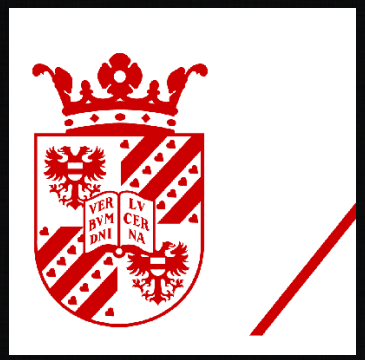
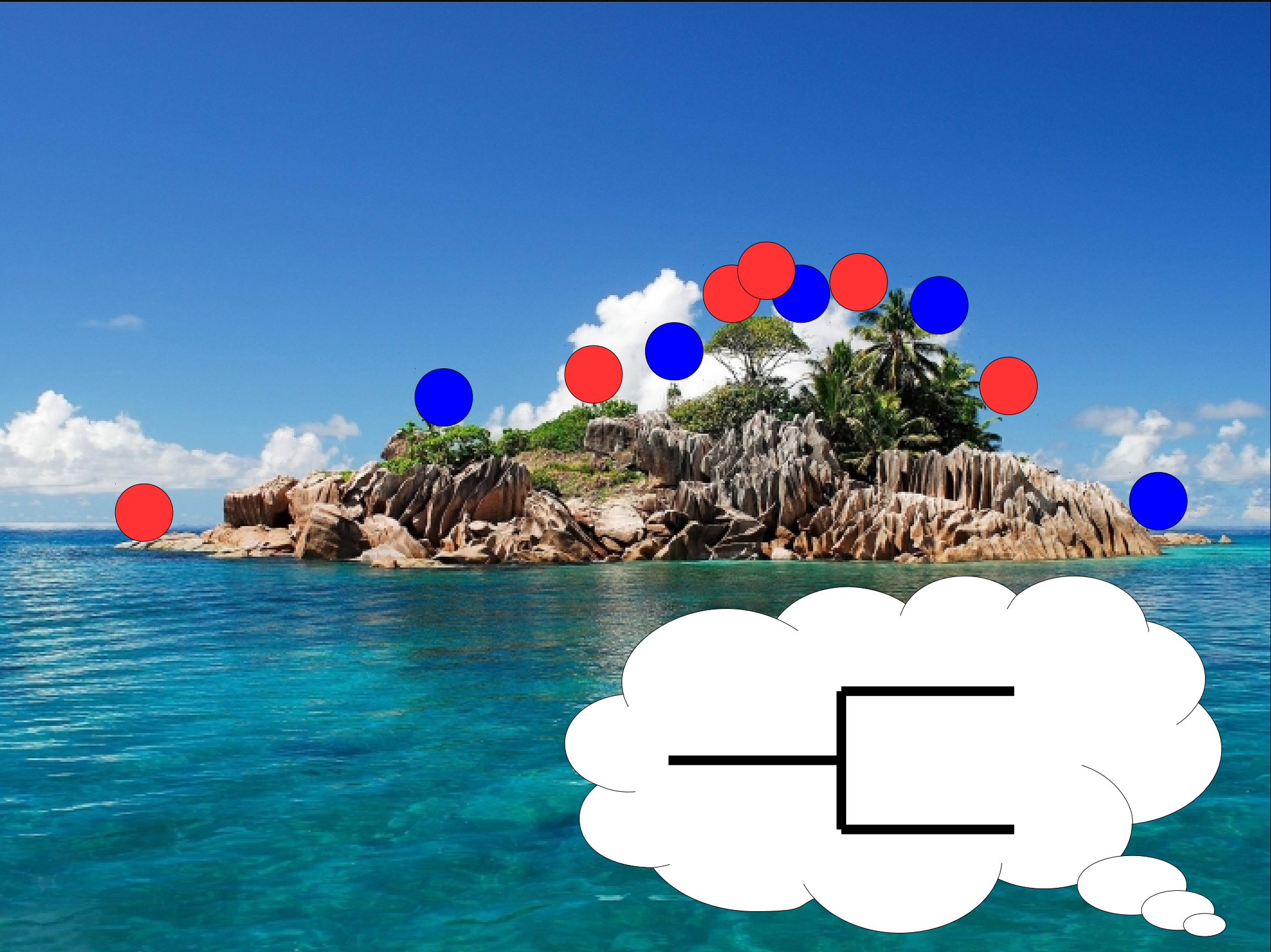
Ignoring incipient species

TRES meeting 2017-02-13

www.github.com/richelbilderbeek/Science



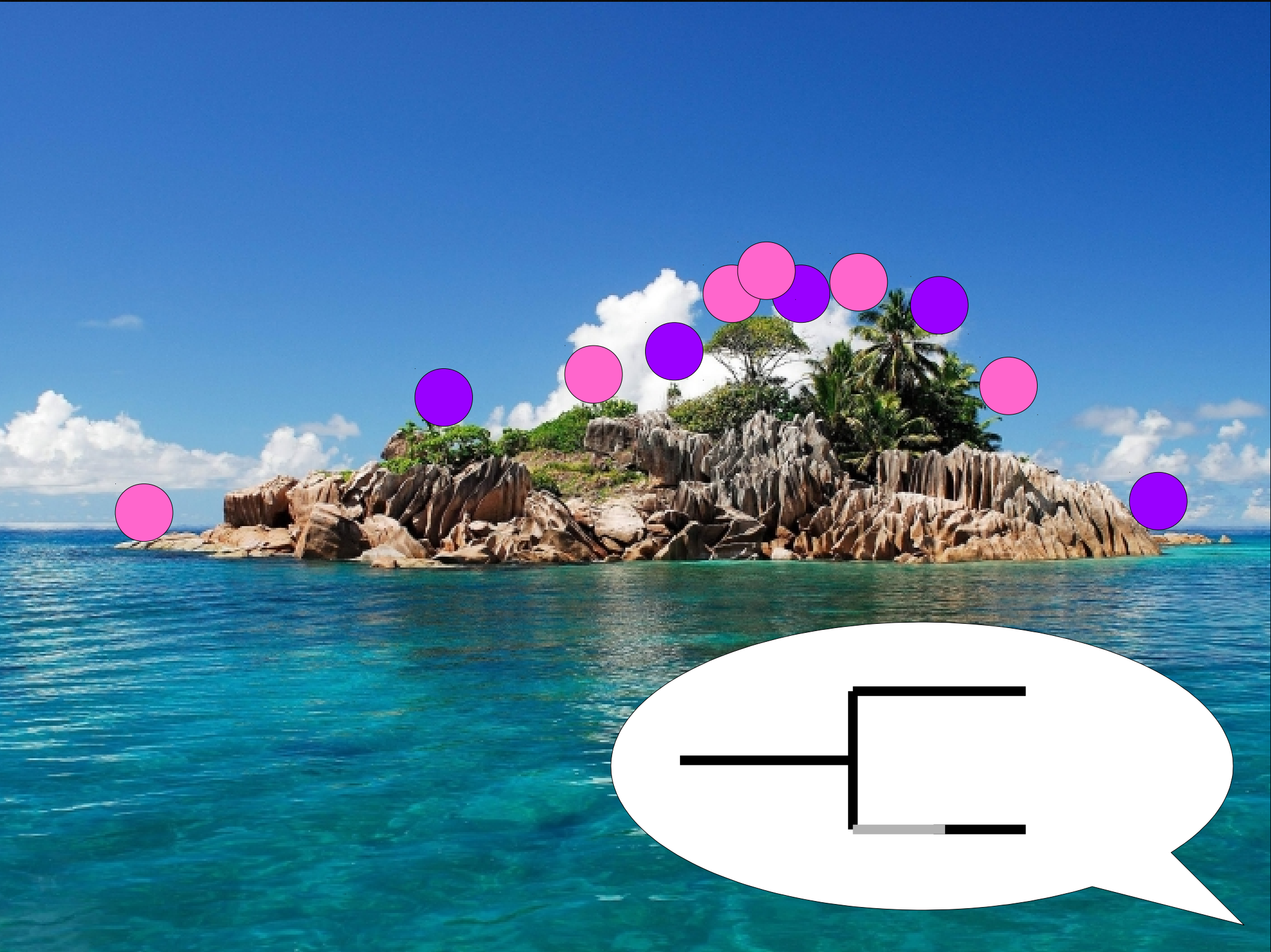


Research question

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

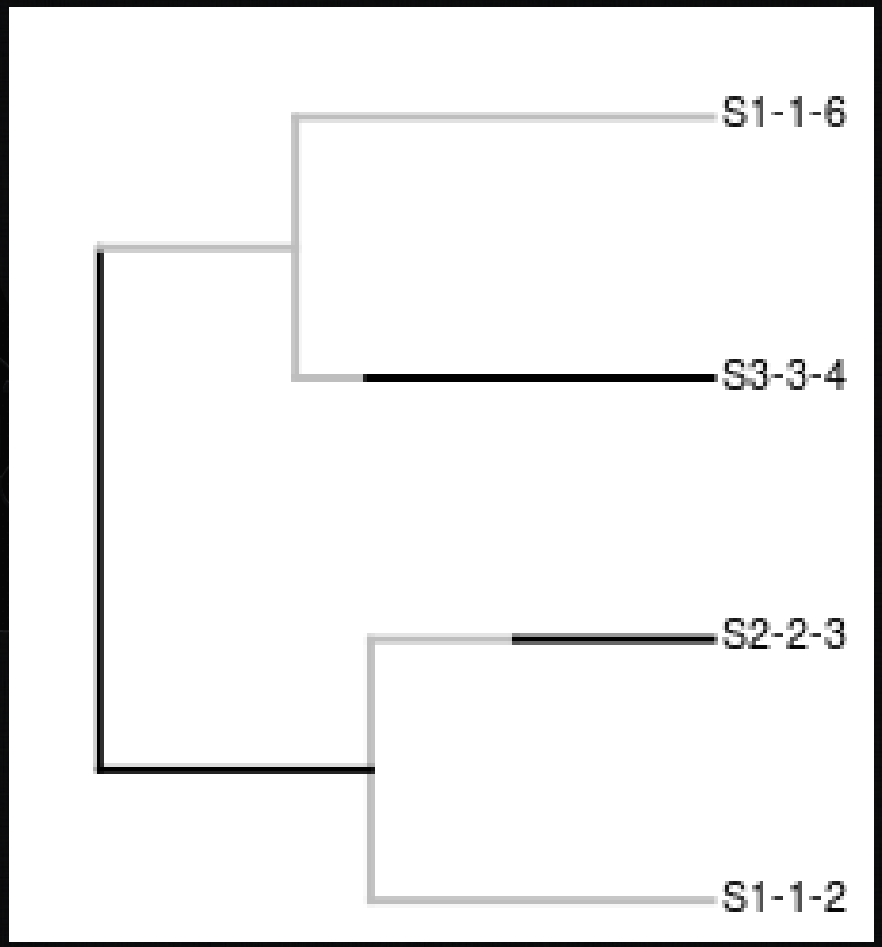
How long does that phase last?

Which species lived when?



Protracted speciation [1]

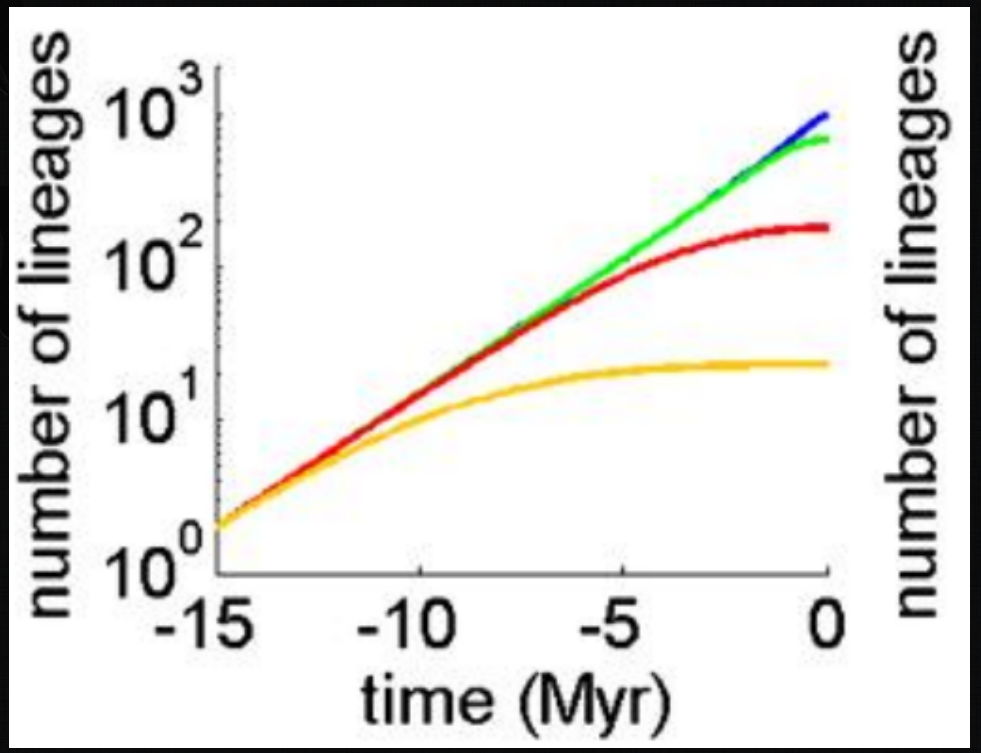
- Extension of Birth-Death (BD) model [2]
- New species are incipient
- Speciation completion rate
  - Incipient → good
  - BD if infinite



[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]



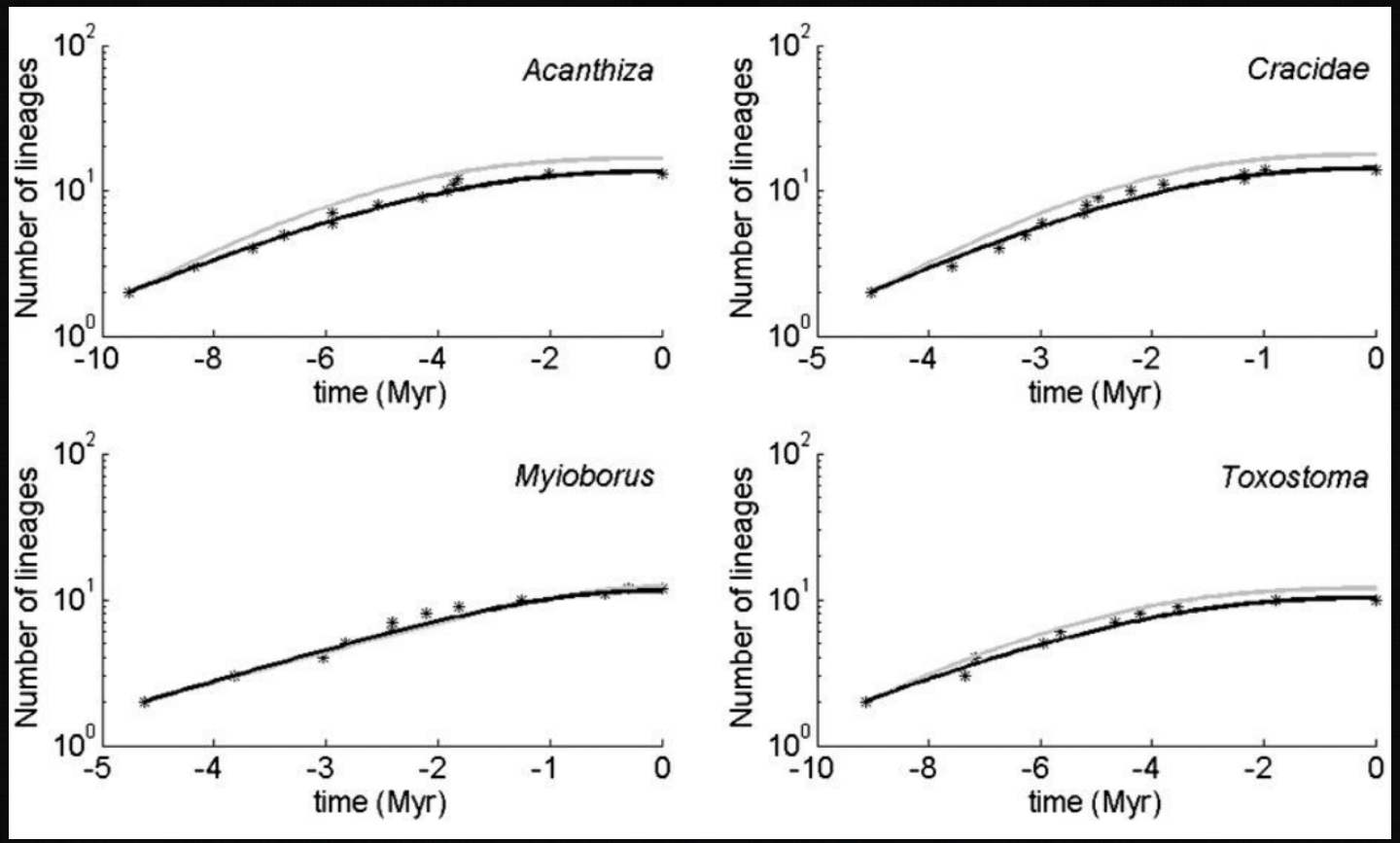
[1] Janzen et al., 2015

Adapted from Etienne & Rosindell, 2012

PBD in nature

Acanthiza nana, Yellow Thornbill

Myioborus torquatus, Collared Whitestart

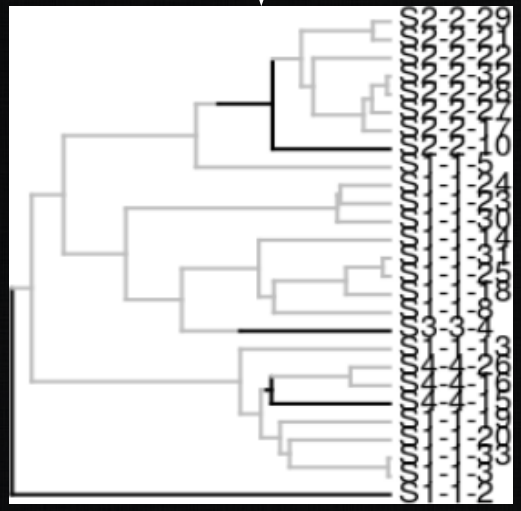


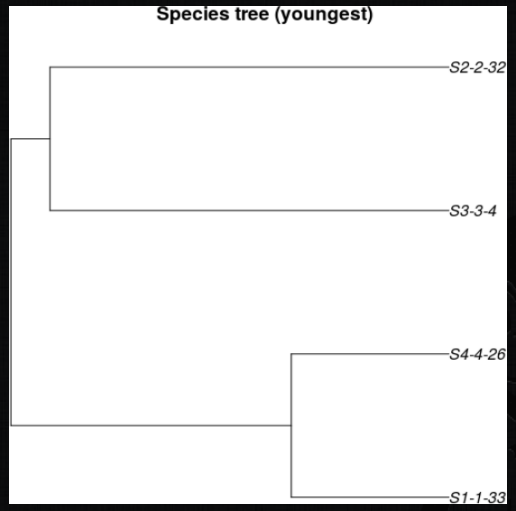
Etienne & Rosindell, 2012

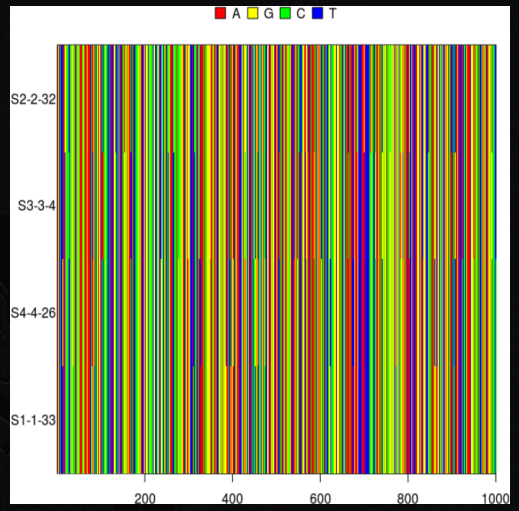
Crax daubentoni, Yellow-knobbed Curassow

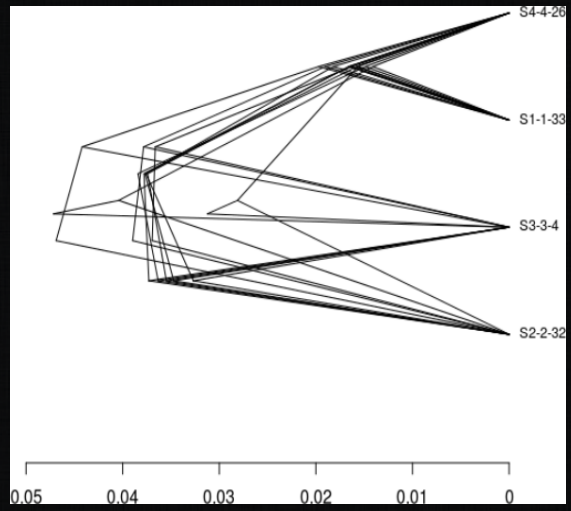
Toxostoma rufum, Brown Thrasher

Approach









Simulate an incipient species tree

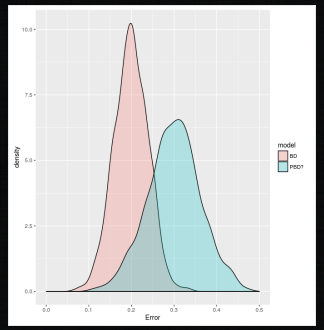
Sample species trees

PBD

Simulate DNA alignments

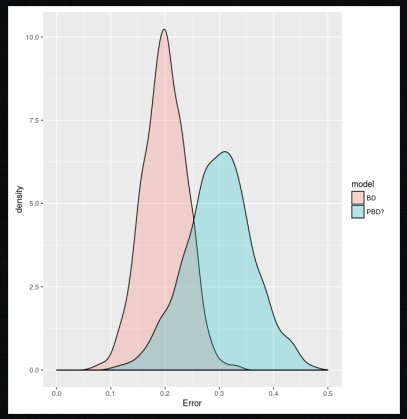
Infer species tree posterior (BEAST2)

BD prior



Measure difference/error (nLTT statistic)

Predictions



Strong protracted-ness

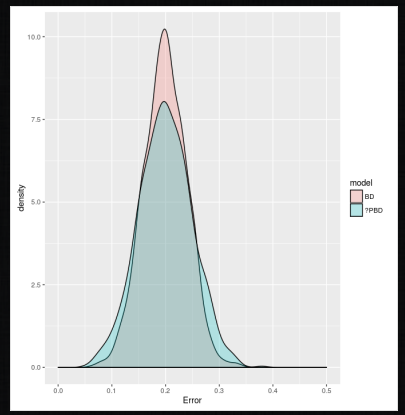
Weak input data

Biologically relevant?

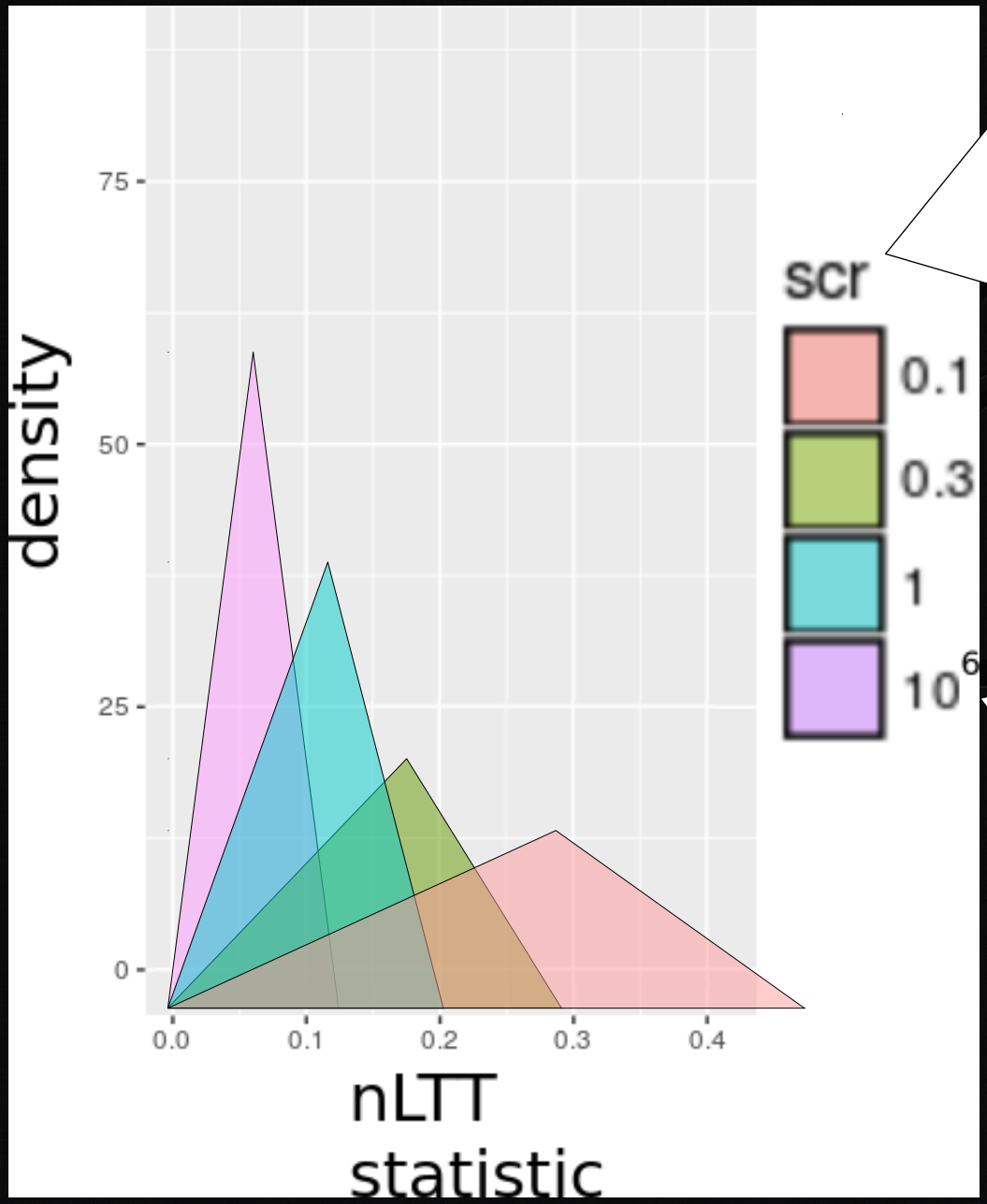
Strong input data

Weak protracted-ness

Parameter space



Effect of SCR, prediction

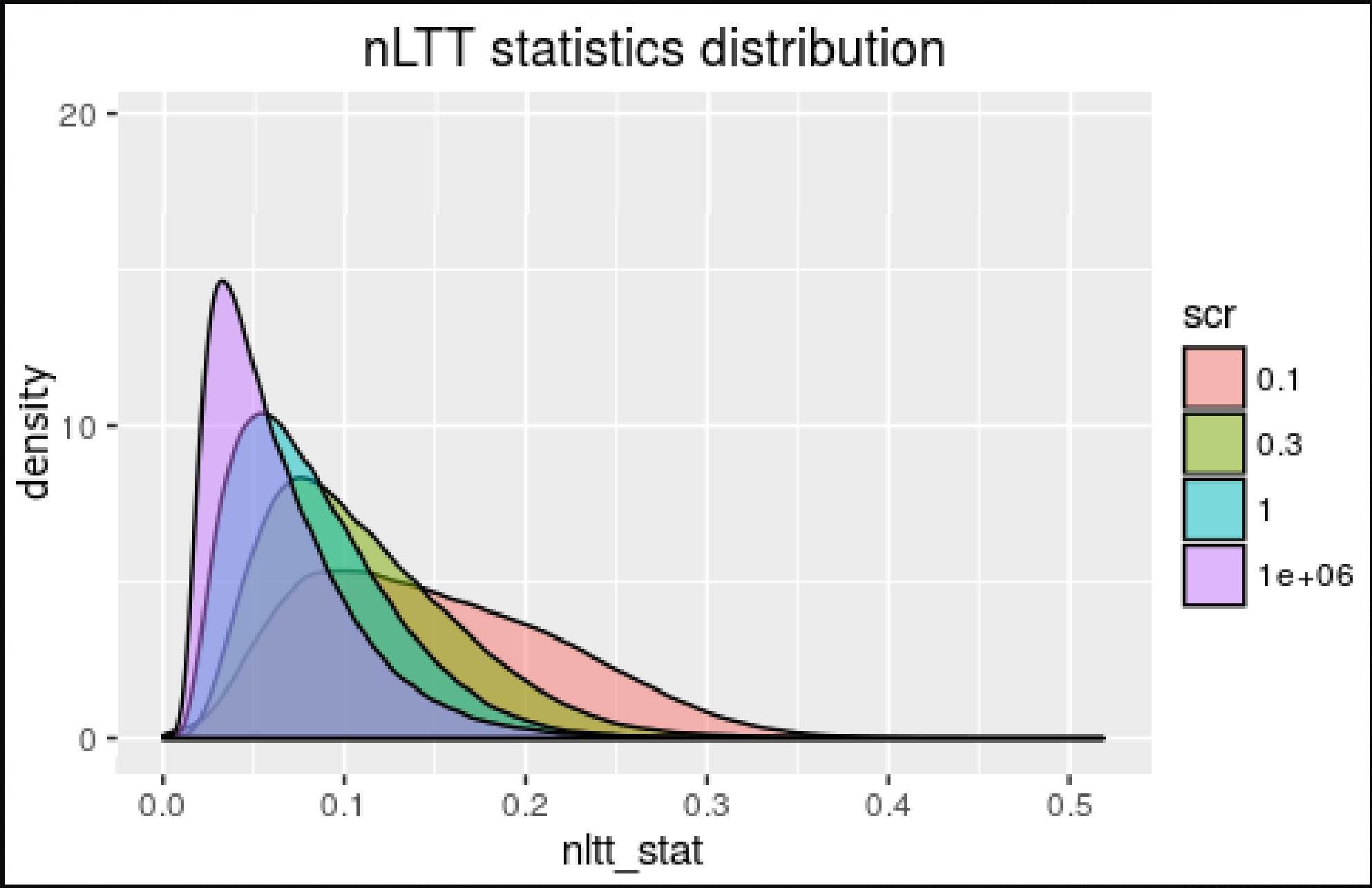


Speciation Completion Rate

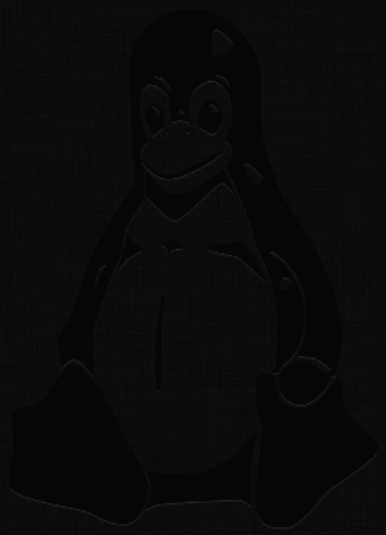
Protracted Birth-Death

Birth-Death (BD) model

Effect of SCR, measured



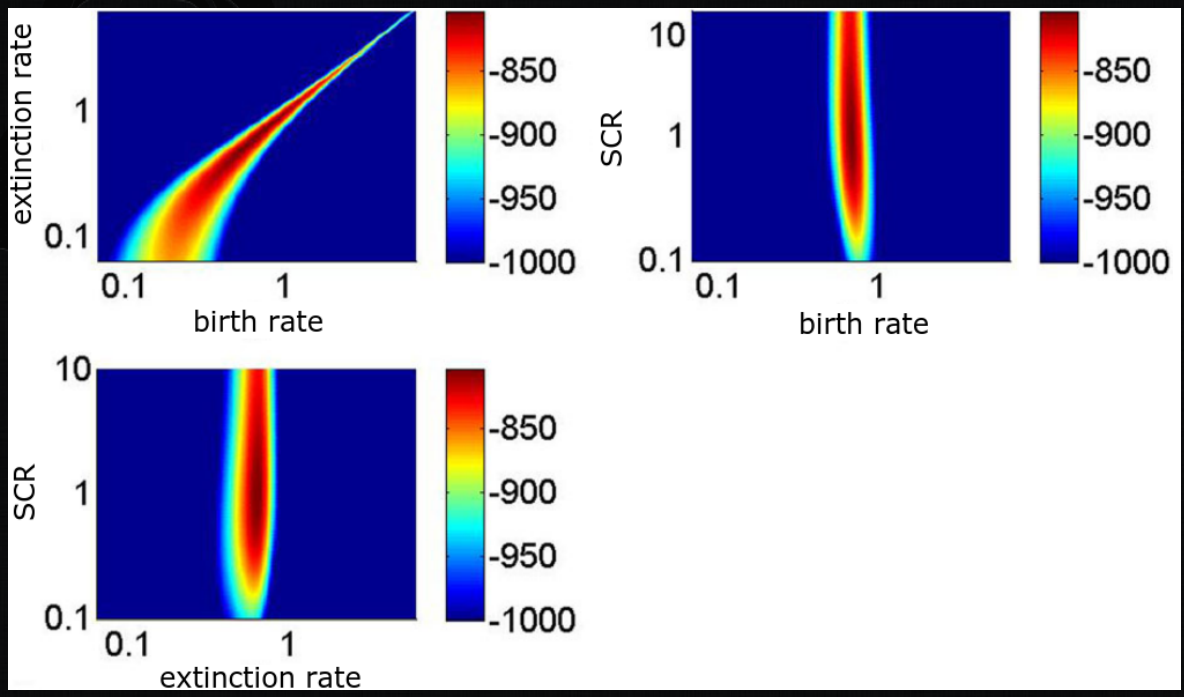
Extinction rates



SCRs in nature

- Birds: 0.04-0.89
- Primates: around 1

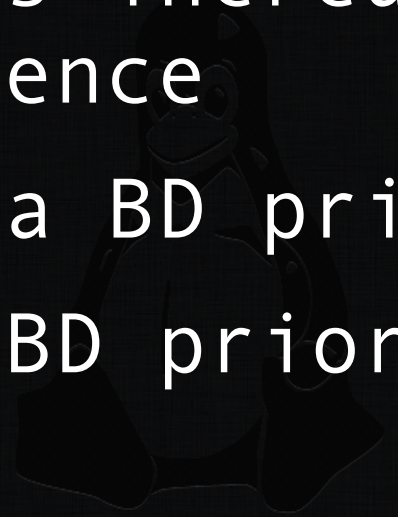
Data set	λ_2 (Myr $^{-1}$)
Acanthiza	0.07
Cracidae	0.16
Myiborus	0.39
Toxostoma	0.06



Adapted from Etienne et al., 2014

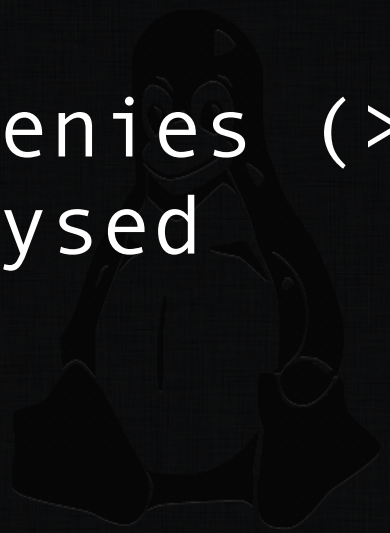
Conclusion

- An increased level of protractedness increases the error made in inference
- For primates a BD prior works fine
- For birds, a BD prior may not be sufficient



Discussion

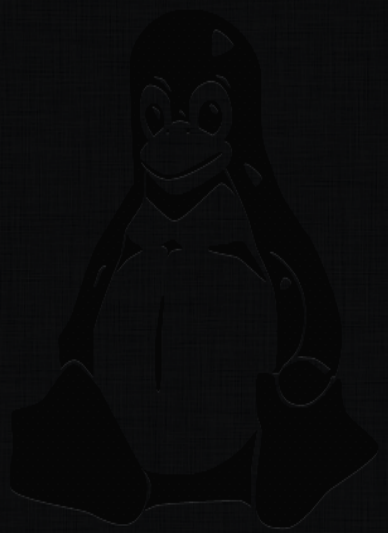
- Only one speciation initiation rate investigated
- Bigger phylogenies (>5000 taxa) were not analysed

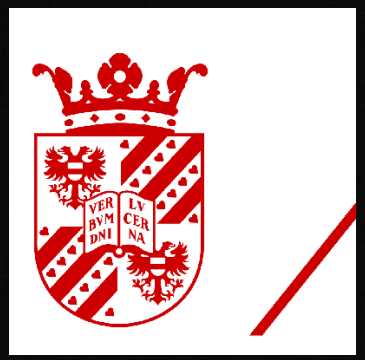


- Run my research:
  - www.gGitHub.com/richelbilderbeek
    - wiritttes: simulation
    - wiritttea: analysis

Acknowledgements

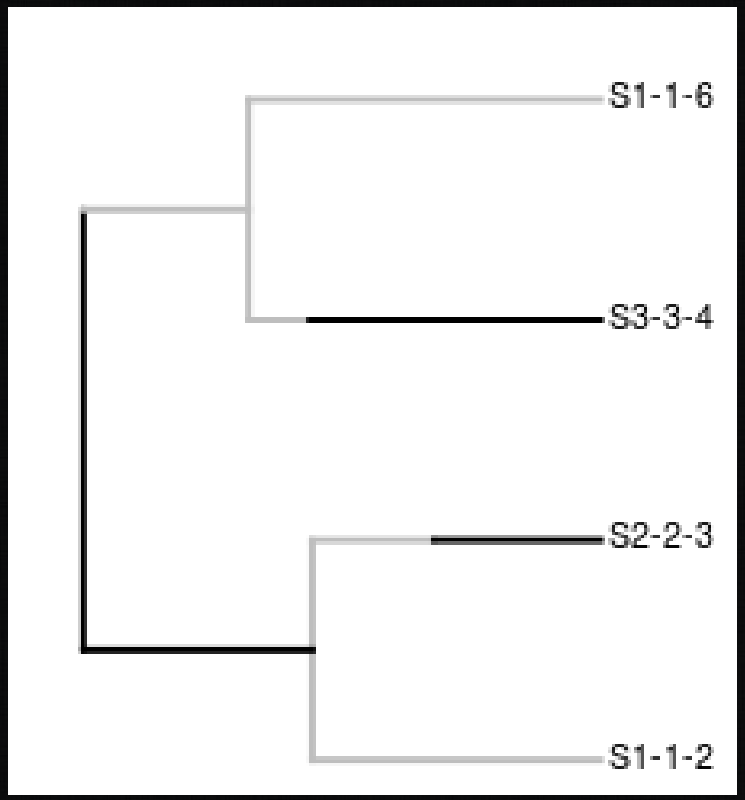
- Rampal Etienne
- Jolien Gay
- Femke Thon

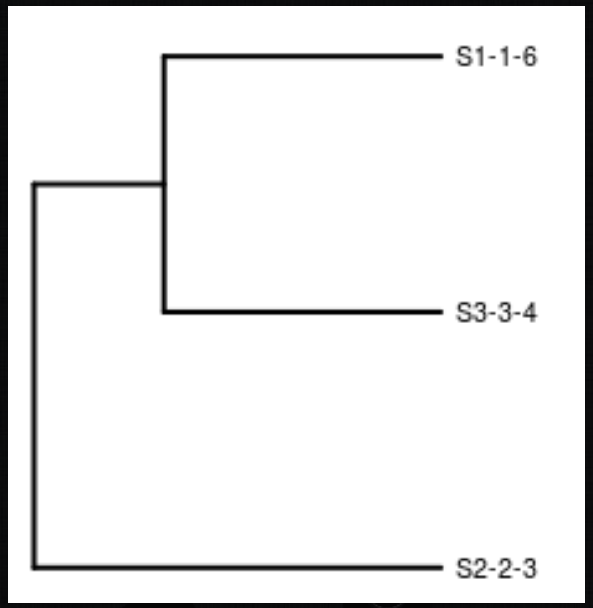


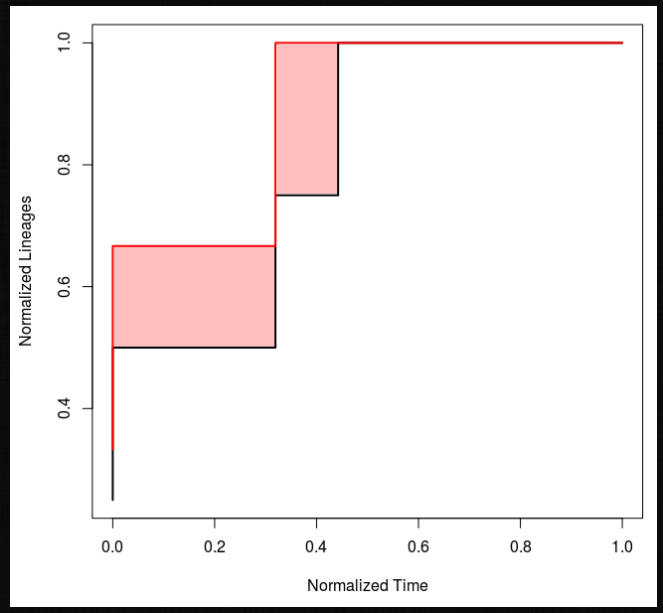


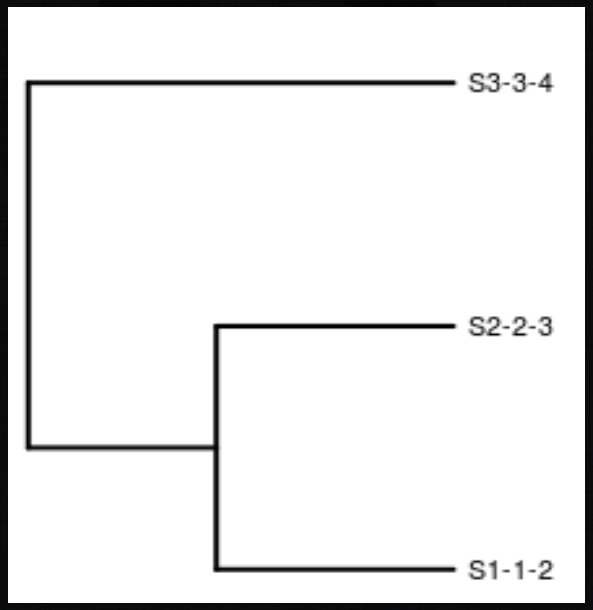
Questions?

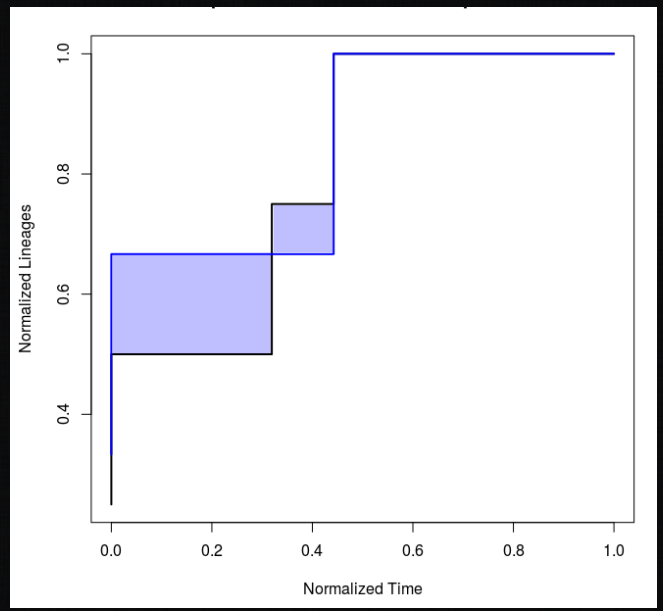
Simulated truth





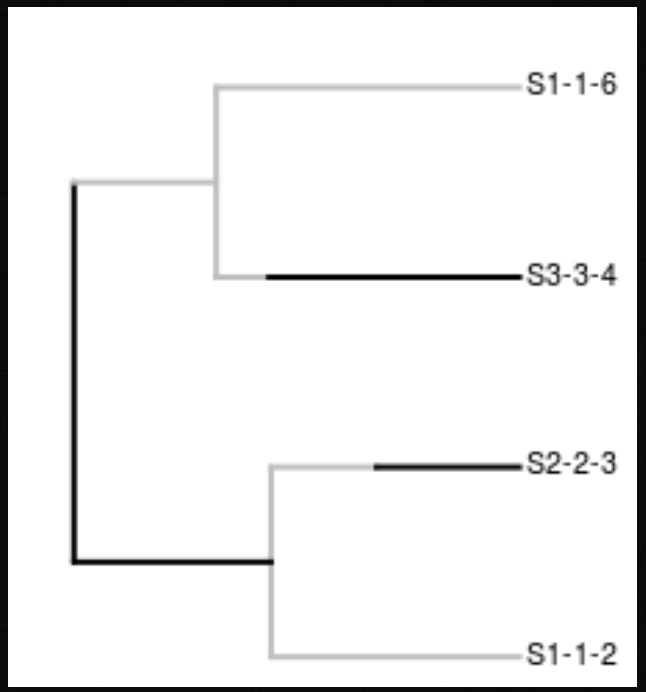


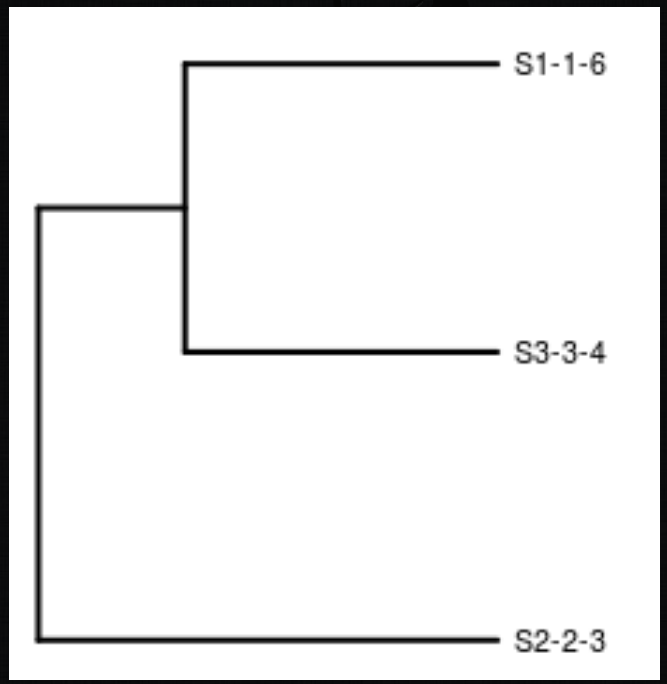


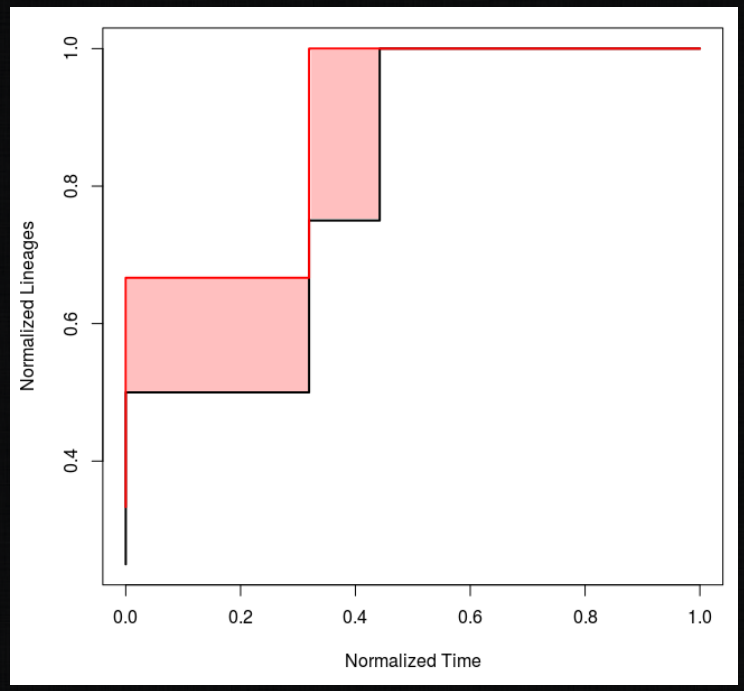


nLTT statistic [1]

- Quantify difference between two phylogenies

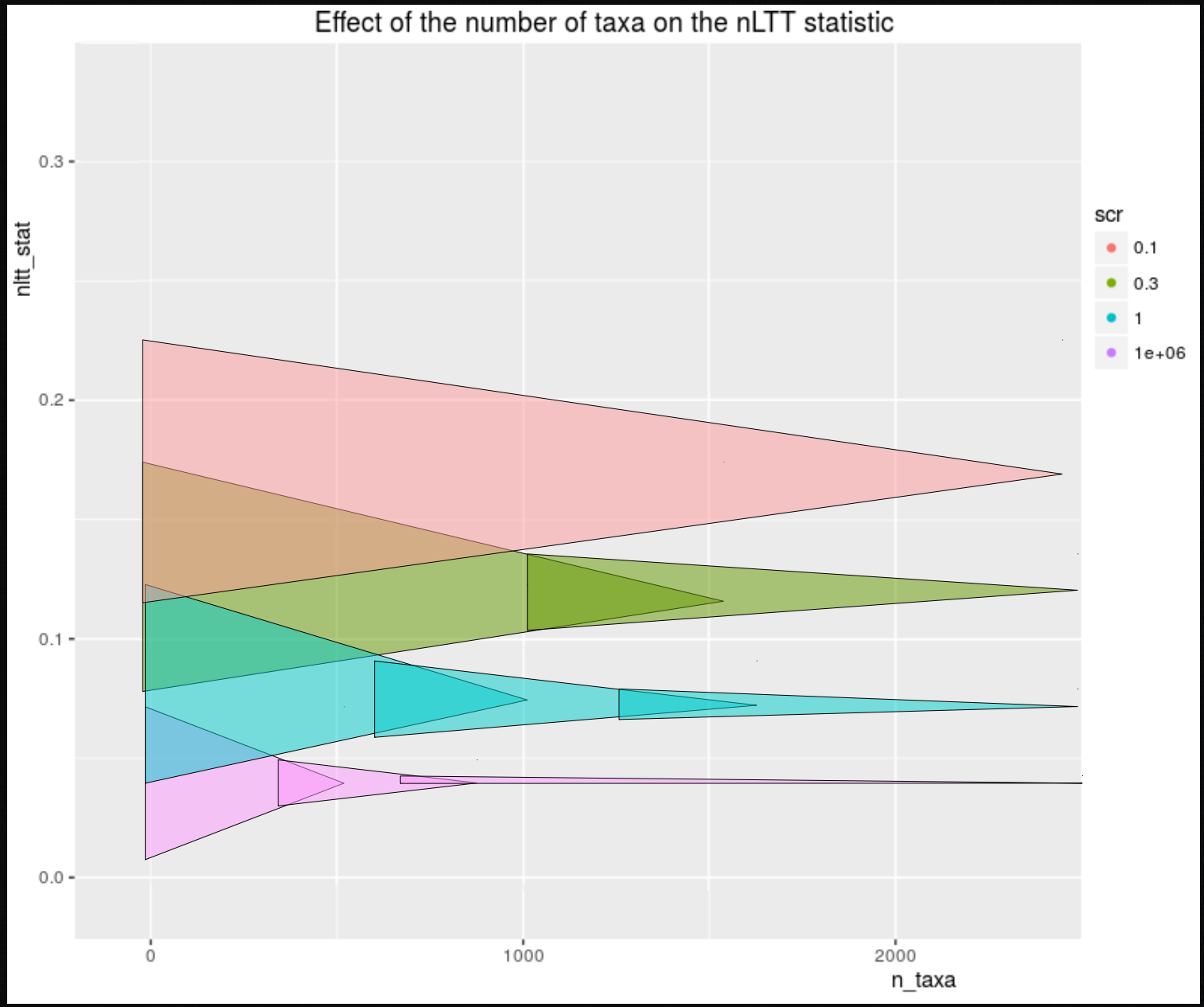






[1] Janzen et al., 2015

Effect of #taxa, expected



Effect of #taxa, measured