

Package ‘MetaboDynamics’

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Title Bayesian analysis of longitudinal metabolomics data

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Description MetaboDynamics is an R-package that provides a framework of probabilistic models to analyze longitudinal metabolomics data. It enables robust estimation of mean concentrations despite varying spread between timepoints and reports differences between timepoints as well as metabolite specific dynamics profiles that can be used for identifying “dynamics clusters” of metabolites of similar dynamics. Provides probabilistic over-representation analysis of KEGG functional modules and pathways as well as comparison between clusters of different experimental conditions.

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MetaboDynamics-package
MetaboDynamics: Bayesian analysis of longitudinal metabolomics data

Description

MetaboDynamics is an R-package that provides a framework of probabilistic models to analyze longitudinal metabolomics data. It enables robust estimation of mean concentrations despite varying spread between timepoints and reports differences between timepoints as well as metabolite specific dynamics profiles that can be used for identifying "dynamics clusters" of metabolites of similar dynamics. Provides probabilistic over-representation analysis of KEGG functional modules and pathways as well as comparison between clusters of different experimental conditions.

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See Also

Useful links:

- <https://github.com/KatjaDanielzik/MetaboDynamics>
- Report bugs at <https://github.com/KatjaDanielzik/MetaboDynamics/issues>

`.calculate_distances` *compare_dynamics()*

Description

`compare_dynamics()`

Usage

`.calculate_distances(group_a, group_b, dynamics)`

Arguments

| | |
|----------|---|
| group_a | dataframe of one cluster of one condition |
| group_b | dataframe of one cluster of a different condition than group_a |
| dynamics | character vector specifying the columns that hold dynamic estimates in data |

Value

matrix of pairwise euclidean distances between two groups of vectors

.calculate_jaccard *Function to calculate Jaccard index on two character vectors of metabolite names*

Description

Function to calculate Jaccard index on two character vectors of metabolite names

Usage

```
.calculate_jaccard(group_a, group_b)
```

Arguments

| | |
|---------|----------------------------------|
| group_a | group of clusters of metabolites |
| group_b | group of clusters of metabolites |

Value

the Jaccard index

.check_fit_dynamics_input
input checks for fit_dynamics_model

Description

input checks for fit_dynamics_model

Usage

```
.check_fit_dynamics_input(  
  model,  
  model_option,  
  data,  
  scaled_measurement,  
  counts,  
  assay,  
  chains,  
  cores,  
  adapt_delta,  
  max_treedepth,  
  iter,  
  warmup  
)
```

Arguments

| | |
|--------------------|---|
| model | which model to fit. Two options are available: "scaled_log": taking in normalized and scaled metabolite concentrations (see scaled measurement) "raw_plus_counts": tailored for in vitro untargeted LC-MS experiments, taking in "raw" (i.e. not normalized and not scaled) metabolite concentrations and cell counts. This model assumes independent measurement (i.e. different wells) of cell counts and metabolite concentrations. Additionally it assumes that cell counts were estimated e.g. by cell counters (i.e. that cells were not counted under the microscope) leading to a small uncertainty of the true cell count. |
| data | concentration table with at least three replicate measurements per metabolite. Must contain columns named "metabolite" (containing names or IDs), "time" (categorical, the same for all conditions), and "condition" or colData of a SummarizedExperiment object Time column needs to be sorted in ascending order |
| scaled_measurement | column of "data" that contains the concentrations per cell, centered and normalized per metabolite and experimental condition (mean=0, sd=1) |
| counts | data frame with at least one replicate per time point and condition specifying the cell counts, must contain columns "time", and "condition" equivalent to the specifications of "data". Must contain a column named "counts" that specifies the cell counts. Model assumes that the replicates of the cell counts and metabolite concentrations are independent of each other (i.e. cell counts were measured in in different wells than metabolite concentrations) |
| assay | if input is a SummarizedExperiment specify the assay that should be used for input, colData has to hold the columns, "condition" and "metabolite", rowData the timepoint specifications, in case of the model "scaled_log" assay needs to hold scaled log-transformed metabolite concentrations (mean=0, sd=1 per metabolite and experimental condition), if model "raw_plus_counts" is chosen must hold the non-transformed and non-scaled metabolite concentrations |
| chains | how many Markov-Chains should be used for model fitting, use at least two, default=4 |

| | |
|---------------|---|
| cores | how many cores should be used for model fitting; this parallelizes the model fitting and therefore speeds it up; default=4 |
| adapt_delta | target average acceptance probability, can be adapted if divergent transitions are reported, default is 0.95 |
| max_treedepth | can be adapted if model throws warnings about hitting max_treedepth, warnings are mostly efficiency not validity concerns and treedepth can be raised, default=10 |
| iter | how many iterations are run, increasing might help with effective sample size being to low, default=2000 |
| warmup | how many iterations the model warms up for, increasing might facilitate efficiency, must be at least 25% of ITER, default=iter/4 |

Value

description error messages

.eu

euclidean distance compare_dynamics()

Description

euclidean distance compare_dynamics()

Usage

.eu(a, b)

Arguments

| | |
|---|--------------------------------------|
| a | a numeric vector |
| b | a numeric vector of same length as a |

Value

euclidean distance between vectors

.get_boot_ph *get bootstraps for clustering of dynamics vectors (cluster_dynamics function)*

Description

get bootstraps for clustering of dynamics vectors (cluster_dynamics function)

Usage

```
.get_boot_ph(x, distance, agglomeration, B)
```

Arguments

| | |
|---------------|---|
| x | posterior of dynamics model |
| distance | distance measure used for hierarchical clustering |
| agglomeration | agglomeration method used for hierarchical clustering |
| B | number of bootstraps |

Value

bootstraps of clustering solution

.hierarchical_clustering
hierarchical clustering

Description

hierarchical clustering

Usage

```
.hierarchical_clustering(  
  data_clust,  
  distance,  
  agglomeration,  
  minClusterSize,  
  deepSplit  
)
```

Arguments

| | |
|----------------|--|
| data_clust | element "mu" of estimates |
| distance | distance method |
| agglomeration | agglomeration method of hierarchical clustering |
| minClusterSize | minimum number of metabolites per of cluster cutreeDynamic |
| deepSplit | rough control over sensitivity of cluster analysis. Possible values are 0:4, the higher the value, the more and smaller clusters will be produced by cutreeDynamic |

Value

list of input data including clustering solution, dendrogram, phylogram

.similarity *Jaccard Index: intersection/union compare_metabolites()*

Description

Jaccard Index: intersection/union compare_metabolites()

Usage

```
.similarity(a, b)
```

Arguments

| | |
|---|----------|
| a | a vector |
| b | a vector |

Value

Jaccard Index of a and b

cluster_dynamics *cluster dynamics profiles of metabolites*

Description

Convenient wrapper function for clustering of metabolite dynamics employing the "hybrid" method of the [dynamicTreeCut](#) package for clustering and [hclust](#) for computing of distance matrix and hierarchical clustering needed as input for [dynamicTreeCut](#). Provides bootstrapping of clustering solution from posterior estimates of the model.

Usage

```
cluster_dynamics(
  data = NULL,
  fit,
  estimates = NULL,
  distance = "euclidean",
  agglomeration = "ward.D2",
  minClusterSize = 1,
  deepSplit = 2,
  B = 1000
)
```

Arguments

| | |
|----------------|---|
| data | data frame or colData of a SummarizedExperiment used to fit dynamics model |
| fit | model fit obtained by <code>fit_dynamics_model()</code> . Needed if data is not a SummarizedExperiment object for which the model fit is saved in "dynamic_fit" of metadata |
| estimates | output of <code>estimates_dynamics</code> function, needed if data is not a SummarizedExperiment object for which the model estimates are saved in "estimates_dynamics" of metadata |
| distance | distance method to be used as input for hierarchical clustering <code>dist</code> can be "euclidean", "maximum", "manhattan", "canberra", "binary" or "minkowski" |
| agglomeration | agglomerative method to be used for hierarchical clustering <code>hclust</code> can be "ward.D", "ward.D2", "single", "complete", "average", "mcquitty", "median" or "centroid" |
| minClusterSize | minimum number of metabolites per of cluster cutreeDynamic |
| deepSplit | rough control over sensitivity of cluster analysis. Possible values are 0:4, the higher the value, the more and smaller clusters will be produced by cutreeDynamic |
| B | number of bootstraps |

Value

a list with one list per condition. The elements per condition are 'data' (mean estimates of mu plus the clustering solution), mean_dendro' the dendrogram of the mean estimates, and mean_phylo' the phylogram of the mean estimates. if data is a [SummarizedExperiment](#) object clustering results are stored in metadata under "cluster" Element 'dynamics' contains column names of time points

See Also

[fit_dynamics_model\(\)](#), [estimates_dynamics\(\)](#), [plot_cluster\(\)](#)

Examples

```
data("longitudinalMetabolomics")
data <- longitudinalMetabolomics[, longitudinalMetabolomics$condition == "A" &
  longitudinalMetabolomics$metabolite %in% c("ATP", "L-Alanine", "GDP")]
data <- fit_dynamics_model(
  data = data,
  scaled_measurement = "m_scaled", assay = "scaled_log",
  max_treedepth = 14, adapt_delta = 0.95, iter = 2000, cores = 1, chains = 1
)
data <- estimates_dynamics(
  data = data
)
data <- cluster_dynamics(data, B = 1000)
S4Vectors::metadata(data)[["cluster"]][["A"]]
plot(S4Vectors::metadata(data)[["cluster"]][["A"]][["mean_dendro"]])
```

compare_dynamics

Comparison of metabolite dynamics clusters under different experimental conditions

Description

Employs a Bayesian model that assumes a normal distribution of Euclidean distances between dynamics vectors (metabolite abundances at different time points) of two clusters that come from different experimental conditions to estimate the mean distance between clusters.

Usage

```
compare_dynamics(data, cores = 4)
```

Arguments

| | |
|-------|--|
| data | result of cluster_dynamics() function: either a list of data frames or a SummarizedExperiment object |
| cores | how many cores should be used for model fitting; this parallelizes the model fitting and therefore speeds it up; default=4 |

Value

a list holding a 1) the model fit 2) dataframe of estimates of the mean distance between #' clusters of different experimental conditions ("mean") and the standard deviation ("sigma"). If data input was a SummarizedExperiment results are stored in metadata(data) under "comparison_dynamics"

See Also

Visualization of estimates [heatmap_dynamics\(\)](#)/ compare metabolite composition of clusters [compare_metabolites\(\)](#)

Examples

```
data("longitudinalMetabolomics")
data <- longitudinalMetabolomics[, longitudinalMetabolomics$condition %in% c("A", "B") &
  longitudinalMetabolomics$metabolite %in% c("ATP", "L-Alanine", "GDP")]
data <- fit_dynamics_model(
  data = data,
  scaled_measurement = "m_scaled", assay = "scaled_log",
  max_treedepth = 14, adapt_delta = 0.95, iter = 2000, cores = 1, chains = 1
)
data <- estimates_dynamics(
  data = data
)
data <- cluster_dynamics(data, B = 1)
data <- compare_dynamics(
  data = data,
  cores = 1
)
S4Vectors::metadata(data)[["comparison_dynamics"]]
```

compare_metabolites *Comparison of metabolite sets between dynamics clusters of different experimental conditions*

Description

Uses the Jaccard Index to compare metabolite names between dynamics clusters of different experimental conditions

Usage

```
compare_metabolites(data)
```

Arguments

data result of [cluster_dynamics\(\)](#) function: either a list of data frames or a SummarizedExperiment object

Value

a data frame of Jaccard indices between data or if data input was a SummarizedExperiment results are stored in `metadata(data)` under "comparison_metabolites"

See Also

Visualization of metabolite similarity `heatmap_metabolites()`/ compare dynamics of clusters `compare_dynamics()`

Examples

```
data("longitudinalMetabolomics")
longitudinalMetabolomics <- compare_metabolites(
  data = longitudinalMetabolomics
)
S4Vectors::metadata(longitudinalMetabolomics)[["comparison_metabolites"]]
```

`diagnostics_dynamics` *Extracts diagnostic criteria from numeric fit of Bayesian model of dynamics*

Description

gathers number of divergences, rhat values, number of effective samples (`n_eff`) and provides plots for diagnostics criteria as well as posterior predictive checks. Output dataframe "model_diagnostics" contains information about experimental condition, number of divergent transitions and rhat and neff values for all timepoints.

Usage

```
diagnostics_dynamics(
  data,
  assay = "scaled_log",
  iter = 2000,
  warmup = iter/4,
  chains = 4,
  fit = metadata(data)[["dynamic_fit"]]
)
```

Arguments

| | |
|--------------------|--|
| <code>data</code> | data frame or a SummarizedExperiment used to fit dynamics model column of "time" that contains time must be numeric, has to contain columns specifying the metabolite named "metabolite", and column specifying the time point named "time", a column named "condition" must specify the experimental condition. |
| <code>assay</code> | of the SummarizedExperiment object that was used to fit the dynamics model |
| <code>iter</code> | number of iterations used for model fit |

| | |
|--------|--|
| warmup | number of warmup iterations used for model fit |
| chains | number of chains used for model fit |
| fit | model fit for which diagnostics should be extracted, is the object that gets returned by <code>fit_dynamics_model()</code> , or if a <code>SummarizedExperiment</code> object the results of <code>fit_dynamics_model()</code> are stored in <code>metadata(data)</code> under "dynamic_fit" |

Value

a list which contains diagnostics criteria of all conditions in a dataframe (named "model_diagnostics") and one dataframe per condition that contains necessary information for Posterior predictive check (named "PPC_condition"). If data is a summarizedExperiment object the diagnostics are stored in `metadata(data)` "diagnostics_dynamics"

See Also

`estimates_dynamics()` parent function `fit_dynamics_model()` visualization functions: `plot_diagnostics()/plot_PPC`

Examples

```
data("longitudinalMetabolomics")
data <- longitudinalMetabolomics[, longitudinalMetabolomics$condition %in% c("A", "B") &
  longitudinalMetabolomics$metabolite == "ATP"]
data <- fit_dynamics_model(
  model = "scaled_log",
  data = data,
  scaled_measurement = "m_scaled", assay = "scaled_log",
  max_treedepth = 14, adapt_delta = 0.95, iter = 2000, cores = 1, chains = 1
)
data <- diagnostics_dynamics(
  data = data, assay = "scaled_log",
  iter = 2000, chains = 1,
  fit = metadata(data)[["dynamic_fit"]]
)
S4Vectors::metadata(data)[["diagnostics_dynamics"]][["model_diagnostics"]]
S4Vectors::metadata(data)[["diagnostics_dynamics"]][["posterior"]]
```

| | |
|---------------------------------|--|
| <code>estimates_dynamics</code> | <i>Extracts parameter estimates from numeric fit of Bayesian model of dynamics</i> |
|---------------------------------|--|

Description

Extracts the mean concentrations (μ) at every time point from the dynamics model fit, the 95% highest density interval (HDI), the estimated standard deviation of metabolite concentrations at every time point (σ), and the pooled standard deviation of every metabolite over all timepoints (λ). Additionally samples from the posterior of μ can be drawn. This can be helpful if p.e. one wants to estimate the clustering precision. λ can be used for clustering algorithms such as `VSClust` that also take the variance into account.

Usage

```
estimates_dynamics(
  data,
  assay = "scaled_log",
  fit = metadata(data)[["dynamic_fit"]],
  model_option = "sd_per_condition"
)
```

Arguments

| | |
|---------------------------|--|
| <code>data</code> | data frame or colData of a SummarizedExperiment used to fit dynamics model, must contain a column named "condition" specifying the experimental condition and a column named "time" specifying the timepoints. If it is a SummarizedExperiment object the dynamic fits must be stored in metadata(data) under "dynamic_fits" (automatically done by fit_dynamics_model()) |
| <code>assay</code> | of the SummarizedExperiment object that was used to fit the dynamics model |
| <code>fit</code> | model fit for which estimates should be extracted |
| <code>model_option</code> | model option that was used for fitting with fit_dynamics_model() . If data is a SummarizedExperiment this is automatically provided by the metadata written by fit_dynamics_model() |

Value

a list of dataframes (one per parameters mu, sigma, lambda, delta_mu and euclidean distance) that contains the estimates: mu: is the estimated mean metabolite abundance sigma: the estimated standard deviation of metabolite abundance lambda: pooled sigma per condition delta_mu: differences of mu between time points euclidean_distances: estimated euclidean distance of time vectors of one metabolite between conditions If data is a summarizedExperiment object the estimates are stored in metadata(data) under "estimates_dynamics"

See Also

Fit the dynamic model [fit_dynamics_model\(\)](#). Diagnostics of the dynamic model [diagnostics_dynamics\(\)](#) Visualization of estimates with [plot_estimates\(\)](#)

Examples

```
data("longitudinalMetabolomics")
data <- longitudinalMetabolomics[, longitudinalMetabolomics$condition == "A" &
  longitudinalMetabolomics$metabolite == "ATP"]
data <- fit_dynamics_model(
  data = data,
  scaled_measurement = "m_scaled", assay = "scaled_log",
  max_treedepth = 14, adapt_delta = 0.95, iter = 2000, cores = 1, chains = 1
)
data <- estimates_dynamics(
  data = data
)
S4Vectors::metadata(data)[["estimates_dynamics"]]
```

fit_dynamics_model *Fits dynamics model*

Description

Employs a hierarchical model that assumes a normal distribution of standardized (mean=0, sd=1) $\log(\text{cpc})$ (cpc = normalized metabolite abundance) values for robust estimation of mean concentrations over time of single metabolites at single experimental conditions. At least three replicates for metabolite concentrations per time point and condition are needed. If cell counts are provided at least one replicate per time point and condition is needed.

Usage

```
fit_dynamics_model(  
  model = "scaled_log",  
  model_option = "sd_per_condition",  
  data,  
  scaled_measurement = "m_scaled",  
  counts = NULL,  
  assay = "scaled_log",  
  chains = 4,  
  cores = 4,  
  adapt_delta = 0.95,  
  max_treedepth = 10,  
  iter = 2000,  
  warmup = iter/4  
)
```

Arguments

| | |
|--------------|---|
| model | which model to fit. Two options are available: "scaled_log": taking in normalized and scaled metabolite concentrations (see scaled measurement) "raw_plus_counts": tailored for in vitro untargeted LC-MS experiments, taking in "raw" (i.e. not normalized and not scaled) metabolite concentrations and cell counts. This model assumes independent measurement (i.e. different wells) of cell counts and metabolite concentrations. Additionally it assumes that cell counts were estimated e.g. by cell counters (i.e. that cells were not counted under the microscope) leading to a small uncertainty of the true cell count. |
| model_option | for each model ("scaled_log" and "raw_plus_counts") two versions are available: "sd_per_time_point" and "sd_per_condition". "sd_per_time_point" is suited for more replicates (at least triplicates) and estimates standard deviations per time point and therefore allows for more sensitive discrimination of changing abundances. high deviations between replicates) or for many metabolites, time points or conditions as it reduces run time due to less parameters. For model details see vignette (browseVignettes("MetaboDynamics")). |

| | |
|--------------------|--|
| data | concentration table with at least three replicate measurements per metabolite. Must contain columns named "metabolite" (containing names or IDs), "time" (categorical, the same for all conditions), and "condition" or colData of a SummarizedExperiment object Time column needs to be sorted in ascending order |
| scaled_measurement | column of "data" that contains the concentrations per cell, centered and normalized per metabolite and experimental condition (mean=0, sd=1), must be numeric |
| counts | data frame with at least one replicate per time point and condition specifying the cell counts, must contain columns "time", and "condition" equivalent to the specifications of "data". Must contain a column named "counts" that specifies the cell counts. Model assumes that the replicates of the cell counts and metabolite concentrations are independent of each other (i.e. cell counts were measured in in different wells than metabolite concentrations) |
| assay | if input is a SummarizedExperiment specify the assay that should be used for input, colData has to hold the columns, "condition" and "metabolite", rowData the timepoint specifications, in case of the model "scaled_log" assay needs to hold scaled log-transformed metabolite concentrations (mean=0,sd=1 per metabolite and experimental condition), if model "raw_plus_counts" is chosen must hold the non-transformed and non-scaled metabolite concentrations |
| chains | how many Markov-Chains should be used for model fitting, use at least two, default=4 |
| cores | how many cores should be used for model fitting; this parallelizes the model fitting and therefore speeds it up; default=4 |
| adapt_delta | target average acceptance probability, can be adapted if divergent transitions are reported, default is 0.95 |
| max_treedepth | can be adapted if model throws warnings about hitting max_treedepth, warnings are mostly efficiency not validity concerns and treedepth can be raised, default=10 |
| iter | how many iterations are run, increasing might help with effective sample size being to low, default=2000 |
| warmup | how many iterations the model warms up for, increasing might facilitate efficiency, must be at least 25% of ITER, default=iter/4 |

Value

returns a list of model fits. One model fit named "condition" per experimental condition. If input is a summarizedExperiment object the dynamic fits are stored metadata(data) under "dynamic_fits". 'model' and 'model_option' are also stored in metadata(data)

See Also

Example data set [longitudinalMetabolomics](#). Get model diagnostics [diagnostics_dynamics\(\)](#) Get model estimates [estimates_dynamics\(\)](#)

Examples

```
## on scaled log-transformed metabolite concentrations
data("longitudinalMetabolomics")
data <- longitudinalMetabolomics[, longitudinalMetabolomics$condition %in% c("A", "B") &
  longitudinalMetabolomics$metabolite == "ATP"]
data <- fit_dynamics_model(
  model = "scaled_log",
  data = data,
  assay = "scaled_log",
  max_treedepth = 14, adapt_delta = 0.95, iter = 2000, cores = 1, chains = 1
)
S4Vectors::metadata(data)[["dynamic_fit"]]
```

| | |
|---------------------|--|
| get_ORA_annotations | <i>Retrieve background and annotation information for over-representation analysis (ORA)</i> |
|---------------------|--|

Description

Uses the package KEGGREST to retrieve background and annotation information needed for over-representation analysis. As KEGGREST only allows 10 queries per second this might take some time to run, depending on the size of the dataset and organism. The user should check afterwards if all functional modules are applicable for the analysis of the dataset (p.e. organism, tissue).

Usage

```
get_ORA_annotations(
  data,
  kegg = "KEGG",
  metabolite_name = "metabolite",
  update_background = TRUE
)
```

Arguments

| | |
|-------------------|--|
| data | data frame to be analyzed with ORA. Must at least contain a column with KEGG IDs or a SummarizedExperiment where the metabolite names or IDs are stored in colData |
| kegg | column name of "data" that holds KEGG IDs |
| metabolite_name | column name of "data" that holds metabolite names |
| update_background | logical. Should the background information be updated? Should be set to TRUE of this is the first time using this function. If TRUE this may take some time. |

Value

a list with dataframes "background" and "annotation" needed for ORA, if data is a SummarizedExperiment [SummarizedExperiment](#) object annotations are stored in metadata(data) under "KEGG_annotations"

See Also

Do over-representation analysis of KEGG functional modules [ORA_hypergeometric\(\)](#)

Examples

```
data("longitudinalMetabolomics")
data <- longitudinalMetabolomics[, longitudinalMetabolomics$condition == "A" &
  longitudinalMetabolomics$metabolite == "ATP"]
data <- get_ORA_annotations(
  data = data,
  kegg = "KEGG",
  metabolite_name = "metabolite",
  update_background = FALSE
)
S4Vectors::metadata(data)[["KEGG_annotations"]]
```

heatmap_dynamics

plot bubble heatmap from the numerical fit of compare_dynamics()

Description

plot bubble heatmap from the numerical fit of compare_dynamics()

Usage

```
heatmap_dynamics(
  estimates = metadata(data)[["comparison_dynamics"]][["estimates"]],
  data
)
```

Arguments

| | |
|-----------|---|
| estimates | dataframe of estimates of the mean distance between clusters of different experimental conditions ("mean") and the standard deviation ("sigma") obtain by function compare_dynamics() |
| data | a dataframe or containing a column specifying the metabolite names to be compared and cluster IDs (column named "cluster") of clusters of similar dynamics, as well as a column "condition" specifying the experimental conditions. to be compared or a SummarizedExperiment storing the same information in metadata(data) under "cluster" |

Value

a bubble heat map where the color of the bubble represents the similarity of two clusters in regards to their dynamics in the color and the size the uncertainty of the similarity. Big bright bubbles mean high similarity with low uncertainty.

See Also

Do calculations for comparison of dynamics between clusters [compare_dynamics\(\)](#)

Examples

```
data("longitudinalMetabolomics")
data <- longitudinalMetabolomics[, longitudinalMetabolomics$condition %in% c("A", "B") &
  longitudinalMetabolomics$metabolite %in% c("ATP", "L-Alanine", "GDP")]
data <- fit_dynamics_model(
  data = data,
  scaled_measurement = "m_scaled", assay = "scaled_log",
  max_treedepth = 14, adapt_delta = 0.95, iter = 2000, cores = 1, chains = 1
)
data <- estimates_dynamics(
  data = data
)
data <- cluster_dynamics(data, B = 1)
data <- compare_dynamics(
  data = data,
  cores = 1
)
S4Vectors::metadata(data)[["comparison_dynamics"]]
heatmap_dynamics(data = data)
```

heatmap_metabolites *plot heatmap from comparison of metabolite composition compare_metabolites()*

Description

plot heatmap from comparison of metabolite composition [compare_metabolites\(\)](#)

Usage

```
heatmap_metabolites(
  distances = metadata(data)[["comparison_metabolites"]],
  data
)
```

Arguments

| | |
|-----------|--|
| distances | dataframe of Jaccard indices between clusters obtained by function <code>compare_metabolites()</code> . If <code>compare_metabolites()</code> was executed on a <code>SummarizedExperiment</code> or a <code>SummarizedExperiment</code> than this is stored in <code>metadata(data)</code> under "comparison_metabolites" |
| data | a dataframe containing the columns "metabolite" specifying the metabolite names to be compared and cluster IDs(column named "cluster") of clusters of similar dynamics, as well as a column "condition" specifying the experimental conditions to be compared |

Value

a heatmap where the color of the tile represents the similarity of two clusters in regards to their metabolite composition. The brighter the color the more similar the metabolite compositions.

See Also

Do calculations for comparison of metabolites between clusters `compare_metabolites()`

Examples

```
data("longitudinalMetabolomics")
longitudinalMetabolomics <- compare_metabolites(
  data = longitudinalMetabolomics
)
heatmap_metabolites(data = longitudinalMetabolomics)
```

| | |
|-----|---|
| IDs | <i>KEGG ID mapping of metabolites in data set longitudinal-Metabolomics</i> |
|-----|---|

Description

Example data set of KEGG ID annotations of metabolites as needed for `ORA_hypergeometric()`

Usage

```
data("IDs")
```

Format

A dataframe

KEGG KEGG ID of metabolites

replicate column that specifies the measurement replicate

longitudinalMetabolomics

A simulated data set of longitudinal concentration tables of metabolites.

Description

A simulated data set of 98 metabolites. 3 replicate measurements of 4 time points and at 2 experimental conditions. Metabolites are in 8 dynamics groups per experimental condition. 4 groups have varying dynamics between conditions. Is represented as a SummarizedExperiment object where concentration tables of each experimental condition are stored in assays (raw concentrations in "concentrations", log-transformed transformations in "log_con" and scaled log-transformed concentrations in "scaled_log") and metabolite names, KEGG IDs, experimental conditions and clustering solutions per experimental condition are stored in colData and timepoint specifications in rowData. ([SummarizedExperiment](#)).

Usage

```
data("longitudinalMetabolomics")
```

Format

A SummarizedExperiment object with concentration tables in assays. RowData contains the time point specification. ColData as specified below.

condition experimental condition

metabolite metabolite name

KEGG KEGG ID of metabolites

replicate column that specifies the measurement replicate

cluster cluster ID that is condition specific for every metabolite

Source

Script used to create simulated data set.seed(1234) # load KEGG database for assignment of metabolite names: data("metabolite_modules")

```
# metabolite_db <- metabolite_modules # Group <- middle_hierarchy
```

```
library(dplyr) library(SummarizedExperiment) library(tidyverse) # Parameters (as before)
```

```
n_features <- 98
```

```
n_groups <- 8 # Number of groups (randomly choose between 6-8)
```

```
n_time_points <- 4 # Number of time points
```

```
n_replicates <- 3 # Number of replicates for all features and time points
```

```
n_conditions <- 2 # Number of experimental conditions
```

```
x_varying_groups <- 4 # Number of groups with varying dynamics across conditions
```

```

condition_names <- c("A","B")
# Probability matrix for assigning metabolites from different database groups to dynamic groups #
# For simplicity, we assume equal probability; customize as needed
group_probabilities <- matrix(c(0.8,rep(0.01,7), #amino acid metabolism rep(0.01,7),0.8, #nucleotide
metabolism 0.1,0.8,0.8,rep(0.1,5), # energy and carbohydrate metabolism runif(5 * length(unique(metabolite_modules$middle_
nrow = n_groups, ncol = length(unique(metabolite_modules$middle_hierarchy))))
# Generate group dynamics (base trends over time) for each condition
group_dynamics <- list()
# Define the base group dynamics for condition 1
group_dynamics[[1]] <- lapply(1:n_groups, function(g) trend <- rnorm(n_time_points, mean = g *
2, sd = 0.5) return(trend) )
# Define varying dynamics for selected groups across other conditions
varying_groups <- sample(1:n_groups, x_varying_groups, replace = FALSE)
for (cond in 2:n_conditions) group_dynamics[[cond]] <- group_dynamics[[1]] for (g in varying_groups)
group_dynamics[[cond]][[g]] <- rnorm(n_time_points, mean = g * 2, sd = 1)
# Assign each feature to a group
feature_to_group <- sample(1:n_groups, n_features, replace = TRUE)
# Initialize a list to store the simulated data
simulated_data <- list()
# Assign metabolite names to features
available_metabolites <- metabolite_modules # Copy of metabolite database to keep track of unused
names
# Simulate data for each feature across all conditions
for (feature in 1:n_features)
# Get the group for this feature
group <- feature_to_group[feature]
# Determine probability of each metabolite database group for this dynamic group
group_probs <- group_probabilities[group, ]
# Subset the metabolite database for selection based on group probabilities
metabolite_candidates <- available_metabolites group_by(middle_hierarchy) mutate(Probability =
group_probs[match(middle_hierarchy, unique(metabolite_modules$middle_hierarchy))]) ungroup()
filter(metabolite
# Randomly sample a metabolite based on these probabilities
metabolite_name <- sample(metabolite_candidates$metabolite, 1, prob = metabolite_candidates$Probability)
# Remove this metabolite from available pool
available_metabolites <- available_metabolites[available_metabolites$metabolite != metabolite_name,
]
# Generate a random base mean for this feature between 0.001 and 1000
base_mean <- runif(1, min = 0.1, max = 1e5)

```

```

# Generate feature-specific variances for each time point
feature_variances <- runif(n_time_points, min = 0.1, max = 2)

# Store data for each condition
for (cond in 1:n_conditions) trend <- group_dynamics[[cond]][[group]] feature_means <- base_mean
* trend / max(abs(trend))

feature_data <- data.frame( metabolite = metabolite_name, # Assign metabolite name here condi-
tion = paste0(condition_names[[cond]]), time = rep(1:n_time_points, each = n_replicates), replicate
= rep(1:n_replicates, times = n_time_points) )

# Generate the actual data points with strictly positive concentrations
feature_data$measurement <- unlist(lapply(1:n_time_points, function(t) rlnorm(n_replicates, mean-
log = log(feature_means[t]), sdlog = feature_variances[t]) ))

simulated_data[[length(simulated_data) + 1]] <- feature_data

rm(base_mean,cond,feature,feature_means,feature_to_group,feature_variances, g,group,group_probs,metabolite_name,n_co
n_time_points,trend,varying_groups,x_varying_groups,available_metabolites,feature_data,group_dynamics,
group_probabilities,metabolite_candidates)

# Combine all features and conditions into one data frame
simulated_data_df <- do.call(rbind, simulated_data)

simulated_data_df <- simulated_data_df group_by(metabolite, condition) mutate( log_m = log10(measurement),
m_scaled = (log_m - mean(log_m)) / sd(log_m) )

# add KEGG IDs name_map_HMDB_CAS <- readr::read_csv("name_map_HMDB_CAS.csv")
longitudinalMetabolomics <- dplyr::left_join(simulated_data_df,name_map_HMDB_CAS[,c("Query","KEGG")],join_by("m
easurement", "KEGG"))

## concentrations temp <- longitudinalMetabolomics temp <- temp select(condition,metabolite,KEGG,time,measurement,rep
pivot_wider(id_cols=c(condition,metabolite,KEGG,replicate), names_from = time, values_from =
measurement) concentrations <- temp ## transform matrix so that conditions are in columns to facil-
itate access ## with colData -> se[,se$condition="A"] concentrations <- t(as.matrix(concentrations))
row.names(concentrations) <- NULL # prepare log_transformed data temp <- longitudinalMetabolomics
temp <- temp select(condition,metabolite,KEGG,time,log_m,replicate) pivot_wider(id_cols=c(condition,metabolite,KEGG,r
names_from = time, values_from = log_m) log_con <- temp log_con <- t(as.matrix(log_con))
row.names(log_con) <- NULL # prepare scaled log_transformed data temp <- longitudinalMetabolomics
temp <- temp select(condition,metabolite,KEGG,time,m_scaled,replicate) pivot_wider(id_cols=c(condition,metabolite,KEG
names_from = time, values_from = m_scaled) scaled_log <- temp scaled_log <- t(as.matrix(scaled_log))
row.names(scaled_log) <- NULL

# simulate cell counts ## I am assuming that all cell counts are from a poisson distribution with the
same ## location parameter (not the case for real life applications). One parameter is just used to
show application of the dynamics model including cell counts

counts <- rbind(rpois(ncol(concentrations),1e5), rpois(ncol(concentrations),1e5), rpois(ncol(concentrations),1e5),
rpois(ncol(concentrations),1e5)) # 882 columns, three entries for same metabolite, four time points

# prepare row and colData ##### row_data <- DataFrame(time_points=c("time_point_1","time_point_2","time_point_3",
"time_point_4")) col_data <- DataFrame(condition=temp$condition,metabolite=temp$metabolite,
KEGG=temp$KEGG,replicate=temp$replicate)

se <- SummarizedExperiment(assays=SimpleList(concentrations=concentrations, log_con=log_con,
scaled_log=scaled_log, cell_counts = counts), rowData = row_data, colData = col_data) # set row

```

```

and colnames ##### rownames(se) <- c("time_point_1","time_point_2","time_point_3", "time_point_4")
colnames(se) <- temp$metabolite

# add metadata ##### metadata(se)[["data origin"]] <- "Simulated data of 98 metabolites with three
concentration observations at four time points and at three different biological conditions. Script to
construct dataset can be seen with ?longitudinalMetabolomics"

data <- se data <- fit_dynamics_model( data = data, scaled_measurement = "m_scaled", assay =
"scaled_log", max_treedepth = 14, adapt_delta = 0.999, iter = 5000, cores = 2, chains = 2 )

data <- estimates_dynamics( data = data ) data <- cluster_dynamics(data,B=10) metadata(data)[["dynamic_fit"]]
<- NULL

data("modules_compounds") data("metabolite_modules") data("IDs") data <- ORA_hygeometric(data
= data, background = modules_compounds, IDs = IDs, annotations = metabolite_modules, tested_column
= "middle_hierarchy")

# save shortened analysis in metadata of se metadata(se)[["estimates_dynamics"]] <- metadata(data)[["estimates_dynamics"]]
metadata(se)[["dynamics"]] <- metadata(data)[["dynamics"]] metadata(se)[["cluster"]] <- metadata(data)[["cluster"]]
metadata(se)[["ORA_middle_hierarchy"]] <- metadata(data)[["ORA_middle_hierarchy"]]

longitudinalMetabolomics <- se usethis::use_data(longitudinalMetabolomics,overwrite = TRUE)

longitudinalMetabolomics_df <- dplyr::left_join(simulated_data_df,name_map_HMDB_CAS[,c("Query","KEGG")],join_b
usethis::use_data(longitudinalMetabolomics_df,overwrite = TRUE)

```

longitudinalMetabolomics_df

A simulated data set of longitudinal concentration tables of metabolites. In contrast to "longitudinalMetabolomics" this dataset is in data frame format. It was simulated with a different seed compared to longitudinalMetabolomics so the results can deviate.

Description

A simulated data set of 98 metabolites. 3 replicate measurements of 4 time points and at 3 experimental conditions. Metabolites are in 8 dynamics groups per experimental condition. 4 groups have varying dynamics between conditions. Is represented as a SummarizedExperiment object where concentration tables of each experimental condition are stored in assays (raw concentrations in "concentrations", log-transformed transformations in "log_con" and scaled log-transformed concentrations in "scaled_log") and metabolite names, KEGG IDs, experimental conditions and clustering solutions per experimental condition are stored in colData and timepoint specifications in rowData. ([SummarizedExperiment](#)).

Usage

```
data("longitudinalMetabolomics")
```

Format

A SummarizedExperiment object with concentration tables in assays. RowData contains the time point specification. ColData as specified below.

```
condition  experimental condition
metabolite metabolite name
KEGG      KEGG ID of metabolites
replicate column that specifies the measurement replicate
cluster   cluster ID that is condition specific for every metabolite
```

Source**Script used to create simulated data**

```
# load KEGG database for assignment of metabolite names: data("metabolite_modules")
# metabolite_db <- metabolite_modules # Group <- middle_hierarchy
library(dplyr) library(SummarizedExperiment) # Parameters (as before)
n_features <- 98
n_groups <- 8 # Number of groups (randomly choose between 6-8)
n_time_points <- 4 # Number of time points
n_replicates <- 3 # Number of replicates for all features and time points
n_conditions <- 2 # Number of experimental conditions
x_varying_groups <- 4 # Number of groups with varying dynamics across conditions
condition_names <- c("A","B")
# Probability matrix for assigning metabolites from different database groups to dynamic groups #
For simplicity, we assume equal probability; customize as needed
group_probabilities <- matrix(c(0.8,rep(0.01,7), #amino acid metabolism rep(0.01,7),0.8, #nucleotide
metabolism 0.1,0.8,0.8,rep(0.1,5), # energy and carbohydrate metabolism runif(5 * length(unique(metabolite_modules$middle_hierarchy)))
nrow = n_groups, ncol = length(unique(metabolite_modules$middle_hierarchy)))
# Generate group dynamics (base trends over time) for each condition
group_dynamics <- list()
# Define the base group dynamics for condition 1
group_dynamics[[1]] <- lapply(1:n_groups, function(g) trend <- rnorm(n_time_points, mean = g *
2, sd = 0.5) return(trend) )
# Define varying dynamics for selected groups across other conditions
varying_groups <- sample(1:n_groups, x_varying_groups, replace = FALSE)
for (cond in 2:n_conditions) group_dynamics[[cond]] <- group_dynamics[[1]] for (g in varying_groups)
group_dynamics[[cond]][[g]] <- rnorm(n_time_points, mean = g * 2, sd = 1)
# Assign each feature to a group
feature_to_group <- sample(1:n_groups, n_features, replace = TRUE)
# Initialize a list to store the simulated data
```

```

simulated_data <- list()
# Assign metabolite names to features
available_metabolites <- metabolite_modules # Copy of metabolite database to keep track of unused
names
# Simulate data for each feature across all conditions
for (feature in 1:n_features)
# Get the group for this feature
group <- feature_to_group[feature]
# Determine probability of each metabolite database group for this dynamic group
group_probs <- group_probabilities[group, ]
# Subset the metabolite database for selection based on group probabilities
metabolite_candidates <- available_metabolites group_by(middle_hierarchy) mutate(Probability =
group_probs[match(middle_hierarchy, unique(metabolite_modules$middle_hierarchy))] ungroup()
filter(metabolite
# Randomly sample a metabolite based on these probabilities
metabolite_name <- sample(metabolite_candidates$metabolite, 1, prob = metabolite_candidates$Probability)
# Remove this metabolite from available pool
available_metabolites <- available_metabolites[available_metabolites$metabolite != metabolite_name,
]
# Generate a random base mean for this feature between 0.001 and 1000
base_mean <- runif(1, min = 0.001, max = 1000)
# Generate feature-specific variances for each time point
feature_variances <- runif(n_time_points, min = 0.1, max = 2)
# Store data for each condition
for (cond in 1:n_conditions) trend <- group_dynamics[[cond]][[group]] feature_means <- base_mean
* trend / max(abs(trend))
feature_data <- data.frame( metabolite = metabolite_name, # Assign metabolite name here condi-
tion = paste0(condition_names[[cond]]), time = rep(1:n_time_points, each = n_replicates), replicate
= rep(1:n_replicates, times = n_time_points) )
# Generate the actual data points with strictly positive concentrations
feature_data$measurement <- unlist(lapply(1:n_time_points, function(t) rlnorm(n_replicates, mean-
log = log(feature_means[t]), sdlog = feature_variances[t]) ))
simulated_data[[length(simulated_data) + 1]] <- feature_data
rm(base_mean,cond,feature,feature_means,feature_to_group,feature_variances, g,group,group_probs,metabolite_name,n_co
n_time_points,trend,varying_groups,x_varying_groups,available_metabolites,feature_data,group_dynamics,
group_probabilities,metabolite_candidates)
# Combine all features and conditions into one data frame
simulated_data_df <- do.call(rbind, simulated_data)
simulated_data_df <- simulated_data_df group_by(metabolite, condition) mutate( log_m = log10(measurement),
m_scaled = (log_m - mean(log_m)) / sd(log_m) )

```

```
# add KEGG IDs name_map_HMDB_CAS <- readr::read_csv("name_map_HMDB_CAS.csv")
longitudinalMetabolomics_df <- dplyr::left_join(simulated_data_df,name_map_HMDB_CAS[,c("Query","KEGG")],join_b
usethis::use_data(longitudinalMetabolomics_df,overwrite = TRUE)
```

| | |
|--------------------|---|
| metabolite_modules | <i>KEGG Query Results of experimental metabolites</i> |
|--------------------|---|

Description

Using the package KEGGREST (<https://www.bioconductor.org/packages/release/bioc/html/KEGGREST.html>) all experimental metabolites (see `data("intra")`) were queried with there KEGG-IDs and all functional modules recorded to which the metabolite is annotated in the KEGG-database.

Usage

```
data("metabolite_modules")
```

Format

A data frame with 348 observations on the following 8 variables.

... 1 row number of the dataframe

metabolite name of the experimental metabolite

KEGG KEGG ID of the experimental metabolite

module_id ID of the KEGG module to which the metabolite is annotated

module_name name of the KEGG module to which the metabolite is annotated

upper_hierarchy name of the highest hierarchy level of module organization

middle_hierarchy name of the middle hierarchy = functional module, p.e. "Amino acid metabolism"

lower_hierarchy name of the lowest level of modules, this often contain only a couple pathways
p.e. "Arginine and proline metabolism"

Source

<https://www.genome.jp/kegg/module.html>

See Also

[modules_compounds](#)

modules_compounds *Background KEGG Query Results Of Functional Modules*

Description

Using the package KEGGREST (<https://www.bioconductor.org/packages/release/bioc/html/KEGGREST.html>) a list of all KEGG-modules (KeggList("module")) including their upper, middle and lower hierarchy as given by the KEGG-database and the corresponding annotated metabolites was queried.

Usage

```
data("modules_compounds")
```

Format

A data frame with 1988 observations on the following 6 variables.

KEGG KEGG ID of a metabolite annotated to a functional module

upper_hierarchy name of the highest hierarchy level of module organization

middle_hierarchy name of the middle hierarchy = functional module, p.e. "Amino acid metabolism"

lower_hierarchy name of the lowest level of modules, this often contain only a couple pathways
p.e. "Arginine and proline metabolism"

module_id the ID of the KEGG functional module

module_name name of the KEGG module

Source

<https://www.genome.jp/kegg/module.html>

See Also

[metabolite_modules](#)

ORA_hypergeometric *OverRepresentationAnalysis with a hypergeometric model*

Description

Testing the hypothesis that certain KEGG modules are over-represented in clusters of metabolites. A module is considered over-represented in a cluster the number of metabolites in a cluster being annotated to a functional module (n_{obs}) is higher than the expected number of metabolites in a cluster of this size being annotated to a functional module (n_{theo}). We can calculate the OvE (Observed versus Expected = n_{obs}/n_{theo}) and show the probabilities of these ratios. $\log(p(OvE)) > 0$ indicates an over-representation of the functional module in the cluster, $\log(p(OvE)) < 0$ an under-representation.

Usage

```
ORA_hypergeometric(  
  background,  
  annotations,  
  data,  
  IDs,  
  tested_column = "middle_hierarchy"  
)
```

Arguments

| | |
|---------------|---|
| background | dataframe that contains KEGG IDs of metabolites that are assigned to functional modules, is incorporated in the package modules_compounds |
| annotations | dataframe that contains information to which functional modules our experimental metabolites are annotated in KEGG, can be constructed by filtering the provided KEGG background modules_compounds for the experimental metabolites |
| data | result of cluster_dynamics() function: either a list of data frames or a SummarizedExperiment object |
| IDs | dataframe with two columns 'metabolite' and 'KEGG' mapping KEGG IDs to metabolites. If function get_ORA_annotations() is used to retrieve IDs these are stored under "KEGG_annotations" of metadata(data) |
| tested_column | column that is in background and annotations and on which the hypergeometric model will be executed |

Value

a dataframe containing the ORA results or if data is SummarizedExperiment [SummarizedExperiment](#) object the output is stored in metadata(data) under "ORA_tested_column"

See Also

Function to obtain data [cluster_dynamics\(\)](#) Function to visualize ORA results [plot_ORA\(\)](#)
[get_ORA_annotations\(\)](#)

Examples

```
data("longitudinalMetabolomics")  
data("modules_compounds")  
head(modules_compounds)  
data("metabolite_modules")  
head(metabolite_modules)  
data("IDs")  
head(IDs)  
  
longitudinalMetabolomics <- ORA_hypergeometric(  
  data = longitudinalMetabolomics,  
  annotations = metabolite_modules,  
  background = modules_compounds,
```

```
  IDs = IDs,  
  tested_column = "middle_hierarchy"  
)  
S4Vectors::metadata(longitudinalMetabolomics)[["ORA_middle_hierarchy"]]
```

plot_cluster

visualize clustering solution of cluster_dynamics()

Description

visualize clustering solution of cluster_dynamics()

Usage

```
plot_cluster(data)
```

Arguments

data result of [cluster_dynamics\(\)](#) function: either a list of data frames or a SummarizedExperiment object

Value

a list of plots. Per experimental condition: 1) a 'bubbletree': a phylogram with numbers on nodes indicating in how many bootstraps of the posterior estimates the same clustering solution was generated, 2) cluster affiliation of metabolites, 3) dynamics of metabolites per cluster, 4) patchwork of 1-3, 5) order of the tips in bubbletree: needed for matching cluster plots and ORA

See Also

[cluster_dynamics\(\)](#)

Examples

```
data("longitudinalMetabolomics")  
plots <- plot_cluster(longitudinalMetabolomics[, longitudinalMetabolomics$condition == "A"])  
  
plots[["trees"]][["A"]]
```

| | |
|------------------|--|
| plot_diagnostics | <i>Plot diagnostic criteria of numerical fit of Bayesian model of dynamics</i> |
|------------------|--|

Description

Plot diagnostic criteria of numerical fit of Bayesian model of dynamics

Usage

```
plot_diagnostics(  
  data,  
  assay = "scaled_log",  
  diagnostics = metadata(data)[["diagnostics_dynamics"]][["model_diagnostics"]],  
  divergences = TRUE,  
  max_treedepth = TRUE,  
  Rhat = TRUE,  
  n_eff = TRUE  
)
```

Arguments

| | |
|---------------|---|
| data | dataframe or colData of a SummarizedExperiment used to fit dynamics model must contain column "time" |
| assay | of the SummarizedExperiment object that was used to fit the dynamics model |
| diagnostics | dataframe containing diagnostics criteria from the numerical fit of Bayesian model of dynamics obtained by function <code>diagnostics_dynamics()</code> |
| divergences | should number of divergent transitions be visualized? |
| max_treedepth | should number of exceeded maximum treedepth be visualized? |
| Rhat | should Rhat be visualized? |
| n_eff | should number of effective samples be visualized? |

Value

plots of diagnostic criteria of numerical fit of Bayesian model of dynamics

See Also

parent function [diagnostics_dynamics\(\)](#) visualization function for posterior predictive check [plot_PPC\(\)](#)

Examples

```

data("longitudinalMetabolomics")
data <- longitudinalMetabolomics[, longitudinalMetabolomics$condition == "A" &
  longitudinalMetabolomics$metabolite %in% c("ATP", "ADP")]
data <- fit_dynamics_model(
  model = "scaled_log",
  data = data,
  scaled_measurement = "m_scaled", assay = "scaled_log",
  max_treedepth = 14, adapt_delta = 0.95, iter = 2000, cores = 1, chains = 1
)
data <- diagnostics_dynamics(
  data = data, assay = "scaled_log",
  iter = 2000, chains = 1,
  fit = metadata(data)[["dynamic_fit"]]
)
plot_diagnostics(data = data, assay = "scaled_log")

```

| | |
|----------------|--|
| plot_estimates | <i>Visualization of parameter estimates from numeric fit of Bayesian model of dynamics</i> |
|----------------|--|

Description

Visualization of parameter estimates from numeric fit of Bayesian model of dynamics

Usage

```

plot_estimates(
  data = NULL,
  estimates = metadata(data)[["estimates_dynamics"]],
  delta_t = TRUE,
  dynamics = TRUE,
  distance_conditions = TRUE
)

```

Arguments

| | |
|---------------------|--|
| data | SummarizedExperiment used to fit dynamics model and extract the estimates |
| estimates | a list of data frames (elements: mu, sigma, lambda, euclidean_distance) that contains the model estimates by estimates_dynamics() or if data is a SummarizedExperiment estimates must be stored in metadata(data) under "estimates_dynamics" |
| delta_t | should differences between time points be plotted? |
| dynamics | should dynamics be plotted? |
| distance_conditions | should differences in metabolite specific dynamic should be plotted? |

Value

Visualization of differences between time points(delta_t) and dynamics profiles of single metabolites

See Also

parent function [estimates_dynamics\(\)](#)

Examples

```
data("longitudinalMetabolomics")
data <- longitudinalMetabolomics[, longitudinalMetabolomics$condition %in% c("A", "B") &
  longitudinalMetabolomics$metabolite %in% c("ATP")]
data <- fit_dynamics_model(
  data = data,
  scaled_measurement = "m_scaled", assay = "scaled_log",
  max_treedepth = 14, adapt_delta = 0.95, iter = 2000, cores = 1, chains = 1
)
data <- estimates_dynamics(
  data = data
)
plot_estimates(data = data, delta_t = TRUE, dynamic = FALSE, distance_conditions = FALSE)
plot_estimates(data = data, delta_t = FALSE, dynamic = TRUE, distance_conditions = FALSE)
plot_estimates(data = data, delta_t = FALSE, dynamic = FALSE, distance_conditions = TRUE)
```

| | |
|----------|---|
| plot_ORA | <i>Plot results of over-representation analysis with ORA_hypergeometric()</i> |
|----------|---|

Description

Plot results of over-representation analysis with `ORA_hypergeometric()`

Usage

```
plot_ORA(
  data,
  tested_column = "middle_hierarchy",
  patchwork = FALSE,
  plot_cluster = NULL
)
```

Arguments

| | |
|---------------|---|
| data | result dataframe from ORA_hypergeometric() or SummarizedExperiment object where the <code>ORA_hypergeometric()</code> results are stored in <code>metadata(data)</code> under "ORA_tested_column" |
| tested_column | KEGG module hierarchy level on which ORA was executed |

patchwork should result be patchworked to results of `plot_cluster()`?
plot_cluster if patchwork = TRUE this needs to be the result of `plot_cluster()`

Value

a plot of the over-representation analysis and lsit of plots suitable to patchwork with cluster visualization if patchwork=TRUE

See Also

do over-representation analysis of KEGG functional modules `ORA_hypergeometric()`

Examples

```
data("longitudinalMetabolomics")
data("modules_compounds")
head(modules_compounds)
data("metabolite_modules")
head(metabolite_modules)
data("IDs")
head(IDs)
# middly hierachy
longitudinalMetabolomics <- ORA_hypergeometric(
  data = longitudinalMetabolomics,
  annotations = metabolite_modules,
  background = modules_compounds,
  tested_column = "middle_hierarchy",
  IDs = IDs
)
plot_ORA(longitudinalMetabolomics)
```

| | |
|----------|---|
| plot_PPC | <i>Plots posterior predictive check of numerical fit of Bayesian dynamics model</i> |
|----------|---|

Description

Plots posterior predictive check of numerical fit of Bayesian dynamics model

Usage

```
plot_PPC(
  posterior = metadata(data)[["diagnostics_dynamics"]],
  data,
  assay = "scaled_log",
  scaled_measurement = "scaled_measurement"
)
```

Arguments

| | |
|--------------------|--|
| posterior | a dataframe that contains necessary information for Posterior predictive check obtained by function <code>diagnostics_dynamics()</code> (named "PPC_condition") |
| data | dataframe or colData of a SummarizedExperiment used to fit dynamics model |
| assay | of the SummarizedExperiment object that was used to fit the dynamics model |
| scaled_measurement | column name of concentration values used to model fit, should be normalized by experimental condition and metabolite to mean of zero and standard deviation of one |

Value

a list of visual posterior predictive check, one per experimental condition

See Also

parent function `diagnostics_dynamics()` visualization function for diagnostics `plot_diagnostics()`

Examples

```
data("longitudinalMetabolomics")
data <- longitudinalMetabolomics[, longitudinalMetabolomics$condition == "A" &
  longitudinalMetabolomics$metabolite %in% c("ATP", "ADP")]
data <- fit_dynamics_model(
  model = "scaled_log",
  data = data,
  scaled_measurement = "m_scaled", assay = "scaled_log",
  max_treedepth = 14, adapt_delta = 0.95, iter = 2000, cores = 1, chains = 1
)
data <- diagnostics_dynamics(
  data = data, assay = "scaled_log",
  iter = 2000, chains = 1,
  fit = metadata(data)[["dynamic_fit"]]
)
plot_PPC(
  data = data, assay = "scaled_log"
)
```

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