

Package ‘seeva’

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Type Package

Title Spatial Evolutionary and Ecological Vicariance Analysis

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Description See <http://www.rci.rutgers.edu/~struwe/seeva/>

Depends ape, phangorn, R2HTML

License GPL (>= 2)

NeedsCompilation no

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checkSeeva	<i>Check and drop taxa for seeva analysis</i>
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Description

This function will drop exclusive taxa from either the data or the tree. It will return a list with the new data.frame and a new tree, where just the taxa in common will be kept.

Usage

```
checkSeeva(data=mydata, tree=mytree)
```

Arguments

data	data.frame - first column should be species names, the other columns the characters
tree	phylo

Value

list

Examples

```
### generating random data ###

rtree(7) -> mytree
data.frame(mytree$tip.label, c(1:7)) -> mydata

### running the function ###

checkSeeva(mydata, mytree) -> checked
checked$data
checked$tree
```

exportSeeva	<i>Export results of seeva</i>
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Description

The function will generate a html with the results of the seeva analysis. If csv=T it also generates a csv with the results. The "cex" options are used to change the sizes (fonts, thermos, etc...) in the plots.

Usage

```
exportSeeva(seeva.out = myseeva, csv = TRUE, p_adj = TRUE, filename = "Seeva_output", cex.nodes = 1
```

Arguments

seeva.out	The output of seevaDisc or seevaCont
csv	logical
filename	character
cex.nodes	numerical
cex.tips	numerical
cex.sign	numerical
adj.sign	numerical
...	see plot.phylo (ape package) for further arguments

Value

Generates a csv or a html in the working directory

Examples

```
## see help of:
```

```
\code{\LinkA{seevaCont}{seevaCont}}
```

pairNnodes	<i>Internal function</i>
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plotSeeva	<i>Plot the "index of divergence" or the Z-score on the tree.</i>
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Description

The function will plot all the characters stored in the seeva output. If pdf=TRUE it will generate a pdf file in the working directory instead.

Usage

```
plotSeeva(seeva.out = myoutput, pdf = FALSE, filename = "Seeva_output", p_adj = TRUE, cex.nodes = 1)
```

Arguments

seeva.out	An output from seevaDisc or seevaCont
pdf	logical
filename	character
cex.nodes	numerical
cex.tips	numerical
cex.sign	numerical
adj.sign	numerical
...	Further arguments can be provided, see plot.phylo from ape package

Value

plot or pdf

Examples

```
## see help of:
```

```
\code{\LinkA{seevaCont}{seevaCont}}
```

seeva

seeva - Spatial Evolutionary and Ecological Vicariance Analysis

Description

In contrast to vicariance biogeography, which assumes geographic separation of populations, the Spatial Evolutionary and Ecological Vicariance Analysis approach allows researchers also to look at ecological vicariance (differences) of sympatric and allopatric species and clades. This method can utilize GIS-derived dataset of collection-associated ecological and environmental data in combination with phylogenetic data to investigate trends in speciation using statistical methods with spatial interpretations. The method can also be used for other kinds of comparisons between groups and clades, in areas such as coevolution, diseases, morphological evolution, and niche comparisons.

Generally, SEEVA works by using measurements gathered from individuals of species or populations, and these measurements are then analyzed statistically for differences between groups (species) and/or clades. Two statistical test are being employed, the Divergence Index (to measure differences between groups or clades) and Fisher's Exact test (the latter to provide a p-value for tests with small sample sizes)

Details

Package: seeva
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License: GPL (>= 2)

Author(s)

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Maintainer: Marcelo Reginato <reginatobio@yahoo.com.br>

References

Struwe, L., P. E. Smouse, E. Heiberg, S. Haag, & R. G. Lathrop. MS (2010). Spatial evolutionary and ecological vicariance analysis (SEEVA), a novel approach to biogeography and speciation research, with an example from Brazilian Gentianaceae. *Journal of Biogeography*, October 2010

<http://www.rci.rutgers.edu/~struwe/seeva/>

See Also

[ape phangorn phangorn R2HTML](#)

 seevaCont

seeva analysis of continuous characters

Description

SEEVA - Mann-Whitney-Wilcoxon Test (scaled)

Usage

```
seevaCont(tree=mytree, data=mydata, permutations=999, node.dist=TRUE)
```

Arguments

tree	phylo
data	data.frame
permutations	numerical
node.dist	logical

Details

If node.dist=TRUE a phylogenetic correction using the number of nodes between pairs of taxa will be applied to the Z-matrix.

Value

list

References

in prep.

Examples

```
#####
### generating data ###
#####
```

```
rtree(7) -> tree
plot(tree)
```

```
sample((c(100:200)/10), 20, replace=T) -> t1
sample((c(100:200)/10), 20, replace=T) -> t2
sample((c(100:200)/10), 20, replace=T) -> t3
sample((c(100:200)/10), 20, replace=T) -> t4
sample((c(100:200)/10), 20, replace=T) -> t5
sample((c(100:200)/10), 20, replace=T) -> t6
sample((c(400:500)/10), 20, replace=T) -> t7
```

```
c(t1,t2,t3,t4,t5,t6,t7) -> values
```

```
species <- c(rep("t1",length(t1)), rep("t2",length(t2)), rep("t3",length(t3)), rep("t4",length(t4)), rep("t5",length(t5)), rep("t6",length(t6)), rep("t7",length(t7)))
data <- data.frame(species=species, variable_1=values, variable_2=sample(values, 140, replace=T))
```

```

data

#pdf("tree.pdf")
plot(tree)
nodelabels(frame="none", col="red", cex=0.8, font=2)
title("Key Tree")
#dev.off()

#pdf("boxplot.pdf")
boxplot(values ~ species, data=data, main="Character")
#dev.off()

summary(data)

#####
### SEEVA ###
#####

## SEEVA-MWW

seevaCont(tree=tree, data=data, permutations=999, node.dist=F) -> results.mww

#####
### Results MWW ###
#####

results.mww

#####
### plotting ###
#####

plotSeeva(seeva.out=results.mww, pdf=F)

plotSeeva(seeva.out=results.mww, pdf=F, cex.tips=1.5, cex.sign=2, edge.color="grey", edge.width=4)

#####
### exporting ###
#####

exportSeeva(seeva.out=results.mww, csv=T, filename="My_results")

### check out your working directory!

### Not sure where is you current working directory?? Type:

getwd()

```

Description

see <http://www.rci.rutgers.edu/~struwe/seeva/>

Usage

```
seevaDisc(tree=mytree, data=mydata, sim.p.value=F)
```

Arguments

tree	phylo
data	data.frame
sim.p.value	Logical

Value

list

Examples

```
### generating random data ###

rtree(10) -> mytree
sample(c("a","b"), 200, replace=T) -> states
rep(mytree$tip.label, 20) -> species
data.frame(species,states) -> mydata

## checking

checkSeeva(mydata,mytree) -> checked
checked$data -> mydata
checked$tree -> mytree

## running seeva

seevaDisc(mytree, mydata, sim.p.value=T) -> results

results

## plotting the key tree (matches the nodes of results)

plot(mytree)
nodelabels(frame="none", col="red")

## plotting the results

results[[1]] -> index.div
which(index.div$p.value_adjusted_bonf < 0.05) -> sign.nodes
index.div[,1] -> labelNodes
labelNodes[sign.nodes]
plot(mytree, cex=0.9)
nodelabels(node=index.div$node, cex=1, thermo=index.div$index_of_divergence, bg=c("blue", "red"))
nodelabels(text="*", node=labelNodes[sign.nodes], frame="none", cex=1.5, adj=c(2,2))
title(names(results[1]))
```


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