Package 'TRONCO'

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Title TRONCO, an R package for TRanslational ONCOlogy

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Imports bnlearn, Rgraphviz, gtools, parallel, foreach, doParallel, iterators, RColorBrewer, circlize, igraph, grid, gridExtra, xtable, gtable, scales, R.matlab, grDevices, graphics, stats, utils, methods

Suggests BiocGenerics, BiocStyle, testthat, knitr, rWikiPathways, magick

Name An R package for the inference of cancer progression models from heterogeneous genomic data

Description The TRONCO (TRanslational ONCOlogy) R package collects algorithms to infer progression models via the approach of Suppes-Bayes Causal Network, both from an ensemble of tumors (cross-sectional samples) and within an individual patient (multi-region or single-cell samples). The package provides parallel implementation of algorithms that process binary matrices where each row represents a tumor sample and each column a single-nucleotide or a structural variant driving the progression; a 0/1 value models the absence/presence of that alteration in the sample. The tool can import data from plain, MAF or GISTIC format files, and can fetch it from the cBioPortal for cancer genomics. Functions for data manipulation and visualization are provided, as well as functions to import/export such data to other bioinformatics tools for, e.g, clustering or detection of mutually exclusive alterations. Inferred models can be visualized and tested for their confidence via bootstrap and cross-validation. TRONCO is used for the implementation of the Pipeline for Cancer Inference (PICNIC).

Encoding UTF-8

License GPL-3

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BugReports https://github.com/BIMIB-DISCo/TRONCO

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Contents

aCML . . . 5
AND . . . 5
annotate.description . . . 6
annotate.stages . . . 6
as.adj.matrix . . . 7
as.alterations . . . 8
as.bootstrap.scores . . . 8
as.colors . . . 9
as.conditional.probs . . . 10
as.confidence . . . 10
as.description . . . 11
as.events . . . 12
as.events.in.patterns . . . 12
as.events.in.sample . . . 13
as.gene . . . 14
as.genes . . . 14
as.genes.in.patterns . . . 15
as.genotypes . . . 16
as.hypotheses . . . 16
as.joint.probs . . . 17
as.kfold.eloss . . . 18
as.kfold.posterr . . . 18
as.kfold.prederr . . . 19
as.marginal.probs . . . 20

as.models . . . 21
as.parameters . . . 21
as.pathway . . . 22
as.patterns . . . 23
as.samples . . . 23
as.selective.advantage.relations . . . 24
as.stages . . . 25
as.types . . . 25
as.types.in.patterns . . . 26
change.color . . . 27
consolidate.data . . . 27
crc_gistic . . . 28
crc_maf . . . 29
crc_plain . . . 29
delete.event . . . 30
delete.gene . . . 31
delete.hypothesis . . . 31
delete.model . . . 32
delete.pattern . . . 33
delete.samples . . . 33
delete.type . . . 34
duplicates . . . 34
ebind . . . 35
enforce.numeric . . . 35
enforce.string . . . 36
events.selection . . . 36
export.graphml . . . 37
export.mutex . . . 38
export.nbs.input . . . 39
extract.MAF.HuGO.Entrez.map . . . 39
genes.table.report . . . 40
has.duplicates . . . 41
has.model . . . 41
has.stages . . . 42
hypothesis.add . . . 42
hypothesis.add.group . . . 43
hypothesis.add.homologous . . . 44
import.genotypes . . . 45
import.GISTIC . . . 45
import.MAF . . . 46
import.model . . . 48
import.mutex.groups . . . 48
intersect.datasets . . . 49
is.compliant . . . 49
join.events . . . 50
join.types . . . 51
keysToNames . . . 51
maf . . . 52

muts . . . 53
nameToKey . . . 53
nevents . . . 54
ngenes . . . 54
nhypotheses . . . 55
npatterns . . . 55
nsamples . . . 56
ntypes . . . 56
oncoprint . . . 57
oncoprint.cbio . . . 59
OR . . . 60
order.frequency . . . 60
pathway.visualization . . . 61
pheatmap . . . 61
rank.recurrents . . . 65
rename.gene . . . 66
rename.type . . . 67
samples.selection . . . 67
sbind . . . 68
ssplit . . . 68
stage . . . 69
TCGA.map.clinical.data . . . 69
TCGA.multiple.samples . . . 70
TCGA.remove.multiple.samples . . . 70
TCGA.shorten.barcodes . . . 71
test_dataset . . . 71
test_dataset_no_hypos . . . 72
test_model . . . 73
test_model_kfold . . . 73
trim . . . 74
tronco.bootstrap . . . 74
tronco.caprese . . . 75
tronco.capri . . . 76
tronco.chowliu . . . 77
tronco.edmonds . . . 78
tronco.gabow . . . 80
tronco.kfold.eloss . . . 81
tronco.kfold.posterr . . . 82
tronco.kfold.prederr . . . 83
tronco.pattern.plot . . . 84
tronco.plot . . . 84
tronco.prim . . . 87
view . . . 88
which.samples . . . 88
XOR . . . 89

Index **90**

aCML *Atypical chronic myeloid leukemia dataset*

Description

This file contains a TRONCO compliant dataset

Usage

```
data(aCML)
```

Format

TRONCO compliant dataset

Value

A standard TRONCO object

Author(s)

Luca De Sano

Source

data from http://www.nature.com/ng/journal/v45/n1/full/ng.2495.html

AND *AND*

Description

AND hypothesis

Usage

```
AND(...)
```

Arguments

...	Atoms of the co-occurance pattern given either as labels or as partielly lifted vectors.

Value

Vector to be added to the lifted genotype resolving the co-occurance pattern

annotate.description *annotate.description*

Description

Annotate a description on the selected dataset

Usage

```
annotate.description(x, label)
```

Arguments

x	A TRONCO compliant dataset.
label	A string

Value

A TRONCO compliant dataset.

Examples

```
data(test_dataset)
annotate.description(test_dataset, 'new description')
```

annotate.stages *annotate.stages*

Description

Annotate stage information on the selected dataset

Usage

```
annotate.stages(x, stages, match.TCGA.patients = FALSE)
```

Arguments

x	A TRONCO compliant dataset.
stages	A list of stages. Rownames must match samples list of x
match.TCGA.patients	Match using TCGA notations (only first 12 characters)

Value

A TRONCO compliant dataset.

Examples

```
data(test_dataset)
data(stage)
test_dataset = annotate.stages(test_dataset, stage)
as.stages(test_dataset)
```

`as.adj.matrix` *as.adj.matrix*

Description

Extract the adjacency matrix of a TRONCO model. The matrix is indexed with colnames/rownames which represent genotype keys - these can be resolved with function `keysToNames`. It is possible to specify a subset of events to build the matrix, a subset of models if multiple reconstruction have been performed. Also, either the prima facie matrix or the post-regularization matrix can be extracted.

Usage

```
as.adj.matrix(x, events = as.events(x), models = names(x$model), type = "fit")
```

Arguments

`x`	A TRONCO model.
`events`	A subset of events as of `as.events(x)`, all by default.
`models`	A subset of reconstructed models, all by default.
`type`	Either the prima facie ('pf') or the post-regularization ('fit') matrix, 'fit' by default.

Value

The adjacency matrix of a TRONCO model.

Examples

```
data(test_model)
as.adj.matrix(test_model)
as.adj.matrix(test_model, events=as.events(test_model)[5:15,])
as.adj.matrix(test_model, events=as.events(test_model)[5:15,], type='pf')
```

as.alterations *as.alterations*

Description

Return a dataset where all events for a gene are merged in a unique event, i.e., a total of gene-level alterations diregarding the event type. Input 'x' is checked to be a TRONCO compliant dataset - see `is.compliant`.

Usage

```
as.alterations(x, new.type = "Alteration", new.color = "khaki", silent = FALSE)
```

Arguments

`x`	A TRONCO compliant dataset.
`new.type`	The types label of the new event type, 'Alteration' by default.
`new.color`	The color of the event `new.type`, default 'khaki'.
`silent`	A parameter to disable/enable verbose messages.

Value

A TRONCO compliant dataset with alteration profiles.

Examples

```
data(muts)
as.alterations(muts)
```

as.bootstrap.scores *as.bootstrap.scores*

Description

Returns a dataframe with all the bootstrap score in a TRONCO model. It is possible to specify a subset of events or models if multiple reconstruction have been performed.

Usage

```
as.bootstrap.scores(x, events = as.events(x), models = names(x$model))
```

Arguments

x	A TRONCO model.
events	A subset of events as of as.events(x), all by default.
models	A subset of reconstructed models, all by default.

Value

All the bootstrap scores in a TRONCO model

Examples

```
data(test_model)
as.bootstrap.scores(test_model)
as.bootstrap.scores(test_model, events=as.events(test_model)[5:15,])
```

---

as.colors *as.colors*

Description

Return the colors associated to each type of event in 'x', which should be a TRONCO compliant dataset - see is.compliant.

Usage

```
as.colors(x)
```

Arguments

x	A TRONCO compliant dataset.

Value

A named vector of colors.

Examples

```
data(test_dataset)
as.colors(test_dataset)
```

as.conditional.probs *as.conditional.probs*

Description

Extract the conditional probabilities from a TRONCO model. The return matrix is indexed with rownames which represent genotype keys - these can be resolved with function `keysToNames`. It is possible to specify a subset of events to build the matrix, a subset of models if multiple reconstruction have been performed. Also, either the observed or fit probabilities can be extracted.

Usage

```
as.conditional.probs(
  x,
  events = as.events(x),
  models = names(x$model),
  type = "observed"
)
```

Arguments

`x`	A TRONCO model.
`events`	A subset of events as of `as.events(x)`, all by default.
`models`	A subset of reconstructed models, all by default.
`type`	observed ('observed')

Details

#' @examples data(test_model) as.conditional.probs(test_model) as.conditional.probs(test_model, events=as.events(test_model)[5:15,])

Value

The conditional probabilities in a TRONCO model.

as.confidence *as.confidence*

Description

Return confidence information for a TRONCO model. Available information are: temporal priority (tp), probability raising (pr), hypergeometric test (hg), parametric (pb), non parametric (npb) or statistical (sb) bootstrap, entropy loss (eloss), prediction error (prederr). Confidence is available only once a model has been reconstructed with any of the algorithms implemented in TRONCO. If more than one model has been reconstructed - for instance via multiple regularizations - confidence information is appropriately nested. The requested confidence is specified via vector parameter `conf`.

Usage

```
as.confidence(x, conf, models = names(x$model))
```

Arguments

x	A TRONCO model.
conf	A vector with any of 'tp', 'pr', 'hg', 'npb', 'pb', 'sb', 'eloss', 'prederr' or 'posterr'.
models	The name of the models to extract, all by default.

Value

A list of matrices with the event-to-event confidence.

Examples

```
data(test_model)
as.confidence(test_model, conf='tp')
as.confidence(test_model, conf=c('tp', 'hg'))
```

---

as.description *as.description*

Description

Return the description annotating the dataset, if any. Input 'x' should be a TRONCO compliant dataset - see `is.compliant`.

Usage

```
as.description(x)
```

Arguments

x	A TRONCO compliant dataset.

Value

The description annotating the dataset, if any.

Examples

```
data(test_dataset)
as.description(test_dataset)
```

as.events *as.events*

Description

Return all events involving certain genes and of a certain type in 'x', which should be a TRONCO compliant dataset - see `is.compliant`.

Usage

```
as.events(x, genes = NA, types = NA, keysToNames = FALSE)
```

Arguments

x	A TRONCO compliant dataset.
genes	The genes to consider, if NA all available genes are used.
types	The types of events to consider, if NA all available types are used.
keysToNames	If TRUE return a list of mnemonic name composed by type + gene

Value

A matrix with 2 columns (event type, gene name) for the events found.

Examples

```
data(test_dataset)
as.events(test_dataset)
as.events(test_dataset, types='ins_del')
as.events(test_dataset, genes = 'TET2')
as.events(test_dataset, types='Missing')
```

as.events.in.patterns *as.events.in.patterns*

Description

Return the list of events present in selected patterns

Usage

```
as.events.in.patterns(x, patterns = NULL)
```

Arguments

x	A TRONCO compliant dataset.
patterns	A list of patterns for which the list will be returned

Value

A list of events present in patterns which consitute CAPRI's hypotheses

Examples

```
data(test_dataset)
as.events.in.patterns(test_dataset)
as.events.in.patterns(test_dataset, patterns='XOR_EZH2')
```

`as.events.in.sample` *as.events.in.sample*

Description

Return a list of events which are observed in the input samples list

Usage

```
as.events.in.sample(x, sample)
```

Arguments

`x`	A TRONCO compliant dataset
`sample`	Vector of sample names

Value

A list of events which are observed in the input samples list

Examples

```
data(test_dataset)
as.events.in.sample(test_dataset, c('patient 1', 'patient 7'))
```

as.gene *as.gene*

Description

Return the genotypes for a certain set of genes and type of events. Input 'x' should be a TRONCO compliant dataset - see `is.compliant`. In this case column names are substituted with events' types.

Usage

```
as.gene(x, genes, types = NA)
```

Arguments

x	A TRONCO compliant dataset.
genes	The genes to consider, if NA all available genes are used.
types	The types of events to consider, if NA all available types are used.

Value

A matrix, subset of `as.genotypes(x)` with colnames substituted with events' types.

Examples

```
data(test_dataset)
as.gene(test_dataset, genes = c('EZH2', 'ASXL1'))
```

as.genes *as.genes*

Description

Return all gene symbols for which a certain type of event exists in 'x', which should be a TRONCO compliant dataset - see `is.compliant`.

Usage

```
as.genes(x, types = NA)
```

Arguments

x	A TRONCO compliant dataset.
types	The types of events to consider, if NA all available types are used.

Value

A vector of gene symbols for which a certain type of event exists

Examples

```
data(test_dataset)
as.genes(test_dataset)
```

---

as.genes.in.patterns *as.genes.in.patterns*

Description

Return the list of genes present in selected patterns

Usage

```
as.genes.in.patterns(x, patterns = NULL)
```

Arguments

x	A TRONCO compliant dataset.
patterns	A list of patterns for which the list will be returned

Value

A list of genes present in patterns which consitute CAPRI's hypotheses

Examples

```
data(test_dataset)
as.genes.in.patterns(test_dataset)
as.genes.in.patterns(test_dataset, patterns='XOR_EZH2')
```

as.genotypes *as.genotypes*

Description

Return all genotypes for input 'x', which should be a TRONCO compliant dataset see `is.compliant`. Function `keysToNames` can be used to translate colnames to events.

Usage

```
as.genotypes(x)
```

Arguments

x	A TRONCO compliant dataset.

Value

A TRONCO genotypes matrix.

Examples

```
data(test_dataset)
as.genotypes(test_dataset)
```

as.hypotheses *as.hypotheses*

Description

Return the hypotheses in the dataset which constitute CAPRI's hypotheses.

Usage

```
as.hypotheses(x, cause = NA, effect = NA)
```

Arguments

x	A TRONCO compliant dataset.
cause	A list of genes to use as causes
effect	A list of genes to use as effects

Value

The hypotheses in the dataset which constitute CAPRI's hypotheses.

Examples

```
data(test_dataset)
as.hypotheses(test_dataset)
```

`as.joint.probs` *as.joint.probs*

Description

Extract the joint probabilities from a TRONCO model. The return matrix is indexed with rownames/colnames which represent genotype keys - these can be resolved with function `keysToNames`. It is possible to specify a subset of events to build the matrix, a subset of models if multiple reconstruction have been performed. Also, either the observed or fit probabilities can be extracted.

Usage

```
as.joint.probs(
  x,
  events = as.events(x),
  models = names(x$model),
  type = "observed"
)
```

Arguments

`x`	A TRONCO model.
`events`	A subset of events as of `as.events(x)`, all by default.
`models`	A subset of reconstructed models, all by default.
`type`	observed

Value

The joint probabilities in a TRONCO model.

Examples

```
data(test_model)
as.joint.probs(test_model)
as.joint.probs(test_model, events=as.events(test_model)[5:15,])
```

as.kfold.eloss *as.kfold.eloss*

Description

Returns a dataframe with all the average/stdev entropy loss score of a TRONCO model. It is possible to specify models if multiple reconstruction have been performed.

Usage

```
as.kfold.eloss(x, models = names(x$model), values = FALSE)
```

Arguments

x	A TRONCO model.
models	A subset of reconstructed models, all by default.
values	If you want to see also the values

Value

All the bootstrap scores in a TRONCO model

Examples

```
data(test_model_kfold)
as.kfold.eloss(test_model_kfold)
as.kfold.eloss(test_model_kfold, models='capri_aic')
```

as.kfold.posterr *as.kfold.posterr*

Description

Returns a dataframe with all the posterior classification error score in a TRONCO model. It is possible to specify a subset of events or models if multiple reconstruction have been performed.

Usage

```
as.kfold.posterr(
  x,
  events = as.events(x),
  models = names(x$model),
  values = FALSE,
  table = FALSE
)
```

Arguments

x	A TRONCO model.
events	A subset of events as of as.events(x), all by default.
models	A subset of reconstructed models, all by default.
values	If you want to see also the values
table	Keep the original table (defaul false)

Value

All the posterior classification error scores in a TRONCO model

Examples

```
data(test_model_kfold)
data(test_model)
as.kfold.posterr(test_model_kfold)
as.kfold.posterr(test_model_kfold, events=as.events(test_model)[5:15,])
```

---

as.kfold.prederr *as.kfold.prederr*

Description

Returns a dataframe with all the prediction error score in a TRONCO model. It is possible to specify a subset of events or models if multiple reconstruction have been performed.

Usage

```
as.kfold.prederr(
  x,
  events = as.events(x),
  models = names(x$model),
  values = FALSE,
  table = FALSE
)
```

Arguments

x	A TRONCO model.
events	A subset of events as of as.events(x), all by default.
models	A subset of reconstructed models, all by default.
values	If you want to see also the values
table	Keep the original table (defaul false)

Value

All the bootstrap scores in a TRONCO model

Examples

```
data(test_model_kfold)
as.kfold.prederr(test_model_kfold)
as.kfold.prederr(test_model_kfold, models='capri_aic')
```

`as.marginal.probs` *as.marginal.probs*

Description

Extract the marginal probabilities from a TRONCO model. The return matrix is indexed with rownames which represent genotype keys - these can be resolved with function `keysToNames`. It is possible to specify a subset of events to build the matrix, a subset of models if multiple reconstruction have been performed. Also, either the observed or fit probabilities can be extracted.

Usage

```
as.marginal.probs(
  x,
  events = as.events(x),
  models = names(x$model),
  type = "observed"
)
```

Arguments

`x`	A TRONCO model.
`events`	A subset of events as of `as.events(x)`, all by default.
`models`	A subset of reconstructed models, all by default.
`type`	observed.

Value

The marginal probabilities in a TRONCO model.

Examples

```
data(test_model)
as.marginal.probs(test_model)
as.marginal.probs(test_model, events=as.events(test_model)[5:15,])
```

as.models *as.models*

Description

Extract the models from a reconstructed object.

Usage

```
as.models(x, models = names(x$model))
```

Arguments

x	A TRONCO model.
models	The name of the models to extract, e.g. 'bic', 'aic', 'caprese', all by default.

Value

The models in a reconstructed object.

Examples

```
data(test_model)
as.models(test_model)
```

as.parameters *as.parameters*

Description

Get parameters of a model

Usage

```
as.parameters(x)
```

Arguments

x	A TRONCO model.

Value

A list of parameters

Examples

```
data(test_model)
as.parameters(test_model)
```

`as.pathway` *as.pathway*

Description

Given a cohort and a pathway, return the cohort with events restricted to genes involved in the pathway. This might contain a new 'pathway' genotype with an alteration mark if any of the involved genes are altered.

Usage

```
as.pathway(
  x,
  pathway.genes,
  pathway.name,
  pathway.color = "yellow",
  aggregate.pathway = TRUE,
  silent = FALSE
)
```

Arguments

`x`	A TRONCO compliant dataset.
`pathway.genes`	Gene (symbols) involved in the pathway.
`pathway.name`	Pathway name for visualization.
`pathway.color`	Pathway color for visualization.
`aggregate.pathway`	If TRUE drop the events for the genes in the pathway.
`silent`	A parameter to disable/enable verbose messages.

Value

Extract the subset of events for genes which are part of a pathway.

Examples

```
data(test_dataset)
p = as.pathway(test_dataset, c('ASXL1', 'TET2'), 'test_pathway')
```

as.patterns *as.patterns*

Description

Return the patterns in the dataset which constitute CAPRI's hypotheses.

Usage

```
as.patterns(x)
```

Arguments

x	A TRONCO compliant dataset.

Value

The patterns in the dataset which constitute CAPRI's hypotheses.

Examples

```
data(test_dataset)
as.patterns(test_dataset)
```

as.samples *as.samples*

Description

Return all sample IDs for input 'x', which should be a TRONCO compliant dataset - see `is.compliant`.

Usage

```
as.samples(x)
```

Arguments

x	A TRONCO compliant dataset.

Value

A vector of sample IDs

Examples

```
data(test_dataset)
as.samples(test_dataset)
```

`as.selective.advantage.relations` *as.selective.advantage.relations*

Description

Returns a dataframe with all the selective advantage relations in a TRONCO model. Confidence is also shown - see `as.confidence`. It is possible to specify a subset of events or models if multiple reconstruction have been performed.

Usage

```
as.selective.advantage.relations(
  x,
  events = as.events(x),
  models = names(x$model),
  type = "fit"
)
```

Arguments

`x`	A TRONCO model.
`events`	A subset of events as of `as.events(x)`, all by default.
`models`	A subset of reconstructed models, all by default.
`type`	Either Prima Facie ('pf') or fit ('fit') probabilities, 'fit' by default.

Value

All the selective advantage relations in a TRONCO model

Examples

```
data(test_model)
as.selective.advantage.relations(test_model)
as.selective.advantage.relations(test_model, events=as.events(test_model)[5:15,])
as.selective.advantage.relations(test_model, events=as.events(test_model)[5:15,], type='pf')
```

as.stages *as.stages*

Description

Return the association sample -> stage, if any. Input 'x' should be a TRONCO compliant dataset - see `is.compliant`.

Usage

```
as.stages(x)
```

Arguments

x	A TRONCO compliant dataset.

Value

A matrix with 1 column annotating stages and rownames as sample IDs.

Examples

```
data(test_dataset)
data(stage)
test_dataset = annotate.stages(test_dataset, stage)
as.stages(test_dataset)
```

as.types *as.types*

Description

Return the types of events for a set of genes which are in 'x', which should be a TRONCO compliant dataset - see `is.compliant`.

Usage

```
as.types(x, genes = NA)
```

Arguments

x	A TRONCO compliant dataset.
genes	A list of genes to consider, if NA all genes are used.

Value

A matrix with 1 column annotating stages and rownames as sample IDs.

Examples

```
data(test_dataset)
as.types(test_dataset)
as.types(test_dataset, genes='TET2')
```

`as.types.in.patterns` *as.types.in.patterns*

Description

Return the list of types present in selected patterns

Usage

```
as.types.in.patterns(x, patterns = NULL)
```

Arguments

`x`	A TRONCO compliant dataset.
`patterns`	A list of patterns for which the list will be returned

Value

A list of types present in patterns which consitute CAPRI's hypotheses

Examples

```
data(test_dataset)
as.types.in.patterns(test_dataset)
as.types.in.patterns(test_dataset, patterns='XOR_EZH2')
```

`change.color` *change.color*

Description

Change the color of an event type

Usage

```
change.color(x, type, new.color)
```

Arguments

`x`	A TRONCO compliant dataset.
`type`	An event type
`new.color`	The new color (either HEX or R Color)

Value

A TRONCO complian dataset.

Examples

```
data(test_dataset)
dataset = change.color(test_dataset, 'ins_del', 'red')
```

`consolidate.data` *consolidate.data*

Description

Verify if the input data are consolidate, i.e., if there are events with 0 or 1 probability or indistinguishable in terms of observations

Usage

```
consolidate.data(x, print = FALSE)
```

Arguments

`x`	A TRONCO compliant dataset.
`print`	A boolean value stating whether to print of not the summary

Value

The list of any 0 probability, 1 probability and indistinguishable.

Examples

```
data(test_dataset)
consolidate.data(test_dataset)
```

`crc_gistic` *GISTIC example data*

Description

This dataset contains an example of GISTIC input of a crc cohort of patients

Usage

```
data(crc_gistic)
```

Format

GISTIC score

Value

A gistic file

Author(s)

Daniele Ramazzotti

Source

data from http://www.nature.com/nature/journal/v487/n7407/full/nature11252.html

crc_maf *MAF example data*

Description

This dataset contains an example of MAF input of a crc cohort of patients

Usage

```
data(crc_maf)
```

Format

Manual Annotated Format

Value

A MAF file

Author(s)

Daniele Ramazzotti

Source

data from http://www.nature.com/nature/journal/v487/n7407/full/nature11252.html

crc_plain *Plain mutation dataset*

Description

This dataset contains an example of plain input of a crc cohort of patients

Usage

```
data(crc_plain)
```

Format

plain data

Value

A plain input

Author(s)

Daniele Ramazzotti

Source

data from http://www.nature.com/nature/journal/v487/n7407/full/nature11252.html

---

`delete.event` *delete.event*

Description

Delete an event from the dataset

Usage

```
delete.event(x, gene, type)
```

Arguments

`x`	A TRONCO compliant dataset.
`gene`	The name of the gene to delete.
`type`	The name of the type to delete.

Value

A TRONCO complian dataset.

Examples

```
data(test_dataset)
test_dataset = delete.event(test_dataset, 'TET2', 'ins_del')
```

`delete.gene` *delete.gene*

Description

Delete a gene

Usage

```
delete.gene(x, gene)
```

Arguments

x	A TRONCO compliant dataset.
gene	The name of the gene to delete.

Value

A TRONCO complian dataset.

Examples

```
data(test_dataset)
test_dataset = delete.gene(test_dataset, 'TET2')
```

`delete.hypothesis` *delete.hypothesis*

Description

Delete an hypothesis from the dataset based on a selected event. Check if the selected event exist in the dataset and delete his associated hypothesis

Usage

```
delete.hypothesis(x, event = NA, cause = NA, effect = NA)
```

Arguments

x	A TRONCO compliant dataset.
event	Can be an event or pattern name
cause	Can be an event or pattern name
effect	Can be an event or pattern name

Value

A TRONCO complian dataset.

Examples

```
data(test_dataset)
delete.hypothesis(test_dataset, event='TET2')
delete.hypothesis(test_dataset, cause='EZH2')
delete.hypothesis(test_dataset, event='XOR_EZH2')
```

---

delete.model *delete.model*

Description

Delete a reconstructed model from the dataset

Usage

```
delete.model(x)
```

Arguments

x	A TRONCO compliant dataset.

Value

A TRONCO complian dataset.

Examples

```
data(test_model)
model = delete.model(test_model)
has.model(model)
```

delete.pattern *delete.pattern*

Description

Delete a pattern and every associated hypotheses from the dataset

Usage

```
delete.pattern(x, pattern)
```

Arguments

x	A TRONCO compliant dataset.
pattern	A pattern name

Value

A TRONCO complian dataset.

Examples

```
data(test_dataset)
delete.pattern(test_dataset, pattern='XOR_EZH2')
```

delete.samples *delete.samples*

Description

Delete samples from selected dataset

Usage

```
delete.samples(x, samples)
```

Arguments

x	A TRONCO compliant dataset.
samples	An array of samples name

Value

A TRONCO complian dataset.

Examples

```
data(test_dataset)
dataset = delete.samples(test_dataset, c('patient 1', 'patient 4'))
```

`delete.type` *delete.type*

Description

Delete an event type

Usage

```
delete.type(x, type)
```

Arguments

`x`	A TRONCO compliant dataset.
`type`	The name of the type to delete.

Value

A TRONCO complian dataset.

Examples

```
data(test_dataset)
test_dataset = delete.type(test_dataset, 'Pattern')
```

`duplicates` *duplicates*

Description

Return the events duplicated in `x`, if any. Input 'x' should be a TRONCO compliant dataset - see `is.compliant`.

Usage

```
duplicates(x)
```

Arguments

`x`	A TRONCO compliant dataset.

Value

A subset of `as.events(x)` with duplicated events.

Examples

```
data(test_dataset)
duplicates(test_dataset)
```

---

ebind *ebind*

Description

Binds events from one or more datasets, which must be defined over the same set of samples.

Usage

```
ebind(..., silent = FALSE)
```

Arguments

`...`	the input datasets
`silent`	A parameter to disable/enable verbose messages.

Value

A TRONCO complian dataset.

---

enforce.numeric *enforce.numeric*

Description

Convert the internal reprensentation of genotypes to numeric, if not.

Usage

```
enforce.numeric(x)
```

Arguments

`x`	A TRONCO compliant dataset.

Value

Convert the internal reprensentation of genotypes to numeric, if not.

Examples

```
data(test_dataset)
test_dataset = enforce.numeric(test_dataset)
```

`enforce.string` *enforce.string*

Description

Convert the internal representation of genotypes to character, if not.

Usage

```
enforce.string(x)
```

Arguments

x	A TRONCO compliant dataset.

Value

Convert the internal reprensentation of genotypes to character, if not.

Examples

```
data(test_dataset)
test_dataset = enforce.string(test_dataset)
```

`events.selection` *events.selection*

Description

select a subset of the input genotypes 'x'. Selection can be done by frequency and gene symbols.

Usage

```
events.selection(
  x,
  filter.freq = NA,
  filter.in.names = NA,
  filter.out.names = NA,
  silent = FALSE
)
```

Arguments

x	A TRONCO compliant dataset.
filter.freq	[0,1] value which constriants the minimum frequence of selected events
filter.in.names	gene symbols which will be included
filter.out.names	gene symbols which will NOT be included
silent	A parameter to disable/enable verbose messages.

Value

A TRONCO compliant dataset.

Examples

```
data(test_dataset)
dataset = events.selection(test_dataset, 0.3)
```

---

export.graphml *export.graphml*

Description

Create a graphML object which can be imported in cytoscape This function is based on the tronco.plot fuction

Usage

```
export.graphml(x, file, ...)
```

Arguments

x	A TRONCO compliant dataset
file	Where to save the output
...	parameters for tronco.plot

Examples

```
data(test_model)
export.graphml(test_model, file='text.xml', scale.nodes=0.3)
```

`export.mutex` *export,mutex*

Description

Create an input file for MUTEX (ref: https://code.google.com/p/mutex/)

Usage

```
export.mutex(
  x,
  filename = "tronco_to_mutex",
  filepath = "./",
  label.mutation = "SNV",
  label.amplification = list("High-level Gain"),
  label.deletion = list("Homozygous Loss")
)
```

Arguments

`x`	A TRONCO compliant dataset.
`filename`	The name of the file
`filepath`	The path where to save the file
`label.mutation`	The event type to use as mutation
`label.amplification`	The event type to use as amplification (can be a list)
`label.deletion`	The event type to use as amplification (can be a list)

Value

A MUTEX example matrix

Examples

```
data(crc_gistic)
dataset = import.GISTIC(crc_gistic)
export.mutex(dataset)
```

export.nbs.input *export.nbs.input*

Description

Create a .mat file which can be used with NBS clustering (ref: http://chianti.ucsd.edu/~mhofree/wordpress/?page_id=26)

Usage

```
export.nbs.input(x, map_hugo_entrez, file = "tronco_to_nbs.mat")
```

Arguments

x	A TRONCO compliant dataset.
map_hugo_entrez	Hugo_Symbol-Entrez_Gene_Id map
file	output file name

extract.MAF.HuGO.Entrez.map *extract.MAF.HuGO.Entrez.map*

Description

Extract a map Hugo_Symbol -> Entrez_Gene_Id from a MAF input file. If some genes map to ID 0 a warning is raised.

Usage

```
extract.MAF.HuGO.Entrez.map(file, sep = "\t")
```

Arguments

file	MAF filename
sep	MAF separator, default \'\t\'

Value

A mapHugo_Symbol -> Entrez_Gene_Id.

genes.table.report *genes.table.report*

Description

Generate PDF and laex tables

Usage

```
genes.table.report(
  x,
  name,
  dir = getwd(),
  maxrow = 33,
  font = 10,
  height = 11,
  width = 8.5,
  fill = "lightblue",
  silent = FALSE
)
```

Arguments

x	A TRONCO compliant dataset.
name	filename
dir	working directory
maxrow	maximum number of row per page
font	document fontsize
height	table height
width	table width
fill	fill color
silent	A parameter to disable/enable verbose messages.

Value

LaTEX code

has.duplicates *has.duplicates*

Description

Return true if there are duplicated events in the TRONCO dataset 'x', which should be a TRONCO compliant dataset - see `is.compliant`. Events are identified by a gene name, e.g., a HuGO_Symbol, and a type label, e.g., c('SNP', 'KRAS')

Usage

```
has.duplicates(x)
```

Arguments

x	A TRONCO compliant dataset.

Value

TRUE if there are duplicated events in `x`.

Examples

```
data(test_dataset)
has.duplicates(test_dataset)
```

has.model *has.model*

Description

Return true if there is a reconstructed model in the TRONCO dataset 'x', which should be a TRONCO compliant dataset - see `is.compliant`.

Usage

```
has.model(x)
```

Arguments

x	A TRONCO compliant dataset.

Value

TRUE if there is a reconstructed model in `x`.

Examples

```
data(test_dataset)
has.model(test_dataset)
```

`has.stages` *has stages*

Description

Return true if the TRONCO dataset 'x', which should be a TRONCO compliant dataset - see `is.compliant` - has stage annotations for samples. Some sample stages might be annotated as NA, but not all.

Usage

```
has.stages(x)
```

Arguments

x	A TRONCO compliant dataset.

Value

TRUE if the TRONCO dataset has stage annotations for samples.

Examples

```
data(test_dataset)
has.stages(test_dataset)
data(stage)
test_dataset = annotate.stages(test_dataset, stage)
has.stages(test_dataset)
```

`hypothesis.add` *hypothesis add*

Description

Add a new hypothesis by creating a new event and adding it to the compliant genotypes

Usage

```
hypothesis.add(
  data,
  pattern.label,
  lifted.pattern,
  pattern.effect = "*",
  pattern.cause = "*"
)
```

Arguments

data	A TRONCO compliant dataset.
pattern.label	Label of the new hypothesis.
lifted.pattern	Vector to be added to the lifted genotype resolving the pattern related to the new hypothesis
pattern.effect	Possibile effects for the pattern.
pattern.cause	Possibile causes for the pattern.

Value

A TRONCO compliant object with the added hypothesis

---

hypothesis.add.group *hypothesis add group*

Description

Add all the hypotheses related to a group of events

Usage

```
hypothesis.add.group(
  x,
  FUN,
  group,
  pattern.cause = "*",
  pattern.effect = "*",
  dim.min = 2,
  dim.max = length(group),
  min.prob = 0,
  silent = FALSE
)
```

Arguments

x	A TRONCO compliant dataset.
FUN	Type of pattern to be added, e.g., co-occurance, soft or hard exclusivity.
group	Group of events to be considered.
pattern.cause	Possibile causes for the pattern.
pattern.effect	Possibile effects for the pattern.
dim.min	Minimum cardinality of the subgroups to be considered.
dim.max	Maximum cardinality of the subgroups to be considered.
min.prob	Minimum probability associated to each valid group.
silent	A parameter to disable/enable verbose messages.

Value

A TRONCO compliant object with the added hypotheses

---

hypothesis.add.homologous
hypothesis.add.homologous

Description

Add all the hypotheses related to homologou events

Usage

```
hypothesis.add.homologous(
  x,
  pattern.cause = "*",
  pattern.effect = "*",
  genes = as.genes(x),
  silent = FALSE
)
```

Arguments

x	A TRONCO compliant dataset.
pattern.cause	Possibile causes for the pattern.
pattern.effect	Possibile effects for the pattern.
genes	List of genes to be considered as possible homologous. For these genes, all the types of mutations will be considered functionally equivalent.
silent	A parameter to disable/enable verbose messages.

Value

A TRONCO compliant object with the added hypotheses

`import.genotypes` *import.genotypes*

Description

Import a matrix of 0/1 alterations as a TRONCO compliant dataset. Input "geno" can be either a dataframe or a file name. In any case the dataframe or the table stored in the file must have a column for each altered gene and a rows for each sample. Colnames will be used to determine gene names, if data is loaded from file the first column will be assigned as rownames. For details and examples regarding the loading functions provided by the package we refer to the Vignette Section 3.

Usage

```
import.genotypes(geno, event.type = "variant", color = "Darkgreen")
```

Arguments

`geno`	Either a dataframe or a filename
`event.type`	Any 1 in "geno" will be interpreted as a an observed alteration labeled with type "event.type"
`color`	This is the color used for visualization of events labeled as of "event.type"

Value

A TRONCO compliant dataset

`import.GISTIC` *import.GISTIC*

Description

Transform GISTIC scores for CNAs in a TRONCO compliant object. Input can be either a matrix, with columns for each altered gene and rows for each sample; in this case colnames/rownames mut be provided. If input is a character an attempt to load a table from file is performed. In this case the input table format should be constitent with TCGA data for focal CNA; there should hence be: one column for each sample, one row for each gene, a column Hugo_Symbol with every gene name and a column Entrez_Gene_Id with every gene\'s Entrez ID. A valid GISTIC score should be any value of: "Homozygous Loss" (-2), "Heterozygous Loss" (-1), "Low-level Gain" (+1), "High-level Gain" (+2). For details and examples regarding the loading functions provided by the package we refer to the Vignette Section 3.

Usage

```
import.GISTIC(
  x,
  filter.genes = NULL,
  filter.samples = NULL,
  silent = FALSE,
  trim = TRUE,
  rna.seq.data = NULL,
  rna.seq.up = NULL,
  rna.seq.down = NULL
)
```

Arguments

x	Either a dataframe or a filename
filter.genes	A list of genes
filter.samples	A list of samples
silent	A parameter to disable/enable verbose messages.
trim	Remove the events without occurrence
rna.seq.data	Either a dataframe or a filename
rna.seq.up	TODO
rna.seq.down	TODO

Value

A TRONCO compliant representation of the input CNAs.

Examples

```
data(crc_gistic)
gistic = import.GISTIC(crc_gistic)
```

---

import.MAF *import.MAF*

Description

Import mutation profiles from a Manual Annotation Format (MAF) file. All mutations are aggregated as a unique event type labeled "Mutation" and assigned a color according to the default of function `import.genotypes`. If this is a TCGA MAF file check for multiple samples per patient is performed and a warning is raised if these occurr. Customized MAF files can be imported as well provided that they have columns Hugo_Symbol, Tumor_Sample_Barcode and Variant_Classification. Custom filters are possible (via filter.fun) to avoid loading the full MAF data. For details and examples regarding the loading functions provided by the package we refer to the Vignette Section 3.

Usage

```
import.MAF(
  file,
  sep = "\t",
  is.TCGA = TRUE,
  filter.fun = NULL,
  to.TRONCO = TRUE,
  irregular = FALSE,
  paste.to.Hugo_Symbol = NULL,
  merge.mutation.types = TRUE,
  silent = FALSE
)
```

Arguments

file	MAF filename
sep	MAF separator, default \'\t\'
is.TCGA	TRUE if this MAF is from TCGA; thus its sample codenames can be interpreted
filter.fun	A filter function applied to each row. This is expected to return TRUE/FALSE.
to.TRONCO	If FALSE returns a dataframe with MAF data, not a TRONCO object
irregular	If TRUE seeks only for columns Hugo_Symbol, Tumor_Sample_Barcode and Variant_Classification
paste.to.Hugo_Symbol	If a list of column names, this will be pasted each Hugo_Symbol to yield names such as PHC2.chr1.33116215.33116215
merge.mutation.types	If TRUE, all mutations are considered equivalent, regardless of their Variant_Classification value. Otherwise no.
silent	A parameter to disable/enable verbose messages.

Value

A TRONCO compliant representation of the input MAF

Examples

```
data(maf)
mutations = import.MAF(maf)
mutations = annotate.description(mutations, 'Example MAF')
mutations = TCGA.shorten.barcodes(mutations)
oncoprint(mutations)
```

`import.model` *import.model*

Description

Add an adjacency matrix as a model to a TRONCO compliant object. Input model can be either a dataframe or a file name.

Usage

```
import.model(tronco_object, model, model.name = "imported_model")
```

Arguments

`tronco_object`	A TRONCO compliant object
`model`	Either a dataframe or a filename
`model.name`	Name of the imported model

Value

A TRONCO compliant object

`import.mutex.groups` *import.mutex.groups*

Description

Create a list of unique Mutex groups for a given fdr cutoff current Mutex version is Jan 8, 2015 (ref: https://code.google.com/p/mutex/)

Usage

```
import.mutex.groups(file, fdr = 0.2, display = TRUE)
```

Arguments

`file`	Mutex results ("ranked-groups.txt" file)
`fdr`	cutoff for fdr
`display`	print summary table of extracted groups

intersect.datasets *intersect.datasets*

Description

Intersect samples and events of two dataset

Usage

```
intersect.datasets(x, y, intersect.genomes = TRUE)
```

Arguments

x	A TRONCO compliant dataset.
y	A TRONCO compliant dataset.
intersect.genomes	If False -> just samples

Value

A TRONCO complian dataset.

Examples

```
data(test_dataset)
```

is.compliant *is.compliant*

Description

Check if 'x' is compliant with TRONCO's input: that is if it has dataframes x$genotypes, x$annotations, x$types and x$stage (optional)

Usage

```
is.compliant(
  x,
  err.fun = "[ERR]",
  stage = !(all(is.null(x$stages)) || all(is.na(x$stages)))
)
```

Arguments

x	A TRONCO compliant dataset.
err.fun	string which identifies the function which called is.compliant
stage	boolean flag to check x$stage datagframe

Value

on error stops the computation

Examples

```
data(test_dataset)
is.compliant(test_dataset)
```

---

join.events *join.events*

Description

Merge a list of events in an unique event

Usage

```
join.events(x, ..., new.event, new.type, event.color)
```

Arguments

x	A TRONCO compliant dataset.
...	A list of events to merge
new.event	The name of the resultant event
new.type	The type of the new event
event.color	The color of the new event

Value

A TRONCO compliant dataset.

Examples

```
data(muts)
dataset = join.events(muts, 'G1', 'G2', new.event='test', new.type='banana', event.color='yellow')
```

join.types *join.types*

Description

For an input dataset merge all the events of two or more distincit types (e.g., say that missense and indel mutations are events of a unique "mutation" type)

Usage

```
join.types(x, ..., new.type = "new.type", new.color = "khaki", silent = FALSE)
```

Arguments

x	A TRONCO compliant dataset.
...	type to merge
new.type	label for the new type to create
new.color	color for the new type to create
silent	A parameter to disable/enable verbose messages.

Value

A TRONCO compliant dataset.

Examples

```
data(test_dataset_no_hypos)
join.types(test_dataset_no_hypos, 'ins_del', 'missense_point_mutations')
join.types(test_dataset_no_hypos, 'ins_del',
     'missense_point_mutations', new.type='mut', new.color='green')
```

keysToNames *keysToNames*

Description

Convert colnames/rownames of a matrix into intelligible event names, e.g., change a key G23 in 'Mutation KRAS'. If a name is not found, the original name is left unchanged.

Usage

```
keysToNames(x, matrix)
```

Arguments

x	A TRONCO compliant dataset.
matrix	A matrix with colnames/rownames which represent genotypes keys.

Value

The matrix with intelligible colnames/rownames.

Examples

```
data(test_model)
adj_matrix = as.adj.matrix(test_model, events=as.events(test_model)[5:15,])$capri_bic
keysToNames(test_model, adj_matrix)
```

---

maf *MAF example data*

Description

This dataset contains a standard MAF input for TRONCO

Usage

```
data(maf)
```

Format

Manual Annotated Format

Value

A standard TRONCO object

Author(s)

Luca De Sano

Source

fake data

muts *Simple mutation dataset*

Description

A simple mutation dataset without hypotheses

Usage

```
data(muts)
```

Format

TRONCO compliant dataset

Value

A standard TRONCO object

Author(s)

Luca De Sano

Source

fake data

nameToKey *nameToKey*

Description

Convert to key an intelligible event names, e.g., change 'Mutation KRAS' in G23. If a name is not found, an error is raised!

Usage

```
nameToKey(x, name)
```

Arguments

x	A TRONCO compliant dataset.
name	A intelligible event name

Value

A TRONCO dataset key name

Examples

```
data(test_model)
adj_matrix = as.adj.matrix(test_model, events=as.events(test_model)[5:15,])$bic
```

---

nevents *nevents*

Description

Return the number of events in the dataset involving a certain gene or type of event.

Usage

```
nevents(x, genes = NA, types = NA)
```

Arguments

x	A TRONCO compliant dataset.
genes	The genes to consider, if NA all available genes are used.
types	The types of events to consider, if NA all available types are used.

Value

The number of events in the dataset involving a certain gene or type of event.

Examples

```
data(test_dataset)
nevents(test_dataset)
```

---

ngenes *ngenes*

Description

Return the number of genes in the dataset involving a certain type of event.

Usage

```
ngenes(x, types = NA)
```

Arguments

x	A TRONCO compliant dataset.
types	The types of events to consider, if NA all available types are used.

Value

The number of genes in the dataset involving a certain type of event.

Examples

```
data(test_dataset)
ngenes(test_dataset)
```

---

nhypotheses *Return the number of hypotheses in the dataset*

Description

Return the number of hypotheses in the dataset

Usage

```
nhypotheses(x)
```

Arguments

x	the dataset.

Examples

```
data(test_dataset)
nhypotheses(test_dataset)
```

---

npatterns *Return the number of patterns in the dataset*

Description

Return the number of patterns in the dataset

Usage

```
npatterns(x)
```

Arguments

x	the dataset.

Examples

```
data(test_dataset)
npatterns(test_dataset)
```

`nsamples` *nsamples*

Description

Return the number of samples in the dataset.

Usage

```
nsamples(x)
```

Arguments

`x`	A TRONCO compliant dataset.

Value

The number of samples in the dataset.

Examples

```
data(test_dataset)
nsamples(test_dataset)
```

`ntypes` *ntypes*

Description

Return the number of types in the dataset.

Usage

```
ntypes(x)
```

Arguments

`x`	A TRONCO compliant dataset.

Value

The number of types in the dataset.

Examples

```
data(test_dataset)
ntypes(test_dataset)
```

---

oncoprint *oncoprint*

Description

oncoPrint : plot a genotype. For details and examples regarding the visualization through oncoprints, we refer to the Vignette Section 4.4.

Usage

```
oncoprint(
  x,
  excl.sort = TRUE,
  samples.cluster = FALSE,
  genes.cluster = FALSE,
  file = NA,
  ann.stage = has.stages(x),
  ann.hits = TRUE,
  stage.color = "YlOrRd",
  hits.color = "Purples",
  null.color = "lightgray",
  border.color = "white",
  text.cex = 1,
  font.column = NA,
  font.row = NA,
  title = as.description(x),
  sample.id = FALSE,
  hide.zeroes = FALSE,
  legend = TRUE,
  legend.cex = 0.5,
  cellwidth = NA,
  cellheight = NA,
  group.by.label = FALSE,
  group.by.stage = FALSE,
  group.samples = NA,
  gene.annot = NA,
  gene.annot.color = "Set1",
  show.patterns = FALSE,
```

```
  annotate.consolidate.events = FALSE,
 txt.stats = paste(nsamples(x), " samples\n", nevents(x), " events\n", ngenes(x),
    " genes\n", npatterns(x), " patterns", sep = ""),
  gtable = FALSE,
  ...
)
```

Arguments

x	A TRONCO compliant dataset
excl.sort	Boolean value, if TRUE sorts samples to enhance exclusivity of alterations
samples.cluster	Boolean value, if TRUE clusters samples (columns). Default FALSE
genes.cluster	Boolean value, if TRUE clusters genes (rows). Default FALSE
file	If not NA write to file the Oncoprint, default is NA (just visualization).
ann.stage	Boolean value to annotate stage classification, default depends on x
ann.hits	Boolean value to annotate the number of events in each sample, default is TRUE
stage.color	RColorbrewer palette to color stage annotations. Default is 'YlOrRd'
hits.color	RColorbrewer palette to color hits annotations. Default is 'Purples'
null.color	Color for the Oncoprint cells with 0s, default is 'lightgray'
border.color	Border color for the Oncoprint, default is white' (no border)
text.cex	Title and annotations cex, multiplied by font size 7
font.column	If NA, half of font.row is used
font.row	If NA, max(c(15 * exp(-0.02 * nrow(data)), 2)) is used, where data is the data visualized in the Oncoprint
title	Oncoprint title, default is as.name(x) - see as.name
sample.id	If TRUE shows samples name (columns). Default is FALSE
hide.zeroes	If TRUE trims data - see trim - before plot. Default is FALSE
legend	If TRUE shows a legend for the types of events visualized. Defualt is TRUE
legend.cex	Default 0.5; determines legend size if legend = TRUE
cellwidth	Default NA, sets autoscale cell width
cellheight	Default NA, sets autoscale cell height
group.by.label	Sort samples (rows) by event label - usefull when multiple events per gene are available
group.by.stage	Default FALSE; sort samples by stage.
group.samples	If this samples -> group map is provided, samples are grouped as of groups and sorted according to the number of mutations per sample - usefull when data was clustered
gene.annot	Genes'groups, e.g. list(RAF=c('KRAS','NRAS'), Wnt=c('APC', 'CTNNB1')). Default is NA.

gene.annot.color	Either a RColorColorbrewer palette name or a set of custom colors matching names(gene.annot)
show.patterns	If TRUE shows also a separate oncoprint for each pattern. Default is FALSE
annotate.consolidate.events	Default is FALSE. If TRUE an annotation for events to consolidate is shown.
txt.stats	By default, shows a summary statistics for shown data (n,m, |G| and |P|)
gtable	If TRUE return the gtable object
...	other arguments to pass to pheatmap

`oncoprint.cbio` *oncoprint.cbio*

Description

export input for cbio visualization at http://www.cbioportal.org/public-portal/oncoprinter.jsp

Usage

```
oncoprint.cbio(
  x,
  file = "oncoprint-cbio.txt",
  hom.del = "Homozygous Loss",
  het.loss = "Heterozygous Loss",
  gain = "Low-level Gain",
  amp = "High-level Gain"
)
```

Arguments

x	A TRONCO compliant dataset.
file	name of the file where to save the output
hom.del	type of Homozygous Deletion
het.loss	type of Heterozygous Loss
gain	type of Gain
amp	type of Amplification

Value

A file containing instruction for the CBio visualization Tool

Examples

```
data(crc_gistic)
gistic = import.GISTIC(crc_gistic)
oncoprint.cbio(gistic)
```

OR *OR*

Description

OR hypothesis

Usage

```
OR(...)
```

Arguments

...	Atoms of the soft exclusive pattern given either as labels or as partielly lifted vectors.

Value

Vector to be added to the lifted genotype resolving the soft exclusive pattern

order.frequency *order.frequency*

Description

Sort the internal genotypes according to event frequency.

Usage

```
order.frequency(x, decreasing = TRUE)
```

Arguments

x	A TRONCO compliant dataset.
decreasing	Inverse order. Default TRUE

Value

A TRONCO compliant dataset with the internal genotypes sorted according to event frequency.

Examples

```
data(test_dataset)
order.frequency(test_dataset)
```

pathway.visualization *pathway.visualization*

Description

Visualise pathways informations

Usage

```
pathway.visualization(
  x,
  title = paste("Pathways:", paste(names(pathways), collapse = ", ", sep = "")),
  file = NA,
  pathways.color = "Set2",
  aggregate.pathways,
  pathways,
  ...
)
```

Arguments

x	A TRONCO complian dataset
title	Plot title
file	To generate a PDF a filename have to be given
pathways.color	A RColorBrewer color palette
aggregate.pathways	Boolean parameter
pathways	Pathways
...	Additional parameters

Value

plot information

pheatmap *A function to draw clustered heatmaps.*

Description

A function to draw clustered heatmaps where one has better control over some graphical parameters such as cell size, etc.

Usage

```
pheatmap(
  mat,
  color = colorRampPalette(rev(brewer.pal(n = 7, name = "RdYlBu")))(100),
  kmeans_k = NA,
  breaks = NA,
  border_color = "grey60",
  cellwidth = NA,
  cellheight = NA,
  scale = "none",
  cluster_rows = TRUE,
  cluster_cols = TRUE,
  clustering_distance_rows = "euclidean",
  clustering_distance_cols = "euclidean",
  clustering_method = "complete",
  cutree_rows = NA,
  cutree_cols = NA,
  treeheight_row = ifelse(cluster_rows, 50, 0),
  treeheight_col = ifelse(cluster_cols, 50, 0),
  legend = TRUE,
  legend_breaks = NA,
  legend_labels = NA,
  annotation_row = NA,
  annotation_col = NA,
  annotation = NA,
  annotation_colors = NA,
  annotation_legend = TRUE,
  drop_levels = TRUE,
  show_rownames = TRUE,
  show_colnames = TRUE,
  main = NA,
  fontsize = 10,
  fontsize_row = fontsize,
  fontsize_col = fontsize,
  display_numbers = FALSE,
  number_format = "%.2f",
  number_color = "grey30",
  fontsize_number = 0.8 * fontsize,
  gaps_row = NULL,
  gaps_col = NULL,
  labels_row = NULL,
  labels_col = NULL,
  filename = NA,
  width = NA,
  height = NA,
  silent = FALSE,
  legend.cex = 1,
  txt.stats = NA,
```

```
  ...
)
```

Arguments

mat	numeric matrix of the values to be plotted.
color	vector of colors used in heatmap.
kmeans_k	the number of kmeans clusters to make, if we want to agggregate the rows before drawing heatmap. If NA then the rows are not aggregated.
breaks	a sequence of numbers that covers the range of values in mat and is one element longer than color vector. Used for mapping values to colors. Useful, if needed to map certain values to certain colors, to certain values. If value is NA then the breaks are calculated automatically.
border_color	color of cell borders on heatmap, use NA if no border should be drawn.
cellwidth	individual cell width in points. If left as NA, then the values depend on the size of plotting window.
cellheight	individual cell height in points. If left as NA, then the values depend on the size of plotting window.
scale	character indicating if the values should be centered and scaled in either the row direction or the column direction, or none. Corresponding values are "row", "column" and "none"
cluster_rows	boolean values determining if rows should be clustered,
cluster_cols	boolean values determining if columns should be clustered.
clustering_distance_rows	distance measure used in clustering rows. Possible values are "correlation" for Pearson correlation and all the distances supported by dist, such as "euclidean", etc. If the value is none of the above it is assumed that a distance matrix is provided.
clustering_distance_cols	distance measure used in clustering columns. Possible values the same as for clustering_distance_rows.
clustering_method	clustering method used. Accepts the same values as hclust.
cutree_rows	number of clusters the rows are divided into, based on the hierarchical clustering (using cutree), if rows are not clustered, the argument is ignored
cutree_cols	similar to cutree_rows, but for columns
treeheight_row	the height of a tree for rows, if these are clustered. Default value 50 points.
treeheight_col	the height of a tree for columns, if these are clustered. Default value 50 points.
legend	logical to determine if legend should be drawn or not.
legend_breaks	vector of breakpoints for the legend.
legend_labels	vector of labels for the legend_breaks.

annotation_row data frame that specifies the annotations shown on left side of the heatmap. Each row defines the features for a specific row. The rows in the data and in the annotation are matched using corresponding row names. Note that color schemes takes into account if variable is continuous or discrete.

annotation_col similar to annotation_row, but for columns.

annotation deprecated parameter that currently sets the annotation_col if it is missing

annotation_colors list for specifying annotation_row and annotation_col track colors manually. It is possible to define the colors for only some of the features. Check examples for details.

annotation_legend boolean value showing if the legend for annotation tracks should be drawn.

drop_levels logical to determine if unused levels are also shown in the legend

show_rownames boolean specifying if column names are be shown.

show_colnames boolean specifying if column names are be shown.

main the title of the plot

fontsize base fontsize for the plot

fontsize_row fontsize for rownames (Default: fontsize)

fontsize_col fontsize for colnames (Default: fontsize)

display_numbers logical determining if the numeric values are also printed to the cells. If this is a matrix (with same dimensions as original matrix), the contents of the matrix are shown instead of original values.

number_format format strings (C printf style) of the numbers shown in cells. For example "%.2f" shows 2 decimal places and "%.1e" shows exponential notation (see more in sprintf).

number_color color of the text

fontsize_number fontsize of the numbers displayed in cells

gaps_row vector of row indices that show shere to put gaps into heatmap. Used only if the rows are not clustered. See cutree_row to see how to introduce gaps to clustered rows.

gaps_col similar to gaps_row, but for columns.

labels_row custom labels for rows that are used instead of rownames.

labels_col similar to labels_row, but for columns.

filename file path where to save the picture. Filetype is decided by the extension in the path. Currently following formats are supported: png, pdf, tiff, bmp, jpeg. Even if the plot does not fit into the plotting window, the file size is calculated so that the plot would fit there, unless specified otherwise.

width manual option for determining the output file width in inches.

height manual option for determining the output file height in inches.

silent do not draw the plot (useful when using the gtable output)

legend.cex	Default 0.5; determines legend size if legend = TRUE
txt.stats	By default, shows a summary statistics for shown data (n,m, |G| and |P|)
...	graphical parameters for the text used in plot. Parameters passed to grid.text, see gpar.

Details

The function also allows to aggregate the rows using kmeans clustering. This is advisable if number of rows is so big that R cannot handle their hierarchical clustering anymore, roughly more than 1000. Instead of showing all the rows separately one can cluster the rows in advance and show only the cluster centers. The number of clusters can be tuned with parameter kmeans_k.

This is a modified version of the original pheatmap (https://cran.r-project.org/web/packages/pheatmap/index.html) edited in accordance with GPL-2.

Value

Invisibly a list of components

- tree_row the clustering of rows as hclust object
- tree_col the clustering of columns as hclust object
- kmeans the kmeans clustering of rows if parameter kmeans_k was specified

Author(s)

Raivo Kolde <rkolde@gmail.com>

Examples

```
# Create test matrix
test = matrix(rnorm(200), 20, 10)
test[1:10, seq(1, 10, 2)] = test[1:10, seq(1, 10, 2)] + 3
test[11:20, seq(2, 10, 2)] = test[11:20, seq(2, 10, 2)] + 2
test[15:20, seq(2, 10, 2)] = test[15:20, seq(2, 10, 2)] + 4
colnames(test) = paste("Test", 1:10, sep = "")
rownames(test) = paste("Gene", 1:20, sep = "")

# Draw heatmaps
pheatmap(test)
```

---

rank.recurrents *rank.recurrents*

Description

Return the first n recurrent events

Usage

```
rank.recurrents(x, n)
```

Arguments

x	A TRONCO compliant dataset.
n	The number of events to rank

Value

the first n recurrent events

Examples

```
data(test_dataset)
dataset = rank.recurrents(test_dataset, 10)
```

---

rename.gene *rename.gene*

Description

Rename a gene

Usage

```
rename.gene(x, old.name, new.name)
```

Arguments

x	A TRONCO compliant dataset.
old.name	The name of the gene to rename.
new.name	The new name

Value

A TRONCO complian dataset.

Examples

```
data(test_dataset)
test_dataset = rename.gene(test_dataset, 'TET2', 'gene x')
```

rename.type *rename.type*

Description

Rename an event type

Usage

```
rename.type(x, old.name, new.name)
```

Arguments

x	A TRONCO compliant dataset.
old.name	The type of event to rename.
new.name	The new name

Value

A TRONCO complian dataset.

Examples

```
data(test_dataset)
test_dataset = rename.type(test_dataset, 'ins_del', 'deletion')
```

samples.selection *samples.selection*

Description

Filter a dataset based on selected samples id

Usage

```
samples.selection(x, samples)
```

Arguments

x	A TRONCO compliant dataset.
samples	A list of samples

Value

A TRONCO compliant dataset.

Examples

```
data(test_dataset)
dataset = samples.selection(test_dataset, c('patient 1', 'patient 2'))
```

`sbind` *sbind*

Description

Binds samples from one or more datasets, which must be defined over the same set of events

Usage

```
sbind(...)
```

Arguments

`...`	the input datasets

Value

A TRONCO complian dataset.

`ssplit` *ssplit*

Description

Split cohort (samples) into groups, return either all groups or a specific group.

Usage

```
ssplit(x, clusters, idx = NA)
```

Arguments

`x`	A TRONCO compliant dataset.
`clusters`	A list of clusters. Rownames must match samples list of x
`idx`	ID of a specific group present in stages. If NA all groups will be extracted

Value

A TRONCO compliant dataset.

stage *Stage information for test_dataset*

Description

This dataset contains stage information for patient in test_dataset

Usage

```
data(stage)
```

Format

Vector of stages

Value

A list of stages

Author(s)

Luca De Sano

Source

fake data

TCGA.map.clinical.data *TCGA.map.clinical.data*

Description

Map clinical data from the TCGA format

Usage

```
TCGA.map.clinical.data(file, sep = "\t", column.samples, column.map)
```

Arguments

file	A file with the clinical data
sep	file delimiter
column.samples	Required columns
column.map	Map to the required columns

Value

a map

`TCGA.multiple.samples` *TCGA.multiple.samples*

Description

Check if there are multiple sample in x, according to TCGA barcodes naming

Usage

```
TCGA.multiple.samples(x)
```

Arguments

x	A TRONCO compliant dataset.

Value

A list of barcodes. NA if no duplicated barcode is found

Examples

```
data(test_dataset)
TCGA.multiple.samples(test_dataset)
```

`TCGA.remove.multiple.samples`
TCGA.remove.multiple.samples

Description

If there are multiple sample in x, according to TCGA barcodes naming, remove them

Usage

```
TCGA.remove.multiple.samples(x)
```

Arguments

x	A TRONCO compliant dataset.

Value

A TRONCO compliant dataset

Examples

```
data(test_dataset)
TCGA.remove.multiple.samples(test_dataset)
```

TCGA.shorten.barcodes *TCGA.shorten.barcodes*

Description

Keep only the first 12 character of samples barcode if there are no duplicates

Usage

```
TCGA.shorten.barcodes(x)
```

Arguments

x	A TRONCO compliant dataset.

Value

A TRONCO compliant dataset

Examples

```
data(test_dataset)
TCGA.shorten.barcodes(test_dataset)
```

---

test_dataset *A complete dataset with hypotheses*

Description

This dataset contains a complete test dataset

Usage

```
data(test_dataset)
```

Format

TRONCO compliant dataset

Value

A standard TRONCO object

Author(s)

Luca De Sano

Source

fake data

---

test_dataset_no_hypos *A complete dataset*

Description

This dataset contains a complete test dataset

Usage

```
data(test_dataset_no_hypos)
```

Format

TRONCO compliant dataset

Value

A standard TRONCO object

Author(s)

Luca De Sano

Source

fake data

test_model — *A complete dataset with a reconstructed model*

Description

This dataset contains a model reconstructed with CAPRI

Usage

```
data(test_model)
```

Format

TRONCO compliant dataset

Value

A standard TRONCO object

Author(s)

Luca De Sano

Source

fake data

test_model_kfold — *A complete dataset with a reconstructed model and crossvalidation informations*

Description

This dataset contains a model reconstructed with CAPRI

Usage

```
data(test_model_kfold)
```

Format

TRONCO compliant dataset

Value

A standard TRONCO object

Author(s)

Luca De Sano

Source

fake data

---

trim *trim*

Description

Deletes all events which have frequency 0 in the dataset.

Usage

```
trim(x)
```

Arguments

x	A TRONCO compliant dataset.

Value

A TRONCO compliant dataset.

Examples

```
data(test_dataset)
test_dataset = trim(test_dataset)
```

---

tronco.bootstrap *tronco bootstrap*

Description

Bootstrap a reconstructed progression model. For details and examples regarding the statistical assesment of an inferred model, we refer to the Vignette Section 7.

Usage

```
tronco.bootstrap(
  reconstruction,
  type = "non-parametric",
  nboot = 100,
  cores.ratio = 1,
  silent = FALSE
)
```

Arguments

reconstruction	The output of tronco.capri or tronco.caprese
type	Parameter to define the type of sampling to be performed, e.g., non-parametric for uniform sampling.
nboot	Number of bootstrap sampling to be performed when estimating the model confidence.
cores.ratio	Percentage of cores to use coresRate * (numCores - 1)
silent	A parameter to disable/enable verbose messages.

Value

A TRONCO compliant object with reconstructed model

Examples

```
data(test_model)
boot = tronco.bootstrap(test_model, nboot = 1, cores.ratio = 0)
```

---

tronco.caprese *tronco caprese*

Description

Reconstruct a progression model using CAPRESE algorithm. For details and examples regarding the inference process and on the algorithm implemented in the package, we refer to the Vignette Section 6.

Usage

```
tronco.caprese(data, lambda = 0.5, silent = FALSE, epos = 0, eneg = 0)
```

Arguments

data	A TRONCO compliant dataset.
lambda	Coefficient to combine the raw estimate with a correction factor into a shrinkage estimator.
silent	A parameter to disable/enable verbose messages.
epos	Error rate of false positive errors.
eneg	Error rate of false negative errors.

Value

A TRONCO compliant object with reconstructed model

Examples

```
data(test_dataset_no_hypos)
recon = tronco.caprese(test_dataset_no_hypos)
```

`tronco.capri` *tronco capri*

Description

Reconstruct a progression model using CAPRI algorithm. For details and examples regarding the inference process and on the algorithm implemented in the package, we refer to the Vignette Section 6.

Usage

```
tronco.capri(
  data,
  command = "hc",
  regularization = c("bic", "aic"),
  do.boot = TRUE,
  nboot = 100,
  pvalue = 0.05,
  min.boot = 3,
  min.stat = TRUE,
  boot.seed = NULL,
  silent = FALSE,
  epos = 0,
  eneg = 0,
  restart = 100
)
```

Arguments

`data`	A TRONCO compliant dataset.
`command`	Parameter to define to heuristic search to be performed. Hill Climbing and Tabu search are currently available.
`regularization`	Select the regularization for the likelihood estimation, e.g., BIC, AIC.
`do.boot`	A parameter to disable/enable the estimation of the error rates give the reconstructed model.
`nboot`	Number of bootstrap sampling (with rejection) to be performed when estimating the selective advantage scores.
`pvalue`	Pvalue to accept/reject the valid selective advantage relations.
`min.boot`	Minimum number of bootstrap sampling to be performed.

min.stat	A parameter to disable/enable the minimum number of bootstrap sampling required besides nboot if any sampling is rejected.
boot.seed	Initial seed for the bootstrap random sampling.
silent	A parameter to disable/enable verbose messages.
epos	Error rate of false positive errors.
eneg	Error rate of false negative errors.
restart	An integer, the number of random restarts.

Value

A TRONCO compliant object with reconstructed model

Examples

```
data(test_dataset)
recon = tronco.capri(test_dataset, nboot = 1)
```

---

tronco.chowliu *Tronco Chow Liu*

Description

Reconstruct a progression model using Chow Liu algorithm combined with probabilistic causation. For details and examples regarding the inference process and on the algorithm implemented in the package, we refer to the Vignette Section 6.

Usage

```
tronco.chowliu(
  data,
  regularization = c("bic", "aic"),
  do.boot = TRUE,
  nboot = 100,
  pvalue = 0.05,
  min.boot = 3,
  min.stat = TRUE,
  boot.seed = NULL,
  silent = FALSE,
  epos = 0,
  eneg = 0
)
```

Arguments

data	A TRONCO compliant dataset.
regularization	Select the regularization for the likelihood estimation, e.g., BIC, AIC.
do.boot	A parameter to disable/enable the estimation of the error rates give the reconstructed model.
nboot	Number of bootstrap sampling (with rejection) to be performed when estimating the selective advantage scores.
pvalue	Pvalue to accept/reject the valid selective advantage relations.
min.boot	Minimum number of bootstrap sampling to be performed.
min.stat	A parameter to disable/enable the minimum number of bootstrap sampling required besides nboot if any sampling is rejected.
boot.seed	Initial seed for the bootstrap random sampling.
silent	A parameter to disable/enable verbose messages.
epos	Error rate of false positive errors.
eneg	Error rate of false negative errors.

Value

A TRONCO compliant object with reconstructed model

Examples

```
data(test_dataset_no_hypos)
recon = tronco.chowliu(test_dataset_no_hypos, nboot = 1)
```

---

tronco.edmonds *Tronco Edmonds*

Description

Reconstruct a progression model using Edmonds algorithm combined with probabilistic causation. For details and examples regarding the inference process and on the algorithm implemented in the package, we refer to the Vignette Section 6.

Usage

```
tronco.edmonds(
  data,
  regularization = "no_reg",
  score = "pmi",
  do.boot = TRUE,
  nboot = 100,
  pvalue = 0.05,
```

```
  min.boot = 3,
  min.stat = TRUE,
  boot.seed = NULL,
  silent = FALSE,
  epos = 0,
  eneg = 0
)
```

Arguments

data	A TRONCO compliant dataset.
regularization	Select the regularization for the likelihood estimation, e.g., BIC, AIC.
score	Select the score for the estimation of the best tree, e.g., pointwise mutual information (pmi), conditional entropy (entropy).
do.boot	A parameter to disable/enable the estimation of the error rates give the reconstructed model.
nboot	Number of bootstrap sampling (with rejection) to be performed when estimating the selective advantage scores.
pvalue	Pvalue to accept/reject the valid selective advantage relations.
min.boot	Minimum number of bootstrap sampling to be performed.
min.stat	A parameter to disable/enable the minimum number of bootstrap sampling required besides nboot if any sampling is rejected.
boot.seed	Initial seed for the bootstrap random sampling.
silent	A parameter to disable/enable verbose messages.
epos	Error rate of false positive errors.
eneg	Error rate of false negative errors.

Value

A TRONCO compliant object with reconstructed model

Examples

```
data(test_dataset_no_hypos)
recon = tronco.edmonds(test_dataset_no_hypos, nboot = 1)
```

`tronco.gabow` *Tronco Gabow*

Description

Reconstruct a progression model using Gabow algorithm combined with probabilistic causation. For details and examples regarding the inference process and on the algorithm implemented in the package, we refer to the Vignette Section 6.

Usage

```
tronco.gabow(
  data,
  regularization = "no_reg",
  score = "pmi",
  do.boot = TRUE,
  nboot = 100,
  pvalue = 0.05,
  min.boot = 3,
  min.stat = TRUE,
  boot.seed = NULL,
  silent = FALSE,
  epos = 0,
  eneg = 0,
  do.raising = TRUE
)
```

Arguments

`data`	A TRONCO compliant dataset.
`regularization`	Select the regularization for the likelihood estimation, e.g., BIC, AIC.
`score`	Select the score for the estimation of the best tree, e.g., pointwise mutual information (pmi), conditional entropy (entropy).
`do.boot`	A parameter to disable/enable the estimation of the error rates give the reconstructed model.
`nboot`	Number of bootstrap sampling (with rejection) to be performed when estimating the selective advantage scores.
`pvalue`	Pvalue to accept/reject the valid selective advantage relations.
`min.boot`	Minimum number of bootstrap sampling to be performed.
`min.stat`	A parameter to disable/enable the minimum number of bootstrap sampling required besides nboot if any sampling is rejected.
`boot.seed`	Initial seed for the bootstrap random sampling.
`silent`	A parameter to disable/enable verbose messages.
`epos`	Error rate of false positive errors.
`eneg`	Error rate of false negative errors.
`do.raising`	Whether to use or not the raising condition as a prior.

Value

A TRONCO compliant object with reconstructed model

Examples

```
data(test_dataset_no_hypos)
recon = tronco.gabow(test_dataset_no_hypos, nboot = 1)
```

`tronco.kfold.eloss` *tronco.kfold.eloss*

Description

Perform a k-fold cross-validation using the function bn.cv to estimate the entropy loss. For details and examples regarding the statistical assesment of an inferred model, we refer to the Vignette Section 7.

Usage

```
tronco.kfold.eloss(
  x,
  models = names(as.models(x)),
  runs = 10,
  k = 10,
  silent = FALSE
)
```

Arguments

`x`	A reconstructed model (the output of tronco.capri or tronco.caprese)
`models`	The names of the selected regularizers (bic, aic or caprese)
`runs`	a positive integer number, the number of times cross-validation will be run
`k`	a positive integer number, the number of groups into which the data will be split
`silent`	A parameter to disable/enable verbose messages.

Examples

```
data(test_model)
tronco.kfold.eloss(test_model, k = 2, runs = 2)
```

`tronco.kfold.posterr` *tronco.kfold.posterr. For details and examples regarding the statistical assesment of an inferred model, we refer to the Vignette Section 7.*

Description

Perform a k-fold cross-validation using the function bn.cv and scan every node to estimate its posterior classification error.

Usage

```
tronco.kfold.posterr(
  x,
  models = names(as.models(x)),
  events = as.events(x),
  runs = 10,
  k = 10,
  cores.ratio = 1,
  silent = FALSE
)
```

Arguments

`x`	A reconstructed model (the output of tronco.capri)
`models`	The names of the selected regularizers (bic, aic or caprese)
`events`	a list of event
`runs`	a positive integer number, the number of times cross-validation will be run
`k`	a positive integer number, the number of groups into which the data will be split
`cores.ratio`	Percentage of cores to use. coresRate * (numCores - 1)
`silent`	A parameter to disable/enable verbose messages.

Examples

```
data(test_model)
tronco.kfold.posterr(test_model, k = 2, runs = 2, cores.ratio = 0)
```

`tronco.kfold.prederr` *tronco.kfold.prederr*

Description

Perform a k-fold cross-validation using the function bn.cv and scan every node to estimate its prediction error. For details and examples regarding the statistical assesment of an inferred model, we refer to the Vignette Section 7.

Usage

```
tronco.kfold.prederr(
  x,
  models = names(as.models(x)),
  events = as.events(x),
  runs = 10,
  k = 10,
  cores.ratio = 1,
  silent = FALSE
)
```

Arguments

`x`	A reconstructed model (the output of tronco.capri)
`models`	The names of the selected regularizers (bic, aic or caprese)
`events`	a list of event
`runs`	a positive integer number, the number of times cross-validation will be run
`k`	a positive integer number, the number of groups into which the data will be split
`cores.ratio`	Percentage of cores to use. coresRate * (numCores - 1)
`silent`	A parameter to disable/enable verbose messages.

Examples

```
data(test_model)
tronco.kfold.prederr(test_model, k = 2, runs = 2, cores.ratio = 0)
```

tronco.pattern.plot *tronco.pattern.plot*

Description

tronco.pattern.plot : plot a genotype

Usage

```
tronco.pattern.plot(
  x,
  group = as.events(x),
  to,
  gap.cex = 1,
  legend.cex = 1,
  label.cex = 1,
  title = paste(to[1], to[2]),
  mode = "barplot"
)
```

Arguments

x	A TRONCO compliant dataset
group	A list of events (see as.events() for details)
to	A target event
gap.cex	cex parameter for gap
legend.cex	cex parameter for legend
label.cex	cex parameter for label
title	title
mode	can be 'circos' or 'barplot'

tronco.plot *tronco.plot*

Description

Plots a progression model from a recostructed dataset. For details and examples regarding the visualization of an inferred model, we refer to the Vignette Section 7.

Usage

```
tronco.plot(
  x,
  models = names(x$model),
  fontsize = NA,
  height = 2,
  width = 3,
  height.logic = 1,
  pf = FALSE,
  disconnected = FALSE,
  scale.nodes = NA,
  title = as.description(x),
  confidence = NA,
  p.min = 0.05,
  legend = TRUE,
  legend.cex = 1,
  edge.cex = 1,
  label.edge.size = NA,
  expand = TRUE,
  genes = NULL,
  relations.filter = NA,
  edge.color = "black",
  pathways.color = "Set1",
  file = NA,
  legend.pos = "bottom",
  pathways = NULL,
  lwd = 3,
  samples.annotation = NA,
  export.igraph = FALSE,
  create.new.dev = TRUE,
  ...
)
```

Arguments

x	A reconstructed model (the output of the inference by a tronco function)
models	A vector containing the names of the algorithms used (caprese, capri_bic, etc)
fontsize	For node names. Default NA for automatic rescaling
height	Proportion node height - node width. Default height 2
width	Proportion node height - node width. Default width 2
height.logic	Height of logical nodes. Defaul 1
pf	Should I print Prima Facie? Default False
disconnected	Should I print disconnected nodes? Default False
scale.nodes	Node scaling coefficient (based on node frequency). Default NA (autoscale)
title	Title of the plot. Default as.description(x)

confidence	Should I add confidence informations? No if NA
p.min	p-value cutoff. Default automatic
legend	Should I visualise the legend?
legend.cex	CEX value for legend. Default 1.0
edge.cex	CEX value for edge labels. Default 1.0
label.edge.size	Size of edge labels. Default NA for automatic rescaling
expand	Should I expand hypotheses? Default TRUE
genes	Visualise only genes in this list. Default NULL, visualise all.
relations.filter	Filter relations to dispaly according to this functions. Default NA
edge.color	Edge color. Default 'black'
pathways.color	RColorBrewer colorser for patways. Default 'Set1'.
file	String containing filename for PDF output. If NA no PDF output will be provided
legend.pos	Legend position. Default 'bottom',
pathways	A vector containing pathways information as described in as.patterns()
lwd	Edge base lwd. Default 3
samples.annotation	= List of samples to search for events in model
export.igraph	If TRUE export the generated igraph object
create.new.dev	If TRUE create a new graphical device when calling trono.plot. Set this to FALSE, e.g., if you do not wish to create a new device when executing the command with export.igraph = TRUE
...	Additional arguments for RGraphviz plot function

Value

Information about the reconstructed model

Examples

```
data(test_model)
tronco.plot(test_model)
```

`tronco.prim` *Tronco Prim*

Description

Reconstruct a progression model using Prim algorithm combined with probabilistic causation. For details and examples regarding the inference process and on the algorithm implemented in the package, we refer to the Vignette Section 6.

Usage

```
tronco.prim(
  data,
  regularization = "no_reg",
  do.boot = TRUE,
  nboot = 100,
  pvalue = 0.05,
  min.boot = 3,
  min.stat = TRUE,
  boot.seed = NULL,
  silent = FALSE,
  epos = 0,
  eneg = 0
)
```

Arguments

`data`	A TRONCO compliant dataset.
`regularization`	Select the regularization for the likelihood estimation, e.g., BIC, AIC.
`do.boot`	A parameter to disable/enable the estimation of the error rates give the reconstructed model.
`nboot`	Number of bootstrap sampling (with rejection) to be performed when estimating the selective advantage scores.
`pvalue`	Pvalue to accept/reject the valid selective advantage relations.
`min.boot`	Minimum number of bootstrap sampling to be performed.
`min.stat`	A parameter to disable/enable the minimum number of bootstrap sampling required besides nboot if any sampling is rejected.
`boot.seed`	Initial seed for the bootstrap random sampling.
`silent`	A parameter to disable/enable verbose messages.
`epos`	Error rate of false positive errors.
`eneg`	Error rate of false negative errors.

Value

A TRONCO compliant object with reconstructed model

Examples

```
data(test_dataset_no_hypos)
recon = tronco.prim(test_dataset_no_hypos, nboot = 1)
```

`view` *view*

Description

Print to console a short report of a dataset 'x', which should be a TRONCO compliant dataset - see `is.compliant`.

Usage

```
view(x, view = 5)
```

Arguments

`x`	A TRONCO compliant dataset.
`view`	The firse `view` events are shown via `head`.

Examples

```
data(test_dataset)
view(test_dataset)
```

`which.samples` *which.samples*

Description

Return a list of samples with specified alteration

Usage

```
which.samples(x, gene, type, neg = FALSE)
```

Arguments

`x`	A TRONCO compliant dataset.
`gene`	A list of gene names
`type`	A list of types
`neg`	If FALSE return the list, if TRUE return as.samples() - list

Value

A list of sample

Examples

```
data(test_dataset)
which.samples(test_dataset, 'TET2', 'ins_del')
which.samples(test_dataset, 'TET2', 'ins_del', neg=TRUE)
```

`XOR` *XOR*

Description

XOR hypothesis

Usage

```
XOR(...)
```

Arguments

...	Atoms of the hard exclusive pattern given either as labels or as partielly lifted vectors.

Value

Vector to be added to the lifted genotype resolving the hard exclusive pattern

Index

aCML, 5
AND, 5
annotate.description, 6
annotate.stages, 6
as.adj.matrix, 7
as.alterations, 8
as.bootstrap.scores, 8
as.colors, 9
as.conditional.probs, 10
as.confidence, 10
as.description, 11
as.events, 12
as.events.in.patterns, 12
as.events.in.sample, 13
as.gene, 14
as.genes, 14
as.genes.in.patterns, 15
as.genotypes, 16
as.hypotheses, 16
as.joint.probs, 17
as.kfold.eloss, 18
as.kfold.posterr, 18
as.kfold.prederr, 19
as.marginal.probs, 20
as.models, 21
as.parameters, 21
as.pathway, 22
as.patterns, 23
as.samples, 23
as.selective.advantage.relations, 24
as.stages, 25
as.types, 25
as.types.in.patterns, 26

change.color, 27
consolidate.data, 27
crc_gistic, 28
crc_maf, 29
crc_plain, 29

delete.event, 30
delete.gene, 31
delete.hypothesis, 31
delete.model, 32
delete.pattern, 33
delete.samples, 33
delete.type, 34
dist, *63*
duplicates, 34

ebind, 35
enforce.numeric, 35
enforce.string, 36
events.selection, 36
export.graphml, 37
export.mutex, 38
export.nbs.input, 39
extract.MAF.HuGO.Entrez.map, 39

genes.table.report, 40
gpar, *65*
grid.text, *65*

has.duplicates, 41
has.model, 41
has.stages, 42
hclust, *63*, *65*
hypothesis.add, 42
hypothesis.add.group, 43
hypothesis.add.homologous, 44

import.genotypes, 45
import.GISTIC, 45
import.MAF, 46
import.model, 48
import.mutex.groups, 48
intersect.datasets, 49
is.compliant, 49

join.events, 50
join.types, 51

keysToNames, 51

maf, 52
muts, 53

nameToKey, 53
nevents, 54
ngenes, 54
nhypotheses, 55
npatterns, 55
nsamples, 56
ntypes, 56

oncoprint, 57
oncoprint.cbio, 59
OR, 60
order.frequency, 60

pathway.visualization, 61
pheatmap, 61

rank.recurrents, 65
rename.gene, 66
rename.type, 67

samples.selection, 67
sbind, 68
sprintf, *64*
ssplit, 68
stage, 69

TCGA.map.clinical.data, 69
TCGA.multiple.samples, 70
TCGA.remove.multiple.samples, 70
TCGA.shorten.barcodes, 71
test_dataset, 71
test_dataset_no_hypos, 72
test_model, 73
test_model_kfold, 73
trim, 74
tronco.bootstrap, 74
tronco.caprese, 75
tronco.capri, 76
tronco.chowliu, 77
tronco.edmonds, 78
tronco.gabow, 80
tronco.kfold.eloss, 81
tronco.kfold.posterr, 82
tronco.kfold.prederr, 83
tronco.pattern.plot, 84
tronco.plot, 84
tronco.prim, 87

view, 88

which.samples, 88

XOR, 89