

```
## Error in loadNamespace(name):  there is no package called 'BiocStyle'
```

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## 1 Introduction

XXX `ggnetworx` extends the `ggtree` [?] package to allow for the visualization of several types of phylogentic networks using the `ggplot2` [?] syntax. More specifically, `ggnetworx` contains functions to plot split (or implicit) networks (unrooted, undirected) and explicit networks (rooted, directed) with reticulations. It offers an alternative to the plot functions already available in `ape` and `phangorn`.

## 2 Getting Started

Load the necessary libraries:

```
library(phangorn)
library(devtools)

## Loading required package: usethis

library(ggplot2)
install_github("YuLab-SMU/ggtree")

## Skipping install of 'ggtree' from a github remote, the SHA1 (6ae936b0)
has not changed since last install.
## Use 'force = TRUE' to force installation

library(ggtree)
install_github("KlausVigo/tangle")

## Skipping install of 'tangle' from a github remote, the SHA1 (5160a05b)
has not changed since last install.
## Use 'force = TRUE' to force installation

library(tangle)
```

## 3 Split Networks

Split networks are data-display objects which allow for the definition of 2 (or more) options for non-compatible splits. Split networks are most often used to visualize consensus networks [?] or neighbor-nets [?]. This can be done either by using the `consensusNet` or `neighbor-net` functions in `phangorn` [?] or by importing nexus files from `SplitsTree` [?].

### 3.1 Data Types

`ggnetworx` accepts three forms of input data for split networks. The following input options all generate a *networx* object for plotting.

1. Nexus file created with SplitsTree [?] and read with the *read.nexus.network* function in phangorn.

```
## read in a split network in nexus format:
fdir <- system.file("extdata/trees", package = "phangorn")
Nnet <- read.nexus.network(file.path(fdir, "woodmouse.nxs"))
```

2. A collection of gene trees (e.g. from RAxML [?]) in one of the following formats:

- Nexus file read with the function *read.nexus*
- Text file in Newick format (one gene tree per line) read with the function *read.tree*

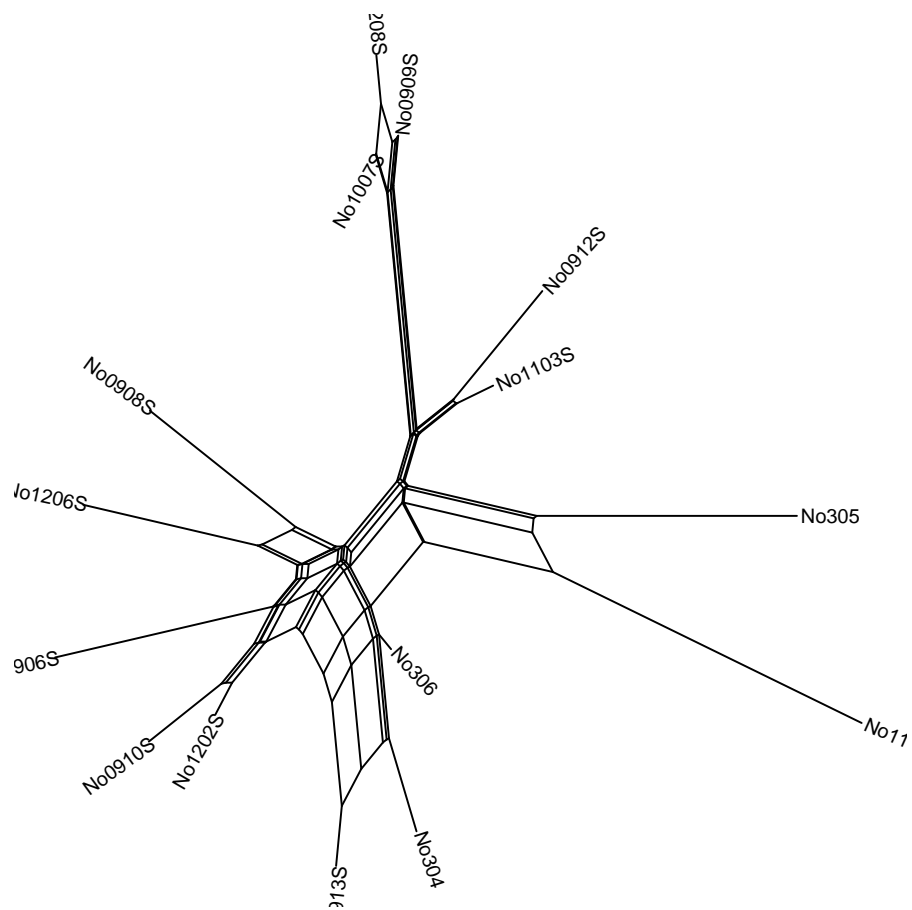
A consensus split network is then computed using the function *consensusNet* in phangorn.

3. Sequences in nexus, fasta or phylip format read with the function *read.phyDat* in phangorn or the function *read.dna* in ape. Distances matrices are then computed for specific models of evolution using the function *dist.ml* in phangorn or *dist.dna* in ape. From the distance matrix, a split network is reconstructed using the function *neighborNet* in phangorn. Optional: branch lengths may be estimated using the function *splitsNetworks* in phangorn.

## 3.2 Plotting a Split Network

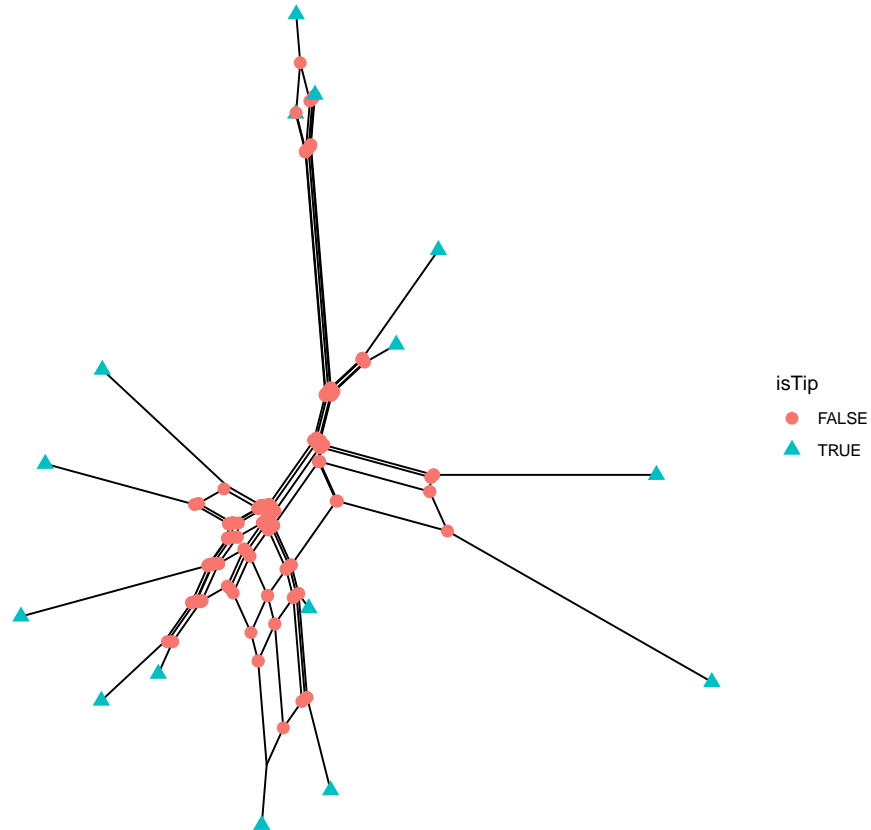
Plot a split network:

```
## plot a split network:
ggsplitnet(Nnet) + geom_tiplab2()
```



Nodes can be annotated with *geom\_point*.

```
ggsplitnet(Nnet) + geom_point(aes(shape=isTip, color=isTip), size=3)
```

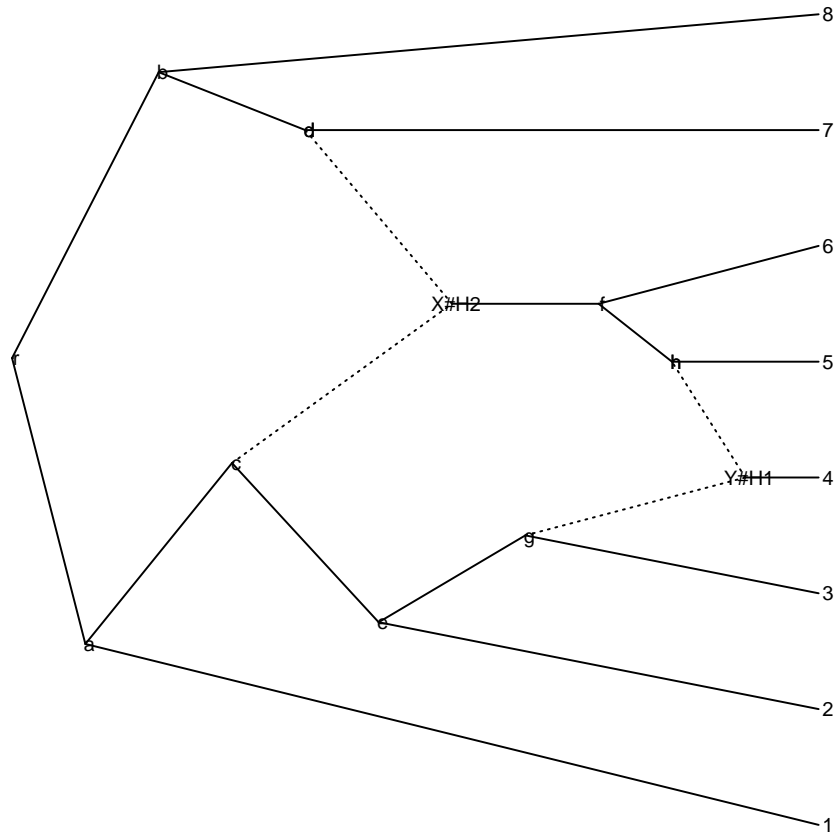


## 4 Plotting Explicit Networks

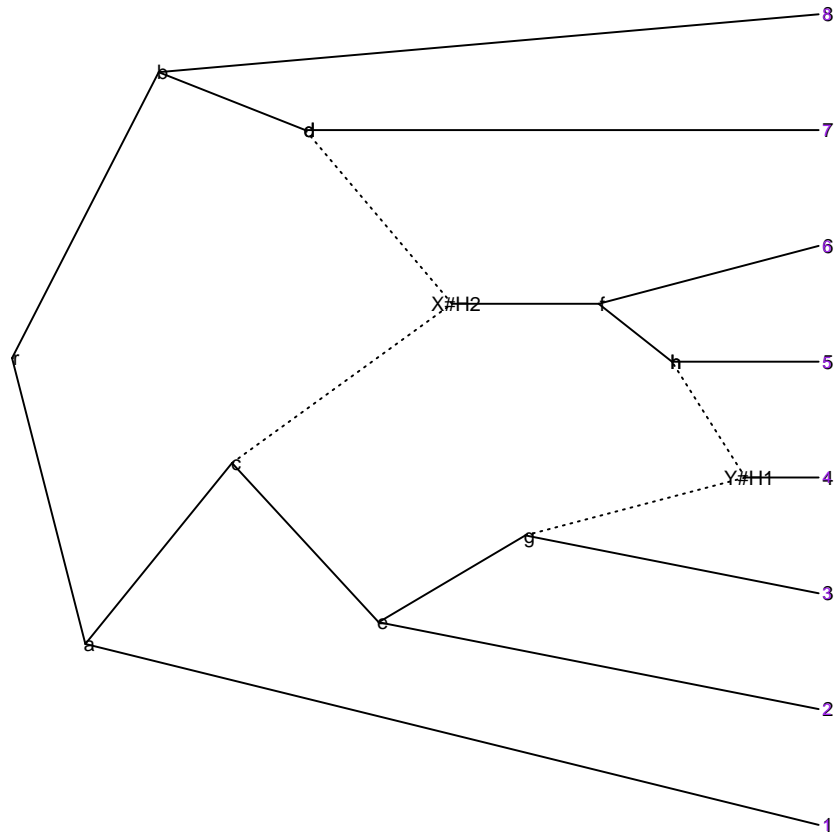
The function `ggevonet` plots explicit networks (phylogenetic trees with reticulations). A recent addition to `ape` [?] made it possible to read in trees in extended newick format [?].

```
## read in an explicit network (example from Fig. 2 in Cardona et al. 2008):
z <- 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;")

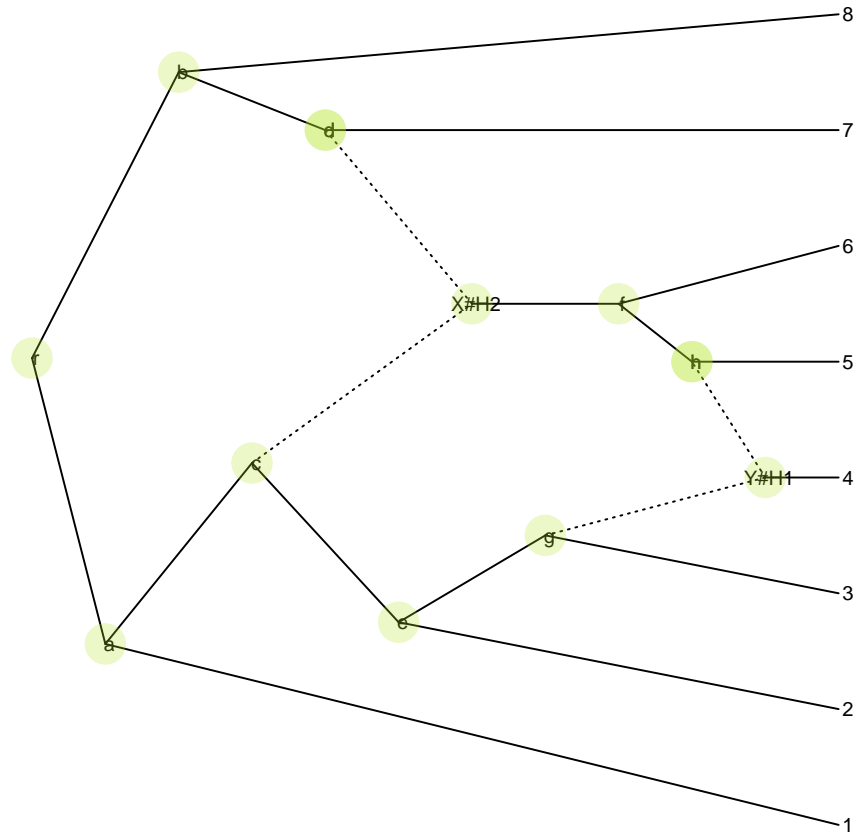
## plot an explicit network:
ggevonet(z) + geom_tiplab() + geom_nodelab()
```



```
p <- ggevonet(z, layout = "slanted") + geom_tiplab() + geom_nodelab()
p + geom_tiplab(size=3, color="purple")
```



```
p + geom_nodepoint(color="#b5e521", alpha=1/4, size=10)
```



## 5 Summary

The split network plots should take most of the functions compatible with unrooted trees in `ggtree`. The explicit network plots are phylogram or slanted. Not all options may work as intended yet.

<https://bioconductor.org/packages/devel/bioc/vignettes/ggtree/inst/doc/treeVisualization.html>



## A Session info

```
sessionInfo()

## R version 3.6.3 (2020-02-29)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS Catalina 10.15.5
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_AU.UTF-8/en_AU.UTF-8/en_AU.UTF-8/C/en_AU.UTF-8/en_AU.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## other attached packages:
## [1] tanggle_0.99.0  ggplot2_3.3.2  devtools_2.3.2  usethis_1.6.3
## [5] phangorn_2.5.5  ape_5.4-1      ggtree_2.3.5.993 knitr_1.30
##
## loaded via a namespace (and not attached):
## [1] Rcpp_1.0.5      lattice_0.20-38  tidyr_1.1.2
## [4] prettyunits_1.1.1 ps_1.3.4        assertthat_0.2.1
## [7] rprojroot_1.3-2 digest_0.6.25    R6_2.4.1
## [10] backports_1.1.10 evaluate_0.14    highr_0.8
## [13] pillar_1.4.6    rlang_0.4.7     lazyeval_0.2.2
## [16] curl_4.3        callr_3.4.4     Matrix_1.2-18
## [19] labeling_0.3    desc_1.2.0      stringr_1.4.0
## [22] igraph_1.2.5    munsell_0.5.0   compiler_3.6.3
## [25] xfun_0.17       pkgconfig_2.0.3 pkgbuild_1.1.0
## [28] tidyselect_1.1.0 tibble_3.0.3    quadprog_1.5-8
## [31] fansi_0.4.1     crayon_1.3.4    dplyr_1.0.2
## [34] withr_2.3.0     grid_3.6.3      nlme_3.1-144
## [37] jsonlite_1.7.1  gtable_0.3.0    lifecycle_0.2.0
## [40] magrittr_1.5    scales_1.1.1    tidytree_0.3.3
## [43] cli_2.0.2       stringi_1.5.3   farver_2.0.3
## [46] fs_1.5.0        remotes_2.2.0   testthat_2.3.2
## [49] ellipsis_0.3.1  rvcheck_0.1.8   generics_0.0.2
## [52] vctrs_0.3.4     fastmatch_1.1-0 tools_3.6.3
## [55] treeio_1.13.1   glue_1.4.2      purrr_0.3.4
## [58] processx_3.4.4  pkgload_1.1.0   parallel_3.6.3
## [61] colorspace_1.4-1 BiocManager_1.30.10 sessioninfo_1.1.1
## [64] aplot_0.0.6     memoise_1.1.0   patchwork_1.0.1
```