

Package ‘CongreveLamsdell2016’

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Title Distance metrics for trees generated by Congreve and Lamsdell (2016)

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).

URL <https://github.com/ms609/CongreveLamsdell2016>

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

Depends R (>= 3.4.0)

Imports Ternary

Suggests ape,
knitr,
phangorn,
Quartet,
TreeSearch (> 0.2.0),
usethis

Remotes ms609/Quartet

LazyData true

ByteCompile true

VignetteBuilder knitr

RoxygenNote 6.1.1

Roxygen list(markdown = TRUE)

R topics documented:

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| | |
|------|--|
| clCI | <i>Congreve Lamsdell consistency indices</i> |
|------|--|

Description

Congreve Lamsdell consistency indices

Usage

clCI

Format

An object of class `numeric` of length 100.

| | |
|-----------|-------------------------------------|
| clColours | <i>Default colours for analyses</i> |
|-----------|-------------------------------------|

Description

Default colours for analyses

Usage

clColours

Format

An object of class `character` of length 8.

clInitializeTernaryQuarts

Initialize ternary plots for quartet plotting

Description

Initialize ternary plots for quartet plotting

Usage

```
clInitializeTernaryQuarts(zoom = 1, padding = 0.1, gridLines = 10,
  fontSize = 1, gridCol = "#EBEBEB", backgroundCol = "#FBFBFD",
  xLim = c(0, 1/zoom) - 0.01, yLim = c(0.5 - (1/zoom), 0.5))
```

```
clInitializeTernarySplits(fontSize = 1, xLim = NULL, yLim = NULL,
  gridCol = "#EBEBEB", backgroundCol = "#FBFBFD", padding = 0.1)
```

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. |

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

<http://datadryad.org/resource/doi:10.5061/dryad.7dq0j>

References

- Congreve, C. R. & Lamsdell, J. C. (2016). Implied weighting and its utility in palaeontological datasets: a study using modelled phylogenetic matrices. *Palaeontology* 59(3), 447–465. doi: [10.1111/pala.12236](https://doi.org/10.1111/pala.12236).
- Congreve, C. R. & Lamsdell, J. C. (2016). Data from: Implied weighting and its utility in palaeontological datasets: a study using modelled phylogenetic matrices. Dryad Digital Repository. doi: [10.5061/dryad.7dq0j](https://doi.org/10.5061/dryad.7dq0j).

clPlotQuartets

Plot results

Description

Plot results

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 <code>names(dataset)</code> . |

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

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, C. R. & Lamsdell, J. C. (2016). Implied weighting and its utility in palaeontological datasets: a study using modelled phylogenetic matrices. *Palaeontology* 59(3), 447–465. doi: [10.1111/pala.12236](https://doi.org/10.1111/pala.12236).

References

- Congreve, C. R. & Lamsdell, J. C. (2016). Implied weighting and its utility in palaeontological datasets: a study using modelled phylogenetic matrices. *Palaeontology* 59(3), 447–465. doi: [10.1111/pala.12236](https://doi.org/10.1111/pala.12236).
- Congreve, C. R. & Lamsdell, J. C. (2016). Data from: Implied weighting and its utility in palaeontological datasets: a study using modelled phylogenetic matrices. Dryad Digital Repository. doi: [10.5061/dryad.7dq0j](https://doi.org/10.5061/dryad.7dq0j).

Examples

```
library(ape) # Contains tree plotting functions
data(clReferenceTree)
plot(clReferenceTree)
```

clResults

Congreve and Lamsdell tree distances

Description

Distance of CL trees from generative tree.

Usage

```
clBremQuartets
clBremPartitions
clMkvPartitions
clMkvQuartets
clBootFreqPartitions
clBootFreqQuartets
clJackFreqPartitions
```

cIJackFreqQuartets

cIBootGcPartitions

cIBootGcQuartets

cIJackGcPartitions

cIJackGcQuartets

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:

- markov: Using the Markov K model in MrBayes.
- equal: Using equal weights in TNT.
- implied1, implied2, implied3, implied5, implied10: Using implied weights in TNT, with the concavity constant (k) set to 1, 2, 3, 5, or 10
- impliedC: 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: * Mk: Posterior probabilities, at 2.5 97.5 * 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)
2. The number of quartets or partitions in total, the same, different, resolved in the estimated tree but not the generative tree (= 0), resolved in the generative tree but not the estimated tree
3. The number of the matrix, from 1 to 100.

Source

Congreve, C. R. & Lamsdell, J. C. (2016). Implied weighting and its utility in palaeontological datasets: a study using modelled phylogenetic matrices. *Palaeontology* 59(3), 447–465. doi: [10.1111/pala.12236](https://doi.org/10.1111/pala.12236).

References

Goloboff, P. A., J. S. Farris, M. Källersjö, B. Oxelman, M. J. Ramírez, and C. A. Szumik. 2003. Improvements to resampling measures of group support. *Cladistics* 19, 324–332. doi: [10.1016/S07483007\(03\)000604](https://doi.org/10.1016/S07483007(03)000604).

See Also

[clMatrices](#), [clReferenceTree](#).

SplitsToPoints

Convert splits data to ternary-plottable points

Description

Convert splits data to ternary-plottable points

Usage

```
SplitsToPoints(itemData)
```

Arguments

itemData A line from clBootGcPartitions or equivalent

Value

Number of partitions resolved in tree 2 only, different, and same in both trees, numbered ready to appear on a ternary plot.

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