

Package ‘CommT’

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Type Package
Title Comparative phylogeographic analysis using the community tree framework
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Depends R (>= 3.0.0)
Imports ape (>= 3.1-4), ggplot2 (>= 1.0.0), gridExtra, phangorn, reshape
Description
Provides functions to measure the difference between constrained and unconstrained gene tree distributions using different tree distance metrics. Constraints are enforced prior to the analysis with this package through the estimation of a tree under the community tree model.
License GPL (>= 2)
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R topics documented:

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CommT-package	<i>Comparative phylogeographic analysis using the community tree framework</i>
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Description
CommT Provides functions to measure the difference between constrained and unconstrained gene tree distributions using different tree distance metrics. Constraints are enforced prior to the analysis with this package through the estimation of a tree under the community tree model.

Author(s)

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References

Gruenstaeudl, M., Reid, N.M., Wheeler, G.R. and Carstens, B.C., 2015. Posterior Predictive Checks of Coalescent Models: P2C2M, an R package. Molecular Ecology Resources, in press.

Examples

```
# Load libraries
# require(ape)

# Load input data
data(post_gt_distrs_BEAST)
data(post_gt_distrs_starBEAST)

# Calculate KF distances
in_data = CommT.kfdist(post_gt_distrs_BEAST, post_gt_distrs_starBEAST)

# Generate ANOVA legend
legend_text = CommT.anova(in_data)

# Generate coordinates for plot
legend_pos = CommT.legendpos(in_data)

# Visualize KF distances
my_plot = CommT.viz(in_data, "my_project", alpha=0.05, legend_text, legend_pos)

# Display plot
my_plot
```

CommT.anova

Conduct ANOVA analysis on tree distance matrix

Description

Function to conduct an ANOVA analysis on the matrix of tree distances generated via function CommT.kfdist().

Usage

```
CommT.anova(in_df)
```

Arguments

in_df a dataframe storing the tree distances inferred via function CommT.kfdist(). This dataframe constitutes a stacked list of distances grouped by genetic locus and is the default output of function CommT.kfdist()

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Examples

```
# Load libraries
# require(ape)

# Load input data
data(post_gt_distrs_BEAST)
data(post_gt_distrs_starBEAST)

# Calculate KF distances
in_data = CommT.kfdist(post_gt_distrs_BEAST, post_gt_distrs_starBEAST)

# Generate ANOVA legend
legend_text = CommT.anova(in_data)
```

CommT.kfdist

*Calculate the tree distance metric***Description**

Function to calculate a selected tree distance metric between posterior gene tree distributions.

Usage

```
CommT.kfdist(post_gt_distrs_BEAST, post_gt_distrs_starBEAST,
             outlier_num = 1, treedist_select = 2)
```

Arguments

post_gt_distrs_BEAST

a multiPhylo object representing the posterior gene tree distribution estimated in the **absence** of a multispecies coalescent model. This object is split into individual lists of trees, whereby each list represents a posterior gene tree distribution inferred under a specific genetic locus. Each list should be named by the respective locus.

post_gt_distrs_starBEAST

a multiPhylo object representing the posterior gene tree distribution estimated in the **presence** of a multispecies coalescent model. This object is split into individual lists of trees, whereby each list represents a posterior gene tree distribution inferred under a specific genetic locus. Each list should be named by the respective locus.

outlier_num

an integer specifying the number of the genetic locus to be used as positive control in the ANOVA calculations employing mixed effects models. The default is 1.

treedist_select

an integer specifying the type of tree distance metric. The selection hereby follows the output order employed in function `treedist` of the R package `phangorn`. The default is 2, which represents the Kuhner-Felsenstein distance.

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References

Kuhner, M.K. and Felsenstein. J., 1994. Simulation comparison of phylogeny algorithms under equal and unequal evolutionary rates. *Molecular Biology and Evolution* 11: 459-468.

Examples

```
# Load libraries
# require(ape)

# Load input data
data(post_gt_distrs_BEAST)
data(post_gt_distrs_starBEAST)

# Calculate KF distances
in_data = CommT.kfdist(post_gt_distrs_BEAST, post_gt_distrs_starBEAST)
```

CommT.legendpos	<i>Infer coordinates for plot legend</i>
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Description

Function to infer the optimal position of the ANOVA legend given the calculated tree distance distributions.

Usage

```
CommT.legendpos(in_data)
```

Arguments

in_data	a dataframe storing the tree distances inferred via function CommT.kfdist(). This dataframe constitutes a stacked list of distances grouped by genetic locus and is the default output of function CommT.kfdist()
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Examples

```
# Load libraries
# require(ape)

# Load input data
data(post_gt_distrs_BEAST)
data(post_gt_distrs_starBEAST)

# Calculate KF distances
in_data = CommT.kfdist(post_gt_distrs_BEAST, post_gt_distrs_starBEAST)

# Generate ANOVA legend
legend_text = CommT.anova(in_data)

# Generate coordinates for plot
legend_pos = CommT.legendpos(in_data)
```

CommT.viz

*Visualize tree distances and ANOVA results***Description**

Function to generate a visualization of both the tree distances and ANOVA results.

Usage

```
CommT.viz(in_df, title_str="a_project_name_here", alpha=0.05, legend_text, legend_pos)
```

Arguments

<code>in_df</code>	a dataframe storing the tree distances inferred via function <code>CommT.kfdist()</code> . This dataframe constitutes a stacked list of distances grouped by genetic locus and is the default output of function <code>CommT.kfdist()</code>
<code>title_str</code>	a string specifying a title for the resulting plot. The default is <code>a_project_name_here</code> .
<code>alpha</code>	a float specifying the alpha-level employed in the ANOVA. The default is <code>0.05</code> .
<code>legend_text</code>	a list specifying the ANOVA results to plotted. It constitutes the default output of function <code>CommT.anova()</code>
<code>legend_pos</code>	a list specifying the plot position. It constitutes the default output of function <code>CommT.legendpos()</code>

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Examples

```
# Load libraries
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# Load input data
data(post_gt_distrs_BEAST)
data(post_gt_distrs_starBEAST)

# Calculate KF distances
in_data = CommT.kfdist(post_gt_distrs_BEAST, post_gt_distrs_starBEAST)

# Generate ANOVA legend
legend_text = CommT.anova(in_data)

# Generate coordinates for plot
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# Visualize KF distances
my_plot = CommT.viz(in_data, "my_project", alpha=0.05, legend_text, legend_pos)
```

post_gt_distrs_BEAST *Data set post_gt_distrs_BEAST*

Description

Posterior gene tree distribution inferred via BEAST

Value

A multiPhylo object; more specifically, a named list of phylo objects

post_gt_distrs_starBEAST
 Data set post_gt_distrs_starBEAST

Description

Posterior gene tree distribution inferred via starBEAST

Value

A multiPhylo object; more specifically, a named list of phylo objects

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