Supplementary information, Section S1

Computational methods for calculating genealogically-sensitive averages and proportions

Contents

1 Introduction

This document provides a guide to calculating genealogically-sensitive proportions and averages. Because a key part of the analysis is the preparation of a phylogenetic tree, considerable space is given over to how such trees can be prepared. Much of the discussion here is an introduction to the functionality of two R packages, *glottoTrees* (Round 2021a) and *phyloWeights* (Round 2021b), which have been specifically written for these tasks.

Since typologists may have little familiarity with R, we begin with a short introduction to it in Section 2. We then discuss the calculation of genealogically-sensitive proportions and averages in Section 3. Section 4 explains how typologists can prepare phylogenetic trees by adapting resources freely available from glottolog.com (Hammarström et al. 2021). Section 5 provides a worked example used in a typological investigation of sonority sequencing by Yin (2020).

2 A short orientation to R

The code presented here runs in R. Here we quickly introduce R objects (such as variables and dataframes) in Section 2.1, R packages in Section 2.2 and how R works with tree objects in Section 2.3. Readers already familiar with the basics of R may wish to skip directly to Section 2.3.

Below, chunks of R code appear against a grey background. The results that R produces from each chunk is shown below it, either as lines of text preceded by `##` or as a plot that R generates, or both. The code within the grey boxes can be copied and pasted into R. Within the code chunks, where a single R command runs longer than one printed line, we have indented the lines after the first; to run these in R, you will need to copy and paste the whole command.

2.1 R objects

In R, values can be assigned to objects (such as variables) using the assignment operator, `<-`:

```
x <- 7.5
y <- 2 / 9
z <- sqrt(2)
a <- "hello"
```

The content of a simple object can be displayed just by entering its name. The `[1]` at the start of the output is telling you this is item number 1 in the object:

```
z
```

```
## [1] 1.414214
```

A common object in R is a one-dimensional vector, such as a sequence of numbers or characters strings. Here is a vector of numbers. The `c()` here is a function, while the numbers `3`, `4`, `5` and `6` are its arguments. The function takes these four individual arguments and returns a single vector.

```
c(3,5,4,6)
```

```
## [1] 3 5 4 6
```

A dataframe is the object in R that most resembles an Excel spreadsheet. It has columns that are named and rows that may or may not be named. Here we see the creation of a dataframe using the function `data.frame()`. In this instance, the first two arguments of the function are a vector of strings, `my_letters`, and a vector of numbers `my_numbers`.[1] These vectors need to be of equal length, as they become the columns of the resulting dataframe. Here we have assigned the result to the object named `my_dataframe`:

```
my_dataframe <- data.frame(my_letters = c("x", "y", "z"),
                           my_numbers = c(7,1,43),
                           stringsAsFactors = FALSE)
```

The contents of `my_dataframe` are displayed like this:

```
my_dataframe
```

```
##   my_letters my_numbers
## 1          x          7
## 2          y          1
## 3          z         43
```

In a dataframe, the contents of any one column will all be of the same class, e.g. all character strings, or all numbers, but as in `my_dataframe`, different columns can contain items of different classes.

2.2 R packages

R provides a range of basic statistical functions, but it is most powerful when extended by the addition of *packages* which contain additional functions. Here we will use the packages *ape* "Analyses of Phylogenetics

[1]The third argument `stringsAsFactors = FALSE` is used to ensure R reads the first argument as character strings, and not as another kind object (which won't be of concern to us here), called a `factor`. If you are using R version 4.0 or later, the argument `stringsAsFactors = FALSE` isn't strictly necessary, since R will assume it by default. In earlier versions of R, it is necessary, since the default assumption was `stringsAsFactors = TRUE`.

and Evolution" (Paradis & Schliep 2018) to work with trees, *dplyr* (Wickham et al. 2021) to manipulate dataframes, *glottoTrees* (Round 2021a) to prepare linguistic phylogenies and *phyloWeights* (Round 2021b) to perform the analysis of genealogically-sensitive averages and proportions.

Packages need to be *installed*, i.e., downloaded and unpacked, just once. Later, they are *loaded* during each work session as needed.

To install the packages we will use, run these commands. You will only ever need to do this once. Since installation involves downloading, you will need an active internet connection.

```
install.packages("dplyr")
install.packages("ape")
install.packages("devtools")
library(devtools)
install_github("erichround/phyloWeights")
install_github("erichround/glottoTrees")
```

To load the installed packages, ready for use, run these commands:

```
library(dplyr)
library(ape)
library(phyloWeights)
library(glottoTrees)
```

2.3 Trees in R

Here we discuss how trees are created, manipulated and plotted in R. Terminology we will use includes: *tips* at the ends of trees, which in a linguistic tree would usually be the languages or lects; the *branches* of a tree; the *interior nodes* or just *nodes* of a tree, where branches join together; and the *root* of the tree, its deepest node. R will represent trees as complex objects, in which the tips, nodes and branches all appear, along with labels for the tips and nodes.

One of the simplest methods of constructing a tree in R begins with a description of the tree using a form a bracketing notation known as the *Newick* standard (Felsenstein n.d.). In its simplest form, a tree is represented in Newick format by a set of tip labels grouped by parentheses, separated by commas, and ending with a semicolon. For example, here is a string that represents a tree with four tips, `A`, `B`, `C` and `D`, which we assign to the object `my_newick`:

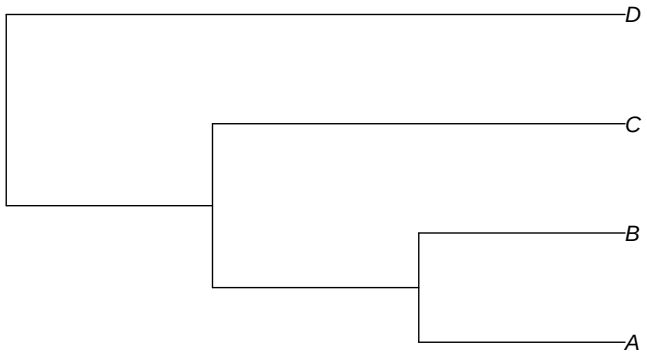
```
my_newick <- "(((A,B),C),D);"
```

A Newick-formatted string can then be converted to a tree object by supplying it as the `text` argument of the function `read.tree()`, from the *ape* package:

```
my_tree <- read.tree(text = my_newick)
```

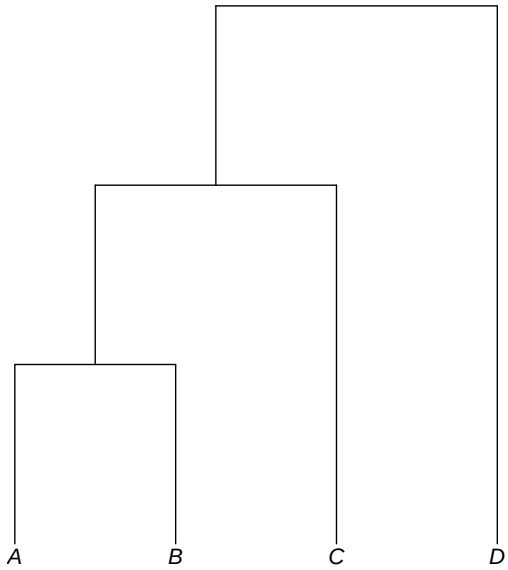
We can plot the tree using the `plot()` function:

```
plot(my_tree)
```



By default, trees in R are plotted horizontally following the convention in biology. The *glottoTrees* package provides a function `plot_glotto()` which plots trees in a more typical, downward-running linguistic format, as below.

```
plot_glotto(my_tree)
```

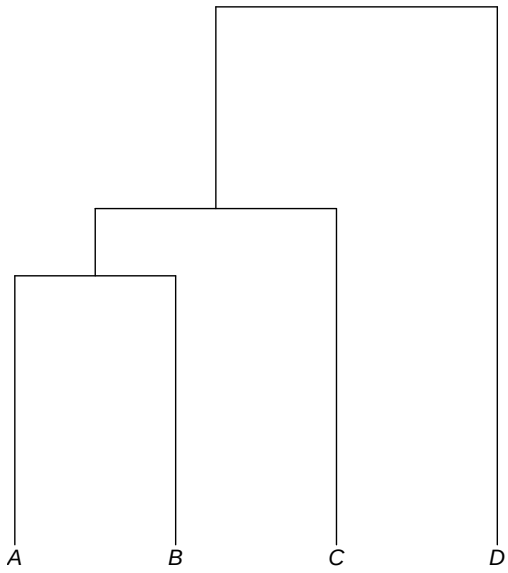


The tree object `my_tree` which we defined above did not include information about branch lengths. In Newick format, branch lengths are written with a preceding colon and appear directly after a language or the closing bracket for a subgroup:

```
my_newick2 <- "(((A:4,B:4):1,C:5):3,D:8);"
```

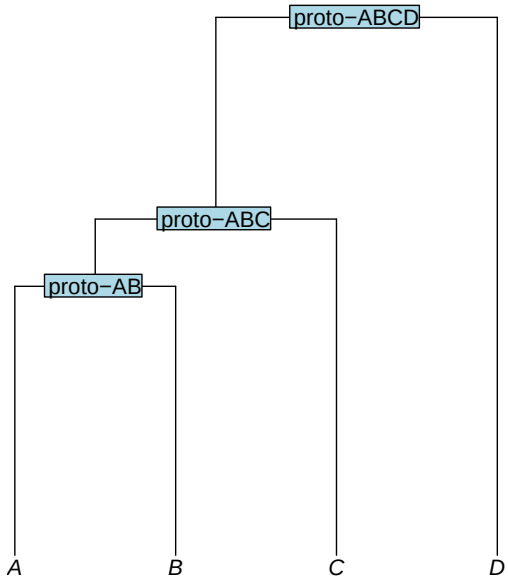
Converting this to a tree object and plotting it:

```
my_tree2 <- read.tree(text = my_newick2)
plot_glotto(my_tree2)
```



Trees can have labels not only for their tips, but also for their internal nodes. In linguistics, an internal node of a tree may be interpreted taxonomically, as representing a subgroup and labeled accordingly, or genealogically, as a proto-language from which the subgroup descends and labeled accordingly. In Newick format, labels for internal nodes are placed directly after a closing parenthesis. For example, here we add labels that reflect a genealogical interpretation of the nodes:

```
my_newick3 <- "(((A:4,B:4)proto-AB:1,C:5)proto-ABC:3,D:8)proto-ABCD;"
my_tree3 <- read.tree(text = my_newick3)
plot_glotto(my_tree3)
```



Technically speaking, trees are represented by R as objects with a customised class called `phylo`.

```
class(my_tree3)
```

```
## [1] "phylo"
```

A `phylo` object stores information about the tree *topology* (i.e., its branching structure), the branch lengths, and the labels of the tips and nodes. In R we often use the `$` operator to access one object that is contained inside another. For instance, the object `y` contained within the larger object `x` would be referred to as `x$y`.

Here are some examples:

```
my_tree3$edge.length
```

```
## [1] 3 1 4 4 5 8
```

```
my_tree3$tip.label
```

```
## [1] "A" "B" "C" "D"
```

```
my_tree3$node.label
```

```
## [1] "proto-ABCD" "proto-ABC"  "proto-AB"
```

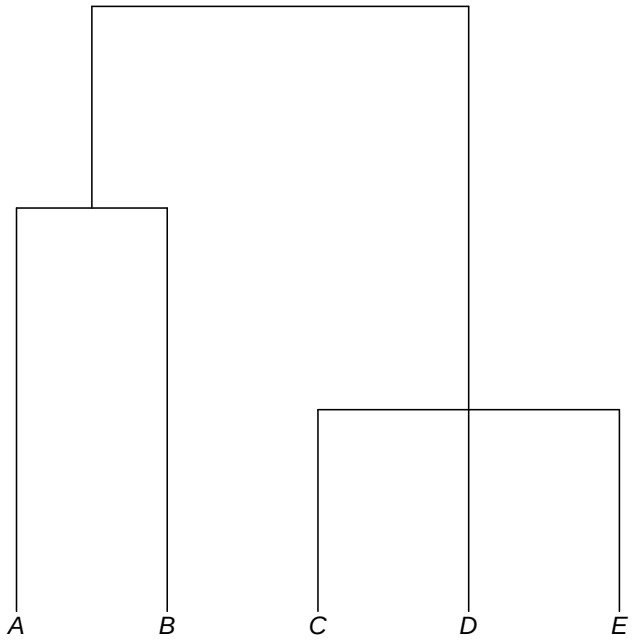
Another object class in R, related to the `phylo` class, is the `multiPhylo` class. Objects of the `multiPhylo` class are used to store multiple `phylo` trees in a single, larger object.

```
newick_a <- "(((A:4,B:4):1,C:5):3,D:8);"
newick_b <- "((A:2,B:2):1,(C:1,D:1,E:1):2);"
tree_a <- read.tree(text = newick_a)
tree_b <- read.tree(text = newick_b)
my_multiPhylo <- c(tree_a, tree_b)
class(my_multiPhylo)
```

```
## [1] "multiPhylo"
```

For reasons we won't go into here, the `phylo` trees inside a `multiPhylo` object are not accessed using the `$` operator but using double square brackets. For example, here we refer to the second tree inside the object `my_multiPhylo` by writing `my_multiPhylo[[2]]`:

```
plot_glotto(my_multiPhylo[[2]])
```



Before concluding this section, a final word is in order about the irrelevance of the left-to-right arrangement of trees. In a tree, there is no meaningful difference between (A,B) and (B,A): in both, A and B are sisters under a shared parent node. Similarly, these are all equivalent: (A,B,C), (A,C,B), (B,A,C), (B,C,A), (C,A,B) and (C,B,A). And likewise, these are all equivalent: (A,(B,C)), (A,(C,B)), ((B,C),A) and ((C,B),A).

3 Genealogically-sensitive averages and proportions

We now turn to the calculation of genealogically-sensitive proportions and averages. To run the code in this and subsequent sections, ensure that the packages described in Section 2.2 have been installed and loaded.

Calculating averages and proportions will require two key components:

1. A `phylo` or `multiPhylo` object containing one or more trees.
2. A dataframe, which (i) contains the typological data to be averaged and (ii) relates that data to the tips of the trees.

The `phylo` or `multiPhylo` object can be manually defined, as described in Section 2.3, can be read from a file,[2] or it can be constructed by using and adjusting materials freely available from glottolog.com, as described below in Section 4.

The dataframe can be manually defined or be read from a file. Perhaps the easiest method is to read from a file that you have created and saved in "CSV" (comma separated value) format. CSV files can be created in commercial spreadsheet software like Excel, and then read by R using the `read.csv()` function like this:

```
my_dataframe <- read.csv("my_csv_file.csv")
```

The dataframe must contain one column named `tip` (note that in R, names of columns and other objects are case sensitive) plus at least one column containing numerical data. The contents of the `tip` column must be the same as the tip labels of the tree(s) in the `phylo` or `multiPhylo` object. The contents of the numerical columns will depend on whether a proportion or an average is desired. To calculate a proportion, fill a numerical column with 1 if the language possesses the property and 0 if it does not. To calculate an average, fill a numerical column with the values of the variable for each language.

As an example, in order to apply these analyses to the four languages in Figure 2a,b,c of the main paper, here are the trees that would be needed, which are placed inside a single `multiPhylo` object:

```
newick_Fig2a <- "(((A:1,B:1,C:1):1,D:2):0.3);"
newick_Fig2b <- "(((A:0.2,B:0.2,C:0.2):1.8,D:2):0.3);"
newick_Fig2c <- "(((A:1.8,B:1.8,C:1.8):0.2,D:2):0.3);"
tree_Fig2a <- read.tree(text = newick_Fig2a)
tree_Fig2b <- read.tree(text = newick_Fig2b)
tree_Fig2c <- read.tree(text = newick_Fig2c)
multiPhylo_Fig2 <- c(tree_Fig2a, tree_Fig2b, tree_Fig2c)
```

The dataframe required is shown below. In addition to the `tip` column, it contains two numerical columns, `is_SOV` and `n_consonants`. As good housekeeping, we recommend using column names of the form `is_X` or `has_X` for columns that contain data for proportions, and names of the form `n_X` for columns that contain counts to be averaged.

```
data_Fig2 <- data.frame(tip = c("A", "B", "C", "D"),
                        is_SOV = c(1, 1, 1, 0),
                        n_consonants = c(18, 20, 22, 40),
                        stringsAsFactors = FALSE)
```

Genealogically-sensitive averages and proportions are obtained using the *phyloWeights* function `phylo_average()`, specifying its arguments `phy` and `data` as in the example below. Here we have assigned the output of this function to a new object `results_Fig2`. We recommend always assigning the output of `phylo_average()` to an object. We will see below how to extract from it the various parts of the results.

```
results_Fig2 <- phylo_average(phy = multiPhylo_Fig2, data = data_Fig2)
```

The function `phylo_average()` may take up to several minutes to run if the tree is large, or many trees are provided. It will return error messages if the inputs provided to it are not what is required.

[2] See online documentation of the *ape* package for reading trees from various common file formats.

The results object will contain several parts, which can be accessed using the `$` operator. In `$phy` will be the tree(s) that were supplied and in `$data` will be the dataframe that was supplied, e.g.:

```
results_Fig2$data
```

```
##   tip is_SOV n_consonants
## 1   A      1           18
## 2   B      1           20
## 3   C      1           22
## 4   D      0           40
```

In `$ACL_weights` is a dataframe containing one column for each tree provided, in which appear the phylogenetic weights obtained using the ACL method. The dataframe also contains all of the non-numeric columns of the input `data` dataframe. In `$BM_weights` is a similar dataframe, with the phylogenetic weights obtained using the BM method:

```
results_Fig2$ACL_weights
```

```
##   tip tree1     tree2     tree3
## 1   A   0.2 0.1724138 0.2380952
## 2   B   0.2 0.1724138 0.2380952
## 3   C   0.2 0.1724138 0.2380952
## 4   D   0.4 0.4827586 0.2857143
```

```
results_Fig2$BM_weights
```

```
##   tip     tree1     tree2     tree3
## 1   A 0.2317460 0.1856200 0.2489451
## 2   B 0.2317460 0.1856200 0.2489451
## 3   C 0.2317460 0.1856200 0.2489451
## 4   D 0.3047619 0.4431401 0.2531646
```

In `$ACL_averages` is a dataframe with one row per tree and one column for each numerical column in the `data` dataframe. These are filled with the genealogically-sensitive averages or proportions obtained using the ACL method. In `$BM_averages` appear the genealogically-sensitive averages or proportions obtained using the BM method:

```
results_Fig2$ACL_averages
```

```
##    tree    is_SOV n_consonants
## 1 tree1 0.6000000     28.00000
## 2 tree2 0.5172414     29.65517
## 3 tree3 0.7142857     25.71429
```

```
results_Fig2$BM_averages
```

```
##    tree    is_SOV n_consonants
## 1 tree1 0.6952381     26.09524
## 2 tree2 0.5568599     28.86280
## 3 tree3 0.7468354     25.06329
```

It is possible to save any of these dataframes to a file using the `write.csv()` function, for example:

```
write.csv(results_Fig2$ACL_averages, file = "my_ACL_averages.csv")
```

4 Using and adapting trees from glottolog.com

Glottolog.com (Hammarström et al. 2021) contains many useful resources for quantitative typology and the package *glottoTrees* (Round 2021a) has been written to help linguists make the most of these resources,

including by modifying them as they desire. This section covers the glottolog data itself and the functionality of *glottoTrees*. We introduce glottolog's genealogical data in Section 4.1, discussing how to locate metadata about languages and families of interest, and how to view glottolog's linguistic family trees. Since genealogically-sensitive averages and proportions require languages to be represented within a single tree, we then discuss how glottolog's individual trees can be combined in Section 4.2. Since typological studies will often examine language varieties at a level of granularity that differs from glottolog's own, in Section 4.3 we discuss how to add and remove languages from trees. In Section 4.4 we discuss how to add branch lengths to trees, since branch lengths are necessary for the calculation of genealogically-sensitive averages and proportions. Section 4.5 discusses how to export trees for use with other software.

4.1 Glottolog's genealogical data

Glottolog provides metadata about the world's language varieties, their division into language families and the hierarchical subgrouping of languages inside those families. Naturally, there are many points of contention in linguistics about what the world's stock of languages and dialects actually is, how it groups into families, and how the families themselves are subgrouped. Glottolog provides one set of answers, and structures them in a way which provides typologists with a basis for carrying out changes to suit their own hypotheses. In later sections we will see how this can be done. In this section we describe glottolog's own global linguistic metadata.

At time of writing, the current version of glottolog is v4.4. The *glottoTrees* package contains a copy of the v4.4 metadata covering language names, language identification codes, family names, geographical groupings, and family trees. The original metadata files that contain this information are currently available at https://glottolog.org/meta/downloads, where a file named `tree_glottolog_newick.txt`[3] contains glottolog's trees, and `languages_and_dialects_geo.csv` provides geographical metadata.

Language metadata can be accessed using the *glottoTrees* function `get_glottolog_languages()`. This function returns a dataframe of close to twenty-six thousand rows. To view it in full, we suggest saving it to a CSV file and opening it in spreadsheet software such as Excel:

```
language_metadata <- get_glottolog_languages()
write.csv(language_metadata, "language_metadata.csv")
```

Here are the first ten rows:

```
language_metadata <- get_glottolog_languages()
head(language_metadata, n = 10)
```

```
##    glottocode isocodes       name name_in_tree position tree            tree_name
## 1    3adt1234          3Ad-Tekles   3Ad-Tekles      tip  391          Afro-Asiatic
## 2    aala1237              Aalawa       Aalawa      tip   94          Austronesian
## 3    aant1238          Aantantara   Aantantara      tip   90 NuclearTransNewGuinea
## 4    aari1238     <NA>       <NA>   Aari-Gayil     node   22           SouthOmotic
## 5    aari1239      aiw        Aari         Aari      tip   22           SouthOmotic
## 6    aari1240      aay     Aariya       Aariya     <NA>   NA                  <NA>
## 7    aasa1238      aas      Aasax        Aasax      tip  391          Afro-Asiatic
## 8    aasd1234            Aasdring     Aasdring      tip  269         Indo-European
## 9    aata1238           Aatasaara    Aatasaara      tip   90 NuclearTransNewGuinea
## 10   abaa1238              Rngaba       Rngaba      tip  345          Sino-Tibetan
```

Listed here are glottolog's languages, dialects, subgroups and families. These entities are identified by a name, an ISO-639-3 code if available (format: three letters) and a glottolog-specific *glottocode* (format: four letters followed by four digits[4]). Also described is the entity's relationship to a glottolog tree: the representation of

[3] Although this file is named `tree_glottolog_newick.txt`, it is not in true Newick format due to its use of square brackets in node and tip labels (Felsenstein n.d.). In *glottoTrees*, the square brackets in glottolog's file are converted to angled brackets (i.e., greater-than and less-than symbols), to bring them into conformity with the Newick standard.

[4] There are two exceptional glottocodes with numbers in the initial four characters: b10b1234 and 3adt1234.

its name in the tree (which may differ slightly from the name used elsewhere by glottolog[5]), its position (as tip or node), and the tree's number and name.

By default, the metadata functions in *glottoTrees*, such as `get_glottolog_languages()`, will return information about the most recent version of glottolog which the package contains. To access older versions, supply the version number via the `glottolog_version` argument:[6]

```
language_metadata_v4.3 <- get_glottolog_languages(glottolog_version = "4.3")
head(language_metadata_v4.3, n = 10)
```

```
##    glottocode isocodes       name name_in_tree position tree             tree_name
## 1    3adt1234          3Ad-Tekles   3Ad-Tekles      tip  186          Afro-Asiatic
## 2    aala1237              Aalawa       Aalawa      tip  205          Austronesian
## 3    aant1238          Aantantara   Aantantara      tip  145 NuclearTransNewGuinea
## 4    aari1238     <NA>       <NA>   Aari-Gayil     node   85           SouthOmotic
## 5    aari1239      aiw        Aari         Aari      tip   85           SouthOmotic
## 6    aari1240      aay     Aariya       Aariya     <NA>   NA                  <NA>
## 7    aasa1238      aas       Aasax        Aasax      tip  186          Afro-Asiatic
## 8    aasd1234             Aasdring     Aasdring      tip  179         Indo-European
## 9    aata1238           Aatasaara    Aatasaara      tip  145 NuclearTransNewGuinea
## 10   abaa1238              Rngaba       Rngaba      tip  329          Sino-Tibetan
```

Briefer metadata about glottolog's language families can be accessed using the *glottoTrees* function `get_glottolog_families()`. This returns a dataframe of 420 rows, so to view it in full, we also suggest saving it to a CSV file and opening it in spreadsheet software. Here are the first ten rows:

```
family_metadata <- get_glottolog_families()
head(family_metadata, n = 10)
```

```
##    tree           tree_name n_tips n_nodes main_macroarea
## 1     1                 Yam     33      18      Papunesia
## 2     2     Mongolic-Khitan     66      25        Eurasia
## 3     3 Kol{PapuaNewGuinea}      2       1      Papunesia
## 4     4       Namla-Tofanma      2       1      Papunesia
## 5     5          Tanahmerah      1       1      Papunesia
## 6     6         Jarawa-Onge      2       1        Eurasia
## 7     7        Ta-Ne-Omotic     29      15         Africa
## 8     8              Pomoan     10       7  North America
## 9     9         WesternDaly     14       7      Australia
## 10   10           Yangmanic      3       1      Australia
```

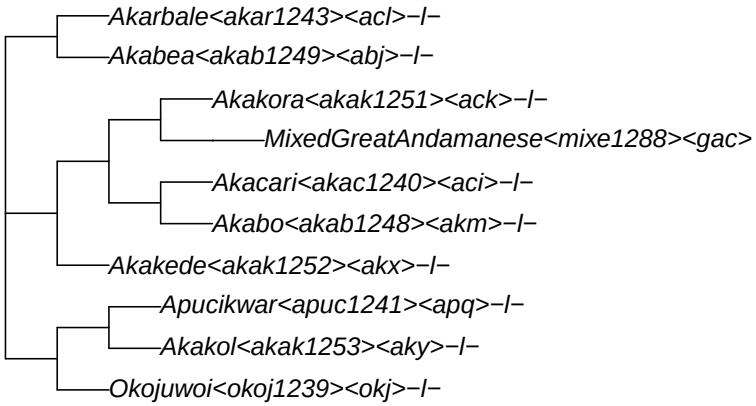
Glottolog v4.4 divides the world's languages into 420 families, including 138 isolates, and it provides a tree for each. Together, the 420 trees contain 8,209 internal nodes and 17,008 tips, many of which represent varieties that would typically be considered dialects. Geographically, glottolog assigns each language variety to one of six *macroareas*: Africa, Australia, Eurasia, Papunesia, South America or North America. The *glottoTrees* metadata includes a column `main_macroarea`. This is the one macroarea which contains more of the family's language varieties than any other. We will see how this information can be useful in Section 4.2.

Glottolog's 420 family trees are stored in a `multiPhylo` object named `glottolog_trees_v4.4`. For example, here is glottolog's representation of the Great Andamanese family, which is tree 340 within the object `glottolog_trees_v4.4`. For readability, we plot this tree horizontally:

```
tree_GA <- glottolog_trees_v4.4[[340]]
plot(tree_GA, x.lim = c(-0.3, 14))
```

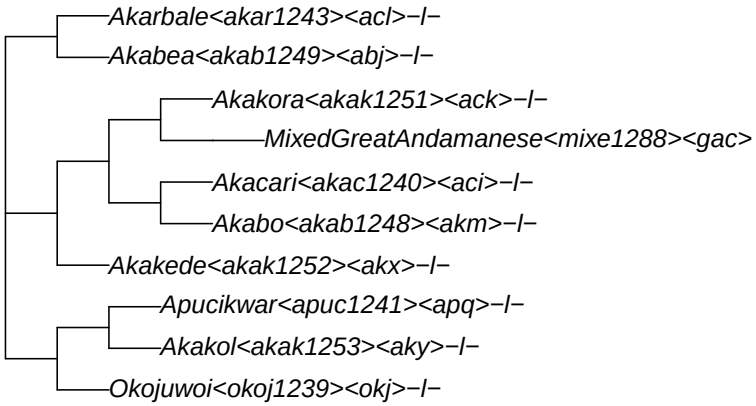
[5]The differences are systematic and are made in order to conform with the permissible Newick format of tree labels: spaces and apostrophes are removed, parentheses are replaced by braces, and commas are replaced by forward slashes.

[6]*glottoTrees* currently contains information from glottolog versions 4.0, 4.1, 4.2, 4.3 and 4.4 (which is current at time of writing). Our intention is to update *glottoTrees* as glottolog updates in the future.



Just above, we obtained the tree for Great Andamanese by referring to its tree number (340) in the `glottolog_trees_v4.4` object. The package *glottoTrees* also provides a function `get_glottolog_trees()` which enables trees to be obtained using the glottolog name for their families, for instance:

```
tree_GA <- get_glottolog_trees("GreatAndamanese")
plot(tree_GA, x.lim = c(-0.3, 14))
```



If you know the name of one or more families and would like to now the number of their trees, use `which_tree()`:

```
which_tree("GreatAndamanese")
```

```
## GreatAndamanese
##             340
```

```
which_tree(c("Turkic", "Tupian", "Tuu"))
```

```
## Turkic Tupian    Tuu
##    217     32     76
```

Both `get_glottolog_trees()` and `which_tree()` allow the usage of a `glottolog_version` argument, to refer to older versions of glottolog. For instance, here are the tree numbers of the same families in version 4.1:

```
which_tree("GreatAndamanese", glottolog_version = "4.1")
```

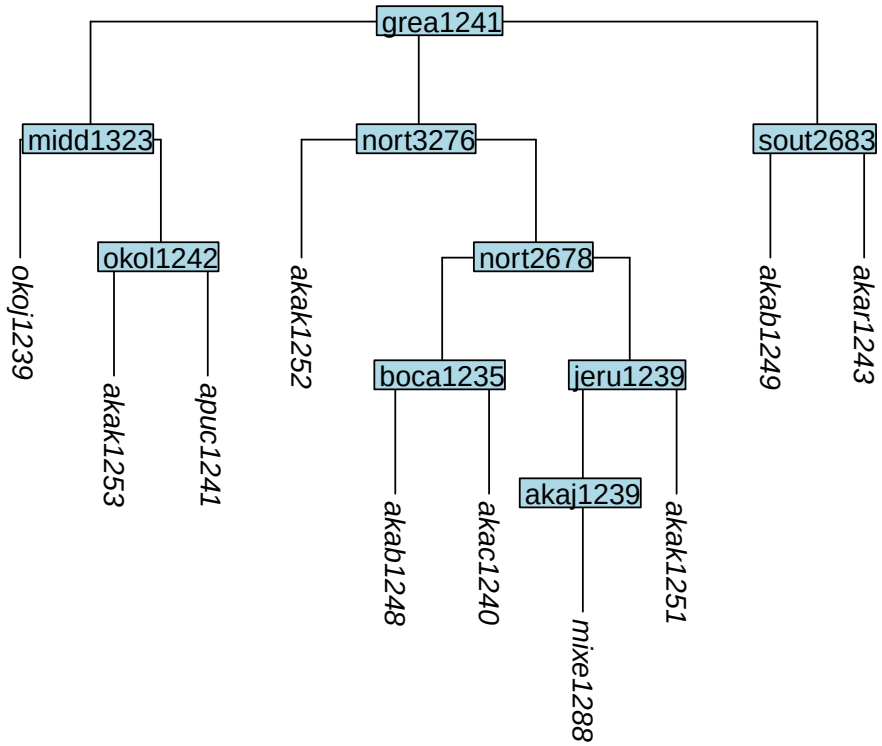
```
## GreatAndamanese
##               6
```

```
which_tree(c("Turkic", "Tupian", "Tuu"), glottolog_version = "4.1")
```

```
## Turkic Tupian    Tuu
##     66    297     80
```

In glottolog's trees, the tip labels are rather long, consisting of a name followed by a glottocode in angled brackets, an ISO code in angled brackets (if one exists) and possibly the string "-l-". Node labels (not shown in the tree above) have the same structure. The *glottoTrees* function `abridge_labels()` will shorten labels to just the glottocode, for example:

```
tree_GA_abr <- abridge_labels(tree_GA)
plot_glotto(tree_GA_abr)
```



The function `abridge_labels()` will issue a warning if there are tip or node labels in which it is unable to identify a glottocode. We will see an example of this shortly below.

In glottolog's trees, the branches are all of equal length. We will discuss how to assign more realistic branch lengths in Section 4.4.

4.2 How to combine trees

As discussed in the main paper, the comparison of languages across language families unavoidably carries a commitment to a genealogical hypothesis, even if that hypotheses is, tacitly, that all families are equally (un)related. Given that making such hypotheses is unavoidable, it will be most beneficial for progress in the field to make them explicit. To enable typologists to explore genealogical hypotheses and to make those hypotheses explicit, *glottoTrees* provides tools for combining multiple glottolog trees into one.

To begin with a small example, here we combine five glottolog families to represent the hypothesised Arnhem group in northern Australia (Green 2003). First we create a `multiPhylo` object containing the five glottolog language families (Gunwinyguan, Mangarrayi-Maran, Maningrida, and the isolates Kungarakany and Gaagudju):

```
arnhem_family_names <-
  c("Gunwinyguan", "Mangarrayi-Maran", "Maningrida", "Kungarakany", "Gaagudju")
multiPhylo_arnhem <- get_glottolog_trees(arnhem_family_names)
```

The *glottoTrees* function `assemble_rake()` enables the trees in a `multiPhylo` object to be assembled into a single tree with a rake structure at its root. Here we apply `assemble_rake()` to our `multiPhylo` object and

assign the resulting, single tree to the object `tree_arnhem`.

```
tree_arnhem <- assemble_rake(multiPhylo_arnhem)
```

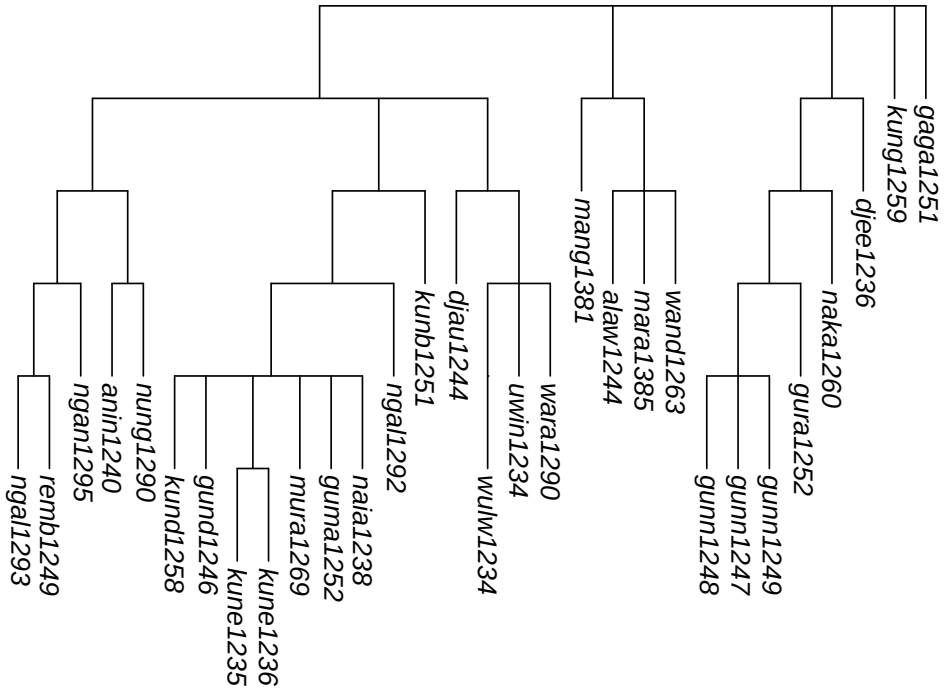
For plotting, it will be convenient to shorten the labels in the tree to just the glottocodes, using `abridge_labels()`. However, the root node in our newly created tree `tree_arnhem` has no label. Accordingly, the function `abridge_labels()` will issue a warning, that it encountered one node without a glottocode. This is not an error message, and `abridge_labels()` still shortens all labels to glottocodes where it can; it is just flagging the fact that it was not able to do so in all cases.

```
tree_arnhem_abr <- abridge_labels(tree_arnhem)
```

```
## Warning in abridge_labels(tree_arnhem): Labels without glottocodes were detected and
## left unchanged for: 0 tip(s); 1 node(s):
```

Plotting the resulting tree enables us to inspect our newly created Arnhem tree. Note how all five families are joined to the root in a rake-like structure, without any additional subgrouping.

```
plot_glotto(tree_arnhem_abr, nodelabels = FALSE)
```



It is possible to give a combined tree more structure, by using `assemble_rake()` iteratively. For instance, suppose we wished to hypothesise that Gunwinyguan, Mangarrayi-Maran and Maningrida form their own subgroup. First, we create a `multiPhylo` object containing those three trees, and combine it into a single rake tree, which we call `tree_A`:

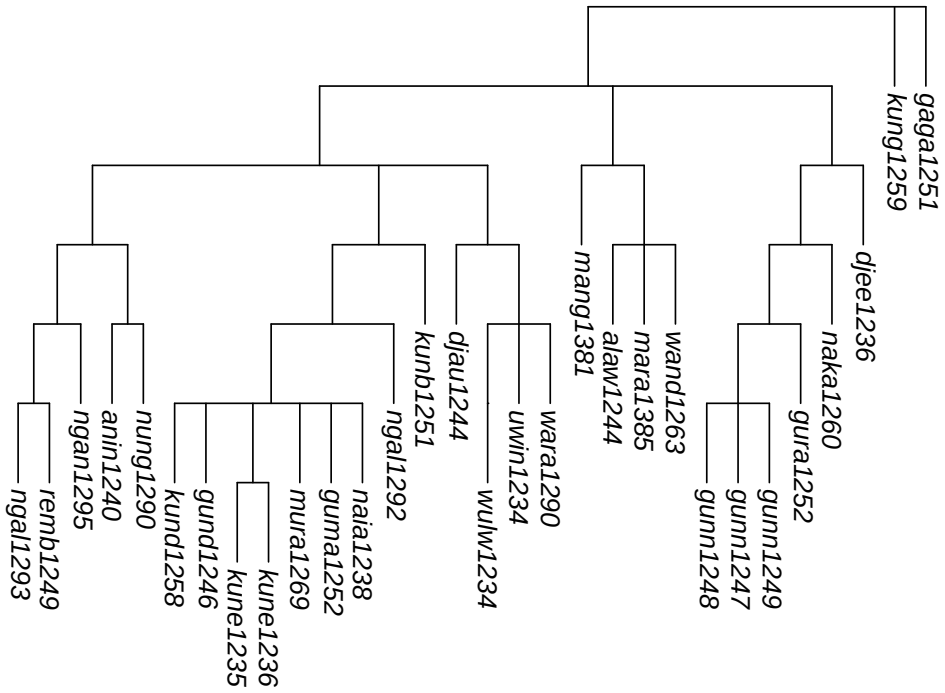
```
multiPhylo_A <- get_glottolog_trees(c("Gunwinyguan", "Mangarrayi-Maran", "Maningrida"))
tree_A <- assemble_rake(multiPhylo_A)
```

Then we create the final tree by combining `tree_A` with the two isolate family trees:

```
multiPhylo_arnhem2 <- c(tree_A, get_glottolog_trees(c("Kungarakany", "Gaagudju")))
tree_arnhem2 <- assemble_rake(multiPhylo_arnhem2)
tree_arnhem2_abr <- abridge_labels(tree_arnhem2)
```

```
## Warning in abridge_labels(tree_arnhem2): Labels without glottocodes were detected and
## left unchanged for: 0 tip(s); 2 node(s): ,
```

```
plot_glotto(tree_arnhem2_abr, nodelabels = FALSE)
```



Typological studies often examine languages from very many families. To group all 420 families into a single 'supertree', *glottoTrees* provides the function `assemble_supertree()`. By default, the function returns a supertree that divides first into glottolog's six macroareas, with an internal node for each, and directly below these macroarea nodes appear all of the glottolog families, grouped by their `main_macroarea` mentioned in Section 4.1 above. This tree is enormous, so we do not plot it here. It is obtained like this:

```
my_supertree <- assemble_supertree()
```

The highest-level, macroarea groupings can also be controlled through the function's argument `macro_groups`. For instance, to group all of the world's families directly into a 420-pronged rake structure, set `macro_groups = NULL`:

```
my_supertree <- assemble_supertree(macro_groups = NULL)
```

It is also possible to group macroareas together, for example, to combine North and South America into a single group. Grouping of macroareas is achieved by setting the `macro_groups` argument to a *list* whose items are the desired groups of macroareas. Each group will then appear as one of the highest-level nodes of the tree, and all of its families below it. For instance, to keep all of glottolog's macroareas separate, but to combine North and South America into a single group, the following code would be used. First we define a list, which we've called `my_list`, within which any groupings containing more than one macroarea are represented as a vector, using the `c()` function:

```
my_list <- list("Africa", "Australia", "Eurasia", "Papunesia",
                c("South America", "North America"))
```

We then use that list as the `macro_groups` argument of `assemble_supertree()`:

```
my_supertree <- assemble_supertree(macro_groups = my_list)
```

Taking a second example, to create a supertree containing only the families whose `main_macroarea` is either Africa or Eurasia, and to place Africa and Eurasia under separate, highest-level nodes, we would use:

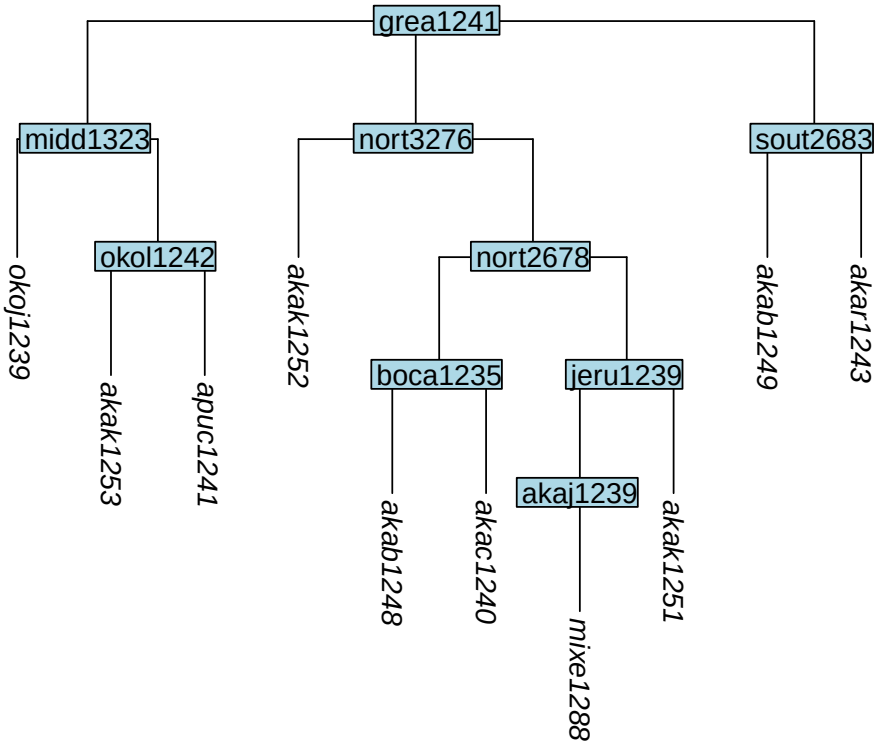
```
my_list <- list("Africa", "Eurasia")
my_supertree <- assemble_supertree(macro_groups = my_list)
```

4.3 How to modify trees

There are several reasons why typologists may wish to use a tree that departs from the glottolog trees. Most commonly, a typological study will cover a set of languages that differs from the set of tips in any single glottolog tree, either through the exclusion of some of the lects that glottolog represents as tips or through the distinction of additional lects. A third case that can arise is when glottolog places one or more dialects at the tree's tips and more a general, language node above them. The typologist may have data that applies to the language (an internal node) rather than the dialects (the tips), yet the calculation of genealogically-sensitive averages and proportions requires one's typological variables to be related to the tips of trees, not to internal nodes. In these cases and many others, the typologist may wish to alter the glottolog tree to suit the purposes of the research. The *glottoTrees* package supplies a set of functions to aid in performing each of these tree manipulations. In the section we introduce them and illustrate their use.

In the following examples, we will make use glottolog's representation of the Great Andamanese family, whose labels we shorten to just the glottocodes using `abridge_labels()`:

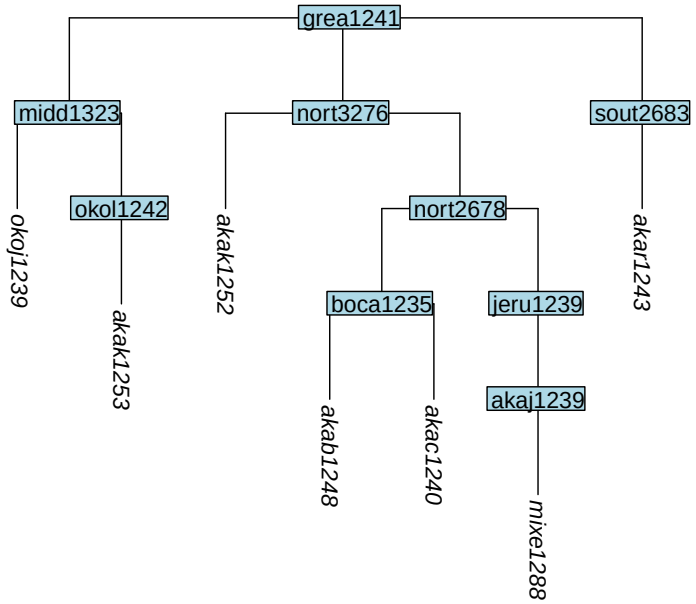
```
tree_GA <- get_glottolog_trees("GreatAndamanese")
tree_GA_abr <- abridge_labels(tree_GA)
plot_glotto(tree_GA_abr)
```



4.3.1 How to remove tips

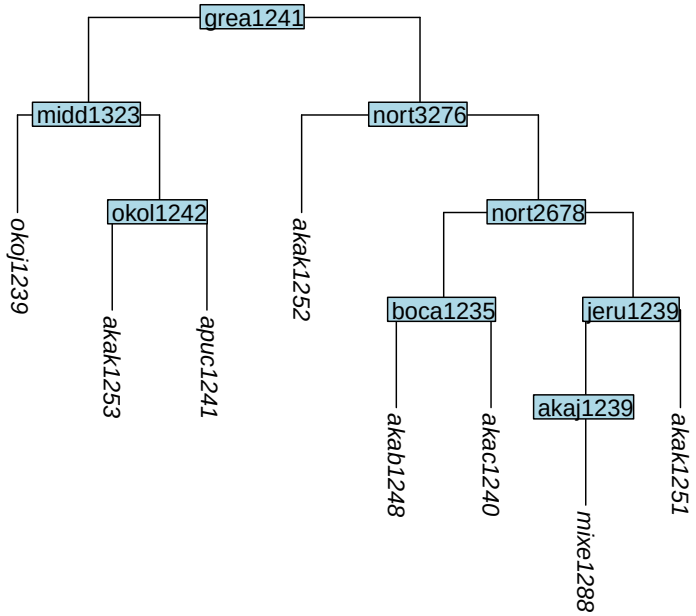
Firstly, we illustrate the removal of tips from a tree. There are two functions in *glottoTrees* for doing this. The function `remove_tip()` works by specifying which tips are to be removed, while the function `keep_tip()` works by specifying which tips are to be retained. First we will remove three of the original ten tips in the Great Andamanese tree. We do this by setting the `label` argument of `remove_tip()` to a vector containing the labels of the tips to be removed. Within the vector, the labels can appear in any order.

```
tree_GAa <- remove_tip(tree_GA_abr, label = c("akab1249", "akak1251", "apuc1241"))
plot_glotto(tree_GAa)
```



In this next example, we remove the tips `akab1249` and `akar1243`. These tips are the only tips that sit below the internal node `sout2683`. This is significant, because it triggers a convention in tree manipulation, that if all tips below a node are removed, then the node is removed also. We see that here:

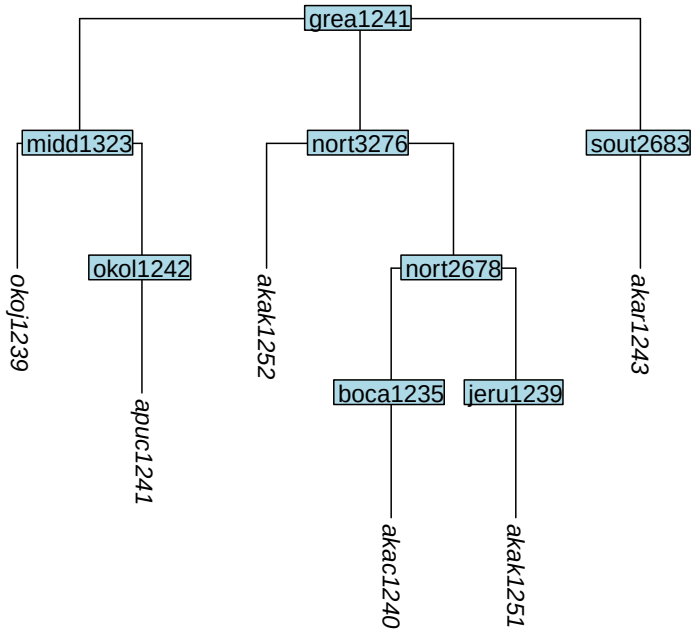
```
tree_GAb <- remove_tip(tree_GA_abr, label = c("akab1249", "akar1243"))
plot_glotto(tree_GAb)
```



We now illustrate the usage of the *glottoTrees* function `keep_tip()`. Here we use it to retain six of the original ten tips in the Great Andamanese. We do this by setting the `label` argument to a vector containing the labels of the six desired tips.

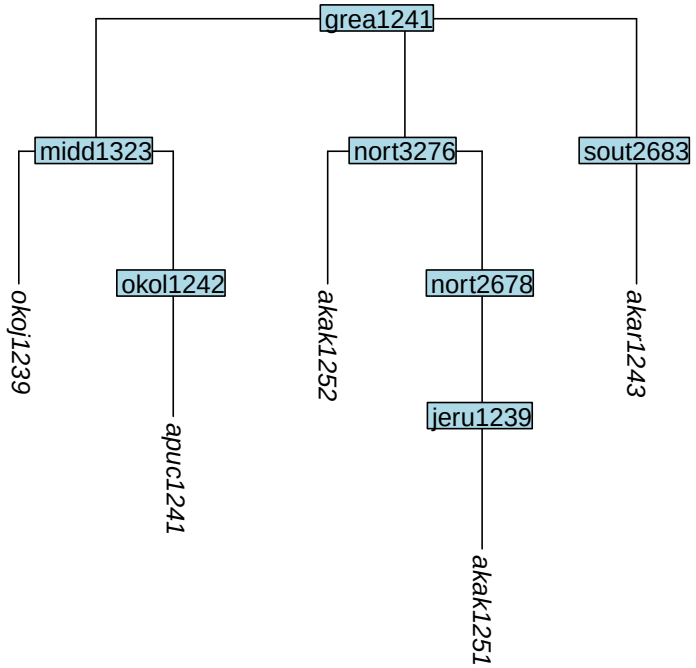
```
tree_GAc <- keep_tip(tree_GA_abr, label = c("akar1243", "akak1251", "akac1240",
                                            "akak1252", "apuc1241", "okoj1239"))
```

```
plot_glotto(tree_GAc)
```



As before, if our use of `keep_tip()` results in a node having all of the tips below it removed, then the node will also be removed automatically. This is illustrated here, where the node `boca1235` is removed automatically because neither of the tips below it are kept:

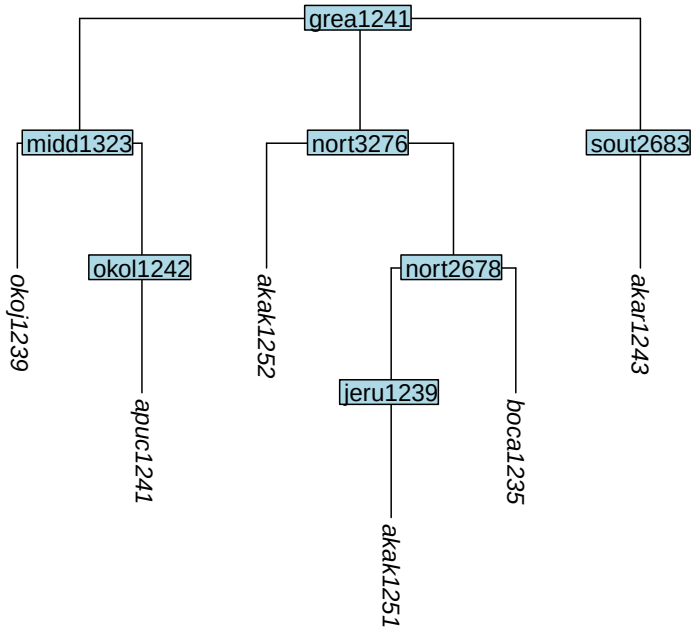
```
tree_GAd <- keep_tip(tree_GA_abr, label = c("akar1243", "akak1251", "akak1252",
                                            "apuc1241", "okoj1239"))
plot_glotto(tree_GAd)
```



4.3.2 How to remove tips and convert nodes to tips

As mentioned earlier, many of the tips in glottolog's trees correspond to dialects, with languages represented as nodes above the dialectal tips. One usage case we foresee is that a typologist will wish to study a set of language varieties, some of which correspond to glottolog's tips and some of which correspond to nodes. The *glottoTrees* function `keep_as_tips()` takes an argument `label` which can contain both tip labels and node labels. Any tips will be kept, and any nodes will be converted into tips, with all of the structure below them being removed. Be mindful when using `keep_as_tips()` that it is not possible to both convert a node into a tip and also retain the structure below it, such as tips that it dominates. Here we keep the same tips as in the tree above, while also converting the node `boca1235` into a tip:[7]

```
tree_GAe <- keep_as_tip(tree_GA_abr, label = c("akar1243", "akak1251", "akak1252",
                                               "apuc1241", "okoj1239", "boca1235"))
plot_glotto(tree_GAe)
```



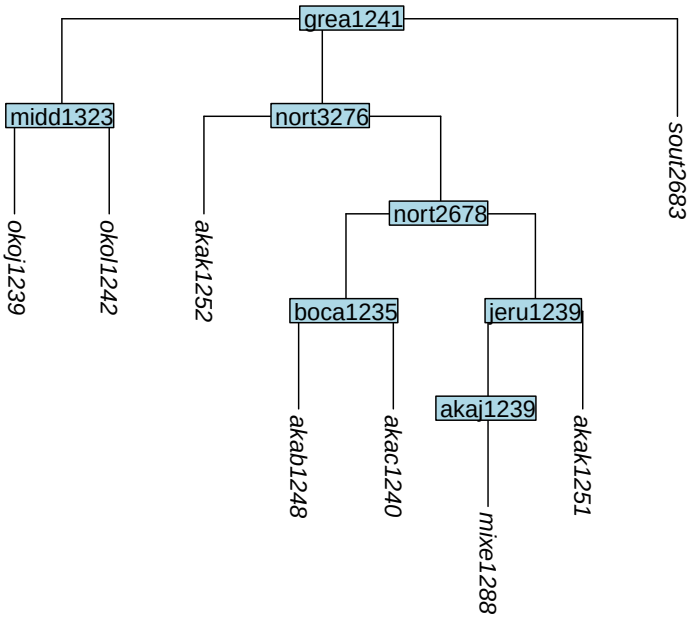
One workflow that we envision for `keep_as_tip()` is that the typologist has prepared a CSV file, one of whose columns is named `tip` and contains the glottocodes of all the language varieties in the study. This CSV file can be loaded in R and assigned to a dataframe, and then its `tip` column can be passed to `keep_as_tip()` as the value of the `labels` argument, like this:

```
my_dataframe <- read.csv("my_data_file.csv", stringsAsFactors = FALSE)
my_new_tree <- keep_as_tip(my_old_tree, label = my_dataframe$tip)
```

To just convert one or more nodes into tips, use `convert_to_tip()`, as we do here to convert the nodes `okol1242` and `sout2683` to tips:

```
tree_GAf <- convert_to_tip(tree_GA_abr, label = c("okol1242", "sout2683"))
plot_glotto(tree_GAf)
```

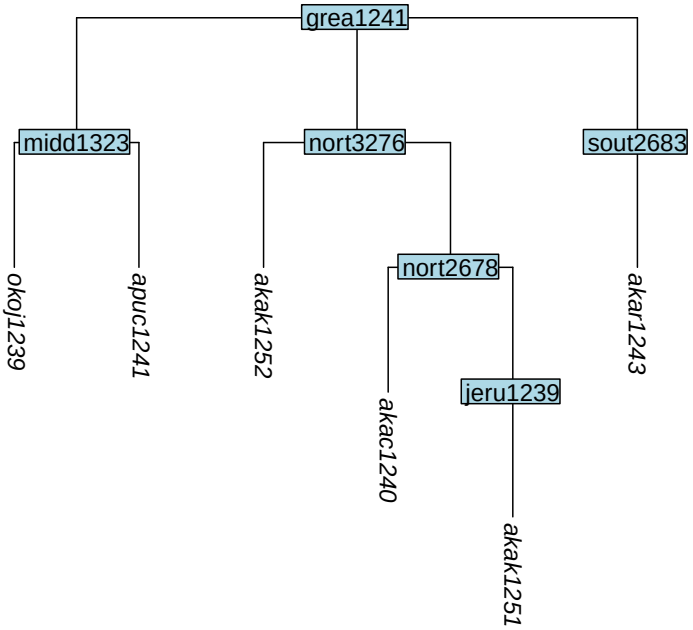
[7] Converting nodes into tips may cause them to move to the left or right in the tree plot. The movement is meaningless, since a subgroup (A, B) is exactly the same as subgroup (B, A). Since the movement is meaningless, it's also harmless.



4.3.3 How to remove internal nodes

Sometimes, the removal of tips will cause one or more of the remaining tips to sit below a node which dominates only it. This reflects that fact that `remove_tip()`, `keep_tip()` and `keep_as_tip()` all preserve the original *depth* of any tips that remain in the tree (the reader may like to confirm this by reviewing the plots above). Depending on the researcher's needs, this outcome may or may not be desirable. If it is undesirable, then non-branching, internal nodes can be removed using the *glottoTrees* function `collapse_node()`. For instance, here we remove two of the non-branching nodes from the tree `tree_GAc` above, by naming them in the `label` argument of `collapse_node()`. In the resulting tree, these nodes have been removed, thus reducing the depth of the tips below them:

```
tree_GAg <- collapse_node(tree_GAc, label = c("boca1235", "okol1242"))
plot_glotto(tree_GAg)
```



When deciding whether to collapse nodes, in can be handy to know which nodes in a tree that have only one child below them. The function `nonbranching_nodes()` will return a vector of all such nodes, for example:

```
nonbranching_nodes(tree_GAc)
```

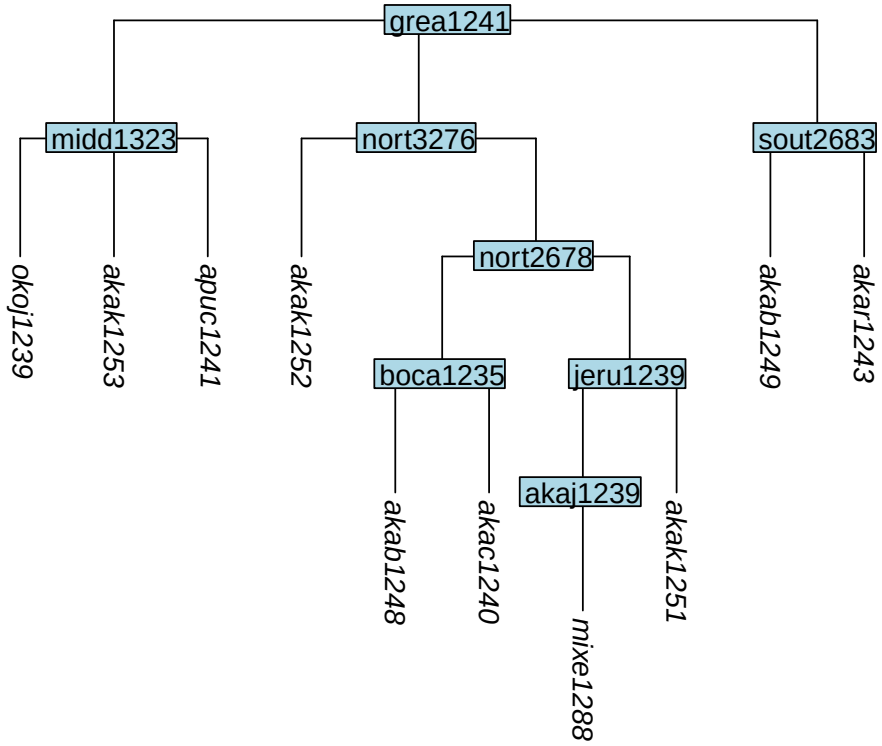
```
## [1] "okol1242" "boca1235" "jeru1239" "sout2683"
```

```
nonbranching_nodes(tree_GAg)
```

```
## [1] "jeru1239" "sout2683"
```

The function `collapse_node()` can also be used to alter a subgrouping hypothesis, and specifically, to remove a layer of subgrouping, converting a nested structure ((A,B),C) into a flat structure (A,B,C). For instance, here we remove the `okol1242` node of the original glottolog Great Andamanese tree, converting its two daughter languages into sisters of `okoj1239`:

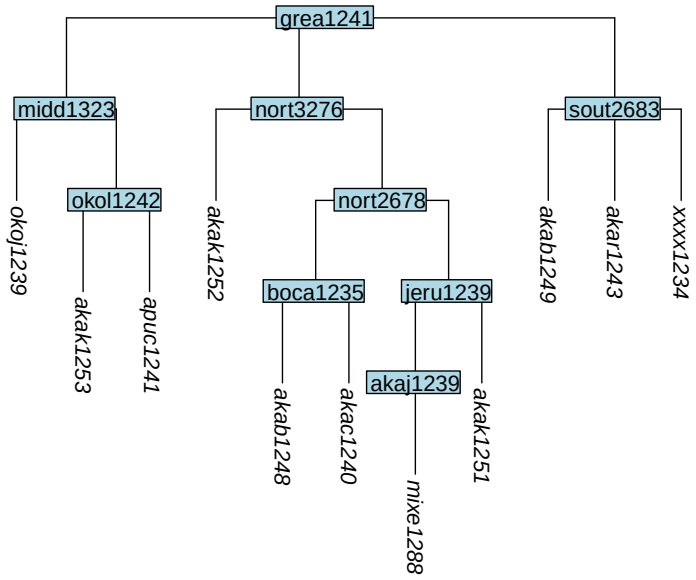
```
tree_GAh <- collapse_node(tree_GA_abr, label= "okol1242")
plot_glotto(tree_GAh)
```



4.3.4 How to add tips

The function `add_tip()` allows tips to be added to a tree. The `label` argument specifies the name of the new tip, while `parent_label` specifies the label of the node below which the new tip should appear. Here we add a tip `xxxx1234` below the node `sout2683`:

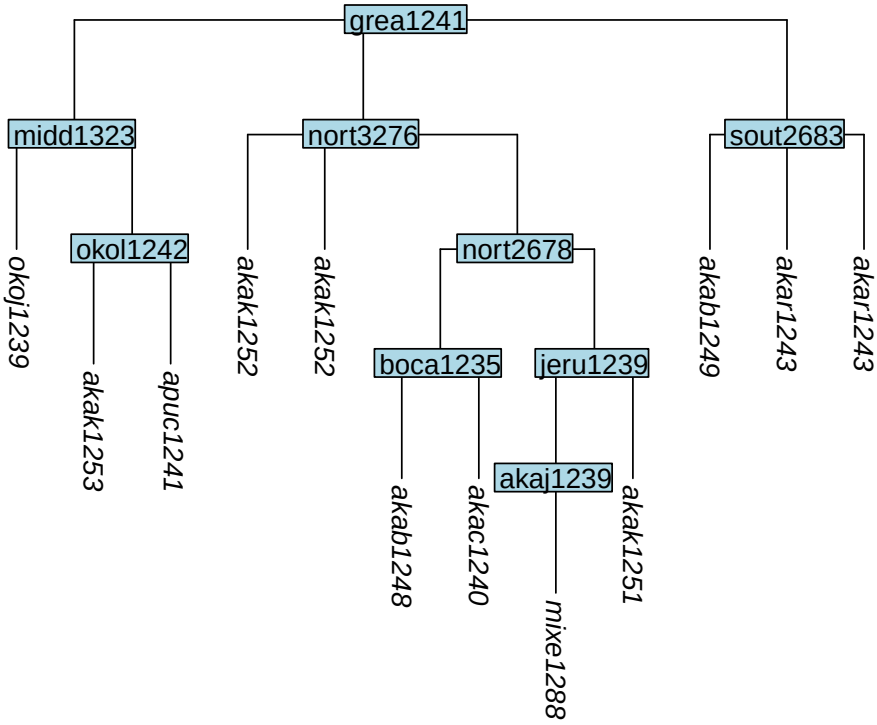
```
tree_GAi <- add_tip(tree_GA_abr, label = "xxxx1234", parent_label = "sout2683")
plot_glotto(tree_GAi)
```



4.3.5 How to clone tips

Next we illustrate the cloning of tips. Cloning tips may be useful when glottolog provides only one glottocode, and thus only one tree tip, corresponding to multiple lects in the typologist's study. To clone a tip, use the function `clone_tip()` and in the `label` argument, provide a vector of the tips to be cloned. Here we clone tips `akar1243` and `akak1252`:

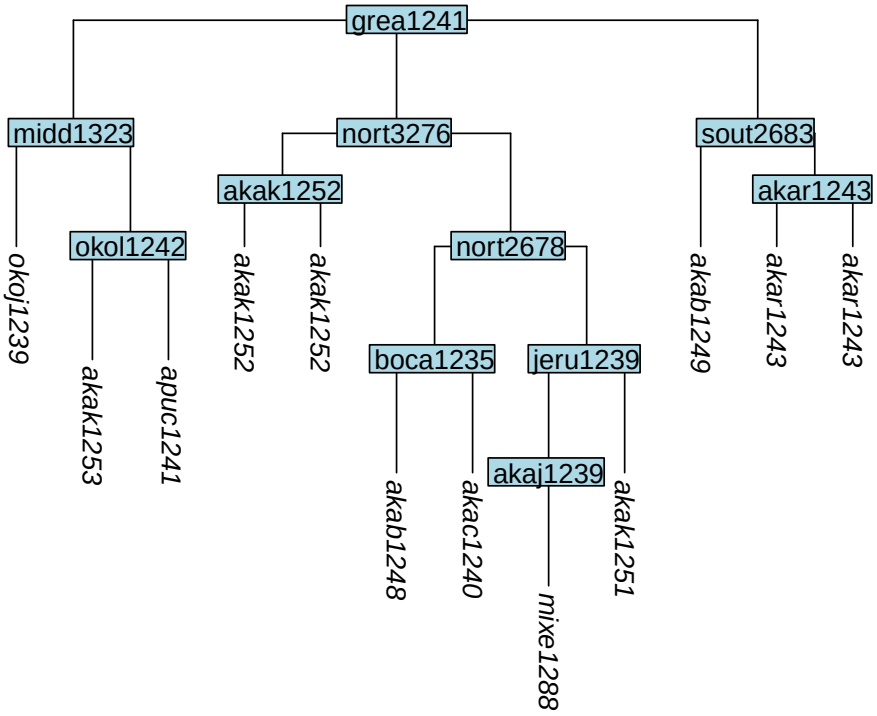
```
tree_GAj <- clone_tip(tree_GA_abr, label = c("akar1243", "akak1252"))
plot_glotto(tree_GAj)
```



By default, clones are added to the tree as sisters directly beneath the parent node of the original tip. An alternative is to create a new subgroup for each set of sister clones, using the `subgroup` argument and setting it to `subgroup = TRUE`. Each newly created subgroup node is given a label that matches the cloned tips it

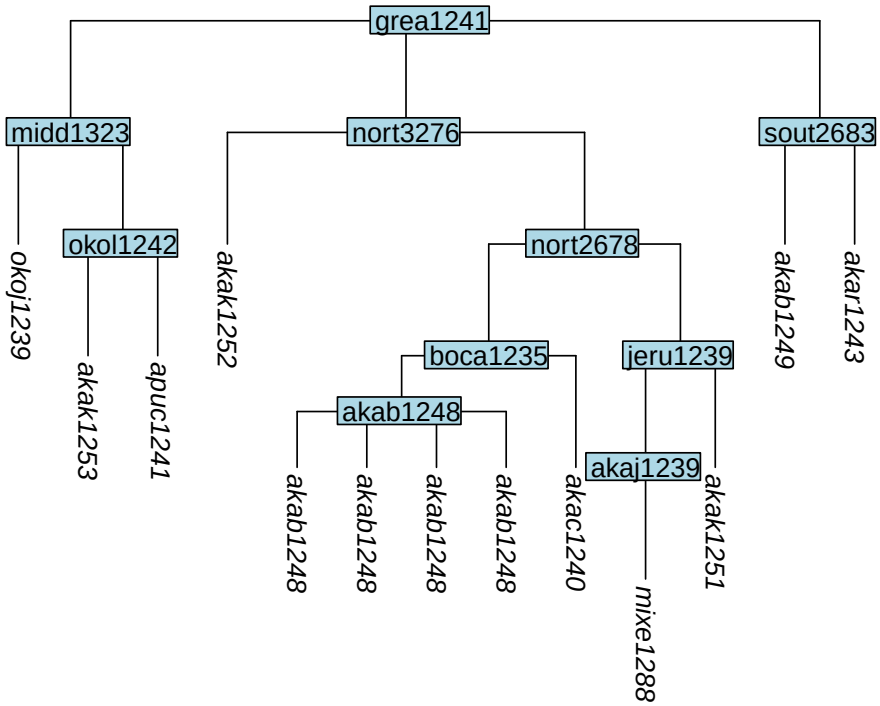
dominates:

```
tree_GAk <- clone_tip(tree_GA_abr, label = c("akar1243", "akak1252"), subgroup = TRUE)
plot_glotto(tree_GAk)
```



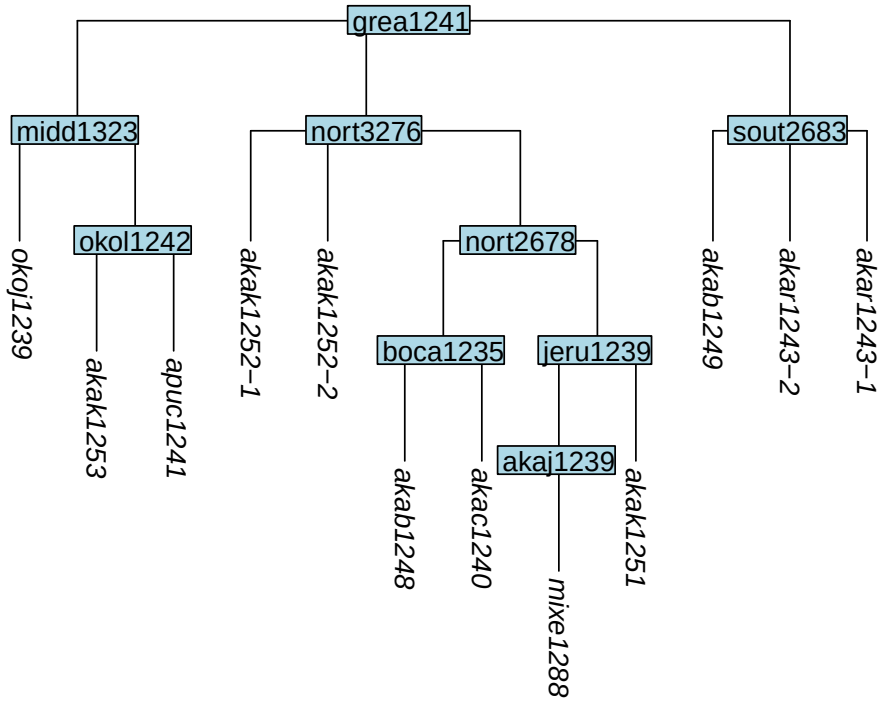
It is also possible to make more than one clone using the `n` argument. Here we create three new clones of `akab1248` and place them in a subgroup:

```
tree_GAl <- clone_tip(tree_GA_abr, label = "akab1248", n = 3, subgroup = TRUE)
plot_glotto(tree_GAl)
```



One of the consequences of cloning tips is that the in the resulting tree, not all tips will have distinct names. The function `apply_duplicate_suffixes()` will add a suffix to any tips with duplicate labels, to make them unique.[8] The suffix will consist of a hyphen followed by a number. Here we add suffixes to the tree `tree_GAj`:

```
tree_GAm <- apply_duplicate_suffixes(tree_GAj)
plot_glotto(tree_GAm)
```

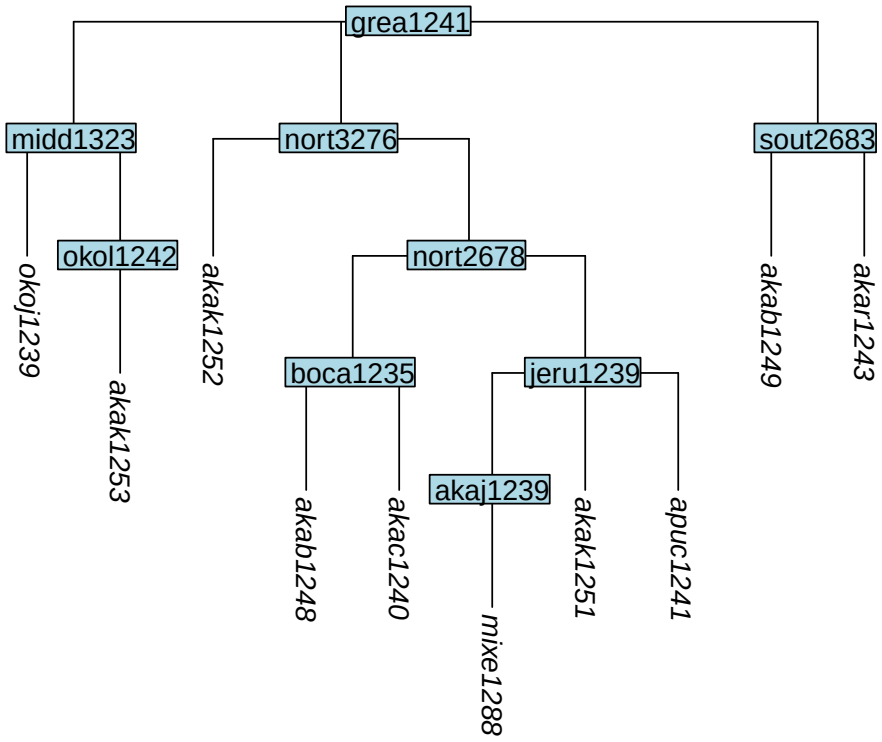


[8] `apply_duplicate_suffixes()` will also add suffixes to any nodes with duplicate labels.

4.3.6 How to move a tip

Using the function `move_tip()`, a tip can be moved to a new position, beneath a new parent node (one of the nodes already in the tree) which is specified with the `parent_label` argument:

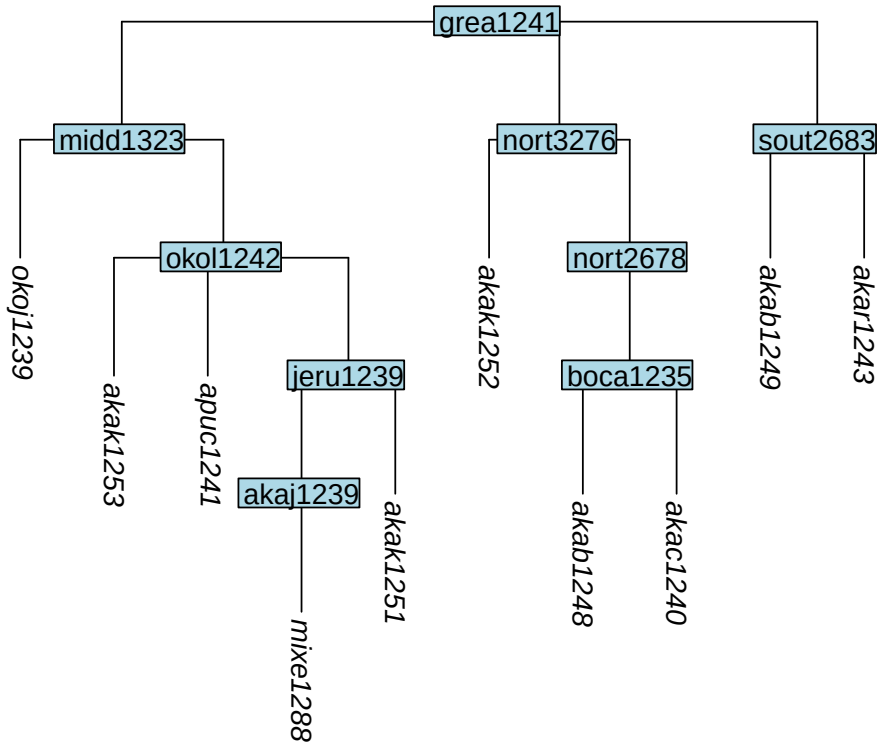
```
tree_GAn <- move_tip(tree_GA_abr, label = "apuc1241", parent_label = "jeru1239")
plot_glotto(tree_GAn)
```



4.3.7 How to move a node and its descendants

In a similar fashion, the function `move_node()` is used to move an internal node, along with all of the structure below it, to a position beneath a new parent node:

```
tree_GAo <- move_node(tree_GA_abr, label = "jeru1239", parent_label = "okol1242")
plot_glotto(tree_GAo)
```



4.3.8 Summary: a general-purpose toolkit for curating trees' topology

The functions `remove_tip()`, `keep_tip()`, `keep_as_tip()`, `convert_to_tip()`, `collapse_node()`, `add_tip()`, `clone_tip()`, `move_tip()` and `move_node()` provide a general-purpose toolkit for modifying a single glottolog tree, or a combined tree, or supertree, to make its set of tips, and the subgrouping of those tips, conform to the set of lects that a typologist is analysing in a typological study.

4.4 How to add branch lengths

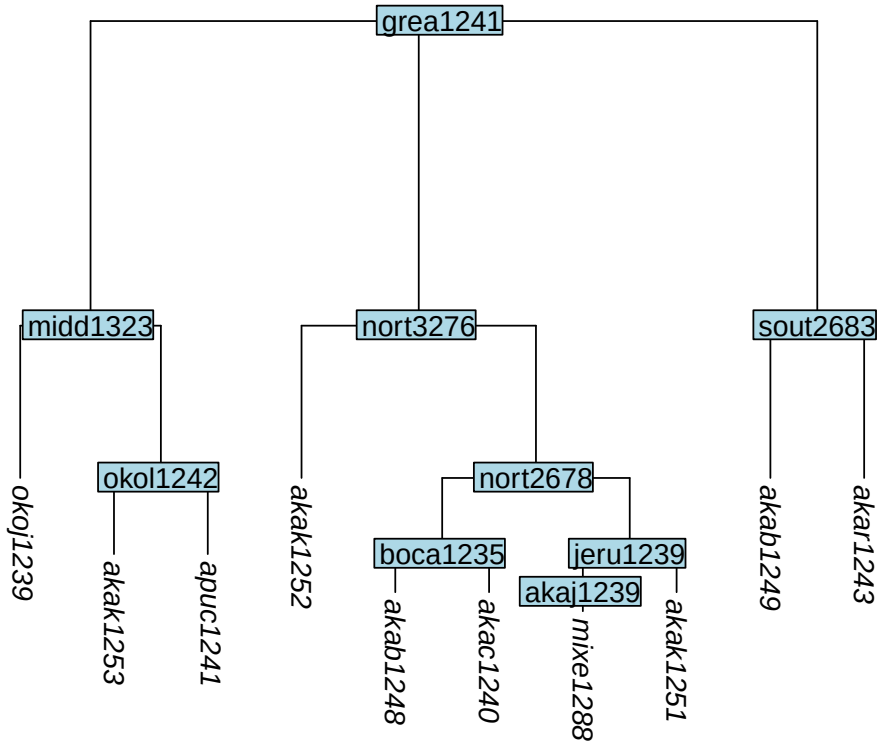
Branch lengths in a tree convey information, and all of the phylogenetic methods discussed in the main paper are sensitive to the information represented by the branch lengths. (To be specific, the methods discussed in the main paper are sensitive to the *relative* lengths of the branches, so multiplying all of the branch lengths in a tree by some constant amount would not affect the results.)

Glottolog's trees contain informative subgrouping structure, but the branch lengths are all equal. Even without knowing what the true branch lengths are for a linguistic tree, we do know that a situation in which all are equal is highly unlikely. A good approximation to the most-likely[9] distribution of branch lengths in a phylogenetic tree, under a variety of assumptions, is exponential (Venditti, Meade & Pagel 2010), i.e., very long branches are rare, and very short ones are frequent. This notion is implemented in the *glottoTrees* package by the function `rescale_branches_exp()`, which sets the deepest branches to length 1/2, then next layer to length 1/4, then the next to 1/8 and so on. This will produce a more plausible set of branch lengths, even in the absence of firm knowledge of exact lengths, and on these grounds we advocate its use if additional information about branch lengths is not available.

Here is an example of the result of applying exponential branch lengths to glottolog's Great Andamanese tree:

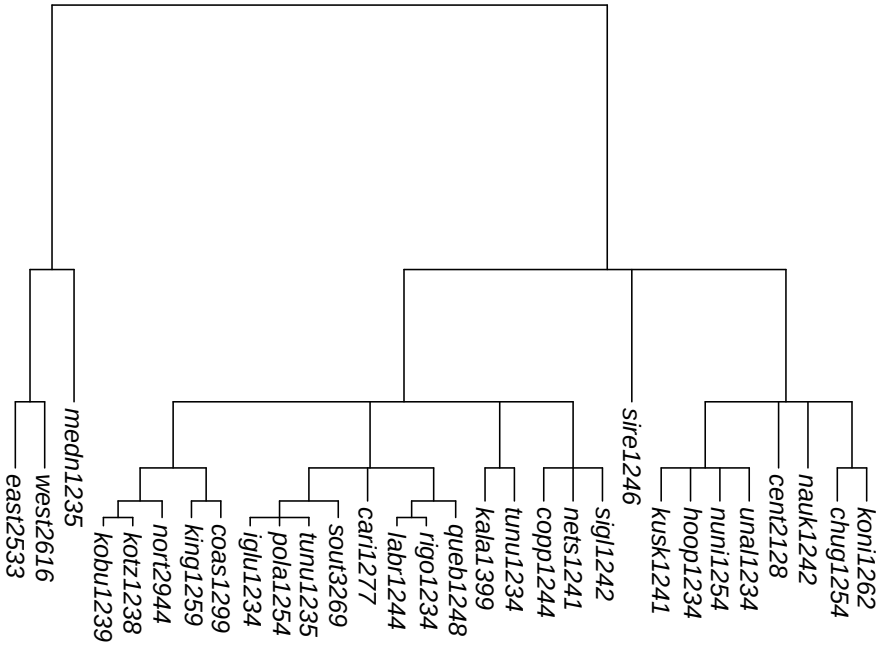
[9] 'Most likely' doesn't mean that we expect to see trees with exactly these branch lengths. Compare this to flipping a coin two million times: although it is unlikely that the outcome will be exactly one million heads and one million tails, it remains true that one million heads and one million tails is the most likely outcome, in the strict sense that it is more likely than any other outcome. The branch lengths discussed here are 'most likely' is a similar sense.

```
tree_GAp <- rescale_branches_exp(tree_GA_abr)
plot_glotto(tree_GAp)
```



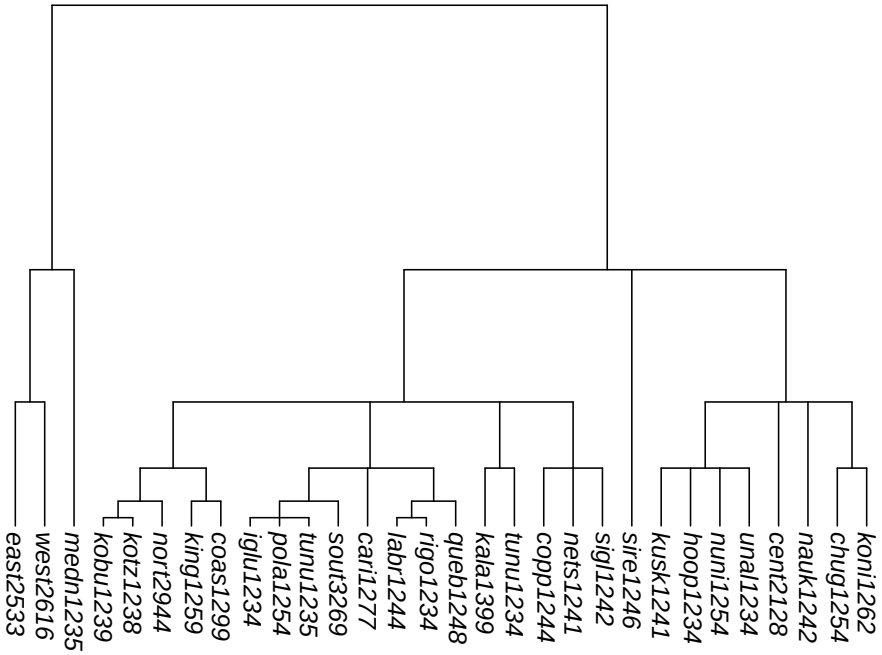
Here is an example of the result of applying them to glottolog's Eskimo-Aleut tree, of 30 tips:

```
tree_EA <- get_glottolog_trees("Eskimo-Aleut")
tree_EA_abr <- abridge_labels(tree_EA)
tree_EAa <- rescale_branches_exp(tree_EA_abr)
plot_glotto(tree_EAa, nodelabels = FALSE)
```



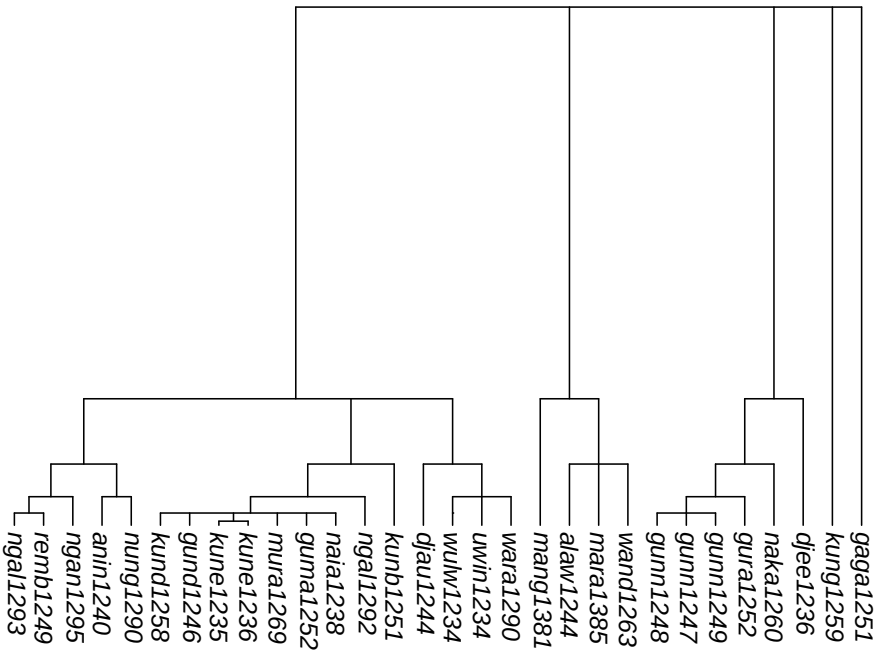
An additional option is to stretch the terminal branches so that all tips are equidistant from the root, creating what is known as an *ultrametric* tree. This is done using the function `ultrametricize()`.

```
tree_EAb <- ultrametricize(tree_EAa)
plot_glotto(tree_EAb, nodelabels = FALSE)
```



An additional function, `rescale_deepest_branches()`, can be used to adjust just the deepest layer of branches. This may be useful where multiple family trees have been joined together, and there is a desire to manipulate the implied closeness or distance between the first-order branches. For example, here we take the hypothesised Arnhem group from Section 4.2. First we assign exponential branch lengths with `set_branch_lengths_exp()`, which sets the deepest branch length to 1/2. Then we triple the distance of the deepest level of relationships by changing the first branch length to 1.5 using `rescale_deepest_branches()`, before ultrametiricising the tree:

```
tree_arnhem_a <- rescale_branches_exp(tree_arnhem_abr)
tree_arnhem_b <- rescale_deepest_branches(tree_arnhem_a, 1.5)
tree_arnhem_c <- ultrametricize(tree_arnhem_b)
plot_glotto(tree_arnhem_c, nodelabels = FALSE)
```



4.5 Exporting trees for use with other software

In R, trees can be saved to file in Newick format using the function `write.tree()` in the *ape* package. Files like this can be opened by other software such as FigTree[10], which can be used to interactively generate tree plots that may be useful for publication and dissemination. For instance, here we write the tree `tree_arnhem_c` to a file whose filename ends in the standard file extension, `.tree`:

```
write.tree(tree_arnhem_c, "my_arnhem_tree.tree")
```

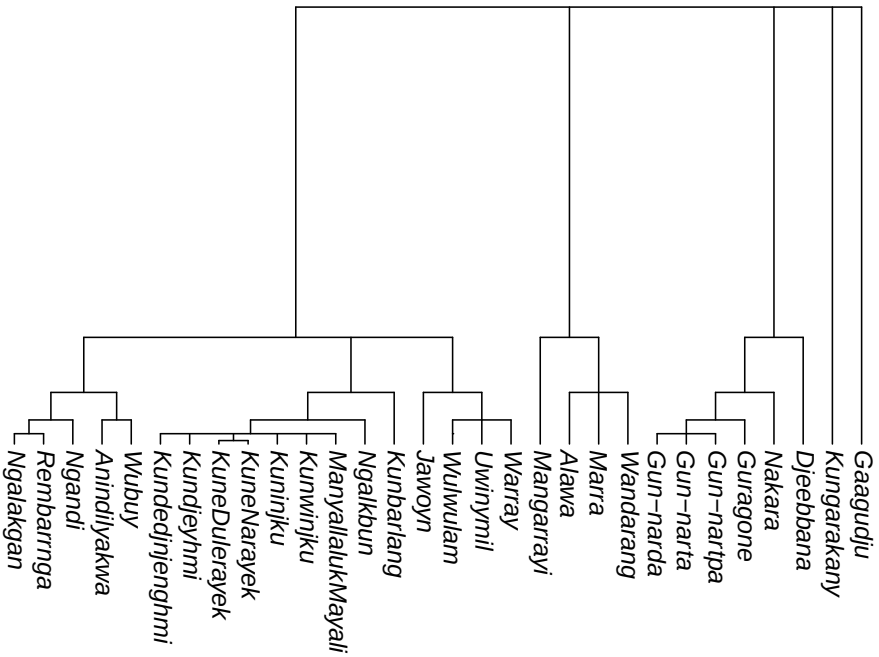
Often it will be desirable to reproduce a tree with labels that are more reader-friendly than glottocodes. *glottoTrees* provides the function `relabel_with_names()`, which will replace full glottolog labels, or labels consisting of just a glottocode, with glottolog's corresponding language, dialect, subgroup or family name. Here we relabel the Arnhem tree by the languages' names. As was the case with `abridge_labels()`, warnings are given by `relabel_with_names()` if a tree contains any nodes that cannot be relabeled in this way; these are not errors, just alerts.

```
tree_arnhem_c_namelabels <- relabel_with_names(tree_arnhem_c)
```

```
## Warning in relabel_with_names(tree_arnhem_c): Labels without glottocodes were detected
## and left unchanged for: 0 tip(s); 1 node(s):
```

```
plot_glotto(tree_arnhem_c_namelabels, nodelabels = FALSE)
```

[10] https://github.com/rambaut/figtree/releases



5 Putting it together: A worked example

In this section we provide a real worked example of the use of the methods described above.

Yin (2020) examined violations of the sonority sequencing principle in 496 languages, and calculated the genealogically-sensitive proportions of languages in which various violations occurred. The language sample consisted of 496 languages in the CLICS2 database (Anderson et al. 2018) and the AusPhon-Lexicon database (Round 2017). The language sample was not balanced in the traditional sense, and phylogenetic methods were used to help produce a principled interpretation of the data.

Yin's raw data consisted of a table of languages' names and glottocodes and indications of whether or not the languages had consonant clusters in word-initial onsets or word-final codas that contained sonority reversals, coded as 1 for yes and 0 for no. This dataset is provided with the *phyloWeights* package as a dataframe named `yin_2020_data` whose columns are `name`, `tip`, `has_onset_violation` and `has_coda_violation`. The first ten rows are shown here:

```
head(yin_2020_data, n = 10)
```

```
##                name      tip has_onset_violation has_coda_violation
## 1            Abkhaz abkh1244                   1                  1
## 2              Abui abui1241                   0                  0
## 3           Achagua acha1250                   0                  1
## 4             Adang adan1251                   0                  1
## 5     Adnyamathanha adny1235                   0                  0
## 6            Adyghe adyg1241                   1                  1
## 7      Hokkaidoainu ainu1240                   0                  0
## 8             Alawa alaw1244                   1                  0
## 9  Standardalbanian alba1267                   1                  1
## 10           Aleut aleu1260                   1                  1
```

5.1 Preparing a tree

The tree for Yin's study was constructed from a glottolog supertree, using glottolog version 4.2. Yin's supertree made use of glottolog's macroareas. Since the language sample covered relatively few families in

the Americas, a single group was used for South America and North America. Additionally, the only African language available in the sample was Arabic, so Africa and Eurasia were grouped together:

```
yin_macro <- list(c("South America", "North America"), c("Africa", "Eurasia"),
                  "Papunesia", "Australia")
supertree <- assemble_supertree(macro_groups = yin_macro, glottolog_version = "4.2")
supertree_abr <- abridge_labels(supertree)
```

```
## Warning in abridge_labels(supertree): Labels without glottocodes were detected and left
## unchanged for: 0 tip(s); 5 node(s): World, SouthAmerica-NorthAmerica, Africa-Eurasia,
## Papunesia, Australia
```

Five tips were cloned, in cases where Yin had data for two varieties corresponding to just one tip in the glottolog supertree:

```
supertree_a <- clone_tip(supertree_abr, subgroup = TRUE,
                         label = c("ayab1239", "basu1242", "biri1256",
                                   "ikar1243", "peri1265"))
supertree_b <- apply_duplicate_suffixes(supertree_a)
```

Eight tips were added, in case where for sister lects (A,B), glottolog placed A as a node above B. In such cases, in new tip A was placed below the existing glottolog node A:

```
supertree_c <- supertree_b
nodes_to_add_as_tips <- c("alor1249", "gami1243", "guri1247", "mand1415",
                          "sins1241", "wang1291", "warl1254", "yand1253")
# Loop through these nodes, and use add_tip() to add the new tip:
for (node_i in nodes_to_add_as_tips) {
  supertree_c <- add_tip(supertree_c, label = node_i, parent_label = node_i)
}
```

From this supertree, the 496 languages in Yin's dataset were kept. The internal node `mada1298` was collapsed, as were all non-branching internal nodes:

```
supertree_d <- keep_as_tip(supertree_c, label = yin_2020_data$tip)
supertree_e <- collapse_node(supertree_d, label = "mada1298")
supertree_f <- collapse_node(supertree_e, label = nonbranching_nodes(supertree_e))
```

Finally, branch lengths were assigned. Branches were first assigned exponential lengths. Then, in order to diminish the importance of the macro groups, the branches above them were shortened to a length of 1/40. The effect of this decision is that the implied distance between families in different macro groups is only marginally greater than between families within a single macro group.

```
supertree_g <- rescale_branches_exp(supertree_f)
yin_2020_tree <- rescale_deepest_branches(supertree_g, 1/40)
```

The resulting tree appears as in Figure 1, which is plotted with the following code:

```
full_names <- yin_2020_data$name[match(yin_2020_tree$tip.label, yin_2020_data$tip)]
name_tree <- yin_2020_tree
name_tree$tip.label <- full_names
plot(ladderize(name_tree, right = FALSE), type = "fan",
     cex = 0.3, label.offset = 0.002, edge.width = 0.5)
```

5.2 Preparing the dataframe of typological data

In order to calculate phylogenetic weights and genealogically-sensitive proportions, in addition to the tree (or a set of trees) we require a dataframe with (a) one column `tip`, whose contents match the tip labels in the trees, and (b) other columns containing numerical data to be averaged. The dataframe `yin_2020_data`

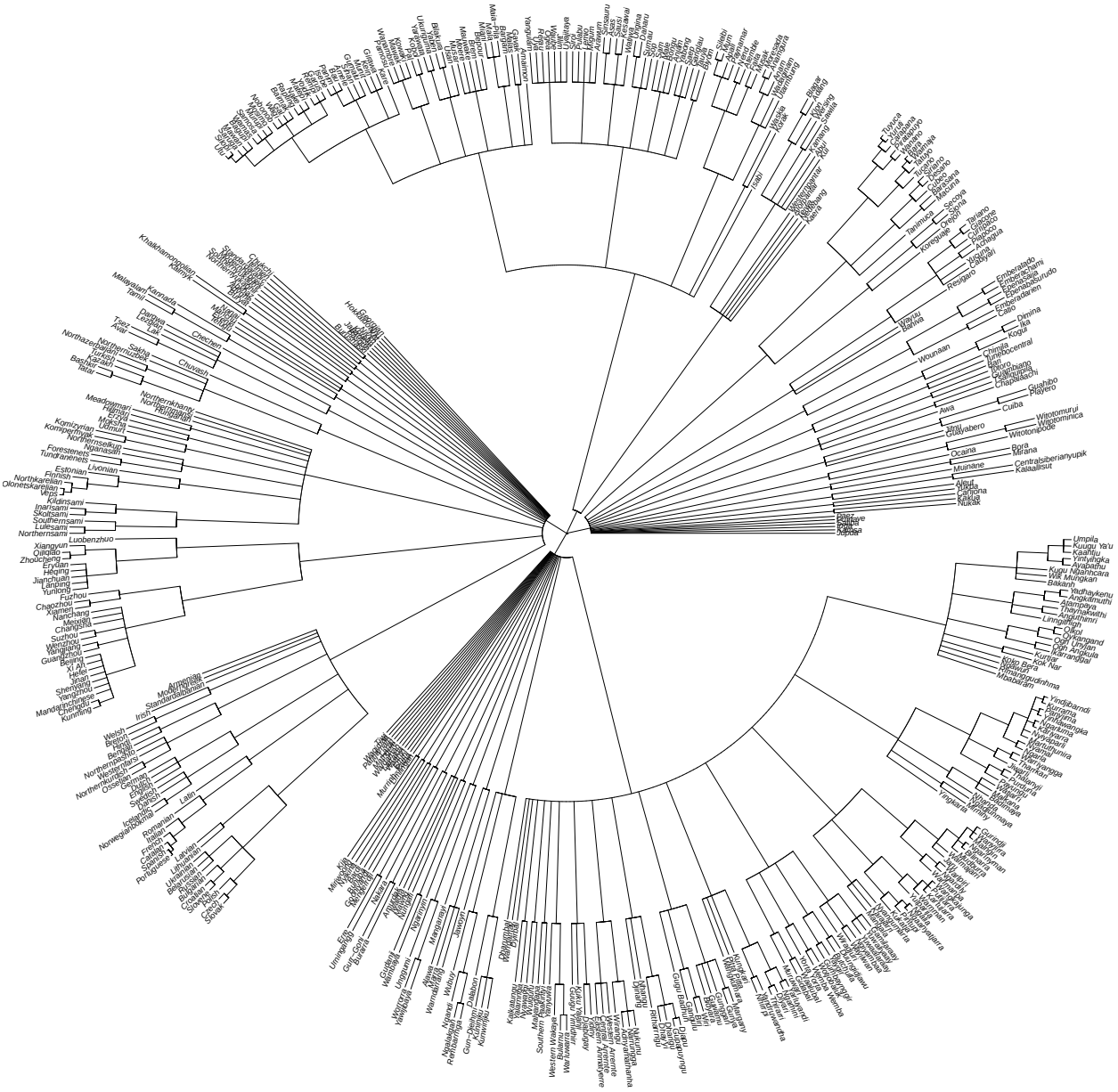


Figure 1: Supertree of 496 languages used in Yin (2020).

has a column `tip` and two columns of numerical data `has_onset_violation` and `has_coda_violation`, and thus it meets the requirements we need. It also contains a column, `names`, of non-numeric data. Columns of non-numeric data (other than `tip`) are ignored by `phylo_average()`, so we do not need to remove them.

5.3 Calculating genealogically-sensitive proportions

The results are calculated using `phylo_average()`, setting its `phy` argument to the tree we have constructed, `yin_2020_tree`, and its `data` argument to the dataframe we have prepared, `yin_2020_data`. A warning is issued altering us that the dataframe contains a non-numeric column that gets ignored:

```
yin_2020_results <- phylo_average(phy = yin_2020_tree, data = yin_2020_data)
```

```
## Warning in phylo_average(phy = yin_2020_tree, data = yin_2020_data): `data` contains
## non-numeric columns other than `tip`, which have been ignored: name.
```

Results are in the format described in Section 3. The first ten rows of phylogenetic weights according to the ACL and BM methods are:

```
head(yin_2020_results$ACL_weights, n = 10)
```

```
##                name      tip        tree1
## 1            Abkhaz abkh1244 0.0069858330
## 2              Abui abui1241 0.0012637162
## 3           Achagua acha1250 0.0002456679
## 4             Adang adan1251 0.0002197767
## 5     Adnyamathanha adny1235 0.0000637717
## 6            Adyghe adyg1241 0.0069858330
## 7      Hokkaidoainu ainu1240 0.0174645825
## 8             Alawa alaw1244 0.0019652742
## 9  Standardalbanian alba1267 0.0023699724
## 10            Aleut aleu1260 0.0085266857
```

```
head(yin_2020_results$BM_weights, n = 10)
```

```
##                name      tip        tree1
## 1            Abkhaz abkh1244 0.0049475265
## 2              Abui abui1241 0.0021424363
## 3           Achagua acha1250 0.0009109899
## 4             Adang adan1251 0.0009391784
## 5     Adnyamathanha adny1235 0.0008929209
## 6            Adyghe adyg1241 0.0049475265
## 7      Hokkaidoainu ainu1240 0.0064304759
## 8             Alawa alaw1244 0.0027423594
## 9  Standardalbanian alba1267 0.0040995307
## 10            Aleut aleu1260 0.0055527679
```

The genealogically-sensitive proportions according to the ACL and BM methods are the following. Recall from the main paper that ACL proportions are more sensitive to languages on outlier branches, and the BM proportions are less so:

```
yin_2020_results$ACL_averages
```

```
##    tree has_onset_violation has_coda_violation
## 1 tree1           0.3711102           0.409806
```

```
yin_2020_results$BM_averages
```

```
##    tree has_onset_violation has_coda_violation
## 1 tree1           0.4014756          0.3847729
```

As a point of comparison, the raw proportions, which are equal to the means of the columns `has_onset_violation` and `has_coda_violation`, are these:

```
mean(yin_2020_data$has_onset_violation)
```

```
## [1] 0.3649194
```

```
mean(yin_2020_data$has_coda_violation)
```

```
## [1] 0.3145161
```

The estimated proportion of languages with onset violations is similar using both the AM and BM methods. The raw proportion is also similar, with all three results in the range of 36–40%. Turning to languages with coda violations, the estimated proportions are also similar using both the AM (41%) and BM (38%) methods, but the raw proportion (31%) is notably lower, illustrating how our understanding of the commonness of typological phenomena can shift once we take genealogy into account.

As we seek to analyse the empirical diversity of attested languages, genealogy must be part of picture. Since the genealogies of human languages are still incompletely known, it is imperative to make our phylogenetic assumptions as explicit and as testable as possible. In this document, we hope have shown that doing so is not only worthwhile, but also feasible and attainable.

6 Using these methods in typological research

We hope that typologists find the arguments in our main paper compelling at the conceptual level and the methods in this supplementary document convenient at the practical level.

If you are interested in trying out the methods described here, please check for updates and additional information at their web pages, https://github.com/erichround/glottoTrees and https://github.com/erichround/phyloWeights.

Through the use of *glottoTrees* and *phyloWeights*, we hope that in the future, linguistic trees and the code used to produce them can be published together with typological studies. This will enable subsequent researchers to replicate the study's findings, and just as importantly, to modify its assumptions by modifying the trees, and thereby to test further hypotheses inspired by the initial research.

If you find these tools useful in your own research, please cite the packages as Round (2021a) and Round (2021b).

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