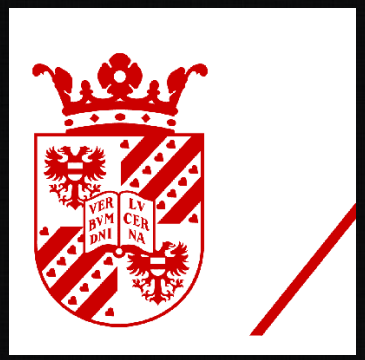
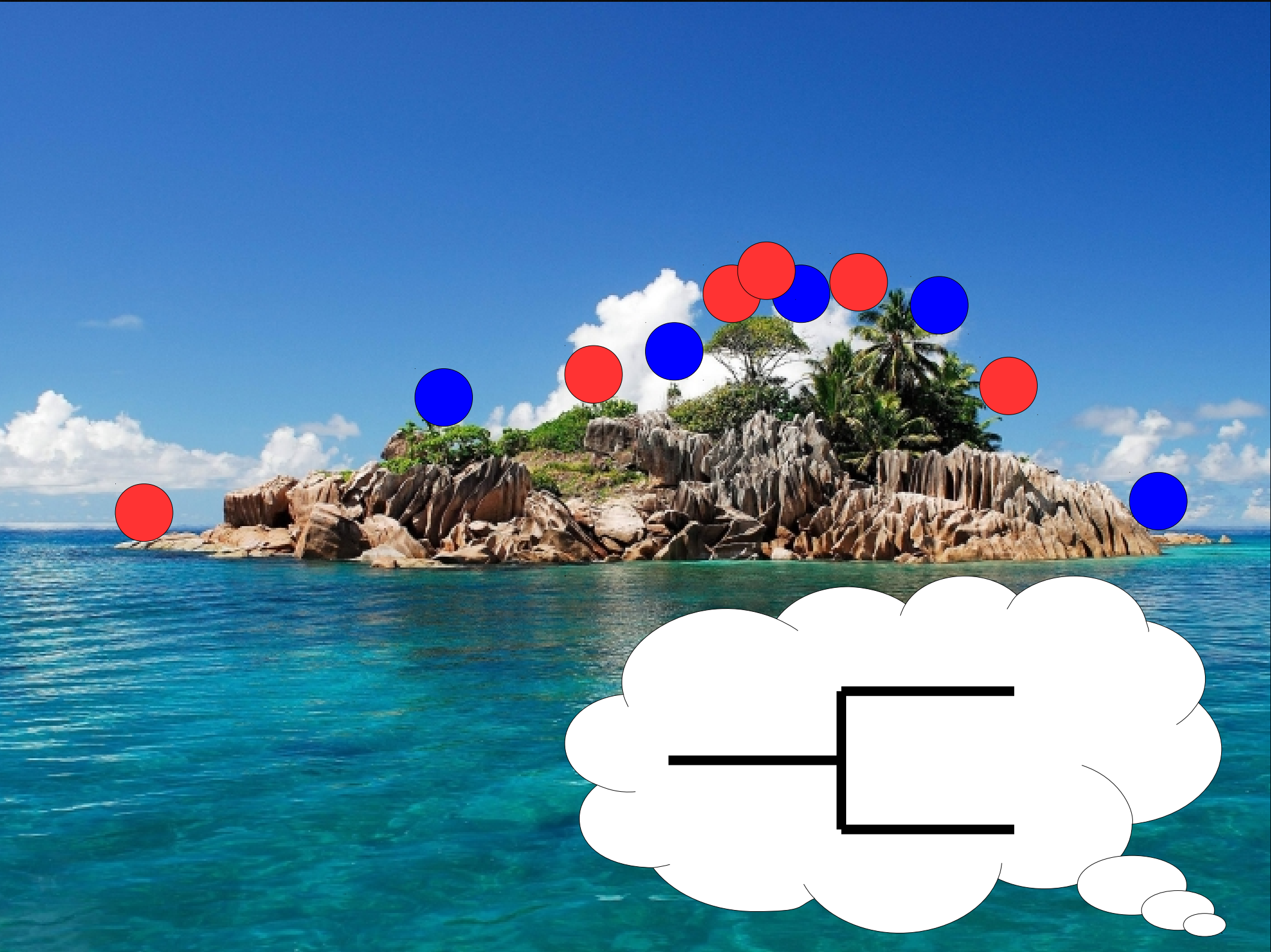
Ignoring incipient species

TRES meeting 2017-02-13

www.github.com/richelbilderbeek/Science



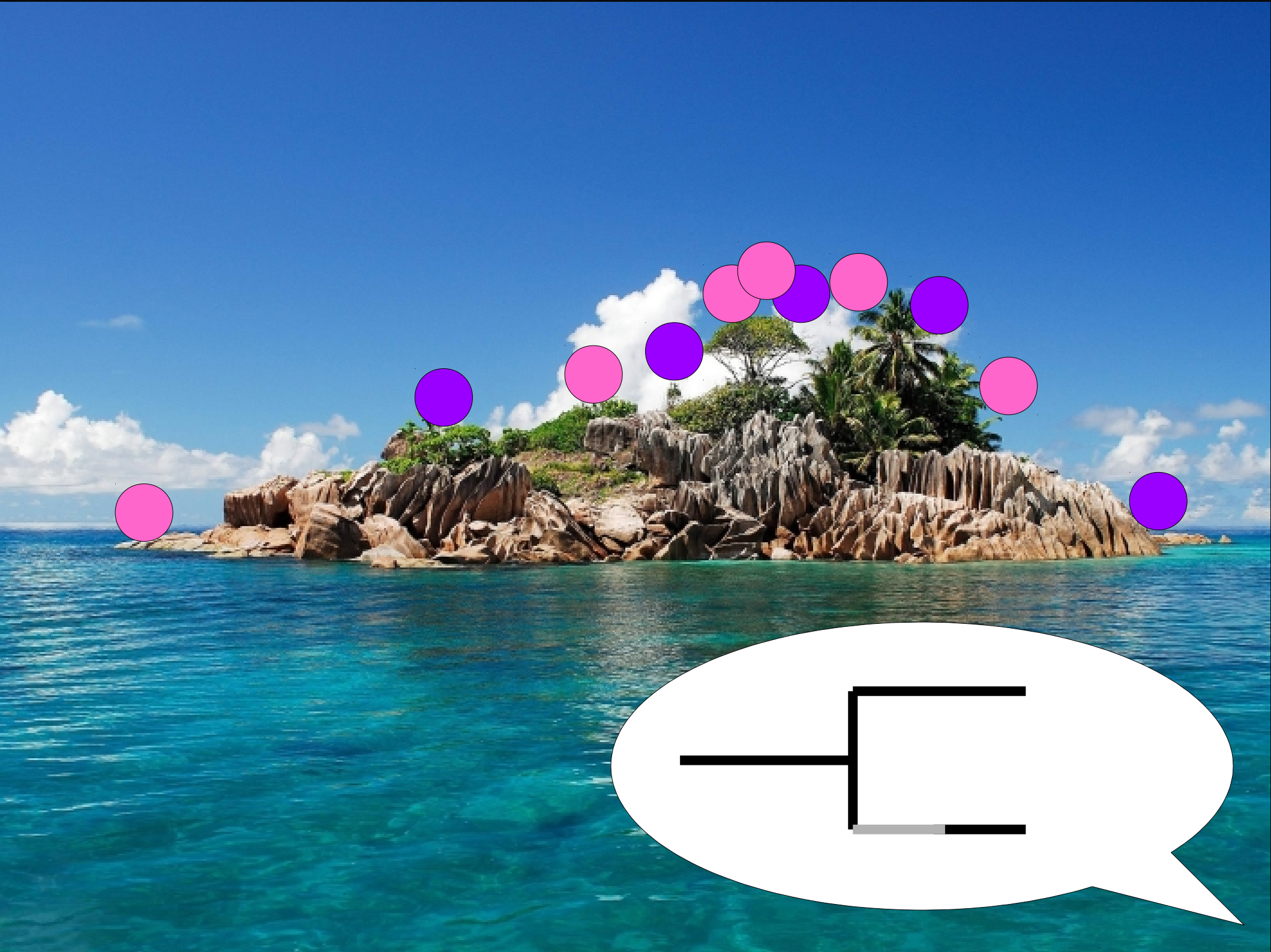


Research question

- What is the effect of ignoring the phase in which species are being formed?

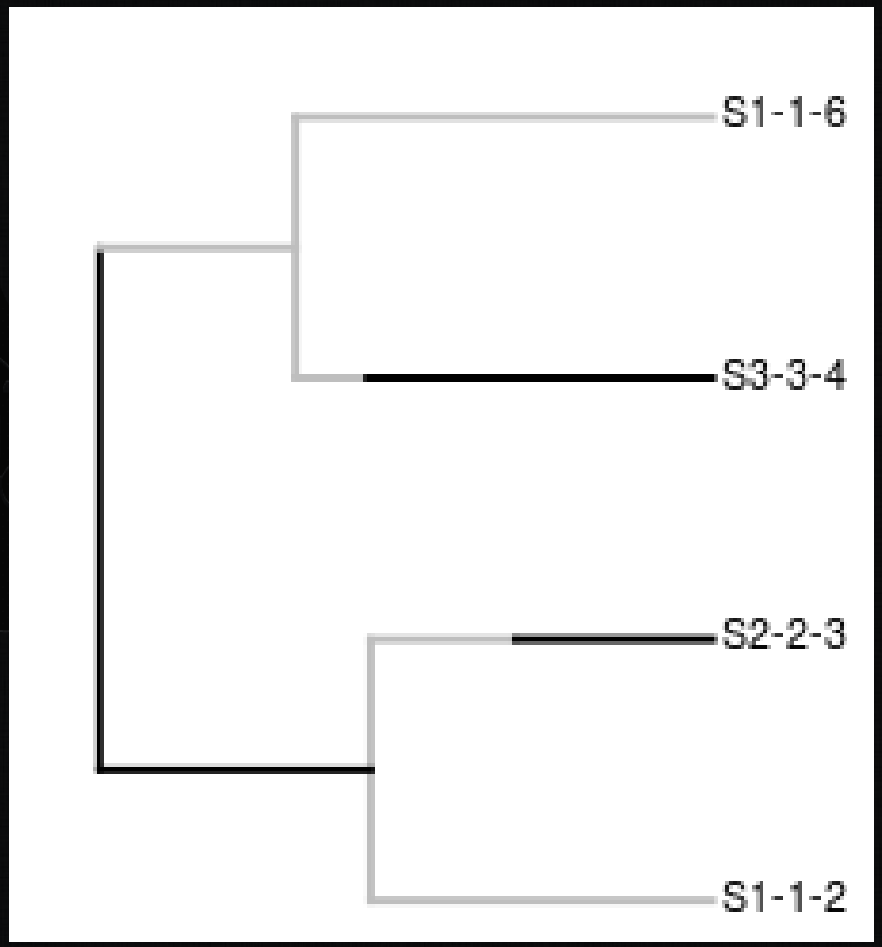
How long does that phase last?

Which species lived when?



Protracted speciation [1]

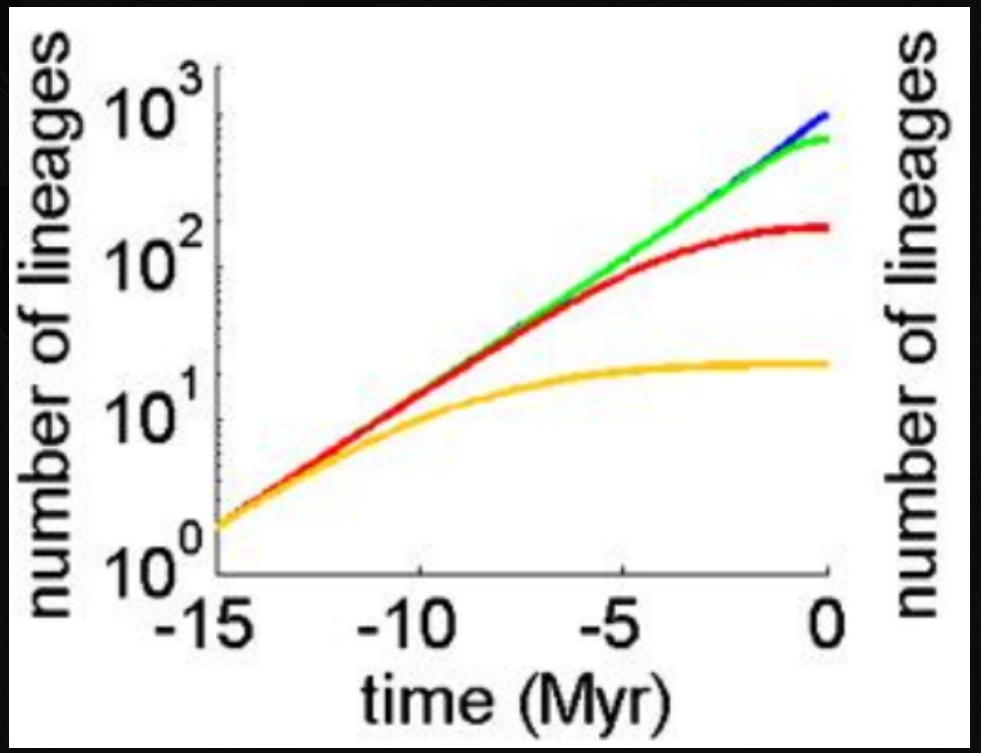
- Extension of Birth-Death (BD) model [2]
- New species are incipient
- Speciation completion rate
  - Incipient → good
  - BD if infinite



[1] Etienne & Rosindell, 2012 [2] Nee et al., 1994

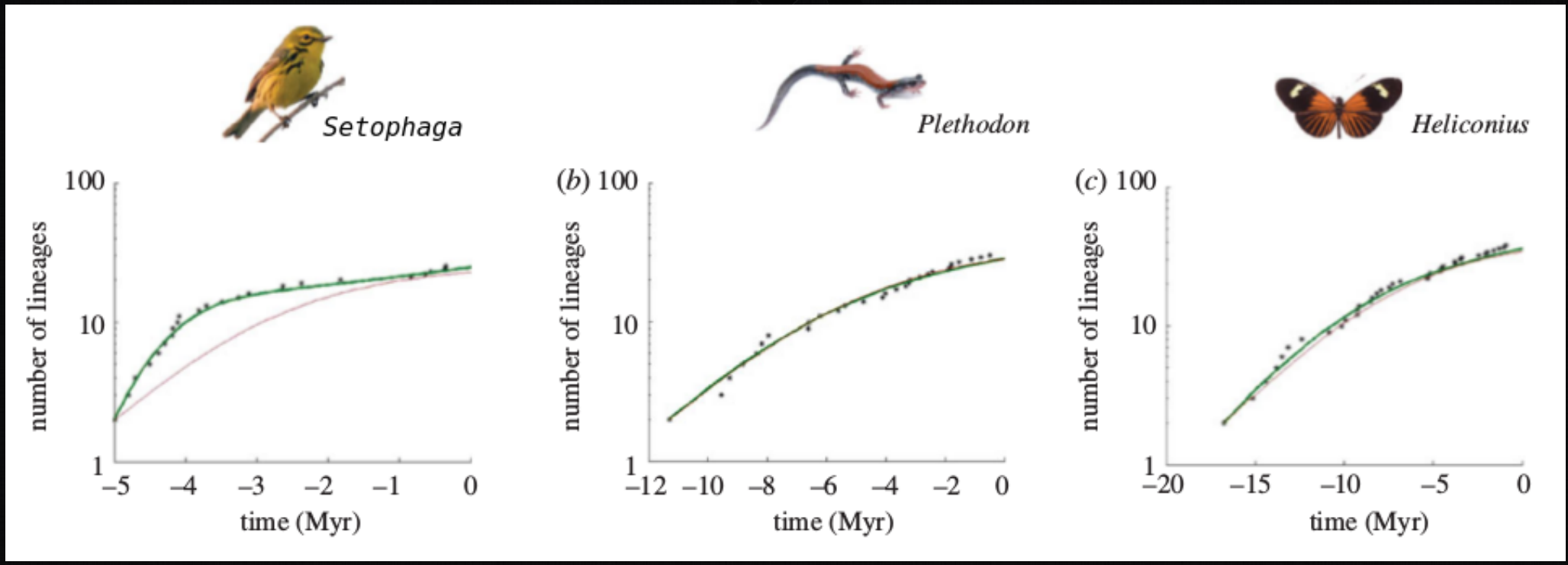
Protracted speciation

- Number of lineages towards the present flattens of
- Difference between two (n)LTT plots: nLTT statistic [1]



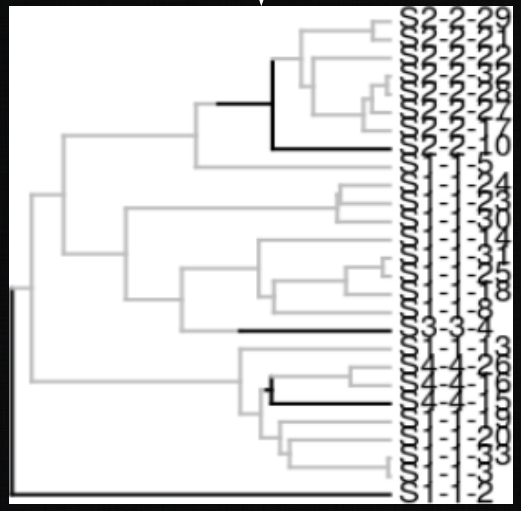
[1] Janzen et al., 2015

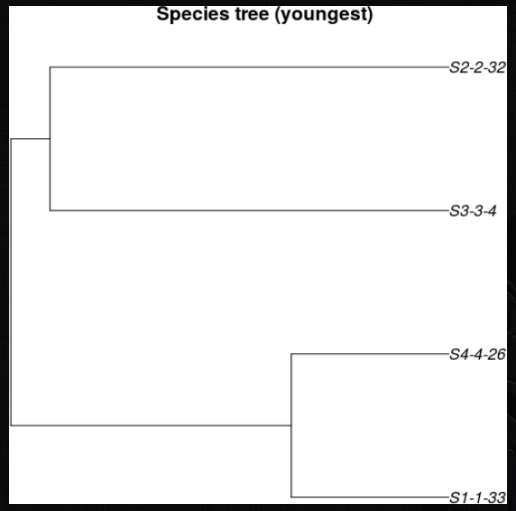
Adapted from Etienne & Rosindell, 2012

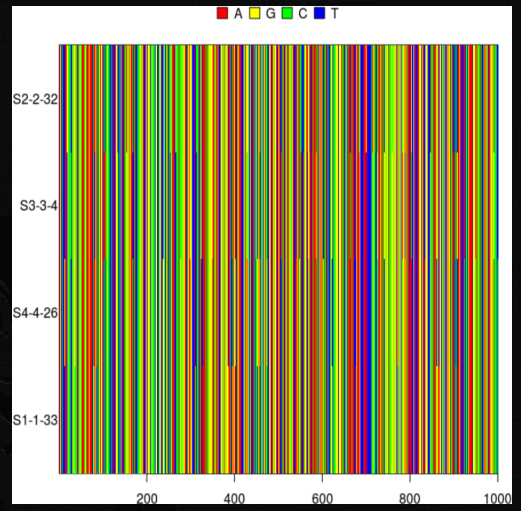


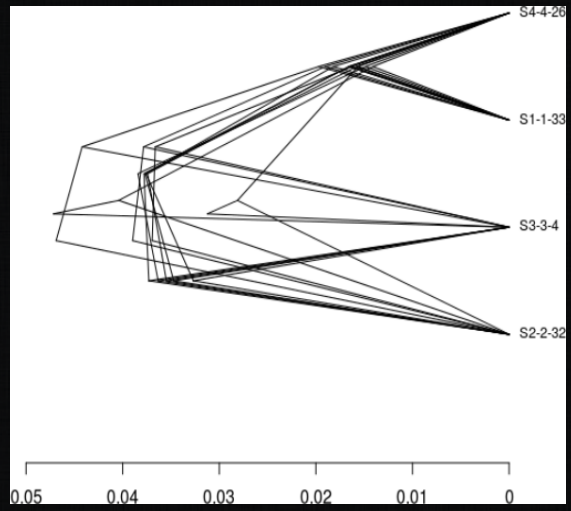
Adapted from Etienne et al., 2012

Approach







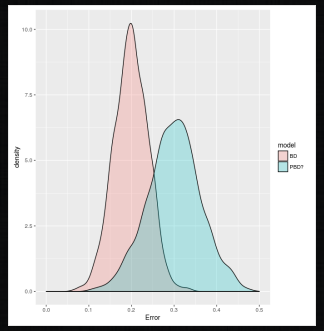


Simulate an incipient species tree

Sample species trees

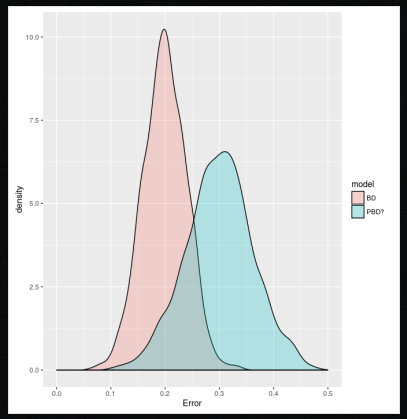
Simulate DNA alignments

Infer species tree posterior (BEAST2)



Measure difference/error (nLTT statistic)

Predictions



Strong protracted-ness

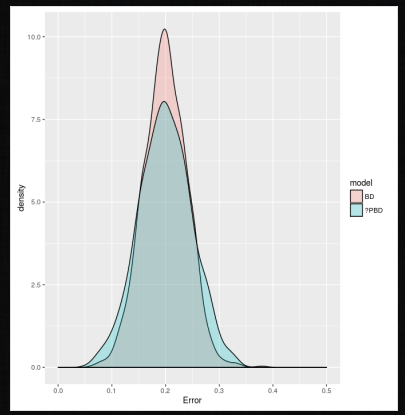
Weak input data

Biologically relevant?

Strong input data

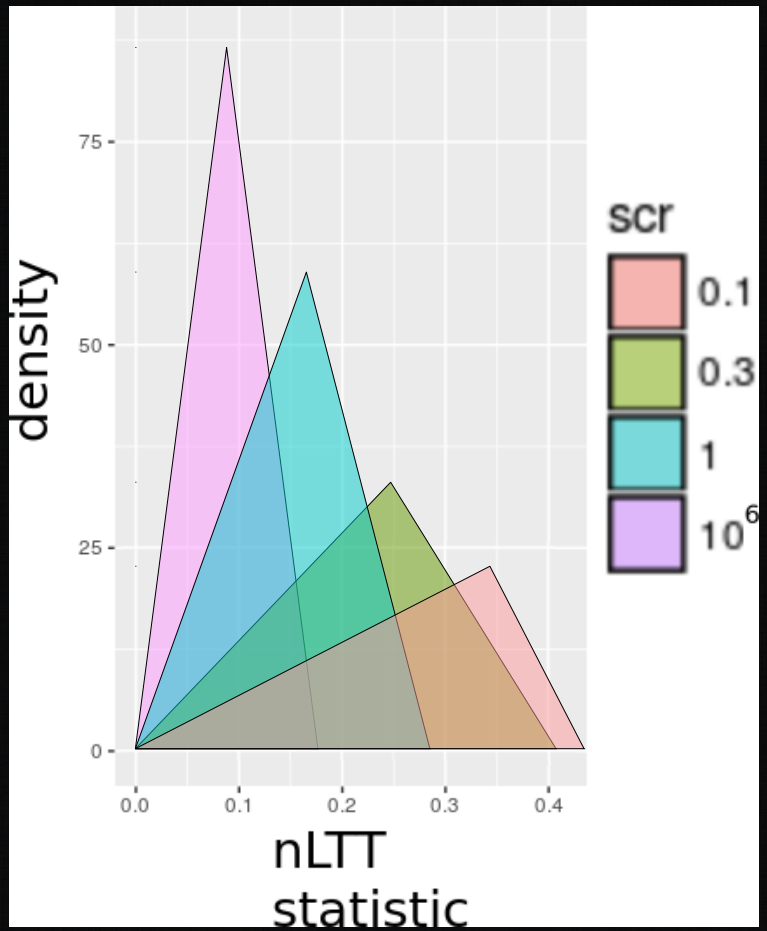
Weak protracted-ness

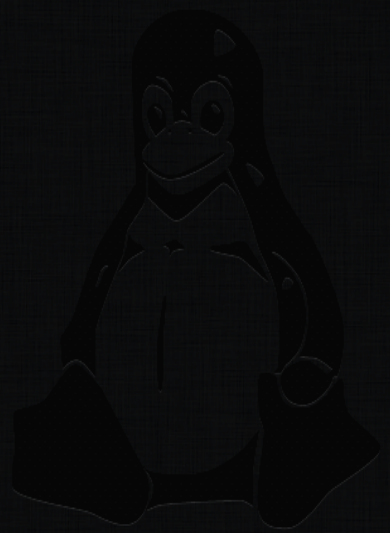
Parameter space



Effect of SCR, prediction

- Infinity: BD
- Small: PBD

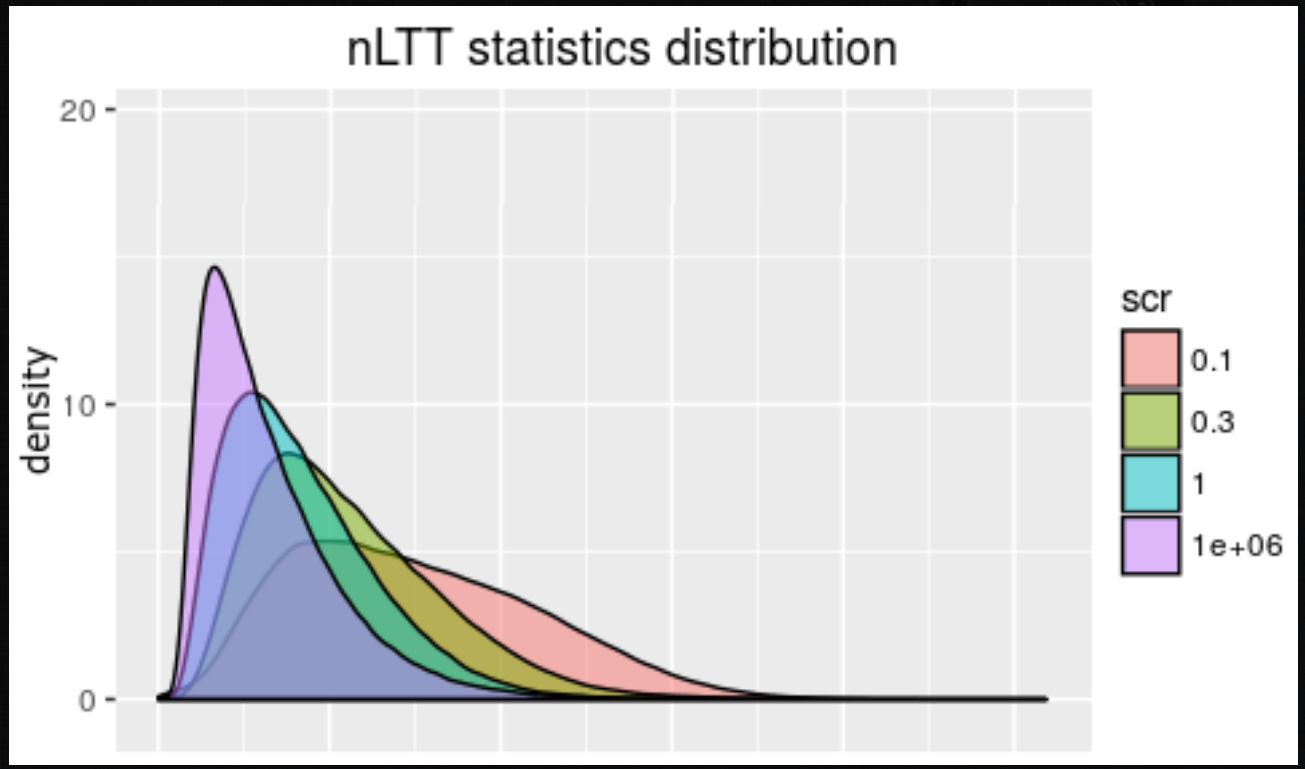




SCR: Speciation Completion Rate
BD: Birth Death model
PBD: Protracted BD model

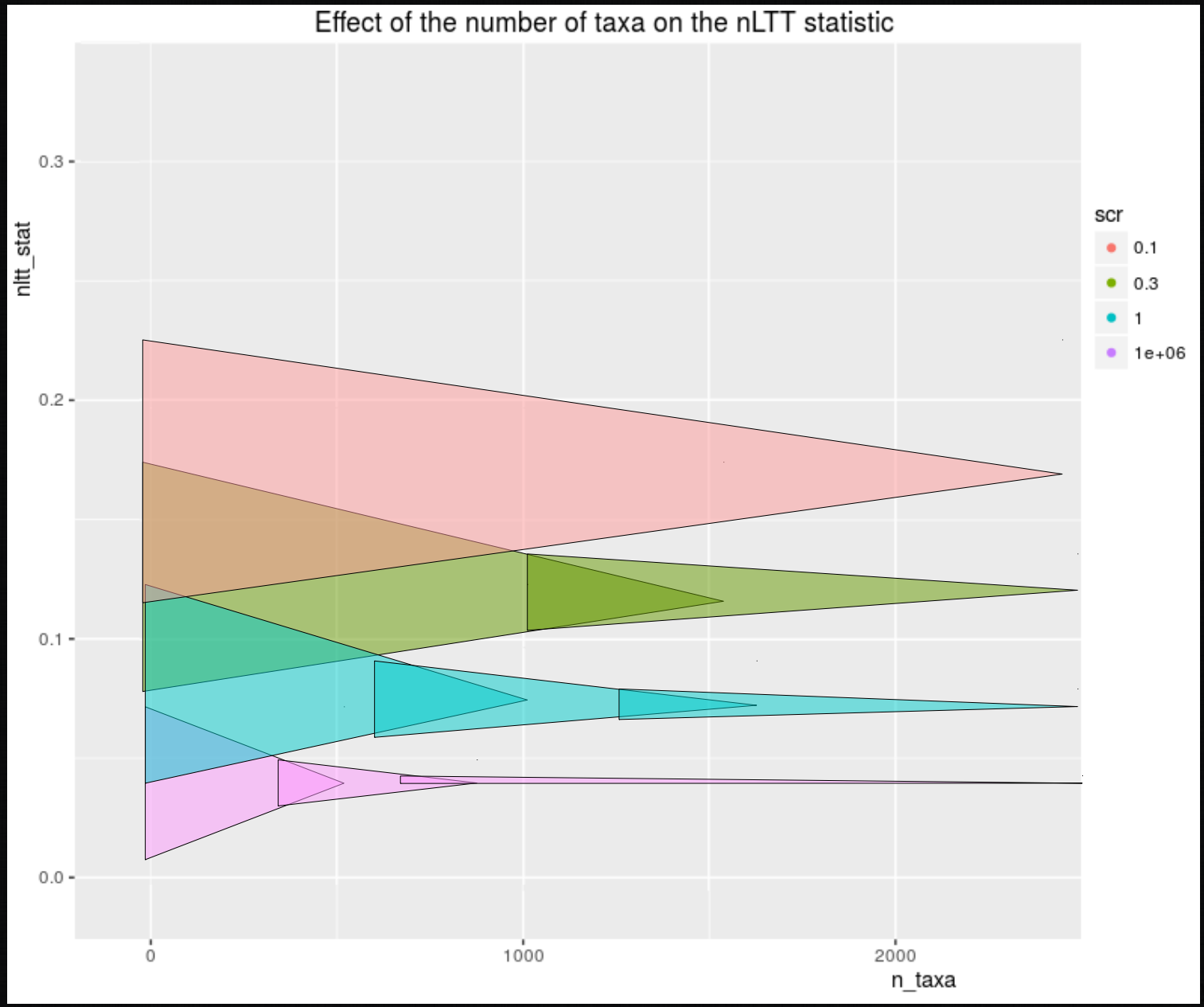
Effect of SCR, measured

- Infinity: BD
- Small: PBD

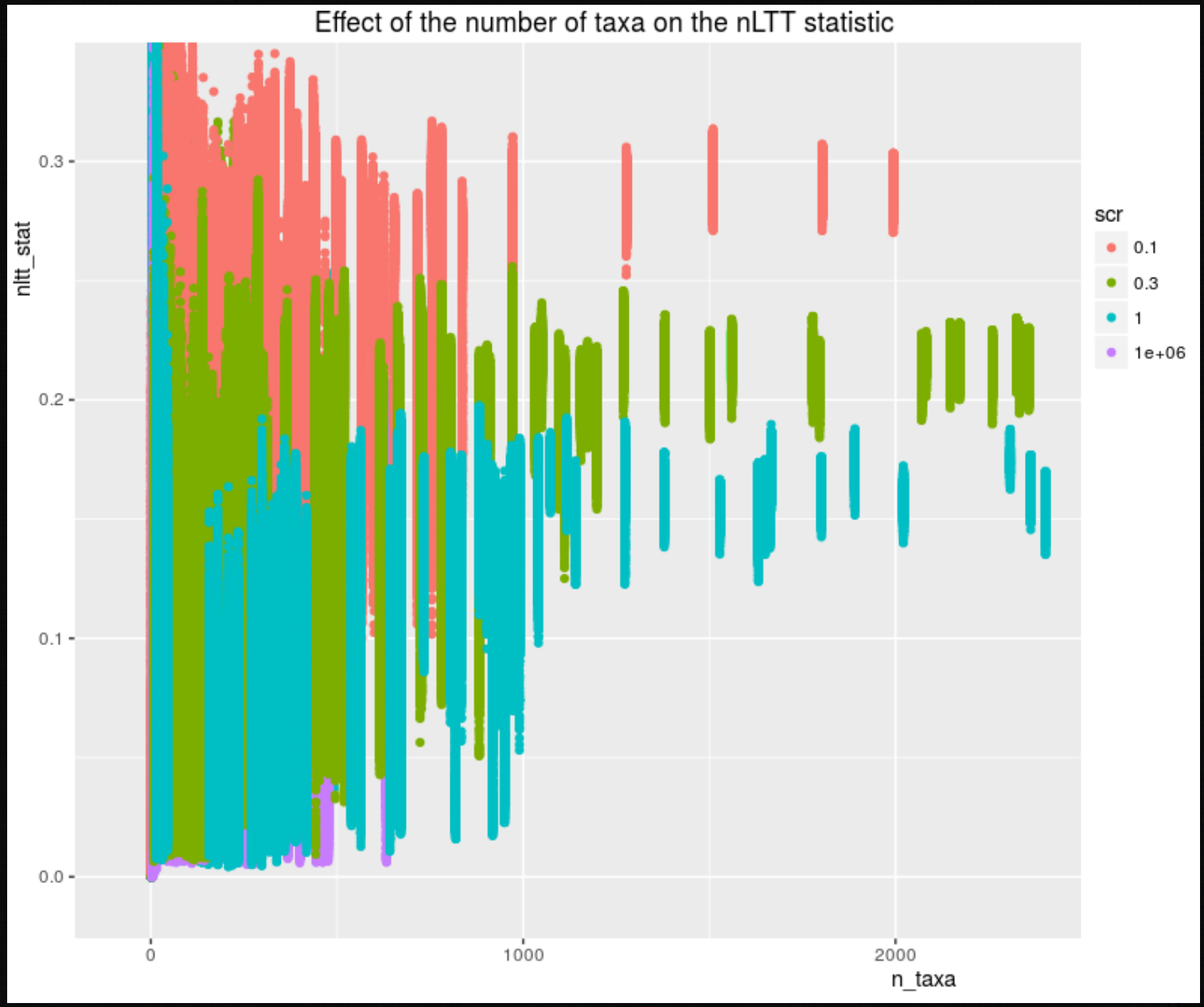


SCR: Speciation Completion Rate
BD: Birth Death model
PBD: Protracted BD model

Effect of #taxa, expected

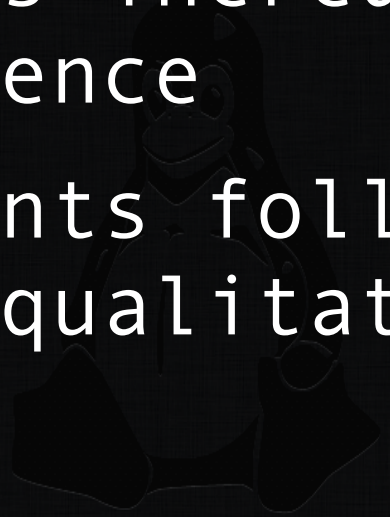


Effect of #taxa, measured



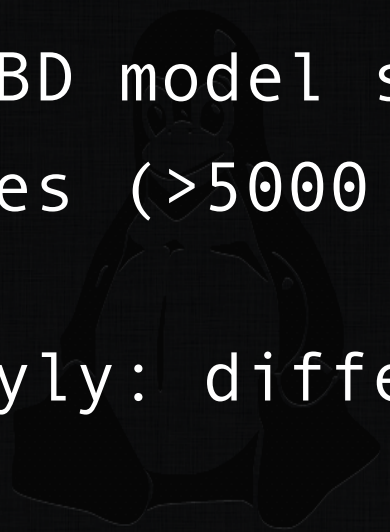
Conclusion

- An increased level of protractedness increases the error made in inference
- The measurements follow the expectations qualitatively



Discussion

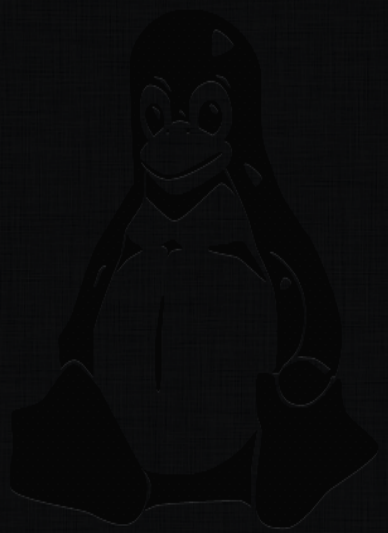
- Comparison with expected error must be measured
- Comparison with BD model stronger
- Bigger phylogenies (>5000 taxa) were not analysed
- Effect of paraphyly: different topology

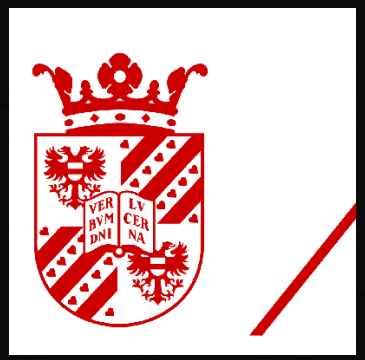


- Check my research:
  - www.GitHub.com/richelbilderbeek
    - wiritttes: simulation
    - wiritttea: analysis

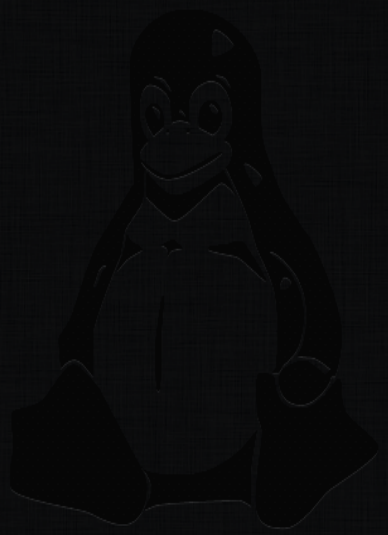
Acknowledgements

- Rampal Etienne
- Jolien Gay
- Femke Thon

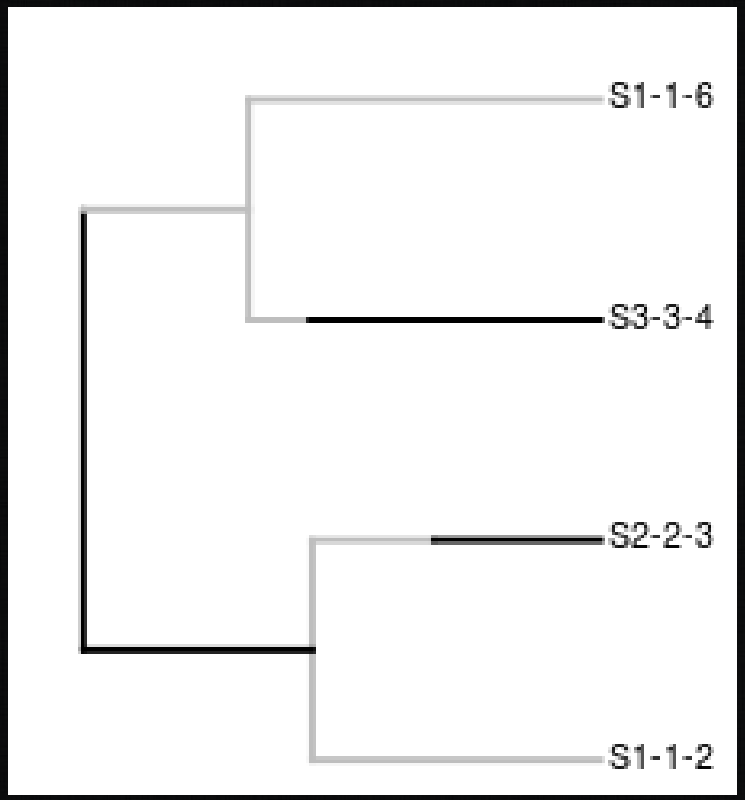


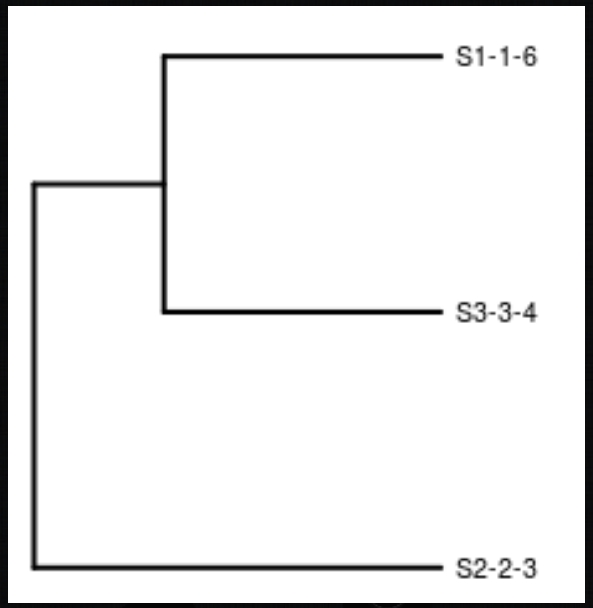


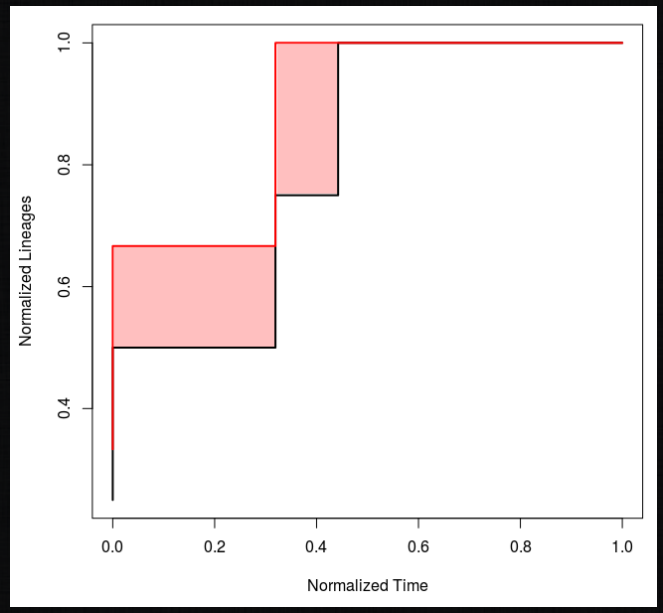
Questions?

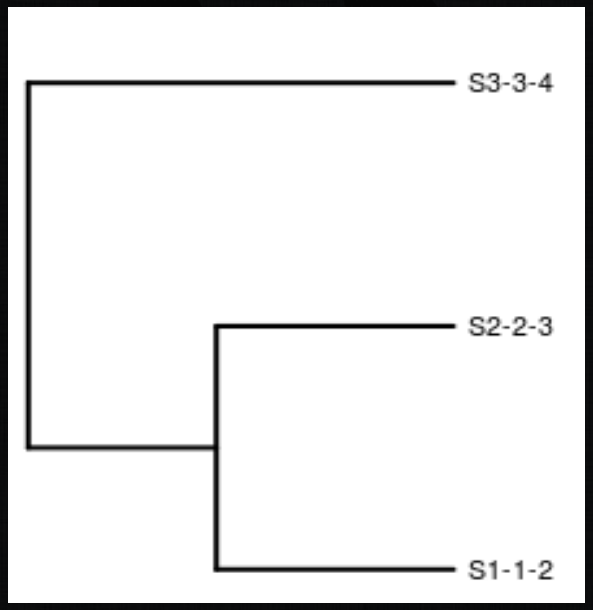


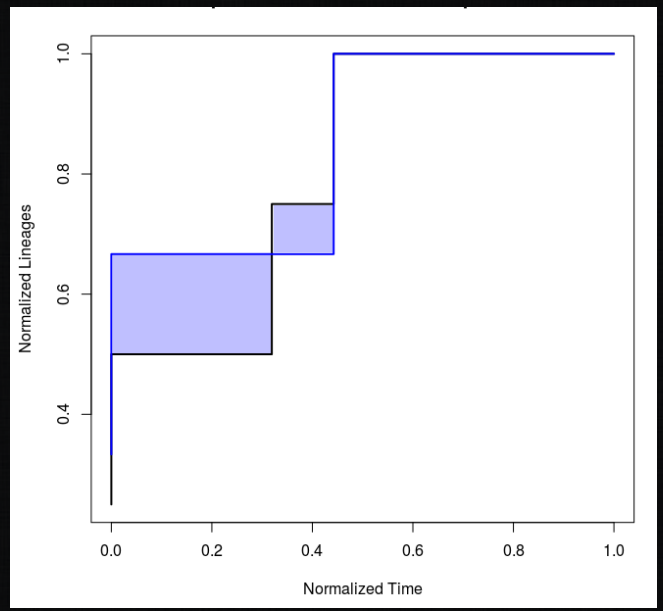
Simulated truth





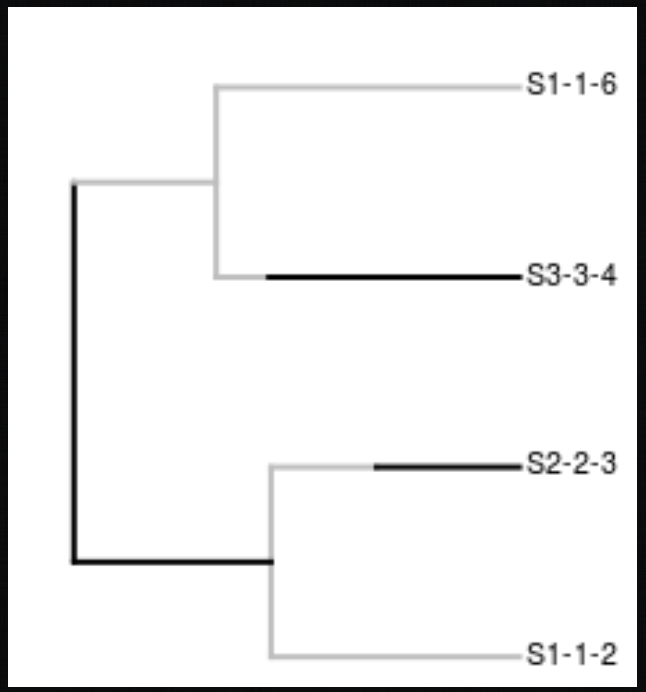


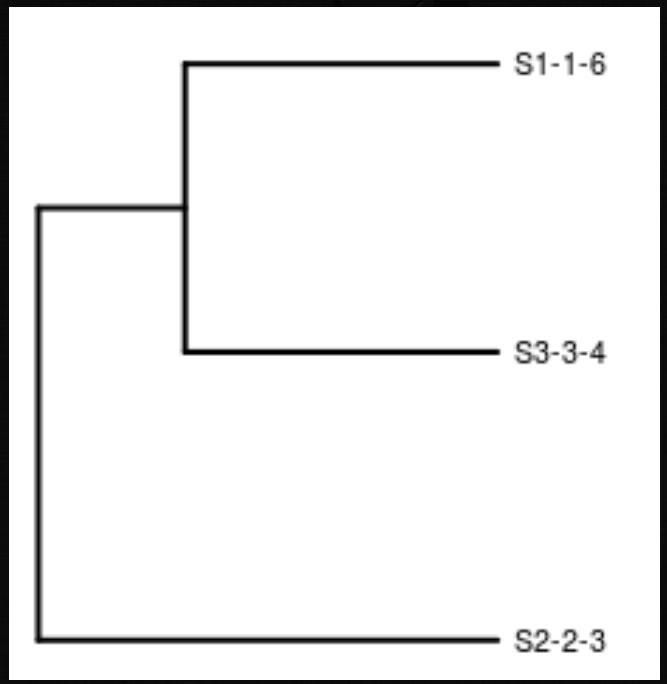


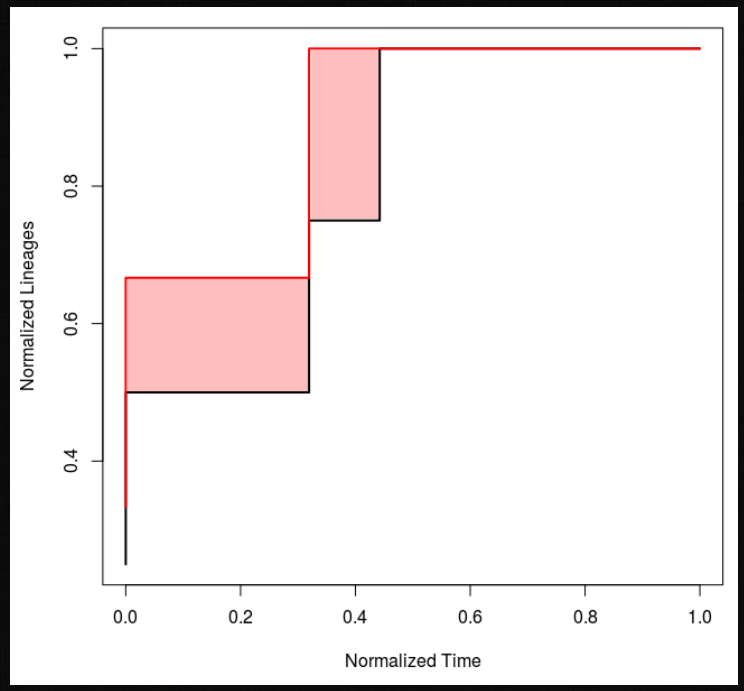


nLTT statistic [1]

- Quantify difference between two phylogenies







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