

# Package ‘CommT’

June 16, 2015

**Type** Package

**Title** Comparative Phylogeographic Analysis using the Community Tree Framework

**Version** 0.1.1

**Date** 2015-06-16

**Author** Michael Gruenstaeudl, PhD

**Maintainer** Michael Gruenstaeudl <mi.gruenstaeudl@gmail.com>

**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 various tree distance metrics. Constraints are enforced prior to this analysis via the estimation of a tree under the community tree model.

**License** GPL (>= 2)

**OS\_type** unix

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2015-06-16 19:51:19

## R topics documented:

CommT-package . . . . .	2
CommT.anova . . . . .	3
CommT.kfdist . . . . .	3
CommT.legendpos . . . . .	5
CommT.viz . . . . .	6
post_gt_distrs_BEAST . . . . .	7
post_gt_distrs_starBEAST . . . . .	7

<b>Index</b>	<b>8</b>
--------------	----------

---

CommT-package

*Comparative phylogeographic analysis using the community tree framework*

---

## Description

**CommT** Provides functions to measure the difference between constrained and unconstrained gene tree distributions using various tree distance metrics. Constraints are enforced prior to this analysis via the estimation of a tree under the community tree model.

## Author(s)

Michael Gruenstaeudl

Maintainer: Michael Gruenstaeudl <mi.gruenstaeudl@gmail.com>

## 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()`

**Author(s)**

Michael Gruenstaeudl

Maintainer: Michael Gruenstaeudl <mi.gruenstaeudl@gmail.com>

**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.

**Author(s)**

Michael Gruenstaedl

Maintainer: Michael Gruenstaedl <mi.gruenstaedl@gmail.com>

**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>
-----------------	--

---

### 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()`

### Author(s)

Michael Gruenstaeudl

Maintainer: Michael Gruenstaeudl <mi.gruenstaeudl@gmail.com>

### 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>

**Author(s)**

Michael Gruenstaeudl

Maintainer: Michael Gruenstaeudl <mi.gruenstaeudl@gmail.com>

**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)
```

---

*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

# Index

CommT (CommT-package), [2](#)

CommT-package, [2](#)

CommT.anova, [3](#)

CommT.kfdist, [3](#)

CommT.legendpos, [5](#)

CommT.viz, [6](#)

post\_gt\_distrs\_BEAST, [7](#)

post\_gt\_distrs\_starBEAST, [7](#)