Package ‘treestructure’

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Type Package

Title Detect Population Structure Within Phylogenetic Trees

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Description Algorithms for detecting population structure from the history of coalescent events recorded in phylogenetic trees. This method classifies each tip and internal node of a tree into disjoint sets characterized by similar coalescent patterns. The methods are described in Volz, E., Wiuf, C., Grad, Y., Frost, S., Dennis, A., & Didelot, X. (2020) <doi:10.1093/sysbio/syaa009>.

License GPL (>= 2)

Suggests ggtree,ggplot2,knitr

Imports ape (>= 5.0)

LinkingTo Rcpp

VignetteBuilder knitr

RoxygenNote 6.1.0

NeedsCompilation yes

Repository CRAN

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Contents

`plot.TreeStructure` *Plot TreeStructure tree with cluster and partition variables*

Description

Plot TreeStructure tree with cluster and partition variables

Usage

```
## S3 method for class 'TreeStructure'
plot(x, use_ggtree = TRUE, ...)
```

Arguments

`x`	A TreeStructure object
`use_ggtree`	Toggle ggtree or ape plotting behaviour
`...`	Additional arguments passed to ggtree or ape::plot.phylo

`trestruct` *Detect cryptic population structure in time trees*

Description

Detect cryptic population structure in time trees

Usage

```
trestruct(tre, minCladeSize = 25, minOverlap = -Inf, nsim = 1000,
  level = 0.01, ncpu = 1, verbosity = 1, debugLevel = 0)
```

Arguments

`tre`	A tree of type ape::phylo. Must be rooted and binary.
`minCladeSize`	All clusters within parititon must have at least this many tips.
`minOverlap`	Threshold time overlap required to find splits in a clade
`nsim`	Number of simulations for computing null distribution of test statistics
`level`	Significance level for finding new split within a set of tips
`ncpu`	If >1 will compute statistics in parallel using multiple CPUs
`verbosity`	If > 0 will print information about progress of the algorithm
`debugLevel`	If > 0 will produce additional data in return value

Details

Estimates a partition of a time-scaled tree by contrasting coalescent patterns. The algorithm is premised on a Kingman coalescent null hypothesis and a test statistic is formulated based on the rank sum of node times in the tree.

Value

A TreeStructure object which includes cluster and partitition assignment for each tip of the tree.

References

E.M. Volz, Wiuf, C., Grad, Y., Frost, S., Dennis, A., Didelot, X.D. (2020) Identification of hidden population structure in time-scaled phylogenies.

Author(s)

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Examples

```
tree <- ape::rcoal(50)
struct <-  trestruct( tree )
```

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