

# Package ‘tanggle’

November 17, 2025

**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](https://doi.org/10.1093/bioinformatics/bty633)> and 'phangorn' Schliep (2011) <[doi:10.1093/bioinformatics/btq706](https://doi.org/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

**License** Artistic-2.0

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

**BugReports** <https://github.com/KlausVigo/tanggle/issues>

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**Author** Klaus Schliep [aut, cre] (ORCID:  
    <<https://orcid.org/0000-0003-2941-0161>>),  
Marta Vidal-Garcia [aut],  
Claudia Solis-Lemus [aut] (ORCID:  
    <<https://orcid.org/0000-0002-9789-8915>>),  
Leann Biancani [aut],  
Eren Ada [aut],  
L. Francisco Henao Diaz [aut],  
Guangchuang Yu [ctb],  
Joshua Justison [aut]

**Maintainer** Klaus Schliep <klaus.schliep@gmail.com>

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| tangle-package | <i>tangle: Visualization of Phylogenetic Networks</i> |
|----------------|-------------------------------------------------------|

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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](https://doi.org/10.1093/bioinformatics/bty633) and 'phangorn' Schliep (2011) [doi:10.1093/bioinformatics/btq706](https://doi.org/10.1093/bioinformatics/btq706).

Author(s)

**Maintainer:** Klaus Schliep <klaus.schliep@gmail.com> (ORCID)

Authors:

- Marta Vidal-Garcia
- Claudia Solis-Lemus <solislemus@wisc.edu> (ORCID)
- Leann Biancani
- Eren Ada

- L. Francisco Henao Diaz
- Joshua Justison

Other contributors:

- Guangchuang Yu [contributor]

## See Also

Useful links:

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

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geom\_splitnet

*geom\_splitnet*

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## 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()
```

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ggevonet

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ggevonet

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## 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 network 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](#), [networkx](#), [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 = "tangle")
nymania <- read.phyDat(file.path(fdir,
                                "Nymania.capensis.ITS.alignment.fasta"), format="fasta")
nnet <- neighborNet(dist.p(nymania))
ggsplitnet(nnet) + geom_tiplab2()
```

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minimize\_overlap

*minimize\_overlap reduces reticulation lines crossing over in plots*

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## 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,
(Xcortezii,Xbirmannii_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)

```

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|                   |                       |
|-------------------|-----------------------|
| node_depth_evonet | <i>Depth of Nodes</i> |
|-------------------|-----------------------|

---

**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)
```

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|                   |                          |
|-------------------|--------------------------|
| swap_hybrid_minor | <i>swap_hybrid_minor</i> |
|-------------------|--------------------------|

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**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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