

# Package ‘CongreveLamsdell2016’

December 10, 2018

**Version** 1.0.0

**Date** 2018-12-10

**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> |
|------|--|

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**Description**

Congreve Lamsdell consistency indices

**Usage**

clCI

**Format**

An object of class `numeric` of length 100.

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

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**Description**

Default colours for analyses

**Usage**

clColours

**Format**

An object of class `character` of length 8.

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clInitializeTernaryQuarts

*Initialize ternary plots for quartet plotting*


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### 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

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clPhyDat

*100 simulated data matrices*


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### 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).

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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 <a href="#">clBootGcQuartets</a>                 |
| tree          | Integer specifying which tree to plot   |
| cex, pch, ... | Graphical parameters to pass to <a href="#">JoinTheDots</a>                   |
| col           | Named vector specifying colour in which to plot each analysis                 |
| col           | Vector specifying colours to use for plotting, 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 | <i>Tree topology for matrix simulation</i> |
|-----------------|--|

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### 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
```

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:

- 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](#).

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|----------------|--|
| SplitsToPoints | <i>Convert splits data to ternary-plottable points</i> |
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**Description**

Convert splits data to ternary-plottable points

**Usage**

```
SplitsToPoints(itemData)
```

**Arguments**

|          |   |
|----------|---|
| itemData | A line from <code>clBootGcPartitions</code> 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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