

Gleesso

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+	<i>overload '+' operator to allow character strings concatenation</i>
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Description

overload '+' operator to allow character strings concatenation

Usage

"+"(e1, e2)

Compute_community_abondance	<i>compute community abundances</i>
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Description

Compute the sum of abundance of species in each community given the abundance matrix by species and the graph community Also compute the p-value of difference of abundance given a contrast vector with to class (2 classes)

Usage

```
Compute_community_abundance(Nodes, abundance, species_taxo, contrast = NULL,
  community_kind = "walktrap_community")
```

Arguments

Nodes: The network node table with the a community attribution column

abundance: The Metagenomic species abundance table

species_taxo: The Metagenomic species taxonomy table

contrast: a boolean vector to form two group of samples. for each community the rank test difference of abundance p-value is calculated between the two groups.

community kind: the algorithm of used to compute the community : "spinglass_community", "walktrap_community"

Value

a table of community abundance and composition

Compute_graph

Compute Glasso

Description

Compute the Glasso model from the MGS abundances on individuals with a true value in the contrast vector.

Usage

```
Compute_graph(MGS_abundance, contrast_vector, fout,
  abundance_treshold = 10^-7, occurence_treshold = 0.05, nlambda = 20,
  lambda.min.ratio = 0.1, lambda = NULL, rep.num = 20)
```

Arguments

contrast_vector : a boolean vector to select a subset of the cohort (the model will be infered on samples with a TRUE value)

MGS_abundance: The Metagenomic species abundance table

fout: where to save the model object

community: Should the community structure be calculated?

nlambda: Number of regularisation parameter that will be tested (see huge::huge() documentation)

lambda.min.ratio: the smallest value of lambda as a fraction of its maximum (see huge::huge() documentation)

occurrence_threshold:
 minimum fraction of samples where a species must be present to be taken into account in the analysis

abundance_threshold:
 minimum mean abundances for a species to be included in the analysis

rep.num:
 Number of subsampling to compute the edge stability with "StarS" (see huge::huge.select documentation)

lambda:
 A sequence of regularisation parameter. If not null, it will override the automatic computation of the lambda sequence (with nlambdas and lambda.min.ratio)

create_graph

Create a gephi format graph from the graphical Lasso model

Description

The Function also compute the community structure of the graph with various algorithms (betweenness community, walktrap community...) community specified by the user

Usage

```
create_graph(file_input, file_output, MGS_by_taxo_species, species_taxo,
             nspins = 20, mod_rep = 10, community = FALSE, additional_info = NULL,
             spinglass_opt = FALSE, variability_threshold = NULL)
```

Arguments

spinglass_opt : Should the number of spin of the spinglass community be optimized?

file_input: emplacement of the GLASSO model object

file_output: where to save the network representation file

MGS_by_taxo_species:
 The Metagenomic species abundance table

species_taxo: The Metagenomic species taxonomy table

nspins: number of spin for the spinglass community detection algorithm

community: Should the community structure be calculated?

additional_info:
 a vector or data.frame containing information to add to the nodes table of the network

variability_threshold:
 The maximum mean variability for graph edge presence. If null, the optimal covariance matrix will correspond to a variability of 0.05

```
generate_graph_from_tables
```

generate_graph_from_tables create a gephi graph from a Nodes table and Glasso model object

Description

generate_graph_from_tables create a gephi graph from a Nodes table and Glasso model object

Usage

```
generate_graph_from_tables(fout, nodes_viz_att, fgraph_model,
  variability_treshold = NULL)
```

```
Gleesso_pipeline
```

Pipeline launcher

Description

Launching the complete glasso analysis (data prep, graph inference, community detection, community abundances computation) Warning : folder shouldn't be indicated with an / at the end

Usage

```
Gleesso_pipeline(data_folder, MGS_file, taxo_file, model_folder, graph_folder,
  contrast_vector, tag_model, tag_graph, community = TRUE, nlambda = 20,
  lambda.min.ratio = 0.1, occurrence_treshold = 0.05,
  abundance_treshold = 10^-7, variability_treshold = NULL,
  analysis_step = NULL, species_mode = TRUE)
```

Arguments

data_folder	: where the community abundance table will be written
contrast_vector	: a boolean vector to select a subset of the cohort (the model will be inferred on samples with a TRUE value)
tag_model	: a tag that will be inserted in output file to recognize the model parameter
tag_graph	: a tag that will be inserted in output file to recognize the graph
species_mode	: should the graph inference be done on MGS (FALSE) or with MGS of the same species merged together (TRUE)
MGS_file:	The Metagenomic species abundance file in the RDS format
model_folder:	where to save the graphical Lasso model object (output of the spiec.easi function)

graph_folder:	where the graphical representation of the model will be saved (in the gephi format)
community:	Should the community structure be calculated?
nlambda:	Number of regularisation parameter that will be tested (see huge::huge() documentation)
lambda.min.ratio:	the smallest value of lambda as a fraction of its maximum (see huge::huge() documentation)
occurence_treshold:	minimum fraction of samples where a species must be present to be taken into account in the analysis
abundance_threshold:	minimum mean abundances for a species to be included in the analysis
variability_treshold:	The maximum mean variability for graph edge presence. If null, the optimal covariance matrix will correspond to a variability of 0.05
analysis_step:	At which step the analysis should be started (0: from scratch, 1: model inferences, 2: save gephi network, 3: Community detection). If NULL (default), the step will be inferred from the files present in the output folders. Use analysis_step=0 to force computation from scratch.

opt_spinglass_com	<i>Computing spinglass communities and their modularity for a range of number of spin We then retrieve the optimal number of spin according to modularity</i>
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Description

Computing spinglass communities and their modularity for a range of number of spin We then retrieve the optimal number of spin according to modularity

Usage

```
opt_spinglass_com(con.grph, mod_rep, nspins)
```

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