

PhD project overview

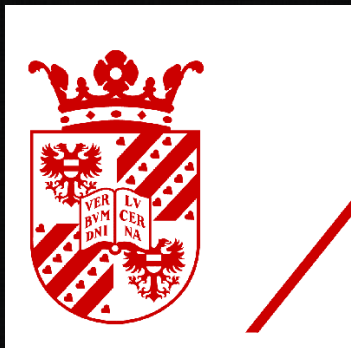
TECE meeting 2016-11-03



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www.github.com/richelbilderbeek/Science

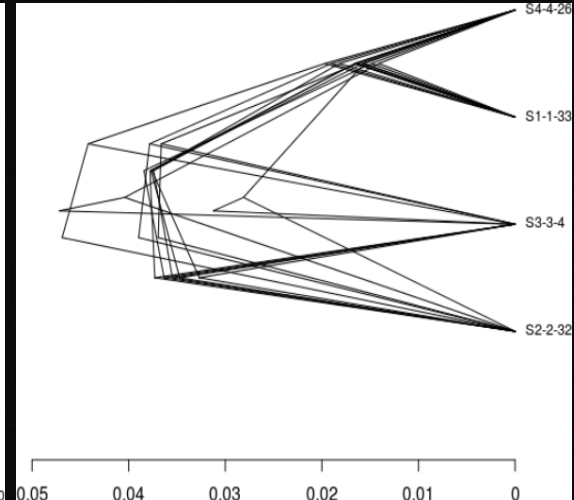
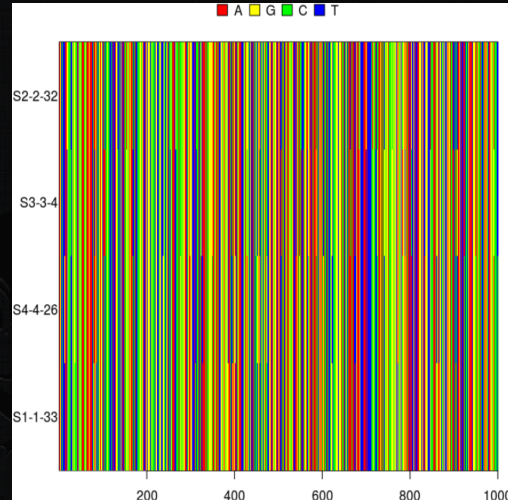
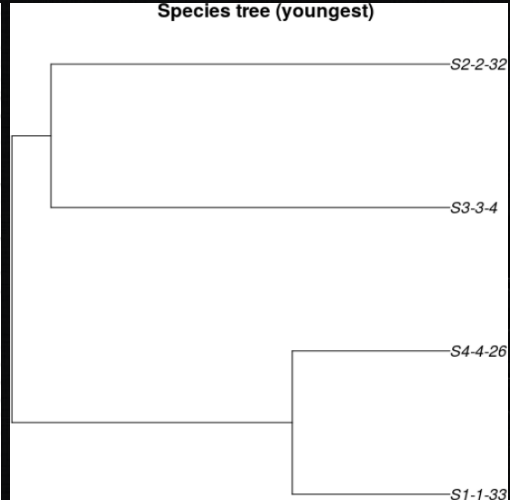
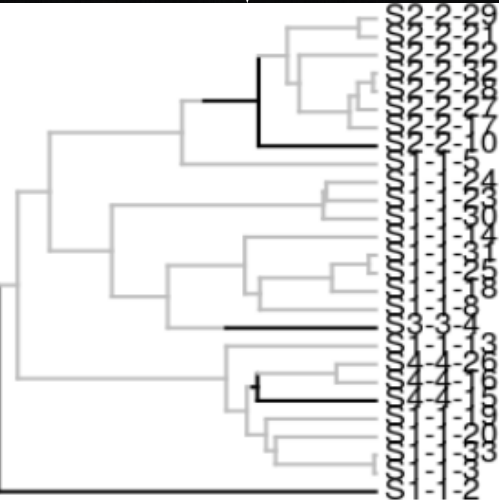


Project 1: BD on PBD

If reproductive isolation takes time to establish, what is the error made today 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

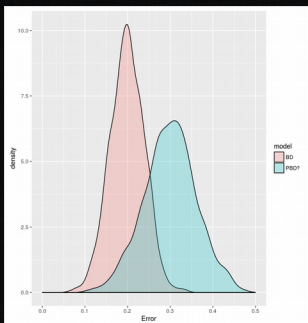


Simulate an
incipient
species tree

Sample species
trees

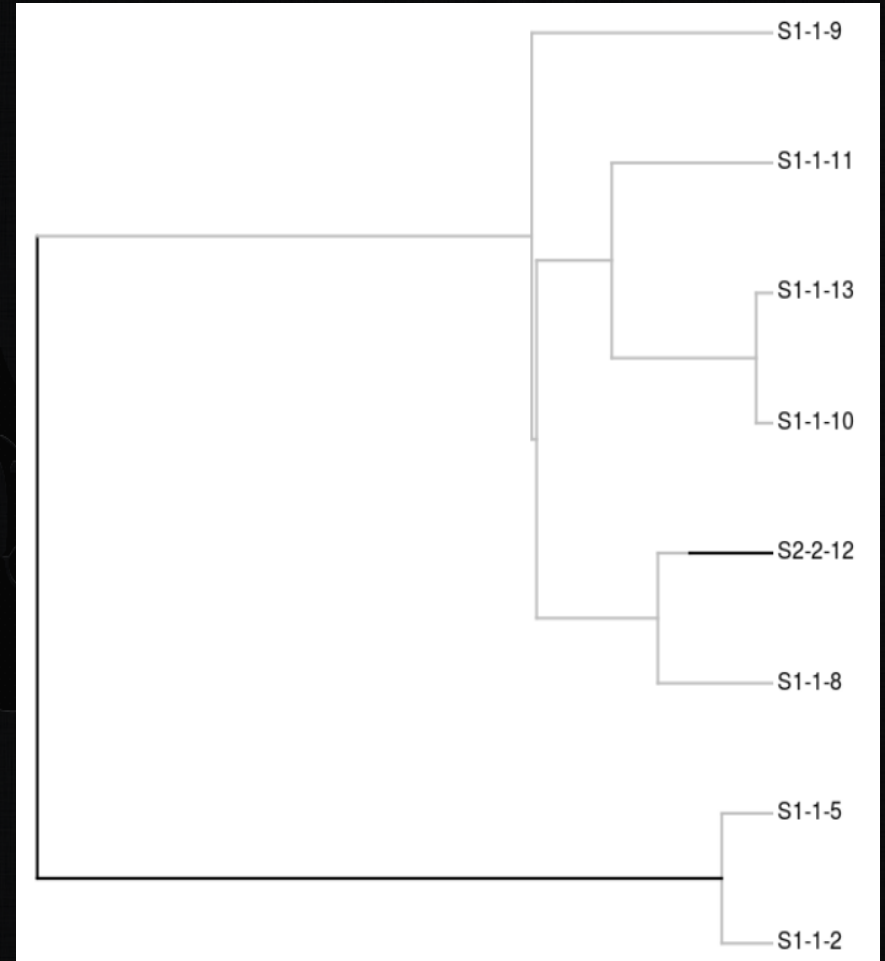
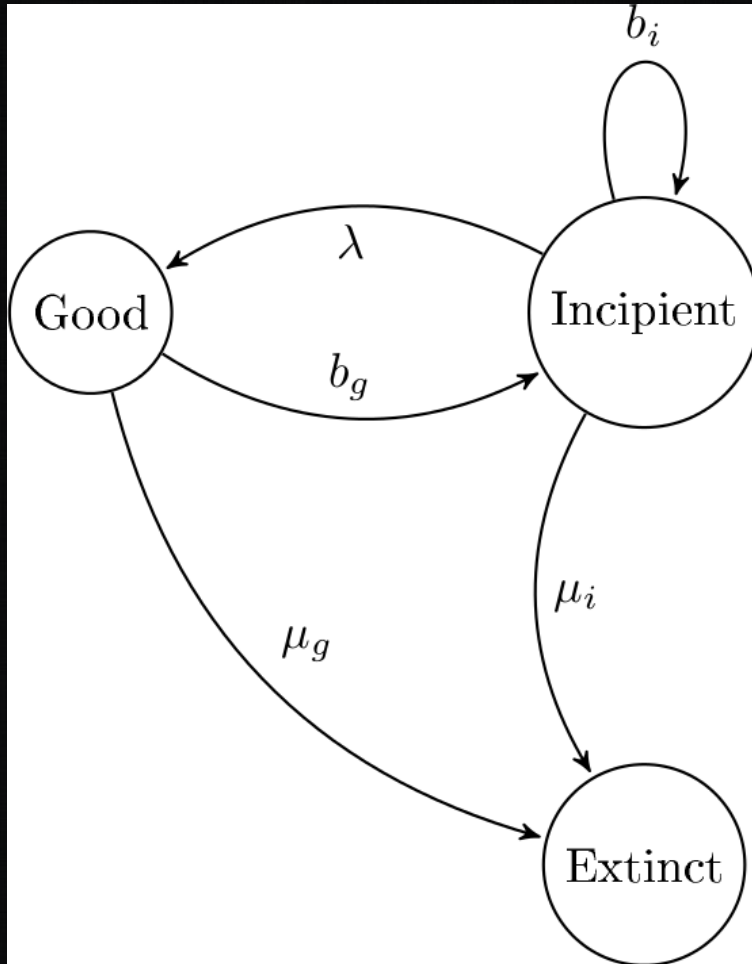
Simulate DNA
alignments

Infer species
tree posterior



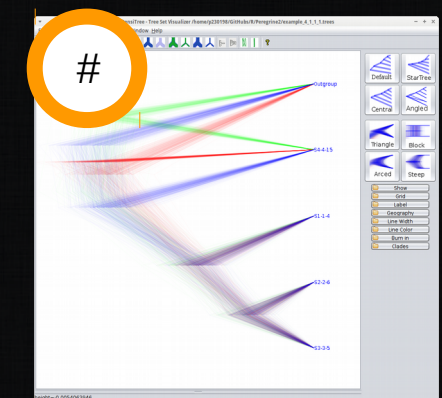
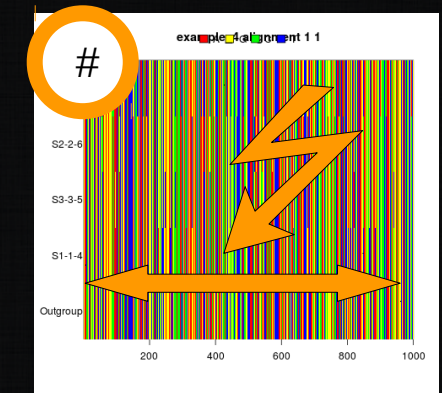
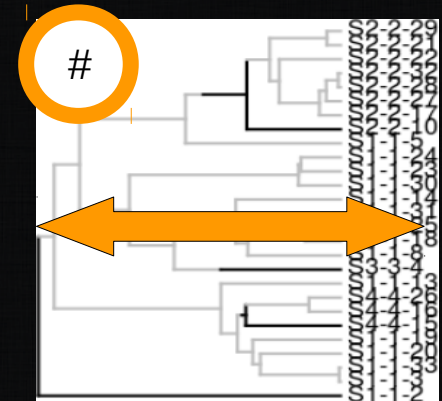
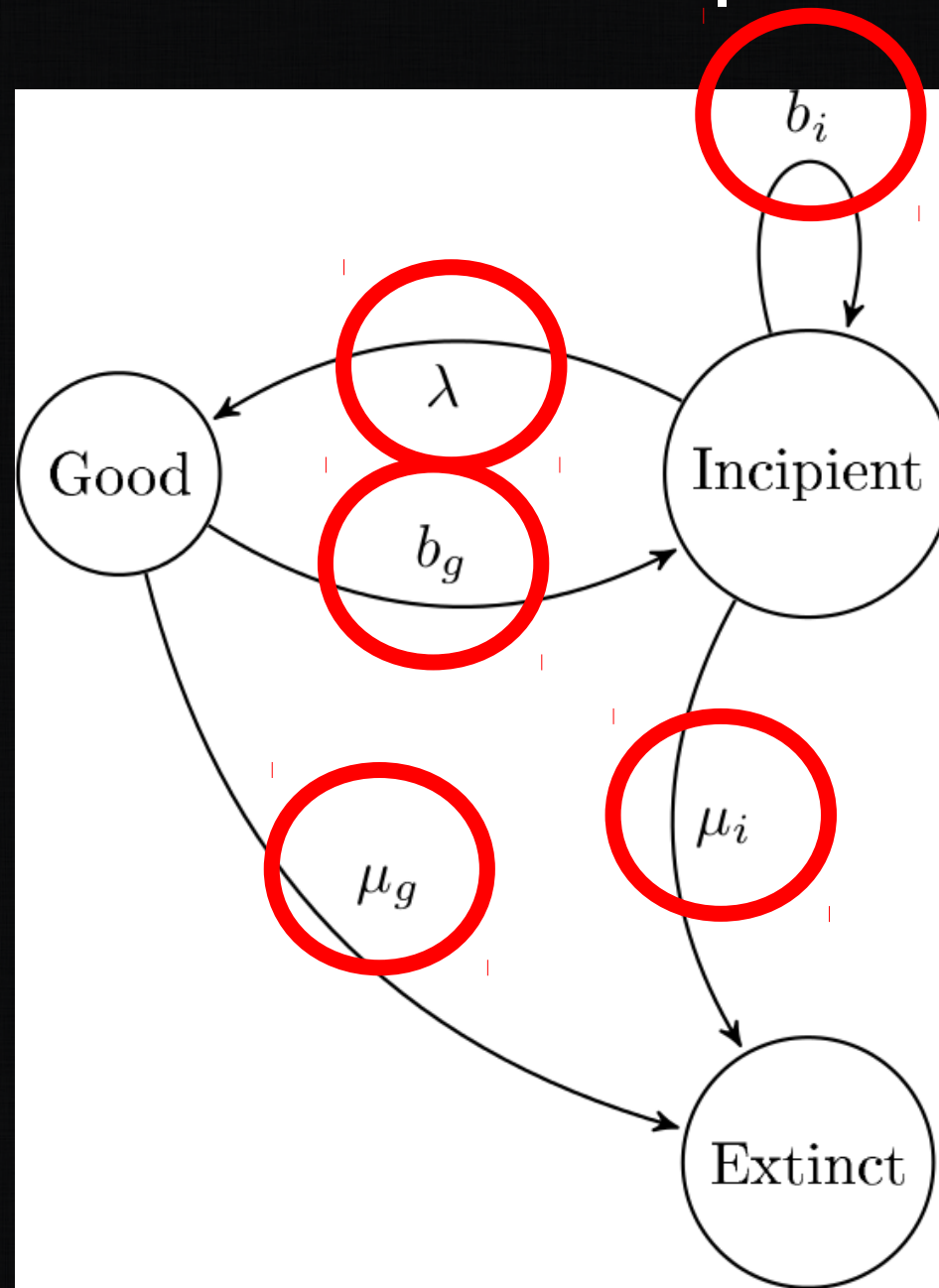
Measure difference/error

PBD model

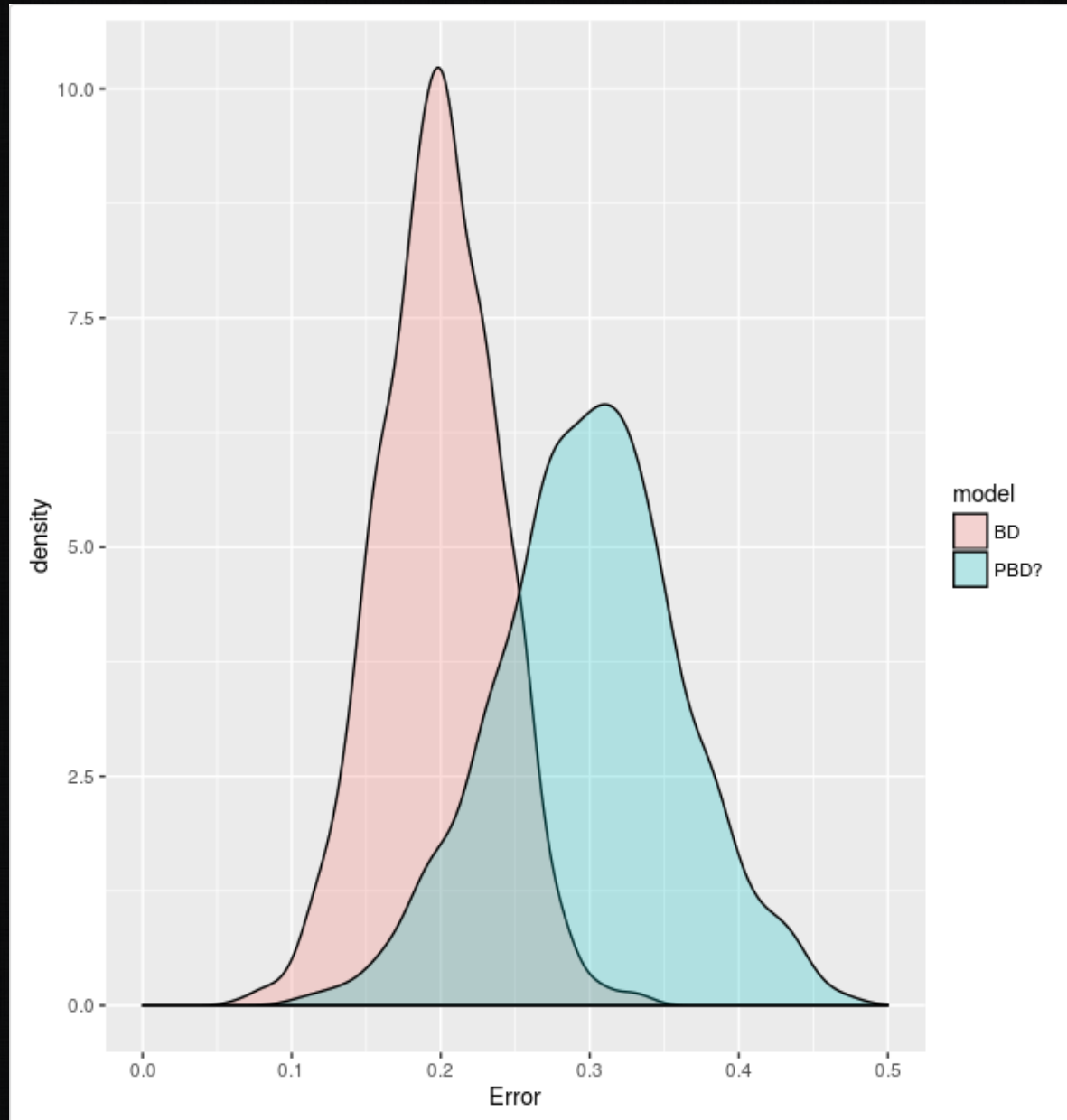


Etienne, Rampal S., and James Rosindell. "Prolonging the past counteracts the pull of the present: protracted speciation can explain observed slowdowns in diversification." *Systematic Biology* (2011): syr091.

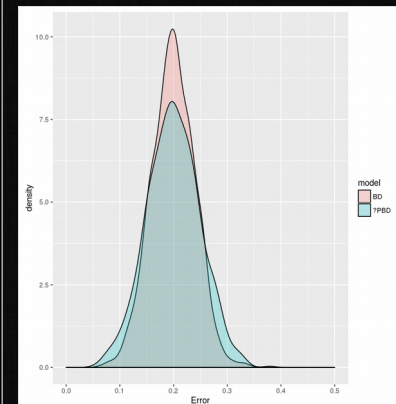
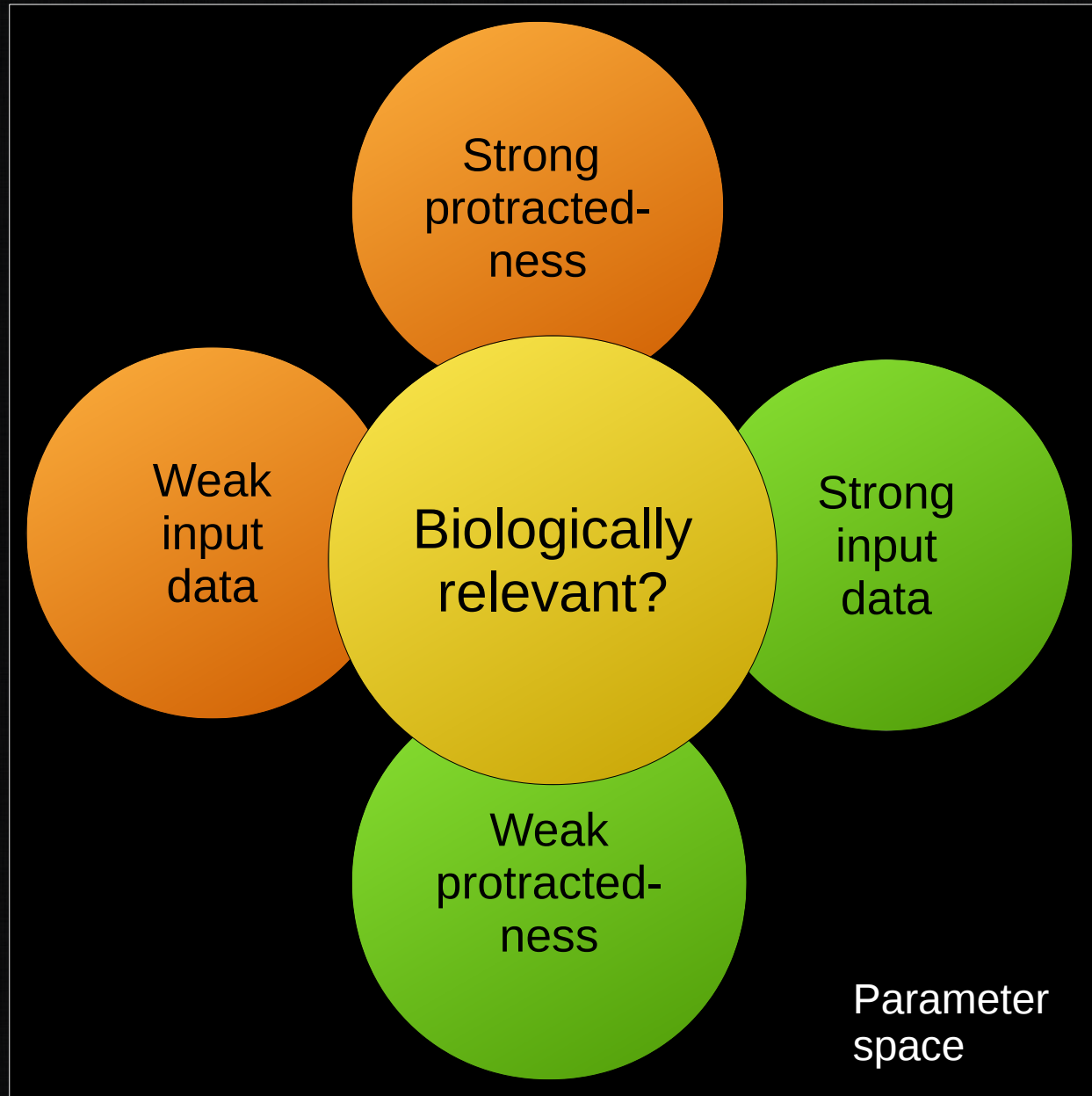
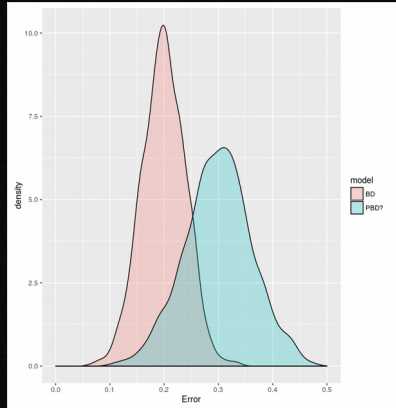
Parameter space



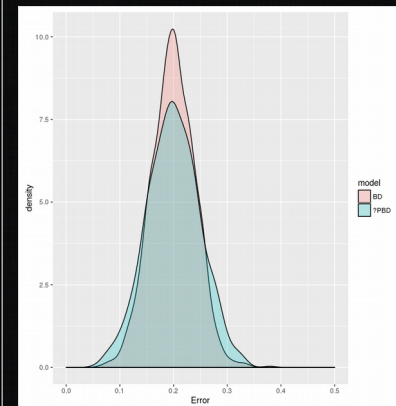
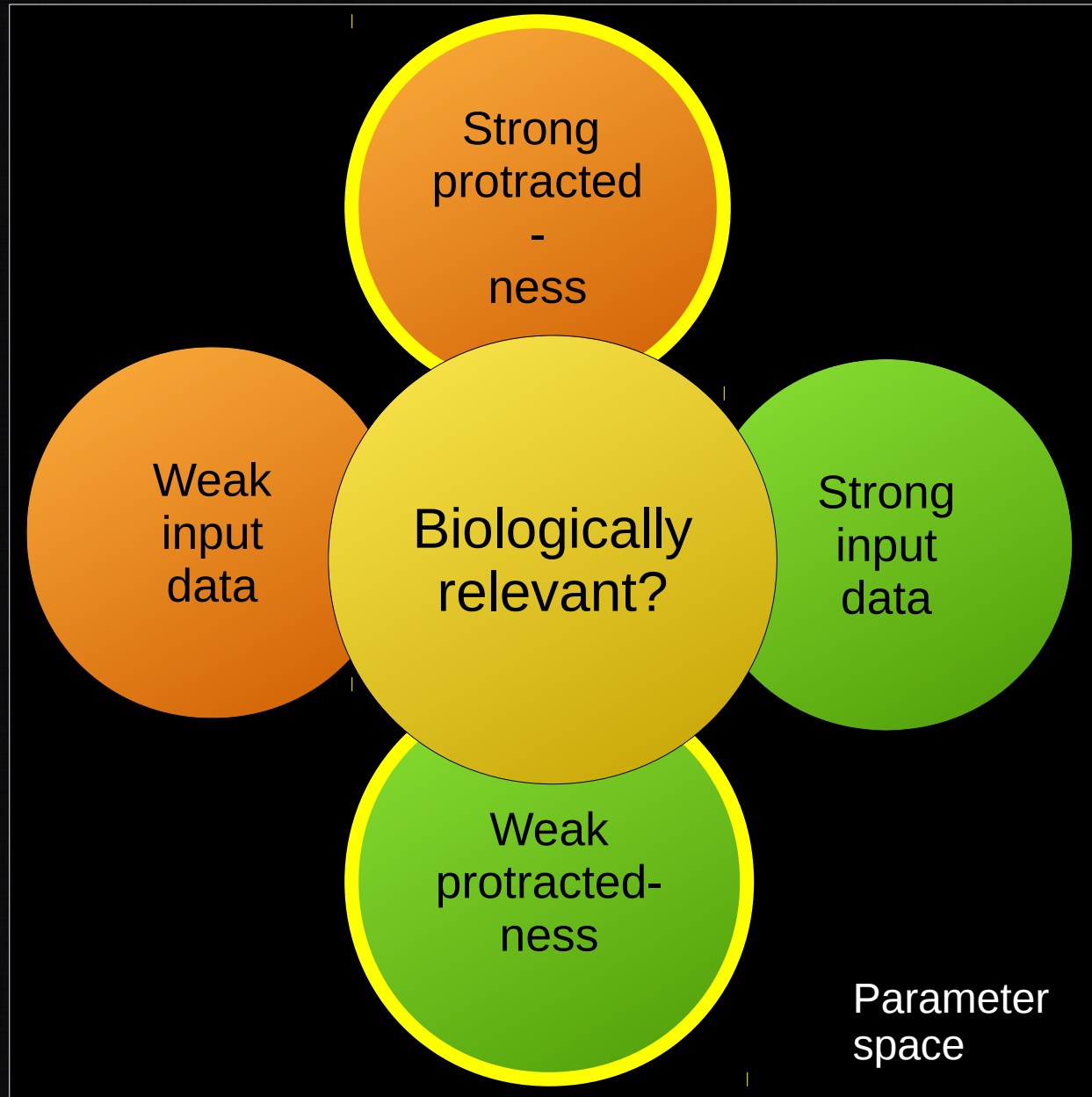
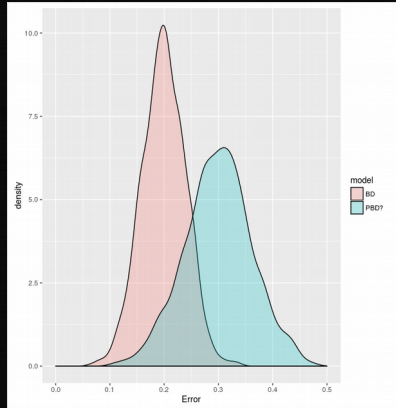
Idealized predictions



Predictions

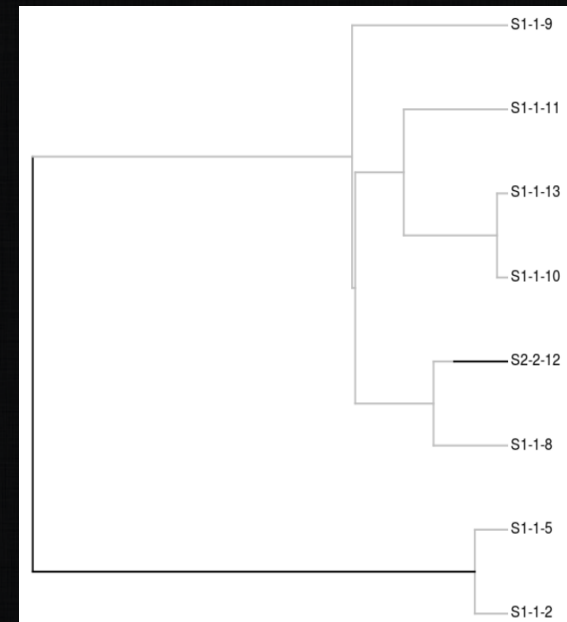


Predictions

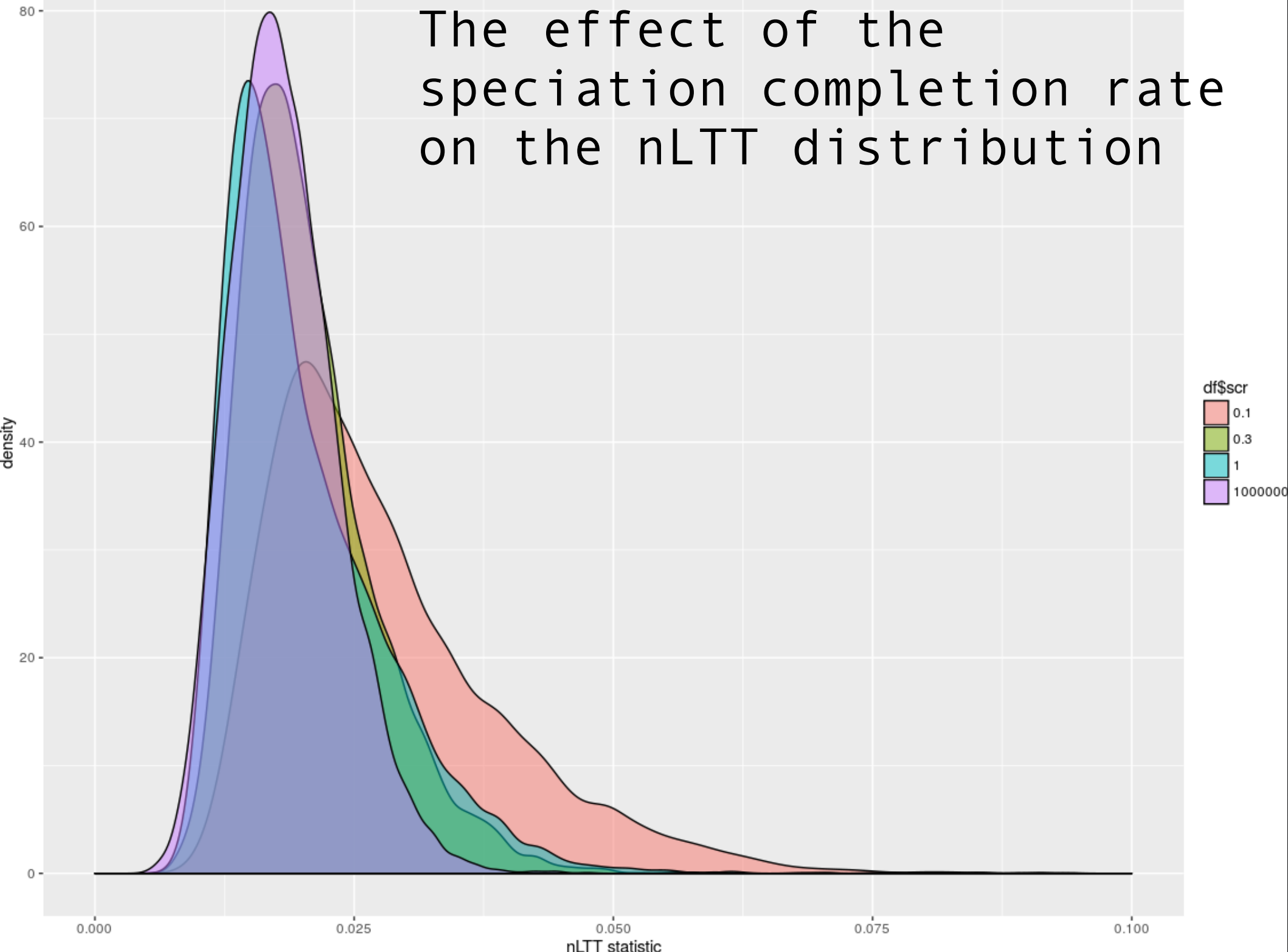


Quick

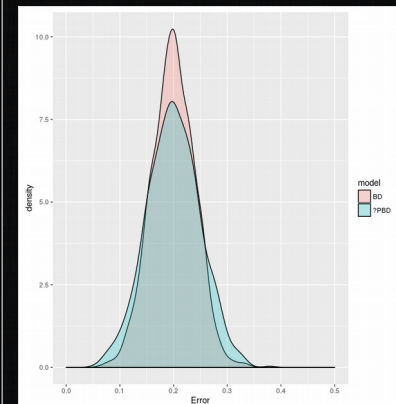
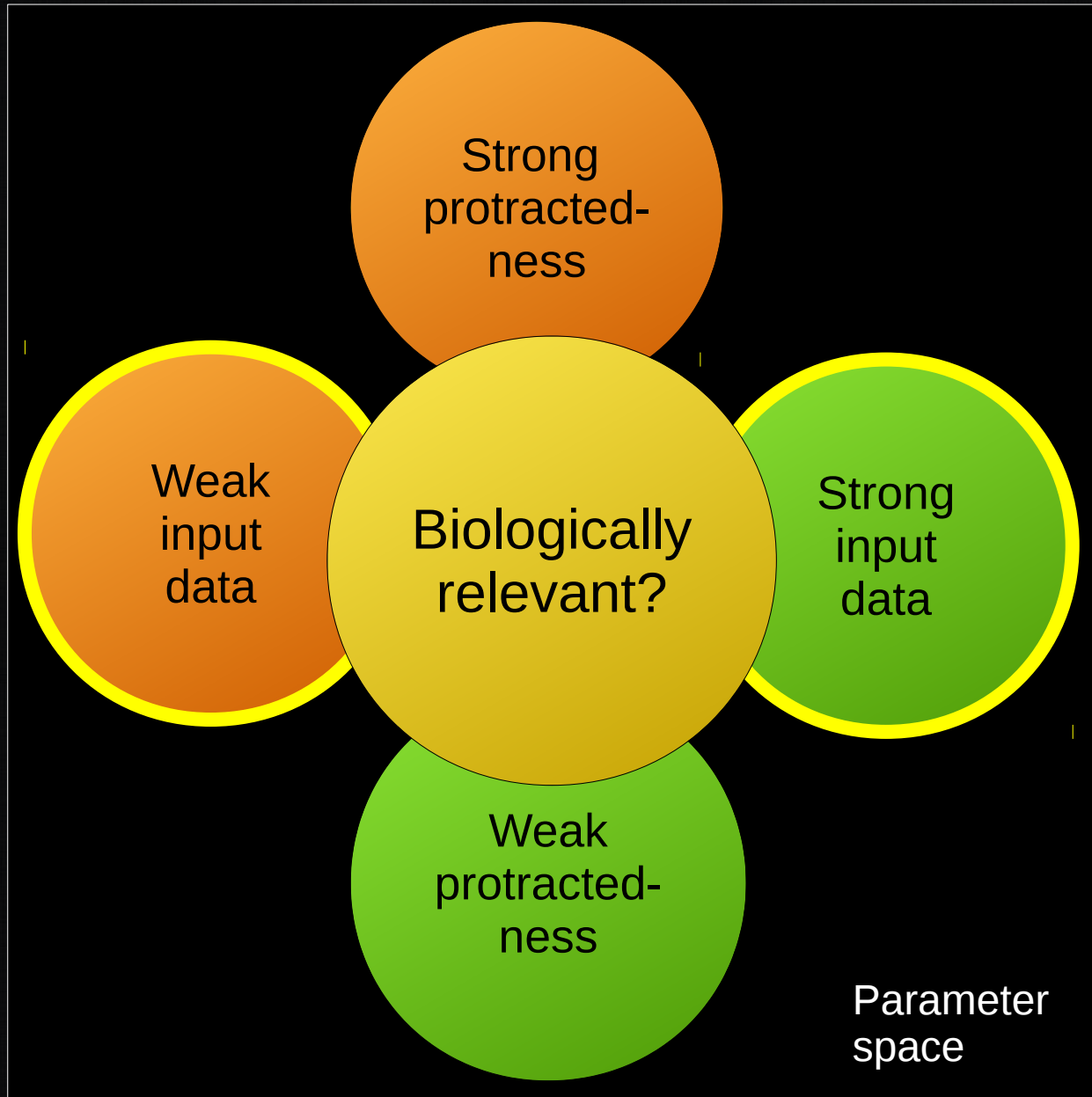
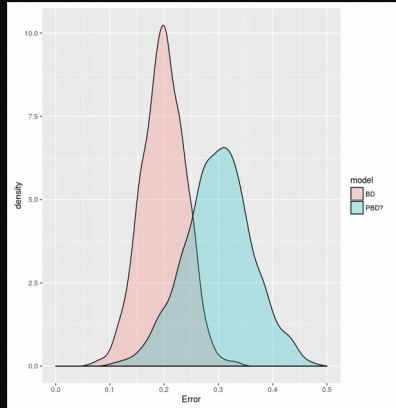
- What is the effect of the speciation completion rate on the nLTT distribution?
 - Low value: long incipient stage
 - High value: short incipient stage
 - Infinite: no infinite stage



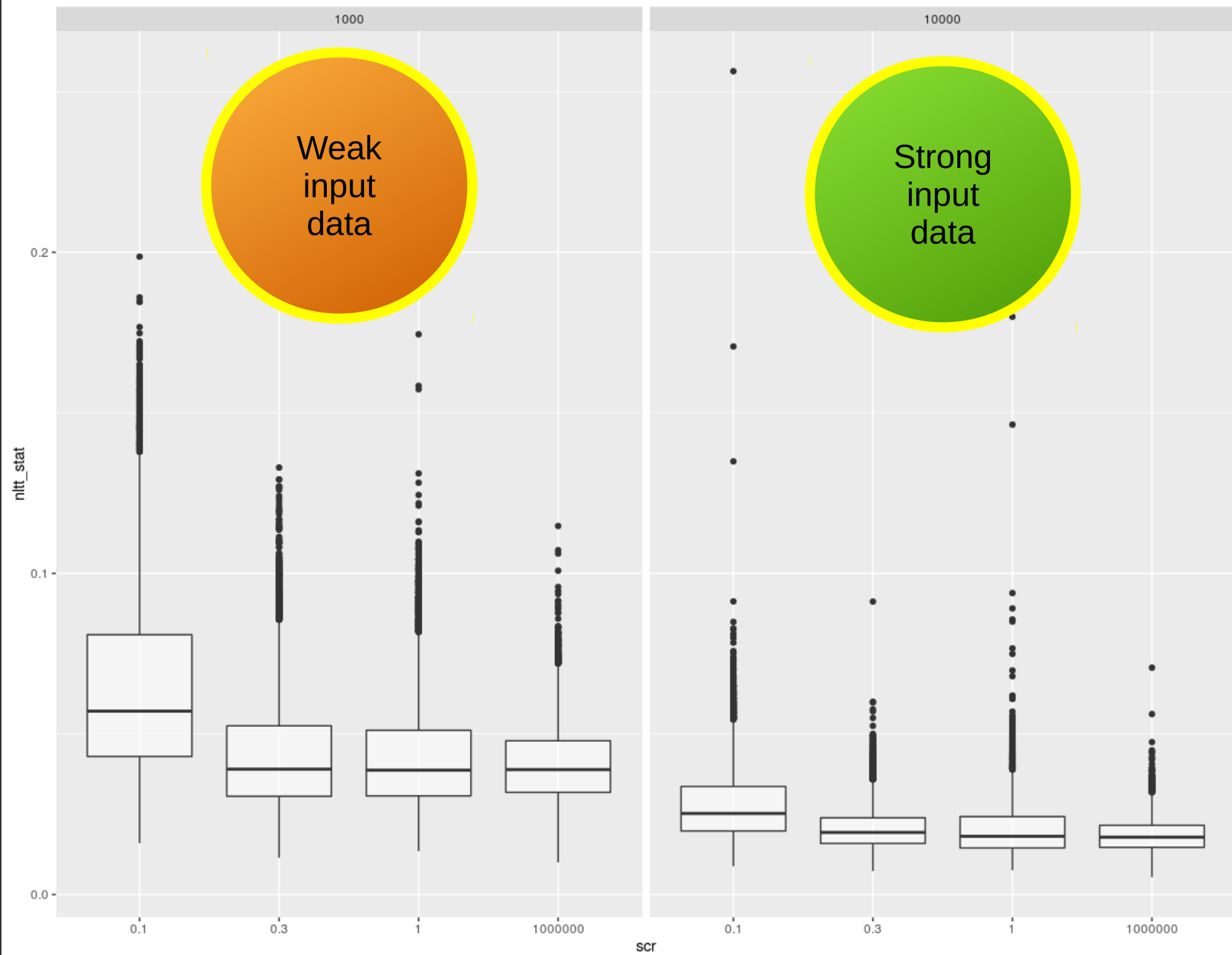
The effect of the speciation completion rate on the nLTT distribution



Predictions

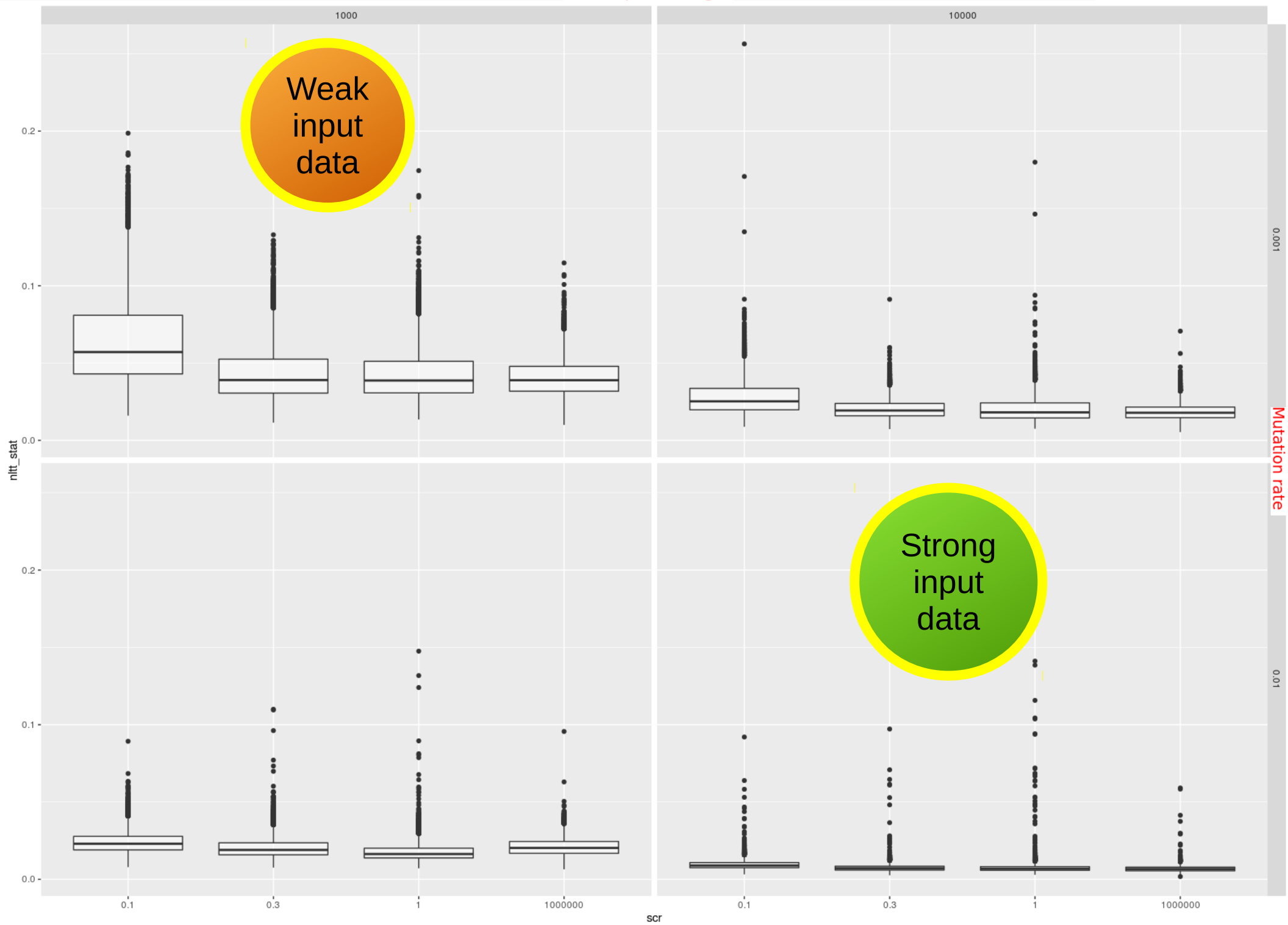


DNA sequence length





DNA sequence length



Sure

- But how do the nLTT statistic distributions look like?



Mutation rate

0.001

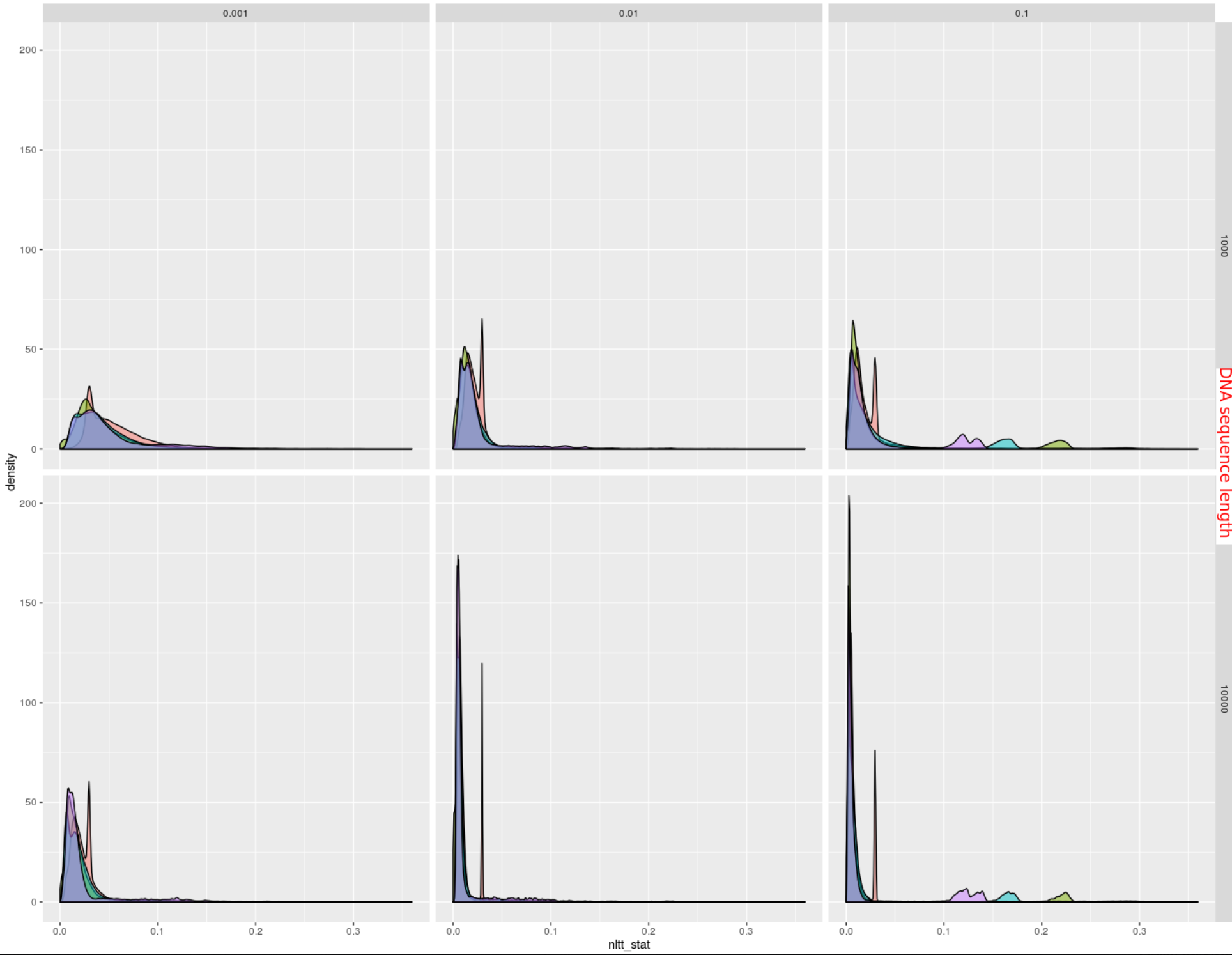
0.01

0.1

1000

10000

DNA sequence length



Conclusion

- Everything is in line with expectations
- Need more replicates to see if bumps are artefacts
- Replicates have run, analysis is running