

Intro to birth-death process in phylogenies

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The packages we will need for these tutorial are

```
library("ape")
library("geiger")
library("TreeSim")
```

```
## Loading required package: laser
```

If you haven't install them you should use the function

```
#install.packages("nameofthepackage")
```

Every time you see "... " that means you need to complete the line of code

Part I: Actual and reconstructed phylogeny simulations

We need a speciation rate b and a extinction rate d

```
#Choose your own parameter values
b= ...
d= ...
```

According to Nee et al.'s paper how should the parameters be rewritten to represent the rate of growth and the strength of the pull of the present?

```
growth.rate= ...
fraction= ... #strength of extinction CHANGE THIS PARAMETER
#b+d turnover rate, what happens on the tips?
```

```
stop("Check your values, if you simulate a phylogeny with these values how do you expect it to look?")
```

Simulate one actual phylogeny with 50 taxa using the function

```
# sim.bd.taxa(n=, numbsim=, lambda=, mu=, frac=, complete=TRUE, stochsampling=FALSE)
# Creates a list of trees simulated
# n= number of tips, numbsim=number of trees (output appears as a list), lambda=birth rate, mu=death ra
```

```
bdtree.actual=sim.bd.taxa( ... )[[1]]
```

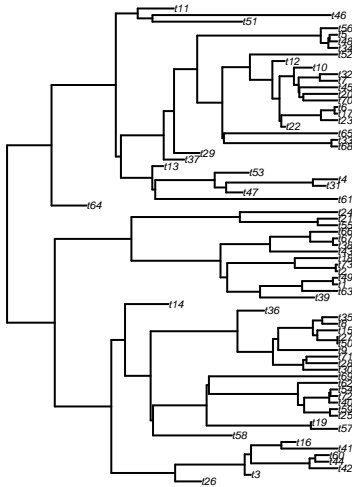
And reconstructed phylogeny (if we have sampled all taxa) is

```

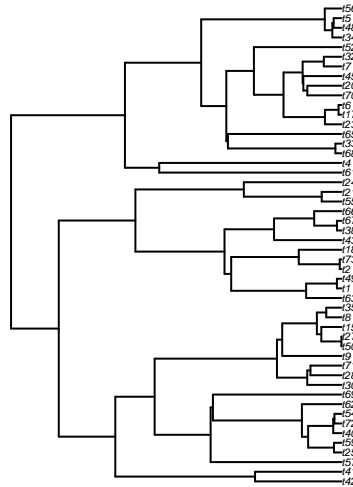
bdtree.reconstructed=drop.extinct(bdtree.actual)
#Plot them size to side
par(mfrow=c(1,2))
plot(...)
plot(...)

```

Actual Phylogeny



Reconstructed Phylogeny



Extra question. How would you simulate a reconstructed phylogeny where not all taxa on the tips have been sampled?

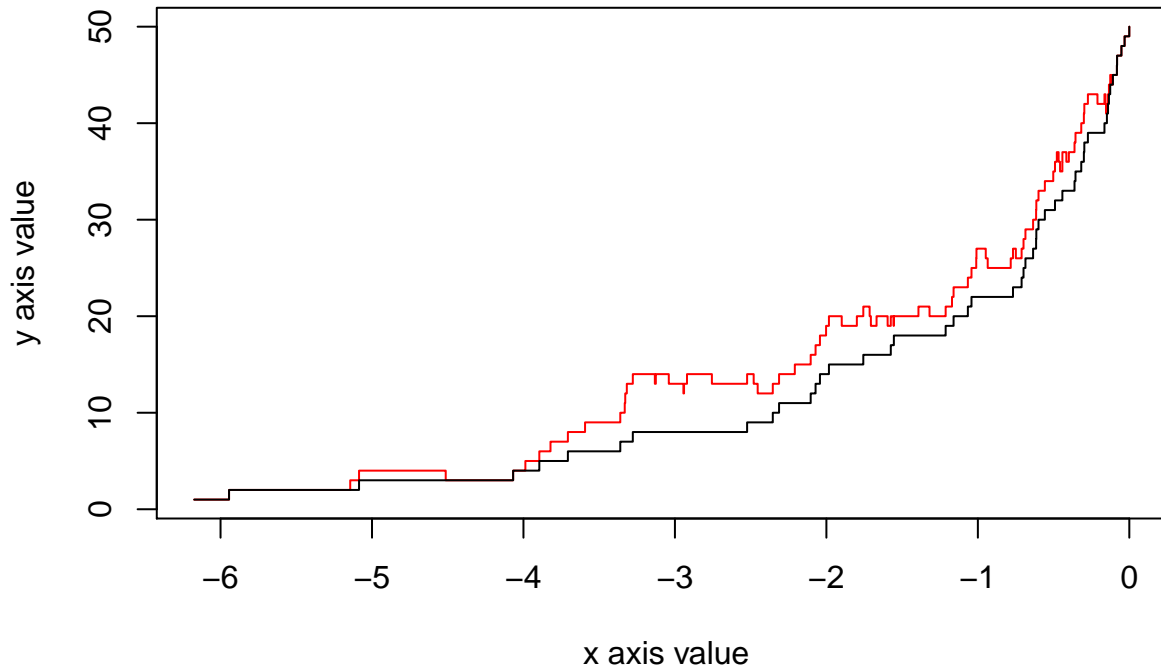
Part 2: Lineage through time (LTT) plot

What are the axes of an LTTplot? Where can we detect the pull of the present? The push of the past? Plot LTT for the actual and the reconstructed phylogeny you simulated in part 1.

```

ltt.plot( ... ,xlab="x axis values",ylab="y axis values",backward=TRUE, col="red")
ltt.lines( ... ,backward=TRUE)
#Another option is plotting in log scale
#gamma test post response

```



Part 3: Speciation and extinction rates estimation

The maximum likelihood estimates of the speciation and extinction rates given our reconstructed phylogeny can be calculated as follows

```
mle=birthdeath(...)
```

To check what the object **mle** has you can use the function

```
str(mle)
```

```
## List of 6
## $ tree: chr "bdtree.reconstructed"
## $ N : int 50
## $ dev : num -162
## $ para: Named num [1:2] 0.684 0.357
## ..- attr(*, "names")= chr [1:2] "d/b" "b-d"
## $ se : Named num [1:2] 0.15 0.129
## ..- attr(*, "names")= chr [1:2] "d/b" "b-d"
## $ CI : num [1:2, 1:2] 0.485 0.243 0.806 0.51
## ..- attr(*, "dimnames")=List of 2
## .. ..$ : chr [1:2] "d/b" "b-d"
## .. ..$ : chr [1:2] "lo" "up"
## - attr(*, "class")= chr "birthdeath"
```

1. How do you extract the maximum likelihood estimates and confidence intervals?
2. Are the estimates close to the values you used to simulate the reconstructed phylogeny?
3. If you have more taxa on the tips, what happens to the mle?

Part 4: Challenge

Simulate a reconstructed phylogeny where the fraction is approximately 1, start with a small sample size and increase towards a 50,000 tip tree. Check what happens with LTT and mle when you increase sample sizes.