The doBy package

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Contents

1 Introduction

The doBy package contains a variety of utility functions. This working document describes some of these functions. The package originally grew out of a need to calculate groupwise summary statistics (much in the spirit of PROC SUMMARY of the SAS system), but today the package contains many different utilities.

2 Data used for illustration

The description of the doBy package is based on the following datasets.

CO2 data The CO2 data frame comes from an experiment on the cold tolerance of the grass species *Echinochloa crus-galli*. To limit the amount of output we modify names and levels of variables as follows

```
data(CO2)
CO2 <- transform(CO2, Treat=Treatment, Treatment=NULL)
levels(CO2$Treat) <- c("nchil","chil")
levels(CO2$Type)  <- c("Que","Mis")
CO2 <- subset(CO2, Plant %in% c("Qn1", "Qc1", "Mn1", "Mc1"))
```

Airquality data The airquality dataset contains air quality measurements in New York, May to September 1973. The months are coded as $5, \dots, 9$. To limit the output we only consider data for two months:

```
airquality <- subset(airquality, Month %in% c(5,6))
```

Dietox data The dietox data are provided in the doBy package and result from a study of the effect of adding vitamin E and/or copper to the feed of slaughter pigs.

3 Working with groupwise data

3.1 The summaryBy function

The summaryBy function is used for calculating quantities like “the mean and variance of x and y for each combination of two factors A and B”. Examples are based on the CO2 data.

3.1.1 Basic usage

The mean and variance of uptake and conc for each value of Plant is obtained by:

```
myfun1 <- function(x){c(m=mean(x), v=var(x))}
summaryBy( conc + uptake ~ Plant, data=CO2, FUN=myfun1)
```

```
  Plant conc.m conc.v uptake.m uptake.v
1   Qn1    435 100950    33.23    67.48
2   Qc1    435 100950    29.97    69.47
3   Mn1    435 100950    26.40    75.59
4   Mc1    435 100950    18.00    16.96
```

Above myfun1() is a function that returns a vector of named values. Note that the values returned by the function has been named as m and v. An alternative specification is:

```
summaryBy( list(c("conc","uptake"), "Plant"), data=CO2, FUN=myfun1)
```

```
  Plant conc.m conc.v uptake.m uptake.v
1   Qn1    435 100950    33.23    67.48
2   Qc1    435 100950    29.97    69.47
3   Mn1    435 100950    26.40    75.59
4   Mc1    435 100950    18.00    16.96
```

If the result of the function(s) are not named, then the names in the output data in general become less intuitive:

```
myfun2 <- function(x){c(mean(x), var(x))}
summaryBy( conc + uptake ~ Plant, data=CO2, FUN=myfun2)
```

```
  Plant conc.FUN1 conc.FUN2 uptake.FUN1 uptake.FUN2
1   Qn1       435    100950       33.23       67.48
2   Qc1       435    100950       29.97       69.47
3   Mn1       435    100950       26.40       75.59
4   Mc1       435    100950       18.00       16.96
```

Another usage is to specify a list of functions each of which returns a single value:

```
summaryBy( conc + uptake ~ Plant, data=CO2, FUN=list( mean, var ) )
```

```
  Plant conc.mean uptake.mean conc.var uptake.var
1   Qn1       435       33.23   100950      67.48
2   Qc1       435       29.97   100950      69.47
3   Mn1       435       26.40   100950      75.59
4   Mc1       435       18.00   100950      16.96
```

Notice that if we specify a list of functions of which some returns a vector with more than one element, then the proper names are not retrieved:

```
summaryBy(uptake˜Plant, data=CO2, FUN=list( mean, var, myfun1 ))
```

```
  Plant uptake.FUN1 uptake.FUN2 uptake.FUN3 uptake.FUN4
1   Qn1       33.23       67.48       33.23       67.48
2   Qc1       29.97       69.47       29.97       69.47
3   Mn1       26.40       75.59       26.40       75.59
4   Mc1       18.00       16.96       18.00       16.96
```

One can “hard code” the function names into the output as

```
summaryBy(uptake˜Plant, data=CO2, FUN=list( mean, var, myfun1 ),
          fun.names=c("mean","var","mm","vv"))
```

```
  Plant uptake.mean uptake.var uptake.mm uptake.vv
1   Qn1       33.23      67.48     33.23     67.48
2   Qc1       29.97      69.47     29.97     69.47
3   Mn1       26.40      75.59     26.40     75.59
4   Mc1       18.00      16.96     18.00     16.96
```

3.1.2 Statistics on functions of data

We may want to calculate the mean and variance for the logarithm of `uptake`, for `uptake+conc` (not likely to be a useful statistic) as well as for `uptake` and `conc`. This can be achieved as:

```
summaryBy(log(uptake) + I(conc+uptake) + conc+uptake ˜ Plant, data=CO2,
          FUN=myfun1)
```

```
  Plant log(uptake).m log(uptake).v conc + uptake.m conc + uptake.v conc.m
1   Qn1         3.467       0.10168           468.2            104747    435
2   Qc1         3.356       0.11873           465.0            105297    435
3   Mn1         3.209       0.17928           461.4            105642    435
4   Mc1         2.864       0.06874           453.0            103157    435
  conc.v uptake.m uptake.v
1 100950    33.23    67.48
2 100950    29.97    69.47
3 100950    26.40    75.59
4 100950    18.00    16.96
```

The names of the variables become involved with this. The user may control the names of the variables directly:

```
summaryBy(log(uptake) + I(conc+uptake) + conc + uptake ˜ Plant, data=CO2,
          FUN=myfun1, var.names=c("log.upt", "conc+upt", "conc", "upt"))
```

```
  Plant log.upt.m log.upt.v conc+upt.m conc+upt.v conc.m conc.v upt.m upt.v
1   Qn1     3.467   0.10168      468.2     104747    435 100950 33.23 67.48
2   Qc1     3.356   0.11873      465.0     105297    435 100950 29.97 69.47
3   Mn1     3.209   0.17928      461.4     105642    435 100950 26.40 75.59
4   Mc1     2.864   0.06874      453.0     103157    435 100950 18.00 16.96
```

If one does not want output variables to contain parentheses then setting `p2d=TRUE` causes the parentheses to be replaced by dots (".").

```
 summaryBy(log(uptake)+I(conc+uptake)~Plant, data=CO2, p2d=TRUE,
  FUN=myfun1)
```

```
  Plant log.uptake..m log.uptake..v conc + uptake.m conc + uptake.v
1   Qn1         3.467       0.10168            468.2            104747
2   Qc1         3.356       0.11873            465.0            105297
3   Mn1         3.209       0.17928            461.4            105642
4   Mc1         2.864       0.06874            453.0            103157
```

3.1.3 Copying variables out with the `id` argument

To get the value of the `Type` and `Treat` in the first row of the groups (defined by the values of `Plant`) copied to the output dataframe we use the `id` argument in one of the following forms:

```
 summaryBy(conc+uptake~Plant, data=CO2, FUN=myfun1, id=~Type+Treat)
```

```
  Plant conc.m conc.v uptake.m uptake.v
1   Qn1    435 100950    33.23    67.48
2   Qc1    435 100950    29.97    69.47
3   Mn1    435 100950    26.40    75.59
4   Mc1    435 100950    18.00    16.96
```

```
 summaryBy(conc+uptake~Plant, data=CO2, FUN=myfun1, id=c("Type","Treat"))
```

```
  Plant conc.m conc.v uptake.m uptake.v
1   Qn1    435 100950    33.23    67.48
2   Qc1    435 100950    29.97    69.47
3   Mn1    435 100950    26.40    75.59
4   Mc1    435 100950    18.00    16.96
```

3.1.4 Using '.' on the left hand side of a formula

It is possible to use the dot (".") on the left hand side of the formula. The dot means "all numerical variables which do not appear elsewhere" (i.e. on the right hand side of the formula and in the `id` statement):

```
 summaryBy(log(uptake)+I(conc+uptake)+. ~Plant, data=CO2, FUN=myfun1)
```

```
  Plant log(uptake).m log(uptake).v conc + uptake.m conc + uptake.v conc.m
1   Qn1         3.467       0.10168            468.2            104747    435
2   Qc1         3.356       0.11873            465.0            105297    435
3   Mn1         3.209       0.17928            461.4            105642    435
4   Mc1         2.864       0.06874            453.0            103157    435
  conc.v uptake.m uptake.v
1 100950    33.23    67.48
2 100950    29.97    69.47
```

```
3 100950    26.40    75.59
4 100950    18.00    16.96
```

3.1.5 Using '.' on the right hand side of a formula

The dot (".") can also be used on the right hand side of the formula where it refers to "all non–numerical variables which are not specified elsewhere":

```
 summaryBy(log(uptake) ~Plant+., data=CO2, FUN=myfun1)
```

```
  Plant Type Treat log(uptake).m log(uptake).v
1   Qn1  Que nchil          3.467       0.10168
2   Qc1  Que  chil          3.356       0.11873
3   Mn1  Mis nchil          3.209       0.17928
4   Mc1  Mis  chil          2.864       0.06874
```

3.1.6 Using '1' on the right hand side of the formula

Using 1 on the right hand side means no grouping:

```
 summaryBy(log(uptake) ~ 1, data=CO2, FUN=myfun1)
```

```
  log(uptake).m log(uptake).v
1         3.224        0.1577
```

3.1.7 Preserving names of variables using `keep.names`

If the function applied to data only returns one value, it is possible to force that the summary variables retain the original names by setting `keep.names=TRUE`. A typical use of this could be

```
 summaryBy(conc+uptake+log(uptake)~Plant,
  data=CO2, FUN=mean, id=~Type+Treat, keep.names=TRUE)
```

```
  Plant conc uptake log(uptake)
1   Qn1  435  33.23       3.467
2   Qc1  435  29.97       3.356
3   Mn1  435  26.40       3.209
4   Mc1  435  18.00       2.864
```

3.2 The `orderBy` function

Ordering (or sorting) a data frame is possible with the `orderBy` function. Suppose we want to order the rows of the the `airquality` data by `Temp` and by `Month` (within `Temp`). This can be achieved by:

```
 x<-orderBy(~Temp+Month, data=airquality)
```

The first lines of the result are:

```
head(x)
```

```
   Ozone Solar.R Wind Temp Month Day
5     NA      NA 14.3   56     5   5
18     6      78 18.4   57     5  18
25    NA      66 16.6   57     5  25
27    NA      NA  8.0   57     5  27
15    18      65 13.2   58     5  15
26    NA     266 14.9   58     5  26
```

If we want the ordering to be by decreasing values of one of the variables, we change the sign, e.g.

```
x<-orderBy(~-Temp+Month, data=airquality)
head(x)
```

```
   Ozone Solar.R Wind Temp Month Day
42    NA     259 10.9   93     6  11
43    NA     250  9.2   92     6  12
40    71     291 13.8   90     6   9
39    NA     273  6.9   87     6   8
41    39     323 11.5   87     6  10
36    NA     220  8.6   85     6   5
```

3.3 The `splitBy` function

Suppose we want to split the `airquality` data into a list of dataframes, e.g. one dataframe for each month. This can be achieved by:

```
x<-splitBy(~Month, data=airquality)
x
```

```
  listentry Month
1         5     5
2         6     6
```

Hence for month 5, the relevant entry-name in the list is '5' and this part of data can be extracted as

```
x[['5']]
```

Information about the grouping is stored as a dataframe in an attribute called `groupid` and can be retrieved with:

```
attr(x,"groupid")
```

```
  Month
1     5
2     6
```

3.4 The sampleBy function

Suppose we want a random sample of 50 % of the observations from a dataframe. This can be achieved with:

```
sampleBy(~1, frac=0.5, data=airquality)
```

Suppose instead that we want a systematic sample of every fifth observation within each month. This is achieved with:

```
sampleBy(~Month, frac=0.2, data=airquality,systematic=T)
```

3.5 The subsetBy function

Suppose we want to select those rows within each month for which the the wind speed is larger than the mean wind speed (within the month). This is achieved by:

```
subsetBy(~Month, subset=Wind>mean(Wind), data=airquality)
```

Note that the statement `Wind>mean(Wind)` is evaluated within each month.

3.6 The transformBy function

The `transformBy` function is analogous to the `transform` function except that it works within groups. For example:

```
transformBy(~Month, data=airquality, minW=min(Wind), maxW=max(Wind),
     chg=sum(range(Wind)*c(-1,1)))
```

3.7 The lapplyBy function

This `lapplyBy` function is a wrapper for first splitting data into a list according to the formula (using splitBy) and then applying a function to each element of the list (using apply).

Suppose we want to calculate the weekwise feed efficiency of the pigs in the `dietox` data, i.e. weight gain divided by feed intake.

```
data(dietox)
dietox <- orderBy(~Pig+Time, data=dietox)
FEfun  <- function(d){c(NA, diff(d$Weight)/diff(d$Feed))}
v      <- lapplyBy(~Pig, data=dietox, FEfun)
dietox$FE <- unlist(v)
```

Technically, the above is the same as

```
dietox <- orderBy(~Pig+Time, data=dietox)
wdata  <- splitBy(~Pig, data=dietox)
v      <- lapply(wdata, FEfun)
dietox$FE <- unlist(v)
```

3.8 The scaleBy function

Standardize the iris data within each value of "Species":

```
x<-scaleBy( list(c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width"),
                   "Species"),     data=iris)
head(x)
```

```
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1      0.26667      0.1899      -0.3570     -0.4365  setosa
2     -0.30072     -1.1291      -0.3570     -0.4365  setosa
3     -0.86811     -0.6015      -0.9328     -0.4365  setosa
4     -1.15181     -0.8653       0.2188     -0.4365  setosa
5     -0.01702      0.4537      -0.3570     -0.4365  setosa
6      1.11776      1.2452       1.3705      1.4613  setosa
```

```
head(iris)
```

```
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          5.1         3.5          1.4         0.2  setosa
2          4.9         3.0          1.4         0.2  setosa
3          4.7         3.2          1.3         0.2  setosa
4          4.6         3.1          1.5         0.2  setosa
5          5.0         3.6          1.4         0.2  setosa
6          5.4         3.9          1.7         0.4  setosa
```

4 Create By–functions on the fly

Create a function for creating groupwise t-tests

```
mydata <- data.frame(y=rnorm(32), x=rnorm(32),
 g1=factor(rep(c(1,2),each=16)), g2=factor(rep(c(1,2), each=8)),
 g3=factor(rep(c(1,2),each=4)))
head(mydata)
```

```
        y        x g1 g2 g3
1 -0.6497 -0.21570  1  1  1
2 -1.2482 -0.41891  1  1  1
3  1.1143  0.17085  1  1  1
4 -1.0461 -0.12209  1  1  1
5 -0.3717 -0.08480  1  1  2
6  0.7251  0.07705  1  1  2
```

```
## Based on the formula interface to t.test
t.testBy1 <- function(formula, group, data, ...){
   formulaFunBy(formula, group, data, FUN=t.test, class="t.testBy1", ...)
 }
## Based on the default interface to t.test
t.testBy2 <- function(formula, group, data, ...){
   xyFunBy(formula, group, data, FUN=t.test, class="t.testBy1", ...)
 }
```

Notice: The optional `class` argument will facilitate that you create your own print / summary methods etc.

```
 t.testBy1(y~g1, ~g2, data=mydata)
```

```
$`1`

        Welch Two Sample t-test

data:  y by g1
t = 0.2337, df = 13.92, p-value = 0.8186
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.8318  1.0351
sample estimates:
mean in group 1 mean in group 2
        -0.3468         -0.4484


$`2`

        Welch Two Sample t-test

data:  y by g1
t = -0.2542, df = 13.82, p-value = 0.8031
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -1.2168  0.9592
sample estimates:
mean in group 1 mean in group 2
         0.2849          0.4137


attr(,"class")
[1] "t.testBy1"
```

```
 t.testBy2(y~x,  ~g2, data=mydata)
```

```
$`1`

        Welch Two Sample t-test

data:  x and y
t = -1.905, df = 28.86, p-value = 0.06677
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -1.0742  0.0382
```

```
sample estimates:
mean of x mean of y
  -0.3976    0.1204


$`2`

        Welch Two Sample t-test

data:  x and y
t = 1.458, df = 29.51, p-value = 0.1555
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -0.1913  1.1432
sample estimates:
mean of x mean of y
   0.3493   -0.1267


attr(,"class")
[1] "t.testBy1"
```

5 Miscellaneous

5.1 Specialize

```
 ff  <- function(a,b=2,c=4){a+b+c}
 ff1 <- specialize(ff, arglist=list(a=1, b=7, yy=123))
 ff1
```

```
function (c = 4)
{
    1 + 7 + c
}
<environment: 0x0000000008bf9328>
```

```
 gg  <- rnorm
 gg1 <- specialize(gg, list(n=10))
 gg1
```

```
function (mean = 0, sd = 1)
.External(C_rnorm, 10, mean, sd)
<environment: 0x0000000008ebe030>
```

Notice that this result is absurd:

```
 f  <- function(a) {a <- a + 1; a}
 f1 <- specialize(f, list(a = 10))
 f1
```

```
function ()
{
    10 <- 10 + 1
    10
}
<environment: 0x0000000008777608>
```

5.2 The firstobs() / lastobs() function

To obtain the indices of the first/last occurences of an item in a vector do:

```
 x <- c(1,1,1,2,2,2,1,1,1,3)
 firstobs(x)
[1]  1  4 10
 lastobs(x)
[1]  6  9 10
```

The same can be done on a data frame, e.g.

```
 firstobs(~Plant, data=CO2)
[1]  1  8 15 22
 lastobs(~Plant, data=CO2)
[1]  7 14 21 28
```

5.3 The which.maxn() and which.minn() functions

The location of the n largest / smallest entries in a numeric vector can be obtained with

```
 x <- c(1:4,0:5,11,NA,NA)
 which.maxn(x,3)
[1] 11 10  4
 which.minn(x,5)
[1] 5 1 6 2 7
```

5.4 Subsequences - subSeq()

Find (sub) sequences in a vector:

```
 x <- c(1,1,2,2,2,1,1,3,3,3,3,1,1,1)
 subSeq(x)
```

```
  first last slength midpoint value
1     1    2       2        2     1
2     3    5       3        4     2
3     6    7       2        7     1
4     8   11       4       10     3
5    12   14       3       13     1
```

```
subSeq(x, item=1)
```

```
  first last slength midpoint value
1     1    2       2        2     1
2     6    7       2        7     1
3    12   14       3       13     1
```

```
subSeq(letters[x])
```

```
  first last slength midpoint value
1     1    2       2        2     a
2     3    5       3        4     b
3     6    7       2        7     a
4     8   11       4       10     c
5    12   14       3       13     a
```

```
subSeq(letters[x],item="a")
```

```
  first last slength midpoint value
1     1    2       2        2     a
2     6    7       2        7     a
3    12   14       3       13     a
```

5.5 Recoding values of a vector - recodeVar()

```
x <- c("dec","jan","feb","mar","apr","may")
src1 <- list(c("dec","jan","feb"), c("mar","apr","may"))
tgt1 <- list("winter","spring")
recodeVar(x,src=src1,tgt=tgt1)
```

```
[1] "winter" "winter" "winter" "spring" "spring" "spring"
```

5.6 Renaming columns of a dataframe or matrix – renameCol()

```
head(renameCol(CO2, 1:2, c("kk","ll")))
```

```
   kk  ll conc uptake Treat
1 Qn1 Que   95   16.0 nchil
2 Qn1 Que  175   30.4 nchil
3 Qn1 Que  250   34.8 nchil
4 Qn1 Que  350   37.2 nchil
5 Qn1 Que  500   35.3 nchil
6 Qn1 Que  675   39.2 nchil
```

```
head(renameCol(CO2, c("Plant","Type"), c("kk","ll")))
```

```
   kk  ll conc uptake Treat
1 Qn1 Que   95   16.0 nchil
2 Qn1 Que  175   30.4 nchil
3 Qn1 Que  250   34.8 nchil
4 Qn1 Que  350   37.2 nchil
5 Qn1 Que  500   35.3 nchil
6 Qn1 Que  675   39.2 nchil
```

5.7 Time since an event - timeSinceEvent()

Consider the vector

```
#yvar <- c(0,0,0,1,0,0,0,0,0,1,0,0,0,0,0,1,0,1,0,0,0,0,0,0,0,0,1,1,0,0,0,0,0)
yvar <- c(0,0,0,1,0,0,0,0,0,1,0,0,0,1,1,0,0,0,0,0)
```

Imagine that ”1” indicates an event of some kind which takes place at a certain time point. By default time points are assumed equidistant but for illustration we define time time variable

```
#tvar <- seq_along(yvar) + c(0.1,0.2,0.3)
tvar <- seq_along(yvar) + c(0.1,0.2)
```

Now we find time since event as

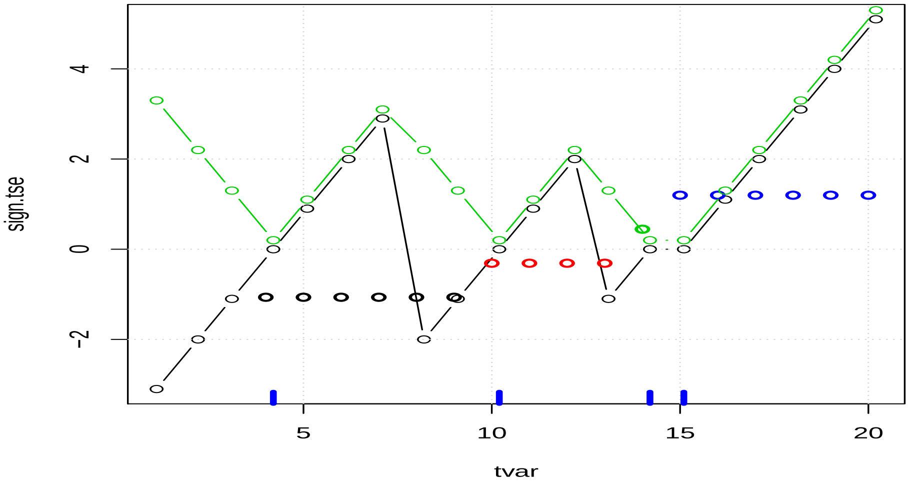
```
tse<- timeSinceEvent(yvar,tvar)
```

```
   yvar tvar abs.tse sign.tse ewin run tae  tbe
1     0  1.1     3.1     -3.1    1  NA  NA -3.1
2     0  2.2     2.0     -2.0    1  NA  NA -2.0
3     0  3.1     1.1     -1.1    1  NA  NA -1.1
4     1  4.2     0.0      0.0    1   1 0.0  0.0
5     0  5.1     0.9      0.9    1   1 0.9 -5.1
6     0  6.2     2.0      2.0    1   1 2.0 -4.0
7     0  7.1     2.9      2.9    1   1 2.9 -3.1
8     0  8.2     2.0     -2.0    2   1 4.0 -2.0
9     0  9.1     1.1     -1.1    2   1 4.9 -1.1
10    1 10.2     0.0      0.0    2   2 0.0  0.0
11    0 11.1     0.9      0.9    2   2 0.9 -3.1
12    0 12.2     2.0      2.0    2   2 2.0 -2.0
13    0 13.1     1.1     -1.1    3   2 2.9 -1.1
14    1 14.2     0.0      0.0    3   3 0.0  0.0
15    1 15.1     0.0      0.0    4   4 0.0  0.0
16    0 16.2     1.1      1.1    4   4 1.1   NA
17    0 17.1     2.0      2.0    4   4 2.0   NA
18    0 18.2     3.1      3.1    4   4 3.1   NA
19    0 19.1     4.0      4.0    4   4 4.0   NA
20    0 20.2     5.1      5.1    4   4 5.1   NA
```

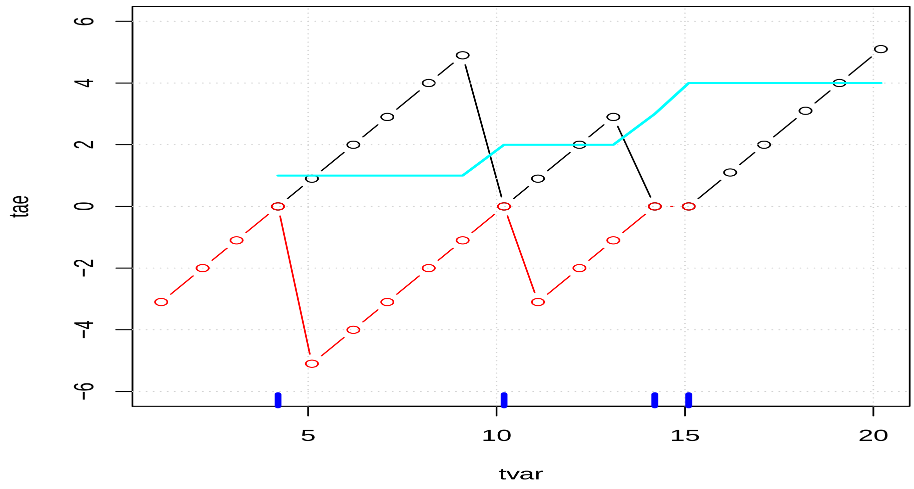
The output reads as follows:

- `abs.tse`: Absolute time since (nearest) event.
- `sign.tse`: Signed time since (nearest) event.
- `ewin`: Event window: Gives a symmetric window around each event.
- `run`: The value of `run` is set to 1 when the first event occurs and is increased by 1 at each subsequent event.
- `tae`: Time after event.
- `tbe`: Time before event.

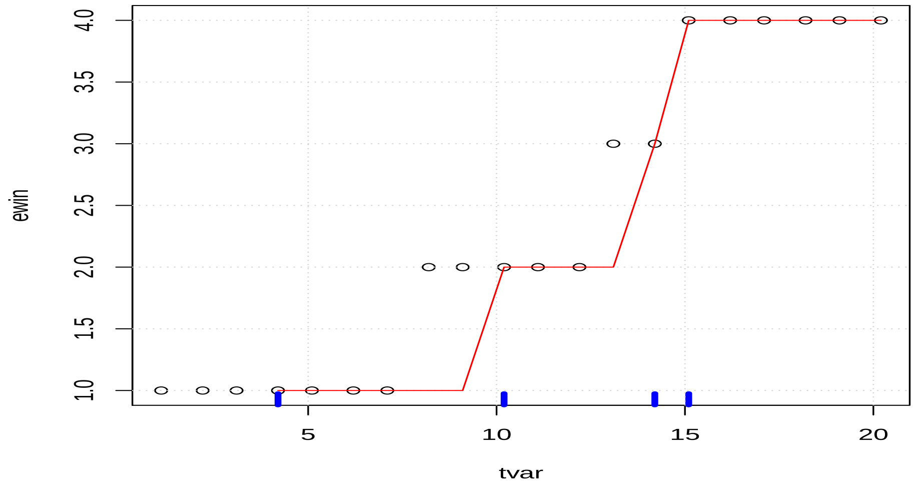
```
plot(sign.tse~tvar, data=tse, type="b")
grid()
rug(tse$tvar[tse$yvar==1], col='blue',lwd=4)
points(scale(tse$run), col=tse$run, lwd=2)
lines(abs.tse+.2~tvar, data=tse, type="b",col=3)
```



```
plot(tae~tvar, data=tse, ylim=c(-6,6),type="b")
grid()
lines(tbe~tvar, data=tse, type="b", col='red')
rug(tse$tvar[tse$yvar==1], col='blue',lwd=4)
lines(run~tvar, data=tse, col='cyan',lwd=2)
```



```
plot(ewin~tvar, data=tse,ylim=c(1,4))
rug(tse$tvar[tse$yvar==1], col='blue',lwd=4)
grid()
lines(run~tvar, data=tse,col='red')
```



We may now find times for which time since an event is at most 1 as

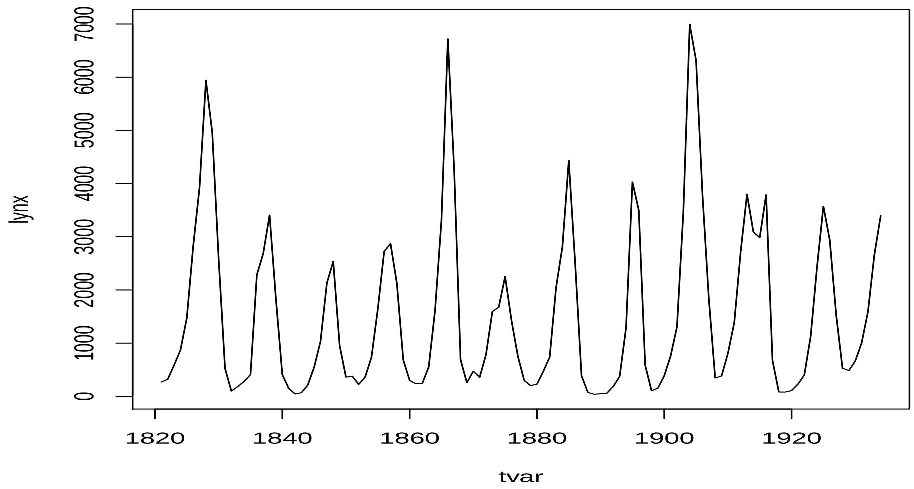
```
tse$tvar[tse$abs<=1]
```

```
[1]  4.2  5.1 10.2 11.1 14.2 15.1
```

5.8 Example: Using subSeq() and timeSinceEvent()

Consider the lynx data:

```
lynx <- as.numeric(lynx)
tvar <- 1821:1934
plot(tvar,lynx,type='l')
```



Suppose we want to estimate the cycle lengths. One way of doing this is as follows:

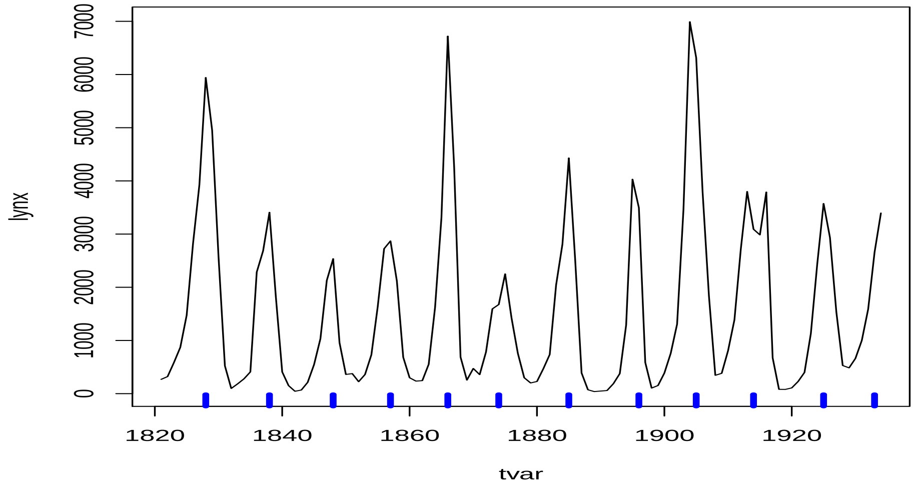
```
yyy <- lynx>mean(lynx)
head(yyy)
```

```
[1] FALSE FALSE FALSE FALSE FALSE  TRUE
```

```
sss <- subSeq(yyy,TRUE)
sss
```

```
   first last slength midpoint value
1      6   10       5        8  TRUE
2     16   19       4       18  TRUE
3     27   28       2       28  TRUE
4     35   38       4       37  TRUE
5     44   47       4       46  TRUE
6     53   55       3       54  TRUE
7     63   66       4       65  TRUE
8     75   76       2       76  TRUE
9     83   87       5       85  TRUE
10    92   96       5       94  TRUE
11   104  106       3      105  TRUE
12   112  114       3      113  TRUE
```

```
plot(tvar,lynx,type='l')
rug(tvar[sss$midpoint],col='blue',lwd=4)
```



Create the 'event vector'

```
yvar <- rep(0,length(lynx))
yvar[sss$midpoint] <- 1
str(yvar)
```

```
num [1:114] 0 0 0 0 0 0 0 1 0 0 ...
```

```
tse <- timeSinceEvent(yvar,tvar)
head(tse,20)
```

```
   yvar tvar abs.tse sign.tse ewin run tae tbe
1     0 1821       7       -7    1  NA  NA  -7
2     0 1822       6       -6    1  NA  NA  -6
3     0 1823       5       -5    1  NA  NA  -5
4     0 1824       4       -4    1  NA  NA  -4
5     0 1825       3       -3    1  NA  NA  -3
6     0 1826       2       -2    1  NA  NA  -2
7     0 1827       1       -1    1  NA  NA  -1
8     1 1828       0        0    1   1   0   0
9     0 1829       1        1    1   1   1  -9
10    0 1830       2        2    1   1   2  -8
11    0 1831       3        3    1   1   3  -7
12    0 1832       4        4    1   1   4  -6
13    0 1833       5        5    1   1   5  -5
14    0 1834       4       -4    2   1   6  -4
15    0 1835       3       -3    2   1   7  -3
16    0 1836       2       -2    2   1   8  -2
17    0 1837       1       -1    2   1   9  -1
18    1 1838       0        0    2   2   0   0
19    0 1839       1        1    2   2   1  -9
20    0 1840       2        2    2   2   2  -8
```

We get two different (not that different) estimates of period lengths:

```
 len1 <- tapply(tse$ewin, tse$ewin, length)
```

```
 1  2  3  4  5  6  7  8  9 10 11 12
13 10  9  9  9  9 11 10  9 10 10  5
```

```
 len2 <- tapply(tse$run, tse$run, length)
```

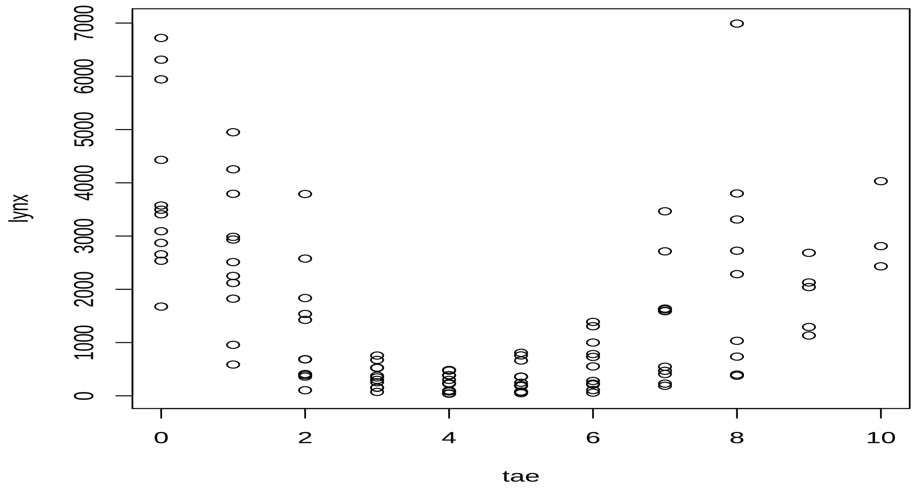
```
 1  2  3  4  5  6  7  8  9 10 11 12
10 10  9  9  8 11 11  9  9 11  8  2
```

```
 c(median(len1),median(len2),mean(len1),mean(len2))
```

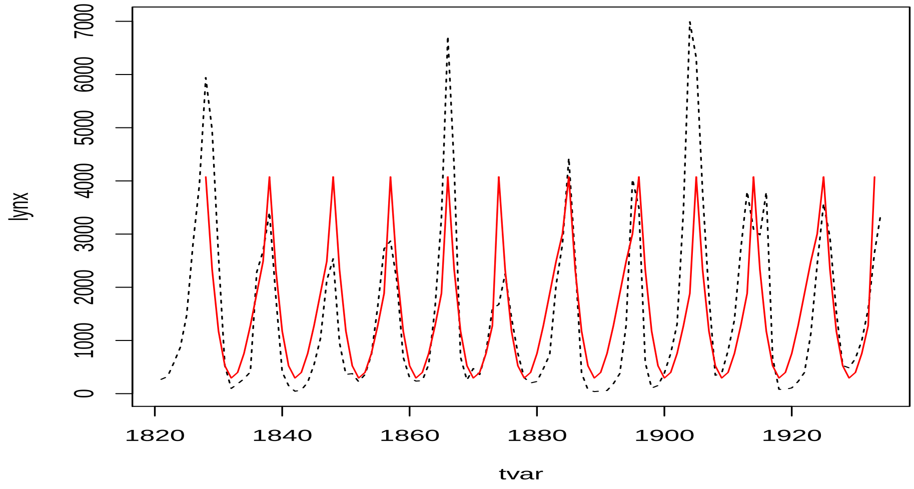
```
[1] 9.500 9.000 9.500 8.917
```

We can overlay the cycles as:

```
 tse$lynx <- lynx
 tse2 <- na.omit(tse)
 plot(lynx~tae, data=tse2)
```



```
 plot(tvar,lynx,type='l',lty=2)
 mm <- lm(lynx~tae+I(tae^2)+I(tae^3), data=tse2)
 lines(fitted(mm)~tvar, data=tse2, col='red')
```



6 Contrasts, estimable functions, LSMEANS

6.1 The esticon function

Consider a linear model which explains Ozone as a linear function of Month and Wind:

```
data(airquality)
airquality <- transform(airquality, Month=factor(Month))
m<-lm(Ozone~Month*Wind, data=airquality)
coefficients(m)
```

```
(Intercept)      Month6      Month7      Month8      Month9        Wind
     50.748     -41.793      68.296      82.211      23.439      -2.368
Month6:Wind Month7:Wind Month8:Wind Month9:Wind
      4.051      -4.663      -6.154      -1.874
```

When a parameter vector β of (systematic) effects have been estimated, interest is often in a particular estimable function, i.e. linear combination $\lambda^\top \beta$ and/or testing the hypothesis $H_0 : \lambda^\top \beta = \beta_0$ where λ is a specific vector defined by the user.

Suppose for example we want to calculate the expected difference in ozone between consequtive months at wind speed 10 mph (which is about the average wind speed over the whole period).

The esticon function provides a way of doing so. We can specify several λ vectors at the same time. For example

```
Lambda <- rbind(
   c(0,-1,0,0,0,0,-10,0,0,0),
   c(0,1,-1,0,0,0,10,-10,0,0),
   c(0,0,1,-1,0,0,0,10,-10,0),
   c(0,0,0,1,-1,0,0,0,10,-10)
   )
esticon(m, Lambda)
```

```
  beta0 Estimate Std.Error t.value  DF Pr(>|t|)   Lower  Upper
1     0   1.2871    10.238  0.1257 106  0.90019 -19.010 21.585
2     0 -22.9503    10.310 -2.2259 106  0.02814 -43.392 -2.509
3     0   0.9954     7.094  0.1403 106  0.88867 -13.069 15.060
4     0  15.9651     6.560  2.4337 106  0.01662   2.959 28.971
```

In other cases, interest is in testing a hypothesis of a contrast $H_0 : \Lambda\beta = \beta_0$ where Λ is a matrix. For example a test of no interaction between `Month` and `Wind` can be made by testing jointly that the last four parameters in `m` are zero (observe that the test is a Wald test):

```
Lambda <- rbind(
   c(0,0,0,0,0,0,1,0,0,0),
   c(0,0,0,0,0,0,0,1,0,0),
   c(0,0,0,0,0,0,0,0,1,0),
   c(0,0,0,0,0,0,0,0,0,1)
   )
esticon(m, Lambda, joint.test=T)
```

```
  X2.stat DF Pr(>|X^2|)
1   22.11  4  0.0001906
```

For a linear normal model, one would typically prefer to do a likelihood ratio test instead. However, for generalized estimating equations of glm–type (as dealt with in the packages geepack and gee) there is no likelihood. In this case `esticon` function provides an operational alternative.

Observe that another function for calculating contrasts as above is the `contrast` function in the Design package but it applies to a narrower range of models than `esticon` does.

6.2 LSMEANS

Marginal means (also called population means or LSMEANS) can be calulated with `lsmeans()`. See the documentation of `lsmeans()` for examples.

7 Acknowledgements

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