

Rational selection of speciation models

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Research lines

- Speciation model comparison
- Fluctuation of neutral traits in time

Speciation

- Speciation has been successful in creating many species
 - 5 ± 3 million [1] and 8.7 ± 1.3 million [2] extant species
 - 100x more species extinct [3]
- Many speciation models, which one fits the data best?

[1] Costello et al., 2013

[2] Sweetlove, 2014

[3] Raup, 1981

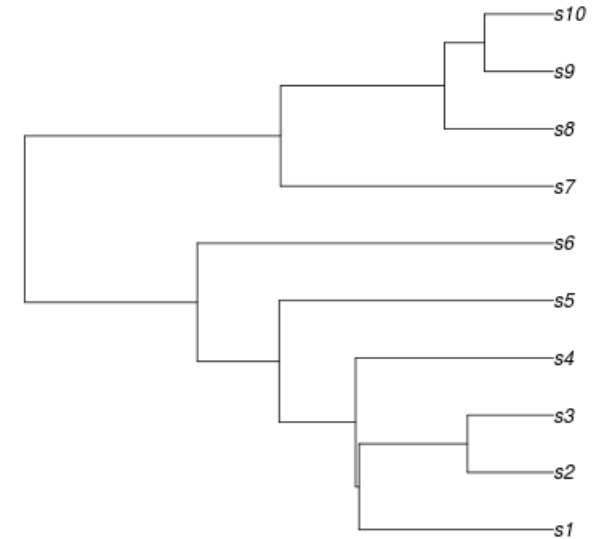
Speciation models

- There are multiple models:
 - Speciation happens at a constant rate
 - Speciation rate changes in time
 - Speciation rate is dependent on the current number of lineages present
 - Speciation itself is a trait
 - Speciation take time
 - Speciation rate is dependent on the age of the lineage

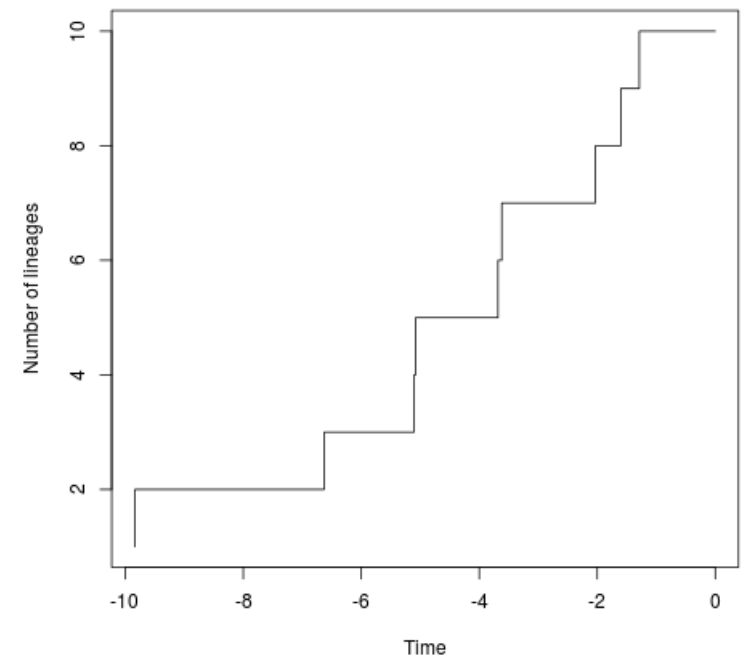
Pure-birth models

- Also called the Yule model, after [1]
- Assumes
 - speciation is constant
 - no extinction
 - speciation is instantaneous
- Simplest model
- Number of lineages changes exponentially

Pure-birth tree, birth rate = 0.2



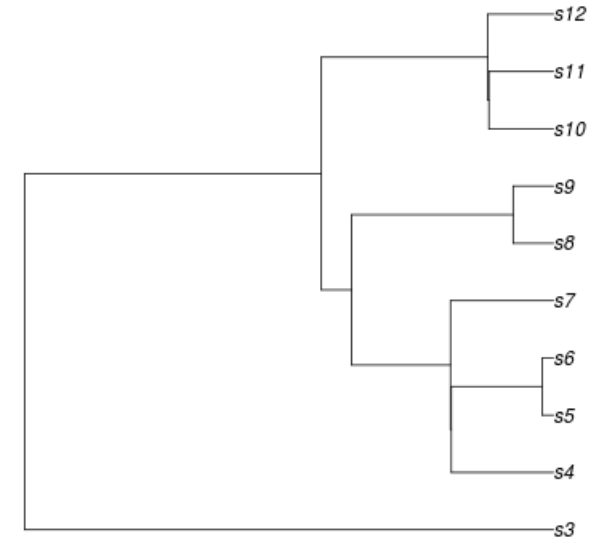
LTT plot of pure-birth tree, birth rate = 0.2



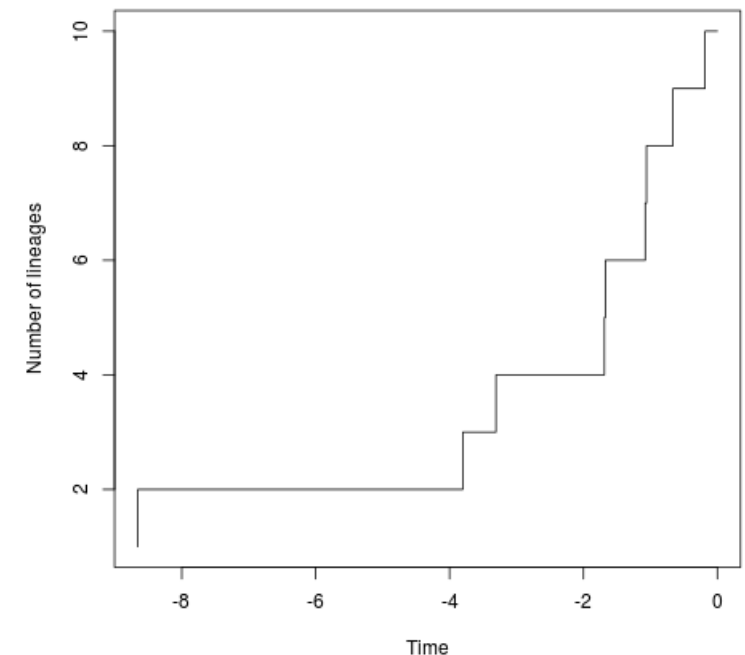
Birth-death (BD) models

- Assumes
 - speciation is constant
 - extinction is constant
 - speciation is instantaneous
 - most taxa sampled
- Suggested as a null model [1-3]
- Number of extant lineages is expected to change exponentially

Reconstructed birth-death tree
birth rate = 0.2 , death rate = 0.1



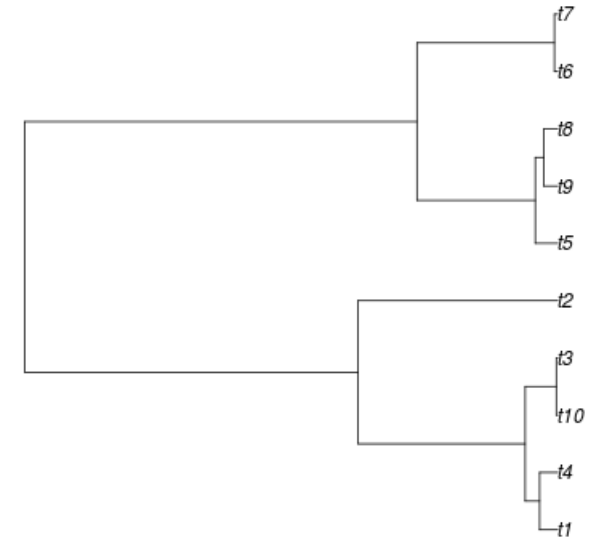
LTT plot of reconstructed birth-death tree
birth rate = 0.2 , death rate = 0.1



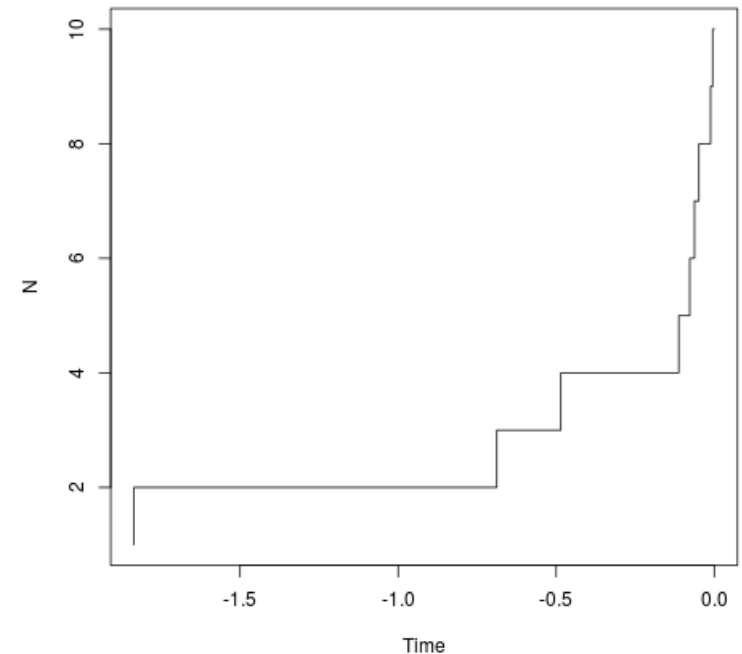
Exponential-growth coalescent model (EGCM)

- Assumes
 - number of lineages grows exponentially
 - speciation is instantaneous
 - small fraction of all taxa sampled

Exponential-size coalescent tree
#sampled: 10, growth rate:0.5

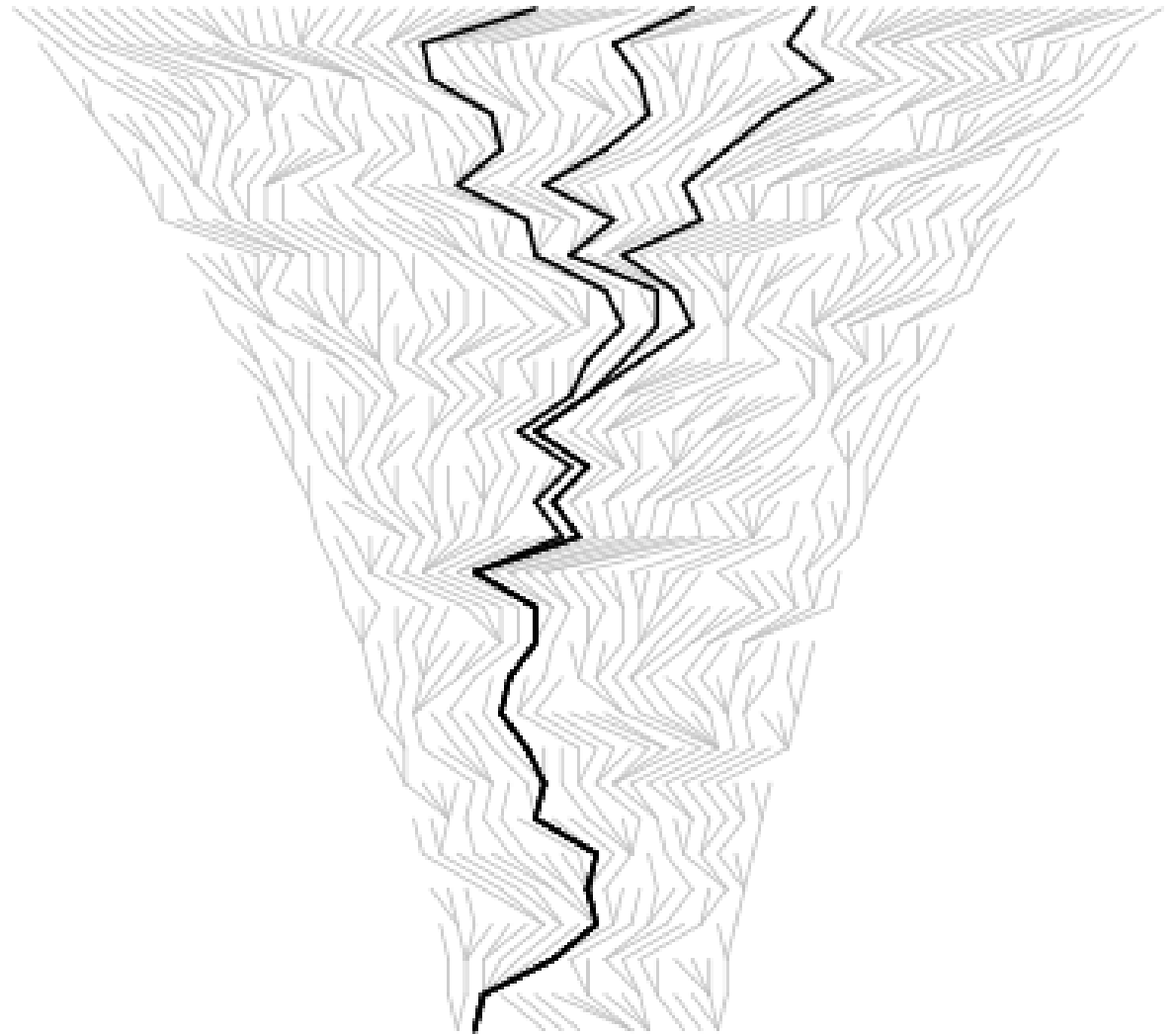


LTT plot of exponential-size coalescent tree
#sampled: 10, growth rate:0.5

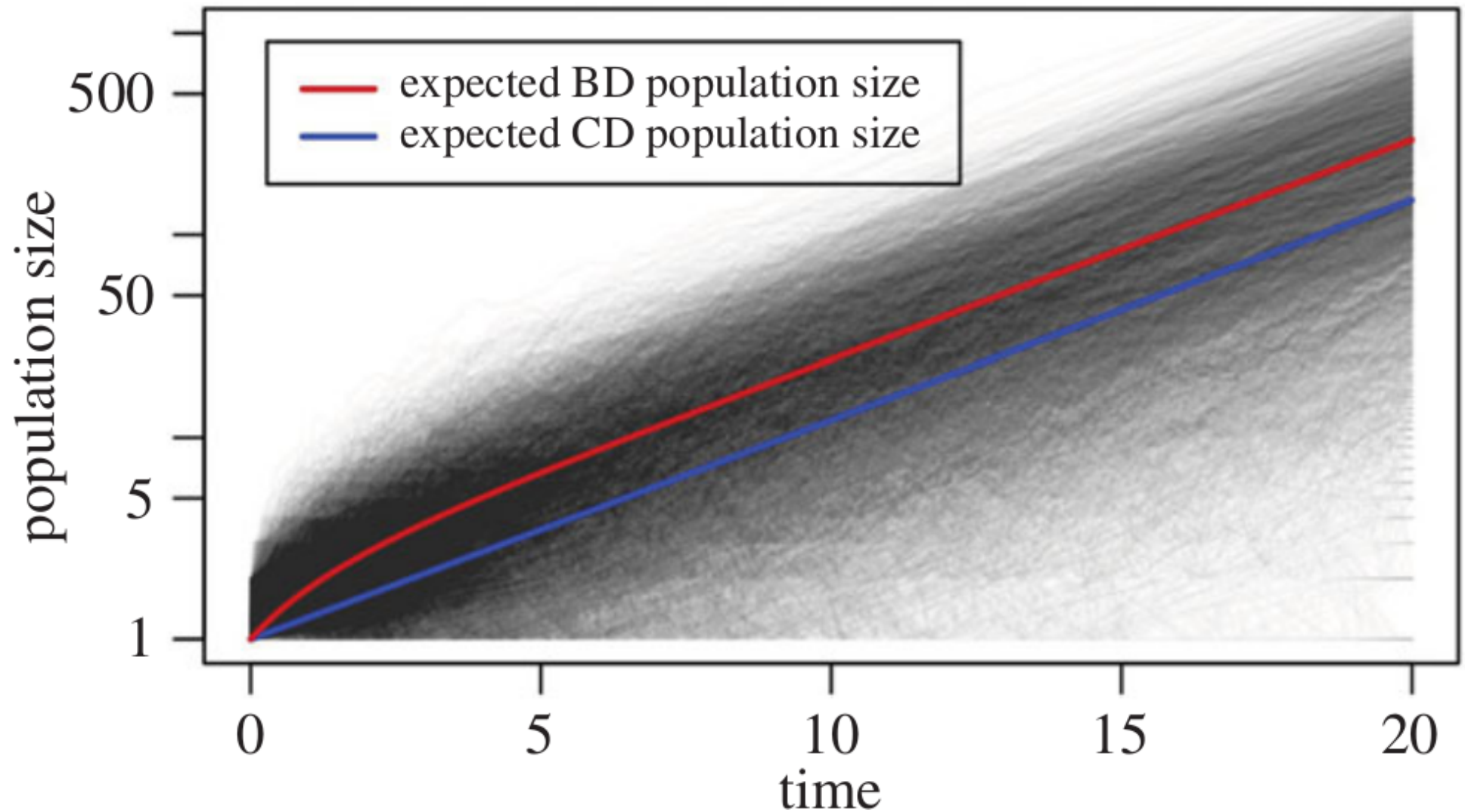


BD versus EGCM

- $N_{\text{BD}}(t) = e^{(\lambda-\mu)t}$
- $N_{\text{EGCM}}(t) = e^{rt}$
- For $\lambda-\mu = r$,
they are
identical?



They are different!

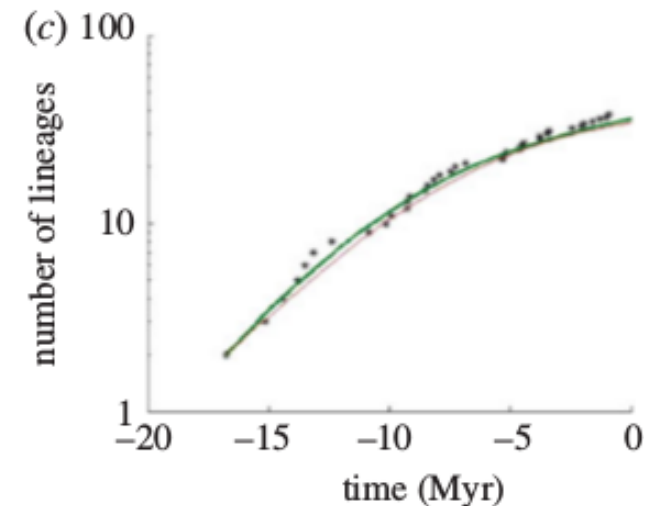
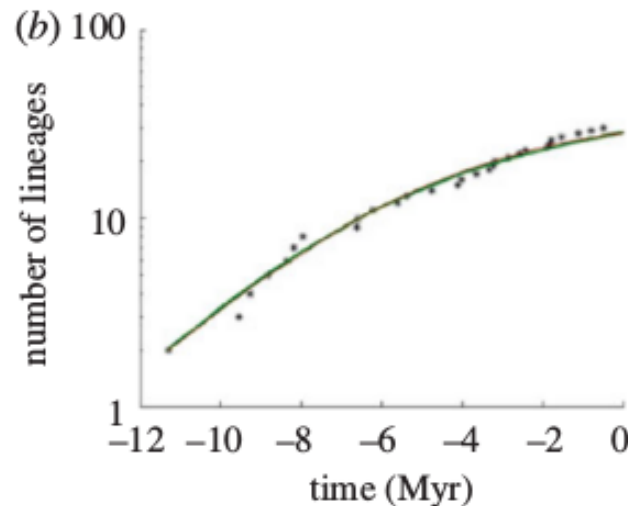
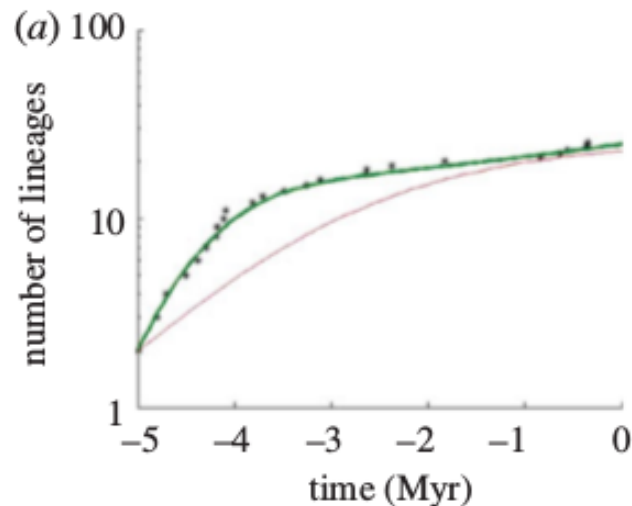


Research project #1

- BD and EGCM were assumed to be the same
- But BD and EGCM differ in practice
- Will conclusions drawn from inferred phylogenies differ?
- Likelihoods cannot be used, but (non-LTT) phylogeny summary statistics can be used

Time dependent birth-death (TDBD) model

- Assumes speciation rate changes with time
- Speciation is caused by an external mechanism, e.g. climate change



Diversity dependent birth-death (DDBD) model

- Assumes speciation rate changes with the number of lineages present
- How different are time- and diversity dependent birth-death models?
 - Investigated by César!

Constant-population coalescence (CPC) model

- Assumes the number of species has reached its (dynamic) equilibrium
- Assumes sample size is smaller than the constant population size



Fisher-Wright individual-based (FWIB) model

- Simulate all individuals from past to present
- Strictly separated generations
- Uses a constant population size

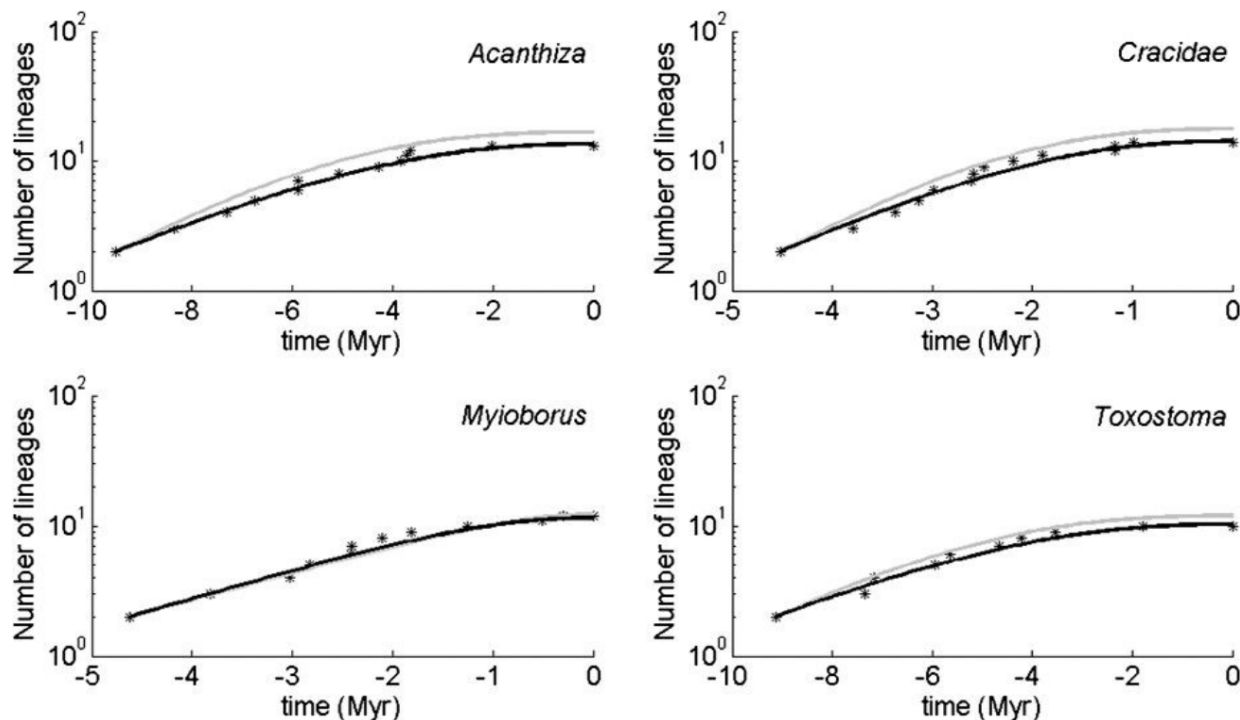


Research project #2

- CPC model is assumed to be complementary to a Fisher-Wright simulation
- Are they really?
- Setup:
 - Run FWIB model
 - Sample with CPC model
 - Should have similar results

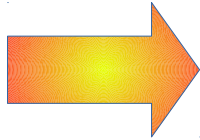
Protracted speciation

- Assumes speciation takes time
- Likelihood function derived recently (Lambert et al., 2015)

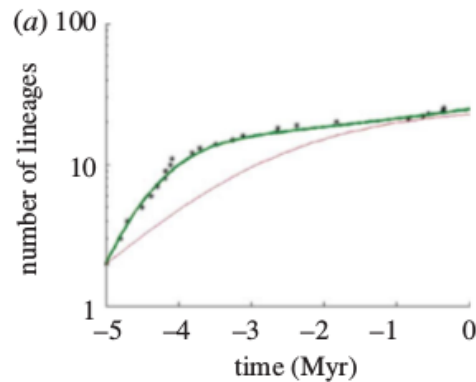


Doesn't this data look similar?

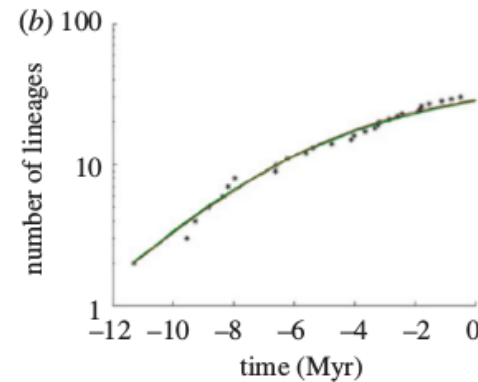
Density
dependent
speciation



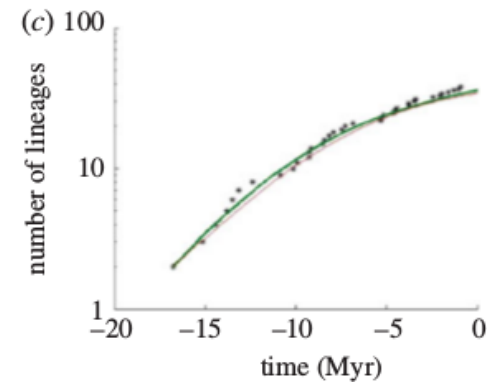
Dendroica



Plethodon

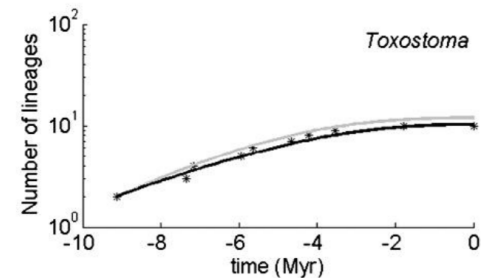
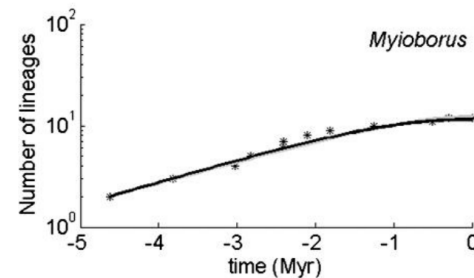
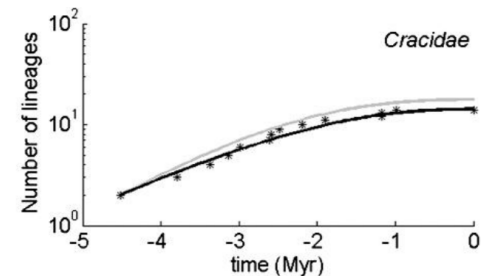
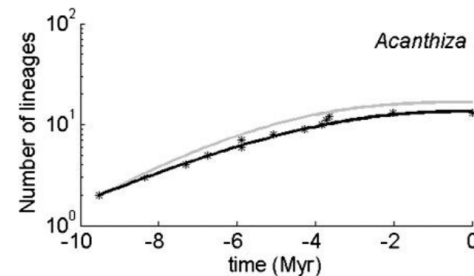
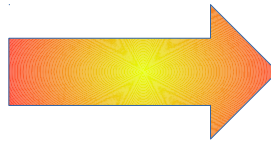


Heliconius



Etienne et al., 2012

Protracted
speciation



Etienne & Rosindell, 2012

Research project #3

- How well do the models fit on the other's data?
- Or: what is the contrast between the two models?
- Setup: compare likelihoods, similar to project of César

Age-specific speciation

- Assumes that speciation decreases with lineage age
- Novel model, similar to the protracted speciation model
- Yield more realistic phylogenies than protracted speciation model [1]
- No likelihood function derived yet (César side project?)

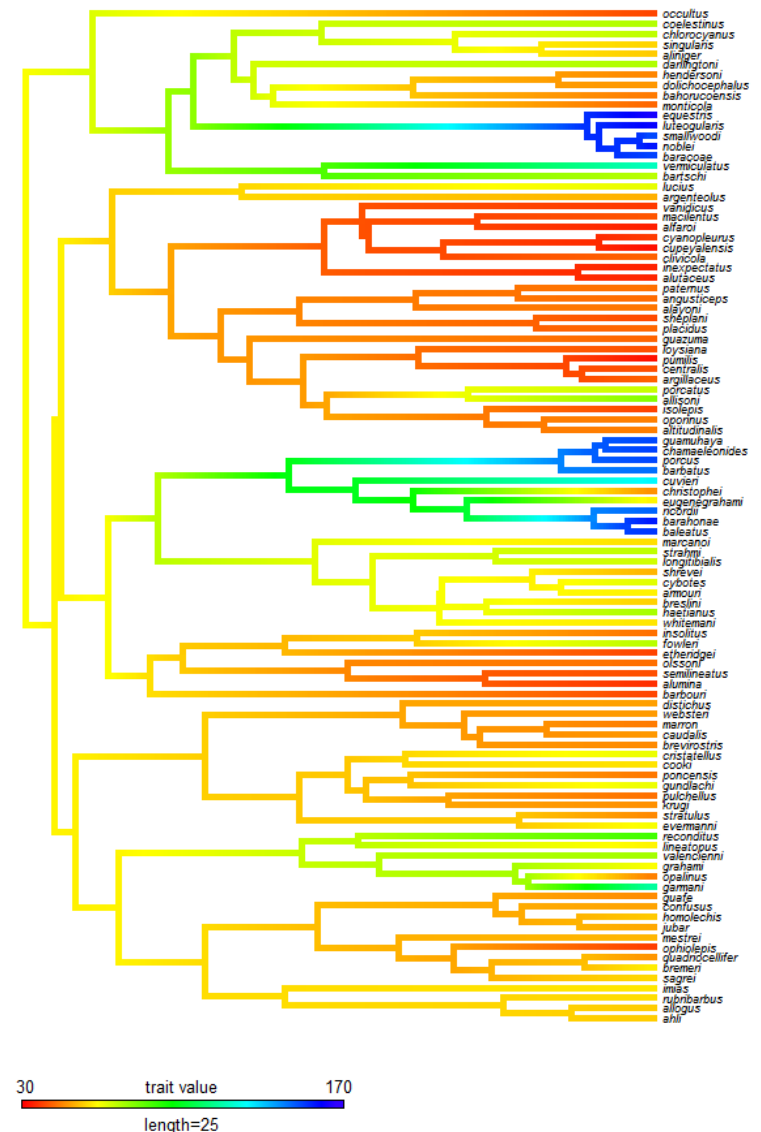
Research project #4

- What is the fit of the age-dependent speciation model to the data?
- Setup:
 - Create phylogenies with both models
 - How well do they fit to the data?

Fluctuations of species traits in time

Fluctuations of neutral traits in time

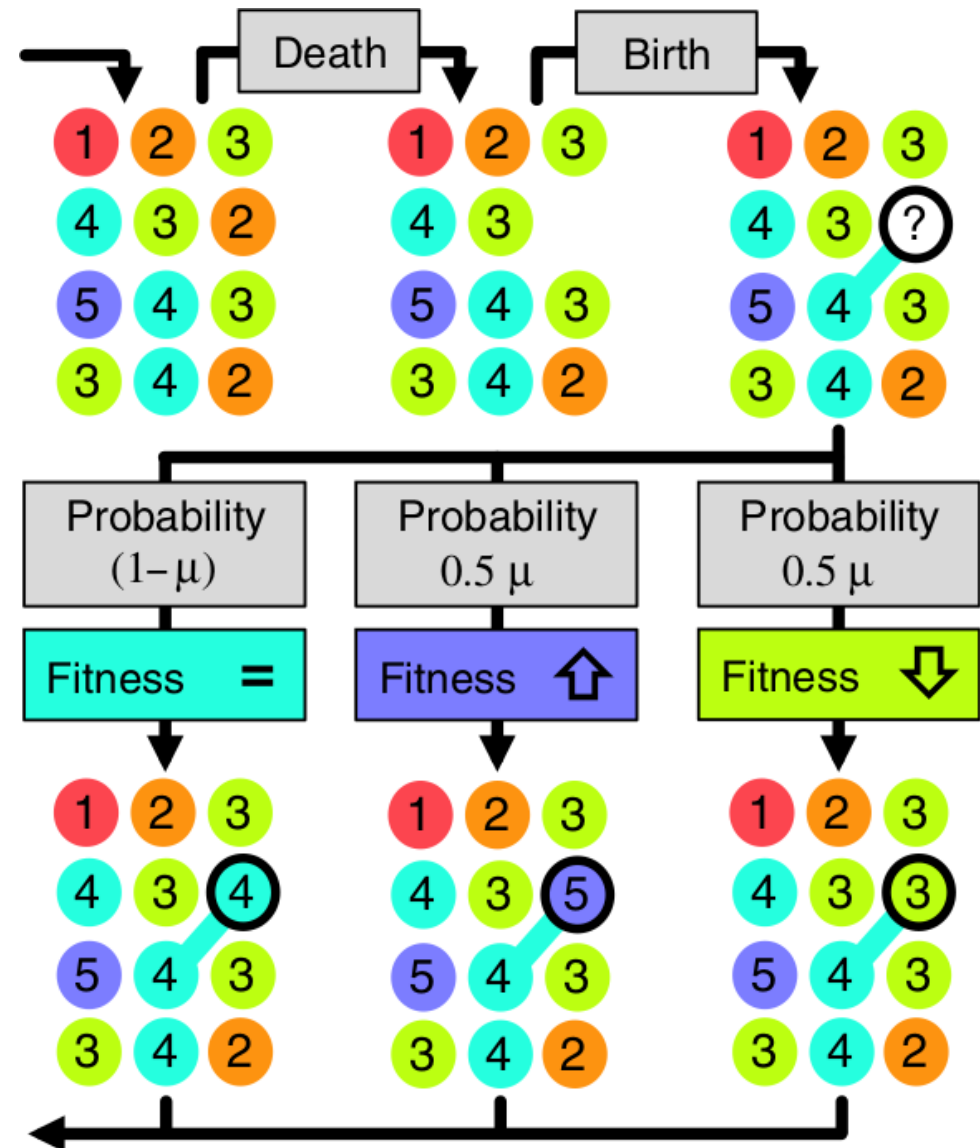
- Traits may be neutral for selection
- This can be detected by measuring the trait value in time
- Is the trait following a Brownian motion? Than it is assumed neutral
- But do neutral traits follow this motion?



Body size in Greater Antillean anoles,
from DiversiTree dataset

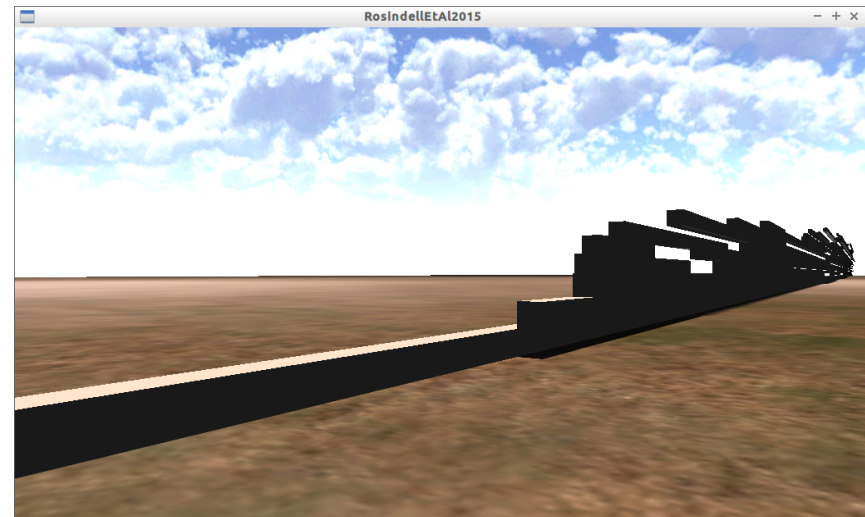
UTEM model

- Individual-based model that adds mild selection to lineages
- Moran model
- Spatially implicit
- Follows the protracted speciation model
- Yields realistic phylogenies



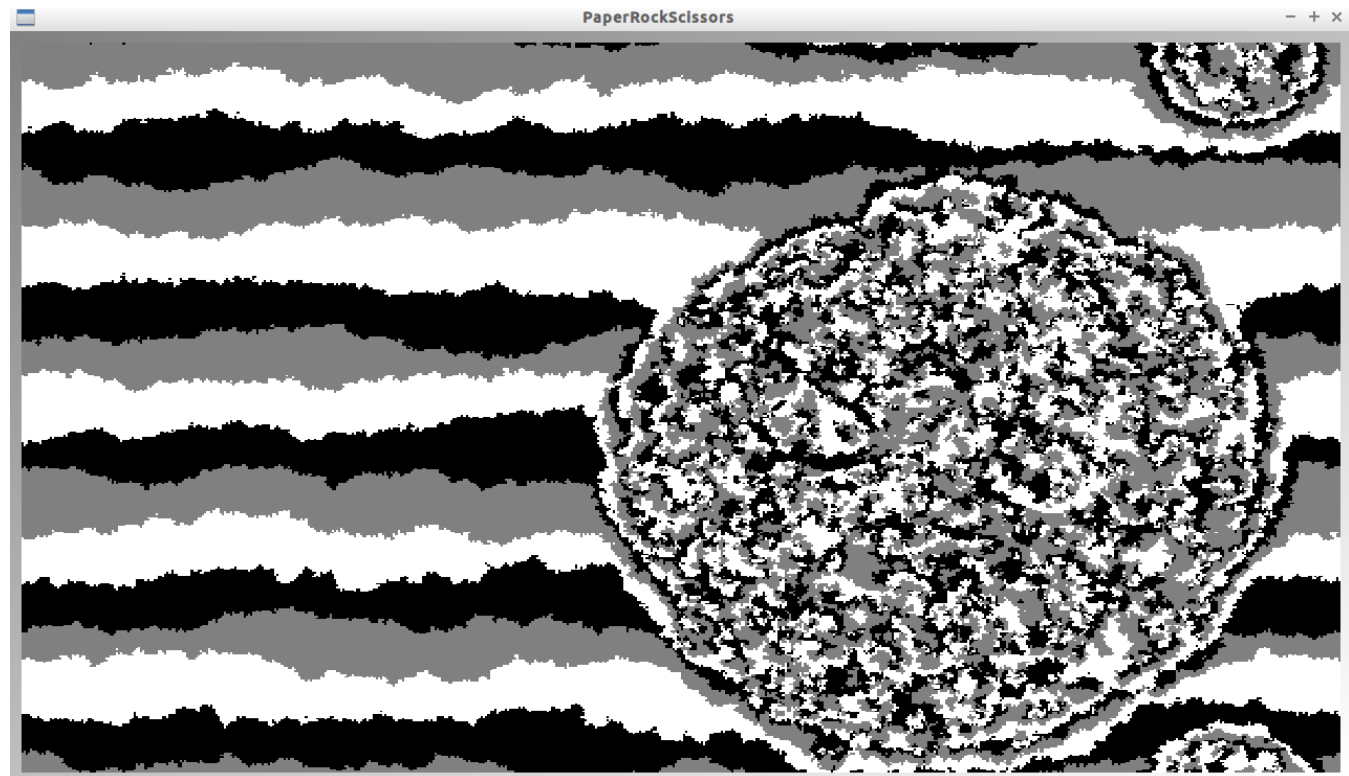
Research project #5

- Hunch: adding a neutral trait to the current behavior might yield something else than a Brownian motion (Rosindell & Harmon, personal communication)
- Possibly also true in simpler simulations!
- Setup: add neutral trait to model, follow it in time, test its motion being Brownian or other



Research project #6

- Hunch: will speciation models still produce realistic phylogenies in a spatial model?
- Setup: take an IBM, add spatiality, check the phylogenies produced



Conclusion

- Cohesive project
 - Approach from multiple angles
 - Overlap between techniques used in different projects

Thanks!

Questions?

References

- Nee, Sean. "Inferring speciation rates from phylogenies." *Evolution* 55.4 (2001): 661-668.
- Nee, Sean, Robert M. May, and Paul H. Harvey. "The reconstructed evolutionary process." *Philosophical Transactions of the Royal Society B: Biological Sciences* 344.1309 (1994): 305-311.
- Yule, G. Udny. "A mathematical theory of evolution, based on the conclusions of Dr. JC Willis, FRS." *Philosophical Transactions of the Royal Society of London. Series B, Containing Papers of a Biological Character* (1925): 21-87.