

# Package ‘cohorttools’

December 3, 2020

**Type** Package

**Title** Cohort Data Analyses

**Version** 0.1.4

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**Depends** R (>= 3.6), Epi, cmprsk, ggplot2

**Imports** stats, survival, DiagrammeR, DiagrammeRsvg, rsvg

**Suggests** knitr, rmarkdown, lattice, mstate, testthat

**Description** Functions to make lifetables and to calculate hazard function estimate using Poisson regression model with splines. Includes function to draw simple flowchart of cohort study. Function `boxesLx()` makes boxes of transition rates between states. It utilizes 'Epi' package 'Lexis' data.

**License** GPL-2

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.1

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2020-12-03 09:20:02 UTC

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boxesLx

*Boxes plot summarizing Lexis object***Description**

Creates boxes graph describing Lexis

**Usage**

```
boxesLx(
  x,
  layout = "circo",
  prop.penwidth = FALSE,
  scale.Y = 1,
  rankdir = "TB",
  node.attr = "shape=box",
  edge.attr = "minlen=1",
  show.loop = FALSE,
  show.persons = FALSE,
  fontsizeN = 14,
  fontsizeL = 8,
  show.gr = TRUE
)
```

**Arguments**

x	Lexis object
layout	Graphviz layout "circo", "dot", "twopi" or, "neato". It determines general layout of graph.
prop.penwidth	use line width relative to incidence. If TRUE linewidths of showing transition rates between states are relative to log of rate.
scale.Y	scale for incidence. Scale factor rates, default is 1.
rankdir	for graph, default is TB. NOTE! this works best with layout "dot"
node.attr	general node attributers. Attributes like shape, color, fillcolor, etc. for nodes. Consult Graphviz documentation for details <a href="https://www.graphviz.org/doc/info/attrs.html">https://www.graphviz.org/doc/info/attrs.html</a> .
edge.attr	general edge (line) attributers. Attributes like color, arrowhead, fontcolor etc. for edges. Consult Graphviz documentation for details <a href="https://www.graphviz.org/doc/info/attrs.html">https://www.graphviz.org/doc/info/attrs.html</a>
show.loop	, should loop (staying in same state be shown), default FALSE
show.persons	, should number of persons be shown (entry->exit), default FALSE
fontsizeN	font size for nodes
fontsizeL	font size for edges
show.gr	should graph be shown. If TRUE, function DiagrammeR::grViz is used to show graph.

**Value**

Character vector containing Graphviz script. This may be used to create graph by `DiagrammeR::grViz` function.

**Author(s)**

Jari Haukka [jari.haukka@helsinki.fi](mailto:jari.haukka@helsinki.fi)

**See Also**

[grViz](#)

**Examples**

```
library(DiagrammeR)
library(survival)
library(Epi)
library(mstate)
data(ebmt3)
bmt <- Lexis(exit = list(tft = rfstime/365.25),
            exit.status = factor(rfsstat, labels = c("Tx", "RD")),
            data = ebmt3)
bmtr <- cutLexis(bmt, cut = bmt$ptime/365.25, precursor.states = "Tx",
                new.state = "PR")

summary(bmtr)
kk<-boxesLx(bmtr)
## Not run:
# Graph to file
gv2image(kk, file="k1", type="pdf")

## End(Not run)
boxesLx(bmtr,layout="dot",rankdir = "LR",show.loop = FALSE,show.persons = TRUE)
boxesLx(bmtr,node.attr='shape=hexagon color=navy style=filled fillcolor=lightblue',
edge.attr = ' color=steelblue arrowhead=vee fontcolor="#8801d7" ',
layout="circo",prop.penwidth=TRUE)
```

---

estim.hazard

*Estimates hazard function using Poisson model*

---

**Description**

Estimates hazard function using Poisson model

**Usage**

```
estim.hazard(  
  time,  
  status,  
  breaks,  
  knots,  
  time.eval = breaks,  
  alpha = 0.05,  
  ...  
)
```

**Arguments**

time	time variables
status	status indicator Lowest value used as censoring. If only one unique value detected, all are assumed events
breaks	time is splitted with these values
knots	knots for natural splines used in estimation of hazard function
time.eval	in which time points hazard function is evaluate.
alpha	significance level for confidence intervals
...	parameters for glm

**Value**

Returns data frame with time and hazard function values with attribute 'estim.hazard.param' containing estimation parameters (breaks and knots)

**Author(s)**

Jari Haukka <jari.haukka@helsinki.fi>

**Examples**

```
library(survival)  
tmp.hz<-estim.hazard(time=lung$time,status=lung$status)  
head(tmp.hz,2)  
attributes(tmp.hz)$estim.hazard.param # estimation parameters
```

---

gv2image

*Function makes image from graphviz code*

---

**Description**

Function makes image from graphviz code

**Usage**

```
gv2image(gv, file = "gv", type = "png", engine = "dot", ...)
```

**Arguments**

gv	character string containing graphviz code
file	file name for image, character string
type	type of ('pdf', 'png', 'ps', 'raw', 'svg', 'webp') as character string
engine	grViz engine, defaults is 'dot'
...	parameters for rsvg_

**Value**

Invisible name of file created.

**Author(s)**

Jari Haukka <jari.haukka@helsinki.fi>

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mkflowchart

*Function makes flowchart in graphviz*


---

**Description**

Function makes flowchart in graphviz

**Usage**

```
mkflowchart(N, text.M, text.P, type = 1)
```

**Arguments**

N	Population sizes
text.M	Text for exclusions, length one less than N
text.P	Text for main boxes, must be same length with N
type	flowchart type (1 or 2)

**Value**

Character string, graphviz language

**Author(s)**

Jari Haukka <jari.haukka@helsinki.fi>

**Examples**

```
DiagrammeR::grViz(mkflowchart(N=c(743,32,20),
text.M=c("Excluded","Excluded \n other with reasons"),
text.P=c("Studies","Relevant studies","Included in final review"),type=1))
```

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mkratetable	<i>Function makes rate table with confidence intervals for crude incidences (rates)</i>
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---

**Description**

Function makes rate table with confidence intervals for crude incidences (rates)

**Usage**

```
mkratetable(formula, data, alpha = 0.05, add.RR = FALSE, lowest.N = 0, ...)
```

**Arguments**

formula	where Surv object is on lhs and marginal variable(s) on rhs. Marginal variables should usually be factors
data	data.frame to be used
alpha	confidence level, default is 0.05
add.RR	should rate ratio (RR) be added
lowest.N	lowest frequency to be shown
...	additional parameter for function survival::pyears

**Value**

table with columns named after marginal variables and n, event, incidence, se, exact.lower95ci and exact.upper95ci variables

**Note**

packages survival is utilized. Frequencies lower than lowest.N replaced by 999999 Person-years scaled by default with 365.25

**Author(s)**

Jari Haukka <jari.haukka@helsinki.fi>

**See Also**

[survival pyears](#)

**Examples**

```
library(survival)
tmp.lt1<-mkratetable(Surv(time,status)~ sex,data=lung)
tmp.lt2<-mkratetable(Surv(time,status)~ sex+ph.ecog,data=lung,add.RR=TRUE,lowest.N=10)
```

---

plotcuminc

*Plots cumulative incidence rates*

---

**Description**

Plots cumulative incidence rates

**Usage**

```
plotcuminc(ftime, fstatus, cencode, pop.length = 50, group, ...)
```

**Arguments**

ftime	failure time variable
fstatus	variable with distinct codes for different causes of failure and also a distinct code for censored observations
cencode	value of fstatus variable which indicates the failure time is censored.
pop.length	number of population sizes shown
group	plots will be made for each group. If missing then treated as all one group
...	additional parameters

**Value**

if missing group ggplot2 object or if group given named list of ggplot2 objects

**Note**

package cmprsk and ggplot2 are utilized

**Author(s)**

Jari Haukka <jari.haukka@helsinki.fi>

**See Also**

[survival pyears](#)

**Examples**

```
set.seed(2)
ss <- rexp(100)
gg <- factor(sample(1:3,100,replace=TRUE),1:3,c('a','b','c'))
cc <- sample(0:2,100,replace=TRUE)
print(plotcuminc(ftime=ss,fstatus=cc,cencode=0))
print(plotcuminc(ftime=ss,fstatus=cc,cencode=0,group=gg))
```

---

plotratetable

*Function makes plot(s) from ratetable*

---

**Description**

Function makes plot(s) from ratetable

**Usage**

```
plotratetable(rt, RR = FALSE)
```

**Arguments**

rt	Rate table produced by function mkratetable
RR	Boolean, if TRUE rate ratios plotted

**Value**

ggplot object, or list if multiple variables in rate table

**Examples**

```
library(ggplot2)
library(survival)
tmp.lt1<-mkratetable(Surv(time,status)~ ph.ecog,data=lung,add.RR = FALSE)
plotratetable(tmp.lt1)
tmp.lt2<-mkratetable(Surv(time,status)~ sex+ph.ecog+cut(age,4),data=lung,add.RR=TRUE,lowest.N=1)
plotratetable(tmp.lt2,TRUE)
```



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