

Package: KINNET (via r-universe)

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Type Package

Title Kinase Interaction NETWORK Generation

Version 0.4.0.9002

Description This package provides the functionality to process PamGene's PamChip Data Output and generate kinase interaction networks from that. This project uses a bayesian algorithm to generate bayesian networks for defining dependence relationships between peptide sequences in the PamChip data. It then uses a novel kinase assignment method to assign upstream kinases to each peptide which is then output as a graph.

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LazyData true

Imports methods, readr, dplyr, tibble, bnlearn, stringr, tidysselect, purrr, tidyr, Rgraphviz, graph, rlang, effectsize

Depends R (>= 2.10)

RoxygenNote 7.1.1

Collate 'assign_kinases.R' 'compare_kinased_graphs.R' 'distances.R' 'equalize_kinase_graphs.R' 'filter_peptides.R' 'make_model.R' 'pamchip_data.R' 'pamchip_data_ptk.R' 'pamchip_data_stk.R' 'probability_matrix.R' 'ptk_methods.R' 'render_kinased_graph.R' 'render_reduced_kinased_graph.R' 'stk_methods.R' 'subset_data.R' 'update_probability_matrix.R'

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

Repository <https://cogdisreslab.r-universe.dev>

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assign_kinases	<i>Assign kinases, given a network and a chip type</i>
----------------	--

Description

Assign kinases, given a network and a chip type

Usage

```
assign_kinases(network, chiptype, identifier = "Gene_Symbol")
```

Arguments

network	A network output from bnlearn
chiptype	Either PTK or STK
identifier	The identifier to use in outputs. Can be either "Gene_Symbol" or "Kinase"

Value

A dataframe with upstream kinases assigned to the peptide

Examples

```
TRUE
```

assign_kinases_guided *Assign kinases, given a network and a chip type and additional essential kinases*

Description

Assign kinases, given a network and a chip type and additional essential kinases

Usage

```
assign_kinases_guided(  
  network,  
  chiptype,  
  identifier = "Gene_Symbol",  
  guided = NULL  
)
```

Arguments

network	A network output from bnlearn
chiptype	Either PTK or STK
identifier	The identifier to use in outputs. Can be either "Gene_Symbol" or "Kinase"
guided	A vector of Kinases or Gene_Symbols that must be included in the network. The vector must be aligned with what was specified in <code>_identifier_</code>

Value

A dataframe with upstream kinases assigned to the peptide

Examples

```
TRUE
```

candidate_kinases *Generate Candidate Kinases Based On Links*

Description

Generate Candidate Kinases Based On Links

Usage

```
candidate_kinases(peptide, arcs, assigned_kinases)
```

Arguments

peptide	Peptide ID
arcs	The arcs in the network
assigned_kinases	The candidate kinases

Value

common kinases

Examples

```
TRUE
```

compare_kinased_graphs
Compare two kinased graphhs

Description

This functions takes two given graphs and compares them to see the changes from one to the other

Usage

```
compare_kinased_graphs(  
  reference,  
  comparison,  
  ref_name = "Reference",  
  comp_name = "Comparison",  
  render = FALSE  
)
```

Arguments

reference	The reference network output from assign_kinases()
comparison	The comparison network output from assign_kinases()
ref_name	Name for the reference network
comp_name	Name for the comparison network
render	logical. Whether a graph should be rendered or not.

Value

A graph object

Examples

```
TRUE
```

equalize_kinase_graphs

Equalize the nodesets of two kinased graphs

Description

Equalize the nodesets of two kinased graphs

Usage

```
equalize_kinase_graphs(reference, comparison)
```

Arguments

reference	a reference result from assign_kinases()
comparison	a comparison result from assign_kinases()

Value

A list with two elements, reference and comparison, that have the same nodesets

Examples

```
TRUE
```

filter_peptides	<i>Return a list of significant peptides</i>
-----------------	--

Description

Return a list of significant peptides

Usage

```
filter_peptides(chipdata, threshold = 0.75)
```

Arguments

chipdata	an object of class PamchipSTK or PamchipPTK
threshold	a lower cutoff for significance

Value

a list of significant peptides for each class

Examples

```
TRUE
```

fit_standardized	<i>Do a standardized fit of expression data from a single peptide's activity</i>
------------------	--

Description

Do a standardized fit of expression data from a single peptide's activity

Usage

```
fit_standardized(expr)
```

Arguments

expr	a dataframe containing the activity data of only one peptide
------	--

Value

a list of three items std_10, std_50 and std_200, of standardized linear coefficients

Examples

```
TRUE
```

get_intersections *Generate Intersections between kinases*

Description

Generate Intersections between kinases

Usage

```
get_intersections(row, column, assigned_kinases)
```

Arguments

row	row peptide
column	column peptide
assigned_kinases	Kinases assigned

Value

common kinases between the two groups

Examples

```
TRUE
```

kinnet_hamming *Calculate the Hamming Distance between two kinased graphs*

Description

Calculate the Hamming Distance between two kinased graphs

Usage

```
kinnet_hamming(reference, comparison)
```

Arguments

reference	a reference result from assign_kinases()
comparison	a comparison result from assign_kinases()

Value

A positive integer

Examples

TRUE

kinnet_normalized_hamming

Calculate Normalized Hamming Distance

Description

Calculate Normalized Hamming Distance

Usage

kinnet_normalized_hamming(reference, comparison)

Arguments

reference a reference result from assign_kinases()

comparison a reference result from assign_kinases()

Value

A positive integer

Examples

TRUE

kinnet_normalized_shd *Calculate Normalized Structural Hamming Distance*

Description

Calculate Normalized Structural Hamming Distance

Usage

kinnet_normalized_shd(reference, comparison)

Arguments

reference a reference result from assign_kinases()

comparison a comparison result from assign_kinases()

Value

A positive integer

Examples

TRUE

kinnet_shd	<i>Calculate the Structural Hamming Distance between two kinased graphs</i>
------------	---

Description

Calculate the Structural Hamming Distance between two kinased graphs

Usage

```
kinnet_shd(reference, comparison)
```

Arguments

reference	a reference result from assign_kinases()
comparison	a comparison result from assign_kinases()

Value

A positive integer

Examples

TRUE

make_model	<i>Generate a bayes net model</i>
------------	-----------------------------------

Description

Generate a bayes net model

Usage

```
make_model(expression, iterations = 200, threshold = NULL, cluster = NULL)
```

Arguments

expression	tbl_df. A tibble with the activity data from the kinome chip.
iterations	numeric. Number of iterations to run the mode.
threshold	numeric. Threshold to use for averaging the network
cluster	cluster. (Optional) a cluster from the package parallel

Value

A list with the strength network dataframe, an averaged network and the threshold used to generate that averaged network.

Examples

```
TRUE
```

PamchipData-class *The Pamchip Data Superclass*

Description

The Pamchip Data Superclass

Value

an object of class PamchipData

Slots

chip_type character. A string

Examples

```
TRUE
```

PamchipData-PTK-class *A representation of the PamChip PTK Data*

Description

A representation of the PamChip PTK Data

Value

An object of class PamchipData-PTK

Slots

BioNavigatorVersion character. A string indicating the version of BioNavigator that generated the dataset

ImageAnalysisDate character. The date the analysis was conducted on.

PamGridVersion character. PamGrid version the chip was run on.

QuantitationType character. The kind of quantitation analysis performed.

SampleData tbl_df. A tibble with the observed activity on each peptide

SampleCharacteristics tbl_df. A tibble with the characteristics of each sample

RefData tbl_df.

PeptideIDs character.

ProcessedData tbl_df.

DataProcessDate character. The date when the data was processed

Examples

TRUE

PamchipData-STK-class *A representation of the PamChip STK Data*

Description

A representation of the PamChip STK Data

Value

An object of class PamchipData-STK

Slots

BioNavigatorVersion character. A string indicating the version of BioNavigator that generated the dataset

ImageAnalysisDate character. The date the analysis was conducted on.

PamGridVersion character. PamGrid version the chip was run on.

QuantitationType character. The kind of quantitation analysis performed.

SampleData tbl_df. A tibble with the observed activity on each peptide

SampleCharacteristics tbl_df. A tibble with the characteristics of each sample

RefData tbl_df.

PositiveControlData tbl_df.

PeptideIDs character.

DataProcessDate character. The date when the data was processed

Examples

TRUE

PamchipData_PTK	<i>Process a file into a usable structure</i>
-----------------	---

Description

Process a file into a usable structure

Usage

```
PamchipData_PTK(dataset)
```

Arguments

dataset character. Path to a file that holds the output of BioNavigator

Value

An object of class PamchipData-PTK

Examples

TRUE

PamchipData_STK *Process a file into a usable structure*

Description

Process a file into a usable structure

Usage

PamchipData_STK(dataset)

Arguments

dataset character. Path to a file that holds the output of BioNavigator

Value

An object of class PamchipData-STK

Examples

TRUE

ptk_probability_matrix_gene
PTK Peptide to Kinase Probability Matrix for Gene Identifiers

Description

A dataframe with the Bayesian posteriors of finding a given peptide/kinase pair

Usage

ptk_probability_matrix_gene

Format

A dataframe with 991 rows and 3 columns

peptide The peptide ID

kinase Gene Symbol of the kinase

posterior Posterior probability of the pair

ptk_probability_matrix_kinase

PTK Peptide to Kinase Probability Matrix for Kinase Identifiers

Description

A dataframe with the Bayesian posteriors of finding a given peptide/kinase pair

Usage

```
ptk_probability_matrix_kinase
```

Format

A dataframe with 991 rows and 3 columns

peptide The peptide ID

kinase Gene Symbol of the kinase

posterior Posterior probability of the pair

render_kinased_graph *Generate a kinase graph*

Description

Generate a kinase graph

Usage

```
render_kinased_graph(analysis_result, title, render = FALSE)
```

Arguments

analysis_result

Object output from assign_kinases()

title Title of the graph

render logical. Whether a graph should be rendered or not.

Value

a graph object

Examples

```
TRUE
```

render_reduced_kinased_graph
Generate a reduced kianse graph

Description

Generate a reduced kianse graph

Usage

```
render_reduced_kinased_graph(analysis_result, title, render = FALSE)
```

Arguments

analysis_result	Object output from assign_kinases()
title	Title of the graph
render	logical. Whether a graph should be rendered or not.

Value

a graph object

Examples

```
TRUE
```

safely_add_node *Add a node safely to a bn object*

Description

This function takes a bn object and a node and adds it if it's not already in the nodeset.

Usage

```
safely_add_node(net, node)
```

Arguments

net	A bn object
node	A node label

Value

A bn object with the node added

Examples

```
TRUE
```

```
stk_accessors
```

```
STK Data Accessor Functions
```

Description

These functions provide a variety of data setters and getter for the Pamchip objects.

Usage

```
pheno_data(chipdata, ...)

## S4 method for signature ``PamchipData-STK``
pheno_data(chipdata)

exp_data(chipdata, ...)

## S4 method for signature ``PamchipData-STK``
exp_data(chipdata)

classes(chipdata, ...)

## S4 method for signature ``PamchipData-STK``
classes(chipdata)

peptides(chipdata, ...)

## S4 method for signature ``PamchipData-STK``
peptides(chipdata)
```

Arguments

```
chipdata      an object of class PamchipData-STK or PamchipData-PTK
...           Currently unused
```

Details

These functions allow you to get and set the slots of the object.

- `processed_data` accesses the processed and transformed data
- `pheno_data` gives the sample characteristics
- `exp_data` access the actual intensity values
- `classes` gives the unique classes in the chip
- `peptides` gives the reference list of peptides on the chip

Value

The requested object

stk_probability_matrix_gene

STK Peptide to Kinase Probability Matrix for Gene Identifiers

Description

A dataframe with the Bayesian posteriors of finding a given peptide/kinase pair

Usage

stk_probability_matrix_gene

Format

A dataframe with 10428 rows and 3 columns

peptide The peptide ID

kinase Gene Symbol of the kinase

posterior Posterior probability of the pair

stk_probability_matrix_kinase

STK Peptide to Kinase Probability Matrix for Kinase Identifiers

Description

A dataframe with the Bayesian posteriors of finding a given peptide/kinase pair

Usage

stk_probability_matrix_kinase

Format

A dataframe with 10428 rows and 3 columns

peptide The peptide ID

kinase Gene Symbol of the kinase

posterior Posterior probability of the pair

`subset_data`*Subset The Kinome Data*

Description

Subset the Kinome data to a given list of peptides and conditions

Usage

```
subset_data(chipdata, peptides, class)
```

Arguments

<code>chipdata</code>	Pamchip-PTK. A Pamchip-PTK Object with all the data available
<code>peptides</code>	character. A vector of peptides of interest
<code>class</code>	character. A specification of the sample class you want to filter to

Value

A tibble with the filtered and asinh transformed data

Examples

```
TRUE
```

`update_probability_matrix`*Calculated Updated Probabilities of each peptide/kinase pair*

Description

Calculated Updated Probabilities of each peptide/kinase pair

Usage

```
update_probability_matrix(  
  chiptype,  
  assignment_df,  
  identifier = "Gene_Symbol",  
  guided = NULL  
)
```

Arguments

chiptype character. Either "STK" or "PTK"
assignment_df tbl_df. A tibble with the potential kianse assignments
identifier The identifier to use in outputs. Can be either "Gene_Symbol" or "Kinase"
guided A vector of Kinases or Gene_Symbols that must be included in the network.
 The vector must be aligned with what was specified in `_identifier_`

Value

an updated dataframe with the probabilities

Examples

TRUE

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