

Progress

TECE meeting 2016-07-14



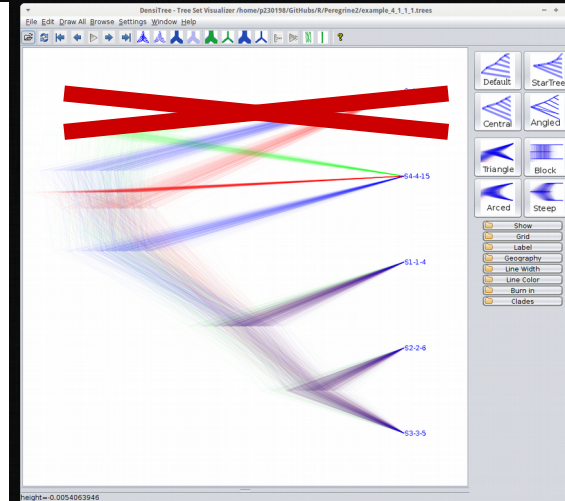
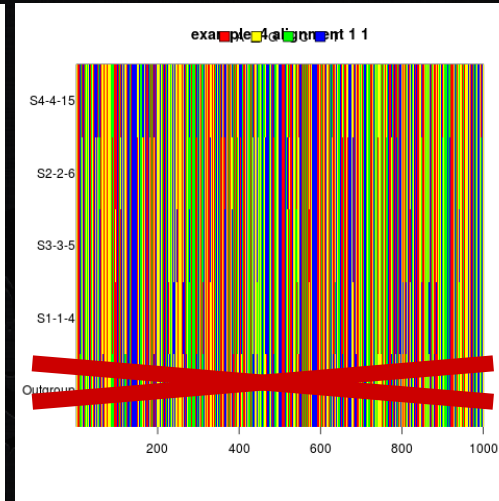
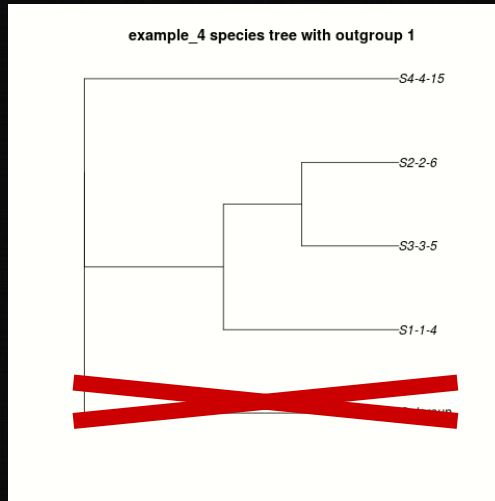
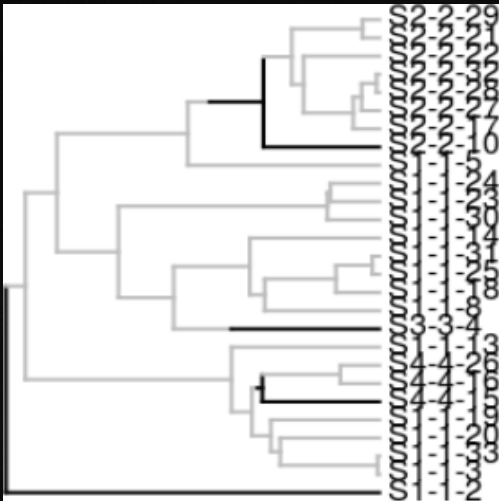
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www.github.com/richelbilderbeek/Science

Research question

If speciation in nature takes time, what is the error made in inferring a phylogeny?

- Under which conditions does it hurt?
- Are these conditions relevant and/or realistic?
- Tool used: BEAST2, assumes speciation is instantaneous

Approach



Simulate an
incipient
species tree

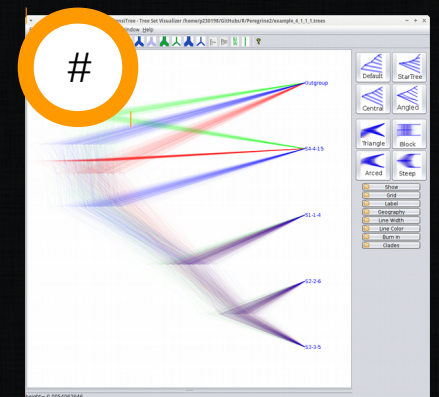
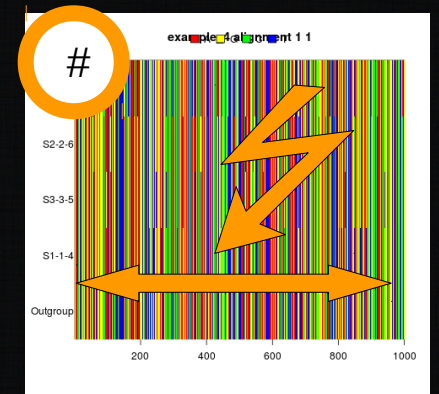
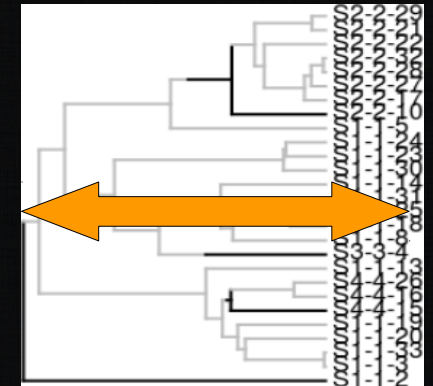
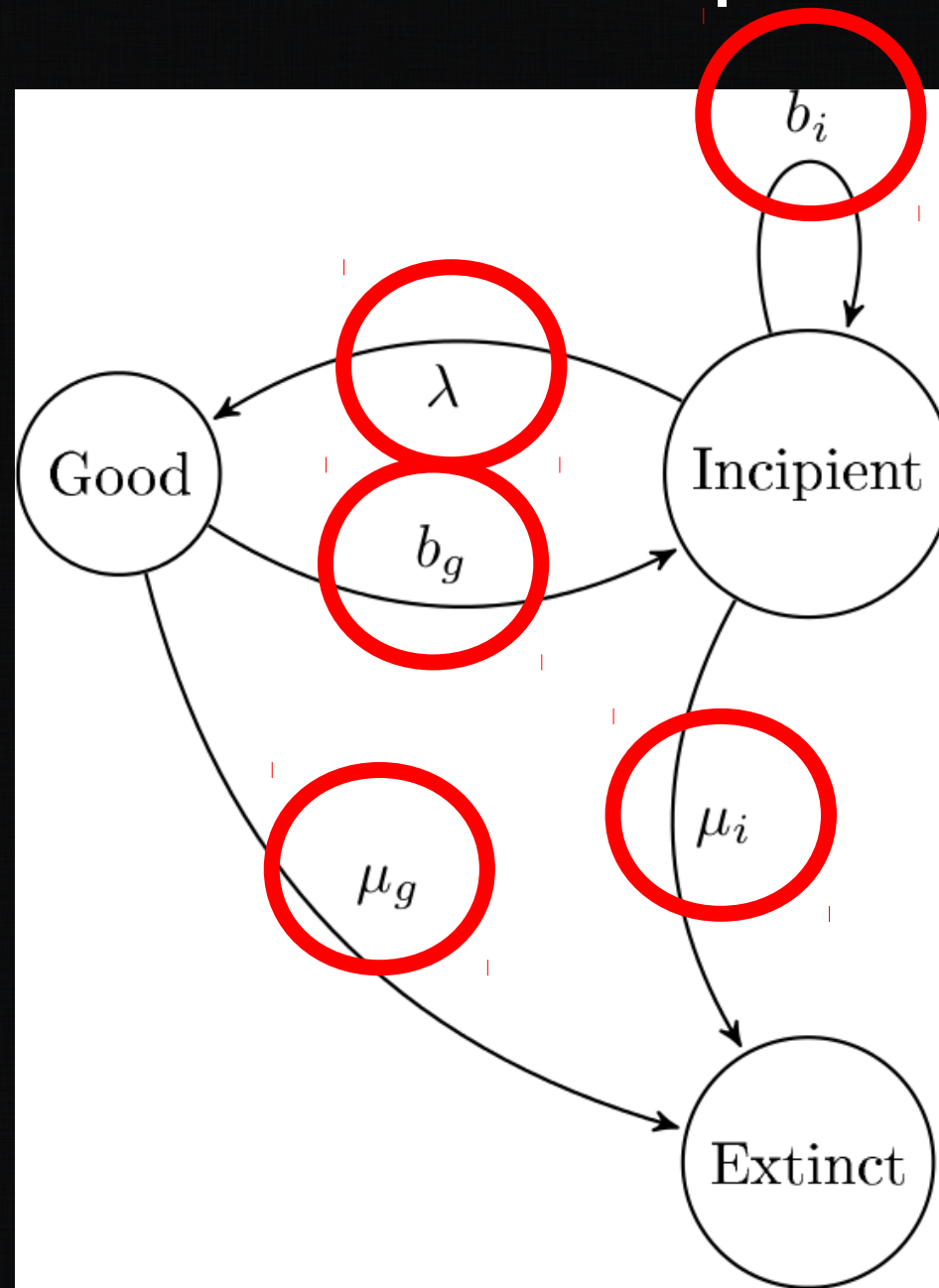
Sample species
trees

Simulate DNA
alignments

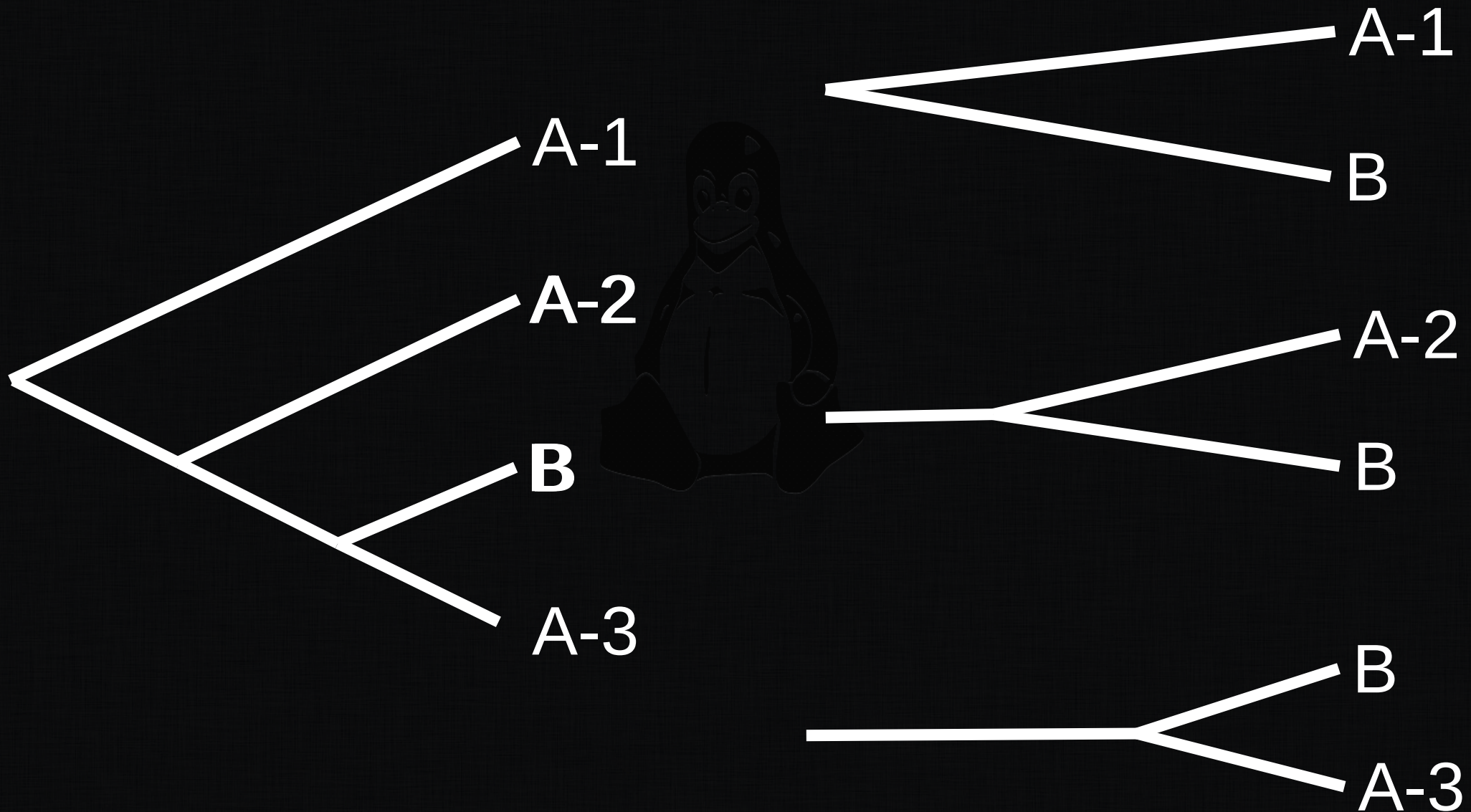
Infer species
tree posterior

Measure difference/error

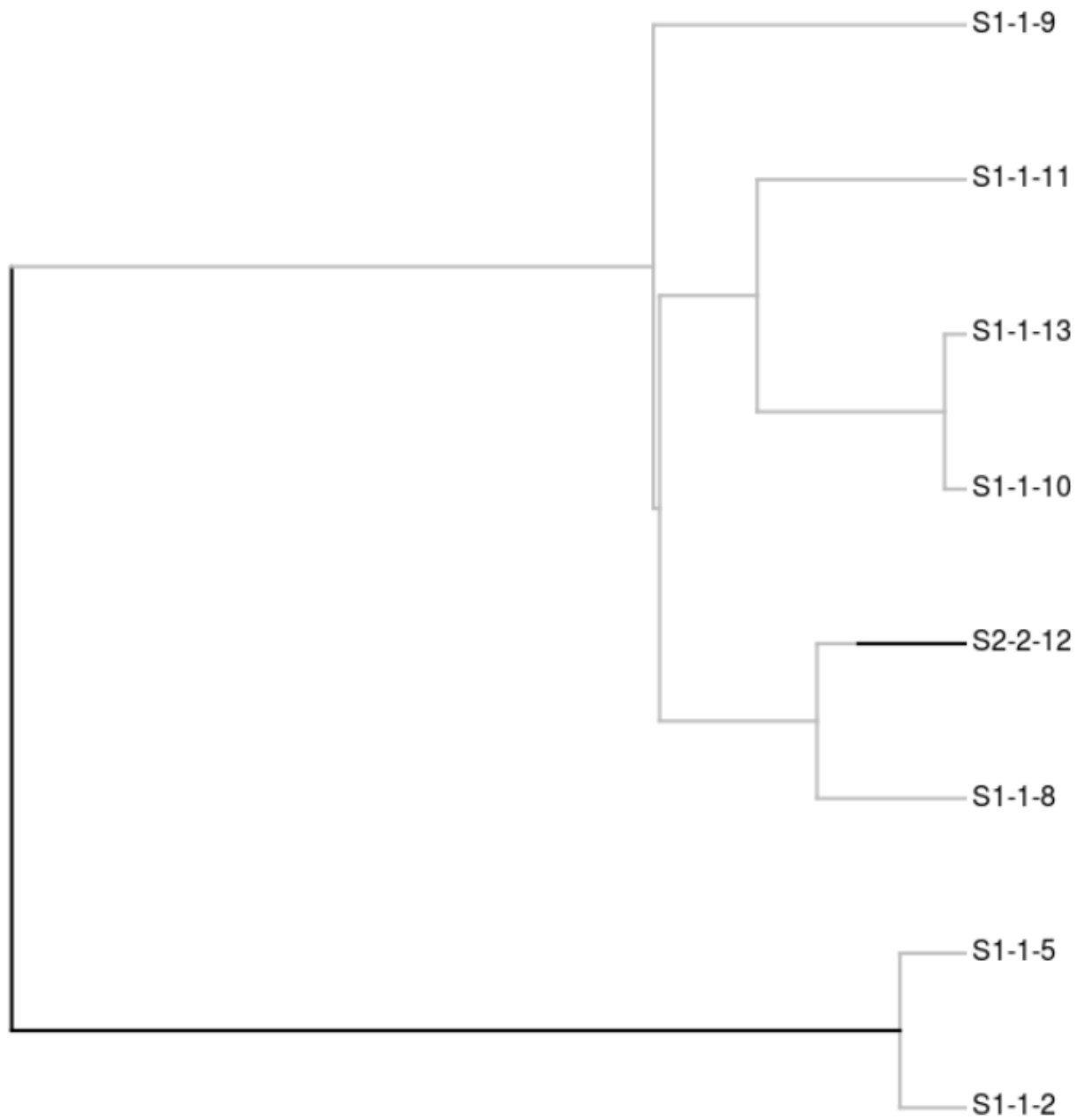
Parameter space



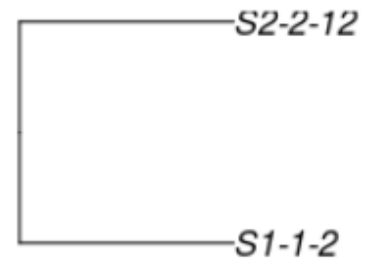
Sampling



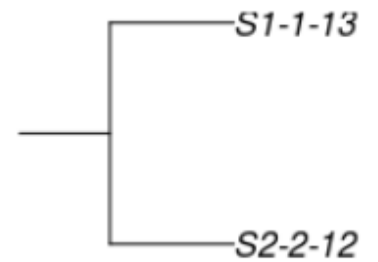
Sampling



oldest

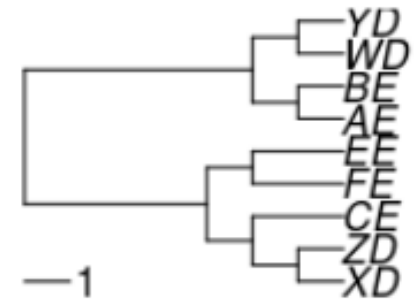


youngest

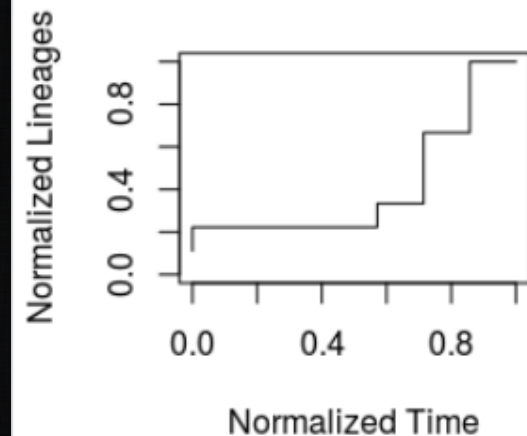


nLTT

- Normalized Lineages-Through-Time

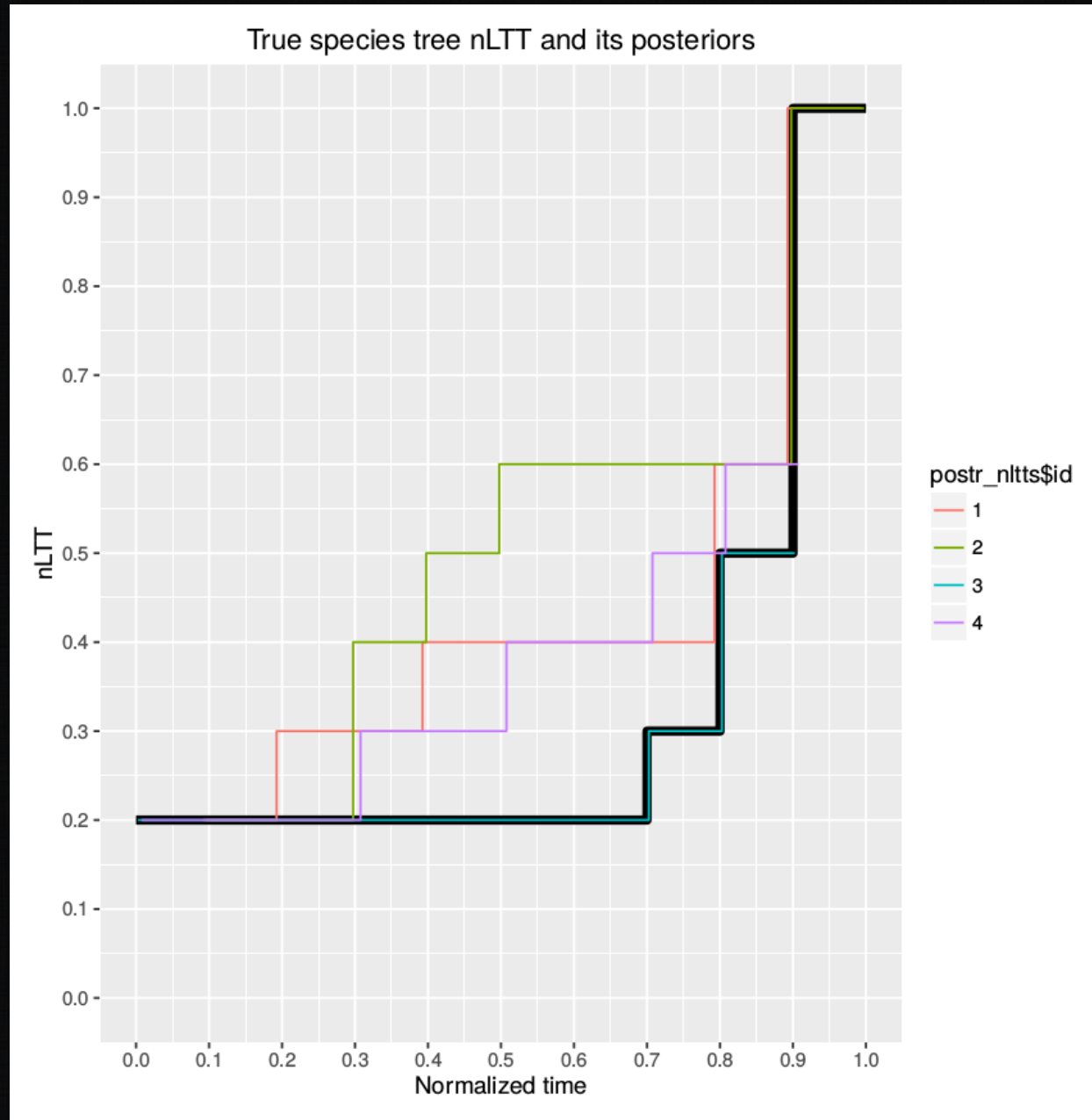


Janzen, Thijs, Sebastian Höhna, and Rampal S. Etienne. "Approximate Bayesian computation of diversification rates from molecular phylogenies: introducing a new efficient summary statistic, the nLTT." *Methods in Ecology and Evolution* 6.5 (2015): 566-575.

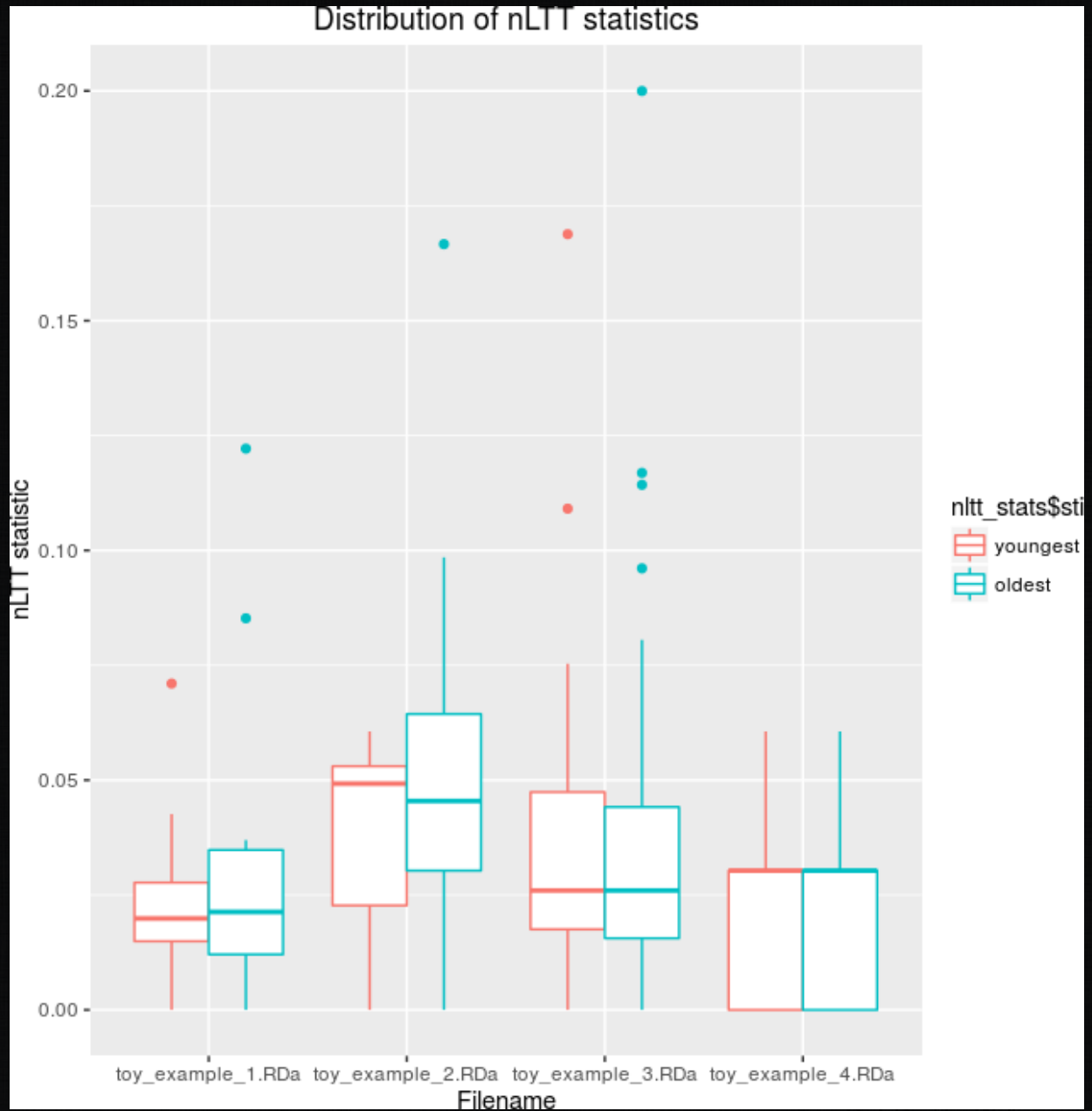


NLTT statistic

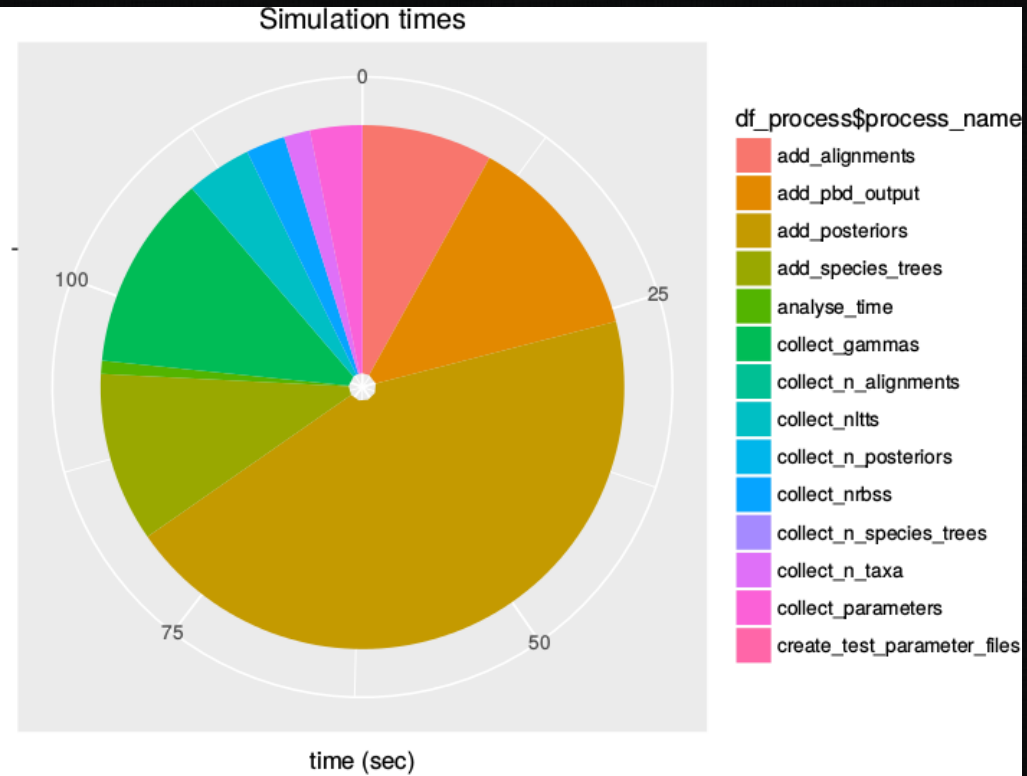
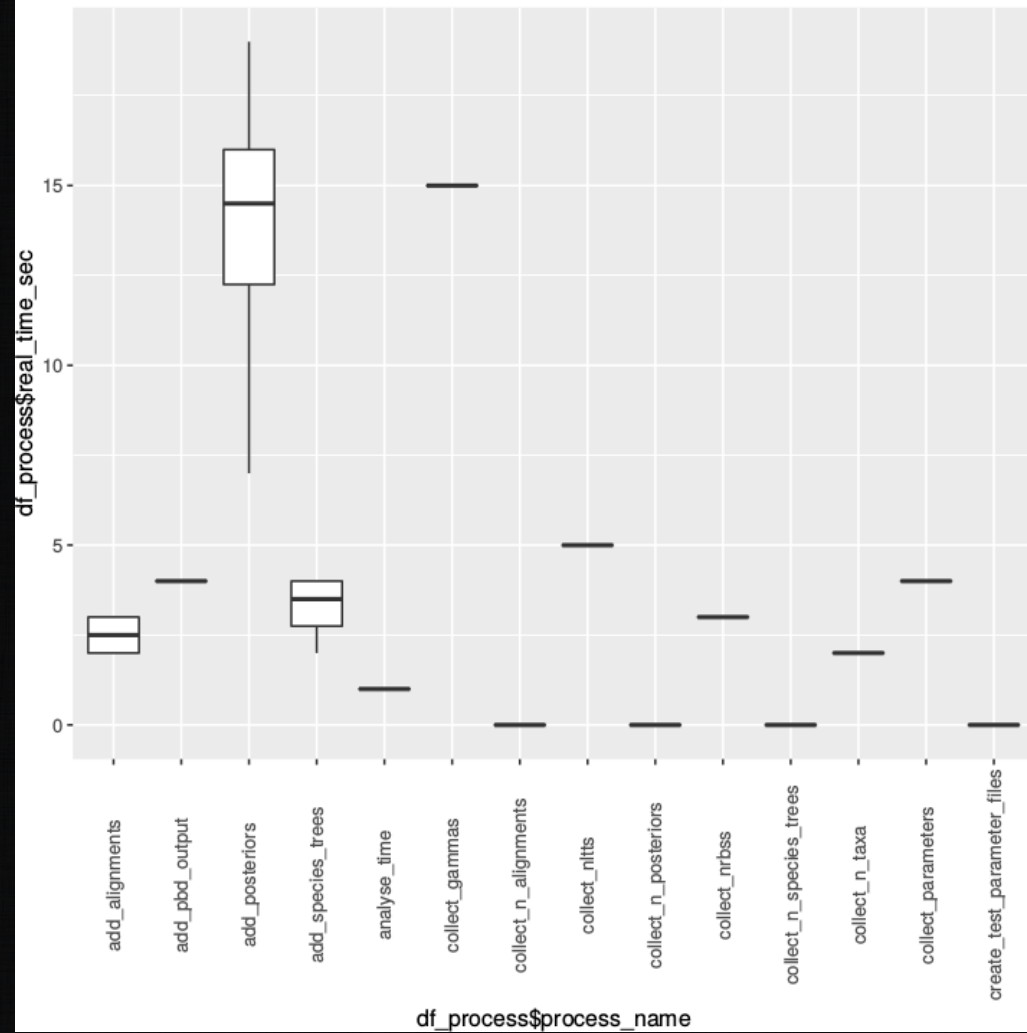
- Surface between two nLTT curves



NLTT statistic measured



Time measurements



Work in progress

- Under which parameters can I simulate?
- Measure the nLTT statistics for those parameters
- Finish article