

Package ‘agalmar’

October 25, 2015

Title A Collection of Tools for Analyzing Agalma Expression Projects

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Description A Collection of tools for analyzing agalma expression projects. See <https://bitbucket.org/caseywdunn/agalma>

Depends R (>= 3.2.2)

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LazyData true

Collate 'utility_functions.R'
'agalmar.R'

Imports hutan,
edgeR,
seriation,
ape

Suggests testthat,
roxygen2,
devtools,
knitr

VignetteBuilder knitr

R topics documented:

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agalmar	<i>agalmar: A Collection of Tools for Analyzing Agalma Expression Projects</i>
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Description

The agalmar package contains a collection of tools for analyzing expression and phylogenetic data exported from Agalma. See <https://bitbucket.org/caseywdunn/agalma>

apply_normalizations	<i>Takes a DGEList object, and returns a matrix of normalized counts</i>
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Description

Takes a DGEList object, and returns a matrix of normalized counts

Usage

```
apply_normalizations(dge)
```

Arguments

dge	edgeR DGEList object, to which normalizations have been applied
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Value

matrix of normalized counts

decompose_orthologs	<i>Decomposes a gene tree into a list of subtrees that have no duplication events. Assumes notung style node annotations.</i>
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Description

Decomposes a gene tree into a list of subtrees that have no duplication events. Assumes notung style node annotations.

Usage

```
decompose_orthologs(phy)
```

Arguments

phy	The tree, as an ape phylo object
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Value

The subtrees as a list of phylo object

Expression	<i>Construct an Expression object from list of experiment data and meta-data provided by Agalma.</i>
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Description

Construct an Expression object from list of experiment data and metadata provided by Agalma.

Usage

```
Expression(data_list)
```

Arguments

`data_list` A list containing the expression data

Value

An Expression object

Expression-class	<i>An S4 class to represent gene expression data for multiple samples for a given species. Assumes that all expression data are derived from mapping to the same reference. Applies to data for g genes across s samples.</i>
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Description

An S4 class to represent gene expression data for multiple samples for a given species. Assumes that all expression data are derived from mapping to the same reference. Applies to data for g genes across s samples.

Slots

`species` The species

`dge` an edgeR DGEList object holding data for all samples. Expression matrix of dimension g,s.

`lengths` Summary of length, in bp, of transcripts for each gene. Length g.

`individuals` Factors indicating which individual each sample is from. Length s.

`treatments` Factors indicating which treatment applies to each sample. Length s.

`id` Factors indicating the unique id of each sample. Length s.

`samples` Factors indicating the unique library id of each sample. Length s.

`sample_prep` Sample prep strategy. Length s.

`genome_type` Character indicating genome type, eg nuclear. See agalma documentation. Length g.

`molecule_type` Character indicating encoded molecule type, eg protein. See agalma documentation. Length g.

`blast_hit` Blast hit. Length g.

`rRNA` Fraction of reads in sample that are rRNA. Length s.

`protein` Fraction of reads in sample that are protein coding. Length s.

get_lane	<i>Get lane from Illumina fastq sequence header</i>
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Description

Get lane from Illumina fastq sequence header

Usage

```
get_lane(header)
```

Arguments

Header	character strings
--------	-------------------

Value

Lane character strings

get_run	<i>Get run from Illumina fastq sequence header</i>
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Description

Get run from Illumina fastq sequence header

Usage

```
get_run(header)
```

Arguments

Header	character strings
--------	-------------------

Value

Run character strings

get_tip_info	<i>Parse species and sequence id from a phy</i>
--------------	---

Description

Parse species and sequence id from a phy

Usage

```
get_tip_info(phy)
```

Arguments

phy The tree, as an ape phylo object. Tip names must have 'species@id' format.

Value

Dataframe with one row per tip, a species column, and an id column

has_species	<i>Returns true if all species are in the tree tips</i>
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Description

Returns true if all species are in the tree tips

Usage

```
has_species(phy, species)
```

Arguments

phy The tree, as an ape phylo object

Value

logical

node_support	<i>Parse support from node name</i>
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Description

Parse support from node name

Usage

```
node_support(node_name)
```

Arguments

node_name	A character string of format 'n38047889-N-83', where 'n38047889-N' is nothing annotation and '83' is node support.
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Value

Numeric indicating node support

parse_gene_tree	<i>Parses newick text to a gene tree</i>
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Description

Parses newick text to a gene tree

Usage

```
parse_gene_tree(tree_text)
```

Arguments

tree_text	Text representation of a newick tree in newick format.
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Value

phy The tree, as an ape phylo object

plot_matrix	<i>Plots a matrix</i>
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Description

Plots a matrix

Usage

```
plot_matrix(m, ...)
```

Arguments

m	The matrix
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species	<i>Get species</i>
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Description

Get species

Usage

```
species(object)
```

Arguments

object	An Expression object
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Value

Character string with species

summary_frame	<i>Summarize experiment.</i>
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Description

Summarize experiment.

Usage

```
summary_frame(object)
```

Arguments

object	An Expression object
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Value

A data frame that summarizes each sample in the experiment

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