

Package ‘MSCquartets’

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Title Analyzing gene trees through quartets under the multispecies coalescent model

Version 0.5.3

Description A package for analyzing and using quartets displayed on a collection of gene trees, primarily to make inferences about the species tree or network under the multispecies coalescent (MSC) model.

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Rdpack

RdMacros Rdpack

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dataGeneTreeSample	<i>Simulated gene tree dataset from species tree</i>
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Description

A text file dataset containing 1000 gene trees on 9 taxa simulated under the MSC on a species tree

Format

A text file with 1000 metric Newick gene trees on the taxa t1-t9

Details

This simulated dataset was produced by SimPhy (Mallo et al. 2016), using the species tree

```
((((t5:5000,t6:5000):5000,t4:10000):2500,t7:12500):7500,((t8:3000,t9:3000):5000,((t1:4000,t2:4000):2500,t3:6500):1500):12000);
```

with a population size of 10,000 throughout the tree.

File is accessed as `system.file("extdata", "dataGeneTreeSample", package="MSCquartets")`, for example via the ape command:

```
gts=read.tree(file = system.file("extdata", "dataGeneTreeSample", package="MSCquartets"))
```

References

Mallo D, De Oliveira Martins L, Posada D (2016). "SimPhy: Phylogenomic Simulation of Gene, Locus, and Species Trees." *Syst. Biol.*, **65**(2), 334-344. doi: [10.1093/sysbio/syv082](https://doi.org/10.1093/sysbio/syv082), <http://dx.doi.org/10.1093/sysbio/syv082>.

dataHeliconiusMartin	<i>Heliconius gene tree dataset</i>
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Description

A text file dataset for *Heliconius* butterflies containing 2909 gene trees on 7 taxa, with 4 individuals sampled for each of 3 of the taxa, for a total of 16 leaves per gene tree. This is a subset of the data of Martin et al. (2013).

Format

A text file with 2909 metric Newick gene trees each with 16 leaves labelled:

chioneus.553, chioneus.560, chioneus.564, chioneus.565,
ethilla.67, hecale.273, melpomeneFG.13435, melpomeneFG.9315,
melpomeneFG.9316, melpomeneFG.9317, pardalinius.371, rosina.2071,
rosina.531, rosina.533, rosina.546, sergestus.202

Details

File is accessed as `system.file("extdata", "dataHeliconiusMartin", package="MSCquartets")`, for example via the ape command:

```
gts = read.tree(file=system.file("extdata", "dataHeliconiusMartin", package="MSCquartets"))
```

Source

<http://datadryad.org/resource/doi:10.5061/dryad.dk712>

References

Martin S, K.K. D, Nadeau N, Salazar C, Walters J, Simpson F, Blaxter M, Manica A, Mallet J, Jiggins C (2013). "Genome-wide evidence for speciation with gene flow in *Heliconius* butterflies." *Genome Res*, **23**, 1817-1828.

dataYeastRokas	<i>Yeast gene tree dataset</i>
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Description

A text file dataset for Yeast containing 106 gene trees on 8 taxa (7 yeasts and 1 outgroup). This is a subset of the data of Rokas et al. (2003).

Format

A text file with 106 topological Newick gene trees on the taxa: Sbay, Scas, Scer, Sklu, Skud, Smik, Spar, and Calb (outgroup)

Details

File is accessed as `system.file("extdata", "dataYeastRokas", package="MSCquartets")`, for example via the ape command:

```
gts=read.tree(file = system.file("extdata", "dataYeastRokas", package="MSCquartets"))
```

Source

<https://wiki.rice.edu/confluence/download/attachments/8898533/yeast.trees?version=1&modificationDate=1360603275797&api=v2>

References

Rokas A, Williams B, Carrol S (2003). "Genome-scale approaches to resolving incongruence in molecular phylogenies." *Nature*, **425**, 798–804.

estimateEdgeLengths	<i>Estimate edge lengths on a species tree from gene tree quartet counts</i>
---------------------	--

Description

Estimate edge lengths, in coalescent units, on a species tree from a table of all resolved quartet counts from a collection of gene trees.

Usage

```
estimateEdgeLengths(tree, rqt, terminal = 1, method = "simpleML",  
  lambda = 1/2)
```

Arguments

tree	a phylo object, giving a resolved tree on which to estimate edge lengths
rqt	a resolved quartet table, as from <code>quartetTableResolved</code> , in which all taxa on tree appear
terminal	an edge length to assign to terminal edges, whose lengths cannot be estimated
method	"simpleML" or "simpleBayes",
lambda	a positive parameter for the "simpleBayes" method

Details

While the argument tree may be rooted or unrooted, metric or topological, only its unrooted topology will be used.

Counts of quartets for all those quartets which define a single edge on the tree (i.e., whose internal edge is the single edge on the unrooted input tree) are summed, and from this an estimate of the branch length is computed. If method= "simpleML" this is the maximum likelihood estimate. If method="simpleBayes" this is the Bayesian estimate of Theorem 2 of Sayyari and Mirarab (2016), using parameter lambda. Using lambda=1/2 gives a flat prior on [1/3,1] for the probability of the quartet displayed on the species tree.

These methods are referred to as 'simple' since they use only the quartets defining a single edge of the species tree. Quartets with central edges composed of several edges in the species tree are ignored.

Note that branch length estimates may be 0 (if the count for the quartet displayed on the input tree is not dominant), positive, or Inf (if the counts for quartet topologies not displayed on the input tree are all 0, and method="simpleML").

Value

an unrooted metric tree with the same topology as tree

References

Sayyari E, Mirarab S (2016). "Fast Coalescent-Based Computation of Local Branch Support from Quartet Frequencies." *Mol. Biol. Evol.*, **33**(7), 1654-1668.

Examples

```
gtrees=read.tree(file=system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
taxanames=taxonNames(gtrees)
QT=quartetTable(gtrees,taxanames)
RQT=quartetTableResolved(QT)
DQT=quartetTableDominant(RQT)
tree=QDS(DQT)
write.tree(tree)
metricMTree=estimateEdgeLengths(tree,RQT,method="simpleML")
write.tree(metricMTree)
metricBTree=estimateEdgeLengths(tree,RQT,method="simpleBayes")
write.tree(metricBTree)
```

HolmBonferroni

Apply Holm-Bonferroni method to adjust for multiple tests

Description

Apply the Holm-Bonferroni method to adjust for multiple hypothesis tests performed on quartets from a data set of gene trees.

Usage

```
HolmBonferroni(pTable, model, alpha = 0.05)
```

Arguments

pTable	a table of quartets with p-values, as computed by <code>quartetTreeTestInd</code> or <code>quartetStarTestInd</code>
model	one of "T1", "T3", or "star", where pTable contains a column p_model of p-values
alpha	a critical value, for rejection of adjusted p-values less than or equal to alpha

Details

When p-values are computed for each quartet using `quartetTreeTestInd` or `quartetStarTestInd`, multiple comparisons are being done for one dataset. The Holm-Bonferroni method (Holm 1979) adjusts these p-values upward, controlling the familywise error rate. The probability of at least one false discovery (rejection of the null hypothesis) is no more than the significance level.

Value

the same table, with rows reordered, and 2 new columns of 1) adjusted p-values, and 2) "Y" or "N" for indicating "reject" or "fail to reject"

References

Holm S (1979). "A simple sequentially rejective multiple test procedure." *Scand. J. Statist.*, **6**(2), 65-70.

See Also

[quartetTreeTestInd](#), [quartetStarTestInd](#)

Examples

```
gtrees=read.tree(file=system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
taxanames=taxonNames(gtrees)
QT=quartetTable(gtrees,taxanames)
RQT=quartetTableResolved(QT)
pTable=quartetTreeTestInd(RQT,"T3")
pTable[1:10,]
HBpTable=HolmBonferroni(pTable,"T3",.05)
HBpTable[1:10,]
```

MSCquartets

Multispecies Coalescent Model Quartet Package

Description

A package for analyzing quartets displayed on gene trees, under the multispecies coalescent (MSC) model.

Details

This package contains routines to analyze a collection of gene trees through the displayed quartets on them.

Recall that a quartet count concordance factor (qcCF) for a set of 4 taxa is the triple of counts of the three possible resolved quartet trees on those taxa across some set of gene trees. The major routines in this package can:

1. Tabulate all qcCFs for a collection of gene trees.
2. Perform hypothesis tests of whether one or more qcCFs are consistent with the MSC model on a species tree (Mitchell et al. 2019).
3. Infer a species tree using the qcCFs via the QDC and WQDC methods (Rhodes 2019; Yourdkhani and Rhodes 2020).
4. Infer a level-1 species network via the NANUQ method (Allman et al. 2019).

As discussed in the cited works, the inference methods for species trees and networks are statistically consistent under the MSC and Network MSC respectively.

Several gene tree data sets, simulated and empirical, are included.

References

- Rhodes J (2019). “Topological metrizations of trees, and new quartet methods of tree inference.” *IEEE/ACM Trans. Comput. Biol. Bioinform.*, **vol(num)**, pp-qq.
- Mitchell J, Allman E, Rhodes J (2019). “Hypothesis testing near singularities and boundaries.” *Electron. J. Statist.*, **13**(1), 2150-2193.
- Allman E, Baños H, Rhodes J (2019). “NANUQ: A method for inferring species networks from gene trees under the coalescent model.” *Algorithms for Molecular Biology*, **vol(num)**, pp-qq.
- Yourdkhani S, Rhodes J (2020). “Inferring species trees from weighted quartets.” *unknown journal*, **vol(num)**, pp-qq.

NANUQ

Apply NANUQ network inference algorithm to gene tree data

Description

Apply the NANUQ algorithm of Allman et al. (2019) to infer a hybridization network from a collection of gene trees, under the level-1 network multispecies coalescent (NMSC) model.

Usage

```
NANUQ(genedata, outfile = "NANUQdist", alpha = 0.05, beta = 0.95,
      taxanames = NULL, plot = TRUE)
```

Arguments

genedata	gene tree data that may be supplied in one of 3 ways: <ol style="list-style-type: none"> 1. as a character string giving the name of a file containing Newick gene trees, 2. as a multiPhylo object containing the gene trees, or 3. as a table of quartets on the gene trees, as produced by a previous call to NANUQ or quartetTableResolved, which has columns only for taxa, quartet counts, and possibly p_T3 and p_star.
outfile	a character string giving an output file name stub, to which will be appended an alpha and beta value and ".nex", for saving the NANUQ distance matrix; if NULL then distance matrix not computed
alpha	a value or vector of significance levels for judging p-values testing a null hypothesis of no hybridization for each quartet; a smaller value applies a more liberal test for a tree (more trees), hence a stricter requirement for suspecting hybridization
beta	a value or vector of significance levels for judging p-values testing a null hypothesis of a star tree for each quartet; a smaller value applies a more liberal test for a star tree (more polytomies), hence a stricter requirement for suspecting a resolved tree; if vectors, alpha and beta must have the same length
taxanames	if genedata is a file or a multiPhylo object, a vector of some of the taxa names on the gene trees which will be the only ones analyzed, if NULL all taxa on the first gene tree are used; if genedata is a quartet table, this argument is ignored and all taxa in the table are used
plot	TRUE produces simplex plots of hypothesis test results, FALSE omits plots

Details

This function

1. counts displayed quartets across gene trees to form quartet count concordance factors (qcCFs),
2. applies appropriate hypothesis tests to judge quartet qcCFs as representing putative hybridization, resolved trees, or unresolved (star) trees using alpha and beta as significance levels, and
3. computes the appropriate distance table under the level-1 network quartet distance, writing it to a file.

The distance table file can then be opened in the external software SplitsTree or within R using the package phangorn to obtain a circular split system under the Neighbor-Net algorithm, which is then depicted as a splits graph. The splits graph should be interpreted via the theory of Allman et al. (2019) to infer the level-1 species network, or to conclude the data does not arise from the NMSC on such a network.

If alpha and beta are vectors, they must have the same length k. Then the i-th entries are paired to produce k plots and k output files. This is equivalent to k calls to NANUQ with scalar values of alpha and beta.

A call of NANUQ with genedata given as a table previously output from NANUQ is equivalent to a call of NANUQdist. If genedata is a table previously output from quartetTableResolved which lacks columns of p-values for hypothesis tests, these will be appended to the table output by NANUQ.

If plots are produced, each point represents an empirical quartet concordance factor, color-coded to represent test results

Usually, an initial call to NANUQ will not give a good analysis, as values of alpha and beta are likely to need some adjustment based on inspecting the data. Saving the returned table from NANUQ will

allow for the results of the time-consuming computation of quartet counts and p-values to be saved, for input to further calls of NANUQ with new choices of alpha and beta.

Value

a table of quartets and p-values for judging fit to the MSC on quartet trees (returned invisibly); this table can be used as input to NANUQ or NANUQdist with new choices of alpha and beta, without re-tallying quartets on the gene trees. A distance table to be used as input for SplitsTree is written to a nexus file.

References

Allman E, Baños H, Rhodes J (2019). “NANUQ: A method for inferring species networks from gene trees under the coalescent model.” *Algorithms for Molecular Biology*, **vol**(num), pp-qq.

See Also

[quartetTable](#), [quartetTableDominant](#), [quartetTreeTestInd](#), [quartetStarTestInd](#), [NANUQdist](#), [quartetTestPlot](#), [pvalHist](#)

Examples

```
pTable=NANUQ(system.file("extdata", "dataYeastRokas",package="MSCquartets"), alpha=.0001, beta=.95)
NANUQ(pTable, alpha=.05, beta=.95)
# The distance table was written to an output file for opening in SplitsTree.
# Alternately, to use the experimental phangorn implementation of NeighborNet
# within R enter the following additional lines:
dist=NANUQdist(pTable, alpha=.05, beta=.95)
nn=neighborNet(dist)
par(mai=c(0,0,0,0))
plot(nn,"2D")
```

NANUQdist

Compute NANUQ distance and write to file

Description

Computes the quartet distance tables for the NANUQ algorithm of Allman et al. (2019), using precomputed p-values for quartets, for each of several levels specified. Distance tables are written to files, in nexus format.

Usage

```
NANUQdist(pTable, outfile = "NANUQdist", alpha = 0.05, beta = 0.95,
plot = TRUE)
```

Arguments

pTable	a table of quartets and p-values, as previously computed by NANUQ, or by both <code>quartetTreeTestInd</code> and <code>quartetStarTestInd</code> , with columns "p_T3" and "p_star"
outfile	a character string giving an output file name stub, to which will be appended an alpha and beta value and ".nex", for saving the distance matrix; if NULL then the distance matrix is not written to a file
alpha	a value or vector of significance levels for judging p-values testing a null hypothesis of no hybridization for each quartet; a smaller value applies a more liberal test for a tree (more trees), hence a stricter requirement for suspecting hybridization
beta	a value or vector of significance levels for judging p-values testing a null hypothesis of a star tree for each quartet; a smaller value applies a more liberal test for a star tree (more polytomies), hence a stricter requirement for suspecting a resolved tree; if vectors, alpha and beta must have the same length
plot	TRUE produces simplex plots of hypothesis tests, FALSE omits plots

Details

If plots are produced, each point represents an empirical quartet concordance factor, color-coded to represent test results giving interpretation as network, resolved tree, or star tree.

If alpha and beta are vectors, they must be of the same length k. Then the i-th entries are paired to produce k plots and k distance tables/output files. This is equivalent to k calls to NANUQdist with scalar values of alpha and beta.

Value

a NANUQ distance table, or a list of such tables if alpha and beta are vectors (returned invisibly)

References

Allman E, Baños H, Rhodes J (2019). "NANUQ: A method for inferring species networks from gene trees under the coalescent model." *Algorithms for Molecular Biology*, **vol**(num), pp-qq.

See Also

[NANUQ](#), [quartetTreeTestInd](#), [quartetStarTestInd](#)

Examples

```
pTable=NANUQ(system.file("extdata","dataYeastRokas",package="MSCquartets"), alpha=.0001, beta=.95)
NANUQdist(pTable, alpha=.05, beta=.95)
```

nexusDist	<i>Write a distance table to a file in nexus format</i>
-----------	---

Description

Write a distance table to a file in nexus format.

Usage

```
nexusDist(distMatrix, outfilename)
```

Arguments

distMatrix	a square matrix giving a distance table, with rows and columns labeled by taxon names
outfilename	the name of an output file

Value

None

Examples

```
gtrees=read.tree(file=system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
QT=quartetTable(gtrees)
RQT=quartetTableResolved(QT)
DQT=quartetTableDominant(RQT)
Dist=quartetDist(DQT)
nexusDist(Dist,"outputfile")
```

powerDivStat	<i>Power divergence statistic of Cressie & Read</i>
--------------	---

Description

Computes any of the family of power-divergence statistics for multinomial data of Cressie and Read (1984), to compare observed and expected counts. Includes Likelihood Ratio and Chi-squared statistics as special cases.

Usage

```
powerDivStat(obs, expd, lambda)
```

Arguments

obs	observation vector
expd	expected vector
lambda	statistic parameter (e.g., 0=Likelihood Ratio, 1=Chi-squared)

Value

value of statistic

References

Cressie N, Read T (1984). “Multinomial Goodness-Of-Fit Tests.” *J. Royal Stat. Soc. B*, **46**(3), 440-464.

Examples

```
obs=c(10,20,30)
expd=c(20,20,20)
powerDivStat(obs,expd,0)
```

pvalHist	<i>Plot histogram of log p-values in table</i>
----------	--

Description

Graphical exploration of extreme p-values from quartet hypothesis tests, to aid in choosing critical values for hypothesis tests. Log base 10 of p-values exceeding some minimum are plotted, to explore gaps in the tail of the distribution.

Usage

```
pvalHist(pTable, model, pmin = 0)
```

Arguments

pTable	a quartet table with p-values such as from quartetTreeTestInd or from quartetStarTestInd
model	one of "T1", "T3", or "star", where pTable contains a column p_model of p-values
pmin	include only p-values above pmin

Details

When exploring possible critical values for the hypothesis tests in the NANUQ algorithm, use model= "T3" to choose values for alpha which distinguishes treelikeness from hybridization, and model= "star" to choose values for beta which distinguishes polytomies from resolved trees. In general, alpha should be chosen to be small and beta to be large so that most quartets are interpreted as resolved trees.

See Also

[NANUQ](#), [NANUQdist](#)

Examples

```
pTable=NANUQ(system.file("extdata","dataYeastRokas",package="MSCquartets"), alpha=0, beta=.95)
pvalHist(pTable,"T3")
NANUQdist(pTable, alpha=10^-5, beta=.95)
NANUQdist(pTable, alpha=10^-3, beta=.95)
```

QDC	<i>Compute Quartet Distance Consensus tree from gene tree data</i>
-----	--

Description

Compute the Quartet Distance Consensus (Rhodes 2019) estimate of an unrooted topological species tree from gene tree data.

Usage

```
QDC(genetreedata, taxanames = NULL, omit = FALSE, metric = FALSE)
```

Arguments

genetreedata	gene tree data either in one of 3 forms: <ol style="list-style-type: none"> 1. a character string giving the name of a file containing gene trees in Newick, 2. a multiPhylo object containing gene trees, or 3. a resolved quartet table, such as produced by quartetTableResolved
taxanames	list of taxa on which to construct tree; can be subset of those on trees; if NULL, uses taxa on first gene tree; this argument is ignored if genetreedata is a resolved quartet table
omit	TRUE ignores unresolved quartets, FALSE treats them as 1/3 of each resolution.
metric	if FALSE return topological tree; if TRUE return metric tree with edge lengths estimated by estimateEdgeLengths with lambda=0.

Details

This function is a wrapper which performs the steps of reading in a collection of gene trees, tallying quartets, computing the quartet distance between taxa, building a tree which consistently estimates the unrooted species tree topology under the MSC, and then possibly estimating edge lengths using the "simpleML" method.

Value

an unrooted topological tree of type phylo

References

Rhodes J (2019). "Topological metrizations of trees, and new quartet methods of tree inference." *IEEE/ACM Trans. Comput. Biol. Bioinform.*, **vol**(num), pp-qq.

See Also

[quartetTable](#), [quartetTableResolved](#), [quartetTableDominant](#), [quartetDist](#), [QDS](#), [WQDC](#), [WQDCrecursive](#), [estimateEdgeLengths](#)

Examples

```
stree=QDC(system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
write.tree(stree)
streeMetric=QDC(system.file("extdata","dataGeneTreeSample",package="MSCquartets"), metric=TRUE)
write.tree(streeMetric)
```

QDS	<i>Compute Quartet Distance Supertree</i>
-----	---

Description

Apply the Quartet Distance Supertree method of Rhodes (2019) to a table specifying a collection of quartets on n taxa.

Usage

```
QDS(dqt, method = fastme.bal)
```

Arguments

- dqt an (n choose 4) x n (or n+1) matrix of form output by [quartetTableDominant](#); (Note: the n+1th column of dqt is ignored)
- method tree building method function ([fastme.bal](#), [nj](#), etc.)

Details

This function is a wrapper which runs [quartetDist](#) and then builds a tree.

Value

An unrooted metric tree of type "phylo". Edge lengths are not in interpretable units.

References

Rhodes J (2019). "Topological metrizations of trees, and new quartet methods of tree inference." *IEEE/ACM Trans. Comput. Biol. Bioinform.*, **vol**(num), pp-qq.

See Also

[quartetTableDominant](#), [quartetDist](#), [QDC](#), [WQDS](#), [WQDC](#), [WQDCrecursive](#)

Examples

```
gtrees=read.tree(file=system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
tnames=taxonNames(gtrees)
QT=quartetTable(gtrees,tnames)
RQT=quartetTableResolved(QT)
DQT=quartetTableDominant(RQT)
tree=QDS(DQT)
write.tree(tree)
```

quartetDist

*Compute quartet distance between taxa***Description**

Compute the Quartet Distance of Rhodes (2019) from a table specifying a collection of quartets on n taxa.

Usage

```
quartetDist(dqt)
```

Arguments

dqt an $(n \text{ choose } 4) \times n$ (or $n+1$) matrix of form output by `quartetTableDominant`;
(Note: the $n+1$ th column of dqt is ignored.)

Value

a pairwise distance matrix on n taxa

References

Rhodes J (2019). "Topological metrizations of trees, and new quartet methods of tree inference." *IEEE/ACM Trans. Comput. Biol. Bioinform.*, **vol**(num), pp-qq.

See Also

[quartetTableDominant](#), [QDS](#), [QDC](#), [quartetWeightedDist](#)

Examples

```
gtrees=read.tree(file=system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
tnames=taxonNames(gtrees)
QT=quartetTable(gtrees,tnames)
RQT=quartetTableResolved(QT)
DQT=quartetTableDominant(RQT)
Dist=quartetDist(DQT)
tree=NJ(Dist)
write.tree(tree)
```

quartetNetworkDist	<i>Compute network quartet distance between taxa</i>
--------------------	--

Description

Produce network quartet distance table for the NANUQ algorithm, from a table of quartets and p-values, and specified levels of quartet hypothesis tests. The network quartet distance, which is described more fully by Allman et al. (2019), generalizes the quartet distance of Rhodes (2019).

Usage

```
quartetNetworkDist(pTable, alpha0, beta0)
```

Arguments

pTable	a table of quartets and p-values, as computed by NANUQ, or <code>quartetTreeTestInd</code> and <code>quartetStarTestInd</code>
alpha0	a scalar significance level for judging p_T3 indicating hybridization on quartet; smaller value gives fewer hybridization calls
beta0	a scalar significance level for judging p_star indicating star quartet tree; smaller value gives fewer resolved tree calls

Value

a distance table

References

Allman E, Baños H, Rhodes J (2019). “NANUQ: A method for inferring species networks from gene trees under the coalescent model.” *Algorithms for Molecular Biology*, **vol(num)**, pp-qq.

Rhodes J (2019). “Topological metrizations of trees, and new quartet methods of tree inference.” *IEEE/ACM Trans. Comput. Biol. Bioinform.*, **vol(num)**, pp-qq.

See Also

[NANUQ](#), [NANUQdist](#)

quartetStarTest	<i>Hypothesis test for quartet counts fitting a star tree under the MSC</i>
-----------------	---

Description

Perform hypothesis test for star tree for a vector of quartet counts to fit expected frequencies of (1/3,1/3,1/3). The test performed is a standard chi-square.

Usage

```
quartetStarTest(obs)
```


Arguments

obs vector of 3 counts of resolved quartet frequencies

Value

p-value

Examples

```
obs=c(16,72,12)
quartetStarTest(obs)
```

quartetStarTestInd	<i>Multiple independent hypothesis tests for gene quartet counts fitting a star species tree under the MSC</i>
--------------------	--

Description

Perform hypothesis test for star species tree for all quartet counts in an input table, as if the quartets are independent.

Usage

```
quartetStarTestInd(rqt)
```

Arguments

rqt Table of resolved quartet counts, as produced by `quartetTableResolved`, or `quartetTreeTestInd`

Details

This function assumes all quartets are resolved. The test performed is described in `quartetStarTest`.

Value

The same table as the input `rqt` with column "p_star" appended, containing p-values for judging fit to MSC on a star tree

See Also

[quartetStarTest](#), [quartetTreeTest](#), [quartetTreeTestInd](#), [quartetTableResolved](#), [quartetTestPlot](#)

Examples

```
gtrees=read.tree(file=system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
taxanames=taxonNames(gtrees)
QT=quartetTable(gtrees,taxanames)
RQT=quartetTableResolved(QT)
pTable=quartetStarTestInd(RQT)
quartetTablePrint(pTable)
```

quartetTable

Produce table of counts of quartets displayed on trees

Description

Compiles table of counts of topological quartets displayed on a collection of trees.

Usage

```
quartetTable(trees, taxonnames = NULL, epsilon = 0, random = 0)
```

Arguments

trees	multi phylo object containing un/rooted metric/topological trees
taxonnames	vector of n names of taxa of interest; if NULL then taken from taxa on trees[[1]]
epsilon	minimum for branch lengths to be treated as non-zero
random	number of random subsets of 4 taxa to consider; if 0, use all n choose 4 subsets

Details

The taxa on the trees may be any set overlapping with taxonnames. Branch lengths of non-negative size less than or equal to epsilon are treated as zero, giving polytomies.

Error if any branch length <0; Warnings if some of taxonnames are missing on some trees, or if some 4-taxon set is on no trees.

If random>0, then for efficiency it should be much smaller than the number of possible 4 taxon subsets.

Value

A (n choose 4)x(n+4) matrix (or (random)x(n+4) matrix) encoding 4 taxon subsets of taxonnames and counts of each of the quartets 12|34, 13|24, 14|23, 1234 across the trees. Columns are labeled by taxa names and quartet names("12|34", etc.). 1s and 0s in taxon columns indicate the taxa in quartet. Quartet 12|34 means first and second indicated taxa form cherry, 13|24 means first and third form cherry, 14|23 means first and fourth form cherry, and 1234 means the quartet is unresolved

See Also

[quartetTableResolved](#), [quartetTableDominant](#)

Examples

```
gtrees=read.tree(file=system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
tnames=taxonNames(gtrees)
QT=quartetTable(gtrees,tnames)
RQT=quartetTableResolved(QT)
DQT=quartetTableDominant(RQT)
```

quartetTableCollapse *Produce small quartet table by combining some taxa*

Description

Form a smaller resolved quartet table by lumping some taxa into a composite taxon.

Usage

```
quartetTableCollapse(rqt, taxaA, taxaB)
```

Arguments

rqt	a resolved quartet table, as from <code>quartetTableResolved</code>
taxaA	a vector of taxon names in rqt to be included in the output table
taxaB	a vector of taxon names in rqt to form new composite taxon in the output table

Details

This function is needed for the recursive calls in `WQDSrec`. It should only be applied to a resolved quartet table which includes counts for all possible quartets on the taxa (though counts can be zero).

Value

a resolved quartet table with $\text{length}(\text{taxaA})+1$ taxa. The composite taxon is named as the concatenation of the sorted names in `taxaB`

See Also

[WQDCrecursive](#)

quartetTableDominant *Produce table of dominant quartets, with estimates of internal edge lengths*

Description

Converts table of counts of resolved quartets on n taxa to show only dominant one, with maximum likelihood estimate of internal edge weight under the MSC.

Usage

```
quartetTableDominant(rqt, bigweights = "infinite")
```

Arguments

rqt	a table, as produced by <code>quartetTableResolved</code> of size $(n \text{ choose } 4) \times (n+3)$;
bigweights	"infinite" or "finite", to indicate whether the weight (internal edge length) of a quartet for which only one topology appears is given as Inf or a finite, but large, numerical value

Value

An $(n \text{ choose } 4) \times (n+1)$ array with dominant quartet topology encoded by 1,1,-1,-1 in taxon columns, with signs indicating cherries. Column "weight" contains the maximum likelihood estimate, under MSC model on a 4-taxon tree, of the quartets' central edge lengths, in coalescent units.

See Also

[quartetTable](#), [quartetTableResolved](#)

Examples

```
gtrees=read.tree(file=system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
tnames=taxonNames(gtrees)
QT=quartetTable(gtrees, tnames)
RQT=quartetTableResolved(QT)
DQT=quartetTableDominant(RQT)
```

quartetTablePrint	<i>Print a quartet table with nice formatting</i>
-------------------	---

Description

Print a quartet table with the taxa in each quartet shown by name.

Usage

```
quartetTablePrint(qt)
```

Arguments

qt	a table such as returned by <code>quartetTable</code> , <code>quartetTableResolved</code> , or <code>quartetTableDominant</code> , possibly with extra columns added by other functions
----	---

Examples

```
gtrees=read.tree(file=system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
tnames=taxonNames(gtrees)
QT=quartetTable(gtrees,tnames)
quartetTablePrint(QT)
RQT=quartetTableResolved(QT)
quartetTablePrint(RQT)
pTable=quartetTreeTestInd(RQT,"T3")
quartetTablePrint(pTable)
DQT=quartetTableDominant(RQT)
quartetTablePrint(DQT)
```

quartetTableResolved *Modify quartet table to only show resolved quartets*

Description

Converts table of all quartet counts, including unresolved ones, by either dropping unresolved ones, or distributing them uniformly among the three resolved counts.

Usage

```
quartetTableResolved(qt, omit = FALSE)
```

Arguments

qt	table, as produced by <code>quartetTable</code> for n taxa, with n+4 columns
omit	TRUE deletes unresolved quartets column; FALSE redistributes unresolved counts as (1/3,1/3,1/3) to resolved counts

Value

A table of with n+3 columns, similar to qt, showing only resolved quartet counts

See Also

[quartetTable](#), [quartetTableDominant](#)

Examples

```
gtrees=read.tree(file=system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
tnames=taxonNames(gtrees)
QT=quartetTable(gtrees,tnames)
RQT=quartetTableResolved(QT)
DQT=quartetTableDominant(RQT)
```

quartetTestPlot *Produce simplex plot of results of quartet hypothesis test results*

Description

Plot a 2-d probability simplex, with points for all quartet count vectors. Colors indicate rejection or failure to reject for tests at specified levels.

Usage

```
quartetTestPlot(pTable, test, alpha = 0.05, beta = 1)
```

Arguments

pTable	table of quartets and p-values, as produced by <code>quartetTreeTestInd</code> , <code>quartetStarTestInd</code> , or <code>NANUQ</code>
test	model to use, for tree null hypothesis; options are "T1" or "T3"
alpha	significance level for tree test with null hypothesis given by test
beta	significance level for test with null hypothesis star tree; test results plotted only if $\beta < 1$

Details

This function must be supplied with a table of quartets and p-values. The plot may show results of either the T1 or T3 test, with or without a star tree test (depending on whether a "p_star" column is in the table). The p-values must be supplied by previous calls to `quartetTreeTestInd` (for "T1" or "T3" p-values) and `quartetStarTestInd` (for "star" p-values). The `NANUQ` and `NANUQdist` functions include calls to these tree test functions.

Value

None

See Also

[quartetTreeTestInd](#), [quartetStarTestInd](#), [NANUQ](#), [NANUQdist](#)

Examples

```
gtrees=read.tree(file=system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
taxanames=taxonNames(gtrees)
QT=quartetTable(gtrees,taxanames)
RQT=quartetTableResolved(QT)
stree="((((t5,t6),t4),t7),((t8,t9),((t1,t2),t3))); "
pTable=quartetTreeTestInd(RQT,"T1",speciestree=stree)
pTable=quartetStarTestInd(pTable)
quartetTestPlot(pTable, "T1", alpha=.05, beta=.95)
```

<code>quartetTreeErrorProb</code>	<i>Bayesian posterior probability of error in 4-taxon unrooted species tree topology estimate</i>
-----------------------------------	---

Description

Computes Bayesian posterior probability that the ML estimate of 4-taxon species tree topology from gene quartet topology counts is incorrect, under the assumption that the counts arise from some species tree.

Usage

```
quartetTreeErrorProb(obs, model = "T3")
```

Arguments

obs	vector of counts for 3 topologies
model	"T3" or "T1", for the models of Mitchell et al. (2019) describing an unspecified species tree topology ("T3"), or the topology corresponding to the first entry of obs ("T1")

Details

The Jeffreys prior is used for internal branch length, along with the uniform prior on the resolved topology.

Value

posterior probability

References

Mitchell J, Allman E, Rhodes J (2019). "Hypothesis testing near singularities and boundaries." *Electron. J. Statist.*, **13**(1), 2150-2193.

Examples

```
obs <- c(28, 32, 30)
quartetTreeErrorProb(obs, model="T1")
quartetTreeErrorProb(obs, model="T3")
```

quartetTreeTest

Hypothesis test for quartet counts fitting a tree under the MSC

Description

Test the hypothesis $H_0 = T1$ or $T3$ model of Mitchell et al. (2019), vs. $H_1 =$ everything else. $T1$ is for a specific tree topology, and $T3$ for any tree topology.

Usage

```
quartetTreeTest(obs, model = "T3", lambda = 0,
  smallcounts = "approximate", bootstraps = 10^4, method = "MLest")
```

Arguments

obs	vector of 3 counts of resolved quartet frequencies,
model	"T1" or "T3", for the models of Mitchell et al. (2019),
lambda	parameter for power-divergence statistic (e.g., 0 for likelihood ratio statistic, 1 for Chi-squared statistic)
smallcounts	"bootstrap" or "approximate", method of obtaining p-value when some counts are small
bootstraps	number of samples for bootstrapping
method	"MLtest", "conservative", or "bootstrap"

Details

This function implements two of the versions of the test given by Mitchell et al. (2019) as well as parametric bootstrapping, with other procedures for when some counts are small. Due to the singularities and boundaries of the models, when the topology and/or the internal quartet branch length is not specified by the null hypothesis these are more accurate tests than, say, a chi-squared with one degree of freedom which assumes no model boundary or singularity near the data.

If method="MLtest", this uses the test by that name described in Section 7 of Mitchell et al. (2019). For both the T1 and T3 models the test is slightly anticonservative over a small range of true internal edges of the quartet species tree. Although the test generally performs well in practice, it lacks a uniform asymptotic guarantee over the full parameter space for either T1 or T3.

If method="conservative", a conservative test described by Mitchell et al. (2019) is used. For model T3 this uses the χ^2_1 distribution (the "least favorable" approach), while for model T1 it uses the Minimum Adjusted Bonferroni, based on precomputed values from simulations. These conservative tests are asymptotically guaranteed to reject the null hypothesis at most at a specified level, but at the expense of increased type II errors.

If method="bootstrap", then parametric bootstrapping is done, based on parameter estimates of the quartet topology and internal edge length. The bootstrap sample size is given by the bootstrap argument.

When some expected topology counts are small, the methods "MLest" and "conservative" are not appropriate. The argument smallcounts determines whether bootstrapping or an approximate method that uses precomputed p-values is used. These both involve estimates of the quartet topology and internal edge length.

The returned p-value should be taken with caution when there is a small sample size, e.g. less than 30 gene trees.

For model T1, the first entry of obs is treated as the count of gene quartets concordant with the species tree.

The returned value of t is a consistent estimator, but not the MLE, of the internal edge length in coalescent units. Although consistent, the MLE for t is biased. Our consistent estimator is still biased, but with less bias than the MLE. See Mitchell et al. (2019) for more discussion on dealing with the bias of parameter estimates in the presence of boundaries and/or singularities of parameter spaces.

Value

(p-value, t) where t is a consistent estimator of the internal edge length in coalescent units, possibly Inf.

References

Mitchell J, Allman E, Rhodes J (2019). "Hypothesis testing near singularities and boundaries." *Electron. J. Statist.*, **13**(1), 2150-2193.

See Also

[quartetTreeTestInd](#)

Examples

```
obs=c(17,72,11)
quartetTreeTest(obs,"T3")
quartetTreeTest(obs,"T1")
```

quartetTreeTestInd	<i>Multiple independent hypothesis tests for quartet counts fitting a species tree under the MSC</i>
--------------------	--

Description

Perform a tree hypothesis test for all quartet counts in an input table, as if the quartets are independent.

Usage

```
quartetTreeTestInd(rqt, model = "T3", lambda = 0,
  smallcounts = "approximate", bootstraps = 10^4, method = "MLest",
  speciestree = NULL)
```

Arguments

rqt	table of resolved quartet counts, as produced by <code>quartetTableResolved</code> , or <code>quartetStarTestInd</code>
model	"T1" for a specific species tree topology, or "T3" for any species tree topology, with these models explained more fully by Mitchell et al. (2019)
lambda	power divergence statistic parameter (e.g., 0 for likelihood ratio statistic, 1 for Chi-squared statistic)
smallcounts	"bootstrap" or "approximate", method of obtaining p-value when some counts are small
bootstraps	number of samples for bootstrapping
method	"MLest", "conservative", or "bootstrap"
speciestree	species tree, in Newick as text, to determine quartet for T1 test; required for model="T1", ignored for model="T3"

Details

This function assumes all quartets are resolved. The test performed is described in `QuartetTreeTest`.

Value

If model="T3", a copy of rqt with a new column "p_T3" appended with p-values for each quartet; If model="T1", a copy of rqt with 2 columns appended: "p_T1" with p-values, and "qindex" giving index of quartet consistent with specified species tree, i.e., 1 if abcd on species tree, 2 if acldb, 3 if adlbc

References

Mitchell J, Allman E, Rhodes J (2019). "Hypothesis testing near singularities and boundaries." *Electron. J. Statist.*, **13**(1), 2150-2193.

See Also

[quartetTreeTest](#), [quartetTestPlot](#), [quartetStarTestInd](#), [quartetTableResolved](#)

Examples

```
gtrees=read.tree(file=system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
taxanames=taxonNames(gtrees)
QT=quartetTable(gtrees,taxanames)
RQT=quartetTableResolved(QT)
pTable3=quartetTreeTestInd(RQT,"T3")
quartetTablePrint(pTable3)
stree=stree="((((t5,t6),t4),t7),((t8,t9),((t1,t2),t3)));")
pTable1=quartetTreeTestInd(RQT,"T1",speciestree=stree)
quartetTablePrint(pTable1)
```

quartetWeightedDist	<i>Compute the Weighted Quartet Distance between taxa</i>
---------------------	---

Description

Compute the Weighted Quartet Distance between taxa of Yourdkhani and Rhodes (2020) from a table specifying a collection of quartets on n taxa and the quartets' internal branch lengths.

Usage

```
quartetWeightedDist(dqt)
```

Arguments

dqt an $(n \text{ choose } 4) \times n+1$ matrix of the form output by quartetTableDominant

Value

A pairwise distance matrix on n taxa

References

Yourdkhani S, Rhodes J (2020). "Inferring species trees from weighted quartets." *unknown journal*, vol(num), pp-qq.

See Also

[quartetTableDominant](#), [WQDSAdjustLengths](#), [WQDS](#), [WQDC](#), [WQDCrecursive](#), [quartetWeightedDist](#)

Examples

```
gtrees=read.tree(file=system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
tnames=taxonNames(gtrees)
QT=quartetTable(gtrees,tnames)
RQT=quartetTableResolved(QT)
DQT=quartetTableDominant(RQT,bigweights="finite")
D=quartetWeightedDist(DQT)
tree=NJ(D)
stree=WQDSAdjustLengths(tree)
write.tree(stree)
```

simplexCoords	<i>Convert 3-d coordinates to 2-d simplex coordinates</i>
---------------	---

Description

Convert from 3-d Cartesian coordinates to 2-d coordinates suitable for plotting in simplex.

Usage

```
simplexCoords(v)
```

Arguments

v	vector of 3 non-negative numbers, not summing to 0
---	--

Value

2-d coordinates to plot normalized point in simplex

See Also

[simplexLabels](#), [simplexPoint](#), [simplexPrepare](#), [simplexSegment](#), [simplexText](#)

Examples

```
simplexCoords(c(15,65,20))
```

simplexLabels	<i>Label vertices of 2-d simplex</i>
---------------	--------------------------------------

Description

Add labels to vertices of the simplex.

Usage

```
simplexLabels(top = "", left = "", right = "")
```

Arguments

top	label for top
left	label for left bottom
right	label for right bottom

Value

None

See Also

[simplexPoint](#), [simplexPrepare](#), [simplexSegment](#), [simplexText](#), [simplexCoords](#)

Examples

```
simplexPrepare("T3", "Example Plot")
simplexLabels("ab|cd", "ac|bd", "ad|bc")
```

simplexPoint	<i>Plot point in 2-d simplex</i>
--------------	----------------------------------

Description

Normalizes a point given in 3-d non-normalized coordinates, then plots it in the 2-d simplex.

Usage

```
simplexPoint(v, ...)
```

Arguments

<code>v</code>	a 3-d point in non-negative orthant, coordinates not summing to 0
<code>...</code>	other options to pass to <code>graphics::points</code> function

Value

None

See Also

[simplexLabels](#), [simplexPrepare](#), [simplexSegment](#), [simplexText](#), [simplexCoords](#)

Examples

```
simplexPrepare("T3", "Example Plot")
simplexPoint(c(15, 65, 20), pch=3, col="blue")
```

simplexPrepare	<i>Draw 2-d probability simplex, with model lines for T3 or T1 model</i>
----------------	--

Description

Outline the 2-d simplex, and draw the T1 or T3 model points for quartet frequencies. The models are described more fully by Mitchell et al. (2019).

Usage

```
simplexPrepare(model = "T3", maintitle = NULL, titletext = NULL)
```

Arguments

model	"T1" or "T3", for 1-tree or 3-tree model
maintitle	main title for plot
titletext	additional text for title

Value

None

References

Mitchell J, Allman E, Rhodes J (2019). "Hypothesis testing near singularities and boundaries." *Electron. J. Statist.*, **13**(1), 2150-2193.

See Also

[simplexLabels](#), [simplexPoint](#), [simplexSegment](#), [simplexText](#), [simplexCoords](#)

Examples

```
simplexPrepare("T3",maintitle="Main title",titletext="further text")
```

simplexSegment	<i>Plot line segment in 2-d simplex</i>
----------------	---

Description

Normalizes two points in 3-d, and draws line segment between them in 2-d simplex.

Usage

```
simplexSegment(v, w, ...)
```

Arguments

`v, w` 3-d endpoints of line segment in non-negative orthant, coords not summing to 0
`...` other options to pass to `graphics::segments` function

Value

None

See Also

[simplexLabels](#), [simplexPoint](#), [simplexPrepare](#), [simplexText](#), [simplexCoords](#)

Examples

```
simplexPrepare("T3", "Example Plot")
simplexSegment(c(15,65,20), c(15,70, 15), col="green")
```

simplexText

Add text at a point in 2-d simplex

Description

Add text to a 2-d simplex plot, at specified location.

Usage

```
simplexText(v, label = "", ...)
```

Arguments

`v` a 3-d point in non-negative orthant, coordinates not summing to 0
`label` text to add to plot
`...` other options to pass to `graphics` text function

Value

None

See Also

[simplexLabels](#), [simplexPoint](#), [simplexPrepare](#), [simplexSegment](#), [simplexCoords](#)

Examples

```
simplexPrepare("T3", "Example Plot")
simplexText(c(15,65,20), "tree ac|bd")
```

T1density	<i>Probability density function for Model T1 of Mitchell et al. (2019), Proposition 5.2</i>
-----------	---

Description

Value of probability density function for Model T1 of Mitchell et al. (2019), Proposition 5.2.

Usage

T1density(x, mu0)

Arguments

x	statistic value (e.g., likelihood ratio stat, or other power divergence stat)
mu0	parameter of density function

Value

value of density function

References

Mitchell J, Allman E, Rhodes J (2019). “Hypothesis testing near singularities and boundaries.” *Electron. J. Statist.*, **13**(1), 2150-2193.

See Also

[T3density](#)

T3density	<i>Probability density function for Model T3 of Mitchell et al. (2019), Proposition 4.2</i>
-----------	---

Description

Value of probability density function for Model T3 of Mitchell et al. (2019), Proposition 4.2.

Usage

T3density(x, mu0, alpha0, beta0)

Arguments

x	statistic value (e.g., LR stat, or other power divergence stat)
mu0	parameter of density function
alpha0	parameter of density function
beta0	parameter of density function

Value

value of density function

References

Mitchell J, Allman E, Rhodes J (2019). “Hypothesis testing near singularities and boundaries.” *Electron. J. Statist.*, **13**(1), 2150-2193.

See Also

[T1density](#)

taxonNames	<i>Get all taxon names from a collection of trees</i>
------------	---

Description

Create a vector of all taxa appearing on a collection of trees, with no repeats.

Usage

```
taxonNames(trees)
```

Arguments

trees a multiphylo object containing a collection of trees

Value

a vector of unique names of taxa appearing on the trees

Examples

```
gtrees=read.tree(file=system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
tnames=taxonNames(gtrees)
```

WQDC	<i>Compute Weighted Quartet Distance Consensus tree from gene tree data.</i>
------	--

Description

Compute the Weighted Quartet Distance Consensus (Yourdkhani and Rhodes 2020) estimate of a species tree from gene tree data. This is a consistent estimator of the unrooted species tree topology and all internal branch lengths.

Usage

```
WQDC(genetreedata, taxanames = NULL, omit = FALSE, terminal = 1)
```


Arguments

<code>genetreedata</code>	gene tree data in one of the 3 forms <ol style="list-style-type: none"> 1. a character string giving the name of a file containing gene trees in Newick 2. a <code>multiphylo</code> object containing gene trees, 3. a resolved quartet table, as produced by <code>quartetTableResolved</code>
<code>taxanames</code>	list of taxa on which to construct tree; may be subset of those on gene trees; ignored if <code>genetreedata</code> given as resolved quartet table
<code>omit</code>	TRUE leaves out unresolved quartets, FALSE treats them as 1/3 of each resolution; ignored if <code>genetreedata</code> given as resolved quartet table
<code>terminal</code>	non-negative branch length to supply for terminal branches, whose length cannot be inferred by WQDC

Details

This function is a wrapper which performs the steps of reading in a collection of gene trees, tallying quartets, estimating quartet internal branch lengths, computing the weighted quartet distance between taxa, building a tree, and adjusting edge lengths, to give a consistent estimate of the metric species tree (in coalescent units) under the multispecies coalescent model.

If the gene tree data indicates some quartets experienced little to no incomplete lineage sorting, this algorithm tends to be less topologically accurate than QDC (which infers no metric information) or WQDCrecursive (which gives better topologies, and reasonable shorter edge lengths, though long edge lengths may still be unreliable).

Value

an unrooted metric tree of type "phylo"

References

Yourdkhani S, Rhodes J (2020). "Inferring species trees from weighted quartets." *unknown journal*, vol(num), pp-qq.

See Also

[quartetTable](#), [quartetTableResolved](#), [quartetTableDominant](#), [quartetWeightedDist](#), [WQDCrecursive](#), [WQDS](#), [QDC](#)

Examples

```
stree=WQDC(system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
write.tree(stree)
```

WQDCrecursive	<i>Compute the Recursive Weighted Quartet Distance Consensus tree from gene tree data</i>
---------------	---

Description

Infer a metric species tree from counts of quartets displayed on a collection of gene trees, as described by Yourdkhani and Rhodes (2020). Edge lengths are in coalescent units.

Usage

```
WQDCrecursive(rqt, stopAt = 2, terminal = 1)
```

Arguments

rqt	a resolved quartet table as produced by <code>quartetTableResolved</code>
stopAt	a non-negative branch length; recursive calls stop when the longest branch in a recursively examined subtree is smaller than this value
terminal	non-negative branch length to supply for terminal branches, whose lengths cannot be inferred by WQDCrecursive

Details

The algorithm counts quarets displayed on the gene trees, builds a tree using WQDS, determines the split corresponding to the longest edge in that tree, and then recursively builds trees on the taxa in each split set together with a 'composite taxon' formed by all taxa in the other split set. This approach is slower than non-recursive WQDC, but increases topological accuracy. Shorter branch lengths tend to be more accurately estimated.

This function must be called with its argument a resolved quartet table (not a dominant quartet table) of size $(n \text{ choose } 4) \times (n+3)$. Its recursive nature requires building smaller resolved quartet tables on split sets with an additional composite taxon.

Value

an unrooted metric tree, of type "phylo"

References

Yourdkhani S, Rhodes J (2020). "Inferring species trees from weighted quartets." *unknown journal*, vol(num), pp-qq.

See Also

[quartetTableResolved](#), [quartetTable](#), [QDC](#), [QDS](#), [quartetTableCollapse](#)

Examples

```
gtrees=read.tree(file=system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
taxanames=taxonNames(gtrees)
QT=quartetTable(gtrees,taxanames)
RQT=quartetTableResolved(QT)
stree=WQDCrecursive(RQT)
write.tree(stree)
```

WQDS	<i>Compute the Weighted Quartet Distance Supertree</i>
------	--

Description

Apply the Weighted Quartet Distance Supertree method of Yourdkhani and Rhodes (2020) to a collection of quartets on n taxa together with internal quartet branch lengths, specified by a table.

Usage

```
WQDS(dqt, method = fastme.bal)
```

Arguments

dqt	an (n choose 4) x n+1) matrix of form output by <code>quartetTableDominant</code>
method	tree building method function (<code>fastme.bal</code> , <code>NJ</code> , etc.)

Details

This function is a wrapper which runs `quartetWeightedDist`, builds a tree, and then adjusts edge lengths with `WQDSAdjustLengths`.

Value

an unrooted metric tree, of type "phylo"

References

Yourdkhani S, Rhodes J (2020). "Inferring species trees from weighted quartets." *unknown journal*, vol(num), pp-qq.

See Also

[quartetTableDominant](#), [quartetWeightedDist](#), [WQDSAdjustLengths](#), [WQDC](#), [WQDCrecursive](#), [QDS](#)

Examples

```
gtrees=read.tree(file=system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
tnames=taxonNames(gtrees)
QT=quartetTable(gtrees,tnames)
RQT=quartetTableResolved(QT)
DQT=quartetTableDominant(RQT,bigweights= "finite")
tree=WQDS(DQT)
write.tree(tree)
```

WQDSAdjustLengths	<i>Adjust edge lengths on tree built from Weighted Quartet distance to estimate metric tree</i>
-------------------	---

Description

Modify edge lengths of a tree built from a distance table produced by `quartetWeightedDist`, to remove scaling factors related to the size of the split associated to the edge.

Usage

```
WQDSAdjustLengths(tree)
```

Arguments

tree	an unrooted metric tree, of type "phylo"
------	--

Details

As explained by Yourdkhani and Rhodes (2020), a metric tree produced from the weighted quartet distance has edge lengths inflated by a factor dependent on the associated split size. Removing these factors yields a consistent estimate of the metric species tree displaying the weighted quartets, if such a tree exists.

This function should not be used on trees output from WQDS, WQDC, or WQDCrecursive, as their edges are already adjusted. It can be used on trees built from the distance computed by `quartetWeightedDist`.

Value

an unrooted metric tree, of type "phylo"

References

Yourdkhani S, Rhodes J (2020). "Inferring species trees from weighted quartets." *unknown journal*, vol(num), pp-qq.

See Also

[WQDS](#), [WQDC](#)

Examples

```
gtrees=read.tree(file=system.file("extdata","dataGeneTreeSample",package="MSCquartets"))
tnames=taxonNames(gtrees)
QT=quartetTable(gtrees,tnames)
RQT=quartetTableResolved(QT)
DQT=quartetTableDominant(RQT,bigweights="finite")
D=quartetWeightedDist(DQT)
tree=NJ(D)
stree=WQDSAdjustLengths(tree)
write.tree(stree)
```

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