Package ‘CongreveLamsdell2016’

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Version 1.0.2

Title Distance Metrics for Trees Generated by Congreve and Lamsdell

Description Includes the 100 datasets simulated by Congreve and Lamsdell (2016) 
<doi:10.1111/pala.12236>, and analyses of the partition and quartet distance of 
reconstructed trees from the generative tree, as analysed by Smith (2019) 


BugReports https://github.com/ms609/Quartet/issues

Copyright Data from Congreve & Lamsdell (2016) released under a CC0 
license <doi:10.5061/dryad.7dq0j/1>.

License GPL (>= 2)

Encoding UTF-8

Language en-GB

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NeedsCompilation no

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clCI  Consistency indices

Description
Consistency indices of Congreve & Lamsdell datasets.

Usage
clCI

Format
An object of class numeric of length 100.

clColours  Default colours for analyses.

Description
Default colours for analyses.

Usage
clColours

Format
An object of class character of length 8.
clInitializeTernaryQuarts

Initialize ternary plots for quartet plotting

Description

Sets up a blank ternary plot ready for analytical results to be added.

Usage

clInitializeTernaryQuarts(zoom = 1, padding = 0.1, gridLines = 10,
  fontSize = 1, gridCol = "#DBDBDB", backgroundCol = "#FDFDFE",
  xLim = c(0, 1/zoom) - 0.01, yLim = c(0.5 - (1/zoom), 0.5),
  isometric = TRUE)

clInitializeTernarySplits(fontSize = 1, xLim = NULL, yLim = NULL,
  gridCol = "#DBDBDB", backgroundCol = "#FDFDFE", padding = 0.1,
  isometric = TRUE)

Arguments

  zoom               Level of magnification (times), used to adjust ticks and scale.
  padding            Padding, passed to TernaryPlot.
  gridLines          Number of grid lines, passed to TernaryPlot as grid.lines.
  fontSize           Font size, passed to TernaryPlot as lab.cex.
  gridCol            Colour, passed to TernaryPlot as grid.col.
  backgroundCol      Background colour, passed to TernaryPlot as col.
  xLim, yLim         x and y limits, passed to TernaryPlot as xlim, ylim.
  isometric          Logical specifying whether plot should be isometric, passed to TernaryPlot as isometric.

Functions

  • clInitializeTernarySplits: Initialize ternary plots for partition plotting.
**clPhyDat**

*100 Simulated Data Matrices*

**Description**

Contains the 100 simulated matrices generated by Congreve & Lamsdell (2016) using a heterogeneous Markov-k model, generated from the clReferenceTree topology, with all branches sharing an equal length.

**Usage**

- clPhyDat

**clMatrices**

**Format**

- clPhyDat: A list with 100 entries, each comprising a phyDat object of 55 characters for 22 taxa.

- clMatrices: A list with 100 entries, each comprising a list of character tokens for each simulated character, as read from raw nexus files using ape::read.nexus.data. The four dummy 'characters' have been removed.

**Source**


**References**


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**clPlotQuartets**

*Plot results*

**Description**

Plots the results of the analyses of the Congreve & Lamsdell (2016) datasets.
Usage

clPlotQuartets(dataset, tree, cex = 1.1, pch = 2,
    col = CongreveLamsdell2016::clColours, ...)

clPlotAverageQuartets(dataset, cex = 1.1, pch = 2,
    col = CongreveLamsdell2016::clColours, ...)

clPlotTheseAverageQuartets(dataset, cex = 1.1, pch = 2,
    col = "black", ...)

clPlotSplits(dataset, tree, cex = 1.1, pch = 2,
    col = CongreveLamsdell2016::clColours, ...)

clPlotTheseAverageSplits(dataset, cex = 1.1, pch = 2, col = "black",
    ...)

clPlotTheseBestAverageSplits(dataset, cex = 1.1, pch = 2,
    col = "black", ...)

clPlotAverageSplits(dataset, cex = 1.1, pch = 2,
    col = CongreveLamsdell2016::clColours, ...)

clPlotBestAverageSplits(dataset, cex = 1.1, pch = 2,
    col = CongreveLamsdell2016::clColours, ...)

Arguments

- **dataset**: Dataset to plot, for example `clBootGcQuartets`.
- **tree**: Integer specifying which tree to plot.
- **cex, pch, ...**: Graphical parameters to pass to `JoinTheDots`.
- **col**: Named vector specifying colours to use to plot each analysis, named to match names(dataset).

Value

Returns **invisible**.

Functions

- `clPlotAverageQuartets`: Plots average across all 100 trees.
- `clPlotTheseAverageQuartets`: Plot average for single dataset across all 100 trees.
- `clPlotSplits`: Splits equivalent of `clPlotQuartets`.
- `clPlotTheseAverageSplits`: Splits equivalent of `clPlotTheseAverageQuartets`.
- `clPlotTheseBestAverageSplits`: Splits equivalent of `clPlotTheseBestAverageQuartets`.
- `clPlotAverageSplits`: Splits equivalent of `clPlotAverageQuartets`.
- `clPlotBestAverageSplits`: Splits equivalent of `clPlotAverageQuartets`. 
Author(s)

Martin R. Smith

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clReferenceTree  Tree topology for matrix simulation

Description

The tree topology used to generate the matrices in clMatrices Congreve & Lamsdell (2016).

Usage

clReferenceTree

Format

A single phylogenetic tree saved as an object of class phylo.

Source

Congreve & Lamsdell (2016).

References


Examples

data(clReferenceTree)
if (requireNamespace('ape', quietly = TRUE)) plot(clReferenceTree)
clResults

Congreve and Lamsdell tree distances

Description
Distance of CL trees from generative tree.

Usage
clBremQuartets
clBremPartitions
clMkvPartitions
clMkvQuartets
clBootFreqPartitions
clBootFreqQuartets
clJackFreqPartitions
clJackFreqQuartets
clBootGcPartitions
clBootGcQuartets
clJackGcPartitions
clJackGcQuartets

Format
An object of class list of length 7.

Details
For each of the 100 matrices generated by Congreve & Lamsdell (2016), I conducted phylogenetic analysis under different methods:

- **Mkv**: using the Markov K model in MrBayes;
- **eq**: using equal weights in TNT;
- **k1, k2, k3, k5, kX**: using implied weights in TNT, with the concavity constant (k) set to 1, 2, 3, 5, or 10;
• **kC**: by taking the strict consensus of all trees recovered by implied weights parsimony analysis under the \(k\) values 2, 3, 5 and 10 (but not 1).

For each analysis, I recorded the strict consensus of all optimal trees, and also the consensus of trees that were suboptimal by a specified degree.

I then calculated, of the total number of quartets or partitions that were resolved in the reference tree, how many were the same or different in the tree that resulted from the phylogenetic analysis, and how many were not resolved in this tree \((r2)\).

The data object contains a list whose elements are named after the methods, as listed above.

Each list entry is a three-dimensional array, whose dimensions are:

1. The suboptimality of the tree. Different measures of node support are employed:
   - **Mkv**: Posterior probabilities, at 2.5% intervals (50%, 52.5%, ..., 97.5%, 100%).
   - **Brem**: Bremer supports: the consensus of all trees that are (equal weights) 0, 1, ..., 19, 20 steps less optimal than the optimal tree (implied weights: the consensus of all trees that are 0.73^(19:0) less optimal than the optimal tree).
   - **Boot**: Bootstrap supports (symmetric resampling, \(p = 0.33\)).
   - **Jack**: Jackknife supports \((p = 0.36)\).

Boot and Jack results are reported both as the frequency of splits among replicates, and using the gc (Groups Present / Contradicted) measure (Goloboff et al. 2003); frequency columns correspond to 100%, 97.5%, 95% ... 0% support; gc columns correspond to 100%, 95%, ... 0% present, 5%, 10%, ... 100% contradicted.

2. Counts of the condition of each quartet or partition:
   - **Q**: The total number of quartets defined on 22 taxa.
   - **N**: The total number of partitions present, counting each tree separately.
   - **P1**: The number of partitions in tree 1 (the reconstructed tree).
   - **P2**: The number of partitions in tree 2 (the generative tree).
   - **s**: The number of quartets or partitions resolved identically in each tree. * **d**: The number of quartets resolved differently in each tree.
   - **d1**: The number of partitions resolved in tree 1, but contradicted by tree 2.
   - **d2**: The number of partitions resolved in tree 2, but contradicted by tree 1.
   - **r1**: The number of partitions or quartets resolved in tree 1 that are neither present in nor contradicted by tree 2.
   - **r2**: The number of partitions or quartets resolved in tree 2 that are neither present in nor contradicted by tree 1.
   - **u**: The number of quartets that are not resolved in either tree.

3. The number of the matrix, from 1 to 100.

**Source**

References


See Also

clMatrices, clReferenceTree.
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