**Main simulation -> simulations\_script.R**

1) Set parameter values

2) Use functions\_M-C\_bifurcation.R and list\_append\_function.R

3) While loop to test what seed produces good results in the simulation (for either positive or negative interactions, create seed list, generate seed and try simulation, if good results then store the seed, and store the results as list\_res\_pos\_list.Rdata or list\_res\_neg\_list.Rdata in folder (Data) for different number of simulations.

Results of the simulation:

res\_sim <- list(simulation\_number = paste0("simulation", **successful\_sim**), seed = **seed**, parameters = **pars**, presence\_matrix = simulation$**pres**, traits\_df = simulation$**traits**, parentage\_matrix = simulation$**anc**, extinxction\_matrix = simulation$**extinct**)

**Generate tree -> phylo\_stats.R**

1) set the number of steps and the maximum species number

2) use tree\_functions.R and phylo\_functions.R

3) Create phylogenetic distance matrix with the function get\_dist\_mat (using the anc, ntimesteps and species number, it fills a time-distance matrix between all the species by

- first, testing whether an ancestor and new species belong to any related group

- second, assigning a new group of related species

- third, record the time-distance of the related species by creating pairwise combinations between the species of the group (nsteps – anc\_rev[loop\_position, 1])

4) Use the distance matrix generated in (3) to run the function hclust(), which conducts a hierarchical cluster analyses on a dissimilarity structure.

5) convert clust to tree format with as.phylo() to produce the tree and save it.

The code below the line:

# Plot phylogenetic tree of existing species at the end of the simulation

Plots a phylogenetic tree for a given timestep using the “press” table. In this case, for the last one. I could use this code to, instead of plotting, saving a phylogenetic tree at each timestep with the present species, so using the function hclust on get\_dist\_mat.

AF\_functions\_M-C\_bifurcation.R

I create trees from step > 50, because step > 4 was not working and I just went up to test if they ar ebeing saved good. They are, but now I need to start saving them from somewhere…how to determine from when? It can be from the moment I have X species, instead of from X step.