

## TNT scripts

The master script is a Windows batch file (*winanalyze.bat*). It runs by double-clicking on it; requires that all the scripts and binaries (either command-line version, or GUI version), as well as the dataset (*dromaeodat.tnt*, *flightadat.tnt*, *sizedat.tnt*), are in the same directory as the batch file. Likewise for the *malinanalyze* script (which runs under either Mac or Linux, and assumes that the TNT binary is called "tnt"), which you can also run in the background, by opening a terminal, going to the directory where the script is placed, and typing:

```
maclinaanalyze & <enter>
```

as this runs in the background, you can close the terminal (or log-off your remote connection) and the process will continue running.

The scripts used produce three types of files.

*.tre	tree files, in parenthetical notation, to be opened with TNT
*.svg	image files (scalable vector graphics), opened with any browser
*.txt	text files, with info on the runs

If you wish to erase all the results produced by previous runs, just double-click (in Windows) in the batch file *clean.bat*. The results under extended equal weights are indicated as XIW, and those under equal weights as EW.

## Tree files

The files *trees\_XIW.tre* and *trees\_EW.tre* contain the individual trees found by the search; *nozeroboot\_XIW.tre* and *nozeroboot\_EW.tre*, the trees produced by no-zero-weight symmetric resampling with 1 as initial random seed (the fixed random seed is needed so that the resampled datasets which produced these trees can subsequently be reproduced). The other tree-files are self-explanatory.

## Image Files

The files *prop\_trend\_char\_0/1\_up/dn.svg* contain a diagram with proportional size changes mapped on the tree, with decreases estimated conservatively (dn) or liberally (up), from one of the XIW trees. The rest of the SVG files produced by the scripts have names that should be self-explanatory.

## Text files

The files *run\_results\_XIW.txt* and *run\_results\_EW.txt* contain the general results for the runs (including legends for floating taxa in *pruned\_consensus\_XIW.svg* and *pruned\_consensus\_EW.svg*). These files, in addition to info on timing and search results, also contain legends of pruned taxa in the strict consensus, rates of asymmetry, lists of synapomorphies, information on character conflict, and on characters responsible for the different locations of the rogue taxa. The file *combination\_EW-XIW.txt* contains the legends for floating taxa indicated in the SVG diagram *combination\_EW-XIW.svg*. The files called *floaters* (or some combination thereof) contain lists of floating taxa (which are used internally by the scripts); in principle, you don't need the contents of these files.

## Scripts (and Usage)

To repeat our analysis, there is no need to use the scripts individually; running the master scripts *winanalyze* or *maclinanlyze* (as indicated above) is sufficient for that. This section explains how to use the TNT scripts individually, or for other datasets. Note that the scripts must be run sequentially; initial scripts produce results that are used by subsequent scripts (they are described below in the order in which they must be run).

### *fullanalysis.run*

The script to do initial tree-searches. To use it, read the data set, then type *fullanalysis* and the name you want to give the run (e.g. EW or XIW; if you use "TEST" as name, it does a quick test analysis). Note that to make the analysis equal weights, you need to set implied weights off (with *piwe-*;) prior to running this script, because implied weights is left ON after reading the dataset in *Dromaeodat.tnt*. (the master scripts *winanalyze* and *maclinanlyze* do this automatically).

### ***improvecombin.run***

A script to identify rogues in tree-files; it assumes that the tree files have been names as in ***fullanalysis.run***. Takes as argument(s) the name(s) of the run(s) you want o improve (can improve more than one at a a time, e.g. ***improvecombin EW XIW***). Called automatically by fullanalysis (to improve the strict consensus of the optimal trees found), and by the master script (***winanalyze***, ***maclinanalyze***) to find the rogues between EW and XIW.

### ***apotable.run***

It produces a list of synapomorphies common to a set of trees, plotted on a tree-diagram (colored and labelled with taxonomy), using character names. It takes two arguments, first one is the width of columns to use, second one is the name of the run to diagnose (it assumes that the tree files have been names as in ***fullanalysis.run***). Called by ***winanalyze*** and ***maclinanalyze***.

### ***gogogo.run***

Produce resampled trees. Takes as argument the name of the run (EW, XIW). The trees are produced with no-zero-weight symmetric resampling; note that these trees are subsequently used to identify rogue taxa, with the script ***bothprunes.run***; if you change settings for the resampling (e.g. the up/dn probability), then you need to also modify ***bothprunes.run***.

### ***bothprunes.run***

Find taxa that decrease group supports for a "base" run (e.g. XIW), and calculate the group supports for the base run, and for the same groups on an alternative run; display in a tree-diagram colored and labeled with taxonomy. Save results to file ***supports\_improved-BASE\_n\_ALTERNATIVE.svg***. The trees must have been produced with ***gogogo.run***; the script also assumes that you have previously created a file called ***combined\_floaters.txt*** with a list of the taxa that need to be pruned for improving the consensus of EW and XIW (which the master batch files do by calling ***improvecombin.run***). If you change the settings for resampling in this file, you must also change the same settings in ***gogogo.run***.

### ***combinem.run***

Using the list of taxa in ***combined\_floaters.txt***, produce a consensus of EW and XIW, with rogues pruned, and save it as a colored and labelled tree-diagram.

### ***rcstrct.run***

Based on values stored in the file ***flightdat.tnt*** (morphological variables used to calculate wing loading and specific lift), optimize the trees produced by the previous runs (these must be pruned to contain only the taxa for which morphological variables are available; the batch files ***maclinanalyze*** and ***winanalyze*** do that automatically, prior to calling ***rcstrct.run***). Plot values on a color scale that switches from blue to red, depending on the values. First argument is Po,m value, second argument is min/max, third argument (optional) is lim (to use the values of the formulae only for those nodes reconstructed to have vaned feathers; nodes for which feathers could be vaned or not, are given the minimum or maximum values, depending whether the second argument is min or max).

### ***ptrends.run***

Script used to calculate trends of (proportional) change in size. Must be used for the dataset in ***sizedat.tnt***. Output goes to file ***prop\_trend\_char\_n\_up/dn.svg*** (where ***n***=character number, file ***sizedat.tnt*** contains two alternative codings for the size).