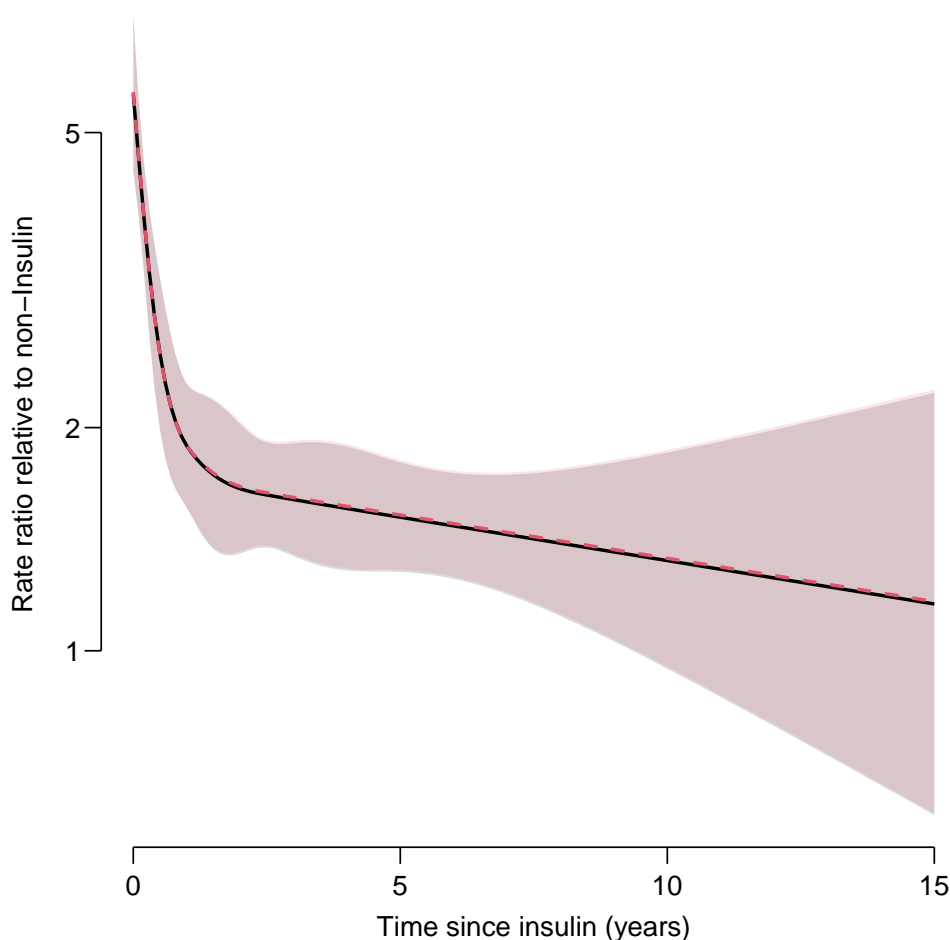


Figure 2.4: *Insulin duration effect (state `Ins`) relative to no insulin (state `DM`), black from Poisson model, red from Cox model. The shape is the same as the previous figure, but the RR is now relative to non-insulin, instead of relative to insulin users at 2 years duration. The estimates from the Cox model and the Poisson model are virtually identical, and so are the standard errors, so the two shaded areas overlap almost perfectly.* `./flup-IeffR`

insulin (the `lex.Cst` estimate), and decreases to about 1.5 in the long term.

Both figure 2.3 and 2.4 indicate a declining RR by insulin duration, but only from figure 2.2 it is visible that mortality actually is *increasing* by age after some 2 years after insulin start. This point would not be available if we had only fitted a Cox model where we did not have access to the baseline hazard as a function of age.

2.6 Age×duration interaction

The model we fitted assumes that the RR is the same regardless of the age at start of insulin — the hazards are multiplicative. Sometimes this is termed the proportional hazards assumption: For *any* fixed age the HR is the same as a function of time since insulin, and vice versa.

A more correct term would be “main effects model” — there is no interaction between

age (the baseline time scale) and other covariates. So there is really no need for the term “proportional hazards”; well defined and precise statistical terms for it has existed for eons.

2.6.1 Age at insulin start

In order to check the consistency of the multiplicative assumption across the spectrum of age at insulin inception, we can fit an interaction model. One approach to this would be using a non-linear effect of age at insulin inception (for convenience we use the same knots as for age) — note that the prediction data frames would be the same as we used above, because we do not compute age at insulin use as a separate variable, but rather enter it as the difference between current age (`age`) and insulin duration (`tfI`).

At first glance we might think of doing:

```
> imx <- glm.Lexis(tsNA20(dmCs),
+                 formula = ~ Ns(age          , knots = a.kn)
+                 + Ns(          tfI, knots = i.kn)
+                 + Ns(age - tfI, knots = a.kn)
+                 + lex.Cst + sex)
stats::glm Poisson analysis of Lexis object tsNA20(dmCs) with log link:
Rates for transitions:
DM->Dead
Ins->Dead
```

But this will fit a model where rate-ratio between persons with and without insulin at start of insulin (`tfI = 0`) will be the same at any age, which really is not the type of interaction we want.

We want the `age-tfI` term to be specific for the insulin exposed so we may use one of two other approaches, that are conceptually alike but mathematically different:

```
> Im <- glm.Lexis(tsNA20(dmCs),
+               formula = ~ Ns( age          , knots = a.kn)
+               + Ns(          tfI, knots = i.kn)
+               + Ns((age - tfI) * (lex.Cst == "Ins"), knots = a.kn)
+               + lex.Cst + sex)
stats::glm Poisson analysis of Lexis object tsNA20(dmCs) with log link:
Rates for transitions:
DM->Dead
Ins->Dead
```

```
> im <- glm.Lexis(tsNA20(dmCs),
+               formula = ~ Ns(age          , knots = a.kn)
+               + Ns(          tfI, knots = i.kn)
+               + lex.Cst:Ns(age - tfI, knots = a.kn)
+               + lex.Cst + sex)
stats::glm Poisson analysis of Lexis object tsNA20(dmCs) with log link:
Rates for transitions:
DM->Dead
Ins->Dead
```

```
> ci.exp(Im)
```

	exp(Est.)	2.5%	97.5%
(Intercept)	0.03088138	0.01046829	0.09109982
Ns(age, knots = a.kn)1	4.36095300	3.63069492	5.23809120
Ns(age, knots = a.kn)2	5.37618161	4.64510861	6.22231494
Ns(age, knots = a.kn)3	17.52217422	14.80810326	20.73368776

```

Ns(age, knots = a.kn)4      8.51763269  7.51690215  9.65159120
Ns(tfI, knots = i.kn)1     0.29229727  0.19032360  0.44890751
Ns(tfI, knots = i.kn)2     0.36963226  0.27665205  0.49386227
Ns(tfI, knots = i.kn)3     0.11597729  0.05899550  0.22799589
Ns(tfI, knots = i.kn)4     0.41241661  0.32492909  0.52346024
Ns((age - tfI) * (lex.Cst == "Ins"), knots = a.kn)1 0.76407224  0.49576920  1.17757698
Ns((age - tfI) * (lex.Cst == "Ins"), knots = a.kn)2 0.64838981  0.43769969  0.96049722
Ns((age - tfI) * (lex.Cst == "Ins"), knots = a.kn)3 0.67976574  0.48532535  0.95210660
Ns((age - tfI) * (lex.Cst == "Ins"), knots = a.kn)4 0.62110018  0.44015278  0.87643530
lex.CstIns                 4.84459292  1.62770586 14.41911653
sexF                       0.67510419  0.62304697  0.73151093

```

```
> ci.exp(im)
```

	exp(Est.)	2.5%	97.5%
(Intercept)	0.02141302	0.01950572	0.02350682
Ns(age, knots = a.kn)1	1.24869568	0.50321454	3.09856088
Ns(age, knots = a.kn)2	2.58134392	1.02999946	6.46926211
Ns(age, knots = a.kn)3	4.84490068	1.39504621	16.82601074
Ns(age, knots = a.kn)4	4.50406059	3.11359484	6.51547899
Ns(tfI, knots = i.kn)1	0.30787963	0.20021601	0.47343799
Ns(tfI, knots = i.kn)2	0.39668886	0.29607127	0.53150059
Ns(tfI, knots = i.kn)3	0.13254967	0.06713624	0.26169793
Ns(tfI, knots = i.kn)4	0.48371543	0.37104360	0.63060141
lex.CstIns	7.65601701	5.70091060	10.28161999
sexF	0.67478542	0.62271396	0.73121111
lex.CstDM:Ns(age - tfI, knots = a.kn)1	3.66854761	1.44954903	9.28443346
lex.CstIns:Ns(age - tfI, knots = a.kn)1	2.17805096	0.93906275	5.05174546
lex.CstDM:Ns(age - tfI, knots = a.kn)2	2.07263078	0.81719621	5.25675264
lex.CstIns:Ns(age - tfI, knots = a.kn)2	1.08639467	0.50381932	2.34261238
lex.CstDM:Ns(age - tfI, knots = a.kn)3	3.58067023	1.01917025	12.58003686
lex.CstIns:Ns(age - tfI, knots = a.kn)3	2.13656386	0.78459198	5.81818988
lex.CstDM:Ns(age - tfI, knots = a.kn)4	1.90423667	1.29006762	2.81079628
lex.CstIns:Ns(age - tfI, knots = a.kn)4	1.00000000	1.00000000	1.00000000

The first model (*Im*) has a common age-effect (`Ns(age, ...)`) for persons with and without insulin and a RR depending on insulin duration `tfI` and age at insulin (`age-tfI`). Since the linear effect of these two terms are in the model as well, a linear trend in the RR by current age (`age`) is accommodated as well.

The second model (*im*) allows age-effects that differ non-linearly between persons with and without insulin, because the interaction term `lex.Cst:Ns(age-tfI...` for persons not on insulin is merely an age term (since `tfI` is coded 0 for all follow-up not on insulin).

We can compare the models fitted:

```
> anova(imx, Im, im, test = 'Chisq')
```

```
Analysis of Deviance Table
```

```

Model 1: cbind(trt(Lx$lex.Cst, Lx$lex.Xst) %in% trnam, Lx$lex.dur) ~ Ns(age,
  knots = a.kn) + Ns(tfI, knots = i.kn) + Ns(age - tfI, knots = a.kn) +
  lex.Cst + sex
Model 2: cbind(trt(Lx$lex.Cst, Lx$lex.Xst) %in% trnam, Lx$lex.dur) ~ Ns(age,
  knots = a.kn) + Ns(tfI, knots = i.kn) + Ns((age - tfI) *
  (lex.Cst == "Ins"), knots = a.kn) + lex.Cst + sex
Model 3: cbind(trt(Lx$lex.Cst, Lx$lex.Xst) %in% trnam, Lx$lex.dur) ~ Ns(age,
  knots = a.kn) + Ns(tfI, knots = i.kn) + lex.Cst:Ns(age -
  tfI, knots = a.kn) + lex.Cst + sex
Resid. Df Resid. Dev Df Deviance Pr(>Chi)

```

```

1  228734      25096
2  228733      25087  1   8.9631 0.002755 **
3  228730      25082  3   4.6804 0.196749

```

```
---
```

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

so we see that the models indeed are different, and moreover that the last model with a more elaborate interaction does not provide substantial further improvement, by allowing non-linear RR along the age-scale.

We can illustrate the different estimated rates from the three models in figure 2.5, p. 30:

```

> pxi <- ci.pred(imx, ndI)
> pxa <- ci.pred(imx, ndA)
> pli <- ci.pred(Im , ndI)
> pia <- ci.pred(Im , ndA)
> pii <- ci.pred(im , ndI)
> pia <- ci.pred(im , ndA)
> par(mar = c(3, 3, 1, 1), mgp = c(3, 1, 0)/1.6, las = 1, bty = "n")
> matshade(ndI$age, cbind(pxi, pli, pii)*1000, plot = T, log = "y",
+         xlab = "Age", ylab = "Mortality per 1000 PY",
+         lty = 1, lwd = 2, col = c("blue", "forestgreen", "red"), alpha = 0.1)
> matshade(ndA$age, cbind(pxa, pia, pia)*1000,
+         lty = 1, lwd = 2, col = c("blue", "forestgreen", "red"), alpha = 0.1)

```

We can also plot the RRs only from these models (figure 2.6, p. 31); for this we need the reference frames, and the machinery from `ci.exp` allowing a list of two data frames:

```

> ndR <- transform(ndI, tfI = 0, lex.Cst = "DM")
> cbind(head(ndI), head(ndR))
  tfI ai sex lex.Cst  age tfI ai sex lex.Cst  age
1  NA 40  M   Ins   NA  0 40  M   DM   NA
2 0.0 40  M   Ins 40.0  0 40  M   DM 40.0
3 0.1 40  M   Ins 40.1  0 40  M   DM 40.1
4 0.2 40  M   Ins 40.2  0 40  M   DM 40.2
5 0.3 40  M   Ins 40.3  0 40  M   DM 40.3
6 0.4 40  M   Ins 40.4  0 40  M   DM 40.4

> Rxi <- ci.exp(imx, list(ndI, ndR))
> Rii <- ci.exp(im , list(ndI, ndR))
> Rli <- ci.exp(Im , list(ndI, ndR))
> par(mar = c(3, 3, 1, 1), mgp = c(3, 1, 0)/1.6, las = 1, bty = "n")
> matshade(ndI$age, cbind(Rxi, Rli, Rii), plot = T, log = "y",
+         xlab = "Age (years)", ylab = "Rate ratio vs, non-Insulin",
+         lty = 1, lwd = 2, col = c("blue", "forestgreen", "red"), alpha = 0.1)
> abline(h = 1)
> abline(h = ci.exp(imx, subset = "lex.Cst")[, 1], lty = "25", col = "blue")

```

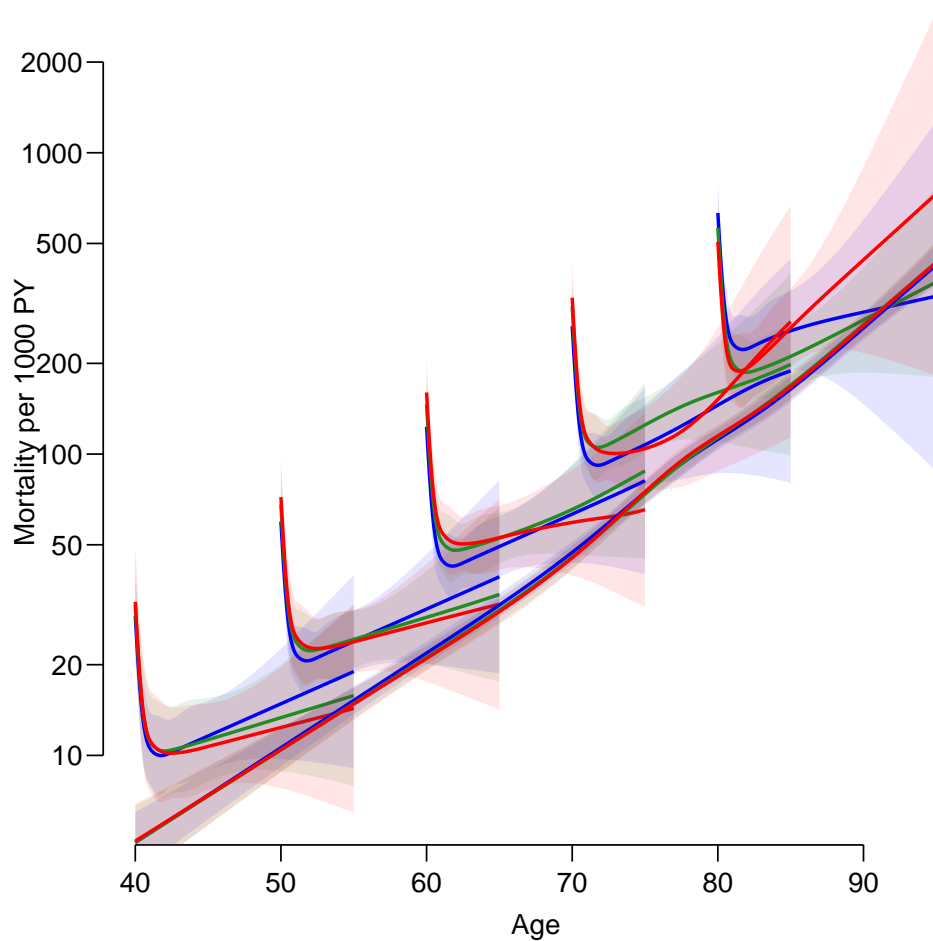


Figure 2.5: *Age at insulin as interaction between age and duration, for persons starting insulin at ages 40, 50, ... and persons not on insulin. Blue curves are from the naive interaction model `imx` with identical RR at `tfI = 0` at any age; green curves are from the interaction model with age at insulin, from the model `Im` with only linear differences by age, and red lines from the full interaction model `im`.*

`./flup-dur-int`

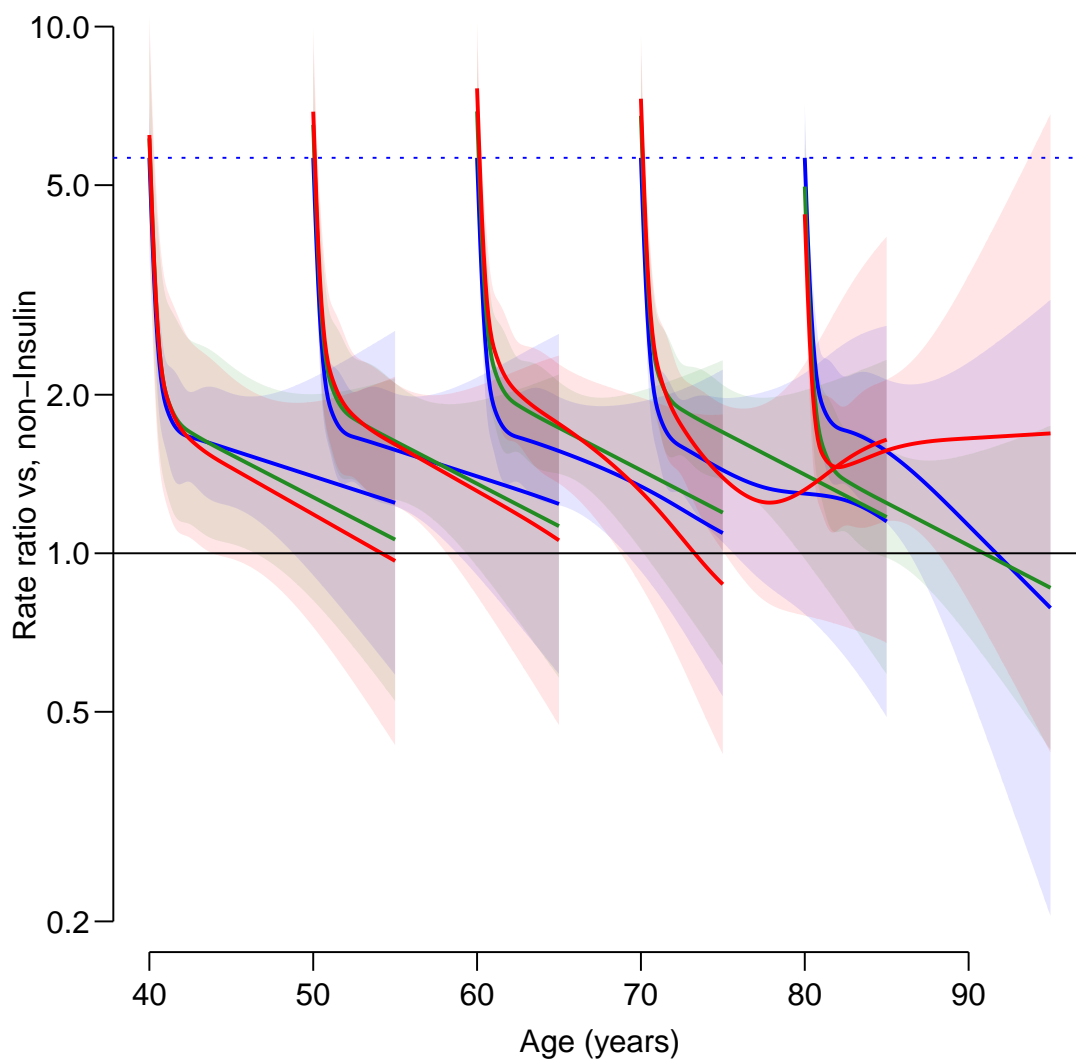


Figure 2.6: *RR from three different interaction models. The horizontal dotted line is at the estimated effect of `lex.Cst`, to illustrate that the first model (blue) constrains this initial HR to be constant across age. The green curves are the extended interaction model, and the red the full one.*

`./flup-dur-int-RR`

2.6.2 General interaction

As a final illustration we may want to explore a different kind of interaction, not defined from the duration — here we simplify the interaction by not using the second-last knot in the interaction terms — figure 2.7, p. 33. Note again that the prediction code is the same:

```
> gm <- glm.Lexis(tsNA20(dmCs),
+               formula = ~ Ns(age, knots = a.kn)
+               + Ns(tfI, knots = i.kn)
+               + lex.Cst:Ns(age, knots = a.kn):Ns(tfI, knots = i.kn)
+               + lex.Cst + sex)
stats::glm Poisson analysis of Lexis object tsNA20(dmCs) with log link:
Rates for transitions:
DM->Dead
Ins->Dead
> pgi <- ci.pred(gm, ndI)
> pga <- ci.pred(gm, ndA)
> par(mar = c(3, 3, 1, 1), mgp = c(3, 1, 0)/1.6, las = 1, bty = "n")
> matshade(ndI$age, cbind(pgi, pii)*1000, plot = T,
+         lty = c("solid", "21"), lend = "butt", lwd = 2, log = "y",
+         xlab = "Age (years)", ylab = "Mortality rates per 1000 PY",
+         alpha = c(0.2, 0.1), col = c("black", "red"))
> matshade(ndA$age, cbind(pga, pia)*1000,
+         lty = c("solid", "21"), lend = "butt", lwd = 2,
+         alpha = c(0.2, 0.1), col = c("black", "red"))
```

This is in figure 2.7, p. 33.

2.6.3 Evaluating interactions

Here we see that the interaction effect is such that in the older ages the length of insulin use has an increasing effect on mortality.

Even though there is no statistically significant interaction between age and time since start of insulin, it would be illustrative to show the RR as a function of age at insulin and age at follow-up:

```
> ndR <- transform(ndI, lex.Cst = "DM", tfI = 0)
> iRR <- ci.exp(im, ctr.mat = list(ndI, ndR))
> gRR <- ci.exp(gm, ctr.mat = list(ndI, ndR))
> par(mar = c(3, 3, 1, 1), mgp = c(3, 1, 0)/1.6, las = 1, bty = "n")
> matshade(ndI$age, cbind(gRR, iRR), lty = 1, log = "y", plot = TRUE,
+         xlab = "Age (years)", ylab = "Rate ratio: Ins vs. non-Ins",
+         col = c("black", "red"), lwd = 2)
> abline(h = 1)
```

This is in figure 2.8, p. 34.

The advantage of the parametric modeling (be that with age at insulin or general spline interaction) is that it is straight-forward to *test* whether we have an interaction.

2.7 Separate models

In the above we insisted on making a joint model for the DM→Dead and the Ins→Dead transitions, but with the complications demonstrated it would actually have been more sensible to model the two transitions separately:

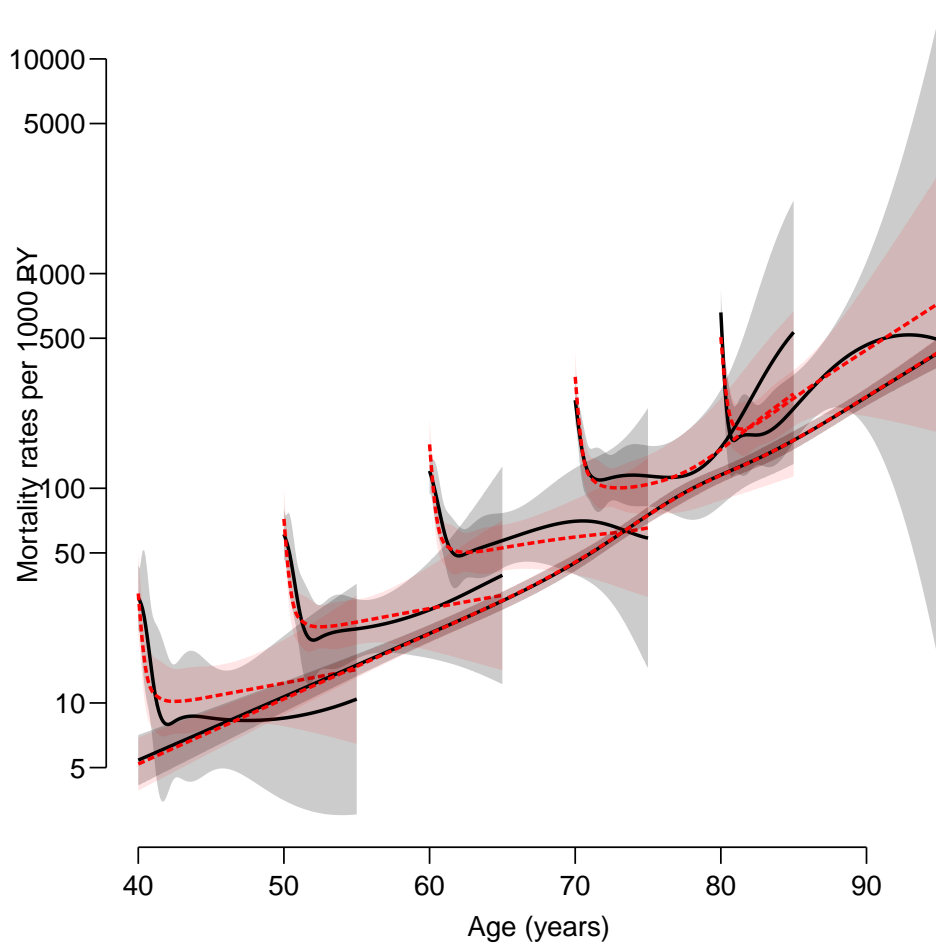


Figure 2.7: *Spline-by-spline interaction between age and duration (model `gm`, black), and the interaction using a non-linear effect of age at entry (model `im`, red), corresponding to the red curves in figure 2.5.*

`./flup-splint`

```
> dmd <- glm.Lexis(dmCs,
+                 from = "DM", to = "Dead",
+                 formula = ~ Ns(age, knots = a.kn)
+                 + sex)
stats::glm Poisson analysis of Lexis object dmCs with log link:
Rates for the transition:
DM->Dead
> ind <- glm.Lexis(dmCs,
+                 from = "Ins", to = "Dead",
+                 formula = ~ Ns(age, knots = a.kn)
+                 + Ns(tfI, knots = i.kn)
+                 + Ns(age - tfI, knots = a.kn)
+                 + sex)
stats::glm Poisson analysis of Lexis object dmCs with log link:
Rates for the transition:
Ins->Dead
> ini <- ci.pred(ind, ndI)
> dmi <- ci.pred(dmd, ndI)
> dma <- ci.pred(dmd, ndA)
```

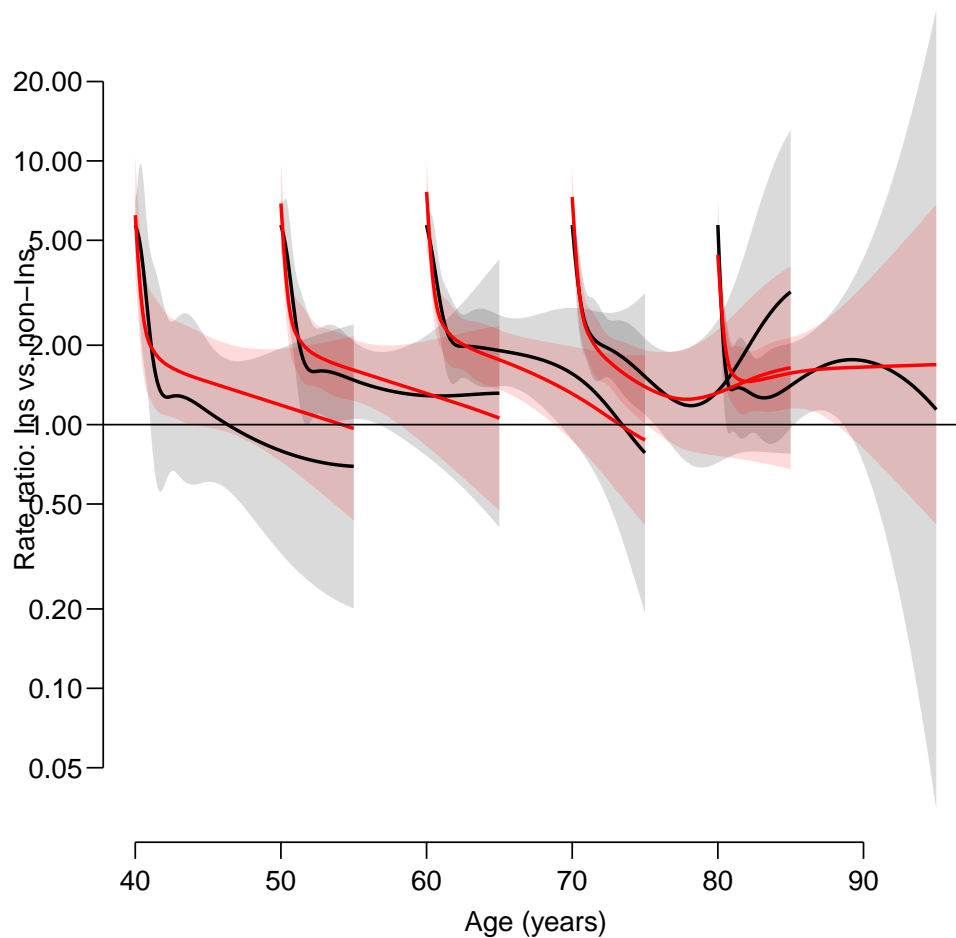


Figure 2.8: *The effect of duration of insulin use at different ages of follow-up (and age at insulin start). Estimates are from the model with an interaction term using a non-linear effect of age at insulin start (model im, red) and using a general spline interactions (model gm, black). It appears that the general interaction over-models a bit.* ./flup-RR-int

The estimated mortality rates are shown in figure ??, p. ??, using:

```
> par(mar = c(3, 3, 1, 1), mgp = c(3, 1, 0)/1.6, las = 1, bty = "n")
> matshade(ndI$age, ini * 1000, plot = TRUE, log = "y",
+         xlab = "Age (years)", ylab = "Mortality rates per 1000 PY",
+         lwd = 2, col = "red")
> matshade(ndA$age, dma*1000,
+         lwd = 2, col = "black")
```

The estimated RRs can now be computed exploiting the fact that the estimates from the two models are uncorrelated, and hence qualify for `ci.ratio` (this and the previous graph appear in figure 2.9, p. 35)

```
> par(mar = c(3, 3, 1, 1), mgp = c(3, 1, 0)/1.6, las = 1, bty = "n")
> matshade(ndI$age, ci.ratio(ini, dmi), plot = TRUE, log = "y",
+         xlab = "Age (years)", ylab = "RR insulin vs. no insulin",
+         lwd = 2, col = "red")
> abline(h = 1)
```

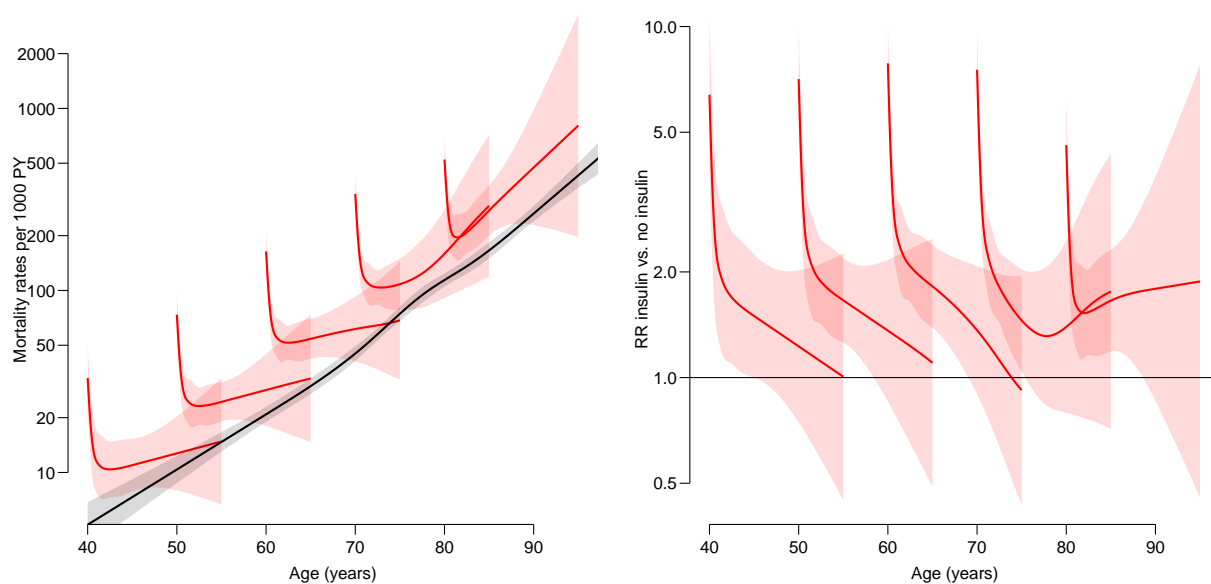


Figure 2.9: *Left panel: Mortality rates from separate models for the two mortality transitions; the DM→Dead transition modeled by age alone; Ins→Dead transition modeled with spline effects of current age, time since insulin and age at insulin. Right panel: Mortality HR of insulin vs. no insulin.*

Chapter 3

More states

3.1 Subdividing states

It may be of interest to subdivide the states following the intermediate event according to whether the event has occurred or not. This will enable us to address the question of the fraction of the patients that ever go on insulin.

This is done by the argument `split.states = TRUE`.

```
> dmCs <- cutLexis(data = dmS2,
+                 cut = dmS2$doins,
+                 timescale = "per",
+                 new.state = "Ins",
+                 new.scale = "tfl",
+                 split.states = TRUE)
> summary(dmCs)
```

Transitions:

	To								
From	DM	Ins	Dead	Dead(Ins)	Records:	Events:	Risk time:	Persons:	
DM	35135	1694	2048	0	38877	3742	45885.49	9899	
Ins	0	5762	0	451	6213	451	8387.77	1791	
Sum	35135	7456	2048	451	45090	4193	54273.27	9996	

We can illustrate the numbers and the transitions (figure 3.1, p. 37)

```
> boxes(dmCs, boxpos = list(x = c(15, 15, 85, 85),
+                             y = c(85, 15, 85, 15)),
+       scale.R = 1000, show.BE = TRUE)
> legendbox(50, 50)
```

Note that it is only the mortality rates that we have been modeling, namely the transitions `DM→Dead` and `Ins→Dead(Ins)`. If we were to model the cumulative risk of using insulin we would also need a model for the `DM→Ins` transition. Subsequent to that we would then compute the probability of being in each state conditional on suitable starting conditions. With models where transition rates depend on several time scales this is not a trivial task. This is treated in more detail in the vignette on `simLexis`.

3.2 Multiple intermediate events

We may be interested in starting either insulin or OAD (oral anti-diabetic drugs), thus giving rise to more states and more time scales. This can be accomplished by the

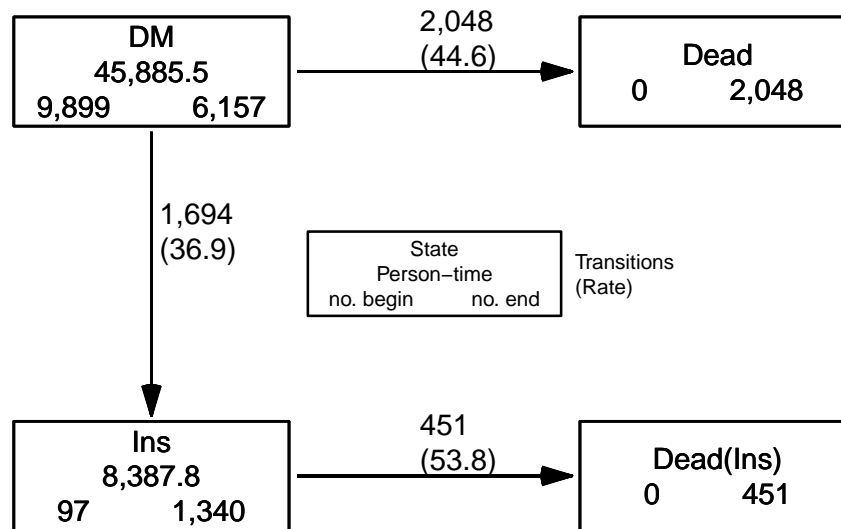


Figure 3.1: *Transitions between 4 states: the numbers in the boxes are person-years (middle), and below the number of persons who start, respectively end their follow-up in each of the states.*

./flup-box4

mcutLexis function, that generalizes cutLexis:

```
> dmM <- mcutLexis(dmL,
+               timescale = "per",
+               wh = c("doins", "dooad"),
+               new.states = c("Ins", "OAD"),
+               new.scales = c("tfI", "tfO"),
+               ties.resolve = TRUE)
```

NOTE: Precursor states set to DM

NOTE: 15 records with tied events times resolved (adding 0.01 random uniform), so results are only reproducible if the random number seed was set.

```
> summary(dmM, t = T)
```

Transitions:

From	To	DM	Dead	OAD	Ins	OAD-Ins	Ins-OAD	Records:	Events:	Risk time:	Persons:
DM		2830	1056	2957	689	0	0	7532	4702	22920.17	7532
OAD		0	992	3327	0	1005	0	5324	1997	22965.30	5324
Ins		0	152	0	462	0	172	786	324	3883.14	786
OAD-Ins		0	266	0	0	739	0	1005	266	3770.55	1005
Ins-OAD		0	33	0	0	0	139	172	33	734.11	172
Sum		2830	2499	6284	1151	1744	311	14819	7322	54273.27	9996

Timescales:

```
per  age  tfD  tfI  tfO
""   ""   ""  "Ins" "OAD"
```

We see that we now have two time scales defined as entry since into states.

```
> wh <- c(subset(dmM, lex.Cst == "Ins-OAD")$lex.id[1:2],
+         subset(dmM, lex.Cst == "OAD-Ins")$lex.id[1:2])
> subset(dmM, lex.id %in% wh)
```

```

lex.id   per   age  tfD  tfI  tfO lex.dur lex.Cst lex.Xst sex   dobth   dodm
  18 1996.75 61.72 0.00  NA  NA   1.17    DM    OAD  M 1935.024 1996.746
  18 1997.92 62.89 1.17  NA  0.00  8.08    OAD OAD-Ins  M 1935.024 1996.746
  18 2005.99 70.97 9.25 0.00 8.08   4.00 OAD-Ins OAD-Ins  M 1935.024 1996.746
  25 2003.69 60.34 0.00  NA  NA   1.88    DM    OAD  F 1943.347 2003.689
  25 2005.57 62.22 1.88  NA  0.00  3.07    OAD OAD-Ins  F 1943.347 2003.689
  25 2008.64 65.29 4.95 0.00 3.07   1.36 OAD-Ins OAD-Ins  F 1943.347 2003.689
  20 2009.25 53.22 0.00  NA  NA   0.03    DM    Ins  F 1956.029 2009.247
  20 2009.28 53.25 0.03 0.00  NA   0.01    Ins Ins-OAD  F 1956.029 2009.247
  20 2009.29 53.26 0.04 0.01 0.00   0.71 Ins-OAD Ins-OAD  F 1956.029 2009.247
  38 2008.37 63.93 0.00  NA  NA   0.09    DM    Ins  M 1944.434 2008.366
  38 2008.46 64.02 0.09 0.00  NA   0.21    Ins Ins-OAD  M 1944.434 2008.366
  38 2008.67 64.24 0.31 0.21 0.00   1.33 Ins-OAD  Dead  M 1944.434 2008.366
dodth   dooad   doins     dox
  NA 1997.915 2005.995 2009.997
  NA 1997.915 2005.995 2009.997
  NA 1997.915 2005.995 2009.997
  NA 2005.570 2008.639 2009.997
  NA 2005.570 2008.639 2009.997
  NA 2005.570 2008.639 2009.997
  NA 2009.287 2009.276 2009.997
  NA 2009.287 2009.276 2009.997
  NA 2009.287 2009.276 2009.997
2009.997 2008.672 2008.459 2009.997
2009.997 2008.672 2008.459 2009.997
2009.997 2008.672 2008.459 2009.997

```

We can also illustrate the transitions to the different states, as in figure 3.2:

```

> boxes(dmM, boxpos = list(x = c(15, 80, 40, 40, 85, 85),
+                             y = c(50, 50, 90, 10, 90, 10)),
+       scale.R = 1000, show.BE = TRUE)

```

We may not be interested in whether persons were prescribed insulin before OAD or vice versa, in which case we would combine the levels with both insulin and OAD to one, regardless of order (figure 3.3):

```

> summary(dmMr <- Relevel(dmM, list('OAD+Ins' = 5:6), first = FALSE))

```

Transitions:

From	To	DM	Dead	OAD	Ins	OAD+Ins	Records:	Events:	Risk time:	Persons:
DM		2830	1056	2957	689	0	7532	4702	22920.17	7532
OAD		0	992	3327	0	1005	5324	1997	22965.30	5324
Ins		0	152	0	462	172	786	324	3883.14	786
OAD+Ins		0	299	0	0	878	1177	299	4504.66	1177
Sum		2830	2499	6284	1151	2055	14819	7322	54273.27	9996

```

> boxes(dmMr, boxpos = list(x = c(15, 50, 15, 85, 85),
+                             y = c(85, 50, 15, 85, 15)),
+       scale.R = 1000, show.BE = TRUE)

```

Diagrams as those in figures 3.2 and 3.3 gives an overview of the possible transitions, which states it might be relevant to collapse, and which transitions to model and how.

The actual modeling of the transition rates is straightforward; split the data along some timescale and then use `glm.Lexis` or `gam.Lexis`, where it is possible to select the transitions modeled. This is also possible with the `coxph.Lexis` function, but it requires that a single time scale be selected as the baseline time scale, and the effect of this will not be accessible.

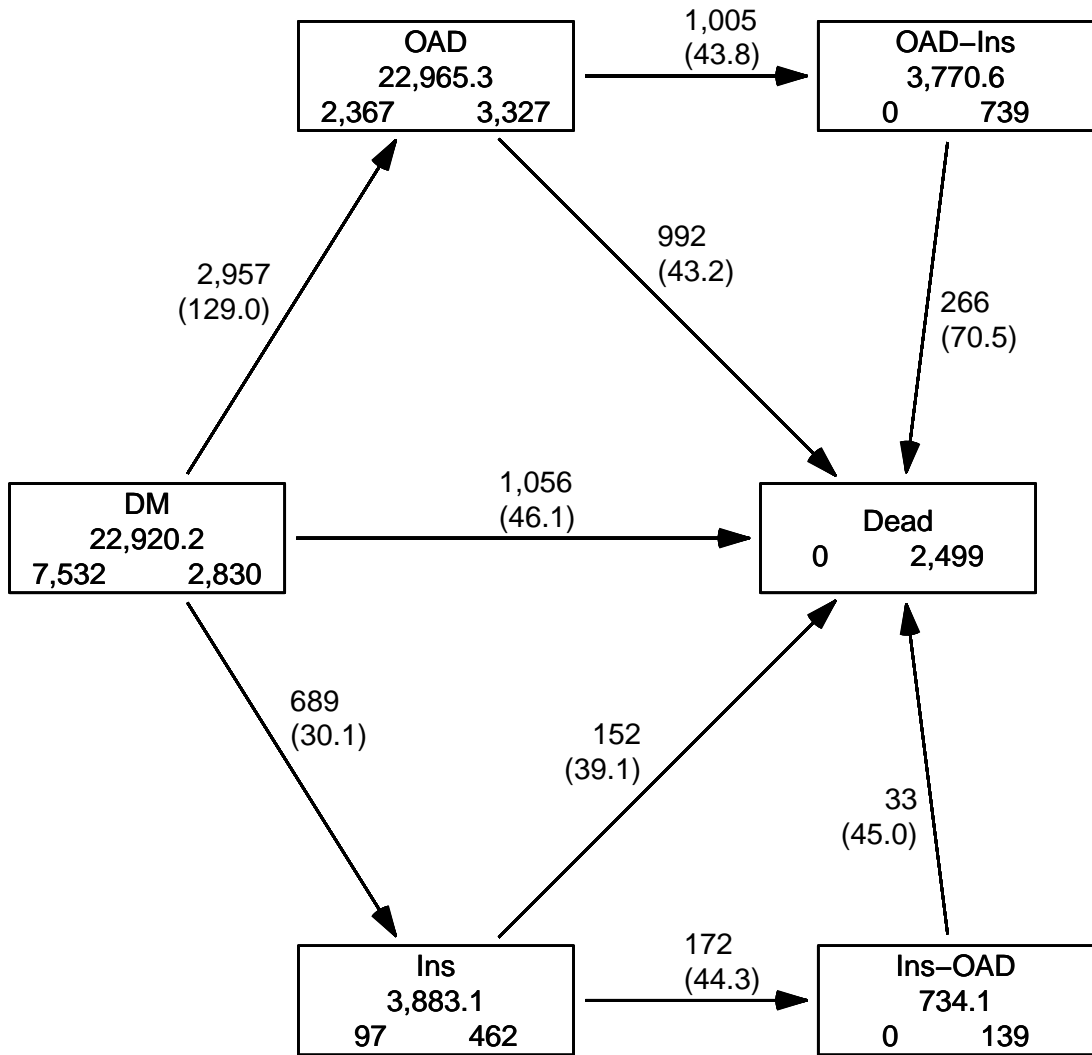


Figure 3.2: Boxes for the dmM object. The numbers in the boxes are person-years (middle), and below the number of persons who start, respectively end their follow-up in each of the states. ./flup-mbox

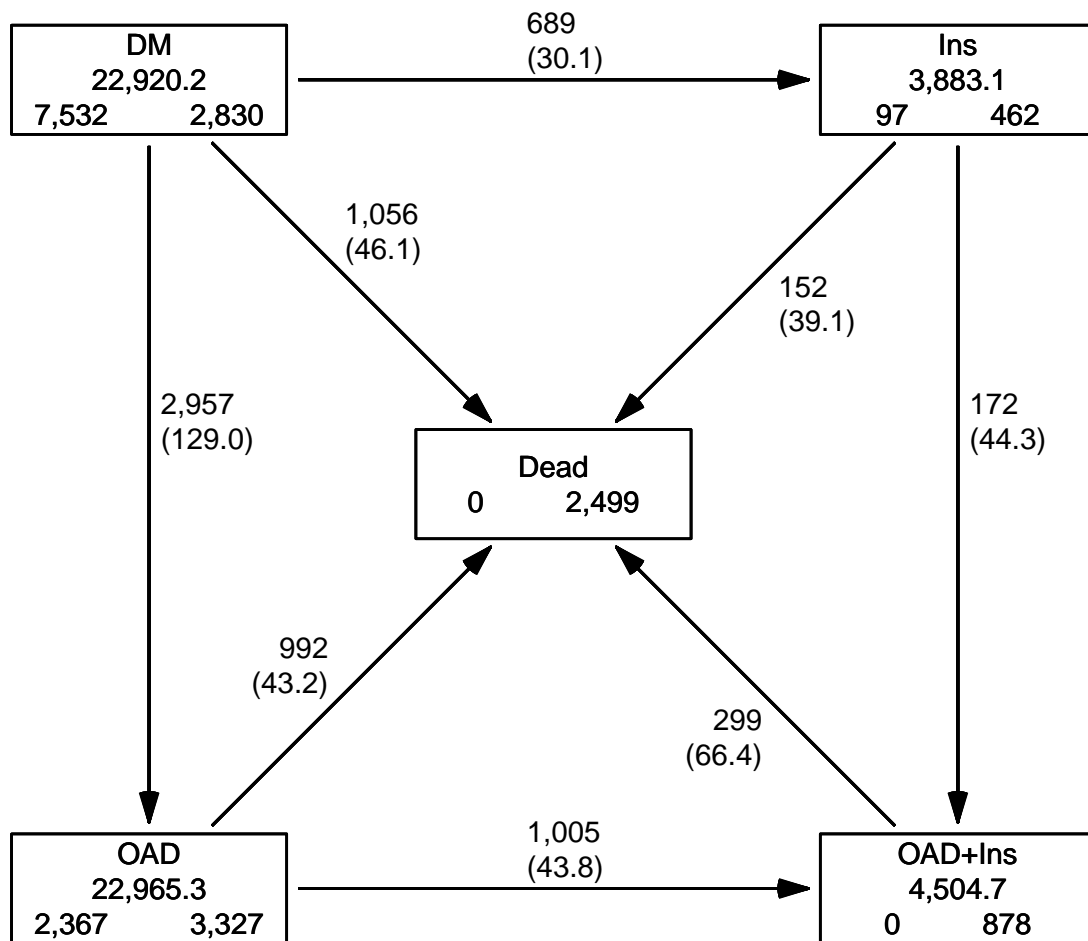


Figure 3.3: Boxes for the `dmMr` object with collapsed states. The numbers in the boxes are person-years (middle), and below the number of persons who start, respectively end their follow-up in each of the states. `./flup-mboxr`

Chapter 4

Lexis functions

The `Lexis` machinery has evolved over time since it was first introduced in a workable version in `Epi_1.0.5` in August 2008.

Over the years there have been additions of tools for handling multistate data. Here is a list of the current functions relating to `Lexis` objects with a very brief description; it does not replace the documentation. Unless otherwise stated, functions named `something.Lexis` (with a “.”) are S3 methods for `Lexis` objects, so you can skip the “.Lexis” in daily use.

Define

`Lexis` defines a `Lexis` object

Cut and split

`cutLexis` cut follow-up at intermediate event

`mcutLexis` cut follow-up at multiple intermediate events, keeping track of history

`rcutLexis` cut follow-up at intermediate, possibly recurring, events, only recording the current state

`countLexis` cut follow-up at intermediate event time and count the no. events so far

`splitLexis` split follow up along a time scale

`splitMulti` split follow up along a time scale — from the `popEpi` package, faster and has simpler syntax than `splitLexis`

`addCov.Lexis` add clinical measurements at a given date to a `Lexis` object

`addDrug.Lexis` add drug exposures to a `Lexis` object

Boxes and plots

`boxes.Lexis` draw a diagram of states and transitions

`legendbox` draw a box explaining the numbers output by `boxes.Lexis`

`plot.Lexis` draw a standard `Lexis` diagram

`points.Lexis` add points to a `Lexis` diagram

`lines.Lexis` add lines to a `Lexis` diagram

`PY.ann.Lexis` annotate life lines in a `Lexis` diagram

Summarize and query

`summary.Lexis` overview of transitions, risk time etc.

`levels.Lexis` what are the states in the `Lexis` object

`nid.Lexis` number of persons in the Lexis object — how many unique values of `lex.id` are present
`entry` entry time
`exit` exit time
`status` status at entry or exit
`timeBand` factor of time bands
`timeScales` what time scales are in the Lexis object
`timeSince` what time scales are defined as time since a given state
`breaks` what breaks are currently defined
`absorbing` what are the absorbing states
`transient` what are the transient states
`preceding, before` which states precede this
`succeeding, after` which states can follow this
`tmat.Lexis` transition matrix for the Lexis object

Manipulate

`subset.Lexis, [` subset of a Lexis object
`merge.Lexis` merges a Lexis objects with a `data.frame`
`cbind.Lexis` bind a `data.frame` to a Lexis object
`rbind.Lexis` put two Lexis objects head-to-foot
`transform.Lexis` transform and add variables
`tsNA20` turn NAs to 0s for time scales
`factorize.Lexis` turn `lex.Cst` and `lex.Xst` into factors with levels equal to the actually occurring values in both
`Relevel.Lexis` reorder and/or combine states
`rm.tr` remove transitions from a Lexis object
`bootLexis` bootstrap sample of *persons* (`lex.id`) in the Lexis object
`unLexis` remove Lexis attributes from a Lexis object

Simulate

`simLexis` simulate a Lexis object from specified transition rate models
`nState, pState` count state occupancy from a simulated Lexis object
`plot.pState, lines.pState` plot state occupancy from a `pState` object

Stack

`stack.Lexis` make a stacked object for simultaneous analysis of transitions — returns a `stacked.Lexis` object
`subset.stacked.Lexis` subsets of a `stacked.Lexis` object
`transform.stacked.Lexis` transform a `stacked.Lexis` object

Interface to other packages

`msdata.Lexis` interface to `mstate` package
`etm.Lexis` interface to `etm` package
`crr.Lexis` interface to `cmprsk` package

Statistical models — these are *not* S3 methods

`glm.Lexis` fit a `glm` model using the `poisreg` family to (hopefully) time split data

`gam.Lexis` fit a gam model (from the `mgcv` package) using the `poisreg` family to
(hopefully) time split data
`coxph.Lexis` fit a Cox model to follow-up in a `Lexis` object

Start time: 2024-09-11, 03:32:06
End time: 2024-09-11, 03:32:30
Elapsed time: 0.4 minutes

References

- [1] B Carstensen and M Plummer. Using Lexis objects for multi-state models in R. *Journal of Statistical Software*, 38(6):1–18, 1 2011.
- [2] S Iacobelli and B Carstensen. Multiple time scales in multi-state models. *Stat Med*, 32(30):5315–5327, Dec 2013.
- [3] M Plummer and B Carstensen. Lexis: An R class for epidemiological studies with long-term follow-up. *Journal of Statistical Software*, 38(5):1–12, 1 2011.