

# Package ‘survtype’

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**Type** Package

**Title** Subtype Identification with Survival Data

**Description** Subtypes are defined as groups of samples that have distinct molecular and clinical features. Genomic data can be analyzed for discovering patient subtypes, associated with clinical data, especially for survival information. This package is aimed to identify subtypes that are both clinically relevant and biologically meaningful.

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**Suggests** maftools, scales, knitr, rmarkdown

**License** Artistic-2.0

**biocViews** Software, StatisticalMethod, GeneExpression, Survival, Clustering, Sequencing, Coverage

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Exprs.survtype	<i>Sample subtype identification via survival information and gene expression data</i>
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**Description**

For discovery of subtypes of samples that are both clinically relevant and biologically meaningful, the Cox regression model and hierarchical clustering are combined.

**Usage**

```
Exprs.survtype(surv.data, time, status, exprs.data, K = 2, num.genes = 100,
              gene.sel = FALSE, gene.sel.opt = list(verbose = FALSE), ...)
```

**Arguments**

surv.data	survival data
time	survival time
status	status indicator
exprs.data	expression data
K	the number of clusters (default: 2)
num.genes	the number of top genes based on the Cox score, before variable selection (default: 100)
gene.sel	a logical value indicating whether or not gene selection for clustering is applied (default: FALSE)
gene.sel.opt	a list of options for the gene selection function "clustvarsel". "verbose" is set to FALSE as default.
...	additional parameters for the "pheatmap"

**Value**

n	the number of subjects in each group
obs	the weighted observed number of events in each group
exp	the weighted expected number of events in each group
chisq	the chi-squared statistic for a test of equality
call	the matched call
fit	fitted survival curves
cluster	a vector of integers indicating the cluster to which each sample is assigned
time	survival time
status	status indicator
surv.data	survival data
exprs.data	expression data

**Author(s)**

Dongmin Jung

## References

Bair, E., & Tibshirani, R. (2004). Semi-supervised methods to predict patient survival from gene expression data. *PLoS biology*, 2(4), e108.

## See Also

survival::Surv, survival::survfit, survival::survdiff, survival::coxph, clustvarsel::clustvarsel, pheatmap::pheatmap

## Examples

```
set.seed(1)
nrows <- 5
ncols <- nrow(ovarian)
counts <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
colnames(counts) <- paste("X", 1:ncols, sep = "")
rownames(ovarian) <- paste("X", 1:ncols, sep = "")
SE <- SummarizedExperiment(assays = SimpleList(counts = counts))
ovarian.survtype <- Exprs.survtype(ovarian, time = "fuptime", status = "fustat",
                                assay(SE), num.genes = 2, scale = "row",
                                clustering_method = "ward.D2")
plot(ovarian.survtype, pval = TRUE)
```

---

gene.clust

*Plots of the heatmap for each cluster of expression data*

---

## Description

Heatmaps of clustered genes for subtypes of samples can be drawn.

## Usage

```
gene.clust(object, K, ...)
```

## Arguments

object	the result of "Exprs.survtype"
K	the number of clusters
...	additional parameters for the "pheatmap"

## Value

Heatmap for each cluster

## Author(s)

Dongmin Jung

## See Also

pheatmap::pheatmap

**Examples**

```

set.seed(1)
nrows <- 5
ncols <- nrow(ovarian)
counts <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
colnames(counts) <- paste("X", 1:ncols, sep = "")
rownames(ovarian) <- paste("X", 1:ncols, sep = "")
SE <- SummarizedExperiment(assays = SimpleList(counts = counts))
ovarian.survtype <- Exprs.survtype(ovarian, time = "fuptime", status = "fustat",
                                assay(SE), num.genes = 5, scale = "row",
                                clustering_method = "ward.D2")
plot(ovarian.survtype, pval = TRUE)
gene.clust(ovarian.survtype, 2, scale = "row", clustering_method = "ward.D2")

```

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MAF.survgroup	<i>Patient group identification via survival data and mutation annotation information</i>
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**Description**

The groups of patients are identified according to whether the variants exist on a single gene. Survival difference between patients with and without mutations is compared.

**Usage**

```

MAF.survgroup(surv.data, time, status, maf, variants = NULL,
              sample.name = "Tumor_Sample_Barcode", gene.name = "Hugo_Symbol",
              variant.type = "Variant_Classification", num.genes = 10,
              significant.genes = 1, ...)

```

**Arguments**

surv.data	survival data
time	survival time
status	status indicator
maf	a MAF file
variants	types of variants on a single gene for mutated samples. samples with any mutations, defined as mutated samples by default.
sample.name	the column name containing sample names (default: "Tumor_Sample_Barcode")
gene.name	the column name containing gene names (default: "Hugo_Symbol")
variant.type	the column name containing variant types (default: "Variant_Classification")
num.genes	the number of top genes based on the number of mutated genes (default: 10)
significant.genes	the number of top genes based on the statistical significance of mutated genes (default: 1)
...	additional parameters for the "ggsurvplot" for the statistically significant genes

**Value**

time	survival time
status	status indicator
surv.data	survival data
maf.matrix	a mutation matrix
summary	a list of number of samples with variants, chi-squared statistics and p-values
cluster	a vector of integers indicating the cluster to which each sample is assigned, for the most significant gene
fit	fitted survival curves, for the most significant gene

**Author(s)**

Dongmin Jung

**See Also**

survival::Surv, survival::survfit, survival::survdiff, survminer::ggsurvplot

**Examples**

```
library(maftools)
laml.maf <- system.file('extdata', 'tcga_laml.maf.gz', package = 'maftools', mustWork = TRUE)
laml.clin <- system.file('extdata', 'tcga_laml_annot.tsv', package = 'maftools', mustWork = TRUE)
laml.maf <- read.csv(laml.maf, sep = "\t")
laml.clinical.data <- read.csv(laml.clin, sep = "\t", row.names = 1)
index <- which(laml.clinical.data$days_to_last_followup == -Inf)
laml.clinical.data <- laml.clinical.data[-index,]
laml.clinical.data <- data.frame(laml.clinical.data)
laml.survgroup <- MAF.survgroup(laml.clinical.data, time = "days_to_last_followup",
                               status = "Overall_Survival_Status", laml.maf,
                               num.genes = 3, significant.genes = 1,
                               pval = TRUE)
```

---

maf2matrix

---

*Convert a MAF file to a mutation matrix*


---

**Description**

Create a mutation matrix using variant types

**Usage**

```
maf2matrix(maf, surv.data = NULL, sample.name = "Tumor_Sample_Barcode",
           gene.name = "Hugo_Symbol", variant.type = "Variant_Classification")
```

**Arguments**

maf	a MAF file
surv.data	survival data for sample names (default: NULL)
sample.name	the column name containing sample names (default: "Tumor_Sample_Barcode")
gene.name	the column name containing gene names (default: "Hugo_Symbol")
variant.type	the column name containing variant types (default: "Variant_Classification")

**Value**

a mutation matrix

**Author(s)**

Dongmin Jung

**Examples**

```
laml.maf <- system.file("extdata", "tcga_laml.maf.gz", package = "maftools")
laml.maf <- read.csv(laml.maf, sep = "\t")
laml.mat <- maf2matrix(laml.maf)
```

---

plot.survtype

*Plot of survival curves of sample subtypes*

---

**Description**

Survival curves for subtypes of samples can be drawn.

**Usage**

```
## S3 method for class 'survtype'
plot(object, ...)
```

**Arguments**

object	object of class "survtype"
...	additional parameters for the "ggsurvplot"

**Value**

Survival curves

**Author(s)**

Dongmin Jung

**See Also**

survminer::ggsurvplot

**Examples**

```
data(ovarian)
ovarian.survtype <- Surv.survtype(ovarian, time = "fuptime", status = "fustat")
plot(ovarian.survtype, pval = TRUE)
```

---

`quantile_normalization`*Normalize a gene expression profile*

---

**Description**

Normalize expression data using quantile normalization

**Usage**

```
quantile_normalization(x)
```

**Arguments**

`x` an expression profile

**Value**

a normalized matrix

**Author(s)**

Dongmin Jung

**Examples**

```
set.seed(1)
nrows <- 10
ncols <- 5
counts <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
normalized.matrix <- quantile_normalization(counts)
```

---

`Single.survgroup`*Patient group identification via survival information and expression of a single gene*

---

**Description**

All midpoints of the expression level or real-valued statistic are investigated to find the best threshold giving the most significant difference between two groups. Any patients having the value greater than the best cutoff are assigned as the "high-score" class. Otherwise, the others belong to the "low-score" class.

**Usage**

```
Single.survgroup(surv.data, time, status, single.gene, intermediate = FALSE,
                 group.names = c("High", "Intermediate", "Low"))
```

**Arguments**

surv.data	survival data
time	survival time
status	status indicator
single.gene	expression level of a single gene
intermediate	a logical value indicating whether or not the intermediate class is considered (default: FALSE)
group.names	the name of clusters for "high-score", "intermediate-score", and "low-score" classes (default: "High", "Intermediate", "Low")

**Value**

time	survival time
status	status indicator
surv.data	survival data
score	a vector of scores
summary	a list of thresholds, chi-squared statistics and p-values
cluster	a vector of clusters to which samples are assigned
fit	fitted survival curves

**Author(s)**

Dongmin Jung

**See Also**

survival::Surv, survival::survfit, survival::survdiff

**Examples**

```
set.seed(1)
nrows <- 1
ncols <- nrow(ovarian)
counts <- matrix(runif(nrows * ncols, 1, 1e4), nrows)
colnames(counts) <- paste("X", 1:ncols, sep = "")
rownames(ovarian) <- paste("X", 1:ncols, sep = "")
Single.ovarian <- Single.survgroup(ovarian, time = "fuptime", status = "fustat", counts[1,])
plot(Single.ovarian, pval = TRUE)
```

---

Surv.survtype

*Sample subtype identification via survival information*

---

**Description**

Any patient who lived longer than the median was considered to be a "low-risk" patient, and any patient that lived less than the median was considered to be a "high-risk" patient. In this manner, we assigned a class label to each observation. For censored data, we can estimate the probability that each censored observation belongs to the "low-risk" and "high-risk" classes, respectively.

**Usage**

```
Surv.survtype(surv.data, time, status)
```

**Arguments**

<code>surv.data</code>	survival data
<code>time</code>	survival time
<code>status</code>	status indicator

**Value**

<code>n</code>	the number of subjects in each group
<code>obs</code>	the weighted observed number of events in each group
<code>exp</code>	the weighted expected number of events in each group
<code>chisq</code>	the chi-squared statistic for a test of equality
<code>call</code>	the matched call
<code>cluster</code>	a vector of clusters to which samples are assigned
<code>time</code>	survival time
<code>status</code>	status indicator
<code>surv.data</code>	survival data
<code>fit</code>	fitted survival curves

**Author(s)**

Dongmin Jung

**References**

Bair, E., & Tibshirani, R. (2004). Semi-supervised methods to predict patient survival from gene expression data. *PLoS biology*, 2(4), e108.

**See Also**

`survival::Surv`, `survival::survfit`, `survival::survdiff`

**Examples**

```
data(ovarian)
ovarian.survtype <- Surv.survtype(ovarian, time = "fuptime", status = "fustat")
```

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