

# PhD project overview

TECE meeting 2016-11-03



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[www.github.com/richelbilderbeek/Science](http://www.github.com/richelbilderbeek/Science)

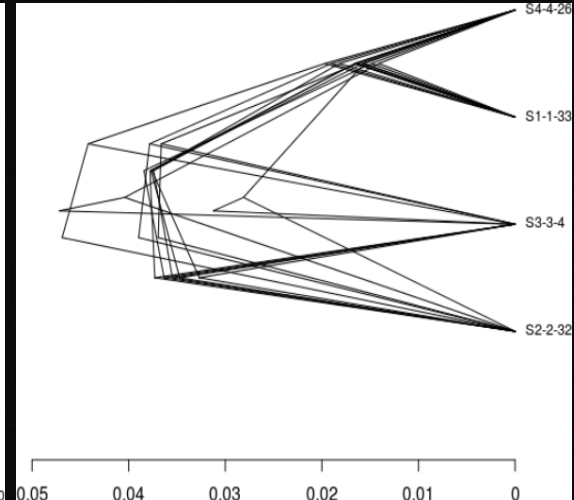
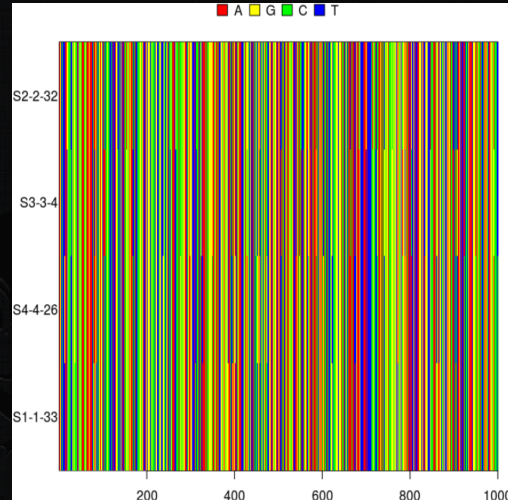
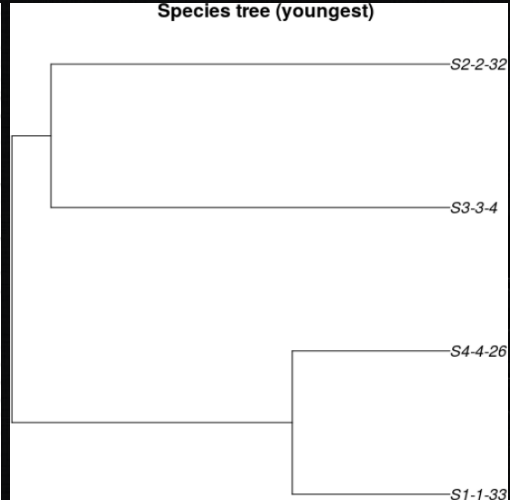
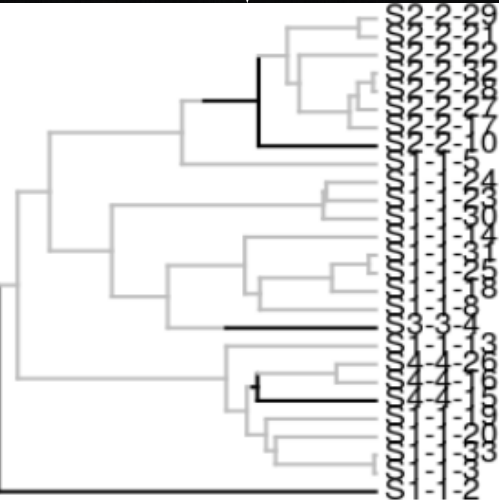
# Project 1: BD on PBD

*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

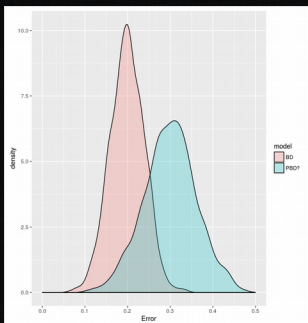


Simulate an  
incipient  
species tree

Sample species  
trees

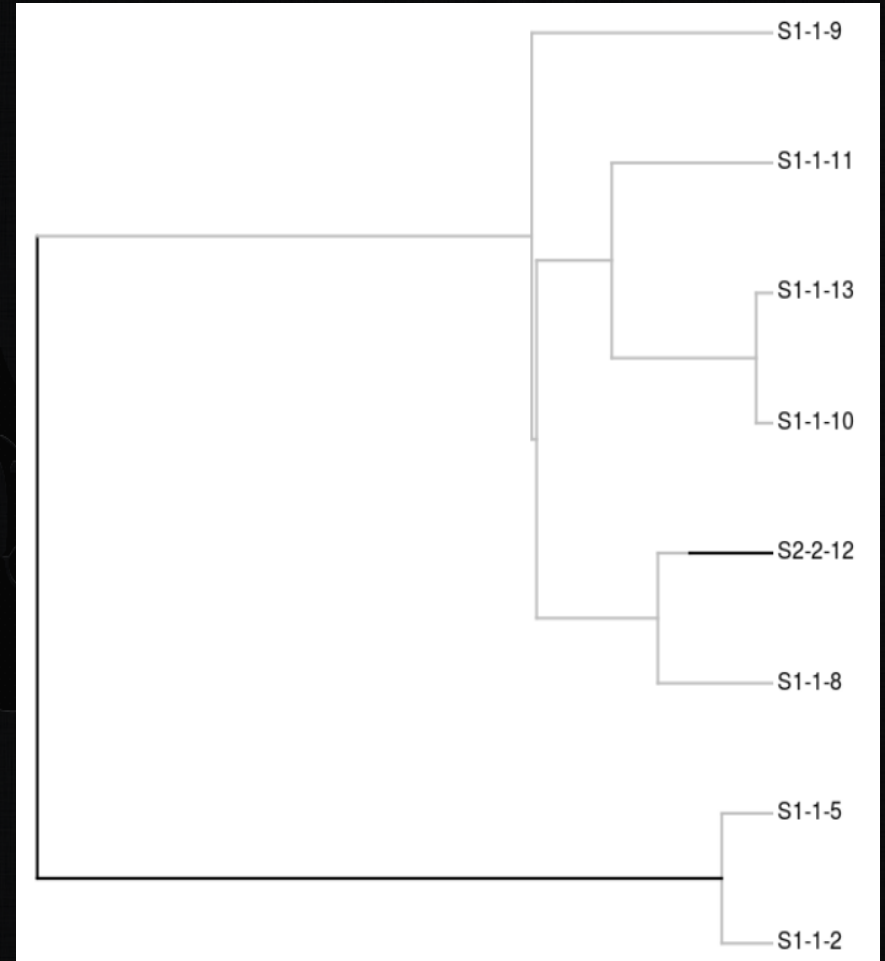
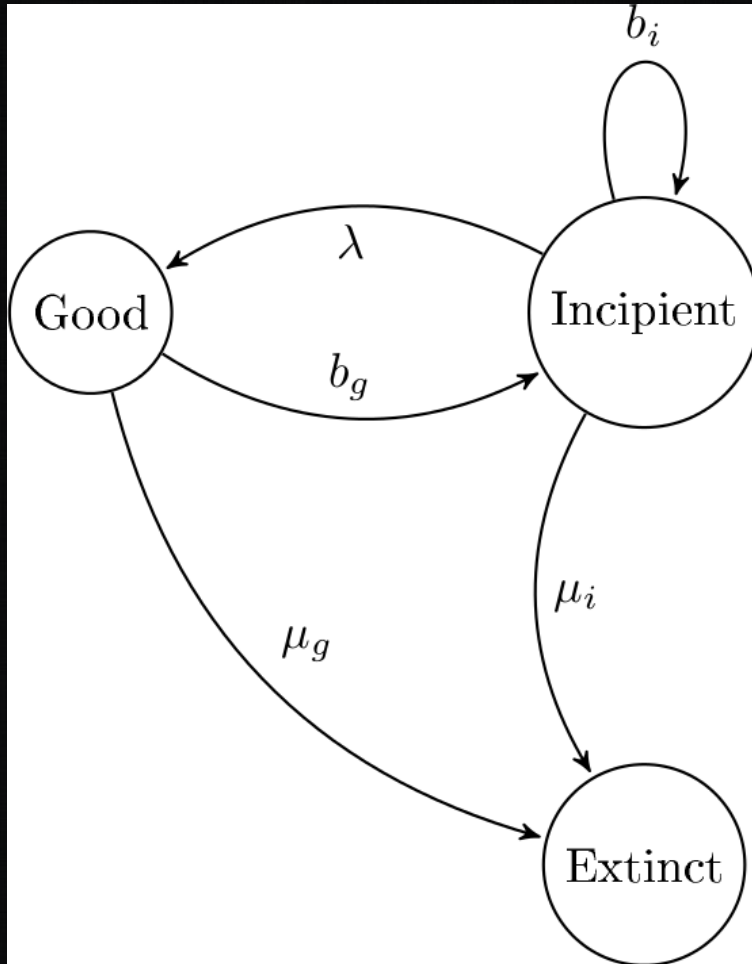
Simulate DNA  
alignments

Infer species  
tree posterior



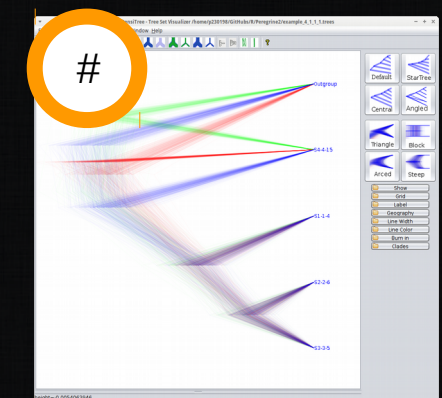
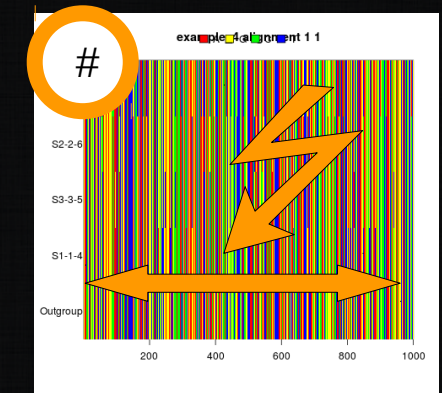
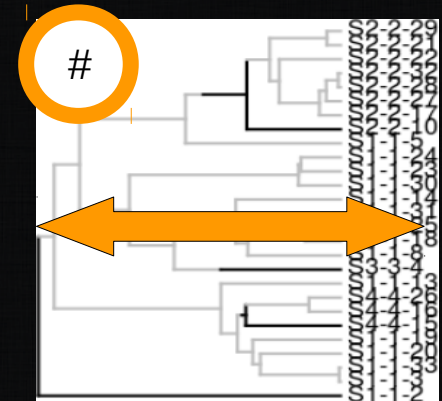
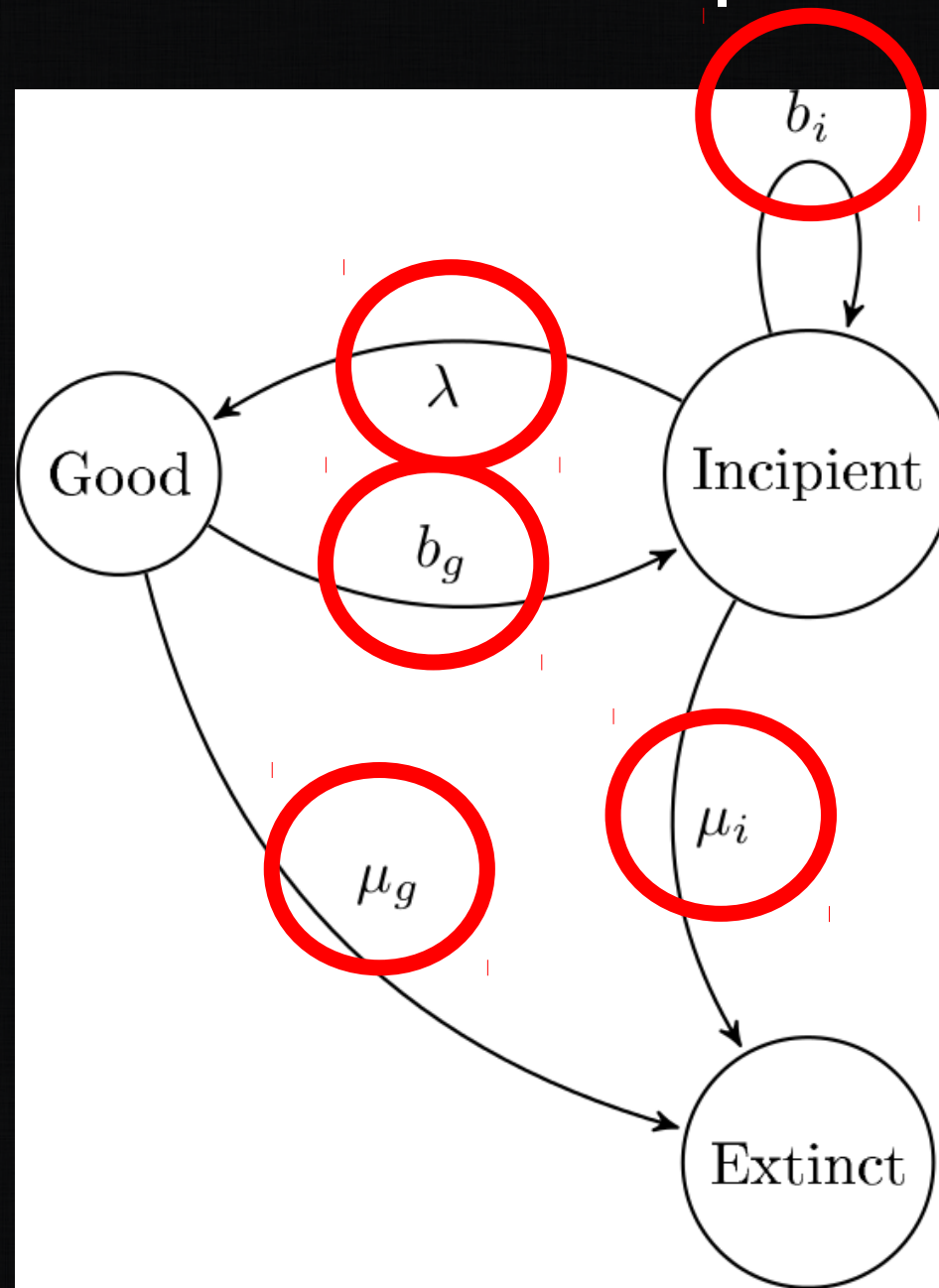
Measure difference/error

# PBD model



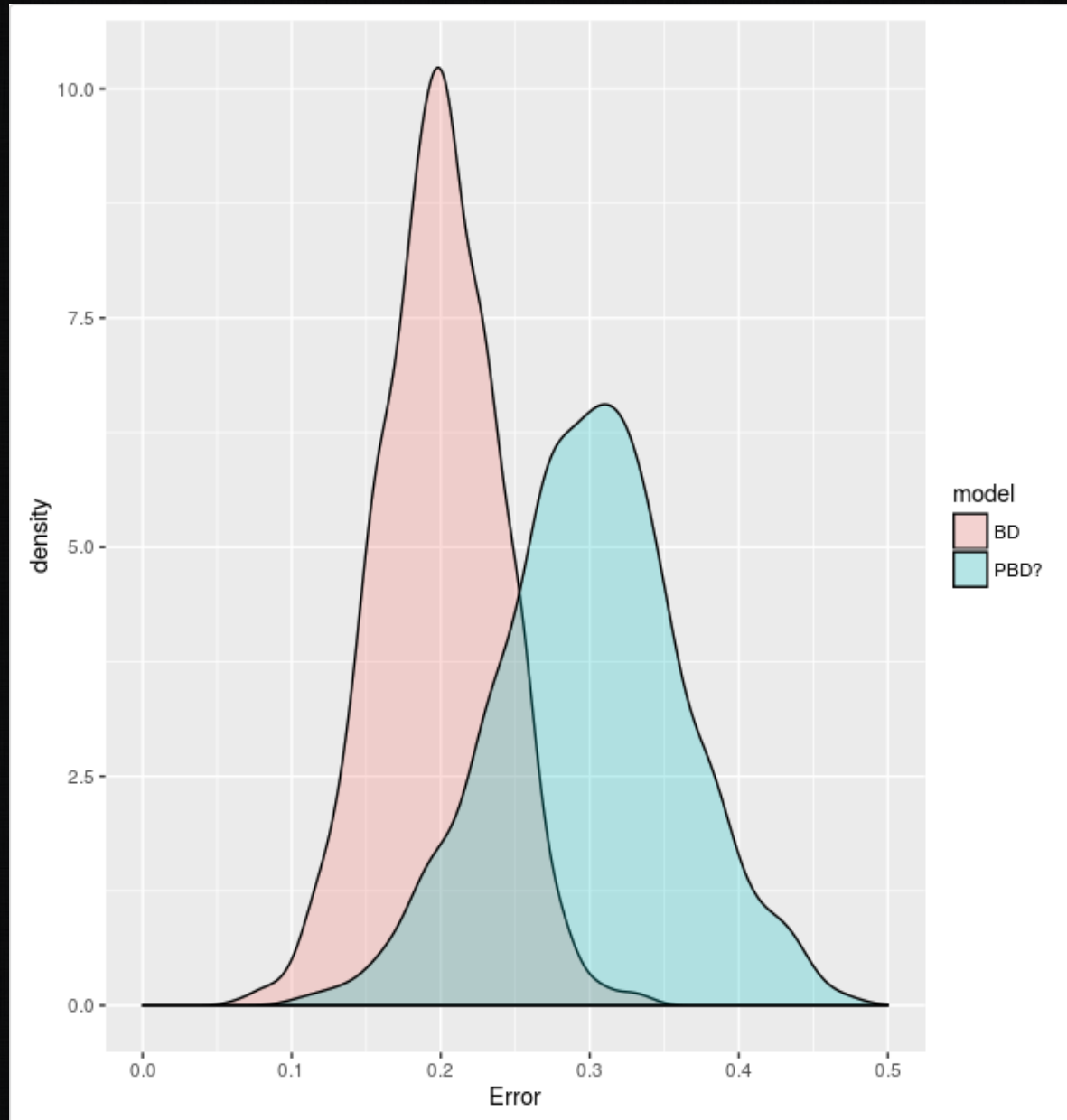
Etienne, Rampal S., and James Rosindell. "Prolonging the past counteracts the pull of the present: protracted speciation can explain observed slowdowns in diversification." *Systematic Biology* (2011): syr091.

# Parameter space

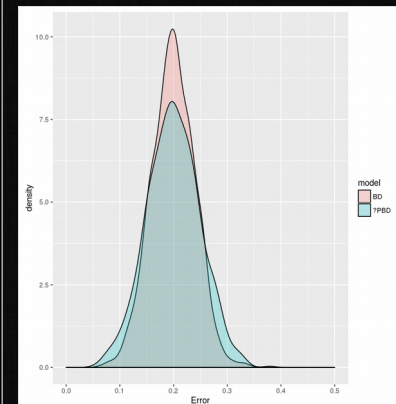
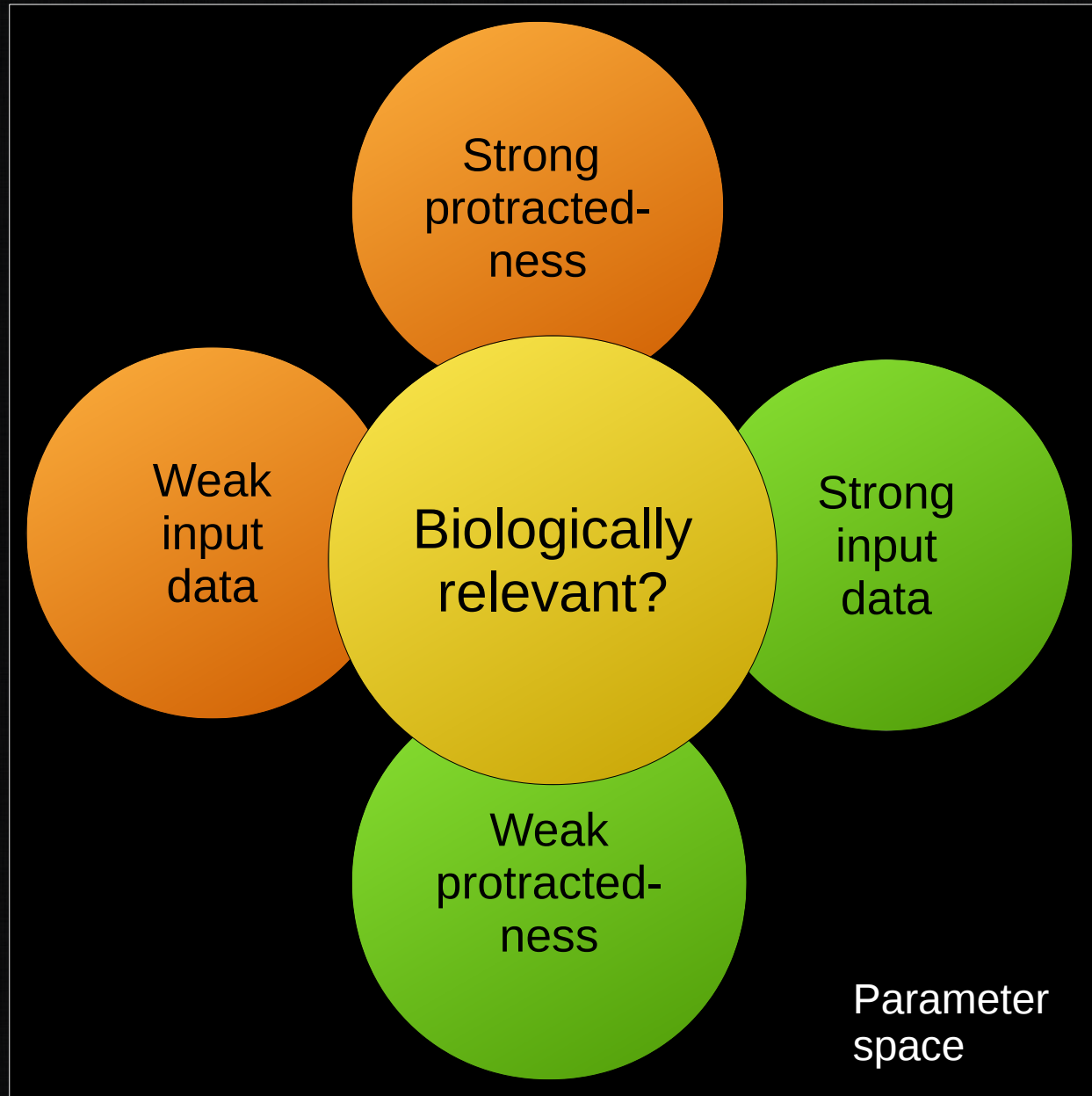
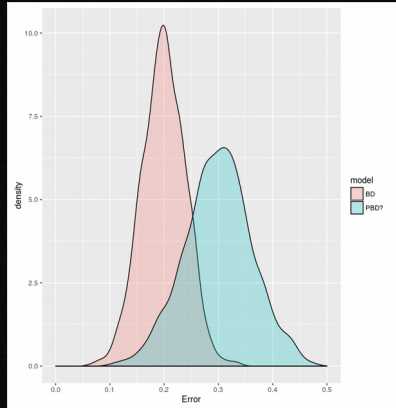




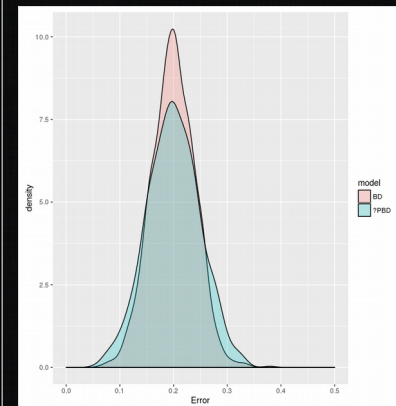
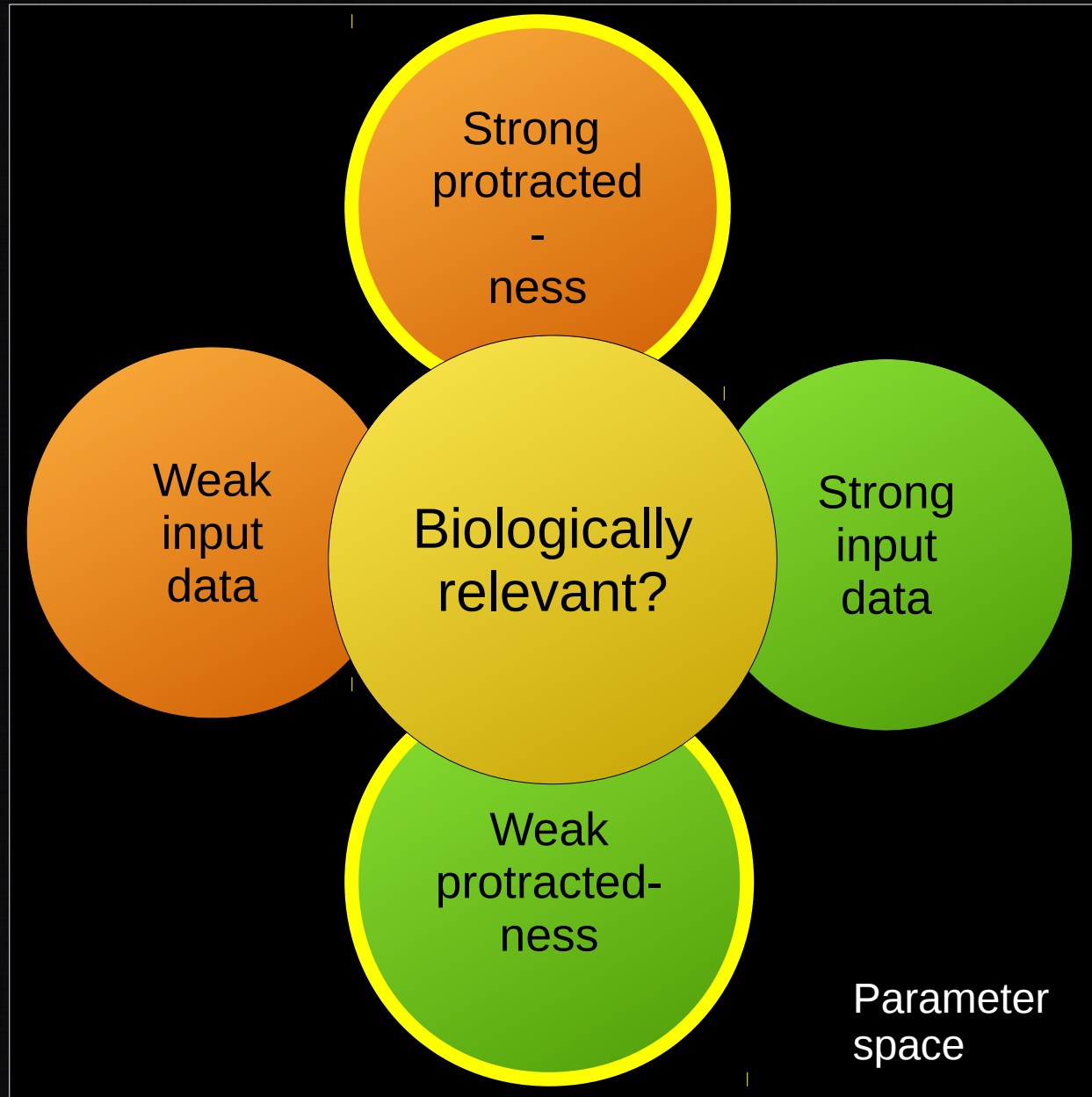
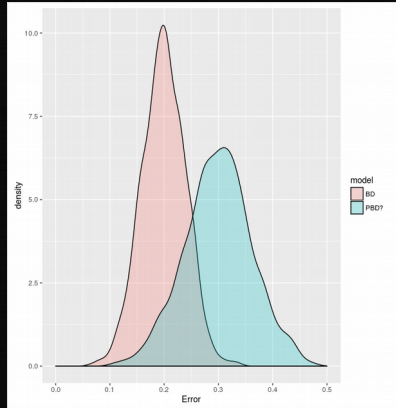
# Idealized predictions



# Predictions



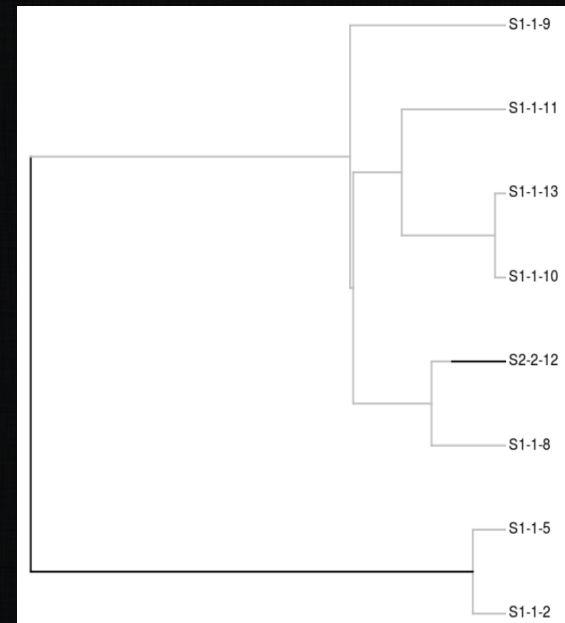
# Predictions



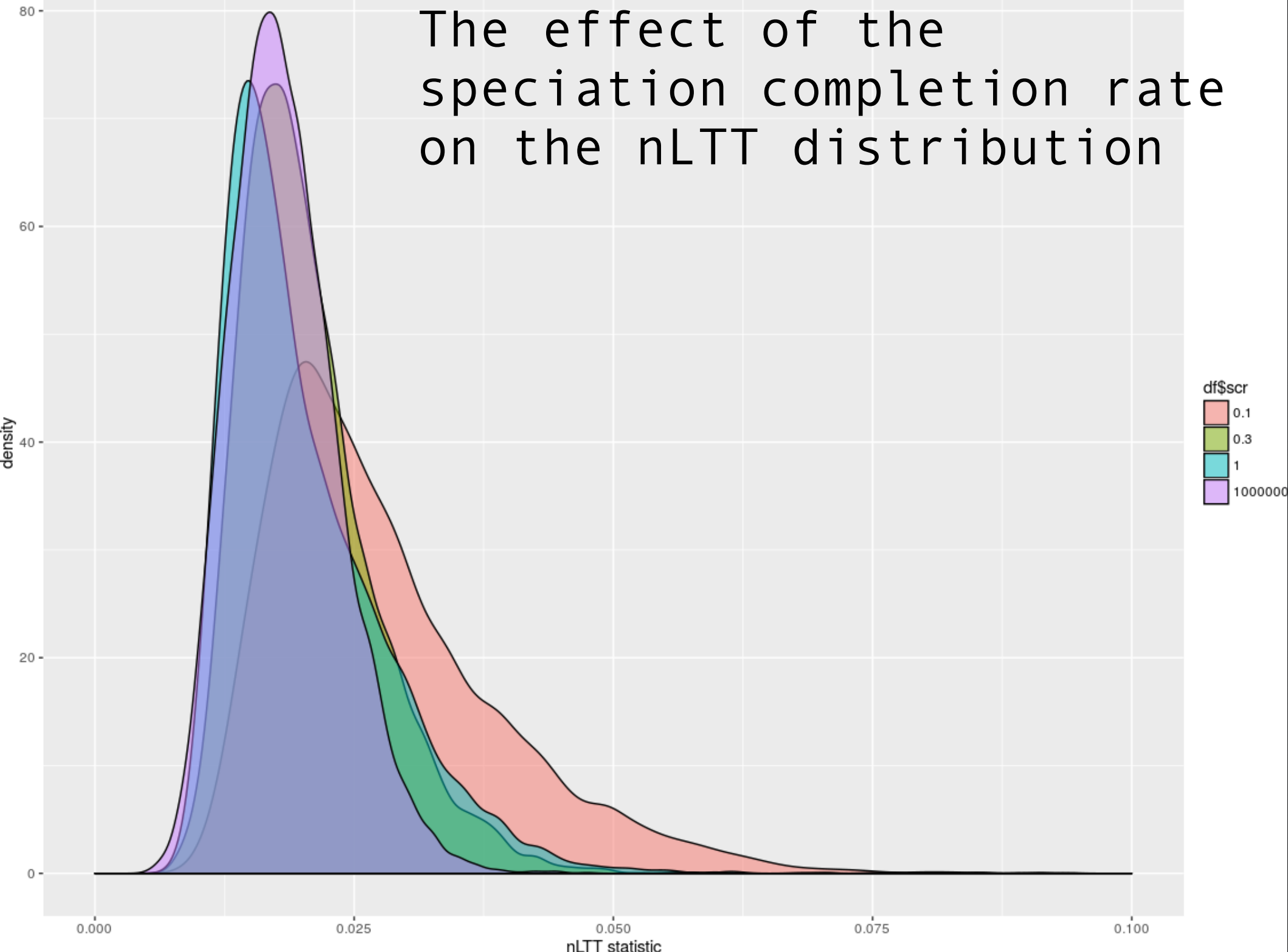


# Quick

- 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

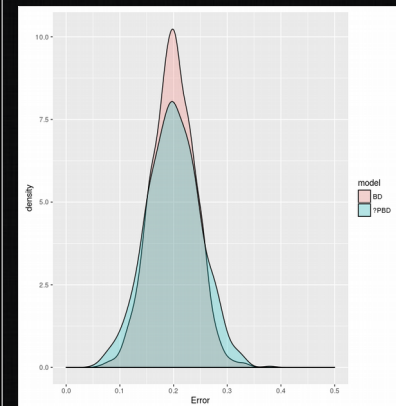
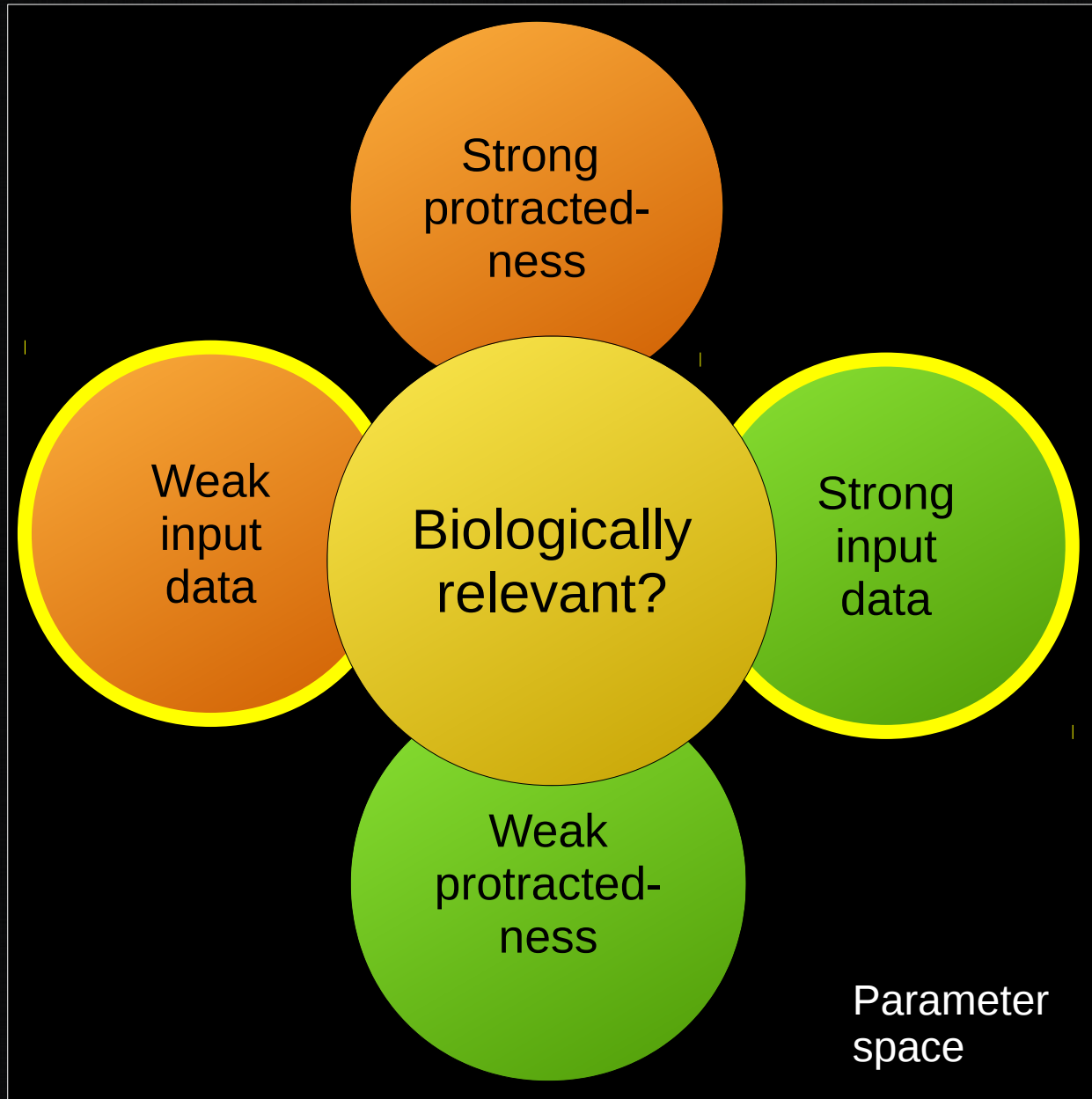
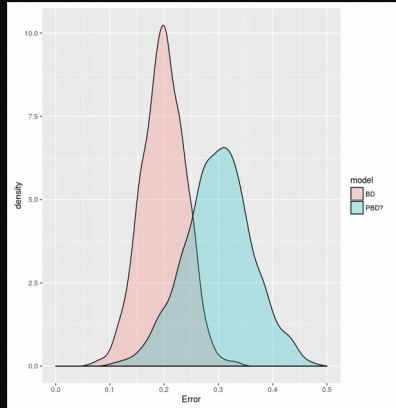


# The effect of the speciation completion rate on the nLTT distribution

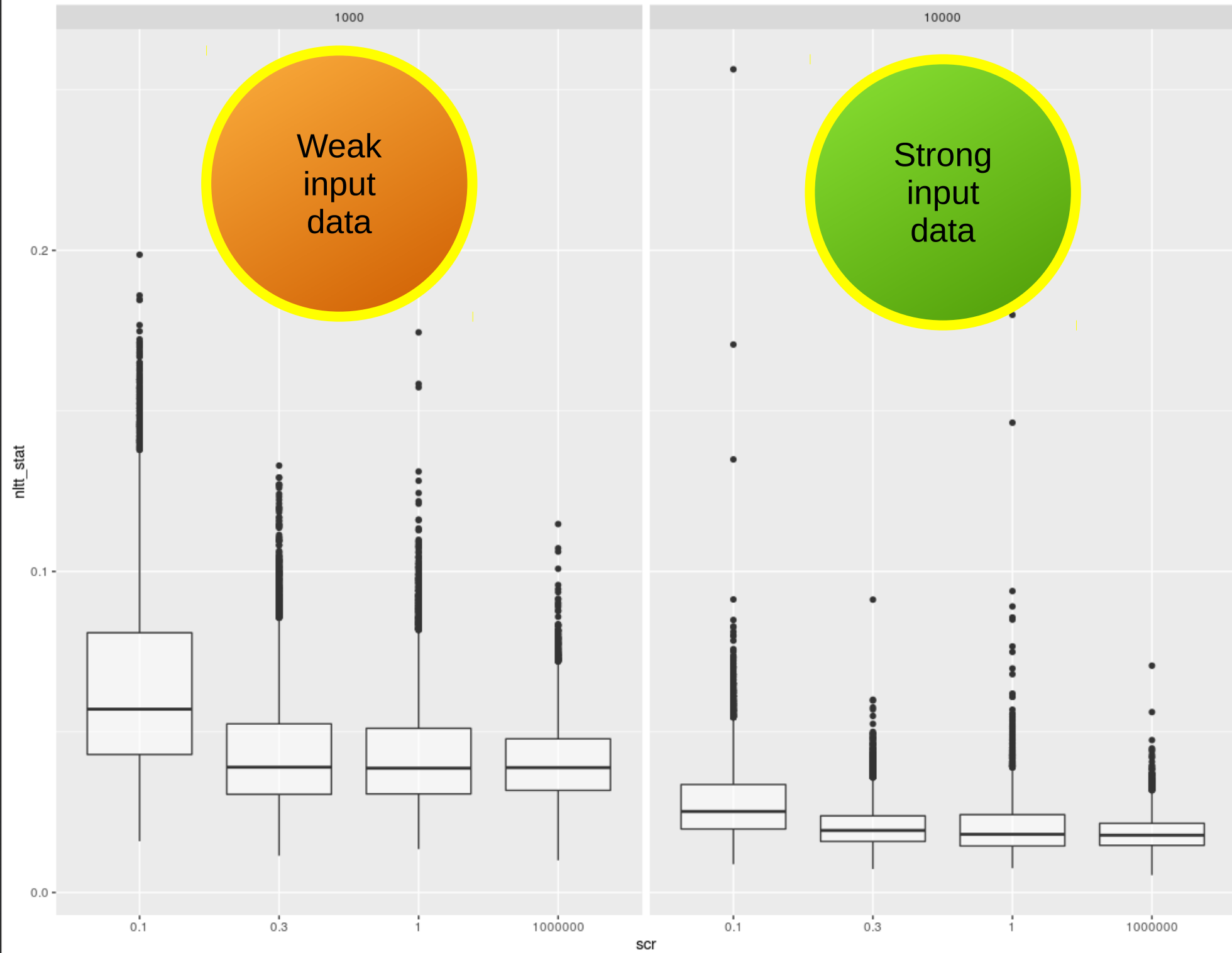




# Predictions



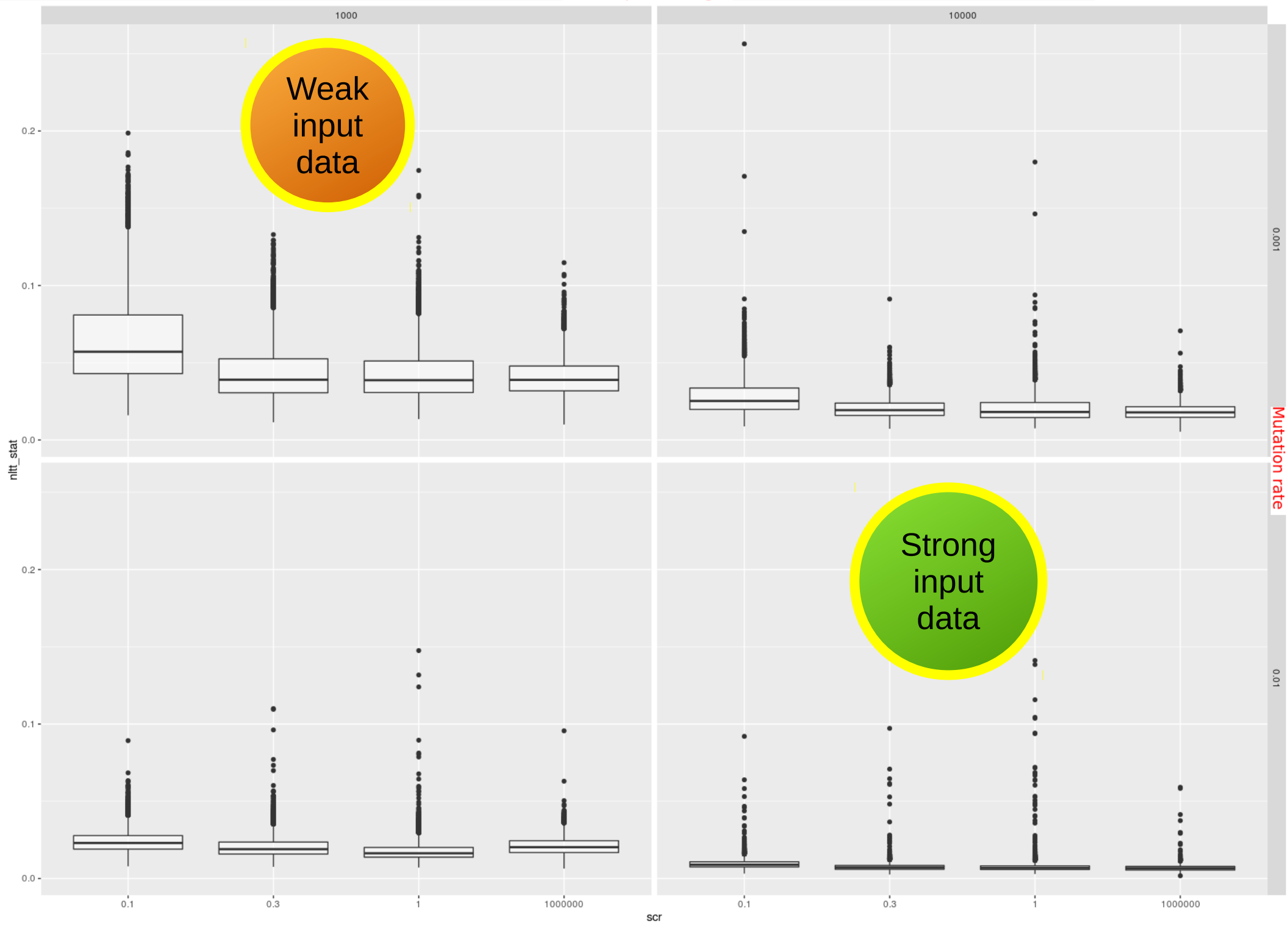
# DNA sequence length







DNA sequence length



# Sure

- But how do the nLTT statistic distributions look like?





Mutation rate

0.001

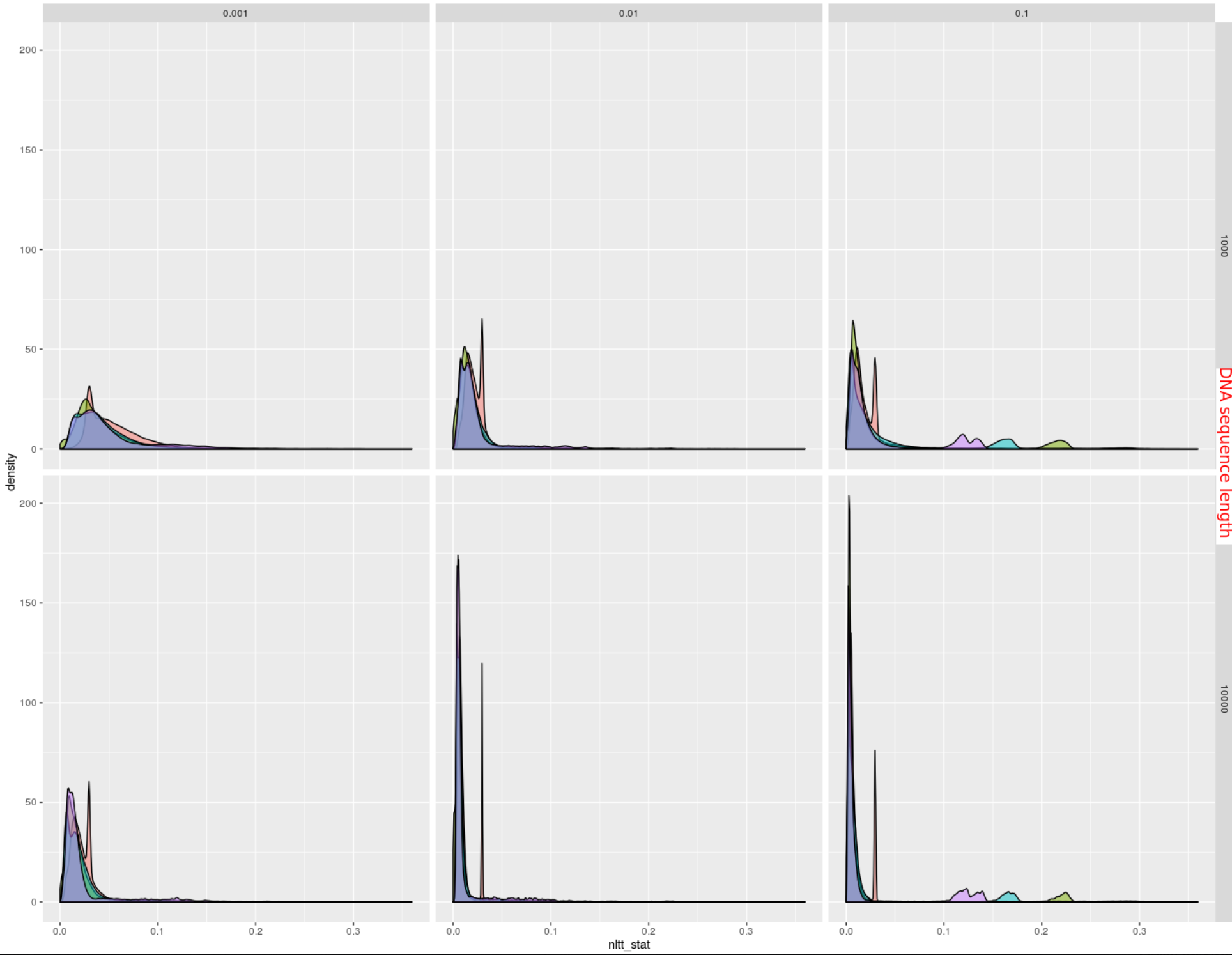
0.01

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