Package 'tanggle'

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Type Package

Title Visualization of Phylogenetic Networks

Version 1.17.0

Description Offers functions for plotting split (or implicit) networks (unrooted, undirected) and explicit networks (rooted, directed) with reticulations extending. 'ggtree' and using functions from 'ape' and 'phangorn'. It extends the 'ggtree' package [@Yu2017] to allow the visualization of phylogenetic networks using the 'ggplot2' syntax. It offers an alternative to the plot functions already available in 'ape' Paradis and Schliep (2019) <doi:10.1093/bioinformatics/bty633> and 'phangorn' Schliep (2011) <doi:10.1093/bioinformatics/btq706>.

Depends R (>= 4.1), ggplot2 (>= 3.0.0), ggtree

Imports ape (>= 5.0), phangorn (>= 2.12), rlang, utils, methods, dplyr

Suggests tinytest, BiocStyle, ggimage, knitr, rmarkdown

VignetteBuilder knitr

biocViews Software, Visualization, Phylogenetics, Alignment, Clustering, MultipleSequenceAlignment, DataImport

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URL https://klausvigo.github.io/tanggle/, https://github.com/KlausVigo/tanggle

BugReports https://github.com/KlausVigo/tanggle/issues

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`tanggle-package` *tanggle: Visualization of Phylogenetic Networks*

Description

Offers functions for plotting split (or implicit) networks (unrooted, undirected) and explicit networks (rooted, directed) with reticulations extending. 'ggtree' and using functions from 'ape' and 'phangorn'. It extends the 'ggtree' package [@Yu2017] to allow the visualization of phylogenetic networks using the 'ggplot2' syntax. It offers an alternative to the plot functions already available in 'ape' Paradis and Schliep (2019) doi:10.1093/bioinformatics/bty633 and 'phangorn' Schliep (2011) doi:10.1093/bioinformatics/btq706.

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See Also

Useful links:

- https://klausvigo.github.io/tanggle/
- https://github.com/KlausVigo/tanggle
- Report bugs at https://github.com/KlausVigo/tanggle/issues

`geom_splitnet` *geom_splitnet*

Description

add splitnet layer

Usage

```
geom_splitnet(layout = "slanted", ...)
```

Arguments

`layout`	one of 'rectangular', 'slanted', 'circular', 'radial' or 'unrooted'
`...`	additional parameter

Value

splitnet layer

Author(s)

Klaus Schliep

Examples

```
data(yeast, package='phangorn')
dm <- phangorn::dist.ml(yeast)
nnet <- phangorn::neighborNet(dm)
ggplot(nnet, aes(x, y))  + geom_splitnet() + theme_tree()
```

ggevonet *ggevonet*

Description

drawing phylogenetic tree from phylo object

Usage

```
ggevonet(tr, mapping = NULL, layout = "slanted", mrsd = NULL,
  as.Date = FALSE, yscale = "none", yscale_mapping = NULL,
  ladderize = FALSE, right = FALSE, branch.length = "branch.length",
  ndigits = NULL, min_crossing = TRUE, ...)
```

Arguments

tr	a evonet object
mapping	aes mapping
layout	one of 'rectangular', 'slanted'
mrsd	most recent sampling date
as.Date	logical whether using Date class in time tree
yscale	y scale
yscale_mapping	yscale mapping for category variable
ladderize	logical
right	logical
branch.length	variable for scaling branch, if 'none' draw cladogram
ndigits	number of digits to round numerical annotation variable
min_crossing	logical, rotate clades to minimize crossings
...	additional parameter

Value

tree

Author(s)

Klaus Schliep

See Also

evonet, ggtree

Examples

```
(enet <- ape::read.evonet(text='((a:2,(b:1)#H1:1):1,(#H1,c:1):2);'))
ggevonet(enet) + geom_tiplab()
ggevonet(enet, layout = "rectangular") + geom_tiplab()
```

---

ggsplitnet *ggsplitnet*

Description

drawing phylogenetic tree from phylo object

Usage

```
ggsplitnet(tr, mapping = NULL, layout = "slanted", mrsd = NULL,
  as.Date = FALSE, yscale = "none", yscale_mapping = NULL,
  ladderize = FALSE, right = FALSE, branch.length = "branch.length",
  ndigits = NULL, angle = 0, ...)
```

Arguments

tr	a networx object
mapping	aes mapping
layout	so far only 'slanted' is supported.
mrsd	most recent sampling date
as.Date	logical whether using Date class in time tree
yscale	y scale
yscale_mapping	yscale mapping for category variable
ladderize	logical
right	logical
branch.length	variable for scaling branch, if 'none' draw cladogram
ndigits	number of digits to round numerical annotation variable
angle	rotate the plot.
...	additional parameter

Value

tree

Author(s)

Klaus Schliep

References

Schliep, K., Potts, A. J., Morrison, D. A. and Grimm, G. W. (2017), Intertwining phylogenetic trees and networks. *Methods Ecol Evol*. **8**, 1212–1220. doi:10.1111/2041-210X.12760

Dress, A.W.M. and Huson, D.H. (2004) Constructing Splits Graphs *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, **1(3)**, 109–115

Bagci, C., Bryant, D., Cetinkaya, B. and Huson, D.H. (2021), Microbial Phylogenetic Context Using Phylogenetic Outlines. *Genome Biology and Evolution*. **13(9)**, evab213

Potts, A.J. and Hedderson, T.A. and Grimm, G.W. (2013), Constructing Phylogenies in the Presence Of Intra-Individual Site Polymorphisms (2ISPs) with a Focus on the Nuclear Ribosomal Cistron, *Systematic Biology*. **63(1)**, 1–16

See Also

ggtree, networx, consensusNet, neighborNet

Examples

```
data(yeast, package='phangorn')
dm <- phangorn::dist.ml(yeast)
nnet <- phangorn::neighborNet(dm)
ggsplitnet(nnet) + geom_tiplab2()

library(phangorn)
fdir <- system.file("extdata/examples", package = "tanggle")
nymania <- read.phyDat(file.path(fdir,
           "Nymania.capensis.ITS.alignment.fasta"), format="fasta")
nnet <- neighborNet(dist.p(nymania))
ggsplitnet(nnet) + geom_tiplab2()
```

`minimize_overlap` *minimize_overlap reduces reticulation lines crossing over in plots*

Description

minimize_overlap reduces reticulation lines crossing over in plots

Usage

```
minimize_overlap(x)
```

Arguments

x	Tree of class 'evonet'

Value

A Tree with rotated nodes of class 'evonet'

Author(s)

L. Francisco Henao Diaz

Examples

```
fishnet <- ape::read.evonet(text='(Xalvarezi,Xmayae,((Xsignum,((Xmonticolus,
(Xclemenciae_F2,#H25)),(((((((((Xgordoni,Xmeyeri),Xcouchianus),Xvariatus),
Xevelynae),(Xxiphidium,#H24)),Xmilleri),Xandersi),Xmaculatus),(((Xmontezumae,
(Xcortezi,(Xbirchmanni_GARC,Xmalinche_CHIC2))),((Xnigrensis,Xmultilineatus),
(Xpygmaeus,Xcontinens))))#H24))),(Xhellerii)#H25));')
fishnet$edge.length <- NULL
new_tre <- minimize_overlap(fishnet)

par(mfrow=c(1,2))
ggevonet(fishnet, min_crossing = FALSE)
ggevonet(new_tre)

net2 <- ape::read.evonet(text='(15,(1,((14,(#H1,(((12,13),(11,#H3)),(7,
    ((10)#H3,(8,9)))))),((((2,3))#H2,(6,(5,(#H2,4)))))#H1)));')
# Cui et al. 2013 Evol.
new_net2 <- minimize_overlap(net2)
ggevonet(net2, min_crossing = FALSE)
ggevonet(new_net2)
```

---

node_depth_evonet *Depth of Nodes*

Description

These functions return the depths or heights of nodes and tips.

Usage

```
node_depth_evonet(x, ...)
```

Arguments

x	an object of class 'evonet'
...	Further arguments passed to or from other methods.

Value

a vector with the depth of the nodes

See Also

node.depth

Examples

```
z <- ape::read.evonet(text = '((1,((2,(3,(4)Y#H1)g)e,
(((Y#H1, 5)h,6)f)X#H2)c)a,((X#H2,7)d,8)b)r;')
nd <- node_depth_evonet(z)
z$edge.length <- nd[z$edge[,1]] - nd[z$edge[,2]]
ggevonet(z)
```

`swap_hybrid_minor` *swap_hybrid_minor*

Description

Swapping the minor edges of an evonet object

Usage

```
swap_hybrid_minor(x, hybrid_nodes, node_times = NULL)
```

Arguments

`x`	evonet object
`hybrid_nodes`	a vector of hybrid nodes to have their minor edges swapped
`node_times`	an optional argument with node times

Value

network

Examples

```
(enet <- ape::read.evonet(text='((a:2,(b:1)#H1:1):1,(#H1,c:1):2);'))
ggevonet(enet) + geom_tiplab()
swapped_enet<-swap_hybrid_minor(enet,6)
ggevonet(swapped_enet) + geom_tiplab()
```

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