

The doBy package

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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.

The doBy package (and this document as a .pdf file) is available from

<http://cran.r-project.org/web/packages/doBy/index.html>

The package is loaded with:

```
library(doBy)
```

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, . . . , 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

For example, 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

Defining the function to return named values as above is the recommended use of `summaryBy`. Note that the values returned by the function has been named as `m` and `v`.

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

3.1.2 Using predefined functions

It is possible use a vector of predefined functions. A typical usage will be by invoking a list of predefined functions:

```
summaryBy(uptake~Plant, data=CO2, FUN=c(mean,var,median))
```

	Plant	uptake.mean	uptake.var	uptake.median
1	Qn1	33.23	67.48	35.3
2	Qc1	29.97	69.47	32.5
3	Mn1	26.40	75.59	30.0
4	Mc1	18.00	16.96	18.9

Slightly more elaborate is

```
mymed <- function(x)c(med=median(x))
summaryBy(uptake~Plant, data=CO2, FUN=c(mean,var,mymed))
```

	Plant	uptake.mean	uptake.var	uptake.mymed
1	Qn1	33.23	67.48	35.3
2	Qc1	29.97	69.47	32.5
3	Mn1	26.40	75.59	30.0
4	Mc1	18.00	16.96	18.9

The naming of the output variables determined from what the functions returns. The names of the last two columns above are imposed by `summaryBy` because `myfun2` does not return named values.

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: as:

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

	Plant	conc.m	conc.v	uptake.m	uptake.v	Type	Treat
1	Qn1	435	100950	33.23	67.48	Que	nchil
2	Qc1	435	100950	29.97	69.47	Que	chil
3	Mn1	435	100950	26.40	75.59	Mis	nchil
4	Mc1	435	100950	18.00	16.96	Mis	chil

3.1.4 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

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

3.1.5 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

3.1.6 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

3.1.7 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

3.1.8 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)	Type	Treat
1	Qn1	435	33.23	3.467	Que	nchil
2	Qc1	435	29.97	3.356	Que	chil
3	Mn1	435	26.40	3.209	Mis	nchil
4	Mc1	435	18.00	2.864	Mis	chil

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

4 Contrasts, estimable functions, LSMEANS

4.1 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 consecutive 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(0,0,0,0,0,0,0,1,0,0),
  c(0,0,0,0,0,0,0,0,1,0),
  c(0,0,0,0,0,0,0,0,0,1),
  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.

4.2 LSMEANS

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

5 Miscellaneous

5.1 The `firstobs()` / `lastobs()` function

To obtain the indices of the first/last occurrences 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
```

5.2 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
```

5.3 Subsequences - `subSeq()`

Find (sub) sequences in a vector:

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

5.4 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"
```

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

```
head(renameCol(C02, 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(C02, 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
```

5.6 Time since an event - timeSinceEvent()

Consider the vector

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

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 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

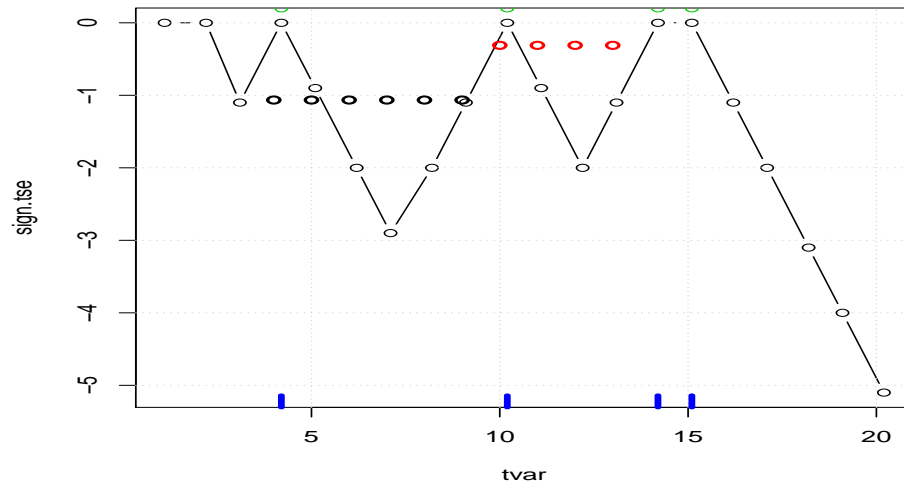
```
tse<- timeSinceEvent(yvar,tvar)
```

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

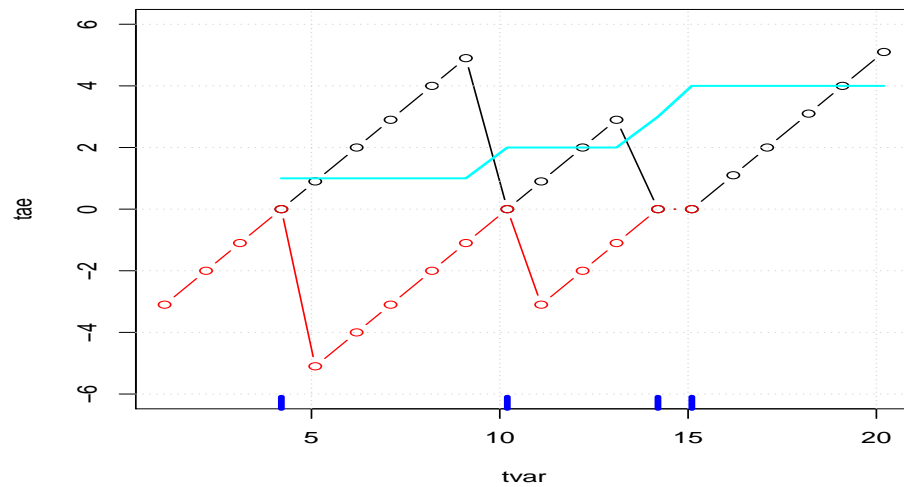
The output reads as follows:

- **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.

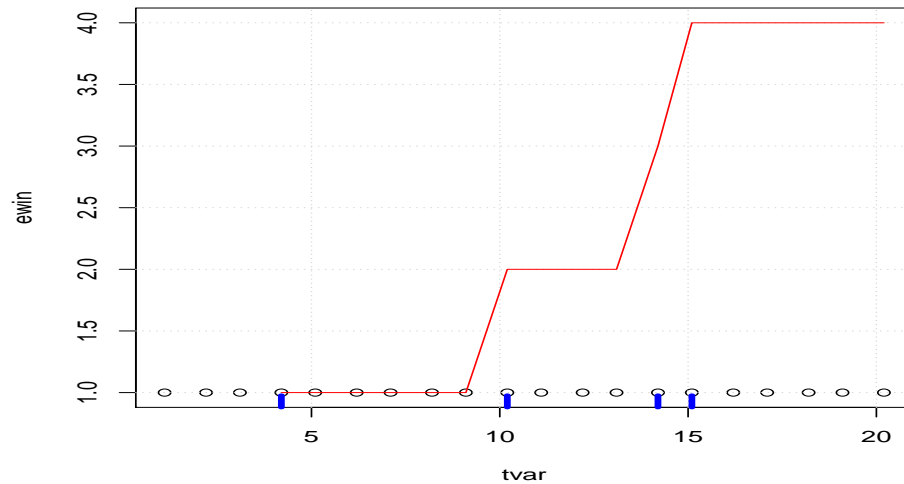
```
plot(sign.tse~tvar, data=tse, type="b")
grid()
rug(tse$tvar[tse$yvar==1], col='blue',lwd=4)
points(scale(tse$run), col=tse$run, lwd=2)
lines(abs.tse+.2~tvar, data=tse, type="b",col=3)
```



```
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

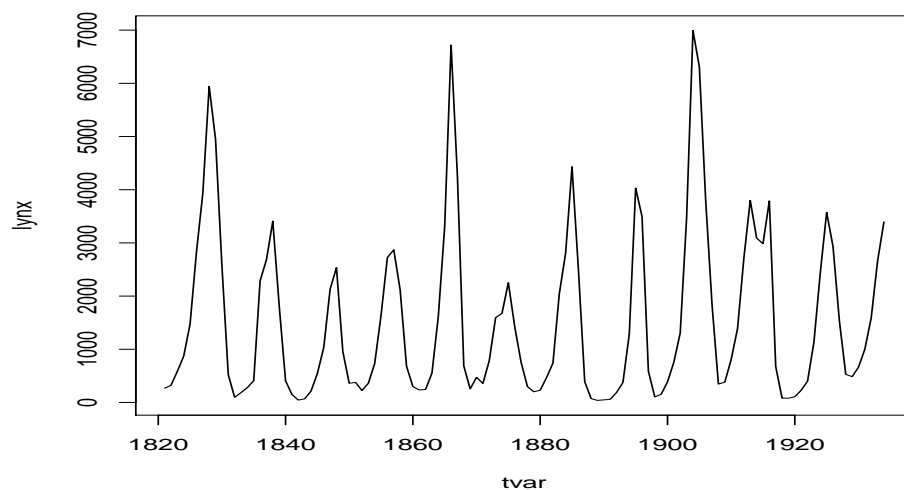
```
tse$tvar[tse$abs<=1]
```

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

5.7 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:

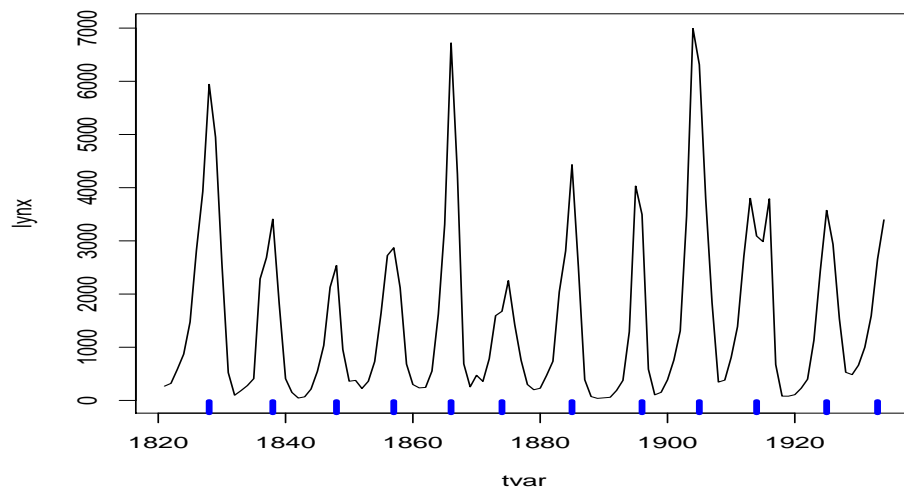
```
yyy <- lynx>mean(lynx)
head(yyy)
```

```
[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 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	2	1	0	0
9	0	1829	1	1	2	1	1	-9
10	0	1830	2	2	2	1	2	-8
11	0	1831	3	3	2	1	3	-7
12	0	1832	4	4	2	1	4	-6
13	0	1833	5	5	2	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	3	2	0	0
19	0	1839	1	1	3	2	1	-9
20	0	1840	2	2	3	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
7 10 10 9 9 8 11 11 9 9 11 8 2

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

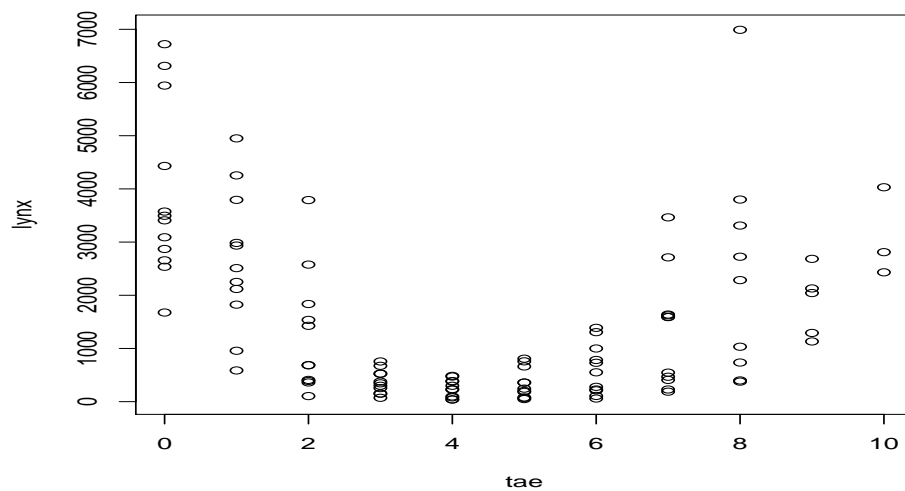
1 2 3 4 5 6 7 8 9 10 11 12
10 10 9 9 8 11 11 9 9 11 8 2

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

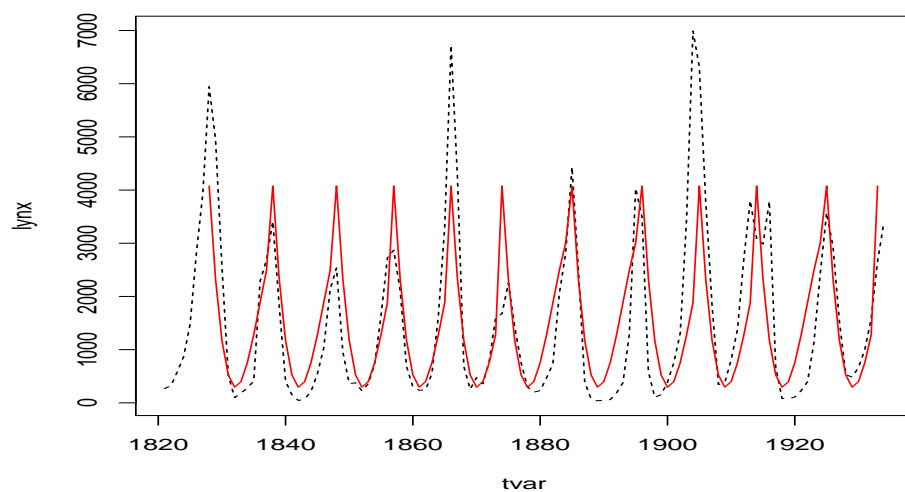
[1] 9.000 9.000 8.769 8.917
```

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')
```



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