

# Phylogeny\_\_construction

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*16/02/2019*

This script builds a set of 100 phylogenies by joining the super trees from xx xx xx together and adding error at each node join based on fossil evidence. This is the set of phylogenies used for the analysis in the paper Healy et al. Beyond the fast-slow continuum.

P.S I cant spell so just go with it.

## Packages and Data

First lets load the packages. Apart from `mulTree`, which is available on github, all other packages are on CRAN

Now let load the demography dataset so that we can match up our species with the phylogeny. For the paper we used a version of COMADRE which was released with the publication, however, check xxx for potential updates.

Now lets load some functions that were built for this job. `Demography_functions` has functions related to calculating demography elements `phylo_bind_functions` has functions to build the phylogenies and include error in the nodes joining together trees.

Lets now upload each of the phylogenies we are going to use to build our superdoooper tree

## Species to match

We run the same code to subset the species in the COMPADRE dataset so that we have the same species in our phylogeny as in our analysis.

We then clean the species names to put it in a formate that can be matched with the phylogeny names.

We now match up the species names from COMADRE with those in the backbone tree

Now we match up the species from the taxinomic groups in our dataset which we dont have a dated phylogeny.

Next we deal with the synomoms in the aves phylogeny

We now start with aves and work backward adding each taxinomic groups and there phylogeny as we meet them. First up is the common ancestor between the two crocodiles species in our analysis

We scale the tree using the Grafen transformation to refect the divergence time for the last common ancestor between our cros species which is between 10.77mya and 16.7mya. See Srikulnath, K; Thapana, W; Muangmai, N (2015). "Role of chromosome changes in Crocodylus evolution and diversity". *Genomics Inform.* 13 (4): 102–111.

We now graft these two sepcies onto the aves tree with error using our `jiggle.bind` function.

Using the last tree we graft on the nest group, the turtles. We use a spit between the Pleurodira and the Cryptodira as 100mya. The common ancestor between aves/cros and turtles was taken from <http://onlinelibrary.wiley.com/doi/10.1111/ede.12081/full>

Next we add the lepidosaurs (add this in from the supp)

Nex the mammals

and one lonely frog

next the fish

Now just the rest of the Bilateral animals

nest add the corals

next we check if the trees are behaving with no jumping forward in time with the nodes.

finally we rename the tips so that they will match the COMADRE species names for the rest of the analysis

and we read out our lovely clean multiphylo object.