

PhD project overview

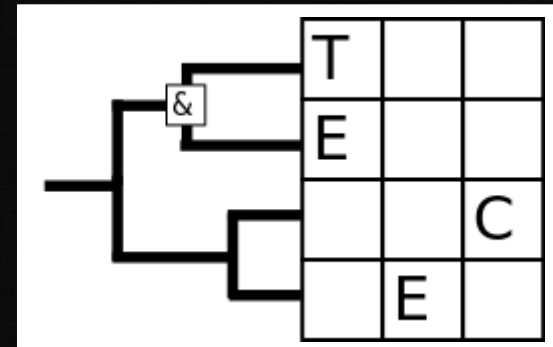
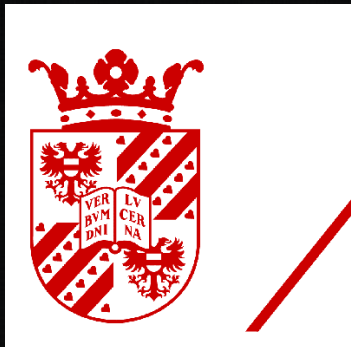
TECE meeting 2016-12-14



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www.github.com/richelbilderbeek/Science

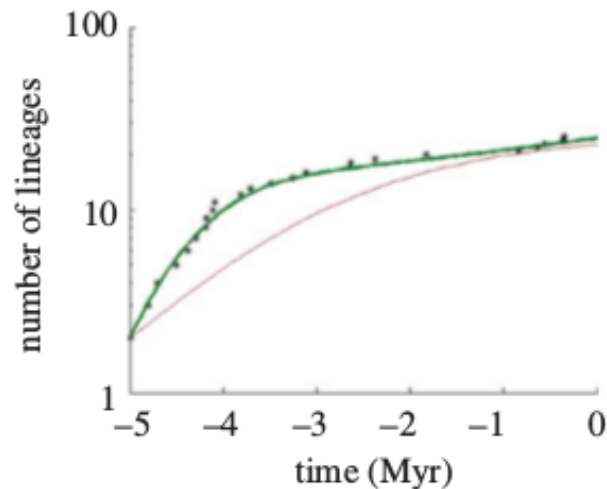


Problem

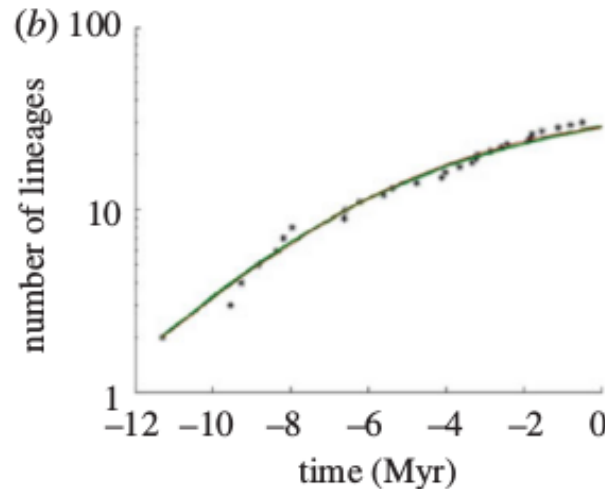
- LTT ('Lineages-through-time') plots flatten out towards the present



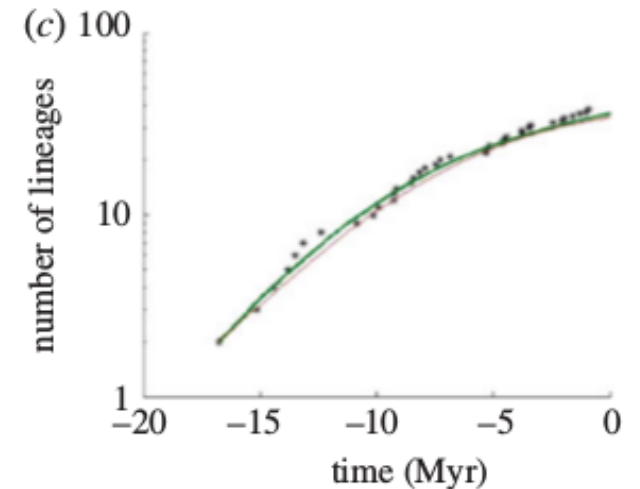
Setophaga



Plethodon



Heliconius



Hypotheses for problem

- Diversity dependence: niches fill up [1]
- Protracted speciations: newly formed species are not directly recognized as such [2, 3]

[1] Etienne et al, 2012

[2] Rosindell & Etienne, 2011

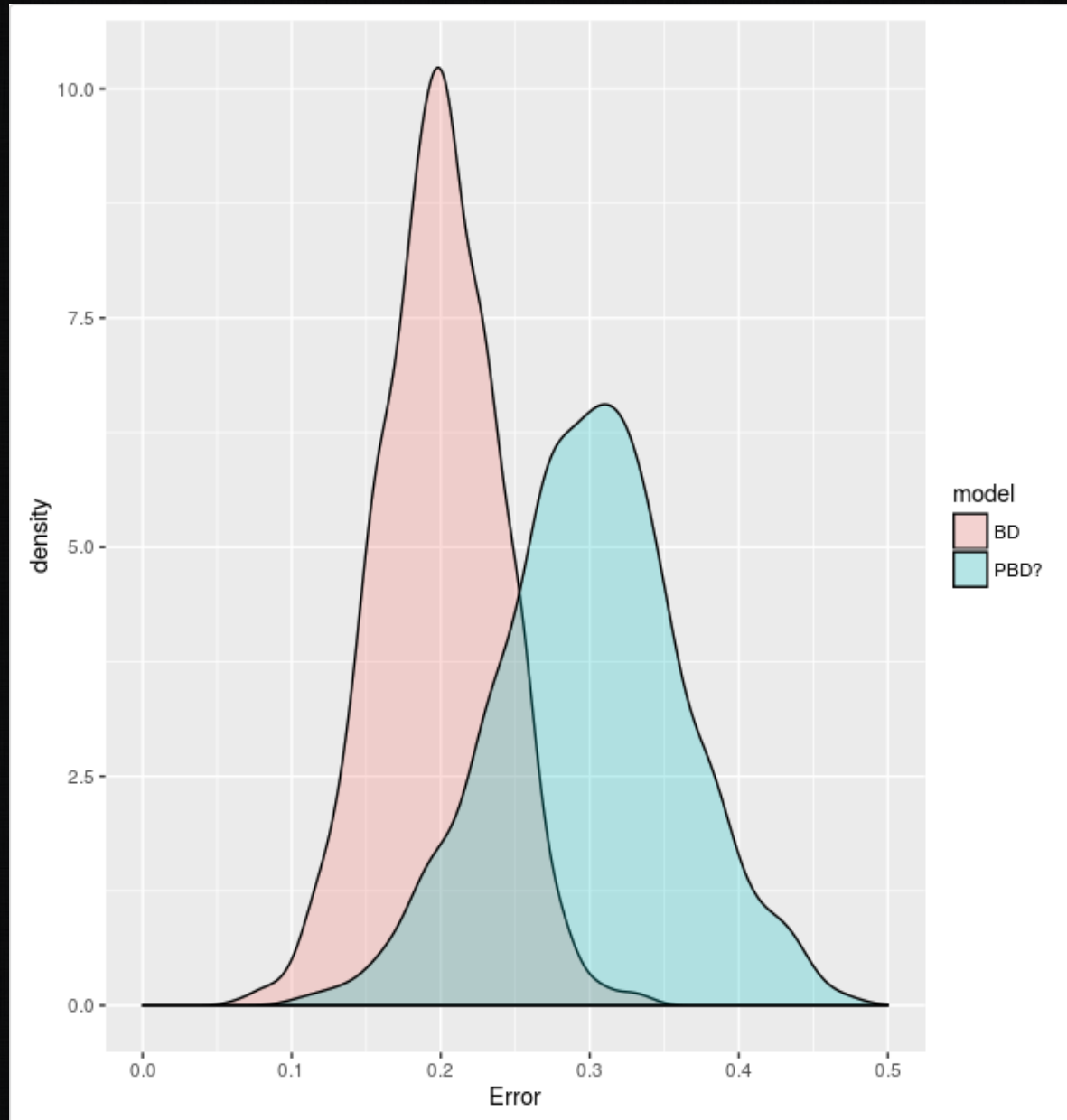
[3] Etienne & Rosindell 2012

Approach

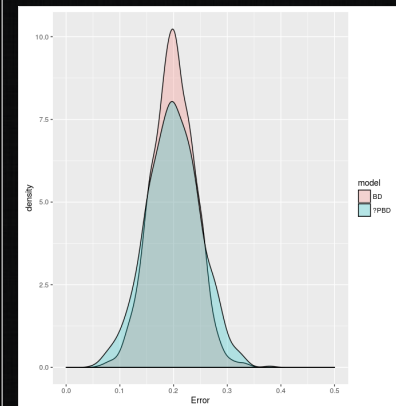
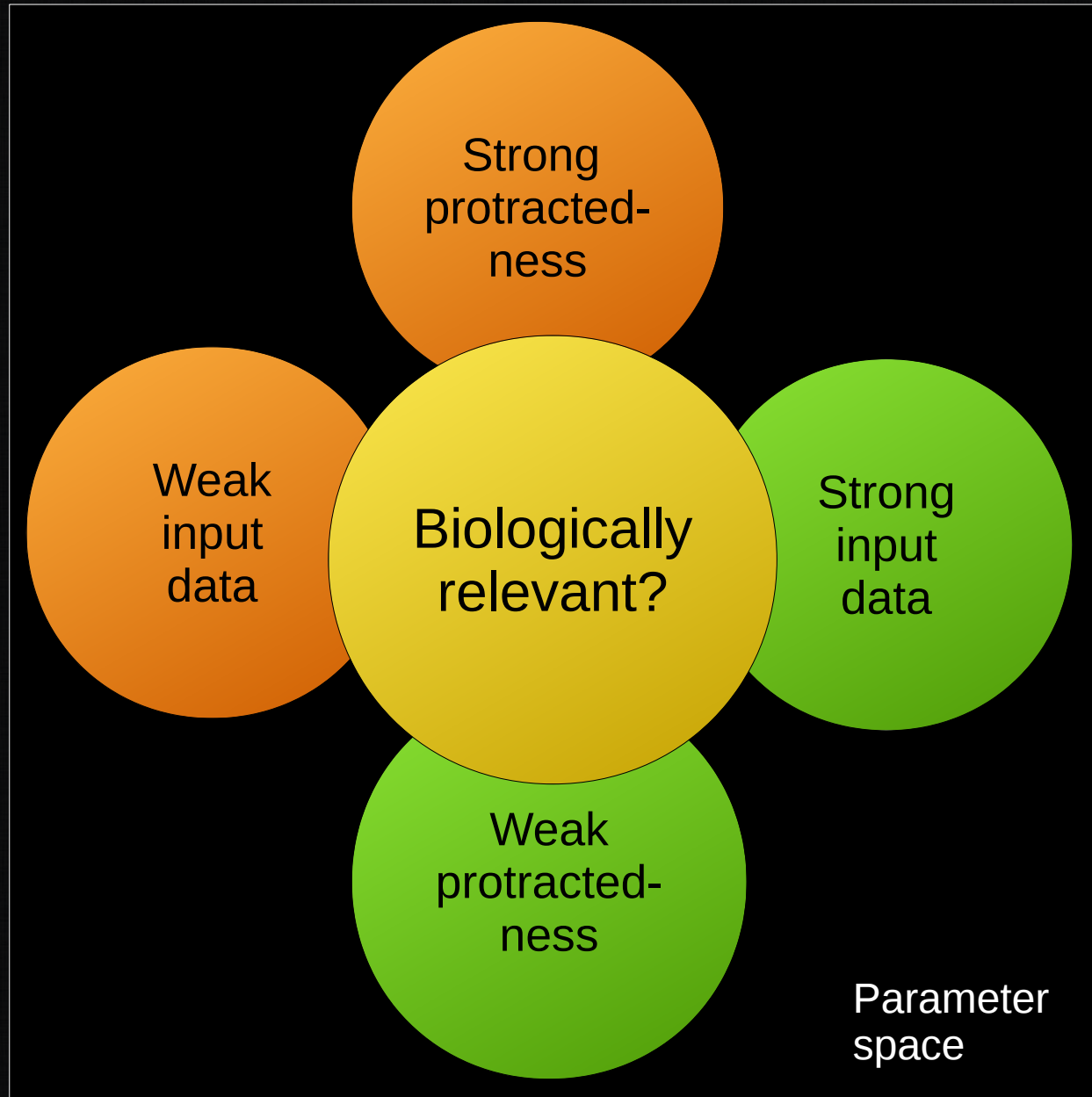
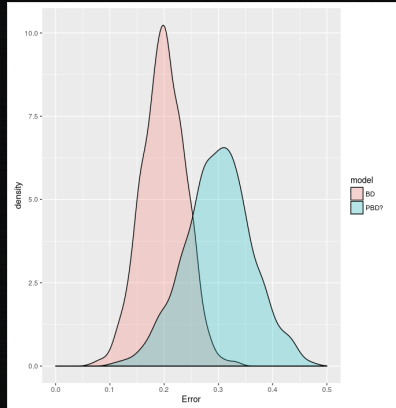
If reproductive isolation takes time to establish, what is the error made today in inferring a phylogeny?

- Simulate protracted phylogenies, 'the truth'
- Simulate DNA, 'as measured in the field'
- Infer phylogeny, using current tools
- Measure difference with nLTT statistic

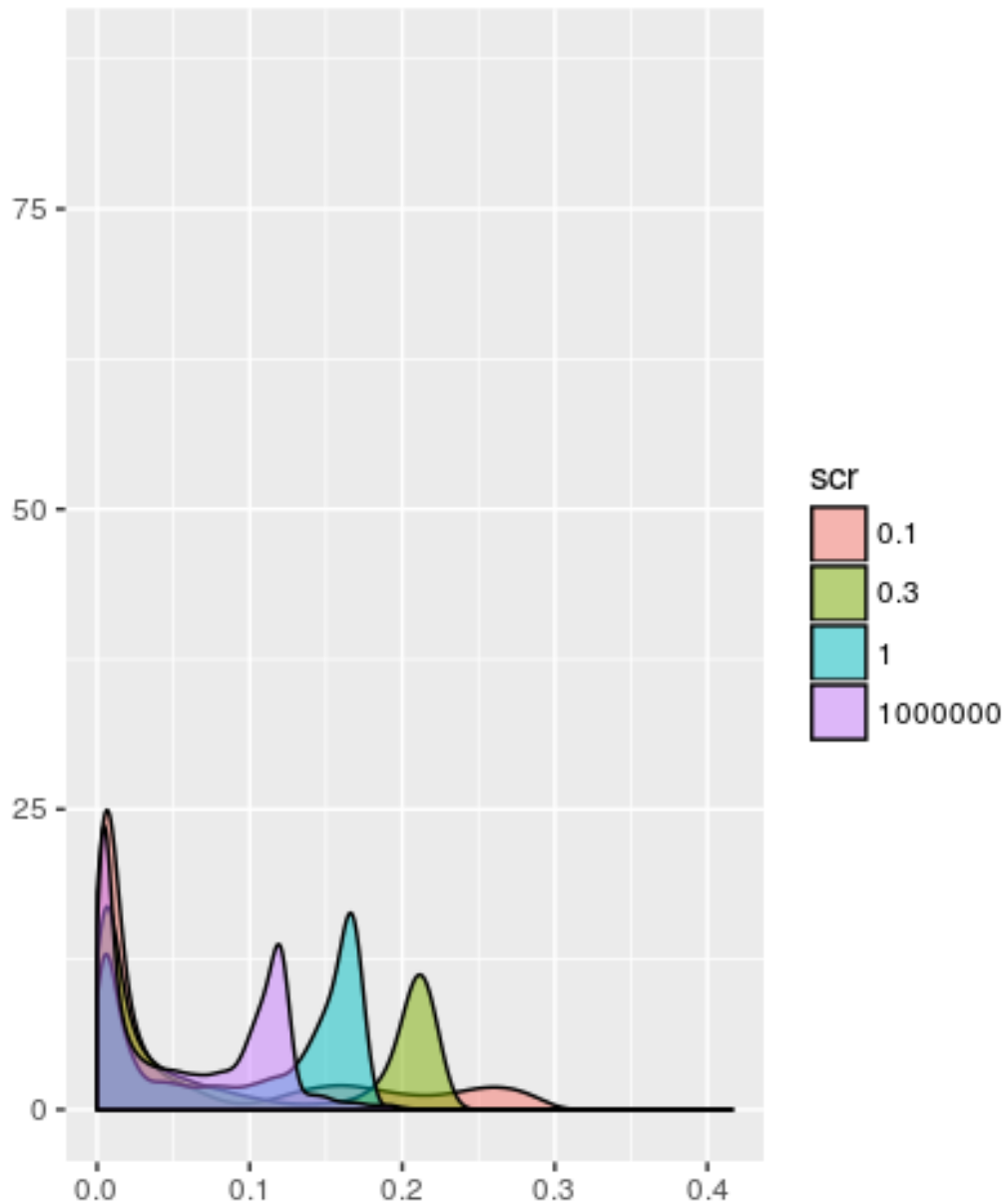
Idealized predictions



Predictions



nLTT stats for
 $\text{erg} = \text{eri} = 0$,
 $\text{sirg} = \text{siri} = 0.5$

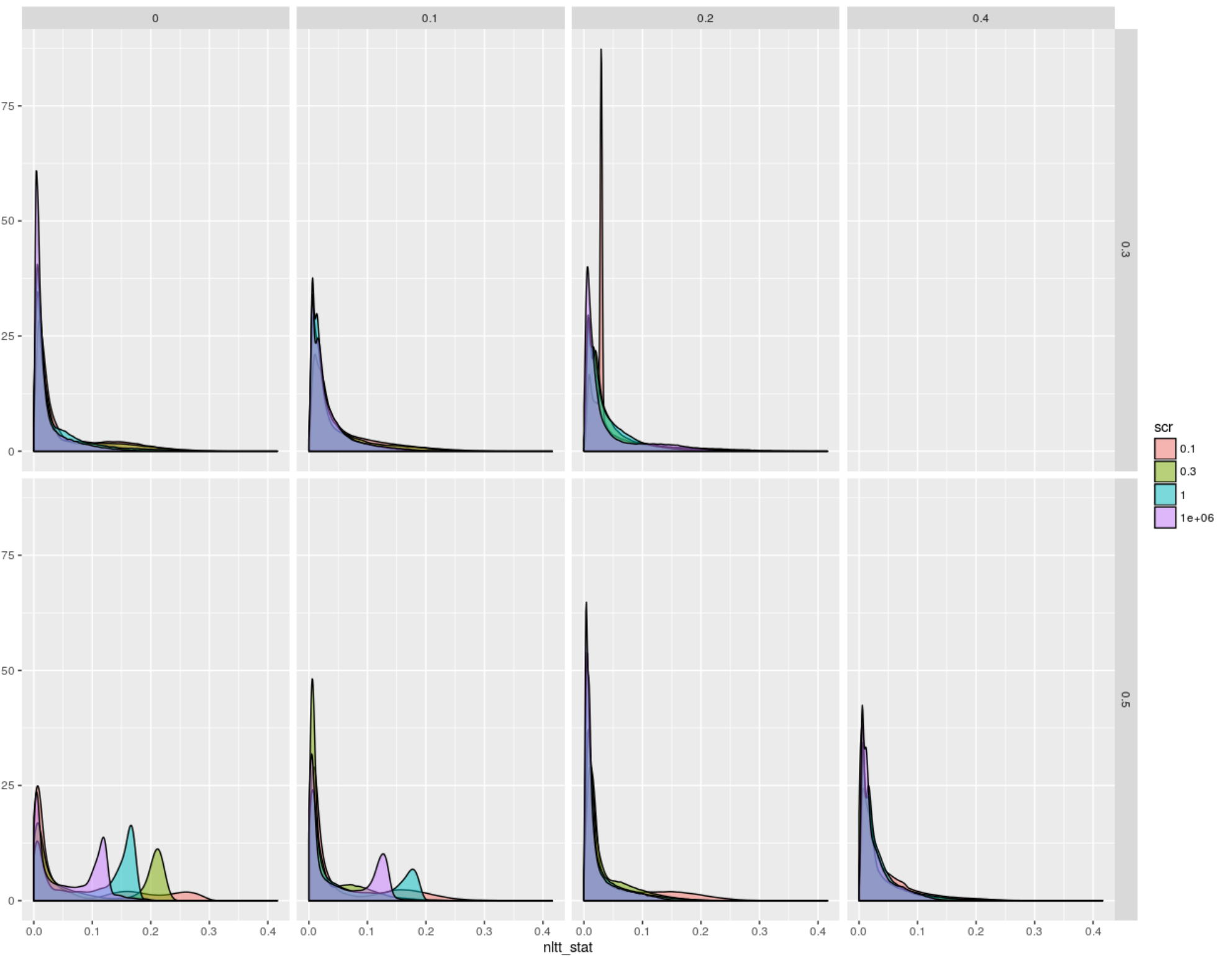


Bumps

- Also in BD model
- Same in all 4 replicates
- Not caused by DNA sequence length
- How does this look for other SIRs and ERs?

SCR: Speciation Completion Rate. PBD model becomes BD for SRC equals infinity

ER: Extinction Rate, Good or Incipient
SIR: Speciation Initiation Rate, Good or Incipient

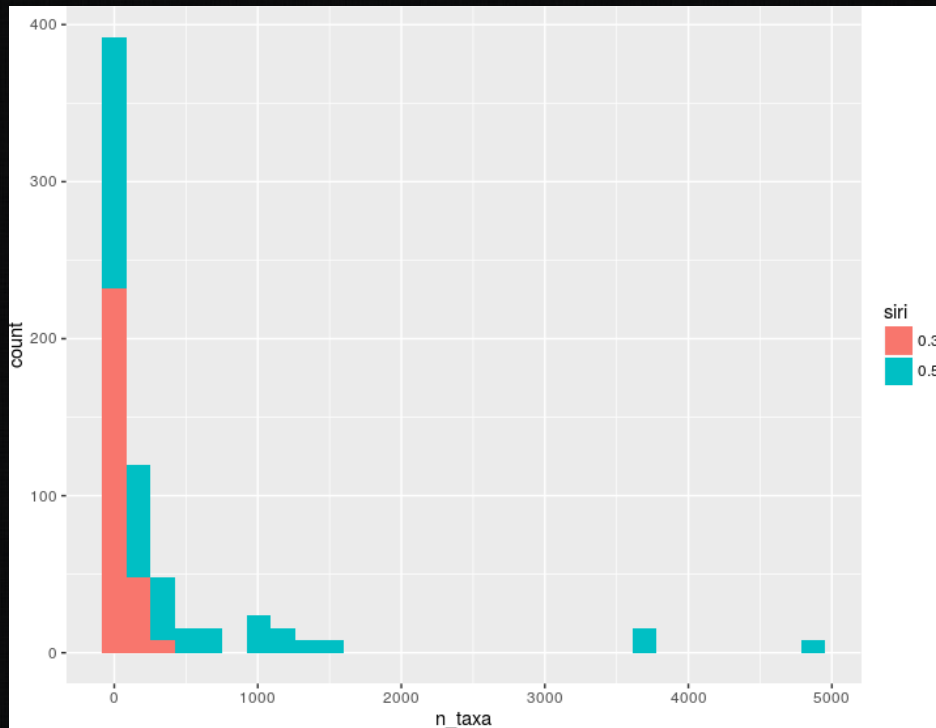


Hypothesis

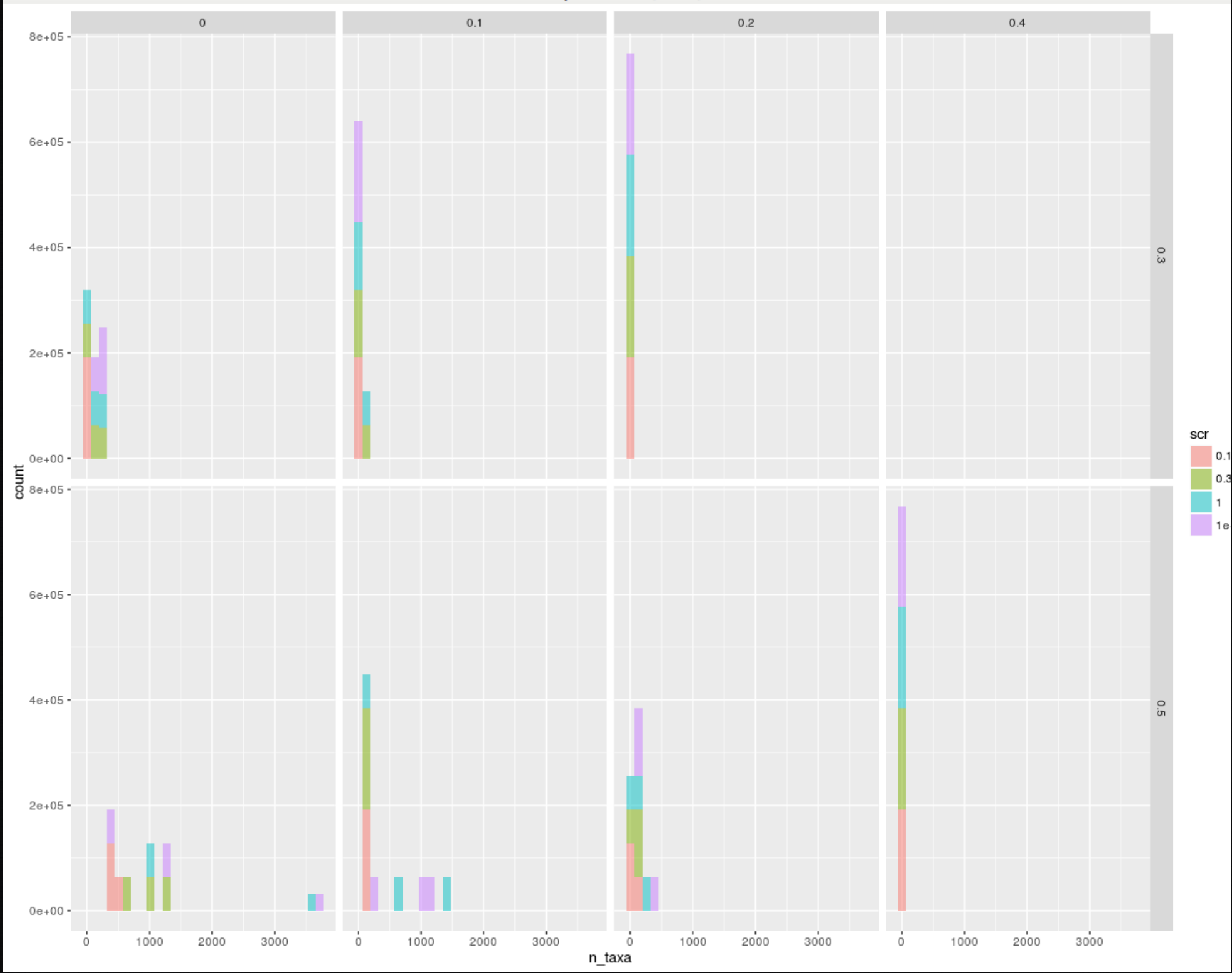
- Too often, a low number of taxa is simulated



Number of taxa



- Is low in general
- Seperate per speciation initiation and extinction rates, as in bump plot



Conclusion

- The more distributed the number of taxa, the more bumps
- Cause is still unknown
 - Bug or feature?

