Package ‘Temporal’

October 12, 2022

Title Parametric Time to Event Analysis
Version 0.3.0
Description Performs maximum likelihood based estimation and inference on time to event data, possibly subject to non-informative right censoring. FitParaSurv() provides maximum likelihood estimates of model parameters and distributional characteristics, including the mean, median, variance, and restricted mean. CompParaSurv() compares the mean, median, and restricted mean survival experiences of two treatment groups. Candidate distributions include the exponential, gamma, generalized gamma, log-normal, and Weibull.

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**CheckArm**

**Description**
Check whether treatment arm is properly formatted.

**Usage**
CheckArm(arm)

**Arguments**
- arm: 0/1, treatment arm.

**Value**
None.

---

**CheckDist**

**Description**
Check whether the distribution selected is available.

**Usage**
CheckDist(dist)

**Arguments**
- dist: String, distribution name.

**Value**
None.
CheckInit  

**Check Initialization**

**Description**
Check whether the initialization is valid.

**Usage**
CheckInit(dist, init)

**Arguments**
- **dist**  
  String, distribution name.
- **init**  
  List of named parameters.

**Value**
None.

CheckStatus  

**Status Check**

**Description**
Function to ensure the status indicator is properly formatted.

**Usage**
CheckStatus(status)

**Arguments**
- **status**  
  0/1 status indicator.

**Value**
None.
**CheckTheta**

**Description**

Function to check the appropriate number of parameters are supplied for the selected distribution. Used by GenData.

**Usage**

CheckTheta(dist, theta)

**Arguments**

- **dist**: String, distribution.
- **theta**: Numeric, parameter vector.

**Value**

None.

---

**CompParaSurv**

**Compare Parametric Survival Distribution**

**Description**

Compares the means and medians of parametric survival distributions fit to two treatment arms. Available distributions include: exponential, gamma, generalized gamma, log-normal, and Weibull.

**Usage**

CompParaSurv(  
data,  
arm_name = "arm",  
dist1 = "weibull",  
dist0 = NULL,  
eps = 1e-06,  
init1 = NULL,  
init0 = NULL,  
maxit = 10,  
report = FALSE,  
reps = NULL,  
sig = 0.05,  
status_name = "status",  
tau = NULL,  
time_name = "time"
)
Arguments

- **data**: Data.frame.
- **arm_name**: Name of the column containing the treatment group, coded as 1 for treatment, 0 for reference.
- **dist1**: Distribution to fit for the target group. Selected from among: exp, gamma, gengamma, log-normal, and weibull.
- **dist0**: Distribution to fit for the reference group. Same choices as for the target group. If omitted, defaults to the distribution specified for the target group.
- **eps**: Tolerance for Newton-Raphson iterations.
- **init1**: Initial parameter values for the target group.
- **init0**: Initial parameter values for the reference group.
- **maxit**: Maximum number of Newton-Raphson iterations.
- **report**: Report fitting progress?
- **reps**: Number of permutation replicates, if requesting permutation p-values.
- **sig**: Significance level, for constructing confidence intervals.
- **status_name**: Name of the status indicator, 1 if observed, 0 if censored.
- **tau**: Optional truncation times for calculating RMST.
- **time_name**: Name of column containing the time to event.

Details

Status should be coded as 0 for censored and 1 for observed. Arm is coded as 0 for reference, 1 for target. Tau is an optional numeric vector of truncation times for calculating restricted mean survival time, which is the area under the survival curve up to the specified truncation point.

Value

An object of class `contrast` containing the following:

- **Model1**: The fitted model for the target group.
- **Model0**: The fitted model for the reference group.
- **Contrast**: Contrasts of means and medians.
- **RMST**: Contrasts of the RMSTs, if ‘tau’ was specified.

Examples

```r
set.seed(100)
# Weibull and Weibull, different means and medians.
n <- 1e3

df1 <- GenData(n = n, dist = "weibull", theta = c(1, 1), p = 0.2)
df1$arm <- 1

df0 <- GenData(n = n, dist = "weibull", theta = c(1, 2), p = 0.2)
```
df0$arm <- 0
data <- rbind(df1, df0)

# Comparison.
comp <- CompParaSurv(data, dist1 = "weibull")

# Add RMST at time 1.
comp <- CompParaSurv(data, dist1 = "weibull", tau = 1)

# Calculate permutation p-values (slow).
comp <- CompParaSurv(data, dist1 = "weibull", tau = 1, reps = 100)

---

**contrast-class**  
*Contrast of Survival Distributions.*

**Description**  
Defines the object class returned by the comparison function.

**Slots**

- **Dist1** Distribution fit to the target group, string.
- **Dist0** Distribution fit to the reference group, string.
- **Model1** Fitted model for the target group, fit.
- **Model0** Fitted model for the reference group, fit.
- **Location** Contrasts of means and medians, data.frame.
- **RMST** Contrasts of RMSTs, data.frame.

---

**ContrastLocs**  
*Contrast Locations*

**Description**

Compare the means and medians of the fitted distributions for two treatment arms.

**Usage**

`ContrastLocs(fit1, fit0, sig = 0.05)`

**Arguments**

- **fit1**  
  Fitted parametric survival distribution for arm 1.
- **fit0**  
  Fitted parametric survival distribution for arm 0.
- **sig**  
  Significance level.
Value
Data.frame contrasting the difference and ratio of the mean and median at each time point.

ContrastRMSTs

Contrast RMSTs

Description
Compare the restricted mean survival times of the fitted distributions for two treatment arms.

Usage
ContrastRMSTs(fit1, fit0, sig = 0.05)

Arguments
- fit1: Fitted parametric survival distribution for arm 1.
- fit0: Fitted parametric survival distribution for arm 0.
- sig: Significance level, for

Value
Data.frame contrasting the difference and ratio of RMSTs at each time point.

DefaultParam

Set Default Parameters

Description
Function to select default parameter values for each distribution.

Usage
DefaultParam(dist)

Arguments
- dist: String, distribution name.

Value
Numeric parameter ist.
### DistProperName

<table>
<thead>
<tr>
<th>DistProperName</th>
<th>Distributions</th>
</tr>
</thead>
</table>

#### Description
DistProperName

#### Usage

DistProperName(dist)

#### Arguments
- **dist**: Argument passed to FitParaSurv

#### Value
String.

### EstDiff

<table>
<thead>
<tr>
<th>EstDiff</th>
<th>Difference of Estimates</th>
</tr>
</thead>
</table>

#### Description
Calculate CIs and p-value for the difference of estimates.

#### Usage

EstDiff(est1, se1, est0, se0, sig = 0.05)

#### Arguments
- **est1**: Arm 1 estimate.
- **se1**: Arm 1 standard error.
- **est0**: Arm 0 estimate.
- **se0**: Arm 0 standard error.
- **sig**: Significance level.

#### Value
Data.frame containing estimated difference, its standard error, lower and upper confidence bounds, and a p-value assessing the null hypothesis of no difference.
EstRatio  

**Ratio of Estimates**

### Description

Calculate CIs and p-value for the ratio of estimates.

### Usage

```r
EstRatio(est1, se1, est0, se0, sig = 0.05)
```

### Arguments

- `est1`: Arm 1 estimate.
- `se1`: Arm 1 standard error.
- `est0`: Arm 0 estimate.
- `se0`: Arm 0 standard error.
- `sig`: Significance level.

### Value

Data.frame containing estimated ratio, its standard error, lower and upper confidence bounds, and a p-value assessing the null hypothesis that the ratio is unity.

---

ExtractObsEst  

**Extract Observed Estimates**

### Description

Helper function for permutation inference.

### Usage

```r
ExtractObsEst(fit1, fit0)
```

### Arguments

- `fit1`: Fitted parametric survival distribution for arm 1.
- `fit0`: Fitted parametric survival distribution for arm 0.

### Value

Numeric vector.
fit-class

Fitted Survival Distribution

Description

Defines the object class returned by fitting functions.

Slots

- **Distribution**: Fitted distribution, string.
- **Parameters**: Parameters, data.frame.
- **Information**: Information components, matrix.
- **Outcome**: Properties of the fitted distribution, data.frame.
- **RMST**: Estimated restricted mean survival times, data.frame.
- **S**: Fitted survival function, function.

FitExp

Exponential Distribution Parameter Estimation

Description

Estimates parameters for exponential event times subject to non-informative right censoring. The exponential distribution is parameterized in terms of the rate $\lambda$:

$$f(t) = \lambda e^{-\lambda t}, t > 0$$

Usage

```R
FitExp(
  data,
  sig = 0.05,
  status_name = "status",
  tau = NULL,
  time_name = "time"
)
```

Arguments

- **data**: Data.frame.
- **sig**: Significance level, for CIs.
- **status_name**: Name of the status indicator, 1 if observed, 0 if censored.
- **tau**: Optional truncation times for calculating RMSTs.
- **time_name**: Name of column containing the time to event.
Value
An object of class fit containing the following:

Parameters  The estimated model parameters.
Information  The observed information matrix.
Outcome    The fitted mean, median, and variance of the time to event distribution.
RMST       The estimated RMSTs, if tau was specified.

Examples
# Generate exponential event time data with 20% censoring.
data <- GenData(n = 1e3, dist = "exp", theta = c(2), p = 0.2)

# Estimate parameters.
fit <- FitParaSurv(data, dist = "exp")

FitGamma

Gamma Distribution Parameter Estimation

Description
Estimates parameters for gamma event times subject to non-informative right censoring. The
gamma distribution is parameterized in terms of the shape $\alpha$ and rate $\lambda$:

$$f(t) = \frac{\lambda}{\Gamma(\alpha)} (\lambda t)^{\alpha-1} e^{-\lambda t}, t > 0$$

Usage
FitGamma(
  data,
  eps = 1e-06,
  init = list(),
  maxit = 10,
  report = FALSE,
  sig = 0.05,
  status_name = "status",
  tau = NULL,
  time_name = "time"
)

Arguments
data        Data.frame.
eps         Tolerance for Newton-Raphson iterations.
init        List with initial values for the 'shape' $\alpha$ and 'rate' $\lambda$.  

`maxit` Maximum number of NR iterations.
`report` Report fitting progress?
`sig` Significance level, for CIs.
`status_name` Name of the status indicator, 1 if observed, 0 if censored.
`tau` Optional truncation times for calculating RMSTs.
`time_name` Name of column containing the time to event.

**Value**

An object of class `fit` containing the following:

- **Parameters** The estimated shape $\alpha$ and rate $\lambda$.
- **Information** The observed information matrix.
- **Outcome** The fitted mean, median, and variance.
- **RMST** The estimated RMSTs, if tau was specified.

**Examples**

```r
# Generate Gamma data with 20% censoring.
data <- GenData(n = 1e3, dist = "gamma", theta = c(2, 2), p = 0.2)

# Estimate parameters.
fit <- FitParaSurv(data, dist = "gamma")
```

---

**FitGammaComplete**  
*Gamma Parameter Estimation without Censoring*

**Description**

Parameter estimation for gamma event times without censoring.

**Usage**

`FitGammaComplete(data, eps = 1e-06)`

**Arguments**

- `data` Data.frame.
- `eps` Tolerance for Newton-Raphson iterations.

**Value**

Numeric vector containing the estimated shape and rate parameters.
**Description**

Estimates parameters for generalized gamma event times subject to non-informative right censoring. The gamma distribution is parameterized in terms of the shape parameters \((\alpha, \beta)\), and the rate \(\lambda\):

\[
f(t) = \frac{\beta \lambda}{\Gamma(\alpha)} (\lambda t)^{\alpha \beta - 1} e^{-\lambda t}, \quad t > 0
\]

**Usage**

```r
FitGenGamma(
  data,
  beta_lower = 0.1,
  beta_upper = 10,
  eps = 1e-06,
  init = list(),
  maxit = 10,
  report = FALSE,
  sig = 0.05,
  status_name = "status",
  tau = NULL,
  time_name = "time"
)
```

**Arguments**

- **data**  
  Data.frame.
- **beta_lower**  
  If dist="gen-gamma", lower limit on possible values for beta.
- **beta_upper**  
  If dist="gen-gamma", upper limit on possible values for beta.
- **eps**  
  Tolerance for Newton-Raphson iterations.
- **init**  
  List with initial values for the shape ‘alpha’, ‘beta’ and rate ‘lambda’ parameters.
- **maxit**  
  Maximum number of NR iterations.
- **report**  
  Report fitting progress?
- **sig**  
  Significance level, for CIs.
- **status_name**  
  Name of the status indicator, 1 if observed, 0 if censored.
- **tau**  
  Optional truncation times for calculating RMSTs.
- **time_name**  
  Name of column containing the time to event.
Value

An object of class fit containing the following:

Parameters  The estimated shape ($\alpha, \beta$) and rate $\lambda$ parameters.
Information  The observed information matrix.
Outcome     The fitted mean, median, and variance.
RMST        The estimated RMSTs, if tau was specified.

Examples

```r
set.seed(103)
# Generate generalized gamma data with 20% censoring.
data <- GenData(n = 1e4, dist = "gen-gamma", theta = c(2, 2, 2), p = 0.2)

# Estimate parameters.
fit <- FitParaSurv(data, dist = "gen-gamma", report = TRUE)
```

---

**FitGenGammaComplete**  
*Generalized Gamma Parameter Estimation without Censoring*

Description

Parameter estimation for generalized gamma event times without censoring.

Usage

`FitGenGammaComplete(data, beta_lower = 0.1, beta_upper = 10)`

Arguments

- **data**  
  Data.frame.
- **beta_lower**  
  Lower limit on possible values for beta.
- **beta_upper**  
  Upper limit on possible values for beta.

Value

Numeric vector containing the estimated shape and rate parameters.
FitLogNormal  

Log-Normal Distribution Parameter Estimation  

Description  
Estimates parameters for log-normal event times subject to non-informative right censoring. The log-normal distribution is parameterized in terms of the location $\mu$ and scale $\sigma$:  

$$f(t) = \phi\left(\frac{\ln t - \mu}{\sigma}\right) \frac{1}{t\sigma}, t > 0$$  

Usage  

FitLogNormal(  
data,  
es = 1e-06,  
init = list(),  
maxit = 10,  
report = FALSE,  
sig = 0.05,  
status_name = "status",  
 tau = NULL,  
time_name = "time"  
)  

Arguments  
data    Data.frame.  
es    Tolerance for Newton-Raphson iterations.  
init    List with initial values for the location ('loc') $\mu$ and 'scale' $\sigma$.  
maxit    Maximum number of NR iterations.  
report    Report fitting progress?  
sig    Significance level, for CIs.  
status_name    Name of the status indicator, 1 if observed, 0 if censored.  
 tau    Optional truncation times for calculating RMSTs.  
time_name    Name of column containing the time to event.  

Value  
An object of class fit containing the following:  

**Parameters**  
The estimated location $\mu$ and scale $\sigma$.  

**Information**  
The observed information matrix.  

**Outcome**  
The fitted mean, median, and variance.  

**RMST**  
The estimated RMSTs, if tau was specified.
Examples

# Generate log-normal data with 20% censoring.
data <- GenData(n = 1e3, dist = "log-normal", theta = c(0, 2), p = 0.2)

# Estimate parameters.
fit <- FitParaSurv(data, dist = "log-normal")

Description

Log-Normal Parameter Estimation without Censoring

Usage

FitLogNormComplete(data)

Arguments

data Data.frame.

Value

Numeric vector containing the estimate location and scale parameters.

Description

Estimates parametric survival distributions using event times subject to non-informative right censoring. Available distributions include: exponential, gamma, generalized gamma, log-normal, and Weibull.

Usage

FitParaSurv(
data,
beta_lower = 0.1,
beta_upper = 10,
dist = "weibull",
eps = 1e-06,
init = NULL,
maxit = 10,
report = FALSE,
sig = 0.05,
status_name = "status",
tau = NULL,
time_name = "time"
)

Arguments

- **data**: Data.frame containing the time to event and status.
- **beta_lower**: If dist="gen-gamma", lower limit on possible values for beta.
- **beta_upper**: If dist="gen-gamma", upper limit on possible values for beta.
- **dist**: String, distribution to fit, selected from among: exp, gamma, gen-gamma log-normal, and weibull.
- **eps**: Tolerance for Newton-Raphson iterations.
- **init**: List of initial parameters. See individual distributions for the expected parameters.
- **maxit**: Maximum number of NR iterations.
- **report**: Report fitting progress?
- **sig**: Significance level, for CIs.
- **status_name**: Name of the status indicator, 1 if observed, 0 if censored.
- **tau**: Optional truncation time for calculating RMSTs.
- **time_name**: Name of column containing the time to event.

Value

An object of class fit containing the following:

- **Parameters**: The estimated shape and rate parameters.
- **Information**: The observed information matrix.
- **Outcome**: The fitted mean, median, and variance.
- **RMST**: The estimated RMSTs, if tau was specified.

See Also

- Between group comparison of survival experience `CompParaSurv`
- Exponential distribution `FitExp`
- Gamma distribution `FitGamma`
- Generalized gamma distribution `FitGenGamma`
- Log-normal distribution `FitLogNormal`
- Weibull distribution `FitWeibull`
Examples

# Generate Gamma data with 20% censoring.
data <- GenData(n = 1e3, dist = "gamma", theta = c(2, 2), p = 0.2)
# Fit gamma distribution.
fit <- FitParaSurv(data, dist = "gamma")

# Generate Weibull data with 10% censoring.
data <- GenData(n = 1e3, dist = "weibull", theta = c(2, 2), p = 0.1)
# Fit weibull distribution, calculate RMST at tau=0.5.
fit <- FitParaSurv(data, dist = "weibull", tau = 0.5)

---

FitWeibull

Weibull Distribution Parameter Estimation

Description

Estimates parameters for Weibull event times subject to non-informative right censoring. The Weibull distribution is parameterized in terms of the shape $\alpha$ and rate $\lambda$:

$$ f(t) = \alpha \lambda t^{\alpha-1} e^{-(\lambda t)^\alpha}, t > 0 $$

Usage

FitWeibull(
    data,
    init = list(),
    sig = 0.05,
    status_name = "status",
    tau = NULL,
    time_name = "time"
)

Arguments

- data: Data.frame.
- init: List containing the initial value for the shape, $\alpha$.
- sig: Significance level, for CIs.
- status_name: Name of the status indicator, 1 if observed, 0 if censored.
- tau: Optional truncation times for calculating RMSTs.
- time_name: Name of column containing the time to event.

Value

An object of class fit containing the following:

- **Parameters**  The estimated shape $\alpha$ and rate $\lambda$.
- **Information** The observed information matrix.
- **Outcome**  The fitted mean, median, and variance.
- **RMST**  The estimated RMSTs, if tau was specified.
Examples

# Generate Weibull data with 20% censoring.
data <- GenData(n = 1e3, dist = "weibull", theta = c(2, 2), p = 0.2)

# Estimate parameters.
fit <- FitParaSurv(data, dist = "weibull")

-----------

**GammaInfo**

*Gamma Observed Information*

**Description**

Observed information for gamma event times without censoring.

**Usage**

GammaInfo(data, shape, rate)

**Arguments**

- **data**: Data.frame.
- **shape**: Shape parameter $\alpha$.
- **rate**: Rate parameter $\lambda$.

**Value**

Numeric information matrix.

-----------

**GammaScore**

*Gamma Profile Score for Shape*

**Description**

Profile score equation for gamma event times without censoring.

**Usage**

GammaScore(data, shape)

**Arguments**

- **data**: Data.frame.
- **shape**: Shape parameter.

**Value**

Numeric score.
Description

Generates data from survival distributions as parameterized in this package, with optional non-informative random right censoring.

Usage

GenData(n, dist = "exp", theta = NULL, p = 0)

Arguments

n Integer sample size.

dist String, distribution name selected from among: "exp","gamma","gen-gamma","log-normal","weibull".

theta Numeric parameter vector. Elements will vary according to the distribution.

p Expected censoring proportion.

Details

The parameter vector theta should contain the following elements, in order, depending on the distribution:

- **Exponential** Rate $\lambda$.
- **Gamma** Shape $\alpha$, rate $\lambda$.
- **Generalized Gamma** Shape 1 $\alpha$, shape 2 $\beta$, rate $\lambda$.
- **Log-Normal** Location $\mu$, scale $\sigma$.
- **Weibull** Shape $\alpha$, rate $\lambda$.

Value

Data.frame including the observation times and status.

Examples

# Gamma event times with shape 2 and rate 2.
# Expected censoring proportion of 20%.
data <- GenData(n = 1e3, dist = "gamma", theta = c(2, 2), p = 0.20)

# Generalized gamma event times with shapes (2,3) and rate 1.
# Expected censoring proportion of 15%.
data <- GenData(n = 1e3, dist = "gen-gamma", theta = c(2, 3, 1), p = 0.15)

# Log-normal event times with location 0 and rate 1.
# Expected censoring proportion of 10%.
data <- GenData(n = 1e3, dist = "log-normal", theta = c(0, 1), p = 0.10)

# Weibull event times with shape 2 and rate 2.
# Expected censoring proportion of 5%.
data <- GenData(n = 1e3, dist = "weibull", theta = c(2, 2), p = 0.05)

GenGammaObsInfo  
Generalized Gamma Observed Information

Description
Observed information for the generalized gamma log likelihood in the absence of censoring.

Usage
GenGammaObsInfo(data, alpha, beta, lambda)

Arguments
  data  Data.frame.
  alpha  First shape parameter.
  beta  Second shape parameter.
  lambda  Rate parameter.

Value
Numeric observed information matrix.

GenGammaProfileLogLik  Generalized Gamma Profile Log Likelihood

Description
Profile log likelihood of the generalized gamma distribution as a function of the second shape parameter $\beta$.

Usage
GenGammaProfileLogLik(data, beta)

Arguments
  data  Data.frame.
  beta  Second shape parameter.

Value
Numeric profile log likelihood.
**GenGammaRate**  

*Generalized Gamma Rate MLE*

---

**Description**

Profile MLE of the generalized gamma rate given the shape parameters.

**Usage**

GenGammaRate(data, alpha, beta)

**Arguments**

- **data**: Data.frame.
- **alpha**: First shape parameter.
- **beta**: Second shape parameter.

**Value**

Numeric MLE of the rate $\lambda$.

---

**GenGammaScore**  

*Generalized Gamma Score Equation*

---

**Description**

Score equation for the generalized gamma log likelihood in the absence of censoring.

**Usage**

GenGammaScore(data, alpha, beta, lambda)

**Arguments**

- **data**: Data.frame.
- **alpha**: First shape parameter.
- **beta**: Second shape parameter.
- **lambda**: Rate parameter.

**Value**

Numeric score vector.
GenGammaShape  Generalized Gamma Shape MLE

Description
Profile MLE of the first shape parameter $\alpha$ of the generalized gamma given the second shape parameter $\beta$.

Usage
GenGammaShape(data, beta)

Arguments
- data: Data.frame.
- beta: Second shape parameter.

Value
Numeric MLE of the rate $\alpha$.

LogNormInfo  Log-Normal Observed Information

Description
Observed information for log-normal event times without censoring.

Usage
LogNormInfo(data, loc, scale, log_scale = FALSE)

Arguments
- data: Data.frame.
- loc: Location parameter.
- scale: Scale parameter.
- log_scale: Is the scale parameter logged?

Value
Numeric score.
**LogNormScore**

**Log-Normal Score Equation**

**Description**
Score equation for log-normal event times without censoring.

**Usage**
LogNormScore(data, loc, scale)

**Arguments**
- data: Data.frame.
- loc: Location parameter.
- scale: Scale parameter.

**Value**
Numeric score.

---

**NewtonRaphson**

**Newton Raphson Estimation**

**Description**
Newton Raphson Estimation

**Usage**
NewtonRaphson(init, obj, eps = 1e-06, maxit = 10, report = FALSE)

**Arguments**
- init: Initial value.
- obj: Objective function.
- eps: Tolerance for Newton-Raphson iterations.
- maxit: Maximum number of NR iterations.
- report: Report fitting progress?

**Value**
Numeric parameter estimate.
NRUpdate  Newton Raphson Update Iteration

**Description**

Newton Raphson Update Iteration

**Usage**

NRUpdate(obj, state)

**Arguments**

- **obj**  Objective function.
- **state**  List containing the parameter vector ‘theta’.

**Value**

List containing the updated parameter vector ‘theta’ and the objective increment ‘delta’.

---

ParaRMST  Restricted Mean Survival Time

**Description**

Calculates the RMST as the area under a fitted parametric survival distribution.

**Usage**

ParaRMST(fit, tau, sig = 0.05)

**Arguments**

- **fit**  Fitted parametric survival distribution.
- **tau**  Numeric vector of truncation times.
- **sig**  Significance level, for CIs.

**Value**

Data.frame containing the estimated RMST at each truncation time.
Examples

# Generate Weibull data with 20% censoring.
data <- GenData(n = 1e3, dist = "weibull", theta = c(2, 0.5), p = 0.2)

# Fit Weibull distribution.
fit <- FitParaSurv(data, dist = "weibull")

# Calculate RMSTs.
rmst <- ParaRMST(fit = fit, tau = c(0.5, 1.0, 1.5, 2.0))

# Generate gamma data with 10% censoring.
data <- GenData(n = 1e3, dist = "gamma", theta = c(2, 2), p = 0.10)

# Fit gamma distribution.
fit <- FitParaSurv(data, dist = "gamma")

# Calculate RMSTs.
rmst <- ParaRMST(fit = fit, tau = c(0.5, 1.0, 1.5, 2.0))

PermP

<table>
<thead>
<tr>
<th>PermP</th>
<th>Permutation P Value</th>
</tr>
</thead>
</table>

Description

Calculates permutation p-values for location and RMST estimates.

Usage

PermP(df1, df0, fit0, fit1, eps, init1, init0, maxit, reps, tau)

Arguments

df1 Target data.frame containing time and status.
df0 Reference data.frame containing time and status.
fit0 Fitted parametric survival distribution for arm 0.
fit1 Fitted parametric survival distribution for arm 1.
eps Tolerance for Newton-Raphson iterations.
init1 Initial parameter values for the target group.
init0 Initial parameter values for the reference group.
maxit Maximum number of Newton-Raphson iterations.
reps Number of permutation replicates.
tau Optional truncation times for calculating RMST.

Value

Numeric vector of permutation p-values.
print.contrast  \hspace{0.5cm} \textit{Print Method for a Contrast of Survival Distributions.}

\section*{Description}

Print method for an object of class \texttt{contrast}.

\section*{Usage}

\begin{verbatim}
## S3 method for class 'contrast'
print(x, ...)
\end{verbatim}

\section*{Arguments}

\begin{itemize}
  \item \texttt{x} \hspace{1cm} A contrast object.
  \item \texttt{...} \hspace{1cm} Unused.
\end{itemize}

print.fit \hspace{0.5cm} \textit{Print Method for Fitted Survival Distributions}

\section*{Description}

Print method for objects of class \texttt{fit}.

\section*{Usage}

\begin{verbatim}
## S3 method for class 'fit'
print(x, ...)
\end{verbatim}

\section*{Arguments}

\begin{itemize}
  \item \texttt{x} \hspace{1cm} An object of class \texttt{fit}.
  \item \texttt{...} \hspace{1cm} Unused.
\end{itemize}
QF  

Quadratic Form

Description
Quadratic Form

Usage
QF(x, A)

Arguments
x  Numeric vector.
A  Numeric matrix.

Value
Numeric scalar.

qWeibull  
Quantile Function for the Weibull Distribution

Description
Quantile function for the Weibull distribution. See FitWeibull for the parameterization.

Usage
qWeibull(p, a = 1, l = 1)

Arguments
p  Probability.
a  Shape.
l  Rate.

Value
Scalar quantile.
rGamma

*Simulation from the Gamma Distribution*

**Description**

Generates gamma event times with shape parameter $\alpha$ and rate parameter $\lambda$. See `FitGamma` for the parameterization. If a censoring proportion $p$ is provided, the event times are subject to non-informative random right censoring.

**Usage**

```r
rGamma(n, a = 1, l = 1, p = 0)
```

**Arguments**

- `n`: Sample size.
- `a`: Shape.
- `l`: Rate.
- `p`: Expected censoring proportion.

**Value**

Data.frame including the observation times and status.

---

rGenGamma

*Simulation from the Generalized Gamma Distribution*

**Description**

Generates generalized gamma event times with shape parameters $(\alpha, \beta)$, and rate parameter $\lambda$. See `FitGenGamma` for the parameterization. If a censoring proportion $p$ is provided, the event times are subject to non-informative random right censoring.

**Usage**

```r
rGenGamma(n, a = 1, b = 1, l = 1, p = 0)
```

**Arguments**

- `n`: Sample size.
- `a`: First shape parameter, $\alpha$.
- `b`: Second shape parameter, $\beta$. For the standard gamma distribution, set $\beta = 1$.
- `l`: Rate.
- `p`: Expected censoring proportion.
Value

Data.frame including the observation times and status indicators.

---

**rLogNormal**  
*Simulation from the Log-Normal Distribution*

Description

Generates log-normal event times with location parameter $\mu$ and scale parameter $\sigma$. See `FitLogNormal` for the parameterization. If a censoring proportion $p$ is provided, the event times are subject to non-informative random right censoring.

Usage

```r
rLogNormal(n, m = 0, s = 1, p = 0)
```

Arguments

- `n` Sample size.
- `m` Location.
- `s` Scale.
- `p` Expected censoring proportion.

Value

Data.frame including the observation time and status.

---

**RoundDF**  
*Round Data Frames*

Description

Round Data Frames

Usage

```r
RoundDF(df, digits = 3)
```

Arguments

- `df` Data.frame.
- `digits` Integer.

Value

Data.frame.
**rWeibull**  
*Simulation from the Weibull Distribution*

**Description**
Generates Weibull event times with shape parameter $\alpha$ and rate parameter $\lambda$. See `FitWeibull` for the parameterization. If a censoring proportion $p$ is provided, the deviates are subject to non-informative random right censoring.

**Usage**
```
   rWeibull(n, a = 1, l = 1, p = 0)
```

**Arguments**
- `n` Sample size.
- `a` Shape.
- `l` Rate.
- `p` Expected censoring proportion.

**Value**
Data.frame including the observation time and status.

**show,contrast-method**  
*Show Method for a Contrast of Survival Distributions.*

**Description**
Show Method for a Contrast of Survival Distributions.

**Usage**
```
   ## S4 method for signature 'contrast'
   show(object)
```

**Arguments**
- `object` An object of class contrast.
**show,fit-method**  

*Show Method for Fitted Survival Distributions*

### Description

Show Method for Fitted Survival Distributions

### Usage

```r
## S4 method for signature 'fit'
show(object)
```

### Arguments

- **object**  
  An object of class `fit`.

**SurvFunc**  

*Survival Functions*

### Description

Constructs the survival function for a parameter distribution.

### Usage

```r
SurvFunc(dist, theta)
```

### Arguments

- **dist**  
  String, distribution name.
- **theta**  
  Numeric parameter vector.

### Details

The parameter vector theta should contain the following elements, in order, according to the distribution:

- **Exponential**  
  Rate λ.
- **Gamma**  
  Shape α, rate λ.
- **Generalized Gamma**  
  Shape 1 α, shape 2 β, rate λ.
- **Log-Normal**  
  Location μ, scale σ.
- **Weibull**  
  Shape α, rate λ.

### Value

Survival function.
Examples

# Survival function for the generalized gamma.
surv <- SurvFunc(dist = "gen-gamma", theta = c(2, 2, 2))

# Evaluation.
surv(1.0)

SurvLogLik

Log Likelihood

Description

Evaluates the log-likelihood for a parametric survival distribution.

Usage

SurvLogLik(
  data,
  dist,
  theta,
  log_scale = FALSE,
  status_name = "status",
  time_name = "time"
)

Arguments

data Data.frame
dist Distribution, from among: "exp", "gamma", "gen-gamma", "log-normal", "weibull".
theta Parameters, which will vary according to the distribution.
log_scale Are strictly positive parameters on log-scale?
status_name Status indicator, coded as 1 if an event was observed, 0 if censored.
time_name Name of column containing the time to event.

Details

The parameter vector theta should contain the following elements, in order, depending on the distribution:

- **Exponential** Rate $\lambda$.
- **Gamma** Shape $\alpha$, rate $\lambda$.
- **Generalized Gamma** Shape 1 $\alpha$, shape 2 $\beta$, rate $\lambda$.
- **Log-Normal** Location $\mu$, scale $\sigma$.
- **Weibull** Shape $\alpha$, rate $\lambda$. 
Temporal: Utilities for Parametric Survival Analysis

Value

Scalar value of the log likelihood.

Examples

# Generate gamma event time data with 10% censoring.
data <- GenData(n = 1e3, dist = "gamma", theta = c(2, 2), p = 0.1)

# Evaluate log likelihood.
ll <- SurvLogLik(data, dist = "gamma", theta = c(2, 2))

# Generate Weibull event time data with 20% censoring.
data <- GenData(n = 1e3, dist = "weibull", theta = c(2, 2), p = 0.2)

# Evaluate log likelihood.
ll <- SurvLogLik(data, dist = "weibull", theta = c(2, 2))

Temporal

Temporal: Utilities for Parametric Survival Analysis

Description

This package performs estimation and inference on parametric survival curves. See FitParaSurv for maximum likelihood estimation of model parameters. See CompParaSurv for contrasting the survival experience of two treatment arms.

Author(s)

Zachary R. McCaw

Weibull Information Matrix.

Description

Information matrix for the Weibull shape and rate parameters.

Usage

WeiInfo(data, shape, rate)

Arguments

data Data.frame.
shape Shape parameter, alpha.
rate Rate parameter, lambda.
WeiInit

**Description**
Weibull Initialization.

**Usage**
```r
WeiInit(data, init)
```

**Arguments**
- `data` Data.frame.
- `init` Initialization list.

**Value**
Numeric initial value for shape.

WeiRate

**Description**
Profile MLE of the Weibull rate as a function of the shape.

**Usage**
```r
WeiRate(data, shape)
```

**Arguments**
- `data` Data.frame.
- `shape` Shape parameter.

**Value**
Numeric rate.
**WeiScore**

*Weibull Profile Score for Shape*

---

**Description**

Profile score equation for the Weibull shape parameter.

**Usage**

`WeiScore(data, shape)`

**Arguments**

- `data` : Data.frame.
- `shape` : Shape parameter.

**Value**

Numeric score.
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