

Package: elect (via r-universe)

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Type Package

Title Estimation of Life Expectancies Using Multi-State Models

Version 1.2

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Description Functions to compute state-specific and marginal life expectancies. The computation is based on a fitted continuous-time multi-state model that includes an absorbing death state; see Van den Hout (2017, ISBN:9781466568402). The fitted multi-state model should be estimated using the 'msm' package using age as the time-scale.

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check.RestrAndConst *Checking the definition of RestrAndConst in elect*

Description

Function to check the definition of RestrAndConst in the elect call.

Usage

```
check.RestrAndConst(x, RestrAndConst, PRINT = FALSE)
```

Arguments

| | |
|---------------|---|
| x | Fitted msm model |
| RestrAndConst | Vector which indexes the independent parameters in model\ \$opt\ \$par w.r.t. to the model parameters |
| PRINT | TRUE for printing the comparison |

Details

Function to help defining the parameter constraints in the elect call\ when the constraint option is used in msm.

Value

TRUE when RestrAndConst is well-defined, FALSE otherwise.

Author(s)

Ardo van den Hout

See Also

[elect](#)

Examples

```
# Fit model with constraints:
Q      <- rbind(c(0,0.01,0.01), c(0,0,0.01), c(0,0,0))
model <- msm(state~age, subject = id, data = electData,
             center = FALSE, qmatrix = Q, deathexact = TRUE,
             fixedpars = c(7,8), covariates = ~age+x)
RestrAndConst <- c(1:6,0,0,7)
check.RestrAndConst(model, RestrAndConst, PRINT= TRUE)

# Usage: elect(x = model, ..., RestrAndConst = RestrAndConst)
```

elect *State-specific and marginal life expectancies*

Description

Estimation of state-specific and marginal life expectancies given a multi-state survival model fitted using the `msm`-package

Usage

```
elect(x, b.covariates, statedistdata, time.scale.msm = "years",
      h, age.max, S = 0, setseed = NULL, RestrAndConst = NULL,
      statedist.covariates = "age", method = "step")
```

Arguments

| | |
|-----------------------------------|---|
| <code>x</code> | Fitted <code>msm</code> model |
| <code>b.covariates</code> | List with specified covariates values (ignore intercept) |
| <code>statedistdata</code> | Data used to estimate prevalence distribution of living states |
| <code>time.scale.msm</code> | Time scale in multi-state model: "years", "months", "weeks", or a value in (0,1] |
| <code>h</code> | Grid parameter for integration where scale is <code>time.scale.msm</code> |
| <code>age.max</code> | Assumed maximum age in same time scale as in fitted model |
| <code>S</code> | Number of replications for estimation of uncertainty ($S=0$ for no estimation) |
| <code>setseed</code> | Seed for the random number generation in the simulation |
| <code>RestrAndConst</code> | Vector which indexes the independent model parameters. Only needed when constraint is used in <code>msm</code> call |
| <code>statedist.covariates</code> | Names of covariates for model for prevalence distribution of living states |
| <code>method</code> | Approximation of integral: "step" for simple step function, "MiddleRiemann" or "Simpson" |

Details

The `elect`-package is an add-on to the `msm`-package for models with one death state. In the `msm` call for fitting the model use `center=FALSE`, and names `state` and `age`. Do not use variables encoded as factor by R. Covariate `age` should be the first entry in `b.covariates`. The other covariates in `b.covariates` should follow the order in the `msm` call. The life expectancies are computed by approximating the integral numerically with a grid defined by `h`. The specification of `statedist.covariates` should be a subset of `b.covariates`.

Value

A list containing the following components:

| | |
|----------|---|
| pnt | Life expectancies derived from MLE of model parameters |
| sim | Simulated life expectancies using the MLE of model parameters |
| h | As specified in <code>elect</code> call |
| covars | Covariates as specified in <code>elect</code> call |
| S | S as specified in <code>elect</code> call |
| sd.model | Fitted model for the prevalence distribution of living states |

Author(s)

Ardo van den Hout and Mei Sum Chan

References

Jackson, C.H. (2011). Multi-State Models for Panel Data: The `msm` Package for R., *Journal of Statistical Software*, 38(8), 1-29.

Van den Hout, A. (2017). *Multi-State Survival Models for Interval-Censored Data*. Boca Raton: CRC/Chapman & Hall.

See Also

[summary.elect](#), [plot.elect](#)

Examples

```
# Fit msm model:
Q      <- rbind(c(0,0.01,0.01), c(0,0,0.01), c(0,0,0))
model <- msm(state~age, subject = id, data = electData,
             center = FALSE, qmatrix = Q, deathexact = TRUE,
             covariates = ~age+x)

# Estimate life expectancies:
sddata <- electData[electData$bsline == 1,]
LEs    <- elect(x = model, b.covariates = list(age = 0, x = 0),
              statedistdata = sddata, h = 0.5, age.max = 50, S = 25)
summary(LEs)
plot(LEs)    # For smoother graphs, increase S
```

| | |
|-----------|---|
| electData | <i>Three-state data for exploring elect</i> |
|-----------|---|

Description

Simulated longitudinal data for a three-state illness-death process.

Usage

```
electData
```

Format

Data frame with 764 rows, grouped by 150 individuals. Simulated interval-censored transition times for living states 1 and 2, and exact times for death state 3. Variables: `id` = identification number, `state` = state, `age` = age in years on a shifted scale (current age minus 70), `x` = binary time-independent covariate (can be interpreted as 0/1 for women/men), `bsline` = baseline record indicator.

Author(s)

Ardo van den Hout

See Also

[elect](#)

Examples

```
# Sample size:
print(length(unique(electData$id)))
# Frequencies number of observation per individual:
print(table(table(electData$id)))
# State table
print(statetable.msm(state, id, data = electData))
```

| | |
|---------|---|
| explore | <i>Data statistics for an age-dependent model</i> |
|---------|---|

Description

Data statistics that are important for fitting an age-dependent multi-state model. Basic summaries and additional information on the age distribution in the data

Usage

```
explore(data = NULL, id = NULL, state = NULL, age = NULL,
        digits = 3, HIST = TRUE, hist.col = c("green", "red",
        "blue"), INFO = FALSE)
```

Arguments

| | |
|-----------------------|---|
| <code>data</code> | Data frame with variables <code>id</code> , <code>state</code> , and <code>age</code> |
| <code>id</code> | Identifier. Specify if data is not provided |
| <code>state</code> | State variable. Specify if data is not provided |
| <code>age</code> | Age or transformed age. Specify if data is not provided |
| <code>digits</code> | Number of digits in the output |
| <code>HIST</code> | TRUE for histograms of the age distribution. FALSE otherwise |
| <code>hist.col</code> | Colours for the three histograms of the age distribution |
| <code>INFO</code> | TRUE for returning a list which links <code>id</code> with time intervals between the subsequent records. FALSE otherwise |

Value

| | |
|------------------------|---|
| <code>intervals</code> | Data frame with variables <code>interval.length</code> and corresponding <code>id</code> (when <code>INFO = TRUE</code>) |
|------------------------|---|

Author(s)

Ardo van den Hout. With thanks to Ying Lou.

Examples

```
explore(electData)
```

| | |
|---------|---|
| hazards | <i>Age-dependent hazards based on a 'msm' model</i> |
|---------|---|

Description

Graph with transition-specific hazard functions derived from an age-dependent model fitted using 'msm'

Usage

```
hazards(x, b.covariates, no.years, trans = NULL,
        max.haz = .5, min.haz = 0, CI = FALSE, col = NULL,
        lty = NULL, lwd = NULL, LEGEND = TRUE,
        location = "topleft", age.shift = 0)
```

Arguments

| | |
|---------------------------|--|
| <code>x</code> | Fitted msm model with age as the Gompertz time scale |
| <code>b.covariates</code> | List with specified covariates values for the prediction (ignore intercept) |
| <code>no.years</code> | Number of years for the prediction |
| <code>trans</code> | Matrix with rows (r,s) for hazard of going from state r to state s. Default to all (r,s)-hazards that are modelled in <code>x</code> |
| <code>max.haz</code> | Upperbound hazard-axis |
| <code>min.haz</code> | Lowerbound hazard-axis |
| <code>CI</code> | TRUE for plotting 95% confidence bands. FALSE otherwise |
| <code>col</code> | Colour for each hazard curve. Example for two curves: <code>col = c("red", "green")</code> |
| <code>lty</code> | Line type for each hazard curve. Example for two curves: <code>lty = c(1, 2)</code> |
| <code>lwd</code> | Width of line for each hazard curve. Example for two curves: <code>lwd = c(2, 2)</code> |
| <code>LEGEND</code> | TRUE for adding a legend. FALSE otherwise |
| <code>location</code> | Location for legend. Default to "topleft". See help file for legend for further details |
| <code>age.shift</code> | Value to shift the age scale in the graph. Useful when age in the model is on a shifted scale. Default to 0. |

Details

This function is an add-on to the functionality in the 'msm' package. A Gompertz model with age as the time scale can be fitted in 'msm' piecewise-constantly by adding age as a covariate. The function `qmatrix.msm` is used by `hazards` repeatedly to take into account the age dependence when calculating the hazards.

Author(s)

Ardo van den Hout. With thanks to Ying Lou.

References

Jackson, C.H. (2011). Multi-State Models for Panel Data: The msm Package for R., *Journal of Statistical Software*, 38(8), 1-29.

Examples

```
# Fit msm model:
Q <- rbind(c(0,0.01,0.01), c(0,0,0.01), c(0,0,0))
model <- msm(state~age, subject = id, data = electData,
             center = FALSE, qmatrix = Q, deathexact = TRUE,
             covariates = ~age+x)
# Plot hazards on original age scale:
hazards(model, b.covariates = list(age = 0, x = 0),
         no.years = 20, max.haz = 0.25, age.shift = -70)
```

`plot.elect`*Plotting of life expectancies*

Description

Graphical representation by smoothed densities of the life expectancies as estimated by `elect`

Usage

```
## S3 method for class 'elect'  
plot(x, which = NULL, kernel = "gaussian", col = "red", lwd = 2, cex.lab = 1, ...)
```

Arguments

| | |
|----------------------|---|
| <code>x</code> | Life expectancies estimated by <code>elect</code> |
| <code>which</code> | Subselection for plotting (following the order in <code>summary</code>). Example: <code>which = c(1,3,5)</code> |
| <code>kernel</code> | Character string for smoothing kernel ("gaussian", "rectangular", "triangular", "epanechnikov", "biweight", "cosine", or "optcosine") |
| <code>col</code> | Colour of curves |
| <code>lwd</code> | Line width of curves |
| <code>cex.lab</code> | Magnification to be used for axis-labels |
| <code>...</code> | Other arguments (not yet implemented) |

Details

Presents distributions of the estimated life expectancies derived from the maximum likelihood estimate of the model parameters. The smoothing is undertaken using the R function `density`.

Author(s)

Ardo van den Hout

See Also

[elect](#)

`plusmin`*Computation of a function of life expectancies*

Description

Compute an additive function of a series of estimated life expectancies

Usage

```
plusmin(x, index = NA, func = "plus", probs = c(0.025, 0.5, 0.975), digits = 3)
```

Arguments

| | |
|---------------------|---|
| <code>x</code> | Life expectancies estimated by <code>elect</code> |
| <code>index</code> | Selection of the life expectancies in the function (following the order in summary) |
| <code>func</code> | Required series of "plus" and "minus". Example: <code>func = c("plus", "plus")</code> |
| <code>probs</code> | Probabilities for the quantiles |
| <code>digits</code> | Number of digits in the output |

Details

This function requires that uncertainty of LEs is estimated; that is, `S` is not 0.

Author(s)

Ardo van den Hout

See Also

[elect](#)

Examples

```
# Fit msm model:
Q      <- rbind(c(0,0.01,0.01), c(0,0,0.01), c(0,0,0))
model <- msm(state~age, subject = id, data = electData,
             center = FALSE, qmatrix = Q, deathexact = TRUE,
             covariates = ~age+x)

# Estimate function of life expectancies:
sddata <- electData[electData$bsline == 1,]
LEs    <- elect(x = model, b.covariates = list(age = 0, x = 1),
               statedistdata = sddata, h = 0.5, age.max = 50, S = 25)
plusmin(LEs, index = c(2,4), func = "plus")
```

| | |
|---------------|---|
| summary.elect | <i>Summarises the estimation of the life expectancies</i> |
|---------------|---|

Description

Summary of estimated state-specific and marginal life expectancies

Usage

```
## S3 method for class 'elect'  
summary(object, probs = c(0.025, 0.5, 0.975),  
        digits = 3, StartStateTotals = FALSE,  
        print = TRUE, sd.model = FALSE,...)
```

Arguments

| | |
|------------------|--|
| object | Life expectancies estimated by elect |
| probs | Numeric vector of probabilities with values in [0,1] for quantiles |
| digits | Number of decimal places in output |
| StartStateTotals | TRUE for output on start-state totals e_r. (for S>0) |
| print | TRUE for printing output to screen, FALSE otherwise |
| sd.model | TRUE for printing a summary of the fitted model for the prevalence |
| ... | Other arguments (not yet implemented) |

Details

A summary for the state-specific and marginal life expectancies as derived in elect. Quantiles are derived from simulation based on the maximum likelihood estimation.

Author(s)

Ardo van den Hout

See Also

[elect](#), [plusmin](#), [plot.elect](#)

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