Package ‘treestructure’

February 17, 2020

Type Package
Title Detect Population Structure Within Phylogenetic Trees
Version 0.1.0
Date 2020-01-20
Author Erik Volz
Maintainer Erik Volz <erik.volz@gmail.com>
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
Date/Publication 2020-02-17 15:20:02 UTC

R topics documented:

plot.TreeStructure .......................................................... 2
treestruct ................................................................. 2

Index 4
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

treestruct  
Detect cryptic population structure in time trees

Description
Detect cryptic population structure in time trees

Usage
treestruct(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 partition 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 partition assignment for each tip of the tree.

References


Author(s)

Erik M Volz <erik.volz@gmail.com>

Examples

tree <- ape::rcoal(50)
struct <- treestruct( tree )
Index

plot.TreeStructure, 2

treestruct, 2