**Package ‘TRONCO’**

**March 23, 2017**

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**Title** TRONCO, an R package for TRanslational ONCOlogy  
**Maintainer** BIMIB Group <tronco@disco.unimib.it>  
**Depends** R (>= 3.3),  
**Imports** bnlearn, Rgraphviz, gtools, parallel, foreach, doParallel, iterators, RColorBrewer, circlize, cgdsr, igraph, grid, gridExtra, xtable, gtable, scales, R.matlab, gRapHD, grDevices, graphics, stats, utils,  
**Suggests** BiocGenerics, BiocStyle, testthat, knitr,  
**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.  
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**License** file LICENSE  
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**BugReports** https://github.com/BIMIB-DISCO/TRONCO  
**biocViews** BiomedicalInformatics, Bayesian, GraphAndNetwork, SomaticMutation, NetworkInference, Network, Clustering, DataImport  
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Description
This file contains a TRONCO compliant dataset

Usage
data(aCML)

Format
TRONCO compliant dataset

Author(s)
Luca De Sano

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

AND hypothesis

Usage

AND(...) 

Arguments

... Atoms of the co-occurrence pattern given either as labels or as partially lifted vectors.

Value

Vector to be added to the lifted genotype resolving the co-occurrence 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

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

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$models), type = "fit")
as.alterations

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

Description

Return a dataset where all events for a gene are merged in a unique event, i.e., a total of gene-level alterations disregarding 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**

**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**

```r
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**

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

---

**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**

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

**Arguments**

- `x` A TRONCO compliant dataset.

**Value**

A named vector of colors.
as.conditional.probs

Examples

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

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

```r
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

```r
# @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

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

\[
\text{as.confidence}(x, \text{conf, models = names}(x$model))
\]

Arguments

\[
x \quad \text{A TRONCO model.}
\]
\[
\text{conf} \quad \text{A vector with any of 'tp', 'pr', 'hg', 'nbp', 'pb', 'sb', 'eloss', 'prederr' or 'posterr'.}
\]
\[
\text{models} \quad \text{The name of the models to extract, all by default.}
\]

Value

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

Examples

\[
\text{data(test_model)}
\]
\[
\text{as.confidence(test_model, conf='tp')}
\]
\[
\text{as.confidence(test_model, conf=c('tp', 'hg'))}
\]

Description

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

Usage

\[
\text{as.description}(x)
\]

Arguments

\[
x \quad \text{A TRONCO compliant dataset.}
\]

Value

The description annotating the dataset, if any.

Examples

\[
\text{data(test_dataset)}
\]
\[
\text{as.description(test_dataset)}
\]
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

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
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)
as.genes

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 \texttt{as.genotypes(x)} with colnames substituted with events’ types.

Examples

data(test_dataset)
as.genes(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 \texttt{is.compliant}.

Usage

\texttt{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

### Description

Return the list of genes present in selected patterns

### Usage

```r
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 constitute CAPRI’s hypotheses

### Examples

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

---

## 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

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

### Arguments

- `x`  
  A TRONCO compliant dataset.

### Value

A TRONCO genotypes matrix.

### Examples

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

Description
Extract the joint probabilities from a TRONCO model. The return matrix is indexed with row-names/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

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

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

```r
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

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

Value
All the posterior classification error scores in a TRONCO model

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

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 (default false).

Value

All the bootstrap scores in a TRONCO model

Examples

```r
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 row-names 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

```r
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

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

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

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

Description

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

Usage

as.patterns(x)

Arguments

x A TRONCO compliant dataset.
as.samples

Value
The patterns in the dataset which constitute CAPRI’s hypotheses.

Examples

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

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

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

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")
```
as.stages

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

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

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

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 constitute CAPRI’s hypotheses
Examples

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

Description

Wrapper for the CGDS package to query the Cbio portal. This can work either automatically, if one sets `cbio.study`, `cbio.dataset` or `cbio.profile`, or interactively otherwise. A list of genes to query with less than 900 entries should be provided. This function returns a list with two dataframe: the gentic profile required and clinical data for the Cbio study. Output is also saved to disk as Rdata file. See also http://www.cbioportal.org.

Usage

cbio.query(cbio.study = NA, cbio.dataset = NA, cbio.profile = NA, genes, file = NA)

Arguments

cbio.study  Cbio study ID
cbio.dataset Cbio dataset ID
cbio.profile Cbio genetic profile ID
genes        A list of < 900 genes to query
file          String containing filename for RData output. If NA no output will be provided

Value

A list with two dataframe: the gentic profile required and clinical data for the Cbio study.

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 compliant dataset.

Examples

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

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 or 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
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

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

Author(s)
  Daniele Ramazzotti

Source
  data from http://www.nature.com/nature/journal/v487/n7407/full/nature11252.html
**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 compliant dataset.

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

**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 compliant dataset.

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

```r
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 compliant dataset.

**Examples**

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

---

**Description**

Delete a reconstructed model from the dataset.

**Usage**

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

**Arguments**

- `x`: A TRONCO compliant dataset.

**Value**

A TRONCO compliant dataset.
**delete.pattern**

**Examples**

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

**Description**

Delete a pattern and every associated hypotheses from the dataset

**Usage**

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

**Arguments**

- `x`: A TRONCO compliant dataset.
- `pattern`: A pattern name

**Value**

A TRONCO compliant dataset.

**Examples**

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

---

**delete.samples**

**Description**

Delete samples from selected dataset

**Usage**

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

**Arguments**

- `x`: A TRONCO compliant dataset.
- `samples`: An array of samples name
### Value
A TRONCO compliant dataset.

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

<table>
<thead>
<tr>
<th>delete.type</th>
<th>delete.type</th>
</tr>
</thead>
</table>

### Description
Delete an event type

### Usage
```r
delete.type(x, type)
```

#### Arguments
- `x`: A TRONCO compliant dataset.
- `type`: The name of the type to delete.

### Value
A TRONCO compliant dataset.

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

<table>
<thead>
<tr>
<th>duplicates</th>
<th>duplicates</th>
</tr>
</thead>
</table>

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

### Usage
```r
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)

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 compliant dataset.

Description

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

Usage

enforce.numeric(x)

Arguments

x A TRONCO compliant dataset.

Value

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

Examples

data(test_dataset)
test_dataset = enforce.numeric(test_dataset)
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 representation of genotypes to character, if not.

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

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 constrains the minimum frequency 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**

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

**Description**

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

**Usage**

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

**Arguments**

- `x`: A TRONCO compliant dataset
- `file`: Where to save the output
- `...`: Parameters for tronco.plot

**Examples**

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

---

**export.mutex**

**Description**

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

**Usage**

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

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

Usage
```r
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

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

Arguments
- `file`: MAF filename
- `sep`: MAF separator, default \"\"\n
Value
A mapHugo_Symbol -> Entrez_Gene_Id.
genes.table.report

**Description**

Generate PDF and LaTeX 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

**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

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

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)
```

**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**: Possible effects for the pattern.
- **pattern.cause**: Possible causes for the pattern.

**Value**

A TRONCO compliant object with the added hypothesis

**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)
```
hypothesis.add.homologous

Arguments

- **x**: A TRONCO compliant dataset.
- **FUN**: Type of pattern to be added, e.g., co-occurrence, soft or hard exclusivity.
- **group**: Group of events to be considered.
- **pattern.cause**: Possible causes for the pattern.
- **pattern.effect**: Possible 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

Description

Add all the hypotheses related to homologous events

Usage

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

Arguments

- **x**: A TRONCO compliant dataset.
- **pattern.cause**: Possible causes for the pattern.
- **pattern.effect**: Possible 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.
- **FUN**: Type of pattern to be added, e.g., co-occurrence, soft or hard exclusivity.
- **silent**: A parameter to disable/enable verbose messages.

Value

A TRONCO compliant object with the added hypotheses
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 row 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 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

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 must 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 consistent 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)
import.MAF

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

Value

A TRONCO compliant representation of the input CNAs.

Examples

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

Usage

```r
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

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 occur. 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.
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.barcode(mutations)
oncoprint(mutations)

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

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.

\( \text{intersect.genomes} \)  
If False -> just samples

Value

A TRONCO compliant dataset.

Examples

```
data(test_dataset)
```

Description

Check if ‘x’ is compliant with TRONCO’s input: that is if it has dataframes \( x$\text{genotypes} \), \( x$\text{annotations} \), \( x$\text{types} \) and \( x$\text{stage} \) (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.

\( \text{err.fun} \)  
string which identifies the function which called is.compliant

\( \text{stage} \)  
boolean flag to check \( x$\text{stage} \) dataframe

Value

on error stops the computation

Examples

```
data(test_dataset)
is.compliant(test_dataset)
```
### join.events

**Description**

Merge a list of events in an unique event

**Usage**

```r
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**

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

### join.types

**Description**

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

**Usage**

```r
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.
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

**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

**Author(s)**
Luca De Sano

**Source**
fake data
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

events

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

Usage
events(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)
events(test_dataset)
Description

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

Usage

\[ \text{ngenes}(x, \text{types} = \text{NA}) \]

Arguments

\begin{itemize}
  \item \textbf{x} \quad \text{A TRONCO compliant dataset.}
  \item \textbf{types} \quad \text{The types of events to consider, if NA all available types are used.}
\end{itemize}

Value

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

Examples

\begin{verbatim}
data(test_dataset)
ngenes(test_dataset)
\end{verbatim}

\hline

\textbf{nhypotheses} \quad \textit{Return the number of hypotheses in the dataset}

\hline

Description

Return the number of hypotheses in the dataset

Usage

\[ \text{nhypotheses}(x) \]

Arguments

\begin{itemize}
  \item \textbf{x} \quad \text{the dataset.}
\end{itemize}

Examples

\begin{verbatim}
data(test_dataset)
nhypotheses(test_dataset)
\end{verbatim}
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

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

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

Usage
oncoprint(x, excl.sort = TRUE, samples.cluster = FALSE,
geens.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.zeros = 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.zeros`  
If TRUE trims data - see trim - before plot. Default is FALSE

`legend`  
If TRUE shows a legend for the types of events visualized. Default 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
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 partially lifted vectors.

Value

  Vector to be added to the lifted genotype resolving the soft exclusive pattern
order.frequency

Description
Sort the internal genotypes according to event frequency.

Usage
order.frequency(x, decreasing = TRUE)

Arguments

<table>
<thead>
<tr>
<th>x</th>
<th>A TRONCO compliant dataset.</th>
</tr>
</thead>
<tbody>
<tr>
<td>decreasing</td>
<td>Inverse order. Default TRUE</td>
</tr>
</tbody>
</table>

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

Examples
data(test_dataset)
order.frequency(test_dataset)

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

<table>
<thead>
<tr>
<th>x</th>
<th>A TRONCO compliant dataset</th>
</tr>
</thead>
<tbody>
<tr>
<td>title</td>
<td>Plot title</td>
</tr>
<tr>
<td>file</td>
<td>To generate a PDF a filename have to be given</td>
</tr>
<tr>
<td>pathways.color</td>
<td>A RColorBrewer color palette</td>
</tr>
<tr>
<td>aggregate.pathways</td>
<td>Boolean parameter</td>
</tr>
<tr>
<td>pathways</td>
<td>Pathways</td>
</tr>
<tr>
<td>...</td>
<td>Additional parameters</td>
</tr>
</tbody>
</table>
pheatmap

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, 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_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 aggregate 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.
pheatmap

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 where 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

```r
# 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**

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**

Description

Rename a gene

Usage

```ename.gene(x, old.name, new.name)
```
**rename.type**

**Arguments**

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

**Value**

A TRONCO compliant dataset.

**Examples**

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

---

**rename.type**

**Description**

Rename an event type

**Usage**

```r
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 compliant dataset.

**Examples**

```r
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**
```r
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 compliant dataset.
Description

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

Usage

```r
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

```r
data(stage)
```

Format

Vector of stages

Author(s)

Luca De Sano

Source

fake 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

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

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

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**

```r
data(test_dataset)
```

**Format**

TRONCO compliant dataset

**Author(s)**

Luca De Sano

**Source**

fake data

---

**test_dataset_no_hypos**  
*A complete dataset*

**Description**

This dataset contains a complete test dataset

**Usage**

```r
data(test_dataset_no_hypos)
```

**Format**

TRONCO compliant dataset

**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

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

Author(s)

Luca De Sano

Source

fake data
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

Description

Bootstrap a reconstructed progression model. For details and examples regarding the statistical
assessment 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 con-
fidence.
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)

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

donco.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)
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

\texttt{tronco.capri(data, command = \texttt{“hc”}, regularization = \texttt{c(“bic”, “aic”), do.boot = TRUE, nboot = 100, pvalue = 0.05, min.boot = 3, min.stat = TRUE, boot.seed = \texttt{NULL}, silent = FALSE, epos = 0, eneg = 0)\n}

Arguments

- \texttt{data} A TRONCO compliant dataset.
- \texttt{command} Parameter to define to heuristic search to be performed. Hill Climbing and Tabu search are currently available.
- \texttt{regularization} Select the regularization for the likelihood estimation, e.g., BIC, AIC.
- \texttt{do.boot} A parameter to disable/enable the estimation of the error rates given the reconstructed model.
- \texttt{nboot} Number of bootstrap sampling (with rejection) to be performed when estimating the selective advantage scores.
- \texttt{pvalue} Pvalue to accept/reject the valid selective advantage relations.
- \texttt{min.boot} Minimum number of bootstrap sampling to be performed.
- \texttt{min.stat} A parameter to disable/enable the minimum number of bootstrap sampling required besides nboot if any sampling is rejected.
- \texttt{boot.seed} Initial seed for the bootstrap random sampling.
- \texttt{silent} A parameter to disable/enable verbose messages.
- \texttt{epos} Error rate of false positive errors.
- \texttt{eneg} Error rate of false negative errors.

Value

A TRONCO compliant object with reconstructed model

Examples

\texttt{data(test_dataset)
recon = tronco.capri(test_dataset, nboot = 1)\n}
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 given the reconstructed model.
nboot: Number of bootstrap sampling (with rejection) to be performed when estimating the selective advantage scores.
pvalue: P-value 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)
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 given 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)
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)
Description
Perform a k-fold cross-validation using the function bn.cv to estimate the entropy loss. For details and examples regarding the statistical assessment 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 assessment 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**

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

---

**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 assessment of an inferred model, we refer to the Vignette Section 7.

**Usage**

```r
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**

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

---

**Description**

`tronco.pattern.plot` : plot a genotype

**Usage**

```r
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'

Description

Plots a progression model from a reconstructed 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, ...)

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. Default 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?
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)

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 first view events are shown via head.

Examples

data(test_dataset)
view(test_dataset)
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

Description
XOR hypothesis

Usage
XOR(...)

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

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