

# Package ‘TRONCO’

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**Title** TRONCO, an R package for TRanslational ONCOlogy

**Depends** R (>= 4.1.0),

**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

**URL** <https://sites.google.com/site/troncopackage/>

**BugReports** <https://github.com/BIMIB-DISCO/TRONCO>

**biocViews** BiomedicalInformatics, Bayesian, GraphAndNetwork,  
SomaticMutation, NetworkInference, Network, Clustering,  
DataImport, SingleCell, ImmunoOncology

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---

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-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	<i>annotate.description</i>
----------------------	-----------------------------

---

**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	<i>annotate.stages</i>
-----------------	------------------------

---

**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	<i>as.alterations</i>
----------------	-----------------------

---

### 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	<i>as.bootstrap.scores</i>
---------------------	----------------------------

---

### 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 <code>as.events(x)</code> , 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	<i>as.conditional.probs</i>
----------------------	-----------------------------

---

### 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

<code>x</code>	A TRONCO model.
<code>events</code>	A subset of events as of <code>as.events(x)</code> , all by default.
<code>models</code>	A subset of reconstructed models, all by default.
<code>type</code>	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	<i>as.confidence</i>
---------------	----------------------

---

### 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	<i>as.events</i>
-----------	------------------

---

**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	<i>as.events.in.patterns</i>
-----------------------	------------------------------

---

**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 constitute 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	<i>as.events.in.sample</i>
---------------------	----------------------------

---

**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	<i>as.genes.in.patterns</i>
----------------------	-----------------------------

---

**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 constitute CAPRI's hypotheses

**Examples**

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

---

as.genotypes	<i>as.genotypes</i>
--------------	---------------------

---

**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	<i>as.hypotheses</i>
---------------	----------------------

---

**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 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**

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

---

as.kfold.eloss	<i>as.kfold.eloss</i>
----------------	-----------------------

---

**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	<i>as.kfold.posterr</i>
------------------	-------------------------

---

**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 <code>as.events(x)</code> , 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)
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	<i>as.kfold.prederr</i>
------------------	-------------------------

---

**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 <code>as.events(x)</code> , 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**

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

---

as.marginal.probs	<i>as.marginal.probs</i>
-------------------	--------------------------

---

**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**

```
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 <code>as.events(x)</code> , 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

<code>x</code>	A TRONCO model.
<code>events</code>	A subset of events as of <code>as.events(x)</code> , all by default.
<code>models</code>	A subset of reconstructed models, all by default.
<code>type</code>	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	<i>change.color</i>
--------------	---------------------

---

**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	<i>consolidate.data</i>
------------------	-------------------------

---

**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	<i>GISTIC example data</i>
------------	----------------------------

---

**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>

---

`data(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>

---

`data(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	<i>delete.gene</i>
-------------	--------------------

---

**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	<i>delete.hypothesis</i>
-------------------	--------------------------

---

**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')
```

---

<code>delete.model</code>	<i>delete.model</i>
---------------------------	---------------------

---

**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	<i>delete.pattern</i>
----------------	-----------------------

---

**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	<i>delete.samples</i>
----------------	-----------------------

---

**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'))
```

---

<code>delete.type</code>	<i>delete.type</i>
--------------------------	--------------------

---

**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')
```

---

<code>duplicates</code>	<i>duplicates</i>
-------------------------	-------------------

---

**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)
```

---

<code>ebind</code>	<i>ebind</i>
--------------------	--------------

---

**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.

---

<code>enforce.numeric</code>	<i>enforce.numeric</i>
------------------------------	------------------------

---

**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	<i>enforce.string</i>
----------------	-----------------------

---

**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	<i>events.selection</i>
------------------	-------------------------

---

**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**

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

**Value**

A TRONCO compliant dataset.

**Examples**

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

---

<code>export.graphml</code>	<i>export.graphml</i>
-----------------------------	-----------------------

---

**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**

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

**Examples**

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

---

export.mutex	<i>export,mutex</i>
--------------	---------------------

---

## 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	<i>export.nbs.input</i>
------------------	-------------------------

---

### Description

Create a .mat file which can be used with NBS clustering (ref: [http://chianti.ucsd.edu/~mhofree/wordpress/?page\\_id=26](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	<i>extract.MAF.HuGO.Entrez.map</i>
-----------------------------	------------------------------------

---

### 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 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	<i>has.duplicates</i>
----------------	-----------------------

---

**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	<i>has.model</i>
-----------	------------------

---

**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)
```

---

<code>has.stages</code>	<i>has stages</i>
-------------------------	-------------------

---

**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)
```

---

<code>hypothesis.add</code>	<i>hypothesis add</i>
-----------------------------	-----------------------

---

**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**

<code>data</code>	A TRONCO compliant dataset.
<code>pattern.label</code>	Label of the new hypothesis.
<code>lifted.pattern</code>	Vector to be added to the lifted genotype resolving the pattern related to the new hypothesis
<code>pattern.effect</code>	Possible effects for the pattern.
<code>pattern.cause</code>	Possible 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-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

---

hypothesis.add.homologous  
*hypothesis.add.homologous*

---

**Description**

Add all the hypotheses related to homologous events

**Usage**

```
hypothesis.add.homologous(  
  x,  
  pattern.cause = "*",  
  pattern.effect = "*",  
  genes = as.genes(x),  
  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.
silent	A parameter to disable/enable verbose messages.

**Value**

A TRONCO compliant object with the added hypotheses

---

import.genotypes	<i>import.genotypes</i>
------------------	-------------------------

---

**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	<i>import.GISTIC</i>
---------------	----------------------

---

**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 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.

**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**

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

---

### 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	<i>import.mutex.groups</i>
---------------------	----------------------------

---

### 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	<i>intersect.datasets</i>
--------------------	---------------------------

---

**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	<i>is.compliant</i>
--------------	---------------------

---

**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 dataframe

**Value**

on error stops the computation

**Examples**

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

---

join.events	<i>join.events</i>
-------------	--------------------

---

**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	<i>join.types</i>
------------	-------------------

---

**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**

```
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	<i>keysToNames</i>
-------------	--------------------

---

**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	<i>MAF example data</i>
-----	-------------------------

---

**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	<i>Simple mutation dataset</i>
------	--------------------------------

---

**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	<i>nameToKey</i>
-----------	------------------

---

**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	<i>nevents</i>
---------	----------------

---

**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	<i>ngenes</i>
--------	---------------

---

**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	<i>Return the number of hypotheses in the dataset</i>
-------------	---

---

**Description**

Return the number of hypotheses in the dataset

**Usage**

```
nhypotheses(x)
```

**Arguments**

x                      the dataset.

**Examples**

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

---

npatterns	<i>Return the number of patterns in the dataset</i>
-----------	---

---

**Description**

Return the number of patterns in the dataset

**Usage**

```
npatterns(x)
```

**Arguments**

x                      the dataset.

**Examples**

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

---

<code>nsamples</code>	<i>nsamples</i>
-----------------------	-----------------

---

**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)
```

---

<code>ntypes</code>	<i>ntypes</i>
---------------------	---------------

---

**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	<i>oncoprint</i>
-----------	------------------

---

**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,
  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

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

---

## 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)
```

<hr/>	
OR	<i>OR</i>
<hr/>	
<b>Description</b>	
OR hypothesis	
<b>Usage</b>	
OR(...)	
<b>Arguments</b>	
...	Atoms of the soft exclusive pattern given either as labels or as partielly lifted vectors.
<b>Value</b>	
Vector to be added to the lifted genotype resolving the soft exclusive pattern	
<hr/>	
order.frequency	<i>order.frequency</i>
<hr/>	

<b>Description</b>	
Sort the internal genotypes according to event frequency.	
<b>Usage</b>	
order.frequency(x, decreasing = TRUE)	
<b>Arguments</b>	
x	A TRONCO compliant dataset.
decreasing	Inverse order. Default TRUE
<b>Value</b>	
A TRONCO compliant dataset with the internal genotypes sorted according to event frequency.	
<b>Examples</b>	
data(test_dataset) order.frequency(test_dataset)	

---

pathway.visualization	<i>pathway.visualization</i>
-----------------------	------------------------------

---

**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	<i>A function to draw clustered heatmaps.</i>
----------	---

---

**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

<code>mat</code>	numeric matrix of the values to be plotted.
<code>color</code>	vector of colors used in heatmap.
<code>kmeans_k</code>	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.
<code>breaks</code>	a sequence of numbers that covers the range of values in <code>mat</code> and is one element longer than <code>color</code> 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.
<code>border_color</code>	color of cell borders on heatmap, use NA if no border should be drawn.
<code>cellwidth</code>	individual cell width in points. If left as NA, then the values depend on the size of plotting window.
<code>cellheight</code>	individual cell height in points. If left as NA, then the values depend on the size of plotting window.
<code>scale</code>	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"
<code>cluster_rows</code>	boolean values determining if rows should be clustered,
<code>cluster_cols</code>	boolean values determining if columns should be clustered.
<code>clustering_distance_rows</code>	distance measure used in clustering rows. Possible values are "correlation" for Pearson correlation and all the distances supported by <a href="#">dist</a> , such as "euclidean", etc. If the value is none of the above it is assumed that a distance matrix is provided.
<code>clustering_distance_cols</code>	distance measure used in clustering columns. Possible values the same as for <code>clustering_distance_rows</code> .
<code>clustering_method</code>	clustering method used. Accepts the same values as <a href="#">hclust</a> .
<code>cutree_rows</code>	number of clusters the rows are divided into, based on the hierarchical clustering (using <code>cutree</code> ), if rows are not clustered, the argument is ignored
<code>cutree_cols</code>	similar to <code>cutree_rows</code> , but for columns
<code>treeheight_row</code>	the height of a tree for rows, if these are clustered. Default value 50 points.
<code>treeheight_col</code>	the height of a tree for columns, if these are clustered. Default value 50 points.
<code>legend</code>	logical to determine if legend should be drawn or not.
<code>legend_breaks</code>	vector of breakpoints for the legend.
<code>legend_labels</code>	vector of labels for the <code>legend_breaks</code> .

<code>annotation_row</code>	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.
<code>annotation_col</code>	similar to <code>annotation_row</code> , but for columns.
<code>annotation</code>	deprecated parameter that currently sets the <code>annotation_col</code> if it is missing
<code>annotation_colors</code>	list for specifying <code>annotation_row</code> and <code>annotation_col</code> track colors manually. It is possible to define the colors for only some of the features. Check examples for details.
<code>annotation_legend</code>	boolean value showing if the legend for annotation tracks should be drawn.
<code>drop_levels</code>	logical to determine if unused levels are also shown in the legend
<code>show_rownames</code>	boolean specifying if column names are be shown.
<code>show_colnames</code>	boolean specifying if column names are be shown.
<code>main</code>	the title of the plot
<code>fontsize</code>	base fontsize for the plot
<code>fontsize_row</code>	fontsize for rownames (Default: <code>fontsize</code> )
<code>fontsize_col</code>	fontsize for colnames (Default: <code>fontsize</code> )
<code>display_numbers</code>	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.
<code>number_format</code>	format strings (C printf style) of the numbers shown in cells. For example <code>"%.2f"</code> shows 2 decimal places and <code>"%.1e"</code> shows exponential notation (see more in <a href="#">sprintf</a> ).
<code>number_color</code>	color of the text
<code>fontsize_number</code>	fontsize of the numbers displayed in cells
<code>gaps_row</code>	vector of row indices that show where to put gaps into heatmap. Used only if the rows are not clustered. See <code>cutree_row</code> to see how to introduce gaps to clustered rows.
<code>gaps_col</code>	similar to <code>gaps_row</code> , but for columns.
<code>labels_row</code>	custom labels for rows that are used instead of rownames.
<code>labels_col</code>	similar to <code>labels_row</code> , but for columns.
<code>filename</code>	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.
<code>width</code>	manual option for determining the output file width in inches.
<code>height</code>	manual option for determining the output file height in inches.
<code>silent</code>	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, lGI and lPI)
...	graphical parameters for the text used in plot. Parameters passed to <code>grid.text</code> , see <code>gpar</code> .

## 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](mailto: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	<i>rename.gene</i>
-------------	--------------------

---

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	<i>rename.type</i>
-------------	--------------------

---

**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 compliant dataset.

**Examples**

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

---

samples.selection	<i>samples.selection</i>
-------------------	--------------------------

---

**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	<i>sbind</i>
-------	--------------

---

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	<i>ssplit</i>
--------	---------------

---

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
<b>Description</b>	
This dataset contains stage information for patient in test_dataset	
<b>Usage</b>	
data(stage)	
<b>Format</b>	
Vector of stages	
<b>Value</b>	
A list of stages	
<b>Author(s)</b>	
Luca De Sano	
<b>Source</b>	
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	<i>TCGA.shorten.barcodes</i>
-----------------------	------------------------------

---

**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	<i>A complete dataset with hypotheses</i>
--------------	---

---

**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	<i>A complete dataset with a reconstructed model</i>
------------	--

---

**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	<i>A complete dataset with a reconstructed model and crossvalidation informations</i>
------------------	---

---

**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 $\text{coresRate} * (\text{numCores} - 1)$
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	<i>tronco caprese</i>
----------------	-----------------------

---

**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.capri(test_dataset_no_hypos)
```

---

tronco.capri	<i>tronco capri</i>
--------------	---------------------

---

## 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

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

<code>min.stat</code>	A parameter to disable/enable the minimum number of bootstrap sampling required besides <code>nboot</code> if any sampling is rejected.
<code>boot.seed</code>	Initial seed for the bootstrap random sampling.
<code>silent</code>	A parameter to disable/enable verbose messages.
<code>epos</code>	Error rate of false positive errors.
<code>eneg</code>	Error rate of false negative errors.
<code>restart</code>	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	<i>Tronco Chow Liu</i>
----------------	------------------------

---

**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**

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

---

**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

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

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

---

**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**

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

**Examples**

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

---

tronco.kfold.posterr	<i>tronco.kfold.posterr. For details and examples regarding the statistical assesment of an inferred model, we refer to the Vignette Section 7.</i>
----------------------	---

---

## 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

<code>x</code>	A reconstructed model (the output of <code>tronco.capri</code> )
<code>models</code>	The names of the selected regularizers ( <code>bic</code> , <code>aic</code> or <code>caprese</code> )
<code>events</code>	a list of event
<code>runs</code>	a positive integer number, the number of times cross-validation will be run
<code>k</code>	a positive integer number, the number of groups into which the data will be split
<code>cores.ratio</code>	Percentage of cores to use. $\text{coresRate} * (\text{numCores} - 1)$
<code>silent</code>	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

<code>x</code>	A reconstructed model (the output of <code>tronco.capri</code> )
<code>models</code>	The names of the selected regularizers (bic, aic or caprese)
<code>events</code>	a list of event
<code>runs</code>	a positive integer number, the number of times cross-validation will be run
<code>k</code>	a positive integer number, the number of groups into which the data will be split
<code>cores.ratio</code>	Percentage of cores to use. $\text{coresRate} * (\text{numCores} - 1)$
<code>silent</code>	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 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,
  create.new.dev = TRUE,
  ...
)
```

**Arguments**

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

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

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

---

<code>view</code>	<i>view</i>
-------------------	-------------

---

**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)
```

---

<code>which.samples</code>	<i>which.samples</i>
----------------------------	----------------------

---

**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	<i>XOR</i>
-----	------------

---

**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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