PhD project overview

TECE meeting 2016-12-14

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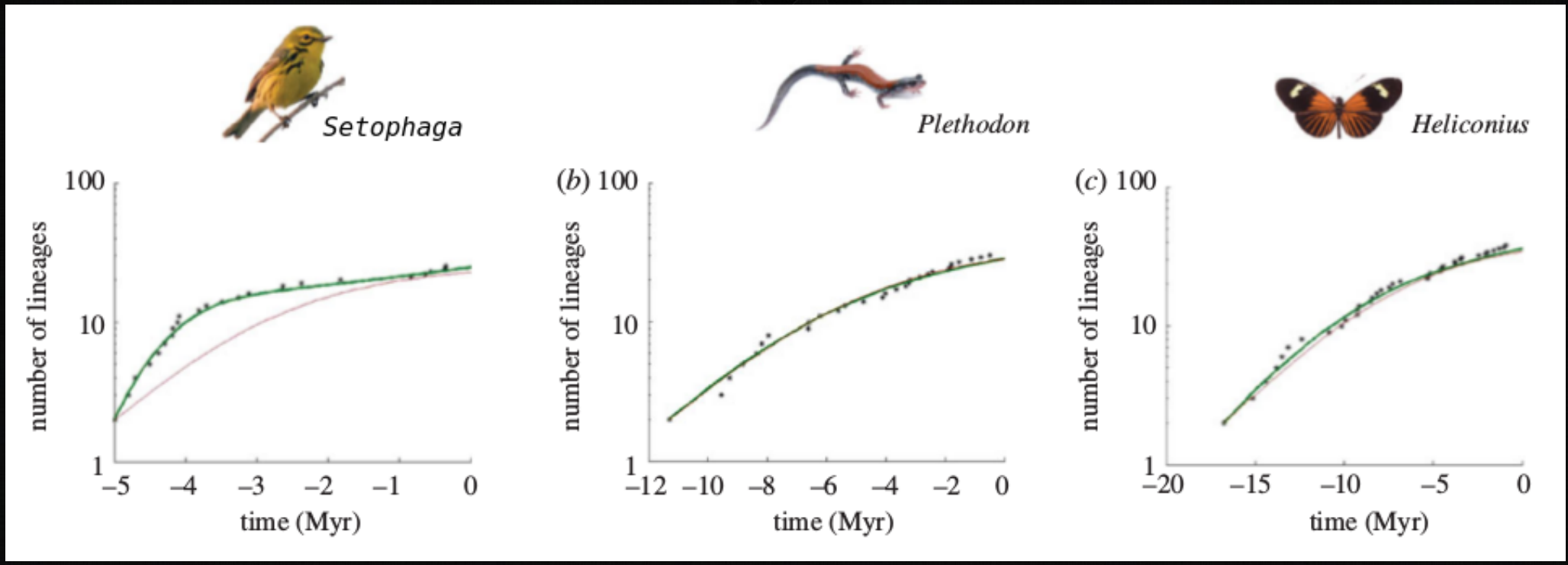
www.github.com/richelbilderbeek/Science

Problem

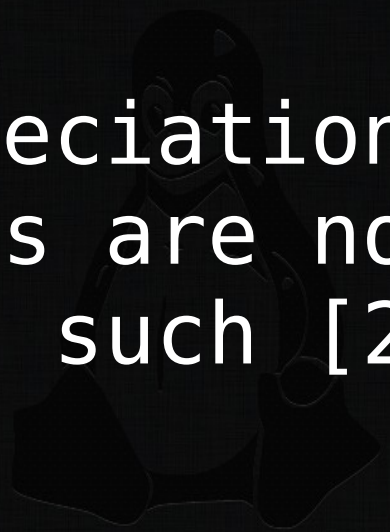
- LTT (‘Lineages-through-time’) plots flatten of towards the present



Adapted from Etienne et al., 2012

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

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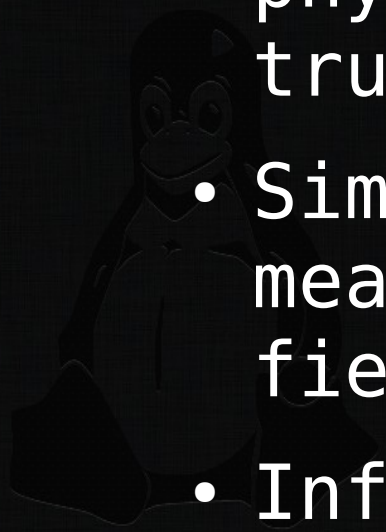
Approach

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

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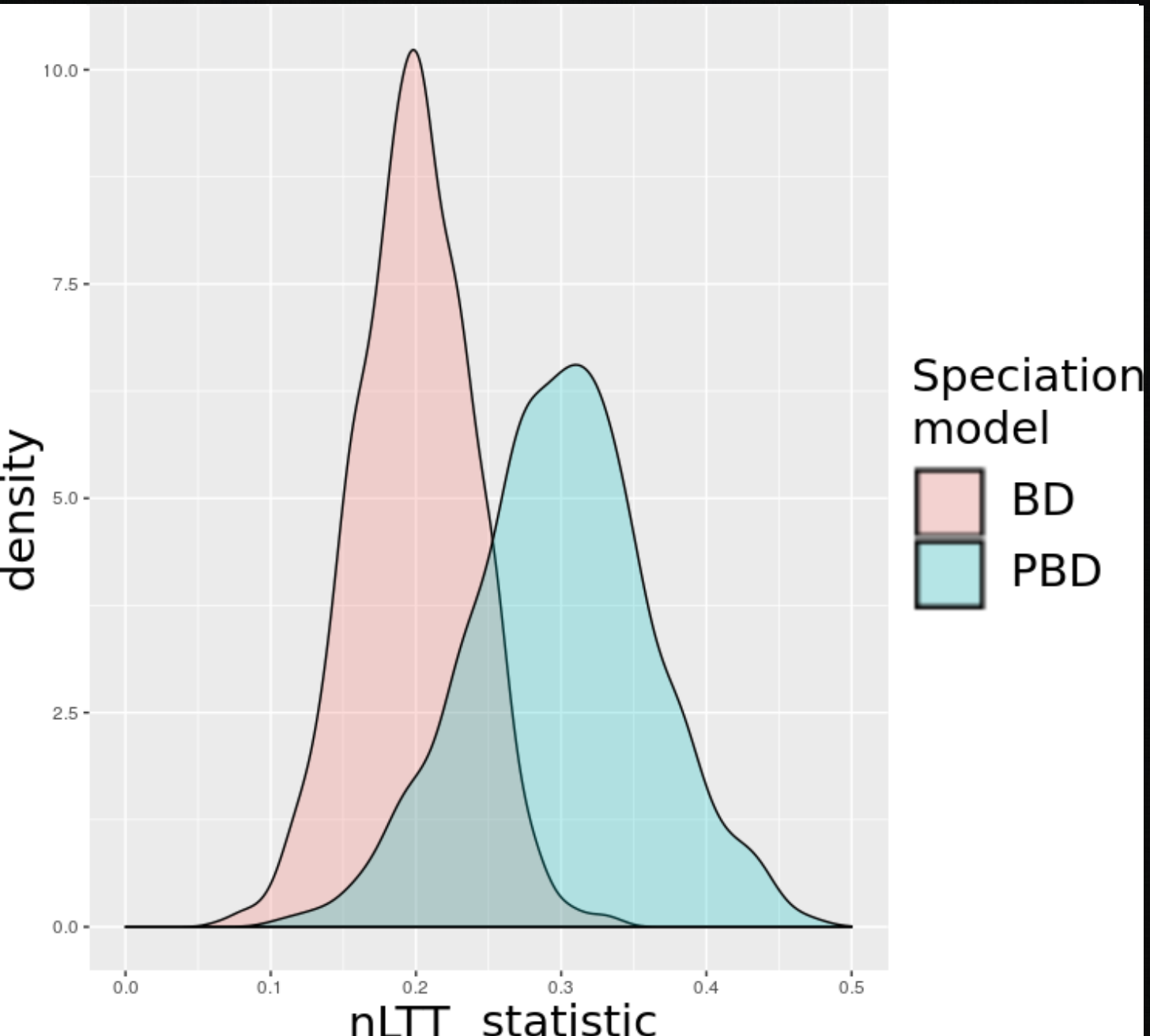
Idealized predictions



BD:
Birth Death

PBD:
Protracted BD

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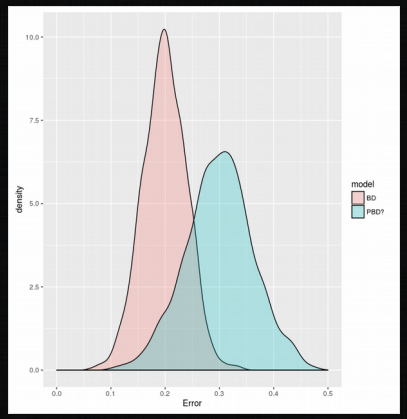
Predictions



Strong protracted-ness

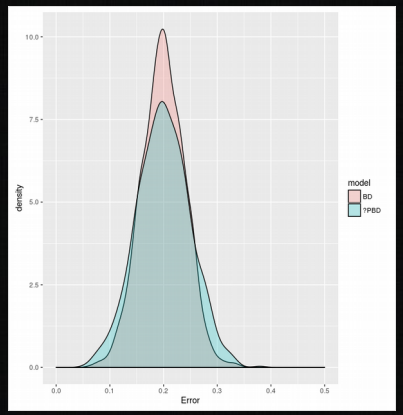
Weak input data

Biologically relevant?

Strong input data

Weak protracted-ness

Parameter space



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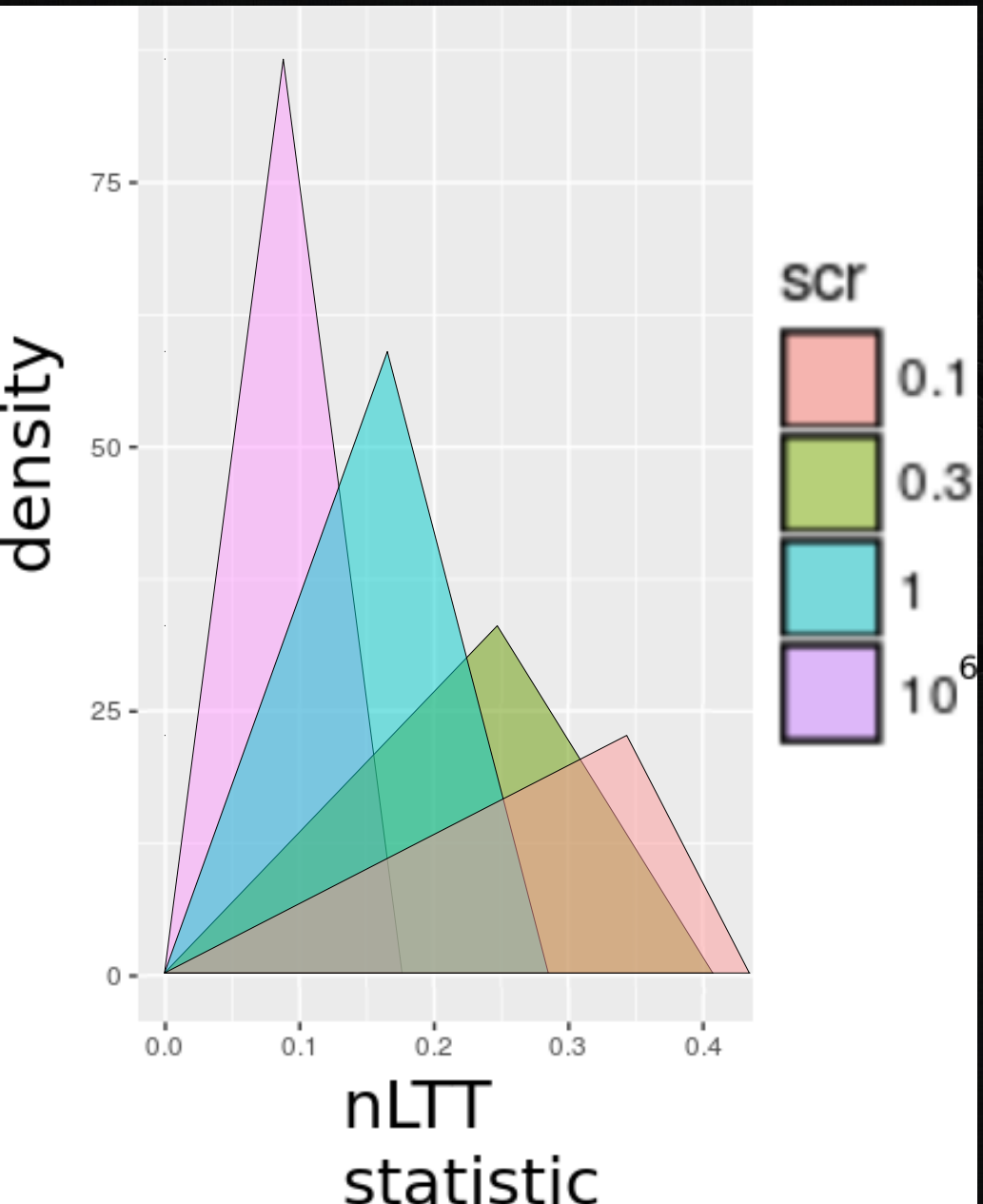
Speciation completion rate



- Infinity: BD
- Small: PBD

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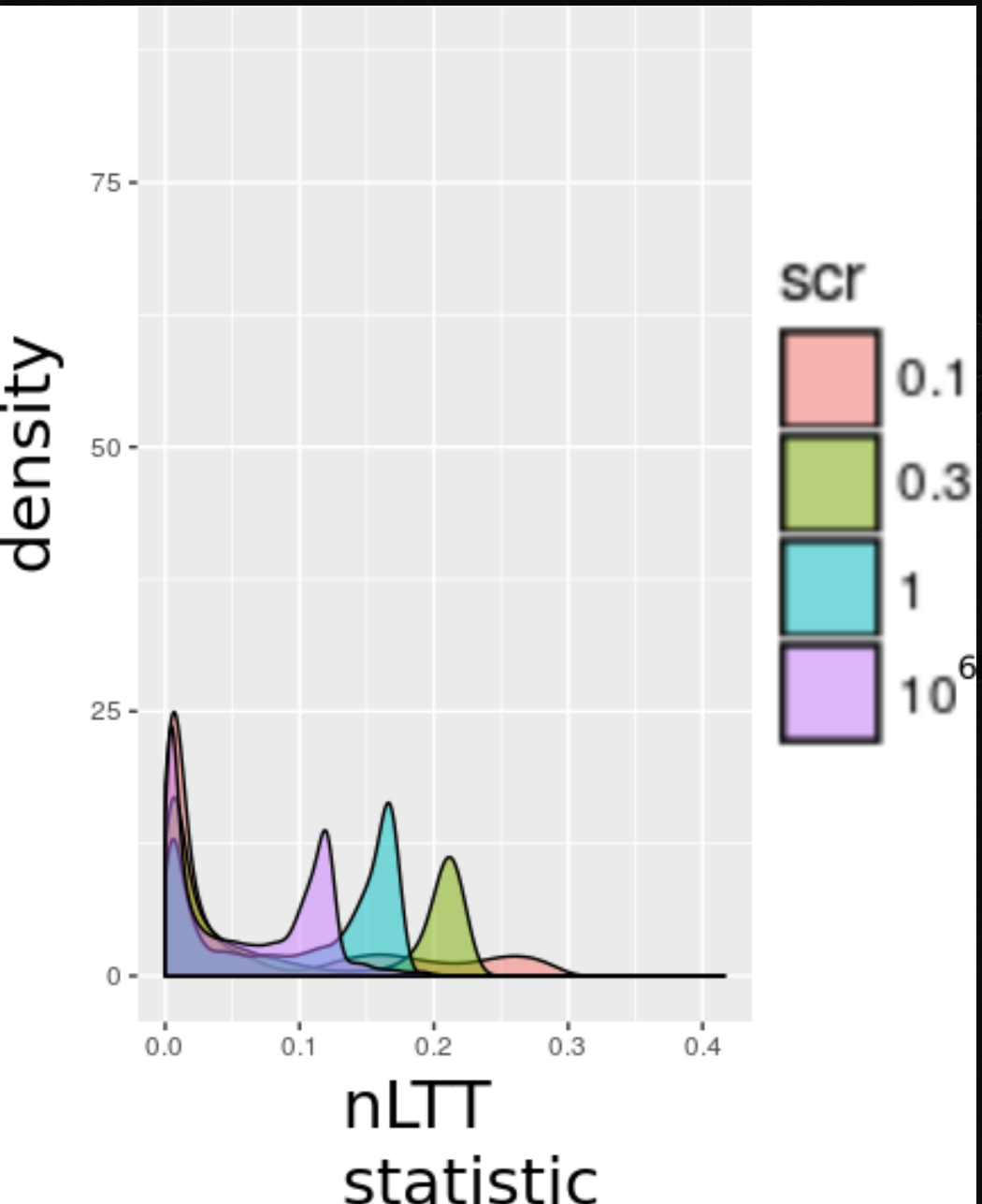
Bimodal distributions



- Here:
  - extinction rate (ER) = 0.0
  - speciation initiation rate (SIR) = 0.5
- And other SIRs and ERs?

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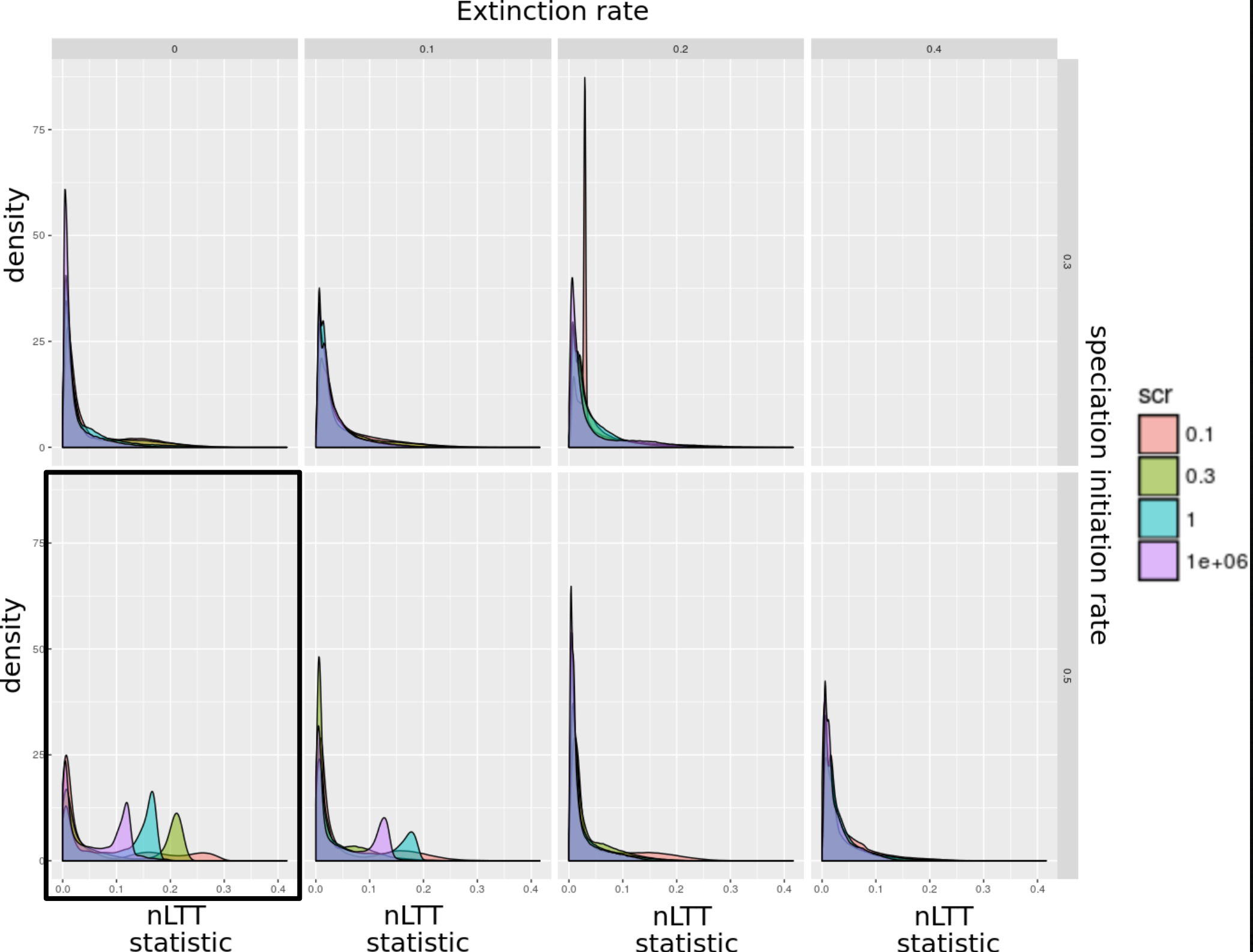
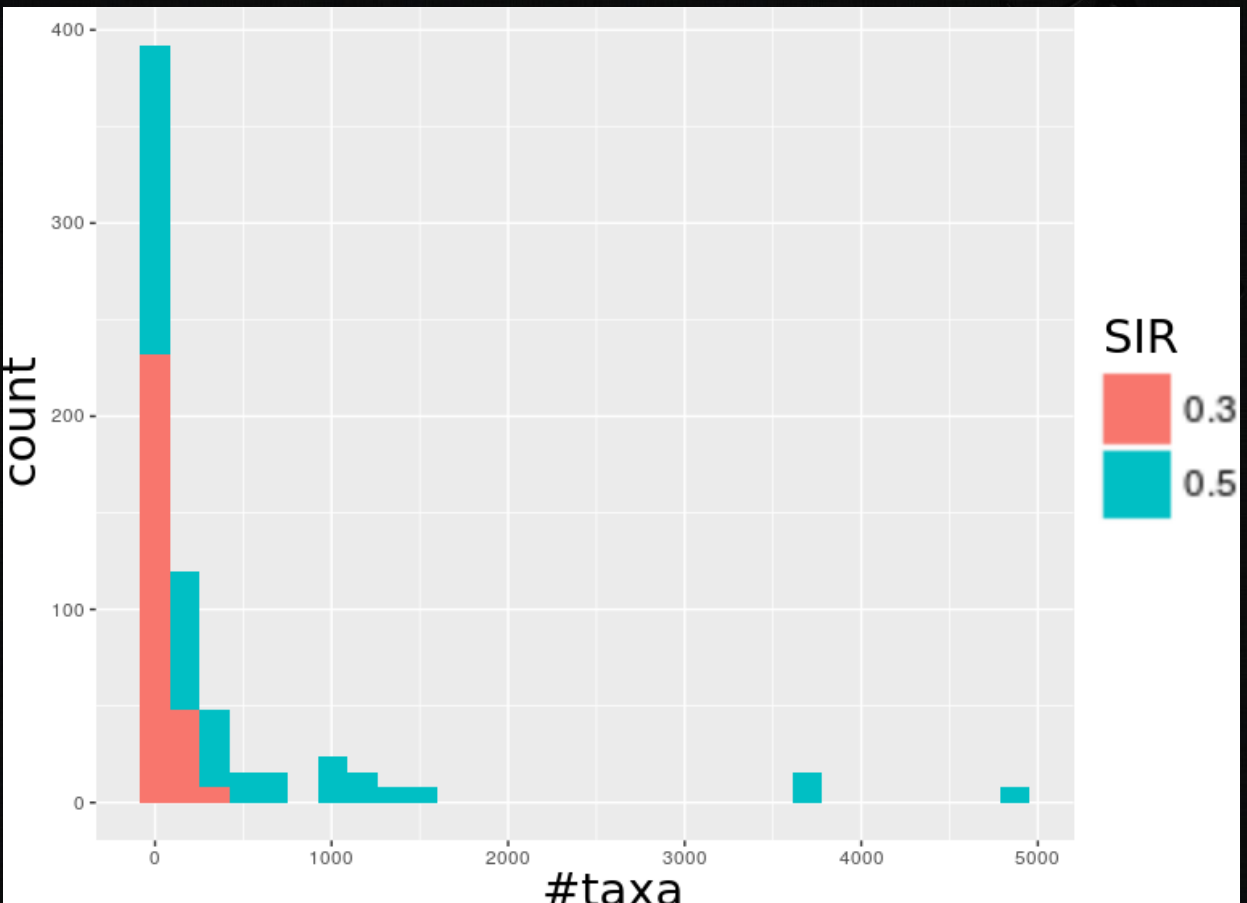

Extinction rate
0
0.1
0.2
0.4
0.3
0.5
speciation initiation rate
density
75
50
25
0
0.0
0.1
0.2
0.3
0.4
nLTT statistic
scr
0.1
0.3
1
1e+06

Hypothesis

- The bimodal distribution is somehow correlated by the number of taxa in the simulated trees?



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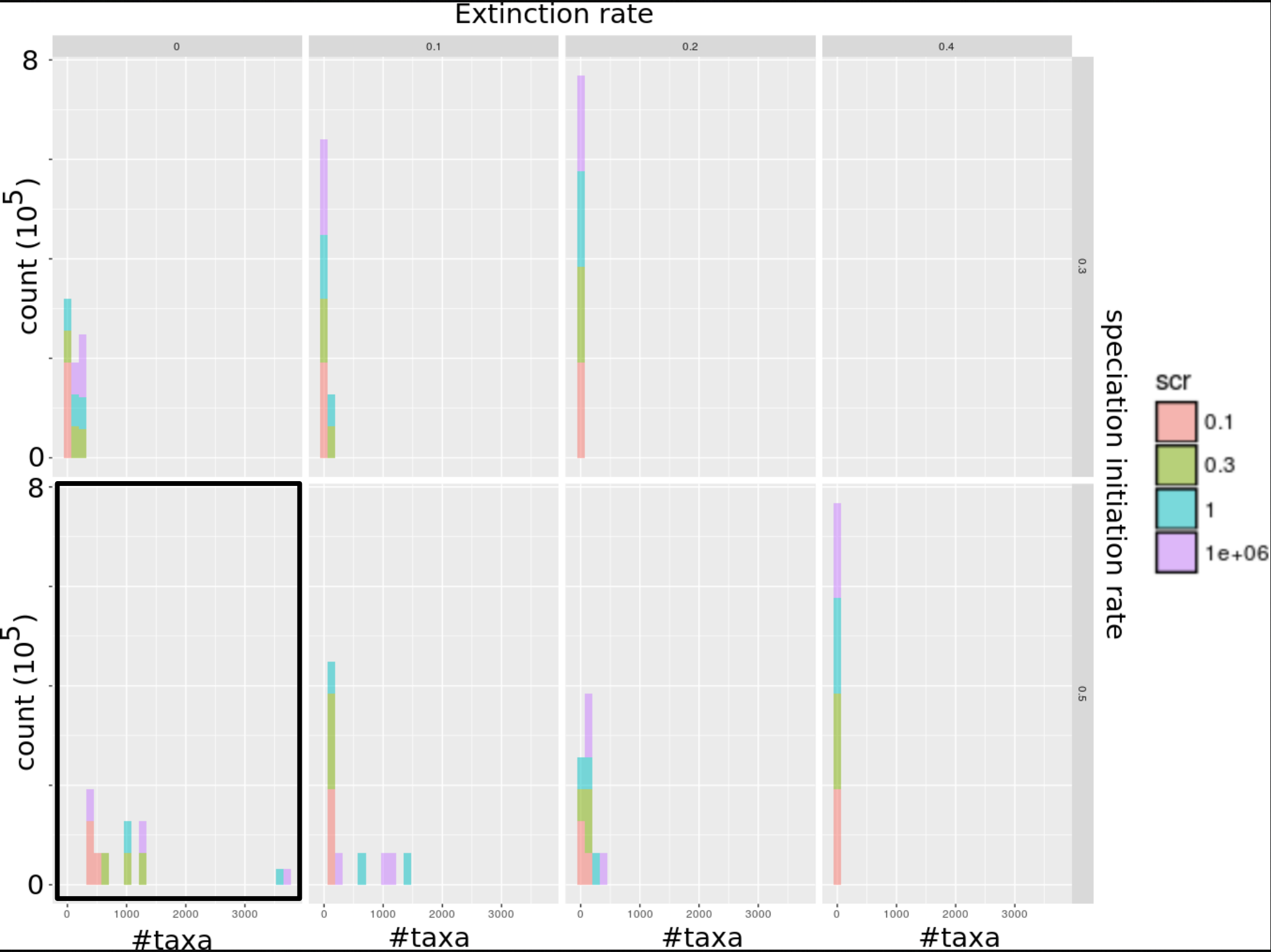
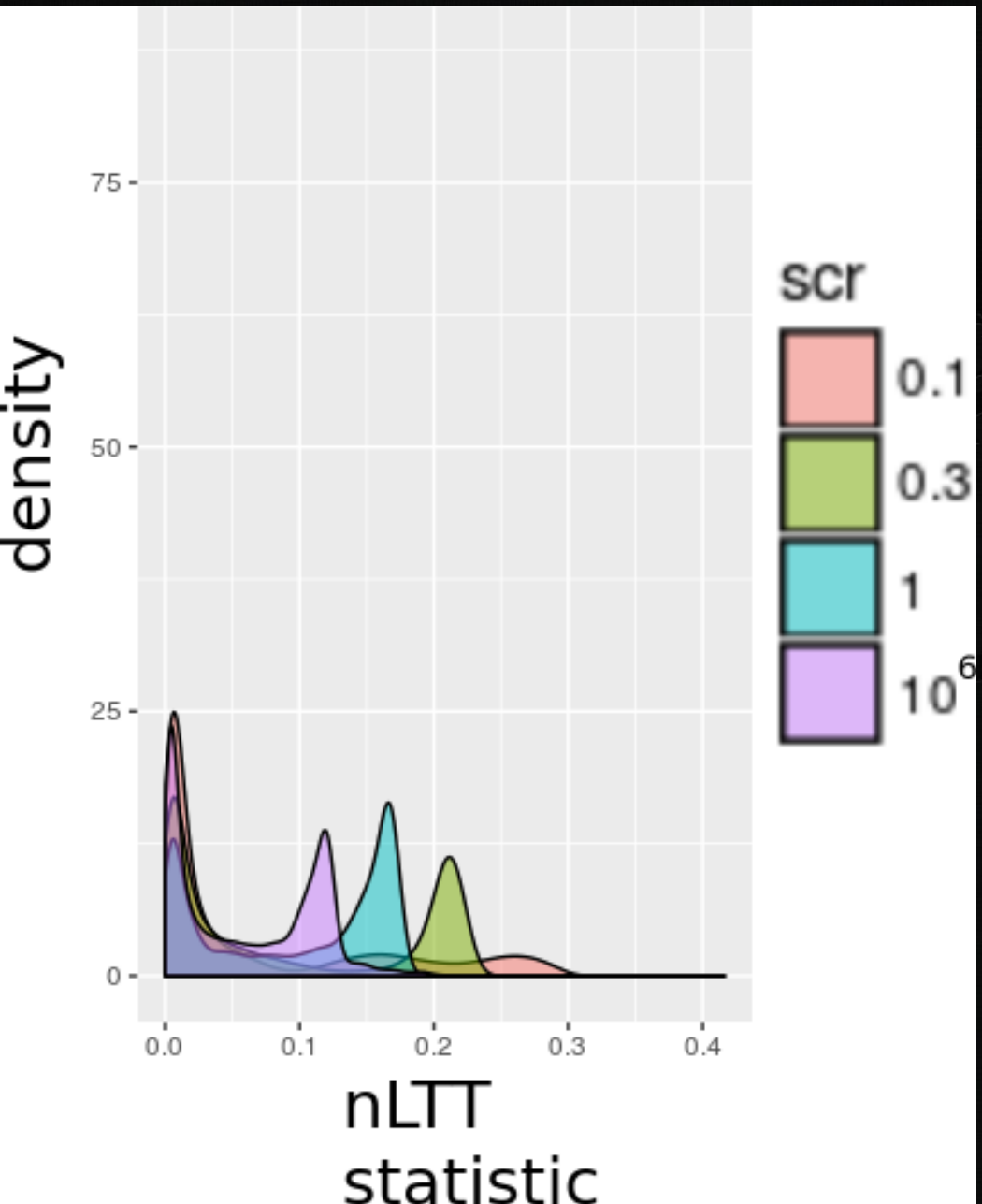
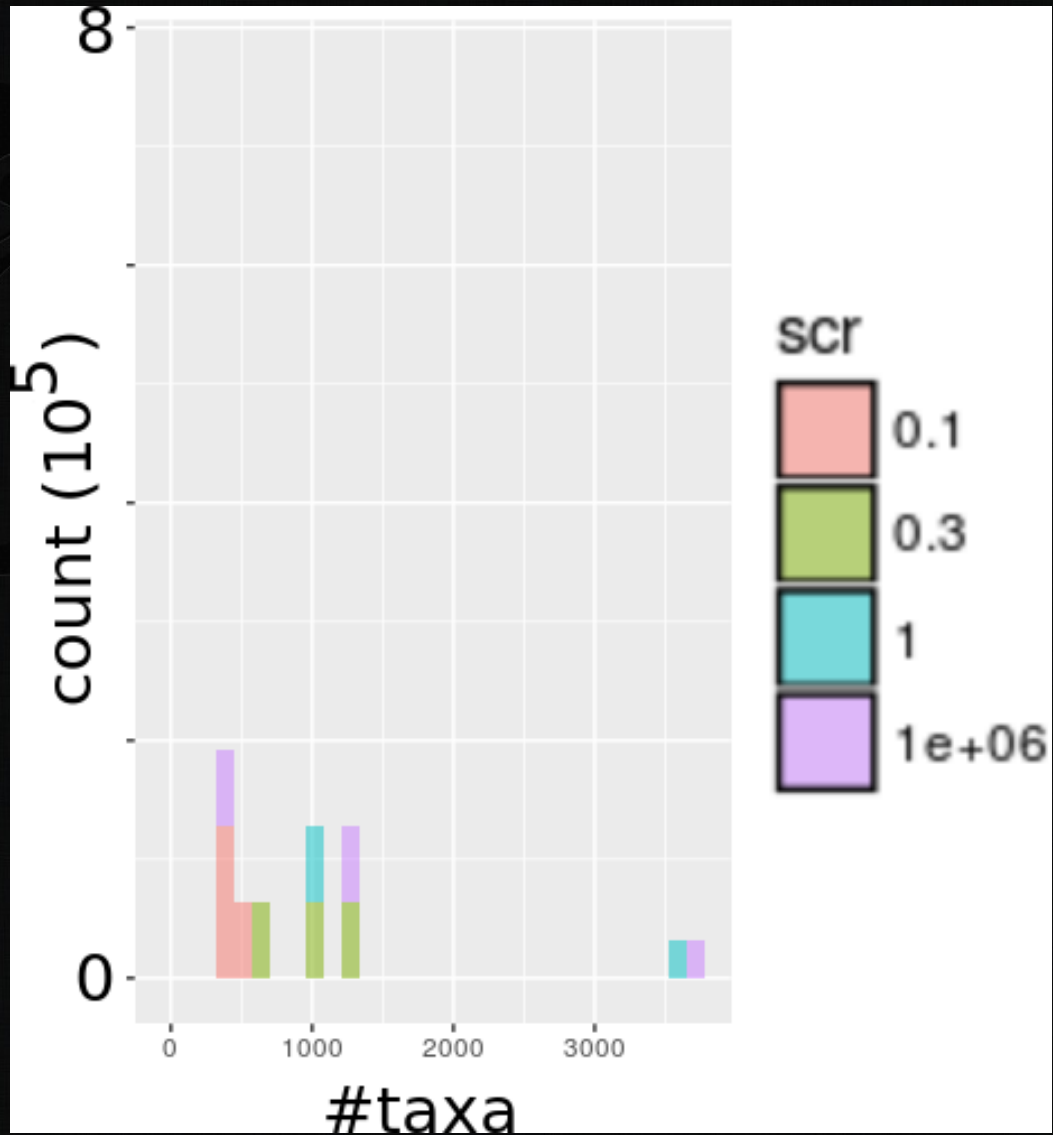
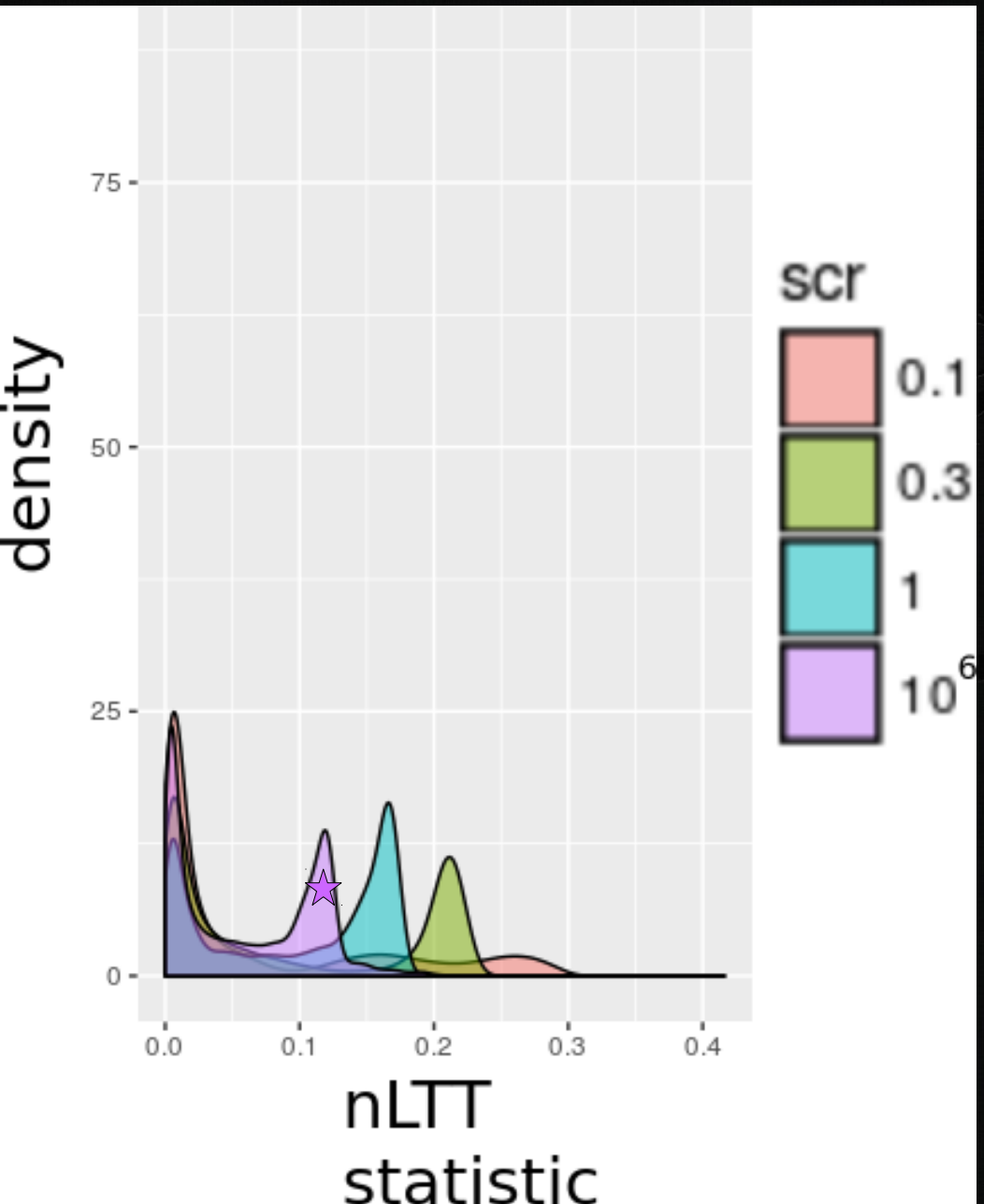

Extinction rate
0
0.1
0.2
0.4
0.3
0.5
speciation initiation rate
count (10^5)
8
0
0
1000
2000
3000
#taxa
scr
0.1
0.3
1
1e+06

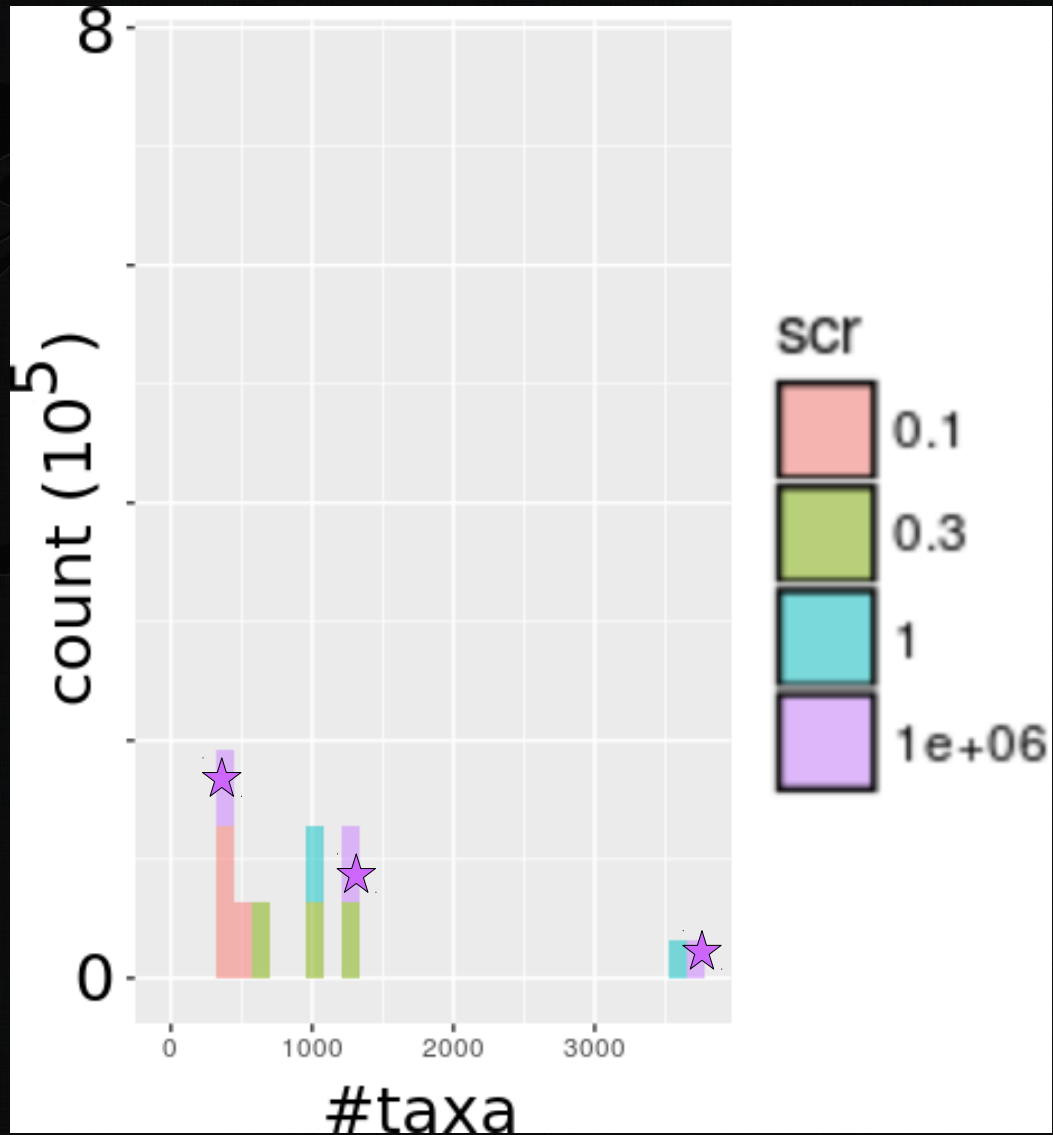
Zooming in


density
75
50
25
0
0.0
0.1
0.2
0.3
0.4
nLTT
statistic
scr
0.1
0.3
1
10^6


count (10^5)
8
0
0
1000
2000
3000
#taxa
scr
0.1
0.3
1
1e+06

Zooming in


density
75
50
25
0
0.0
0.1
0.2
0.3
0.4
nLTT
statistic
scr
0.1
0.3
1
10^6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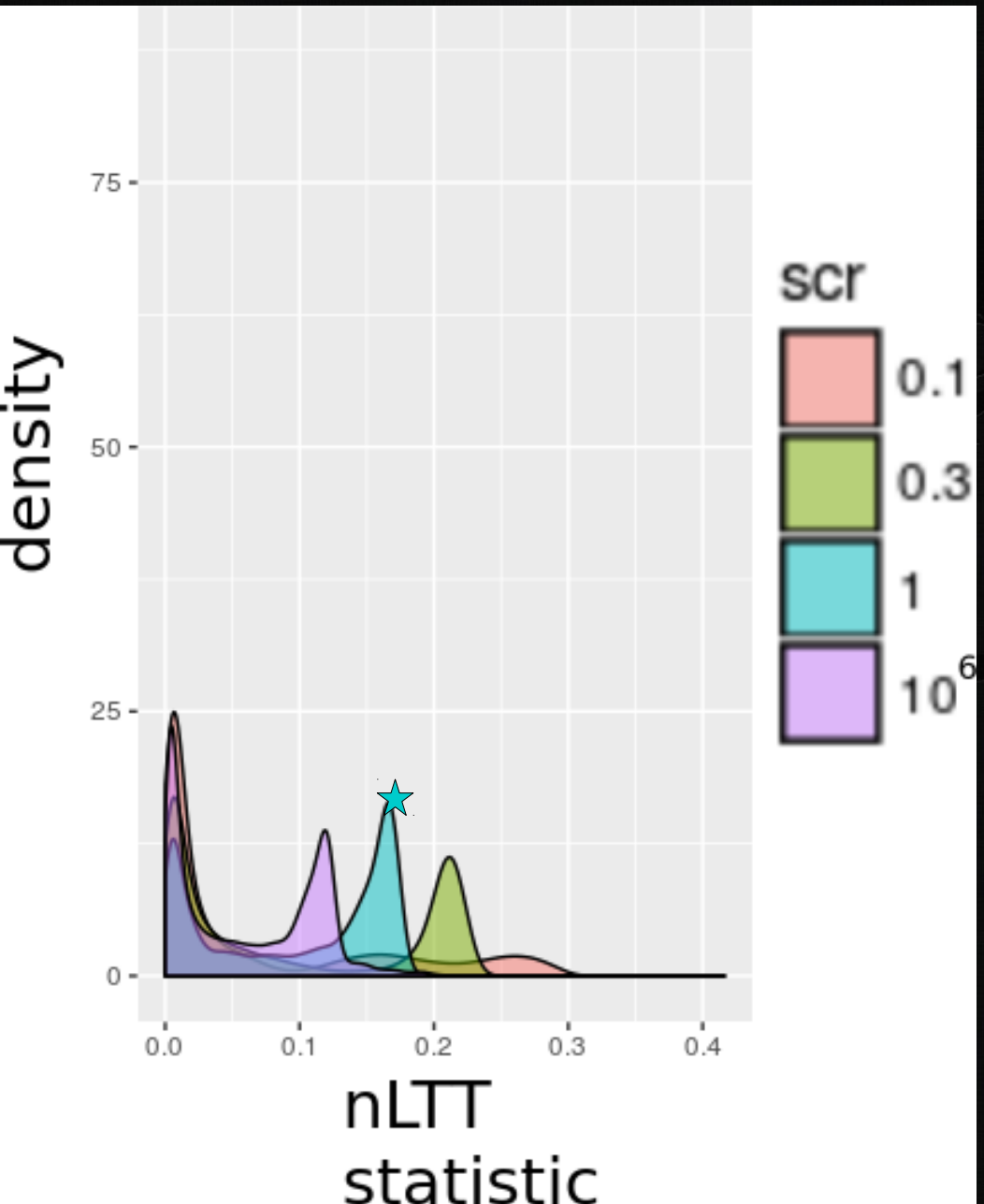
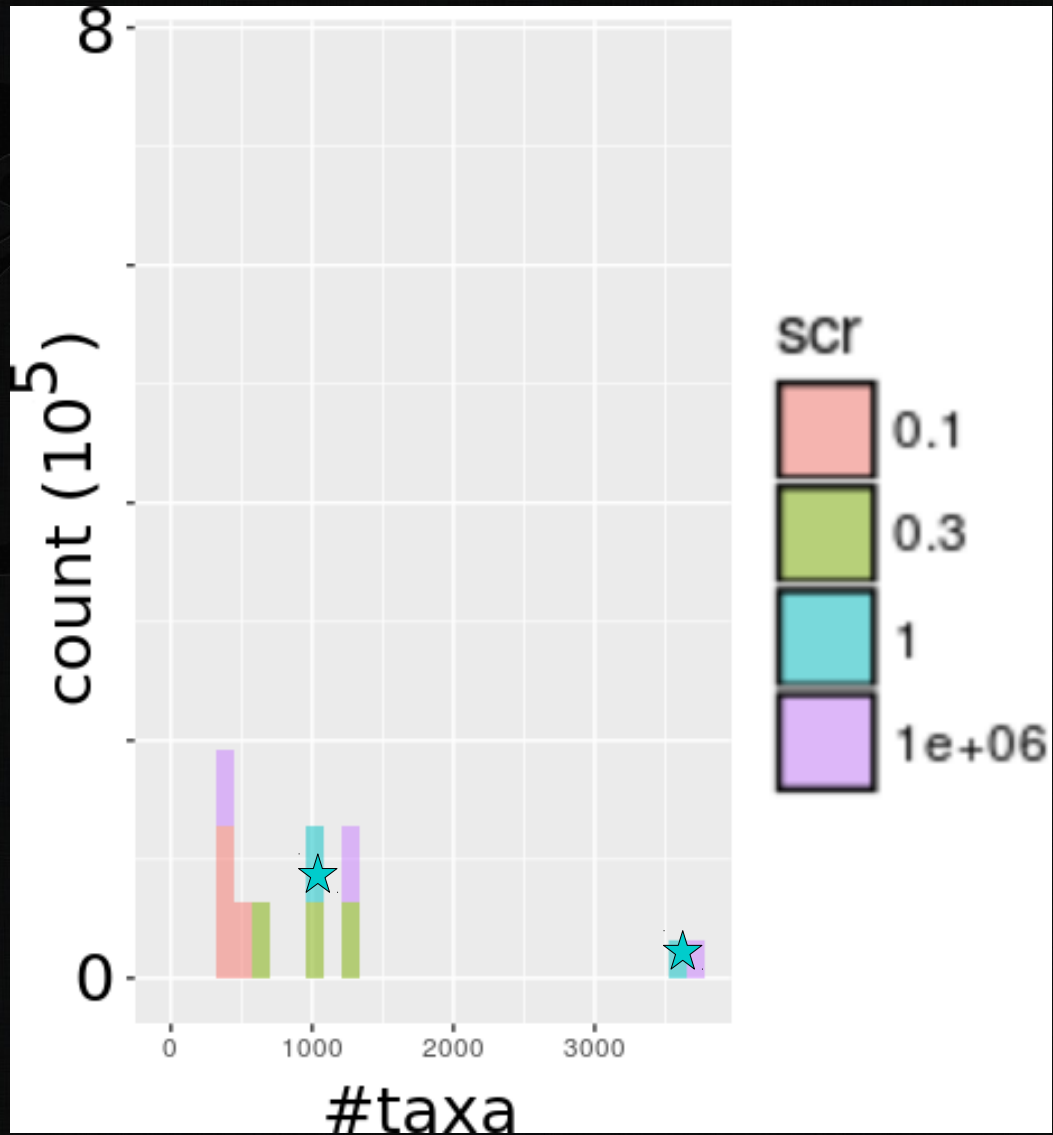
Zooming in


density
75
50
25
0
0.0
0.1
0.2
0.3
0.4
nLTT
statistic
scr
0.1
0.3
1
10^6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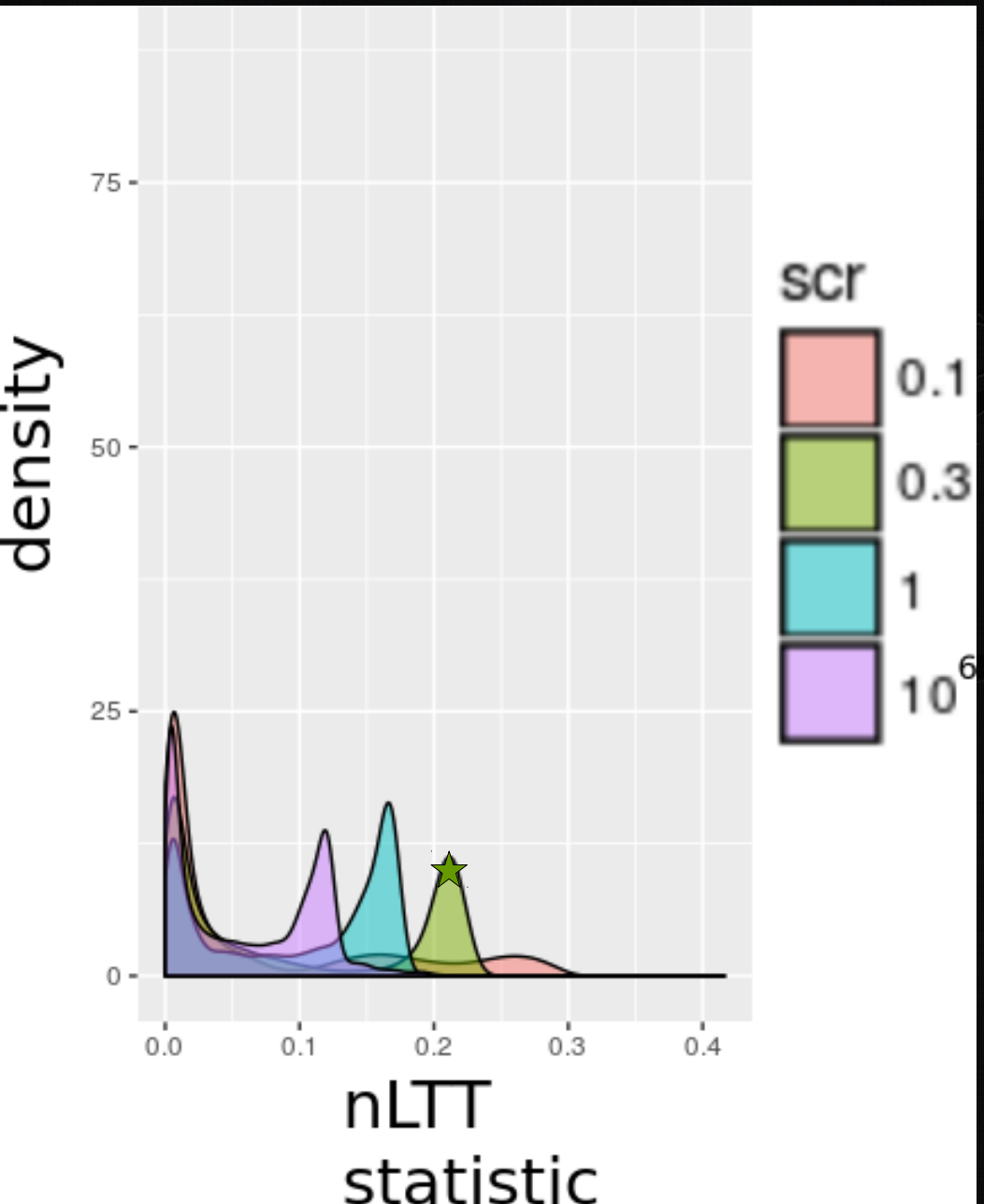
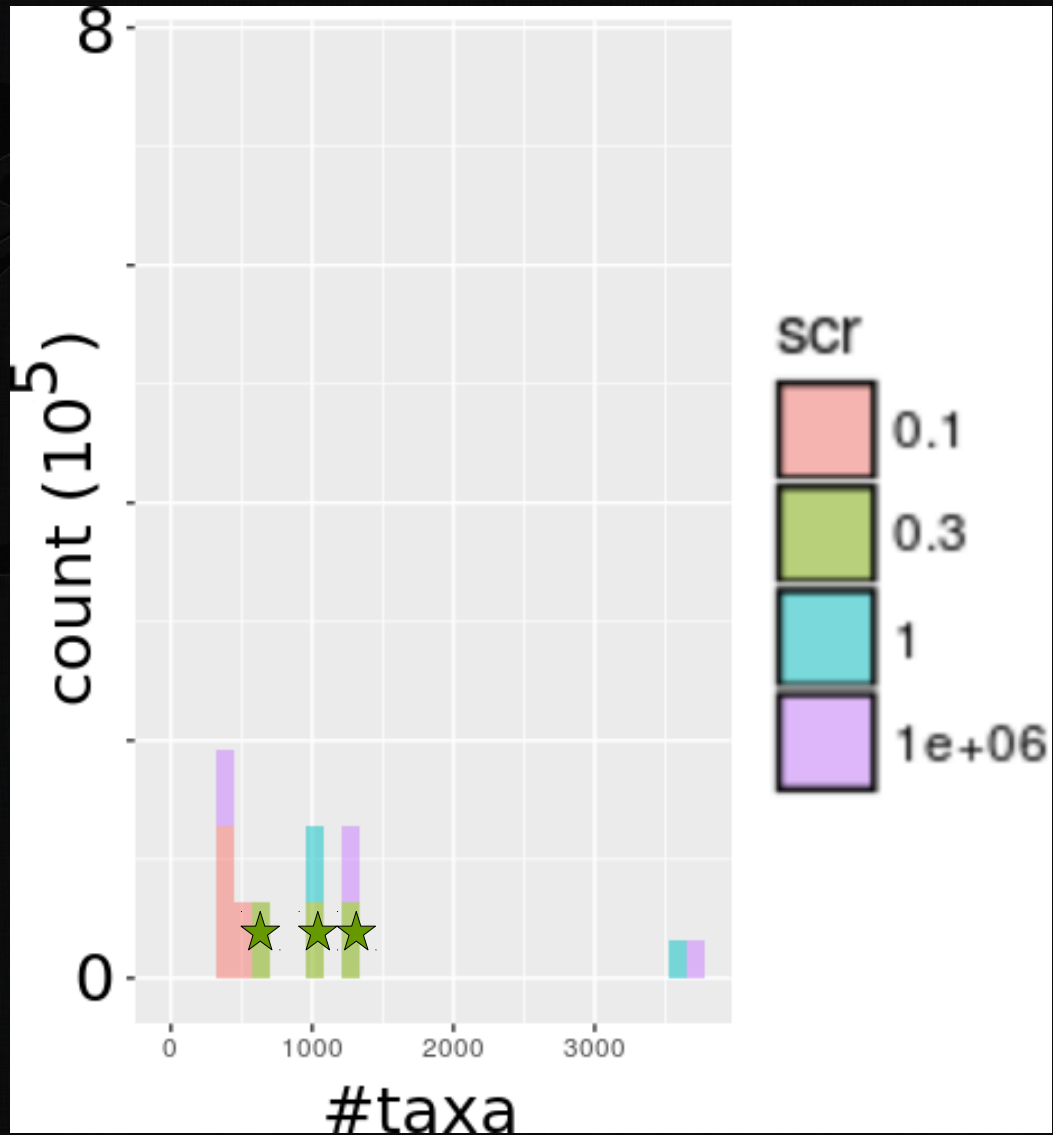
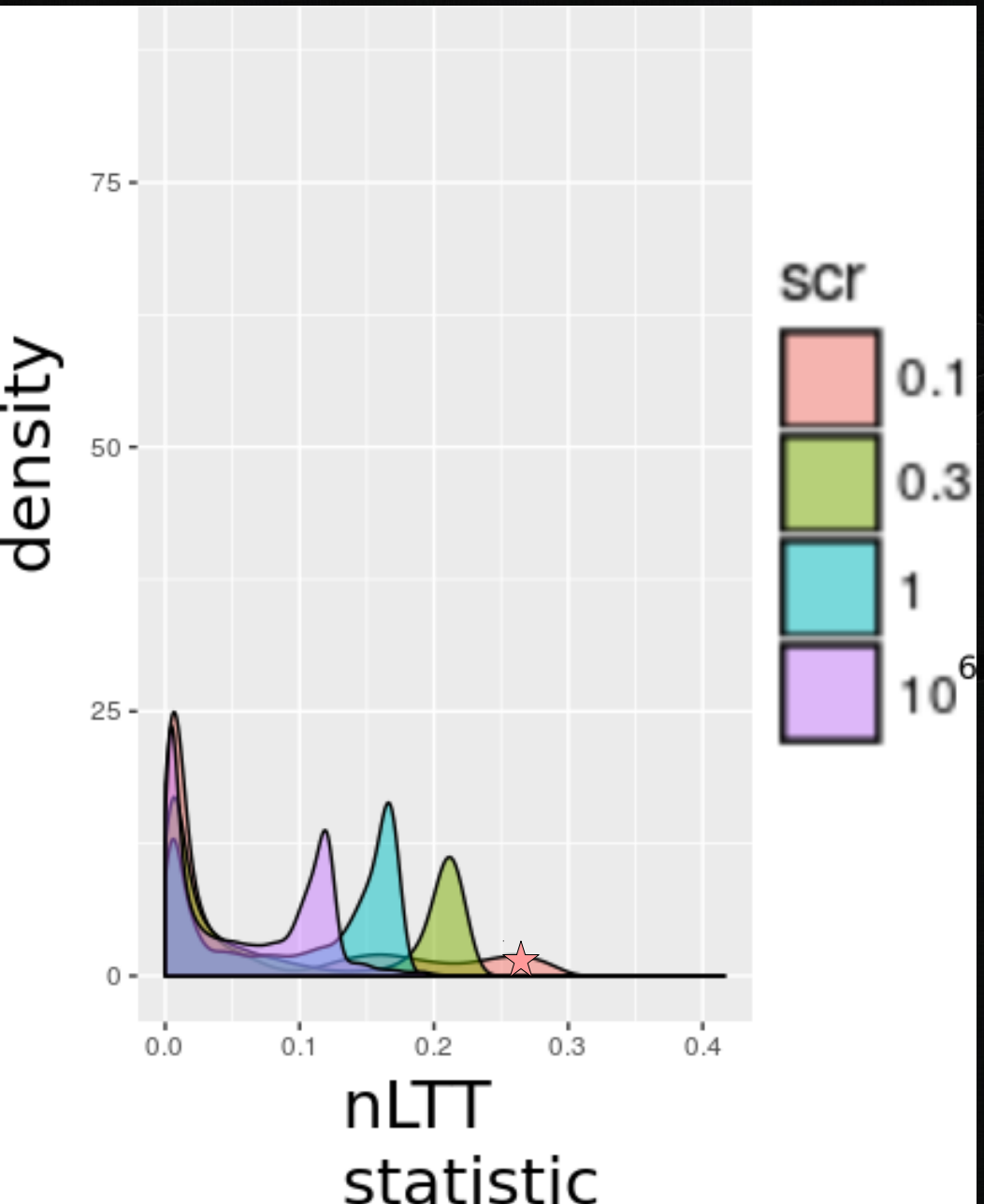
8
0
0
1000
2000
3000
#taxa
scr
0.1
0.3
1
1e+06

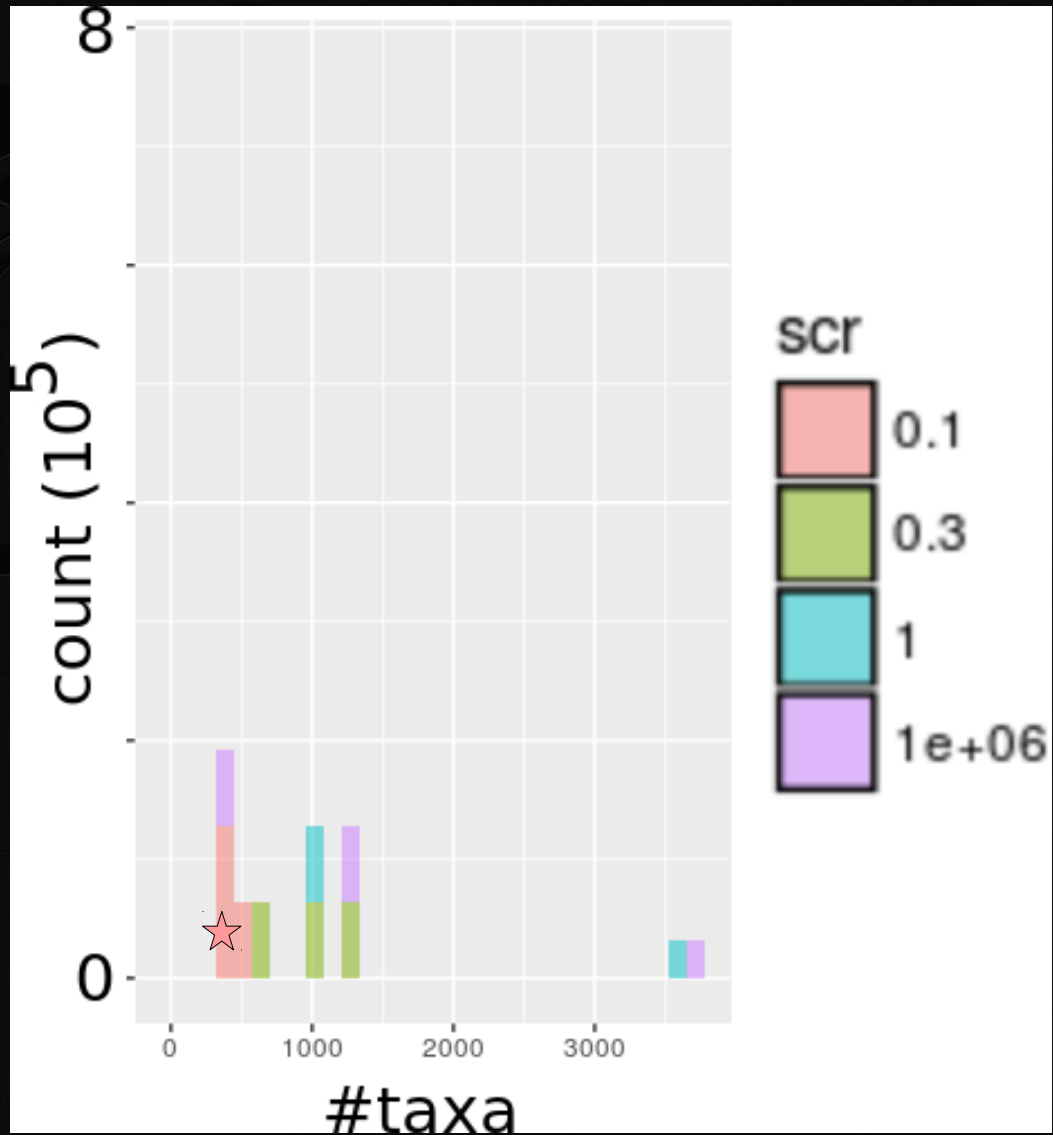
Zooming in


density
75
50
25
0
0.0
0.1
0.2
0.3
0.4
nLTT
statistic
scr
0.1
0.3
1
10^6


count (10^5)
8
0
0
1000
2000
3000
#taxa
scr
0.1
0.3
1
1e+06

Zooming in


density
75
50
25
0
0.0
0.1
0.2
0.3
0.4
nLTT statistic
scr
0.1
0.3
1
10^6


count (10^5)
8
0
0
1000
2000
3000
#taxa
scr
0.1
0.3
1
1e+06

Conclusion

- Bimodal distribution probably caused by distribution of taxa
- More pronounced of DNA sequences contains more information (not shown here)

- Need to simulate a smooth distribution of phylogenies

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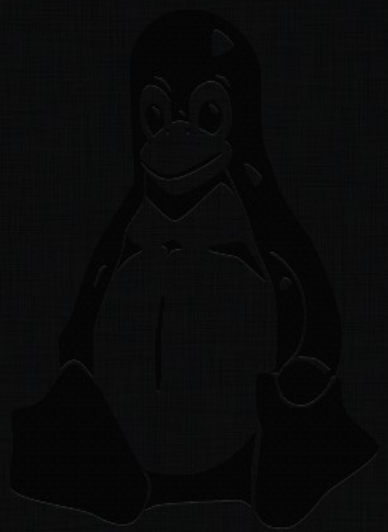
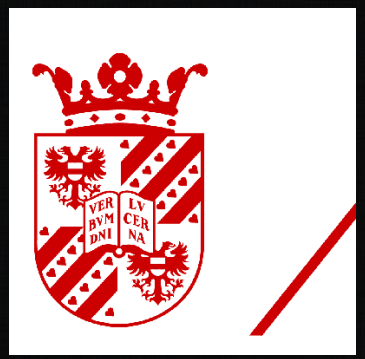
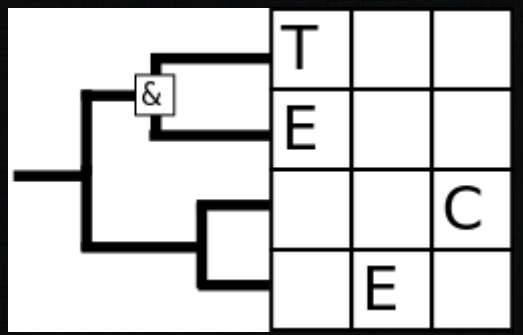
Acknowledgements

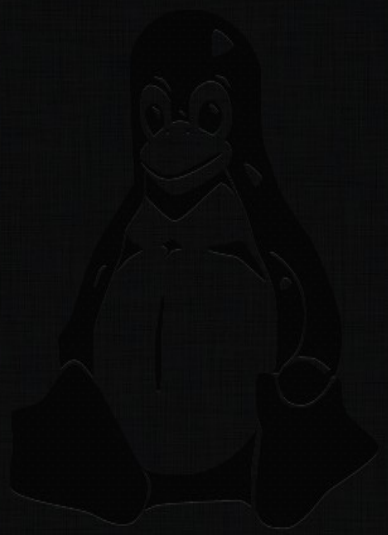
- Rampal
- The Rmy
- TECE
- TRES







Questions?



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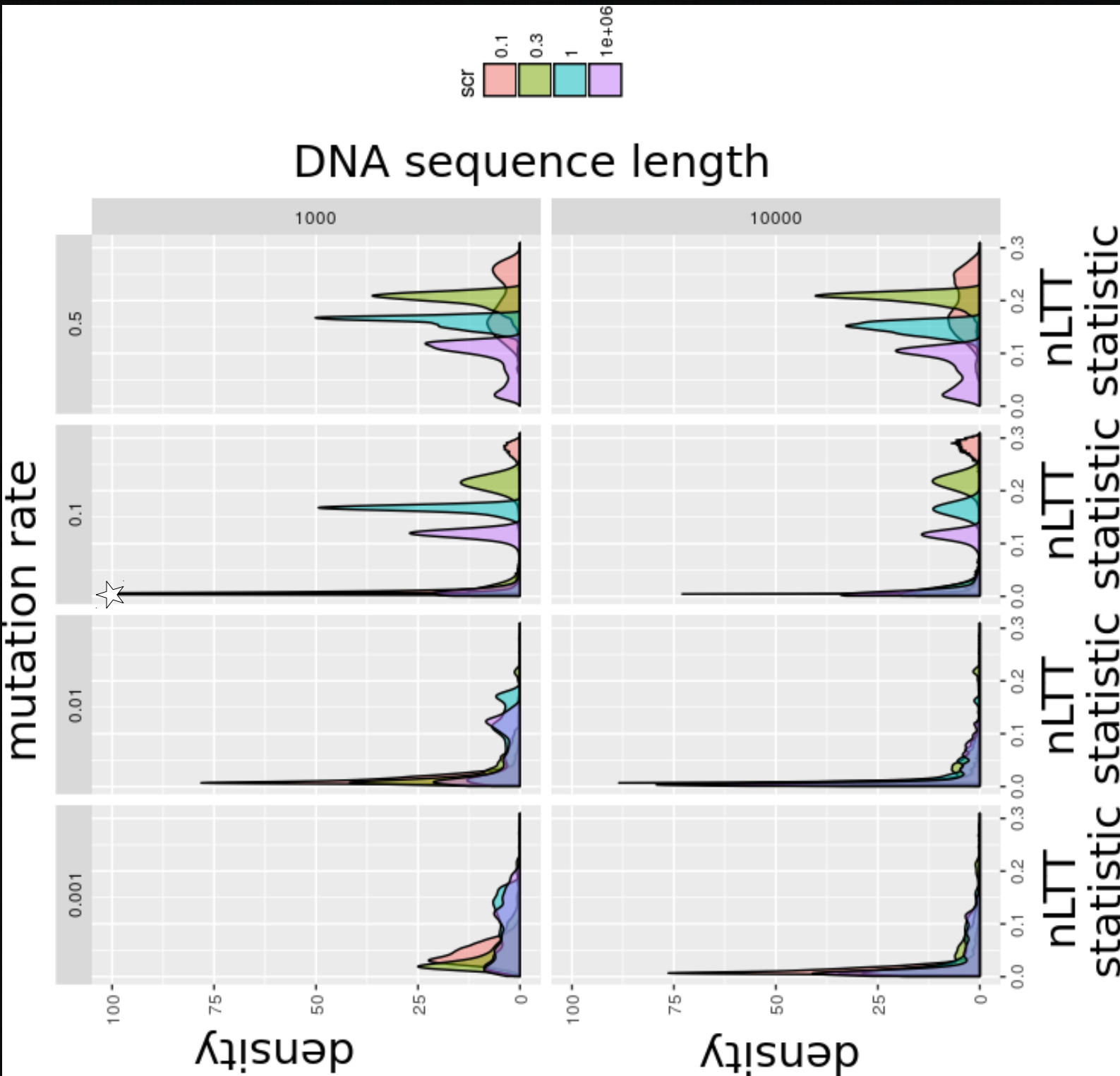
Bimodal distributions get more pronounced with more information on DNA