Package ‘Temporal’

March 16, 2020

Title Parametric Time to Event Analysis
Version 0.2.0
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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bootCI

Description

Bootstrap CIs

Generates bootstrap confidence intervals for location and RMST estimates.
**checkArm**

**Usage**

```
bootCI(d1, d0, tau = NULL, dist1, dist0, B = 2000, sig)
```

**Arguments**

- **d1**: Target data frame containing time and status.
- **d0**: Reference data frame containing time and status.
- **tau**: Optional truncation times for calculating restricted mean survival time.
- **dist1**: String, target distribution.
- **dist0**: String, reference distribution.
- **B**: Number of resamples.
- **sig**: Significance level, for CIs.

**Value**

List containing data frames with the bootstrap CIs for the location and RMST estimates.

---

**checkArm**

**Check Arm**

**Description**

Check whether treatment arm is properly formatted.

**Usage**

```
checkArm(arm, n)
```

**Arguments**

- **arm**: 0/1, treatment arm.
- **n**: Integer, sample size.

**Value**

Logical indication of whether arm was properly formatted.
checkDist  

*Check Distribution*

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

**Usage**  
checkDist(dist)

**Arguments**  

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dist</td>
<td>String, distribution name.</td>
</tr>
</tbody>
</table>

**Value**  
Logical indication of whether the distribution was available.

checkInit  

*Check Initialization*

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

**Usage**  
checkInit(dist, init)

**Arguments**  

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dist</td>
<td>String, distribution name.</td>
</tr>
<tr>
<td>init</td>
<td>Numeric vector, initialization.</td>
</tr>
</tbody>
</table>

**Value**  
Logical indication of whether the initialization was valid.
checkStatus

Status Check

Description
Function to ensure the status indicator is properly formatted

Usage
checkStatus(n, status)

Arguments
n Integer, sample size.
status 0/1 status indicator.

Value
Logical indicator of whether the status indicator was properly formatted.

checkTheta

Check Theta

Description
Function to check the appropriate number of parameters are supplied for the selected distribution.

Usage
checkTheta(dist, theta)

Arguments
dist String, distribution.
theta Numeric, parameter vector.

Value
Logical indication of whether the appropriate number of parameters was provided.
compParaSurv  

**Compare Parametric Survival Distribution**

**Description**

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

**Usage**

```r
compParaSurv(
  time,
  status = NULL,
  arm,
  tau = NULL,
  dist1 = "weibull",
  dist0 = NULL,
  init1 = NULL,
  init0 = NULL,
  boot = NULL,
  perm = NULL,
  sig = 0.05,
  eps = 1e-06,
  maxit = 10,
  report = F
)
```

**Arguments**

- `time`: Observation time.
- `status`: Status indicator, coded as 1 if an event was observed, 0 if censored.
- `arm`: Treatment indicator, coded as 1 for the target group, 0 for the reference group.
- `tau`: Optional truncation times for calculating RMST.
- `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.
- `init1`: Initial parameter values for the target group.
- `init0`: Initial parameter values for the reference group.
- `boot`: If provided, integer number of bootstraps for constructing CIs.
- `perm`: If provided, integer number of permutations for calculating p-values.
- `sig`: Significance level, for CIs.
- `eps`: Tolerance for Newton-Raphson iterations.
compParaSurv

maxit    Maximum number of NR iterations.
report   Report fitting progress?

Details

Status is encoded 0 for censored and 1 for observed. Arm is encoded 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.

See Also

- Fitting function for parametric survival distributions fitParaSurv

Examples

```r
## Not run:
set.seed(100);
# Weibull and Weibull, different means and medians
n = 1e3;
## Target group
d1 = genData(n=n,dist="weibull",theta=c(1,1),p=0.2);
d1$arm = 1;
## Reference group
d0 = genData(n=n,dist="weibull",theta=c(1,2),p=0.2);
d0$arm = 0;
## Overall data set
data = rbind(d1,d0);
## Comparison
comp = compParaSurv(time=data$time,status=data$status,arm=data$arm,tau=0.5,dist1="weibull");

# Gamma and Weibull, same mean, different medians, bootstrap CIs
## Target group
d1 = genData(n=n,dist="gamma",theta=c(2,2),p=0.2);
d1$arm = 1;
## Reference group
d0 = genData(n=n,dist="weibull",theta=c(2,sqrt(pi)/2),p=0.2);
d0$arm = 0;
## Overall data set
data = rbind(d1,d0);
## Comparison
comp = compParaSurv(time=data$time,status=data$status,arm=data$arm,
tau=0.5,dist1="gamma",dist0="weibull",boot=2e3);
```
# Weibull and Log-normal, different means, same median, permutation p.values

## Target group
d1 = genData(n=n,dist="log-normal",theta=c(0,2),p=0.2);
d1$arm = 1;

## Reference group
d0 = genData(n=n,dist="weibull",theta=c(2,sqrt(log(2))),p=0.2);
d0$arm = 0;

## Overall data set
data = rbind(d1,d0);

## Comparison
comp = compParaSurv(time=data$time,status=data$status,arm=data$arm,
                     tau=0.5,dist1="log-normal",dist0="weibull",perm=2e3);

## End(Not run)

defaultParam

**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.

**defaultParam**  
Set Default Parameters

**Description**

Function to select default parameter values for each distribution.

**Usage**

defaultParam(dist)

**Arguments**

- **dist**  String, distribution name.
**estDiff**  

*Difference of Estimates*

**Value**

Numeric parameter vector

**Description**

Calculate CIs and p-value for the difference of estimated parameters

**Usage**

```r
estDiff(t1, s1, t0, s0, sig = 0.05)
```

**Arguments**

- **t1**: Treatment estimate
- **s1**: Treatment standard error
- **t0**: Reference estimate
- **s0**: Reference 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 estimated parameters

**Usage**

```r
estRatio(t1, s1, t0, s0, sig = 0.05)
```

**Arguments**

- **t1**: Treatment estimate
- **s1**: Treatment standard error
- **t0**: Reference estimate
- **s0**: Reference 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.

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.

fit.Exp  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

fit.Exp(time, status, sig = 0.05, tau = NULL)

Arguments

- time: Numeric observation times.
- status: Status indicator, coded as 1 if an event was observed, 0 if censored.
- sig: Significance level, for CIs.
- tau: Optional truncation times for calculating RMSTs.
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.

See Also

- Fitting function for parametric survival distributions `fitParaSurv`

Examples

```r
# Generate exponential data with 20% censoring
data = genData(n=1e3,dist="exp",theta=c(2),p=0.2);
# Estimate
fit = fitParaSurv(time=data$time,status=data$status,dist="exp");
```

---

**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**

```r
fit.Gamma(
    time,
    status,
    sig = 0.05,
    tau = NULL,
    init = NULL,
    eps = 1e-06,
    maxit = 10,
    report = FALSE
)
```
Arguments

- **time**: Numeric observation times.
- **status**: Status indicator, coded as 1 if an event was observed, 0 if censored.
- **sig**: Significance level, for CIs.
- **tau**: Optional truncation times for calculating RMSTs.
- **init**: Vector of initial values for shape $\alpha$ and rate $\lambda$ parameters, respectively.
- **eps**: Tolerance for Newton-Raphson iterations.
- **maxit**: Maximum number of NR iterations.
- **report**: Report fitting progress?

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.

See Also

- Fitting function for parametric survival distributions `fitParaSurv`

Examples

```r
# Generate Gamma data with 20% censoring.
data = genData(n=1e3,dist="gamma",theta=c(2,2),p=0.2);
# Estimate
fit = fitParaSurv(time=data$time,status=data$status,dist="gamma");
```

---

fit.Gamma.Complete

*Gamma Distribution Parameter Estimation without Censoring*

Description

Estimates parameters for gamma event times not subject to censoring.

Usage

`fit.Gamma.Complete(time, eps = 1e-06)`

Arguments

- **time**: Observation times.
- **eps**: Tolerance for Newton-Raphson iterations.
fit.GenGamma

Generalized Gamma Distribution Parameter Estimation

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 \(\lambda\):

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

Usage

fit.GenGamma(
  time,
  status,
  sig = 0.05,
  tau = NULL,
  init,
  bL = 0.1,
  bU = 10,
  eps = 1e-06,
  maxit = 10,
  report = FALSE
)

Arguments

time: Numeric observation times.
status: Status indicator, coded as 1 if an event was observed, 0 if censored.
sig: Significance level, for CIs.
tau: Optional truncation times for calculating RMSTs.
init: Vector of initial values for the shape \(\alpha, \beta\), and rate \(\lambda\) parameters, respectively.
bL: Lower limit on possible values for beta.
bU: Upper limit on possible values for beta.
eps: Tolerance for Newton-Raphson iterations.
maxit: Maximum number of NR iterations.
report: Report fitting progress?

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.
See Also

- Fitting function for parametric survival distributions `fitParaSurv`

Examples

```r
set.seed(103);
# Generalized Gamma data with 20% censoring.
data = genData(n=1e4,dist="gen-gamma",theta=c(2,2,2),p=0.2);
# Estimate
fit = fitParaSurv(time=data$time,status=data$status,dist="gen-gamma",report=TRUE);
```

---

**fit.GenGamma.Complete**  Initialization for Generalized Gamma

**Description**

Initializes the parameters for the generalized gamma distribution via maximum likelihood.

**Usage**

`fit.GenGamma.Complete(time, bL, bU)`

**Arguments**

- `time`: Observed event times.
- `bL`: Lower limit on possible values for beta.
- `bU`: Upper limit on possible values for beta.

**Value**

3x1 numeric vector of estimated parameters, $\alpha, \beta, \lambda$.

---

**fit.LogNormal**  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

fit.LogNormal(
  time,
  status,
  sig = 0.05,
  tau = NULL,
  init = NULL,
  eps = 1e-06,
  maxit = 10,
  report = F
)

Arguments

- time: Numeric observation times.
- status: Status indicator, coded as 1 if an event was observed, 0 if censored.
- sig: Significance level, for CIs.
- tau: Optional truncation times for calculating RMSTs.
- init: Vector of initial values for the location $\mu$ and scale $\sigma$.
- eps: Tolerance for Newton-Raphson iterations.
- maxit: Maximum number of NR iterations.
- report: Report fitting progress?

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.

See Also

- Fitting function for parametric survival distributions fitParaSurv

Examples

# Generate Log-Normal data with 20% censoring.
data = genData(n=1e3,dist="log-normal",theta=c(0,2),p=0.2);
# Estimate
fit = fitParaSurv(time=data$time,status=data$status,dist="log-normal");
fit.Weibull  

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 $\lambda$:

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

Usage

`fit.Weibull(time, status, sig = 0.05, tau = NULL, init = NULL)`

Arguments

- `time` Numeric observation times.
- `status` Status indicator, coded as 1 if an event was observed, 0 if censored.
- `sig` Significance level, for CIs.
- `tau` Optional truncation times for calculating RMSTs
- `init` Numeric vector containing the initial value for $\alpha$.

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.

See Also

- Fitting function for parametric survival distributions `fitParaSurv`

Examples

```r
# Generate Weibull data with 20% censoring
data = genData(n=1e3,dist="weibull",theta=c(2,2),p=0.2);
# Estimate
fit = fitParaSurv(time=data$time,status=data$status,dist="weibull");```
**fitParaSurv**

**Fit Parametric Survival Distribution**

**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**

```r
fitParaSurv(
  time,
  status = NULL,
  dist = "weibull",
  tau = NULL,
  sig = 0.05,
  init = NULL,
  bL = 0.1,
  bU = 10,
  eps = 1e-06,
  maxit = 10,
  report = F
)
```

**Arguments**

- **time**: Numeric observation times.
- **status**: Status indicator, coded as 1 if observed, 0 if censored.
- **dist**: String, distribution to fit, selected from among: exp, gamma, gen-gamma log-normal, and weibull.
- **tau**: Optional truncation time for calculating RMSTs.
- **sig**: Significance level, for CIs.
- **init**: Numeric vector of initial parameters. See individual distributions for parameter order.
- **bL**: If dist="gen-gamma", lower limit on possible values for beta.
- **bU**: If dist="gen-gamma", upper limit on possible values for beta.
- **eps**: Tolerance for Newton-Raphson iterations.
- **maxit**: Maximum number of NR iterations.
- **report**: Report fitting progress?
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 `fit.Exp`
- Gamma distribution `fit.Gamma`
- Generalized gamma distribution `fit.GenGamma`
- Log-normal distribution `fit.LogNormal`
- Weibull distribution `fit.Weibull`

Examples

```r
# Generate Gamma data with 20% censoring
D = genData(n=1e3,dist="gamma",theta=c(2,2),p=0.2);
# Fit gamma distribution
M = fitParaSurv(time=D$time,status=D$status,dist="gamma");

# Generate Weibull data with 10% censoring
D = genData(n=1e3,dist="weibull",theta=c(2,2),p=0.1);
# Fit weibull distribution, calculate RMST at tau=0.5
M = fitParaSurv(time=D$time,status=D$status,dist="weibull",tau=0.5);
```

Description

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

Usage

```r
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 indicators.

Examples

```r
# 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);
```

---

**matInv**  

*Matrix Inverse*

Description

Calculates \( A^{-1} \).

Usage

```r
matInv(A)
```

Arguments

- \( A \)  Numeric matrix.

Value

Numeric matrix.
**matIP**  
*Matrix Inner Product*

**Description**  
Calculates the product $A'B$.

**Usage**  
\[
\text{matIP}(A, B)
\]

**Arguments**  
- **A**  
  Numeric matrix.
- **B**  
  Numeric matrix.

**Value**  
Numeric matrix.

---

**matOP**  
*Matrix Outer Product*

**Description**  
Calculates the outer product $AB'$.

**Usage**  
\[
\text{matOP}(A, B)
\]

**Arguments**  
- **A**  
  Numeric matrix.
- **B**  
  Numeric matrix.

**Value**  
Numeric matrix.
## matQF

### Quadratic Form

**Description**
Calculates the quadratic form $X'AX$.

**Usage**

```
matQF(X, A)
```

**Arguments**

- **X**: Numeric matrix.
- **A**: Numeric matrix.

**Value**
Numeric matrix.

## MMP

### Matrix Matrix Product

**Description**
Calculates the product $AB$.

**Usage**

```
MMP(A, B)
```

**Arguments**

- **A**: Numeric matrix.
- **B**: Numeric matrix.

**Value**
Numeric matrix.
**paraRMST**

*Restricted Mean Survival Time*

**Description**

Calculates the tau-year RMST for a fitted parametric model.

**Usage**

\[
\text{paraRMST}(\text{fit}, \text{sig} = 0.05, \text{tau})
\]

**Arguments**

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

**Value**

Data.table containing the estimated RMST at each truncation time.

**Examples**

```r
# Generate Weibull data with 20% censoring.
data = genData(n=1e3,dist="weibull",theta=c(2,0.5),p=0.2);
fit = fitParaSurv(time=data$time,status=data$status,dist="weibull");
rmst = paraRMST(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 = fitParaSurv(time=data$time,status=data$status,dist="gamma");
rmst = paraRMST(fit,tau=c(0.5,1.0,1.5,2.0));
```

**permP**

*Permutation P Value*

**Description**

Calculates permutation p-values for location and RMST estimates.

**Usage**

\[
\text{permP}(d1, d0, \text{tau}, \text{dist1}, \text{dist0}, B = 1999)
\]
Arguments

d1 Target data.frame containing time and status.
d0 Reference data.frame containing time and status.
tau Optional truncation times for calculating restricted mean survival time.
dist1 String, target distribution.
dist0 String, reference distribution.
B Number of resamples.

Value
List containing data.frames with the bootstrap CIs for the location and RMST estimates.

print.contrast
Print Method for a Contrast of Survival Distributions.

Description
Print method for an object of class contrast.

Usage
## S3 method for class 'contrast'
print(x, ...)

Arguments
x A contrast object.
... Unused.

print.fit
Print Method for Fitted Survival Distributions

Description
Print method for objects of class fit.

Usage
## S3 method for class 'fit'
print(x, ...)

Arguments
x An object of class fit.
... Unused.
qWeibull  
Quantile Function for the Weibull Distribution

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

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

Arguments
p Probability.
 a Shape.
 l Rate.

Value
Scalar quantile.

resample  
Resample Data

Description
Generates a resampled data.frame with replacement.

Usage
resample(data)

Arguments
data Input data.frame

Value
Data.frame resampled from the input.
**rGamma**

*Simulation from the Gamma Distribution*

**Description**
Generates gamma event times with shape parameter $\alpha$ and rate parameter $\lambda$. See `fit.Gamma` 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 indicators.

---

**rGenGamma**

*Simulation from the Generalized Gamma Distribution*

**Description**
Generates generalized gamma event times with shape parameters $(\alpha, \beta)$, and rate parameter $\lambda$. See `fit.GenGamma` 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.
rLogNormal
Simulation from the Log-Normal Distribution

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

Usage
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 times and status indicators.

rWeibull
Simulation from the Weibull Distribution

Description
Generates Weibull event times with shape parameter $\alpha$ and rate parameter $\lambda$. See fit.Weibull 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 times and status indicators.

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

## 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**

```
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 $\lambda$.
- **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**

Survival function.

---

survLogLik  

**Log Likelihood**

**Description**

Evaluates the log-likelihood for a parametric survival distribution.

**Usage**

```
survLogLik(time, status = NULL, dist, theta, log.scale = FALSE)
```
Temporal: Utilities for Parametric Survival Analysis

Arguments

- **time**: Numeric observation times.
- **status**: Status indicator, coded as 1 if an event was observed, 0 if censored.
- **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?

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

Scalar value of the log likelihood.

Examples

```r
# Generate Weibull data with 20% censoring.
data = genData(n=1e3,dist="weibull",theta=c(2,2),p=0.2);
# Log likelihood
ll = survLogLik(time=data$time,status=data$status,dist="weibull",theta=c(2,2));

# Generate Gamma data with 10% censoring.
data = genData(n=1e3,dist="gamma",theta=c(2,2),p=0.1);
# Log likelihood
ll = survLogLik(time=data$time,status=data$status,dist="gamma",theta=c(2,2));
```

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)

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