Package 'PSTDistanceR'

November 13, 2019

Title Computing probabilistic distances between species tree models

Version 0.0.0.9000

Description What the package does (one paragraph).

Depends R (>= 3.4.1)

License What license is it under?

LinkingTo Rcpp

Imports Rcpp

Encoding UTF-8

LazyData true

RoxygenNote 6.1.0

R topics documented:

Compute.Pairwise.SpeciesTree.Distances

> *Compute.Pairwise.SpeciesTree.Distances: function to compute a matrix of pairwise distances among a set of species trees*

Description

returns a list of pairwise distance matrix between all provided specie trees

Usage

```
Compute.Pairwise.SpeciesTree.Distances(list.SpeciesTrees,
  vector.SpeciesTreeNames, string.PathParentDir, string.PathHybridCoal)
```

Arguments

list.SpeciesTrees
                 List of input species trees

Value

vector.Probabilistic.SpeciesTree.Distances Vector containing the three PSTD measures

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Compute.Probabilistic.SpeciesTree.Distances

> *Compute.Probabilistic.SpeciesTree.Distances: function to compute probabilistic species tree distances between two species tree models*

Description

This function returns a vector of length (3): representing the "Hellinger", "Kullback_Leibler", and "Jensen_Shannon" distances between to trees

Usage

```
Compute.Probabilistic.SpeciesTree.Distances(handle.SpeciesTree.Model1,
  handle.SpeciesTree.Model2, string.PathParentDir, string.PathHybridCoal)
```

Arguments

handle.SpeciesTree.Model1
                 Species Tree Model 1

handle.SpeciesTree.Model2
                 Species Tree Model 2

string.PathParentDir
                 Path to a parent directory that will be used for subdirectories

string.PathHybridCoal
                 Path to HYBRID-COAL executable

Value

vector.Probabilistic.SpeciesTree.Distances Vector containing the three PSTD measures

Examples

```
string.SpeciesTree.1a <- "(((A:1,B:1):1,C:2):1,D:3);"
handle.SpeciesTree.1a <- read.tree(text = string.SpeciesTree.1a)

string.SpeciesTree.1b <- "(((A:1,C:1):1,B:2):1,D:3);"
handle.SpeciesTree.1b <- read.tree(text = string.SpeciesTree.1b)
```

```
Compute.Probabilistic.SpeciesTree.Distances(handle.SpeciesTree.Model1 = handle.SpeciesTree.1a,
    handle.SpeciesTree.Model2 = handle.SpeciesTree.1b,
    string.PathParentDir = '~/Desktop/EXAMPLE/SmallTree/',
    string.PathHybridCoal = '/Applications/hybrid-coal-v0.2.1-beta/hybrid-coal')
```

ComputePSTD   *ComputeDistancesPSTD*

Description

Function to compute the probabililistic distance between two gene tree probabilities for the Hellinger (dH, first), KL (dKL, second), and JS (dJS, third) distance measures of Garba et al 2018

IMPORTANT: This function assumes that the two gene tree probability vectors (vectorM1 and vectorM2) are sorted by to be the same. That is, the first gene tree in vectorM1 is also the first gene tree in vectorM2, and so on... The gene tree probability output files of HYBRID-COAL are sorted automatically.

Usage

```
ComputePSTD(vectorM1, vectorM2)
```

Arguments

vectorM1   Vector of the gene tree probabilities for M1

vectorM2   Vector of the gene tree probabilities for M2

Details

`ComputeDistancesPSTD` Computes the probabilistic distances between two probability distributions

Examples

```
vector.GeneTreeProbs.M1 <- Read.GeneTree.Probabilities(string.PathToGeneTreeProbs = '~/Desktop/EXAMPLE/Small
vector.GeneTreeProbs.M2 <- Read.GeneTree.Probabilities(string.PathToGeneTreeProbs = '~/Desktop/EXAMPLE/Small

ComputePSTD(vectorM1 = vector.GeneTreeProbs.M1, vectorM2 = vector.GeneTreeProbs.M2)
```

Pipeline.SpeciesNetworkDistances.ScaleAllBranches

> *Pipeline.SpeciesNetworkDistances.ScaleAllBranches: function to measure phylogenetic distances across a range of branch length scaling between two species tree models*

Description

This function returns a matrix containing the 5 distance metics (3 probabilistic + Robinson-Foulds + BHV)

Usage

```
Pipeline.SpeciesNetworkDistances.ScaleAllBranches(vector.ScaleFactor,
  string.PathParentDir, string.PathHybridCoal,
  handle.SpeciesNetwork.Model1, handle.SpeciesNetwork.Model2)
```

Arguments

vector.ScaleFactor
:   Vector to containing the values to scale the branches of the second species tree model

string.PathParentDir
:   Path to a parent directory that will be used for subdirectories

string.PathHybridCoal
:   Path to HYBRID-COAL executable

handle.SpeciesTree.Model1
:   Species Tree Model 1

handle.SpeciesTree.Model2
:   Species Tree Model 2

Value

XXX

Examples

```
library(phangorn)
library(PSTD)
library(distory)

string.SpeciesTree.1a <- "(((A:1,B:1):1,C:2):1,D:3);"
handle.SpeciesTree.1a <- read.tree(text = string.SpeciesTree.1a)

vector.Gamma <- seq(0.01, 10, 0.01)
handle.Figure1d <- Pipeline.SpeciesTreeDistances.ScaleAllBranches(vector.ScaleFactor = vector.Gamma,
  string.PathParentDir = '~/Desktop/',
  string.PathHybridCoal = '/Applications/hybrid-coal-v0.2.1-beta/hybrid-coal',
  handle.SpeciesTree.Model1 = handle.SpeciesTree.1a,
```

```
      handle.SpeciesTree.Model2 = handle.SpeciesTree.1a)

 plot(handle.Figure1d[,1], ylim = c(0, 0.75), col = "darkblue", type = "l", xaxt='n', yaxt="n", lty = 1)
 axis(1,at=seq(from = 0, to = 1000, by = 50),labels=seq(from = 0, to = 10, by = 0.50))
 axis(2,at=seq(from = 0, to = 0.75, by = 0.10),labels=seq(from = 0, to = 0.75, by = 0.10))
 lines(handle.Figure1d[,2], col = "blue", lty = 2)
 lines(handle.Figure1d[,3], col = "lightblue", lty = 4)
 lines(handle.Figure1d[,5]*0.025, col = "red", lty = 3)
```

Pipeline.SpeciesTreeDistances.ScaleAllBranches

> *Pipeline.SpeciesTreeDistances.ScaleAllBranches: function to measure phylogenetic distances across a range of branch length scaling between two species tree models*

Description

This function returns a matrix containing the 5 distance metics (3 probabilistic + Robinson-Foulds + BHV)

Usage

```
Pipeline.SpeciesTreeDistances.ScaleAllBranches(vector.ScaleFactor,
  string.PathParentDir, string.PathHybridCoal, handle.SpeciesTree.Model1,
  handle.SpeciesTree.Model2)
```

Arguments

vector.ScaleFactor
> Vector to containing the values to scale the branches of the second species tree model

string.PathParentDir
> Path to a parent directory that will be used for subdirectories

string.PathHybridCoal
> Path to HYBRID-COAL executable

handle.SpeciesTree.Model1
> Species Tree Model 1

handle.SpeciesTree.Model2
> Species Tree Model 2

Value

XXX

Examples

```
library(phangorn)
library(PSTD)
library(distory)

string.SpeciesTree.1a <- "(((A:1,B:1):1,C:2):1,D:3);"
handle.SpeciesTree.1a <- read.tree(text = string.SpeciesTree.1a)

vector.Gamma <- seq(0.01, 10, 0.01)
handle.Figure1d <- Pipeline.SpeciesTreeDistances.ScaleAllBranches(vector.ScaleFactor = vector.Gamma,
    string.PathParentDir = '~/Desktop/',
    string.PathHybridCoal = '/Applications/hybrid-coal-v0.2.1-beta/hybrid-coal',
    handle.SpeciesTree.Model1 = handle.SpeciesTree.1a,
    handle.SpeciesTree.Model2 = handle.SpeciesTree.1a)

plot(handle.Figure1d[,1], ylim = c(0, 0.75), col = "darkblue", type = "l", xaxt='n', yaxt="n", lty = 1)
axis(1,at=seq(from = 0, to = 1000, by = 50),labels=seq(from = 0, to = 10, by = 0.50))
axis(2,at=seq(from = 0, to = 0.75, by = 0.10),labels=seq(from = 0, to = 0.75, by = 0.10))
lines(handle.Figure1d[,2], col = "blue", lty = 2)
lines(handle.Figure1d[,3], col = "lightblue", lty = 4)
lines(handle.Figure1d[,5]*0.025, col = "red", lty = 3)
```

Pipeline.SpeciesTreeDistances.ScaleSingleBranch

> *Pipeline.SpeciesTreeDistances.ScaleSingleBranch: function to measure phylogenetic distances across a range of branch length scaling (for a single branch on the second model) between two species tree models*

Description

This function returns a matrix containing the 5 distance metics (3 probabilistic + Robinson-Foulds + BHV) across a range of scaler values

Usage

```
Pipeline.SpeciesTreeDistances.ScaleSingleBranch(vector.ScaleFactor,
  string.PathParentDir, string.PathHybridCoal, handle.SpeciesTree.Model1,
  handle.SpeciesTree.Model2, numeric.BranchToScale)
```

Arguments

vector.ScaleFactor

          Vector to containing the values to scale the branches of the second species tree model

string.PathParentDir

          Path to a parent directory that will be used for subdirectories

string.PathHybridCoal

          Path to HYBRID-COAL executable

handle.SpeciesTree.Model1

          Species Tree Model 1

```
handle.SpeciesTree.Model2
                  Species Tree Model 2
numeric.BranchToScale
                  Number indicating the branch to scale on species tree model 2
```

Value

XXX

```
Read.GeneTree.Probabilities
```
                  Read.GeneTree.Probabilities: function to extract the gene tree proba-
                  bilities from the output of HYBRID-COAL

Description

This function returns a vector of containing gene tree probabilities (assumed to be in the same order when comparing two gene tree probability vectors)

Usage

```
Read.GeneTree.Probabilities(string.PathToGeneTreeProbs)
```

Arguments

```
string.PathToGeneTreeProbs
                  Vector containing a set of likelihoods under model 1
```

Value

vector.GeneTreeProbabilities: vector containing a set of gene tree probabilities

Examples

```
vector.GeneTreeProbs.M1 <- Read.GeneTree.Probabilities(string.PathToGeneTreeProbs = '~/Desktop/EXAMPLE/Small
```

RunHybridCoal   *RunHybridCoal: function to run HYBRID-COAL on a given species tree model, and return a vector of gene tree probabilities for the species tree*

Description

This function returns vector.GeneTreeProbabilities: a vector of gene tree probabilities for the species model (sum ~1.0)

Usage

```
RunHybridCoal(string.PathHybridCoal, handle.SpeciesTree,
   string.PathParentDir, string.SpeciesTree.ModelName)
```

Arguments

string.PathHybridCoal

                Path to HYBRID-COAL executable

handle.SpeciesTree

                Species tree

string.PathParentDir

                Path to a parent directory that will be used for subdirectories

string.SpeciesTree.ModelName

                String giving the name of the species model

Value

vector.GeneTreeProbabilities: vector containing a set of gene tree probabilities for the species tree model

Examples

```
string.SpeciesTree.1a <- "(((A:1,B:1):1,C:2):1,D:3);"
handle.SpeciesTree.1a <- read.tree(text = string.SpeciesTree.1a)

RunHybridCoal(string.PathHybridCoal = '/Applications/hybrid-coal-v0.2.1-beta/hybrid-coal',
   handle.SpeciesTree = handle.SpeciesTree.1a,
   string.PathParentDir = '~/Desktop/EXAMPLE/SmallTree/',
   string.SpeciesTree.ModelName = "Model1a")
```

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