Package ‘vitality’

March 19, 2016

Title Fitting Routines for the Vitality Family of Mortality Models
Version 1.2
Date 2016-03-15
Author Gregor Passolt, James J. Anderson, Ting Li, David H. Salinger, David J. Sharrow
Maintainer David J. Sharrow <dsharrow@uw.edu>
Depends stats
Description Provides fitting routines for four versions of the Vitality family of mortality models.
License GPL (>= 2)
Collate 'dataPrep.R' 'vitality.4p.R' 'vitality.6p.R' 'vitality.k.R'
    'vitality.ku.R' 'vitality.utils.R' 'data_documentation.R'
    'density.R' 'mortality_rate.R' 'package_documentation.R'
NeedsCompilation no
Repository CRAN
Date/Publication 2016-03-19 09:35:55

R topics documented:

daphnia ......................................................... 2
dataPrep ......................................................... 3
ft.4p ............................................................. 4
ft.6p ............................................................. 4
indexFinder ..................................................... 5
logLikelihood.4p ................................................. 5
logLikelihood.6p ................................................. 6
logLikelihood.k ............................................... 7
logLikelihood.ku ............................................... 7
mu.vd.4p ......................................................... 8
mu.vd.6p ......................................................... 9
mu.vd1.4p ....................................................... 9
mu.vd1.6p ....................................................... 10
mu.vd2.4p ....................................................... 11
Sample Daphnia Data

Description

Sample survival data for daphnia. Columns include "days" and "lx" (cumulative survival proportion by day).

Format

data frame
dataPrep

Source

http://cbr.washington.edu/analysis/vitality

Anderson, J.J. (2000). "A vitality-based model relating stressors and environmental properties to organism survival." Ecological Monographs 70(3):445-470 (Figure 5)

dataPrep Function for data preparation

Description

Function to deal with NAs, right truncated data, and datatype (i.e. cumulative survival or incremental mortality).

Usage

dataPrep(time, sdata, datatype, rc.data, returnMatrix = FALSE)

Arguments

<table>
<thead>
<tr>
<th>time</th>
<th>A vector of observation dates</th>
</tr>
</thead>
<tbody>
<tr>
<td>sdata</td>
<td>A vector of survival data of the same length as time</td>
</tr>
<tr>
<td>datatype</td>
<td>either &quot;CUM&quot; for cumulative or &quot;INC&quot; for incremental</td>
</tr>
<tr>
<td>rc.data</td>
<td>Boolean. Is data right-censored?</td>
</tr>
<tr>
<td>returnMatrix</td>
<td>Boolean. False returns a data frame, true returns a matrix. (as in the original), if &quot;matrix&quot; returns a matrix instead, with the &quot;rc.data&quot; column being 0 for FALSE, 1 for TRUE, or 2 for TF</td>
</tr>
</tbody>
</table>

Details

This function is designed for use in the primary vitality model fitting functions in this package. See package documentation.

Value

Returns a data.frame or matrix with columns time, sfract, x1, x2, Ni (incremental survival fraction), rc.data.
ft.4p  

*Density function for 3-parameter (r, s, u)*

**Description**

This function is used in the calculation of the fitted intrinsic \((\mu.vd.4p)\) and total \((\mu.vd.4p)\) mortality rate in the 4-parameter model.

**Usage**

\[
ft.4p(xx, r, s, u)
\]

**Arguments**

- **xx**: age
- **r**: r value
- **s**: s value
- **u**: u value

**Value**

density

**See Also**

`vft.4p, ft.6p`

---

ft.6p  

*Density function for 2-parameters (r, s)*

**Description**

This function is used in the calculation of the fitted intrinsic \((\mu.vd.1.6p)\) and total \((\mu.vd.6p)\) mortality rate in the 6-parameter model.

**Usage**

\[
ft.6p(xx, r, s)
\]

**Arguments**

- **xx**: age
- **r**: r value
- **s**: s value
indexFinder

Value
density

See Also
vft.6p

indexFinder  Finds the first value of a vector that is less than a value.

Description
For use in the primary vitality model fitting functions in this package. See package documentation.

Usage
indexFinder(x, val)

Arguments

- x  Vector to search
- val Threshold

Value
Gives the index of the first value of x that is <= val. returns -1 if no value satisfies the condition

logLikelihood.4p  Log likelihood of 2-process 4-parameter model

Description
Gives the log likelihood of 2-process 6 parameter vitality model.

Usage
logLikelihood.4p(par, xx1, xx2, NNi)

Arguments

- par  vector of parameter(r, s, lambda, beta)
- xx1 xx1 vector
- xx2 xx2 vector
- NNi survival fractions
Details
For use in vitality.4p.

Value
log likelihood

See Also
loglikelihoodN6p

logLikelihood.6p

Log likelihood of 2-process 6-parameter vitality model

Description
Gives the log likelihood of 6-parameter vitality model.

Usage
logLikelihood.6p(par, xx1, xx2, NNi)

Arguments
par vector of parameters (r, s, lambda, beta, alpha, gamma)
xx1 xx1 vector
xx2 xx2 vector
NNi survival fractions

Details
For use in vitality.6p.

Value
log likelihood

See Also
vitality.6p
Description

Gives the log likelihood of 3-parameter vitality model.

Usage

logLikelihood.k(par, xx1, xx2, NNi)

Arguments

par  vector of parameters (r, s, k)
xx1  xx1 vector
xx2  xx2 vector
NNi  survival fractions

Details

For use in vitality.k.

Value

log likelihood

See Also

vitality.k

Description

Gives the log likelihood of 4-parameter vitality model.

Usage

logLikelihood.ku(par, xx1, xx2, NNi)
Arguments

par vector of parameters (r, s, k, u)
xx1 xx1 vector
xx2 xx2 vector
NNi survival fractions

Details

For use in vitality.ku.

Value

log likelihood

See Also

vitality.ku

mu.vd.4p

Total mortality rate for the 2-process 4-parameter vitality model

Description

Gives the total age-specific mortality rates for a given set of the four parameters. See mu.vd1.4p for calculation of intrinsic age-specific mortality rates. See mu.vd2.4p for calculation of extrinsic age-specific mortality rates.

Usage

mu.vd.4p(t, r, s, lambda, beta)

Arguments

t age
r r value
s s value
lambda lambda value
beta beta value

Value

Total age-specific mortality rates

See Also

mu.vd1.4p, mu.vd2.4p
**mu.vd.6p**

*Total mortality rate for the 2-process 6-parameter vitality model*

**Description**

Gives the total age-specific mortality rates for a given set of the six parameters. See `mu.vd1.6p` for calculation of intrinsic age-specific mortality rates. See `mu.vd2.6p` for calculation of extrinsic age-specific mortality rates.

**Usage**

```r
mu.vd.6p(t, r, s, lambda, beta, gamma, alpha)
```

**Arguments**

- `t`: age
- `r`: r value
- `s`: s value
- `lambda`: lambda value
- `beta`: beta value
- `gamma`: gamma value
- `alpha`: alpha value

**Value**

Total age-specific mortality rates

**See Also**

`mu.vd1.6p`, `mu.vd2.6p`

---

**mu.vd1.4p**

*Intrinsic mortality rate for the 2-process 4-parameter vitality model*

**Description**

Gives the intrinsic age-specific mortality rates for a given set of r and s, the intrinsic parameters.

**Usage**

```r
mu.vd1.4p(x, r, s)
```
**Arguments**

- `x`: age
- `r`: r value
- `s`: s value

**Value**

Intrinsic age-specific mortality rates

**See Also**

`mu.vd.4p`, `mu.vd2.4p`

---

**mu.vd1.6p**

*Intrinsic mortality rate for the 2-process 6-parameter vitality model*

**Description**

Gives the intrinsic age-specific mortality rates for a given set of `r` and `s`, the intrinsic parameters.

**Usage**

```r
mu.vd1.6p(x, r, s)
```

**Arguments**

- `x`: age
- `r`: r value
- `s`: s value

**Value**

Vector of intrinsic age-specific mortality rates at age `x`

**See Also**

`mu.vd.6p`, `mu.vd2.6p`
\textit{mu.vd2.4p} \hfill \textit{Extrinsic mortality rate for the 2-process 4-parameter vitality model}

\textbf{Description}

Gives the extrinsic age-specific mortality rates for a given set of $r$ and the extrinsic parameters.

\textbf{Usage}

\texttt{mu.vd2.4p(x, r, lambda, beta)}

\textbf{Arguments}

- \texttt{x} \quad \text{age}
- \texttt{r} \quad \text{r value}
- \texttt{lambda} \quad \text{lambda value}
- \texttt{beta} \quad \text{beta value}

\textbf{Value}

Extrinsic age-specific mortality rates

\textbf{See Also}

\texttt{mu.vd.4p, mu.vd1.4p}

\textit{mu.vd2.6p} \hfill \textit{Extrinsic mortality rate for the 2-process 6-parameter vitality model}

\textbf{Description}

Gives the extrinsic age-specific mortality rates for a given set of $r$ and the extrinsic parameters.

\textbf{Usage}

\texttt{mu.vd2.6p(x, r, lambda, beta, gamma, alpha)}

\textbf{Arguments}

- \texttt{x} \quad \text{age}
- \texttt{r} \quad \text{r value}
- \texttt{lambda} \quad \text{lambda value}
- \texttt{beta} \quad \text{beta value}
- \texttt{gamma} \quad \text{gamma value}
- \texttt{alpha} \quad \text{alpha value}
Value

Vector of extrinsic age-specific mortality rates at ages $x$

See Also

$\text{mu.vd.6p, mu.vd1.6p, mu.vd3.6p, mu.vd4.6p}$

---

**mu.vd3.6p**

Adult extrinsic mortality rate for the 2-process 6-parameter vitality model

Description

Gives the extrinsic age-specific mortality rates for a given set of $r$ and the adult extrinsic parameters.

Usage

$\text{mu.vd3.6p}(x, r, \lambda, \beta)$

Arguments

- $x$: age
- $r$: $r$ value
- $\lambda$: lambda value
- $\beta$: beta value

Value

Vector of adult extrinsic age-specific mortality rates at ages $x$

See Also

$\text{mu.vd.6p, mu.vd1.6p, mu.vd2.6p, mu.vd4.6p}$
Description

Gives the childhood extrinsic age-specific mortality rates for a given set of the childhood extrinsic parameters.

Usage

mu.vd4.6p(x, gamma, alpha)

Arguments

x age
gamma gamma value
alpha alpha value

Value

Vector of childhood extrinsic age-specific mortality rates at ages x

See Also

mu.vd.6p, mu.vd1.6p, mu.vd2.6p, mu.vd3.6p

plotting.4p

Plotting function for 2-process 4-parameter vitality model

Description

This function plots the estimated results from the 4 parameter vitality model. It is used within the function vitality.4p.

Usage

plotting.4p(r.final, s.final, lambda.final, beta.final, mlv, time, sfract, x1, x2, N, ppplot, Iplot, Mplot, tlab, rc.data)
Arguments

- `r.final` : r estimate
- `s.final` : s estimate
- `lambda.final` : lambda estimate
- `beta.final` : beta estimate
- `mlv` : TODO mlv
- `time` : time vector
- `sfrac` : survival fraction
- `x1` : Time 1
- `x2` : Time 2
- `Ni` : Initial population
- `pplot` : Boolean. Plot cumulative survival fraction?
- `iplot` : Boolean. Plot incremental survival?
- `mplot` : Boolean. Plot mortality rate? Note: plotted mortality data is derived from survival data and is approximate
- `tlab` : Character, label for time axis
- `rc.data` : Boolean, right-censored data?

Details

See `vitality.4p` for further description of function arguments.

Only one of `iplot` or `mplot` should be set to TRUE at once.

See Also

`vitality.4p`, `mu.vd.4p`, `mu.vd1.4p`, `mu.vd2.4p`

plotting.6p  Plotting function for 2-process 6-parameter vitality model

Description

This function plots the estimated results from the 6 parameter vitality model. It is used within the function `vitality.6p`.

Usage

`plotting.6p(r.final, s.final, lambda.final, beta.final, gamma.final, alpha.final, mlv, time, sfrac, x1, x2, Ni, pplot, Iplot, Mplot, tlab, rc.data)`
plotting.k

Arguments

- r.final: r estimate
- s.final: s estimate
- lambda.final: lambda estimate
- beta.final: beta estimate
- gamma.final: gamma estimate
- alpha.final: alpha estimate
- mlv: TODO mlv
- time: time vector giving the ages at which calculate the estimated value
- sfract: observed survival fraction
- x1: Time 1
- x2: Time 2
- Ni: Initial population
- pplot: Boolean. Plot cumulative survival fraction?
- lplot: Boolean. Plot incremental survival?
- mplot: Boolean. Plot mortality rate? Note: plotted mortality data is derived from survival data and is approximate
- tlab: Character, label for time axis
- rc.data: Boolean, right-censored data?

Details

See vitality.6p for further description of function arguments.
Only one of lplot or mplot should be set to TRUE at once.

See Also

vitality.6p, mu.vd.6p, mu.vd1.6p, mu.vd2.6p, mu.vd3.6p, mu.vd4.6p

plotting.k  Plotting function for 3-parameter vitality model

Description

This function plots the estimated results from the 3 parameter vitality model. It is used within the function vitality.k.

Usage

plotting.k(r.final, s.final, k.final, mlv, time, sfract, x1, x2, Ni, pplot, tlab, lplot, cplot, lplot, gfit, rc.data)
Arguments

- `r.final`: r estimate
- `s.final`: s estimate
- `k.final`: k estimate
- `mlv`: TODO mlv
- `time`: time vector giving the ages at which calculate the estimated value
- `sfrac`: observed survival fraction
- `x1`: Time 1
- `x2`: Time 2
- `Ni`: Initial population
- `pplot`: Boolean. Plot cumulative survival fraction?
- `iplot`: Boolean. Plot incremental survival?
- `lplot`: Boolean. Plot likelihood functions? Provides likelihood function plotting. Defaults to FALSE. Note: these plots are not "likelihood profiles" in that while one parameter is varied, the others are held fixed, rather than re-optimized. (must also have `pplot=T`.)
- `cplot`: Boolean. Plot likelihood contour plot? Provides a likelihood contour plot for a range of r and s values (can be slow so default is FALSE). Must also have `lplot=T` and `pplot=T` to get contour plots.
- `tlab`: Character, label for time axis. Defaults to "days".
- `gfit`: Provides a Pearson C type test for goodness of fit. Default is FALSE. Must provide the initial study population to compute goodness of fit.
- `rc.data`: Boolean, right-censored data?

Details

See `vitality.k` for further description of function arguments.

See Also

- `vitality.k`

plotting.ku  Plotting function for 4-parameter vitality model

Description

This function plots the estimated results from the 4 parameter vitality model. It is used within the function `vitality.k`. 
plotting.ku

Usage

plotting.ku(r.final, s.final, k.final, u.final, mlv, time, sfract, x1, x2, Ni,
pplot, tlab, lplot, cplot, Iplot, gfit)

Arguments

r.final  r estimate
s.final  s estimate
k.final  k estimate
u.final  u estimate
mlv      TODO mlv
time     time vector giving the ages at which calculate the estimated value
sfract   observed survival fraction
x1       Time 1
x2       Time 2
Ni       Initial population
pplot    Boolean. Plot cumulative survival fraction?
lplot    Boolean. Plot likelihood functions? Provides likelihood function plotting. De-
        faults to FALSE. Note: these plots are not "likelihood profiles" in that while one
         parameter is varied, the others are held fixed, rather than re-optimized. (must
         also have pplot=T.)
cplot    Boolean. Plot likelihood contour plot? Provides a likelihood contour plot for
         a range of r and s values (can be slow so default is FALSE). Must also have
         lplot=T and pplot=T to get contour plots.
tlab     Character, label for time axis. Defaults to "days".
gfit     Provides a Pearson C type test for goodness of fit. Default is FALSE. Must pro-
         vide the initial study population to compute goodness of fit.

Details

See vitality.ku for further description of function arguments.

See Also

vitality.ku
Sample Rainbow Trout Data

Description
Sample survival data for rainbow trout. Columns include "days" and "survival" (cumulative survival proportion by day).

Format
matrix

Source
http://cbr.washington.edu/analysis/vitality

stdErr.4p

Standard errors for 4-parameters: r, s, lambda, beta

Description
Gives the standard errors for the 4 parameter model. Primarily used within vitality.4p.

Usage
stdErr.4p(r, s, k, u, x1, x2, Ni, pop)

Arguments
- r: r value
- s: s value
- k: lambda value
- u: beta value
- x1: age 1 (corresponding 1:(t-1) and 2:t)
- x2: age 2
- Ni: survival fraction
- pop: initial population (total population of the study)

Value
standard error for r, s, lambda, beta
stdErr.6p

Note
if k <= 0, cannot find standard error for k

See Also
vitality.4p

---

stdErr.6p

| stdErr.6p |
| Standard errors for 6-parameters: r, s, lambda, beta, gamma, alpha |

Description
Gives the standard errors for the 6 parameter model. Primarily used within vitality.6p.

Usage
stdErr.6p(r, s, k, u, g, a, x1, x2, Ni, pop)

Arguments
- r: r value
- s: s value
- k: lambda value
- u: beta value
- g: gamma value
- a: alpha value
- x1: age 1 (corresponding 1:(t-1))
- x2: age 2 (corresponding 2:t)
- Ni: age-specific survival fractions
- pop: initial population (total population of the study)

Value
standard error for r, s, lambda, beta, gamma, and alpha.

Note
if k <= 0, cannot find standard error for k

See Also
vitality.6p
**stdErr.k**

*Standard errors for 3-parameters: r, s, k*

**Description**

Gives the standard errors for the 3 parameter model. Primarily used within `vitality.k`.

**Usage**

```
stdErr.k(r, s, k, x1, x2, Ni, pop)
```

**Arguments**

- **r**: r value
- **s**: s value
- **k**: k value
- **x1**: age 1 (corresponding 1:(t-1))
- **x2**: age 2 (corresponding 2:t)
- **Ni**: age-specific survival fractions
- **pop**: initial population (total population of the study)

**Value**

standard error for r, s, k.

**Note**

k is restricted to be >0.

**See Also**

`vitality.k`

---

**stdErr.ku**

*Standard errors for 4-parameters: r, s, k, u*

**Description**

Gives the standard errors for the 4 parameter model. Primarily used within `vitality.k`.

**Usage**

```
stdErr.ku(r, s, k, u, x1, x2, Ni, pop)
```

---
SurvFn.4p

Arguments

- \( r \)  
  r value
- \( s \)  
  s value
- \( k \)  
  k value
- \( u \)  
  u value
- \( x_1 \)  
  age 1 (corresponding \( 1:(t-1) \))
- \( x_2 \)  
  age 2 (corresponding \( 2:t \))
- \( N_i \)  
  age-specific survival fractions
- \( \text{pop} \)  
  initial population (total population of the study)

Value

standard error for \( r, s, k, u \).

Note

\( k \) is restricted to be \( >0 \).

See Also

vitality.ku

---

The cumulative survival distribution function for 2-process 4-parameter vitality model

Description

Gives the cumulative survival proportions at \( xx \) from all processes for a given set of parameter values.

Usage

\[ \text{SurvFn.4p}(xx, r, s, \text{lambda}, \beta) \]

Arguments

- \( xx \)  
  vector of ages
- \( r \)  
  r value
- \( s \)  
  s value
- \( \text{lambda} \)  
  lambda value
- \( \beta \)  
  beta value
Details

Used within vitality.4p for estimating model parameters based on the observed cumulative survival function.

Value

vector of cumulative survival proportions at xx from all processes

See Also

vitality.4p, survProbInc.4p, SurvFn.in.4p, SurvFn.ex.4p

SurvFn.6p

The cumulative survival distribution function for 2-process 6-parameter vitality model

Description

Gives the cumulative survival proportions at xx from all processes for a given set of parameter values.

Usage

SurvFn.6p(xx, r, s, lambda, beta, gamma, alpha)

Arguments

xx vector of ages
r r value
s s value
lambda lambda value
beta beta value
gamma gamma value
alpha alpha value

Details

Used within vitality.6p for estimating model parameters based on the observed cumulative survival function.

Value

vector of cumulative survival proportions at xx from all processes

See Also

vitality.6p, survProbInc.6p, SurvFn.in.6p, SurvFn.ex.6p
The extrinsic cumulative survival distribution function for 2-process 6-parameter vitality model

| Description | Gives the cumulative survival proportions at xx from extrinsic processes for a given set of parameter values. |
| Usage | `SurvFn.ex.4p(xx, r, s, lambda, beta)` |
| Arguments | | |
| xx | vector of ages |
| r | r value |
| s | s value |
| lambda | lambda value |
| beta | beta value |
| Details | Used within `vitality.4p` for estimating model parameters based on the observed cumulative survival function. |
| Value | vector of cumulative survival proportions at xx from extrinsic process |
| See Also | `vitality.4p`, `survProbInc.4p`, `SurvFn.4p`, `SurvFni.4p` |

The extrinsic cumulative survival distribution function for 2-process 6-parameter vitality model

| Description | Gives the cumulative survival proportions at xx from the extrinsic processes for a given set of parameter values. |
Usage

SurvFn.ex.6p(xx, r, s, lambda, beta, gamma, alpha)

Arguments

xx  vector of ages
r   r value
s   s value
lambda  lambda value
beta  beta value
gamma  gamma value
alpha  alpha value

Details

Used within vitality.6p for estimating model parameters based on the observed cumulative survival function.

Value

vector cumulative survival proportions at xx from extrinsic processes

See Also

vitality.6p, survProbInc.6p, SurvFn.6p

SurvFn.h.4p

Intrinsic cumulative survival distribution for 4 parameter model

Description

Gives the intrinsic cumulative survival distribution at xx.

Usage

SurvFn.h.4p(xx, r, s, u)

Arguments

xx  vector of ages
r   r value
s   s value
u   u value
Details
  For use in vitality.4p.

Value
  intrinsic cumulative survival distribution

See Also
  vitality.4p

Description
  Gives the intrinsic cumulative survival distribution at xx.

Usage
  SurvFn.h.6p(xx, r, s)

Arguments
  xx  vector of ages
  r   r value
  s   s value

Details
  For use in vitality.6p.

Value
  intrinsic cumulative survival distribution

See Also
  vitality.6p
SurvFn.in.4p  The intrinsic cumulative survival distribution function for 2-process 4-parameter vitality model

Description
Gives the cumulative survival proportions at xx from intrinsic process for a given set of parameter values.

Usage
SurvFn.in.4p(xx, r, s)

Arguments
- xx: vector of ages
- r: r value
- s: s value

Details
Used within vitality.4p for estimating model parameters based on the observed cumulative survival function.

Value
vector of cumulative survival proportions at xx from intrinsic process

See Also
vitality.4p, survProbInc.4p, SurvFn.4p, SurvFn.ex.4p

SurvFn.in.6p  The intrinsic cumulative survival distribution function for 2-process 6-parameter vitality model

Description
Gives the cumulative survival proportions at xx from the intrinsic process for a given set of parameter values.

Usage
SurvFn.in.6p(xx, r, s)
SurvFn.k

Arguments

- \textbf{xx} vector of ages
- \textbf{r} \textit{r} value
- \textbf{s} \textit{s} value

Details

Used within \texttt{vitality.6p} for estimating model parameters based on the observed cumulative survival function.

Value

vector of cumulative survival proportions at \textbf{xx} from intrinsic process

See Also

\texttt{vitality.6p, survProbInc.6p, SurvFn.6p}

\begin{tabular}{ll}
\textbf{SurvFn.k} & \textit{The cumulative survival distribution function for 3-parameter vitality model} \\
\end{tabular}

Description

Gives the cumulative survival proportions at \textbf{xx} for a given set of parameter values.

Usage

\texttt{SurvFn.k(xx, r, s, k)}

Arguments

- \textbf{xx} vector of ages
- \textbf{r} \textit{r} value
- \textbf{s} \textit{s} value
- \textbf{k} \textit{k} value

Details

Used within \texttt{vitality.k} for estimating model parameters based on the observed cumulative survival function.

Value

cumulative survival proportions at \textbf{xx}
SurvFn.ku

The cumulative survival distribution function for 4-parameter vitality model

Description

Gives the cumulative survival proportions at xx for a given set of parameter values.

Usage

SurvFn.ku(xx, r, s, k, u)

Arguments

xx vector of ages
r r value
s s value
k k value
u u value

Details

Used within vitality.ku for estimating model parameters based on the observed cumulative survival function.

Value

cumulative survival proportions at xx

See Also

vitality.ku, survProbInc.ku
**survProbInc.4p**

Incremental survival probability for 2-process 4-parameter model

**Description**

Calculates the incremental survival probabilities (between xx1 and xx2) for 2-process 4-parameter model.

**Usage**

```
survProbInc.4p(r, s, lambda, beta, xx1, xx2)
```

**Arguments**

- `r`: r value
- `s`: s value
- `lambda`: lambda value
- `beta`: beta value
- `xx1`: xx1 vector
- `xx2`: xx2 vector

**Details**

For use in `vitality.4p`.

**Value**

incremental survival probabilities

**See Also**

`vitality.4p`, `logLikelihood.4p`

---

**survProbInc.6p**

Incremental survival probability for 2-process 6-parameter model

**Description**

Calculates the incremental survival probabilities (between xx1 and xx2) for 2-process 6-parameter model.

**Usage**

```
survProbInc.6p(r, s, lambda, beta, gamma, alpha, xx1, xx2)
```
Arguments

- \( r \): \( r \) value
- \( s \): \( s \) value
- \( \lambda \): \( \lambda \) value
- \( \beta \): \( \beta \) value
- \( \gamma \): \( \gamma \) value
- \( \alpha \): \( \alpha \) value
- \( xx_1 \): \( xx_1 \) vector
- \( xx_2 \): \( xx_2 \) vector

Details

For use in vitality.6p.

Value

incremental survival probabilities

See Also

vitality.6p, logLikelihood.6p

Description

Calculates the incremental survival probabilities (between \( xx_1 \) and \( xx_2 \)) for 3-parameter model.

Usage

\[
\text{survProbInc.k}(r, s, k, xx_1, xx_2)
\]

Arguments

- \( r \): \( r \) value
- \( s \): \( s \) value
- \( k \): \( k \) value
- \( xx_1 \): \( xx_1 \) vector
- \( xx_2 \): \( xx_2 \) vector

Details

For use in vitality.k.
survProbInc.ku

Description
Calculates the incremental survival probabilities (between xx1 and xx2) for 4-parameter model.

Usage
survProbInc.ku(r, s, k, u, xx1, xx2)

Arguments
- r: r value
- s: s value
- k: k value
- u: u value
- xx1: xx1 vector
- xx2: xx2 vector

Details
For use in vitality.ku.

Value
incremental survival probabilities

See Also
vitality.ku, logLikelihood.ku
**swedish_females**  
*Swedish Female Mortality Data*

**Description**  

**Format**  
A `data.frame` object

**Source**  
Human Mortality Database

---

**vft.4p**  
*Vectorized density function*

**Description**  
This function is used in the calculation of the fitted intrinsic (`mu.vd1.4p`) and total (`mu.vd.4p`) mortality rate in the 4-parameter model.

**Usage**  
```
vft.4p(xx, r, s, u)
```

**Arguments**  
- **xx**: vector of ages
- **r**: `r` value
- **s**: `s` value
- **u**: `u` value

**Value**  
vector of densities

**See Also**  
`ft.4p`
vft.6p

Vectorized density function

Description
This function is used in the calculation of the fitted intrinsic ($\mu vd1.6p$) and total ($\mu vd.6p$) mortality rate in the 6-parameter model.

Usage
vft.6p(xx, r, s)

Arguments
xx vector of ages
r r value
s s value

Value
vector of densities

See Also
ft.6p

vitality
Fitting routines for the Vitality family of mortality models.

Description
This package provides support for fitting the vitality family of mortality models that characterize mortality in terms of the loss vitality, an abstract measure of survival capacity. Mortality occurs by two processes. Intrinsic mortality occurs when vitality is depleted by stochastic losses. Extrinsic mortality occurs when a random external challenge exceeds the available vitality. The package contains four model versions:

- vitality.k is a 3-parameter model. Intrinsic mortality is characterized by the mean ($r$) and variability ($s$) in vitality loss rate. Extrinsic mortality is characterized by the frequency ($k$) of lethal random challenges. Model is appropriate to animal mortality data (e.g. Anderson 2000).

- vitality.ku is a 4-parameter model. Intrinsic mortality is characterized by the mean ($r$) and variability ($s$) in the vitality loss rate and the standard deviation of initial vitality ($u$). Extrinsic mortality is characterized by the frequency ($k$) of lethal random challenges. Model is appropriate to animal mortality data (e.g. Li and Anderson 2009).
• **vitality.4p** is a 4-parameter model. Intrinsic mortality is characterized by the mean \((r)\) and variability \((s)\) in the vitality loss rate. Extrinsic mortality is characterized by random challenges of frequency \((\lambda)\) and random magnitude \((\beta)\) exceeding the remaining average vitality. Model is appropriate to adult human mortality data (e.g. Li and Anderson 2013).

• **vitality.6p** is a 6-parameter model. Intrinsic mortality is characterized by the mean \((r)\) and variability \((s)\) in the vitality loss rate. Adult extrinsic mortality is characterized by random challenges of frequency \((\lambda)\) and random magnitude \((\beta)\) exceeding the remaining average vitality. Child extrinsic mortality is characterized by childhood challenges of frequency \((\gamma)\) exceeding childhood vitality development rate \((\alpha)\). Model is appropriate to full lifespan of human mortality data (e.g. Anderson and Li 2015).

Model parameters are estimated on survival or mortality rate data using maximum log likelihood methods based on Salinger et al. (2003).

Version 1.1 adds the versions **vitality.k**, **vitality.ku** and **vitality.6p** to the original code for the **vitality.4p** model previously designated vitality.2ps.

Version 1.2 makes previously invisible functions to produce the survival and mortality rate functions from a given set of parameters (e.g. **SurvFn.4p**, **SurvFn.6p**, **mu.vd.4p**, **mu.vd.6p**) usable. The child mortality rate formula in **mu.vd.6p**, **mu.vd2.6p**, and **mu.vd4.6p** has been updated to improve fit.

### Details

Support for package development was provided by the National Institute of Ageing Grant 1R21AG046760-01, the Bonneville Power Administration, and the University of Washington Center for Statistics and the Social Sciences and Center for Studies in Demography and Ecology.

### References


### Examples

```r
# vitality.k
data(daphnia)
time <- daphnia$days
survival_fraction <- daphnia$lx

results.modk <- vitality.k(time = time,
```
vitality

sdata = survival_fraction,
crc.data=TRUE,
se=FALSE,
gfit=FALSE,
datatype="CUM",
ttol=.00001,
init.params=FALSE,
lower=c(0,-1,0), upper=c(100,50,50),
pplot=TRUE,
tlab="days",
lplot=TRUE,
cplot=TRUE,
iplot=TRUE,
silent=TRUE)

# vitality.ku
data(rainbow_trout_for_k)
time <- rainbow_trout_for_k$days
survival_fraction <- rainbow_trout_for_k$survival

results.modku <- vitality.ku(time = time,
sdata = survival_fraction,
crc.data=TRUE,
se=FALSE,
gfit=FALSE,
datatype="CUM",
ttol=.00001,
init.params=FALSE,
lower=c(0,-1,0,0), upper=c(100,100,50,50),
pplot=TRUE,
tlab="days",
lplot=TRUE,
cplot=TRUE,
iplot=TRUE,
silent=TRUE,
L=0)

# vitality.4p
data(swedish_females)
swe <- swedish_females
initial_age <- 20 # Could be adjusted
time <- initial_age:max(swedish_females$age)
survival_fraction <- swe$lx / swe$lx[1]
survival_fraction <- survival_fraction[time] # when first element <1 data is adjusted
sample_size <- swe$lx[initial_age] # sample size

results.4par <- vitality.4p(time = time,
sdata = survival_fraction,
# init.params=FALSE,
init.params=c(0.012, 0.01, 0.1, 0.1),
lower = c(0, 0, 0, 0), upper = c(100,50,1,50),
crc.data = TRUE,
se = sample_size,
datatype = "CUM",
final_guess = TRUE,
vitality.4p

Fitting routine for the 2-process, 4-parameter vitality model (no childhood hook).

Description

This function provides the fitting routine for the 4-parameter 2-process vitality model. Intrinsic mortality is characterized by the mean (r) and variability (s) in the vitality loss rate. Extrinsic mortality is characterized by random challenges of frequency (lambda) and random magnitude (beta) exceeding the remaining average vitality. Model is appropriate to adult human mortality data (e.g. Li and Anderson 2013).

Usage

vitality.4p(time = 0:(length(sdata)-1), sdata, init.params = FALSE, lower = c(0, 0, 0, 0), upper = c(100,50,100,50), rc.data = FALSE, se = FALSE, datatype = c("CUM", "INC"), ttlol = 1e-06, pplot = TRUE, Iplot = TRUE, Mplot = TRUE, tlab = "years", silent = FALSE)
Arguments

time
Vector. Time component of data: Defaults to $\theta$: (length(sdata)-1).

sdata
Required. Survival or mortality data. The default expects cumulative survival fraction. If providing incremental mortality fraction instead, use option: datatype = "INC". The default also expects the data to represent full mortality. Otherwise, use option: rc.data = T to indicate right censored data. If first element of sdata <1 data will be rescaled.

rc.data
Optional, Boolean. Specifies Right Censored data. If the data does not represent full mortality, it is probably right censored. The default is rc.data = F. A third option is rc.data = "TF". Use this case to add a near-term zero survival point to data which displays nearly full mortality ( <.01 survival at end). If rc.data = F but the data does not show full mortality, rc.data = "TF" will be invoked automatically.

se
Optional, Boolean. Calculates the standard errors for the MLE parameters. Default is FALSE. Set equal to the initial study population to compute standard errors.

datatype
Optional. Defaults to "CUM" for cumulative survival fraction data. Use "INC" - for incremental mortality fraction data.

ttol
Optional. Stopping criteria tolerance. Default is 1e-6. Specify as ttol = .0001. If one of the likelihood plots (esp. for "k") does not look optimal, try decreasing ttol. If the program crashes, try increasing ttol.

init.params
Optional. Please specify the initial param values. specify init.params = c(r, s, lambda, beta) in that order (e.g., init.params = c(.1,.02, .3, 0.12)).

lower
vector of lower parameter bounds in order of c(r, s, lambda, beta). see nlminb

upper
vector of upper parameter bounds in order of c(r, s, lambda, beta). see nlminb

pplot
Optional, Boolean. Plots of cumulative survival for both data and fitted curves? Default TRUE. FALSE Produce no plots. A A third option: pplot = n (n >= 1) extends the time axis of the fitting plots (beyond the max time in data). For example: pplot = 1.2 extends the time axis by 20 Note: the incremental mortality plot is a continuous representation of the appropriately- binned histogram of incremental mortalities.

Iplot
Optional, Boolean. Incremental mortality for both data and fitted curves? Default: FALSE.

Mplot
Optional, Boolean. Plot fitted mortality curve? Default is FALSE. If TRUE 'observed' mortality rates for plotting are approximate and estimated from the input survival data. Depending on time (ages) and the change in mortality over age, these may be unrealistic but the fitted lines are derived from the parameter estimates themselves. For human data, the approximated mortality rates diverge at ages >80. pplot must be set to TRUE and Iplot=FALSE.

tlab
Optional, character. specifies units for x-axis of plots. Default is "days".

silent
Optional, Boolean. Stops all print and plot options (still get most warning and all error messages) Default is FALSE. A third option, "verbose" also enables the trace setting in the ms (minimum sum) S-Plus routine.
vitality.6p

Fitting routine for the 2-process, 6-parameter vitality model (with childhood hook).

Description

This function provides the fitting routine for the 6-parameter 2-process vitality model. Intrinsic mortality is characterized by the mean (r) and variability (s) in the vitality loss rate. Adult extrinsic mortality is characterized by random challenges of frequency (lambda) and random magnitude (beta) exceeding the remaining average vitality. Child extrinsic mortality is characterized by childhood challenges of frequency (gamma) exceeding childhood vitality development rate (alpha). Model is appropriate to full lifespan of human mortality data (e.g. Anderson and Li 2015).
Usage

vitality.6p(time = \theta: (\text{length}(\text{sdata}) - 1), \text{sdata}, \text{init.params} = \text{FALSE}, \text{lower} = \text{c}(0, 0, 0, 0, 0, 0), \text{upper} = \text{c}(100, 50, 100, 50, 50, 10), \text{rc.data} = \text{FALSE}, \text{se} = \text{FALSE}, \text{datatype} = \text{c}("\text{CUM}", "\text{INC}"), \text{ttol} = 1e-06, \text{pplot} = \text{TRUE}, \text{Iplot} = \text{FALSE}, \text{Mplot} = \text{FALSE}, \text{tlab} = "\text{years}", \text{silent} = \text{FALSE})

Arguments

time Vector. Time component of data: Defaults to \theta: (\text{length}(\text{sdata}) - 1). Typically this refers to ages.
sdata Required. Survival or mortality data. The default expects cumulative survival fraction. If providing incremental mortality fraction instead, use option: datatype = "INC". The default also expects the data to represent full mortality. Otherwise, use option: rc.data = T to indicate right censored data.
rc.data Optional, Boolean. Specifies Right Censored data. If the data does not represent full mortality, it is probably right censored. The default is rc.data = F. A third option is rc.data = "TF". Use this case to add a near-term zero survival point to data which displays nearly full mortality ( <.01 survival at end). If rc.data = F but the data does not show full mortality, rc.data = "TF" will be invoked automatically.
se Optional, Boolean. Calculates the standard errors for the MLE parameters. Default is FALSE. Set equal to the initial study population to compute standard errors.
datatype Optional. Defaults to "CUM" for cumulative survival fraction data. Use "INC" for incremental mortality fraction data.
ttol Optional. Stopping criteria tolerance. Default is 1e-6. Specify as ttol = .0001. If one of the likelihood plots (esp. for "k") does not look optimal, try decreasing ttol. If the program crashes, try increasing ttol.
init.params Optional. Please specify the initial param values. specify init.params = c(r, s, lambda, beta, gamma, alpha) in that order (e.g., init.params = c(.1, .02, .3, 0.12, 0.1, 1)).
lower vector of lower parameter bounds in order of c(r, s, lambda, beta, gamma, alpha).
see nlminb
upper vector of upper parameter bounds in order of c(r, s, lambda, beta, gamma, alpha).
see nlminb
pplot Optional, Boolean. Plots of cumulative survival for both data and fitted curves? Default: TRUE. FALSE produces no plots. A third option: pplot = n (n >= 1) extends the time axis of the fitting plots (beyond the max time in data). For example: pplot = 1.2 extends the time axis by 20 Note: the incremental mortality plot is a continuous representation of the appropriately binned histogram of incremental mortalities.
Iplot Optional, Boolean. Incremental mortality for both data and fitted curves? Default: FALSE.
Mplot Optional, Boolean. Plot fitted total, intrinsic, extrinsic (child), and extrinsic (adult) mortality curves? Default: FALSE. If TRUE 'observed' mortality rates for
plotting are approximate and estimated from the input survival data. Depending on time (ages) and the change in mortality over age, the approximated, plotted mortality rates may be inaccurate (e.g. For human mortality data, mortality rates at the oldest ages are underestimated because \( nax \) is assumed to be half the length of the age interval but the true \( nax \) is likely larger). This caveat applies only to the plotted mortality rates (black circles in plot). The plotted, fitted lines are calculated with the parameter estimates themselves and are unaffected by the estimation of the mortality rates for this plot. \( \text{pplot} \) must be set to TRUE and \( \text{Iplot}\) = FALSE.

\[ \text{tlab} \]
Optional, character. specifies units for x-axis of plots. Default is "years".

\[ \text{silent} \]
Optional, Boolean. Stops all print and plot options (still get most warning and all error messages) Default is FALSE. A third option, "verbose" also enables the trace setting in the ms (minimum sum) S-Plus routine.

Value

vector of final MLE \( r, s, \lambda, \beta, \gamma \) and \( \alpha \) parameter estimates. standard errors of MLE parameter estimates (if se = <population> is specified).

References


Examples

data(swedish_females)
swe <- swedish_females
initial_age <- 0
time <- swedish_females$age
survival_fraction <- swe$lx / swe$lx[1]
sample_size <- swe$lx[1] # sample size

results.6par <- vitality.6p(time = time,
                         sdata = survival_fraction,
                         # init.params=FALSE,
                         init.params=c(0.012, 0.01, 0.1, 0.1, 0.1, 1),
                         lower = c(0, 0, 0, 0, 0, 0), upper = c(100,50,1,50,50,50),
                         rc.data = TRUE,
                         se=FALSE,
                         # se = sample_size,
                         datatype = "CUM",
                         tol = 1e-06,
                         pplot = TRUE,
                         Iplot = TRUE,
                         Mplot = TRUE,
                         tlab = "years",
                         ...)
Fitting routine for the 3-parameter vitality model.

Description

This function provides the fitting routine for the 3-parameter vitality model. Intrinsic mortality is characterized by the mean (r) and variability (s) in vitality loss rate. Extrinsic mortality is characterized by the frequency (k) of lethal random challenges. Model is appropriate to animal mortality data (e.g. Anderson 2000).

Usage

```r
vitality.k(time, sdata, rc.data=F, se=F, gfit=F, datatype="Cum", ttol=.000001,
init.params=F, lower=c(0,-1,0), upper=c(100,50,50), pplot=T, tlab="days",
lplot=F, cplot=F, iplot=F, silent=F)
```

Arguments

- **time**: Vector. Time component of data: Defaults to \( (\text{length}(\text{sdata})-1) \). Typically this refers to ages.
- **sdata**: Required. Survival or mortality data. The default expects cumulative survival fraction. If providing incremental mortality fraction instead, use option: `datatype = "INC"`. The default also expects the data to represent full mortality. Otherwise, use option: `rc.data = T` to indicate right censored data.
- **rc.data**: Optional, Boolean. Specifies Right Censored data. If the data does not represent full mortality, it is probably right censored. The default is `rc.data = F`. A third option is `rc.data = "TF"`. Use this case to add a near-term zero survival point to data which displays nearly full mortality ( <.01 survival at end). If `rc.data = F` but the data does not show full mortality, `rc.data = "TF"` will be invoked automatically.
- **se**: Optional, Boolean. Calculates the standard errors for the MLE parameters. Default is FALSE. Set equal to the initial study population to compute standard errors.
- **datatype**: Optional. Defaults to "Cum" for cumulative survival fraction data. Use "INC" for incremental mortality fraction data.
- **ttol**: Optional. Stopping criteria tolerance. Default is 1e-6. Specify as `ttol = .0001`. If one of the likelihood plots (esp. for "k") does not look optimal, try decreasing `ttol`. If the program crashes, try increasing `ttol`.
- **init.params**: Optional. Please specify the initial param values. specify `init.params = c(r, s, k)` in that order (e.g. `init.params = c(.1, .02, .3)`).
- **lower**: vector of lower parameter bounds in order of c(r, s, k). see `nlminb`
- **upper**: vector of upper parameter bounds in order of c(r, s, k). see `nlminb`
vitality.k

pplot Optional, Boolean. Plots of cumulative survival for both data and fitted curves? Default: TRUE. FALSE produces no plots. Note: the incremental mortality plot is a continuous representation of the appropriately binned histogram of incremental mortalities.

iplot Boolean. Plot incremental survival? Must have pplot=TRUE

lplot Boolean. Plot likelihood functions? Provides likelihood function plotting. Defaults to FALSE. Note: these plots are not "likelihood profiles" in that while one parameter is varied, the others are held fixed, rather than re-optimized. (must also have pplot=T and iplot=F.)

cplot Boolean. Plot likelihood contour plot? Provides a likelihood contour plot for a range of r and s values (can be slow so default is FALSE). Must also have lplot=T and pplot=T to get contour plots.

tlab Character, label for time axis. Defaults to "days".

gfit Provides a Pearson C type test for goodness of fit. Default is FALSE. Must provide the initial study population to compute goodness of fit.

silent Optional, Boolean. Stops all print and plot options (still get most warning and all error messages) Default is FALSE. A third option, "verbose" also enables the trace setting in the ms (minimum sum) S-Plus routine.

Value

vector of final MLE r, s, k parameter estimates. standard errors of MLE parameter estimates (if se = <population> is specified).

References


Examples

data(daphnia)
time <- daphnia$days
survival_fraction <- daphnia$lx

results.modk <- vitality.k(time = time,
sdata = survival_fraction,
rc.data=TRUE,
se=FALSE,
gfit=FALSE,
datatype="CUM",
ttol=.000001,
init.params=FALSE,
#init.params=c(0.075, 0.15, 0.001),
lower=c(0,-1,0), upper=c(100,50,50),
pplot=TRUE,
tlab="days",
lplot=TRUE,
lplot=TRUE,
cplot=TRUE,
Fitting routine for the 4-parameter vitality model.

Description

This function provides the fitting routine for the 4-parameter vitality model. Intrinsic mortality is characterized by the mean (r) and variability (s) in the vitality loss rate and the standard deviation of initial vitality (u). Extrinsic mortality is characterized by the frequency (k) of lethal random challenges. Model is appropriate to animal mortality data (e.g. Li and Anderson 2009)

Usage

vitality.ku(time, sdata, rc.data=F, se=F, gfit=F, datatype="CUM", ttol=.000001, init.params=F, lower=c(0,-1,0,0), upper=c(100,100,50,50), pplot=T, tlab="days", lplot=F, cplot=F, iplot=F, silent=F, L=0)

Arguments

time Vector. Time component of data. Typically this refers to ages.
sdata Required. Survival or mortality data. The default expects cumulative survival fraction. If providing incremental mortality fraction instead, use option: datatype = "INC". The default also expects the data to represent full mortality. Otherwise, use option: rc.data = T to indicate right censored data.
rc.data Optional. Boolean. Specifies Right Censored data. If the data does not represent full mortality, it is probably right censored. The default is rc.data = F. A third option is rc.data = "TF". Use this case to add a near-term zero survival point to data which displays nearly full mortality ( <.01 survival at end). If rc.data = F but the data does not show full mortality, rc.data = "TF" will be invoked automatically.
se Optional. Boolean. Calculates the standard errors for the MLE parameters. Default is FALSE. Set equal to the initial study population to compute standard errors.
datatype Optional. Defaults to "CUM" for cumulative survival fraction data. Use "INC" - for incremental mortality fraction data.
ttol Optional. Stopping criteria tolerance. Default is 1e-6. Specify as ttol = .0001. If one of the likelihood plots (esp. for "k") does not look optimal, try decreasing ttol. If the program crashes, try increasing ttol.
init.params Optional. Please specify the initial param values. specify init.params = c(r, s, k, u) in that order (e.g., init.params = c(.1,.02,.3,.25)).
lower vector of lower parameter bounds in order of c(r, s, k, u). see nlminb
upper vector of upper parameter bounds in order of c(r, s, k, u). see nlminb
pplot
Optional, Boolean. Plots of cumulative survival for both data and fitted curves? Default: TRUE. FALSE produces no plots. Note: the incremental mortality plot is a continuous representation of the appropriately binned histogram of incremental mortalities.

iplot
Boolean. Plot incremental survival?

lplot
Boolean. Plot likelihood functions? Provides likelihood function plotting. Defaults to FALSE. Note: these plots are not "likelihood profiles" in that while one parameter is varied, the others are held fixed, rather than re-optimized. (must also have pplot=T.)

cplot
Boolean. Plot likelihood contour plot? Provides a likelihood contour plot for a range of parameter values (can be slow so default is FALSE). Must also have lplot=T and pplot=T to get contour plots.

tlab
Character, label for time axis. Defaults to "days".

gfit
Provides a Pearson C type test for goodness of fit. Default is FALSE. Must provide the initial study population to compute goodness of fit.

silent
Optional, Boolean. Stops all print and plot options (still get most warning and all error messages) Default is FALSE.

L
Number of times of running simulated annealing. Default is 0, use Newton-Ralphson method only.

Value

vector of final MLE r, s, k, u parameter estimates. standard errors of MLE parameter estimates (if se = <population> is specified).

References


Examples

data(rainbow_trout_for_k)
time <- rainbow_trout_for_k$days
survival_fraction <- rainbow_trout_for_k$survival

results.modku <- vitality.ku(time = time,
                           sdata = survival_fraction,
                           rc.data=TRUE,
                           se=FALSE,
                           gfit=FALSE,
                           datatype="CUM",
                           ttol=.000001,
                           init.params=FALSE,
                           lower=c(0,-1,0,0),upper=c(100,100,50,50),
                           pplot=TRUE,
                           tlab="days",
                           lplot=TRUE,)
cplot=TRUE,
Iplot=TRUE,
silent=FALSE,
L=0)
## Index

*Topic **datasets**
  - daphnia, 2
  - rainbow_trout_for_k, 18
  - swedish_females, 32

  daphnia, 2
  dataPrep, 3

  ft. 4p, 4, 32
  ft. 6p, 4, 4, 33

  indexFinder, 5

  logLikelihood.4p, 5, 29
  logLikelihood.6p, 6, 6, 30
  logLikelihood.k, 7, 31
  logLikelihood.ku, 7, 31

  mu.vd.4p, 4, 8, 10, 11, 14, 32, 34
  mu.vd.6p, 4, 9, 10, 12, 13, 15, 33, 34
  mu.vd1.4p, 4, 8, 9, 11, 14, 32
  mu.vd1.6p, 4, 9, 10, 12, 13, 15, 33
  mu.vd2.4p, 8, 10, 11, 14
  mu.vd2.6p, 9, 10, 11, 12, 13, 15, 34
  mu.vd3.6p, 12, 12, 13, 15
  mu.vd4.6p, 12, 13, 15, 34

  nlminb, 37, 39, 41, 43

  plotting.4p, 13
  plotting.6p, 14
  plotting.k, 15
  plotting.ku, 16

  rainbow_trout_for_k, 18

  stderrNTp, 18
  stderrN6p, 19
  stderrNk, 20
  stderrNku, 20
  SurvFn.4p, 21, 23, 26, 34

  SurvFn.6p, 22, 24, 27, 34
  SurvFn.ex.4p, 22, 23, 26
  SurvFn.ex.6p, 22, 23
  SurvFn.h.4p, 24
  SurvFn.h.6p, 25
  SurvFn.in.4p, 22, 23, 26
  SurvFn.in.6p, 22, 26
  SurvFn.k, 27
  SurvFn.ku, 28
  survProbInc.4p, 22, 23, 26, 29
  survProbInc.6p, 22, 24, 27, 29
  survProbInc.k, 28, 30
  survProbInc.ku, 28, 31
  swedish_females, 32

  vft.4p, 4, 32
  vft.6p, 3, 33
  vitality, 33
  vitality-package (vitality), 33
  vitality.4p, 6, 13, 14, 18, 19, 22, 23, 25, 26,
  29, 34, 36
  vitality.6p, 6, 14, 15, 19, 22, 24, 25, 27, 30,
  34, 38
  vitality.k, 7, 15, 16, 20, 27, 28, 30, 31, 33,
  34, 41
  vitality.ku, 8, 16, 17, 20, 21, 28, 31, 33, 34,
  43

  vitalityMpackage (vitality), 33