

Assessing Monophyly in Orobanchaceae Tree v7.3.2

10/16/2018

Load Packages and Files:

```
library(geiger)
```

```
## Loading required package: ape
```

```
## Warning: package 'ape' was built under R version 3.4.2
```

```
require(ape)
```

```
require(MonoPhy)
```

```
## Loading required package: MonoPhy
```

```
## Loading required package: phytools
```

```
## Loading required package: maps
```

```
## Loading required package: phangorn
```

```
## Warning: package 'phangorn' was built under R version 3.4.2
```

```
## Loading required package: RColorBrewer
```

```
## Loading required package: taxize
```

```
## Warning: package 'taxize' was built under R version 3.4.2
```

```
setwd("~/Documents/pyphlawd_local/PyPHLAWD-master_v2/examples/alt_config_oroban2_filtF/Final_SuperMatrix")
```

```
oro_tree <- read.nexus('RAML_bipartitions.12_gene_7.3.fasta.rtp.nssp.tre')
```

```
#plot(oro_tree)
```

Assess monophyly:

```
sol_tip_label <- AssessMonophyly(oro_tree)
```

```
#sol_tip_label
```

Write results to csv file:

```
MonophylyResults <- GetResultMonophyly(sol_tip_label)
```

```
#MonophylyResults
```

```
write.csv(file= 'MonoPhy_result1_7.3.2.csv', MonophylyResults)
```

Using these results I found species whose taxonomy was contentious or where names were incorrect based on GenBank: I changed these names in a new tree:

```
oro_tree2 <- read.nexus('RAML_bipartitions.12_gene_7.3.fasta.rtp.nssp.ncorr.tre')
```

```
sol_tip_label2 <- AssessMonophyly(oro_tree2)
```

```
#sol_tip_label2
```

```
MonophylyResults2 <- GetResultMonophyly(sol_tip_label2)
```

```
#MonophylyResults2
```

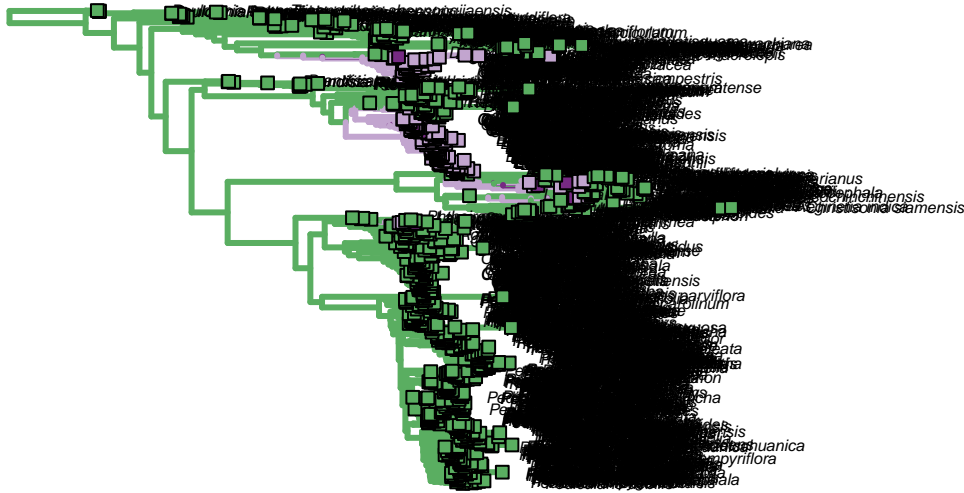
```
write.csv(file= 'MonoPhy_result2_7.3.2.csv', MonophylyResults2)
```

There are still a couple tip which conflict with monophyletic groups. However, I did not find evidence in the literature to change these names:

See table on monophyly and name changes.

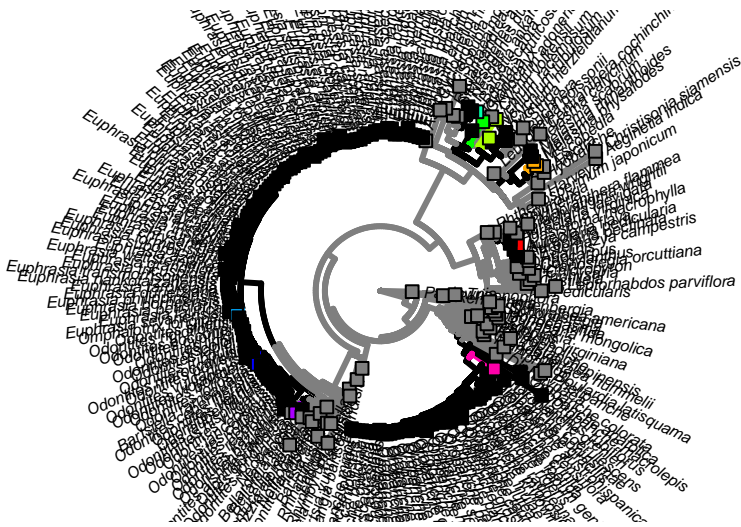
Visualize monophyletic and nonmonophyletic genera:

```
PlotMonophyly(sol_tip_label2, oro_tree2, plot.type='monophyly', ladderize=TRUE, cex=0.5)
```



This tree collapses monophyletic groups in order to highlight where we have conflict (Best viewed as pdf):

```
PlotMonophyly(sol_tip_label2, oro_tree2, taxlevels=1, plot.type='intruders', monocoll=TRUE, cex=0.5, lab
```



```
PlotMonophyly(sol_tip_label2, oro_tree2, taxlevels=1, plot.type='intruders', monocoll=TRUE, cex=0.5, lab
```

Source: <https://cran.r-project.org/web/packages/MonoPhy/vignettes/MonoPhyVignette.html>