

Package ‘vitality’

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Title Fitting Routines for the Vitality Family of Mortality Models

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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'

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daphnia	<i>Sample Daphnia Data</i>
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Description

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

Format

data frame

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	<i>Function for data preparation</i>
----------	--------------------------------------

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

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

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	<i>Density function for 3-parameter (r, s, u)</i>
-------	---

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

```
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	<i>Density function for 2-parameters (r, s)</i>
-------	---

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

```
ft.6p(xx, r, s)
```

Arguments

xx	age
r	r value
s	s value

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

[logLikelihood.6p](#)

logLikelihood.6p	<i>Log likelihood of 2-process 6-parameter vitality model</i>
------------------	---

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](#)

logLikelihood.k	<i>Log likelihood of 3-parameter (r,s,k) model</i>
-----------------	--

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](#)

logLikelihood.ku	<i>Log likelihood of 4-parameter (r,s,k,u) model</i>
------------------	--

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	<i>Total mortality rate for the 2-process 4-parameter vitality model</i>
----------	--

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	<i>Total mortality rate for the 2-process 6-parameter vitality model</i>
----------	--

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

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	<i>Intrinsic mortality rate for the 2-process 4-parameter vitality model</i>
-----------	--

Description

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

Usage

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](#)

<code>mu.vd1.6p</code>	<i>Intrinsic mortality rate for the 2-process 6-parameter vitality model</i>
------------------------	--

Description

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

Usage

`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](#)

mu.vd2.4p	<i>Extrinsic mortality rate for the 2-process 4-parameter vitality model</i>
-----------	--

Description

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

Usage

mu.vd2.4p(x, r, lambda, beta)

Arguments

x	age
r	r value
lambda	lambda value
beta	beta value

Value

Extrinsic age-specific mortality rates

See Also

[mu.vd.4p](#), [mu.vd1.4p](#)

mu.vd2.6p	<i>Extrinsic mortality rate for the 2-process 6-parameter vitality model</i>
-----------	--

Description

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

Usage

mu.vd2.6p(x, r, lambda, beta, gamma, alpha)

Arguments

x	age
r	r value
lambda	lambda value
beta	beta value
gamma	gamma value
alpha	alpha value

Value

Vector of extrinsic age-specific mortality rates at ages x

See Also

[mu.vd.6p](#), [mu.vd1.6p](#), [mu.vd3.6p](#), [mu.vd4.6p](#)

mu.vd3.6p	<i>Adult extrinsic mortality rate for the 2-process 6-parameter vitality model</i>
-----------	--

Description

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

Usage

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

[mu.vd.6p](#), [mu.vd1.6p](#), [mu.vd2.6p](#), [mu.vd4.6p](#)

mu.vd4.6p	<i>Childhood extrinsic mortality rate for the 2-process 6-parameter vitality model</i>
-----------	--

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	<i>Plotting function for 2-process 4-parameter vitality model</i>
-------------	---

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, Ni, pplot, lplot, 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
sfract	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, sfract, x1, x2, Ni, pplot, Iplot, Mplot,
  tlab, rc.data)
```

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?
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.6p](#) for further description of function arguments.

Only one of Iplot 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,Iplot,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
sfract	observed survival fraction
x1	Time 1
x2	Time 2
Ni	Initial population
pplot	Boolean. Plot cumulative survival fraction?
lplot	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.ku](#).

Usage

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

Details

See [vitality.ku](#) for further description of function arguments.

See Also

[vitality.ku](#)

rainbow_trout_for_k	<i>Sample Rainbow Trout Data</i>
---------------------	----------------------------------

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	<i>Standard errors for 4-parameters: r, s, lambda, beta</i>
-----------	---

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

Note

if $k \leq 0$, cannot find standard error for k

See Also

[vitality.4p](#)

stdErr.6p	<i>Standard errors for 6-parameters: r, s, lambda, beta, gamma, alpha</i>
-----------	---

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 $k \leq 0$, cannot find standard error for k

See Also

[vitality.6p](#)

stdErr.k	<i>Standard errors for 3-parameters: r, s, k</i>
----------	--

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	<i>Standard errors for 4-parameters: r, s, k, u</i>
-----------	---

Description

Gives the standard errors for the 4 parameter model. Primarily used within [vitality.ku](#).

Usage

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

Arguments

r	r value
s	s value
k	k value
u	u 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, u.

Note

k is restricted to be >0.

See Also

[vitality.ku](#)

SurvFn.4p	<i>The cumulative survival distribution function for 2-process 4-parameter vitality model</i>
-----------	---

Description

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

Usage

SurvFn.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 all processes

See Also

[vitality.4p](#), [survProbInc.4p](#), [SurvFn.in.4p](#), [SurvFn.ex.4p](#)

SurvFn.6p	<i>The cumulative survival distribution function for 2-process 6-parameter vitality model</i>
-----------	---

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](#)

SurvFn.ex.4p	<i>The extrinsic cumulative survival distribution function for 2-process 4-parameter vitality model</i>
--------------	---

Description

Gives the cumulative survival proportions at xx from extrinsic process 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](#), [SurvFn.in.4p](#)

SurvFn.ex.6p	<i>The extrinsic cumulative survival distribution function for 2-process 6-parameter vitality model</i>
--------------	---

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](#)

SurvFn.h.6p

Intrinsic cumulative survival distribution for 6 parameter model

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	<i>The intrinsic cumulative survival distribution function for 2-process 4-parameter vitality model</i>
--------------	---

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	<i>The intrinsic cumulative survival distribution function for 2-process 6-parameter vitality model</i>
--------------	---

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)
```

Arguments

xx	vector of ages
r	r value
s	s 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 intrinsic process

See Also

[vitality.6p](#), [survProbInc.6p](#), [SurvFn.6p](#)

SurvFn.k	<i>The cumulative survival distribution function for 3-parameter vitality model</i>
----------	---

Description

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

Usage

```
SurvFn.k(xx, r, s, k)
```

Arguments

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

Details

Used within [vitality.k](#) for estimating model parameters based on the observed cumulative survival function.

Value

cumulative survival proportions at xx

See Also

[vitality.k](#), [survProbInc.k](#)

SurvFn.ku	<i>The cumulative survival distribution function for 4-parameter vitality model</i>
-----------	---

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	<i>Incremental survival probability for 2-process 4-parameter model</i>
----------------	---

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	<i>Incremental survival probability for 2-process 6-parameter model</i>
----------------	---

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
xx1	xx1 vector
xx2	xx2 vector

Details

For use in [vitality.6p](#).

Value

incremental survival probabilities

See Also

[vitality.6p](#), [logLikelihood.6p](#)

survProbInc.k

Incremental survival probability for 3-parameter model

Description

Calculates the incremental survival probabilities (between xx1 and xx2) for 3-parameter model.

Usage

```
survProbInc.k(r, s, k, xx1, xx2)
```

Arguments

r	r value
s	s value
k	k value
xx1	xx1 vector
xx2	xx2 vector

Details

For use in [vitality.k](#).

Value

incremental survival probabilities

See Also

[vitality.k](#), [logLikelihood.k](#)

survProbInc.ku

Incremental survival probability for 4-parameter model

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	<i>Swedish Female Mortality Data</i>
-----------------	--------------------------------------

Description

Period life table for Swedish females in the year 2000. Columns follow standard life-table naming conventions.

Format

A data.frame object

Source

Human Mortality Database

vft.4p	<i>Vectorized density function</i>
--------	------------------------------------

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	<i>Vectorized density function</i>
--------	------------------------------------

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	<i>Fitting routines for the Vitality family of mortality models.</i>
----------	--

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 (λ) and random magnitude (β) 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 (λ) and random magnitude (β) exceeding the remaining average vitality. Child extrinsic mortality is characterized by childhood challenges of frequency (γ) exceeding childhood vitality development rate (α). 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

- Anderson, J.J. (2000). "A vitality-based model relating stressors and environmental properties to organism survival." *Ecological Monographs* 70(3):445-470.
- Anderson, J.J. and Li, T. (2015). "A two-process mortality model with extensions to juvenile mortality, populations and evolution." *Population Association of America Annual Meeting 2015* <http://paa2015.princeton.edu/abstracts/153144>
- Li, T. and J.J. Anderson. (2009). "The vitality model: A way to understand population survival and demographic heterogeneity." *Theoretical Population Biology* 76: 118-131.
- Li, T. and J.J. Anderson (2013). "Shaping human mortality patterns through intrinsic and extrinsic vitality processes." *Demographic Research* 28(12): 341-372.
- Salinger, D.H., J.J. Anderson, and O.S. Hamel. (2003). "A parameter estimation routine for the vitality-based survival model." *Ecological Modelling* 166 (3): 287-29

Examples

```
# vitality.k
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,
        lower=c(0,-1,0), upper=c(100,50,50),
        pplot=TRUE,
        tlab="days",
        lplot=TRUE,
        cplot=TRUE,
        lplot=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,
        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,
        lplot=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),
        rc.data = TRUE,
        se = sample_size,
        datatype = "CUM",

```

```

        ttol = 1e-06,
        pplot = TRUE,
        lplot = TRUE,
        mplot = TRUE,
        tlab = "years",
        silent = FALSE)

# vitality.6p
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",
    ttol = 1e-06,
    pplot = TRUE,
    lplot = TRUE,
    mplot = TRUE,
    tlab = "years",
    silent = FALSE)

```

vitality.4p	<i>Fitting routine for the 2-process, 4-parameter vitality model (no childhood hook).</i>
-------------	---

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 (λ) and random magnitude (β) 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"), ttol = 1e-06, pplot = TRUE,
    lplot = FALSE, mplot = FALSE, tlab = "years", silent = FALSE)

```

Arguments

time	Vector. Time component of data: Defaults to 0:(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.

Value

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

References

D.H. Salinger, J.J. Anderson and O. Hamel (2003). "A parameter fitting routine for the vitality based survival model." *Ecological Modeling* 166(3): 287–294.

Li, T. and J.J. Anderson (2013). "Shaping human mortality patterns through intrinsic and extrinsic vitality processes." *Demographic Research* 28(12): 341-372.

Examples

```
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),
                           rc.data = TRUE,
                           se = sample_size,
                           datatype = "CUM",
                           ttol = 1e-06,
                           pplot = TRUE,
                           lplot = TRUE,
                           mplot = TRUE,
                           tlab = "years",
                           silent = FALSE)
```

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 (λ) and random magnitude (β) exceeding the remaining average vitality. Child extrinsic mortality is characterized by childhood challenges of frequency (γ) exceeding childhood vitality development rate (α). Model is appropriate to full lifespan of human mortality data (e.g. Anderson and Li 2015).

Usage

```
vitality.6p(time = 0:(length(sdata)-1), sdata, init.params = FALSE,
  lower = c(0, 0, 0, 0, 0, 0), upper = c(100,50,100,50,50,10), rc.data = FALSE,
  se = FALSE, datatype = c("CUM", "INC"), ttol = 1e-06, pplot = TRUE,
  lplot = FALSE, mplot = FALSE, tlab = "years", silent = FALSE)
```

Arguments

time	Vector. Time component of data: Defaults to 0:(length(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.
lplot	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. `pplot` must be set to `TRUE` and `lplot=FALSE`.

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

`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 , λ , β , γ and α parameter estimates. standard errors of MLE parameter estimates (if `se = <population>` is specified).

References

D.H. Salinger, J.J. Anderson and O. Hamel (2003). "A parameter fitting routine for the vitality based survival model." *Ecological Modeling* 166(3): 287–294.

Anderson, J.J. and T. Li. (2015). "A two-process mortality model with extensions to juvenile mortality, populations and evolution." Population Association of America Annual Meeting 2015 <http://paa2015.princeton.edu/abstracts/153144>

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",
  ttol = 1e-06,
  pplot = TRUE,
  lplot = TRUE,
  mplot = TRUE,
  tlab = "years",
```



```
silent = FALSE)
```

vitality.k

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

```
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, lplot=F, silent=F)
```

Arguments

time	Vector. Time component of data: Defaults to 0:(length(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

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.
lplot	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 lplot=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

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

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,
                           cplot=TRUE,
```

```
Iplot=TRUE,
silent=FALSE)
```

vitality.ku

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.
lplot	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

- Li, T. and J.J. Anderson. (2009). "The vitality model: A way to understand population survival and demographic heterogeneity." *Theoretical Population Biology* 76: 118-131.

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)
```

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