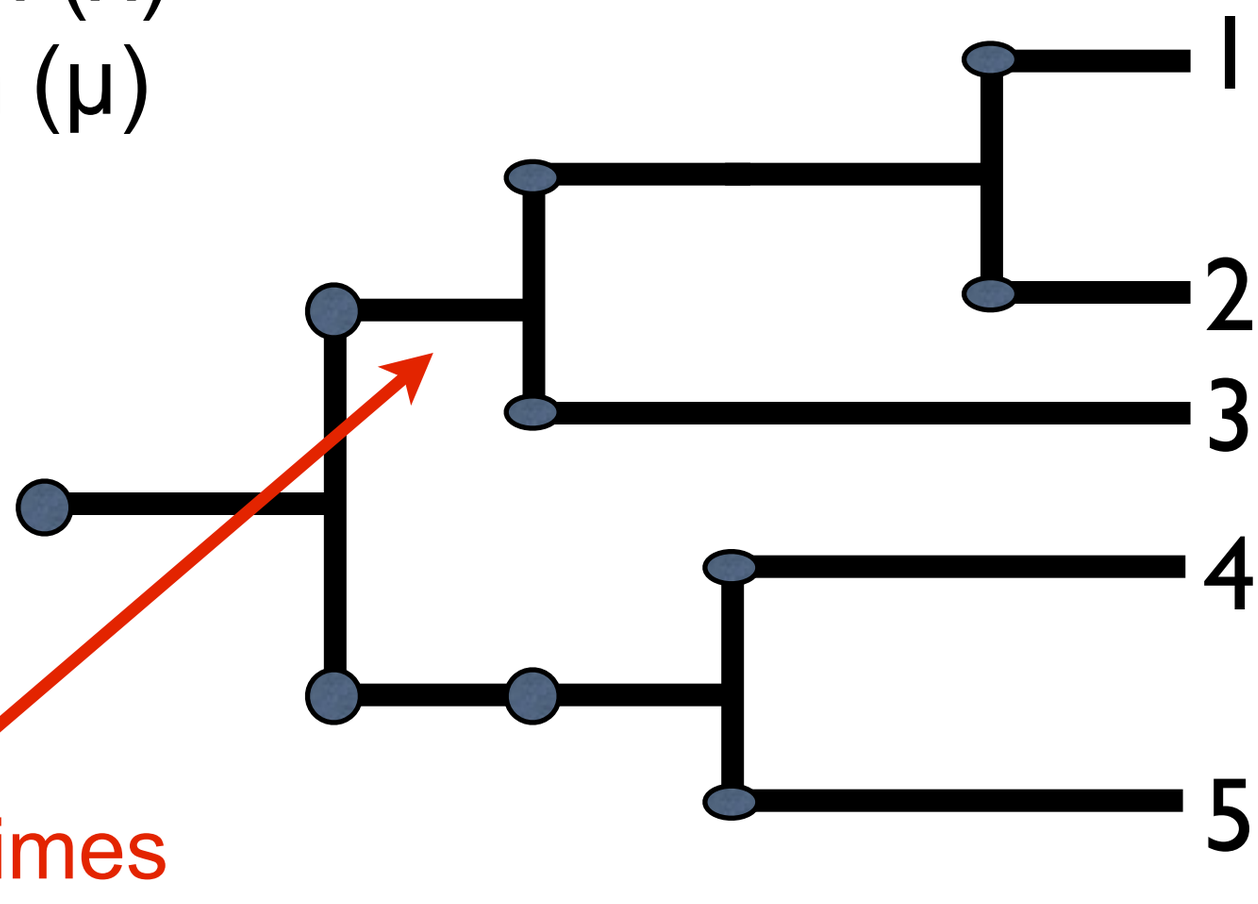
an improvement: the birth-death model

- Assumptions:
  - Speciation and extinction occur randomly
  - Each lineage has an equal and constant rate of speciation, *b*, and extinction, *d*

Nee S., May R.M., Harvey P.H. 1994. The reconstructed evolutionary process. Philos. Trans. R. Soc. Lond. B Biol. Sci. 344:305–311.

Diversification Model

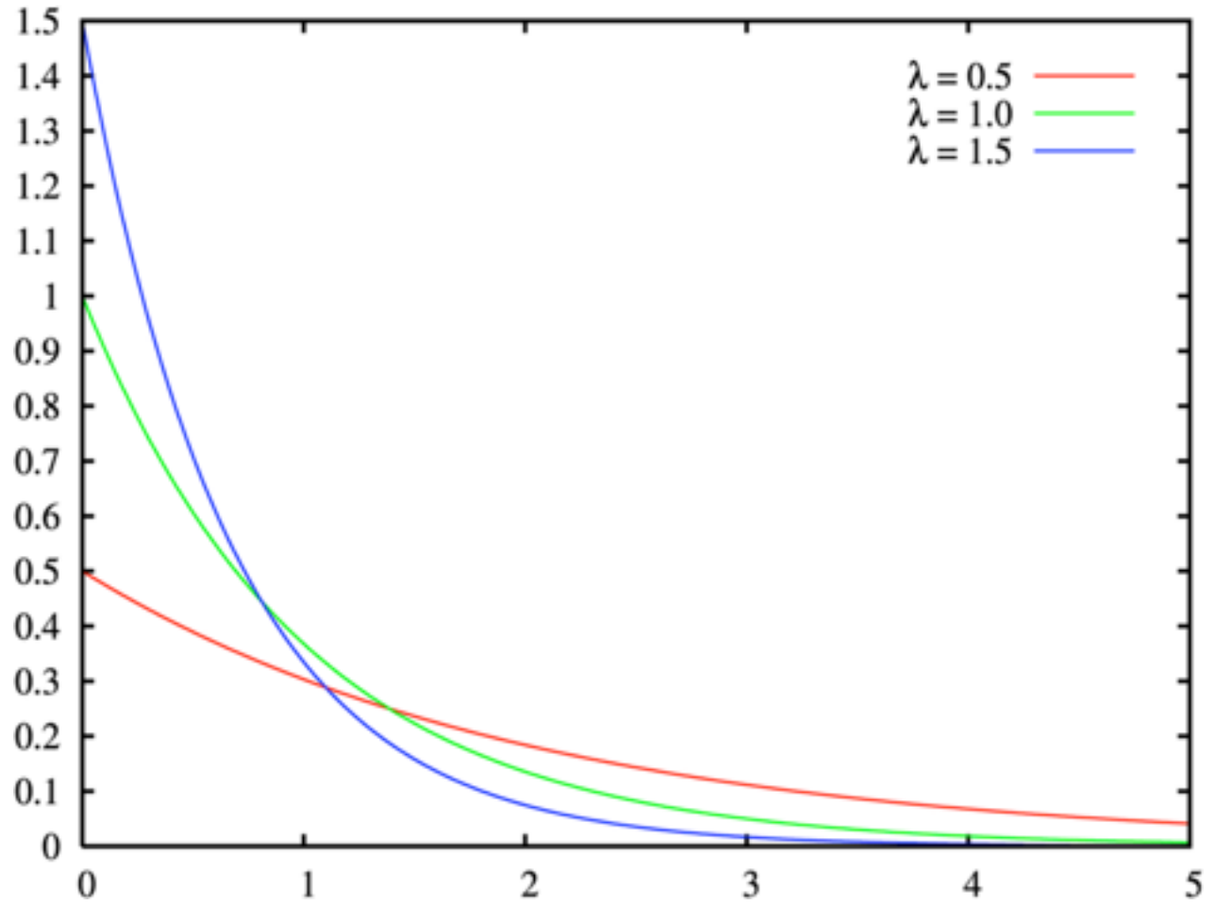
- Model: birth-death
- Every lineage has constant probability of:
  - –speciation (λ)
  - –extinction (μ)



Nee S., May R.M., Harvey P.H. 1994. The reconstructed evolutionary process. Philos. Trans. R. Soc. Lond. B Biol. Sci. 344:305–311.

Waiting times

- Under a birth-death model, the time intervals between successive events are always drawn from exponential distributions



$$f(x;\lambda) = \begin{cases} \lambda e^{-\lambda x} & , \ x \geq 0, \\ 0 & , \ x < 0. \end{cases}$$

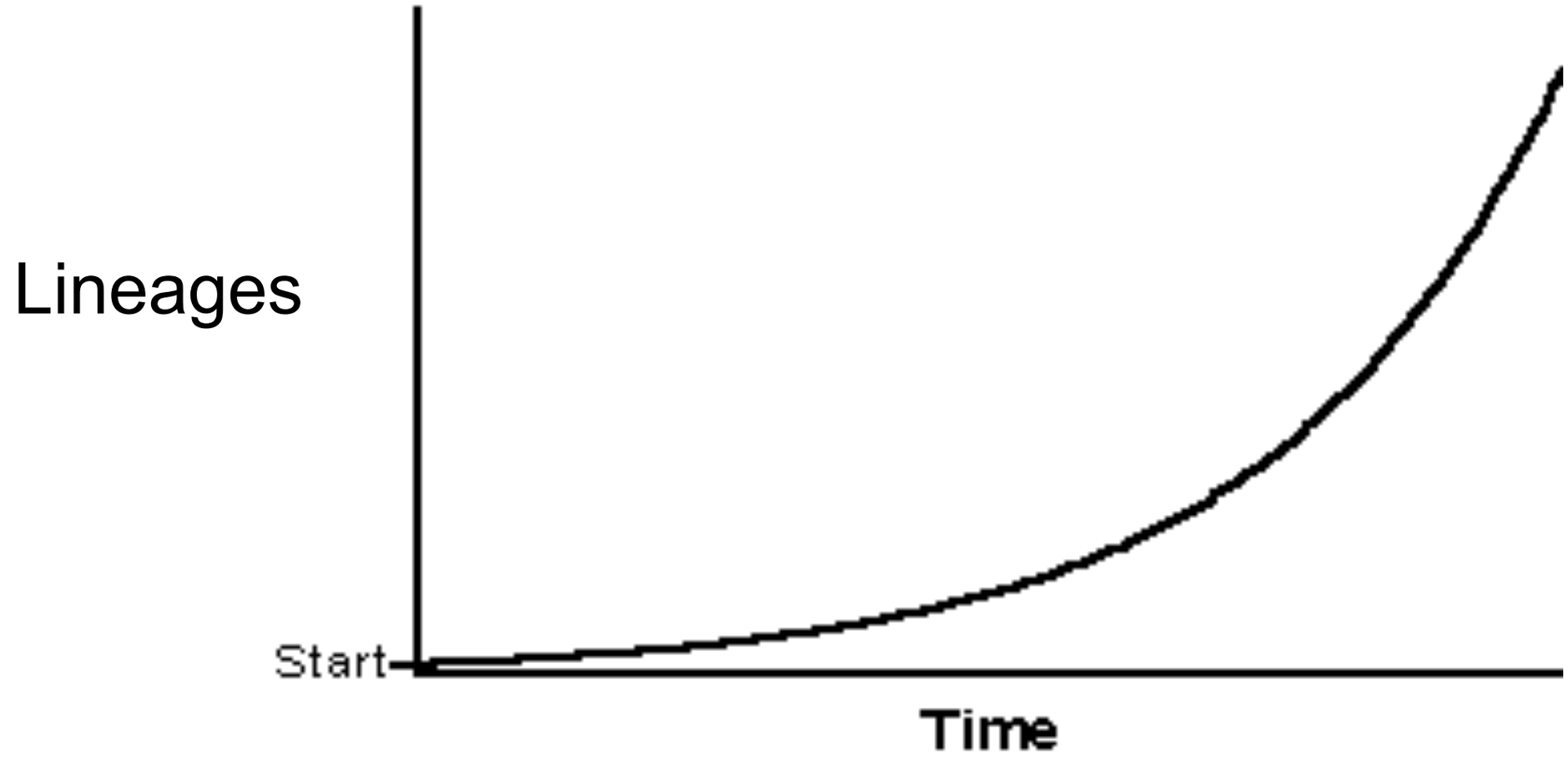
Expected species diversity under a birth-death model:

$$E[N_t] = N_o e^{(b-d)t}$$

N_t = species diversity after time t
N_o = starting species diversity
b = birth rate
d = death rate
t = time

Species Accumulation

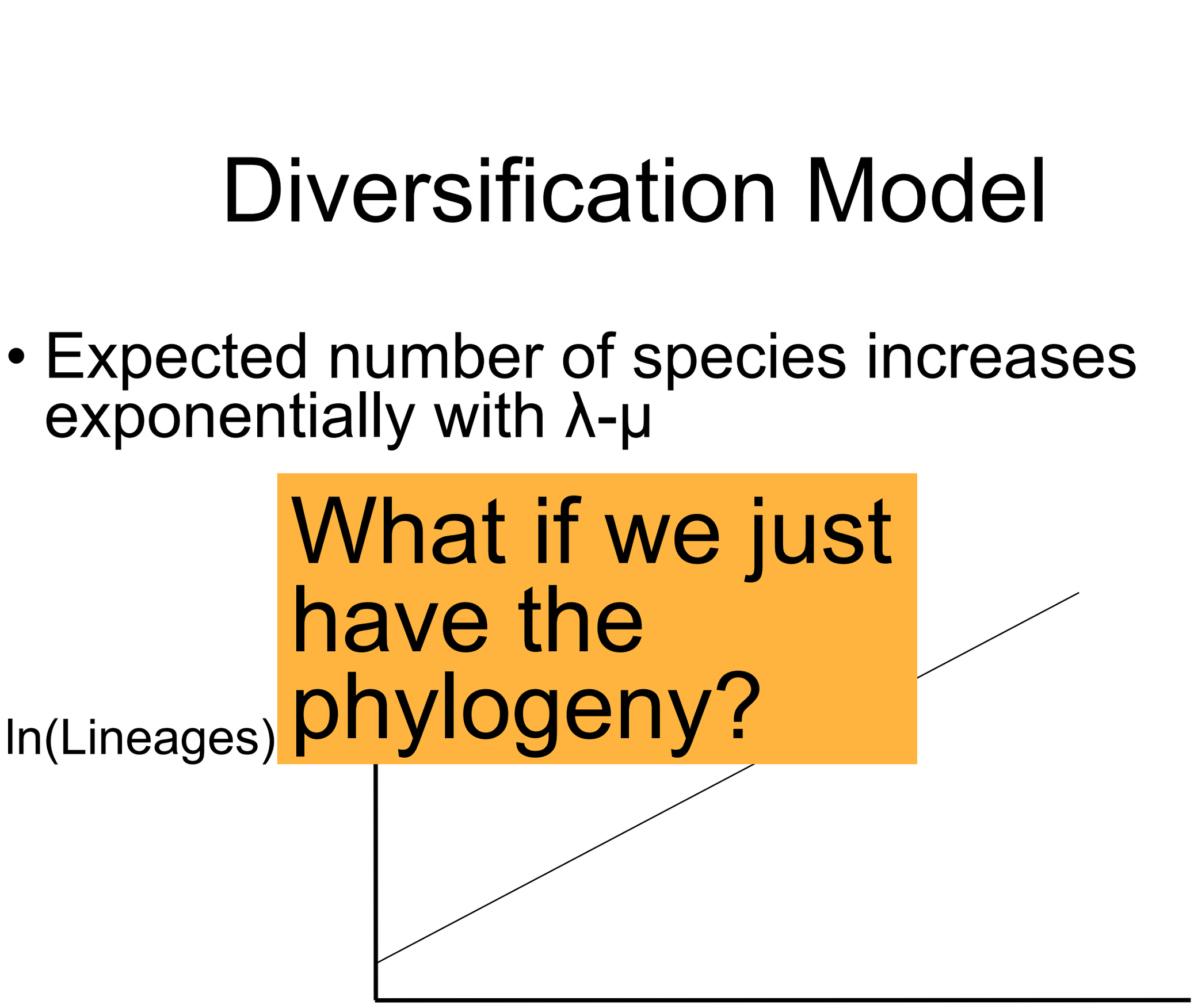
- Expected number of species increases exponentially with λ-μ



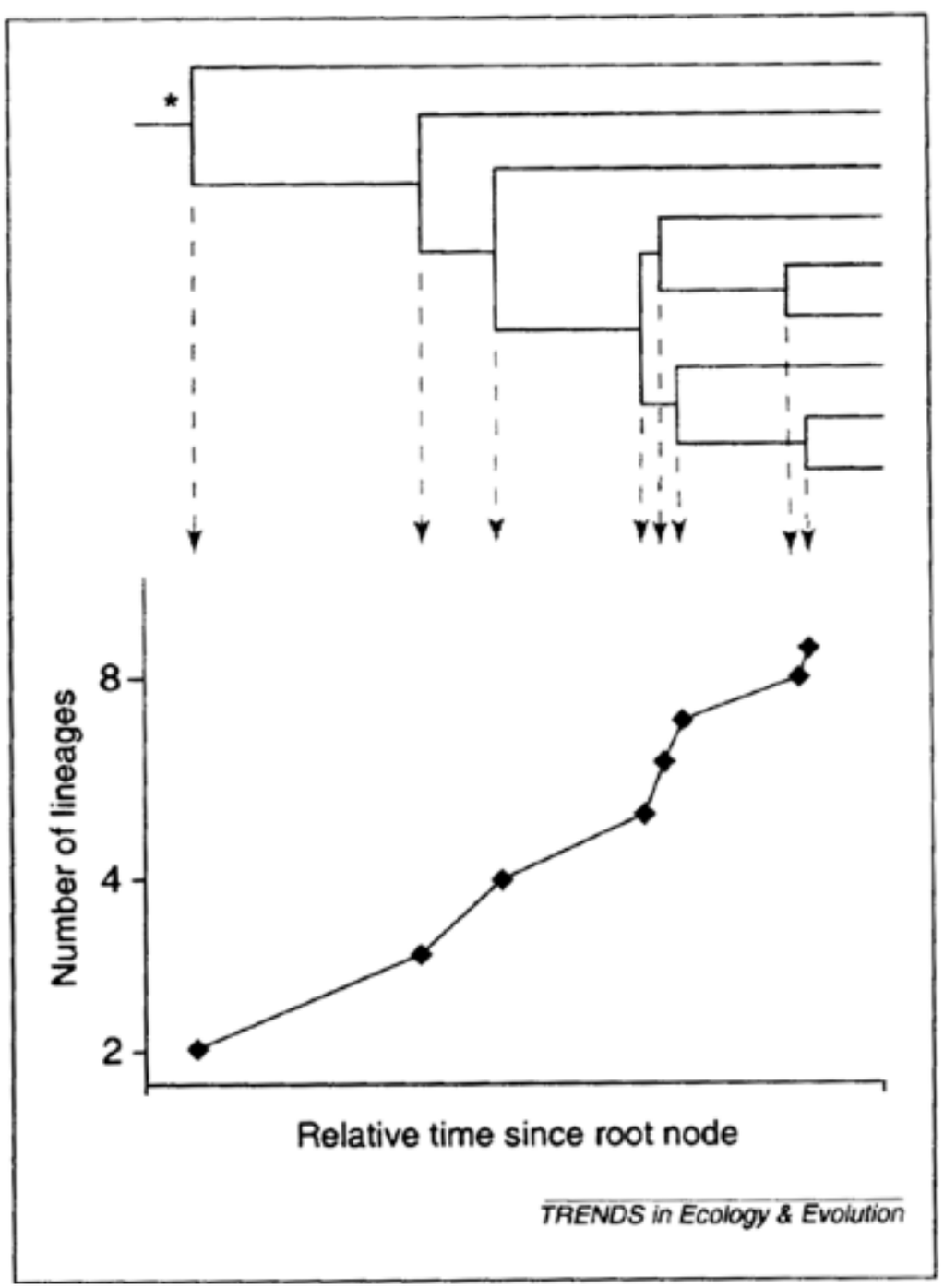
Diversification Model

- Expected number of species increases exponentially with λ-μ

What if we just have the phylogeny?

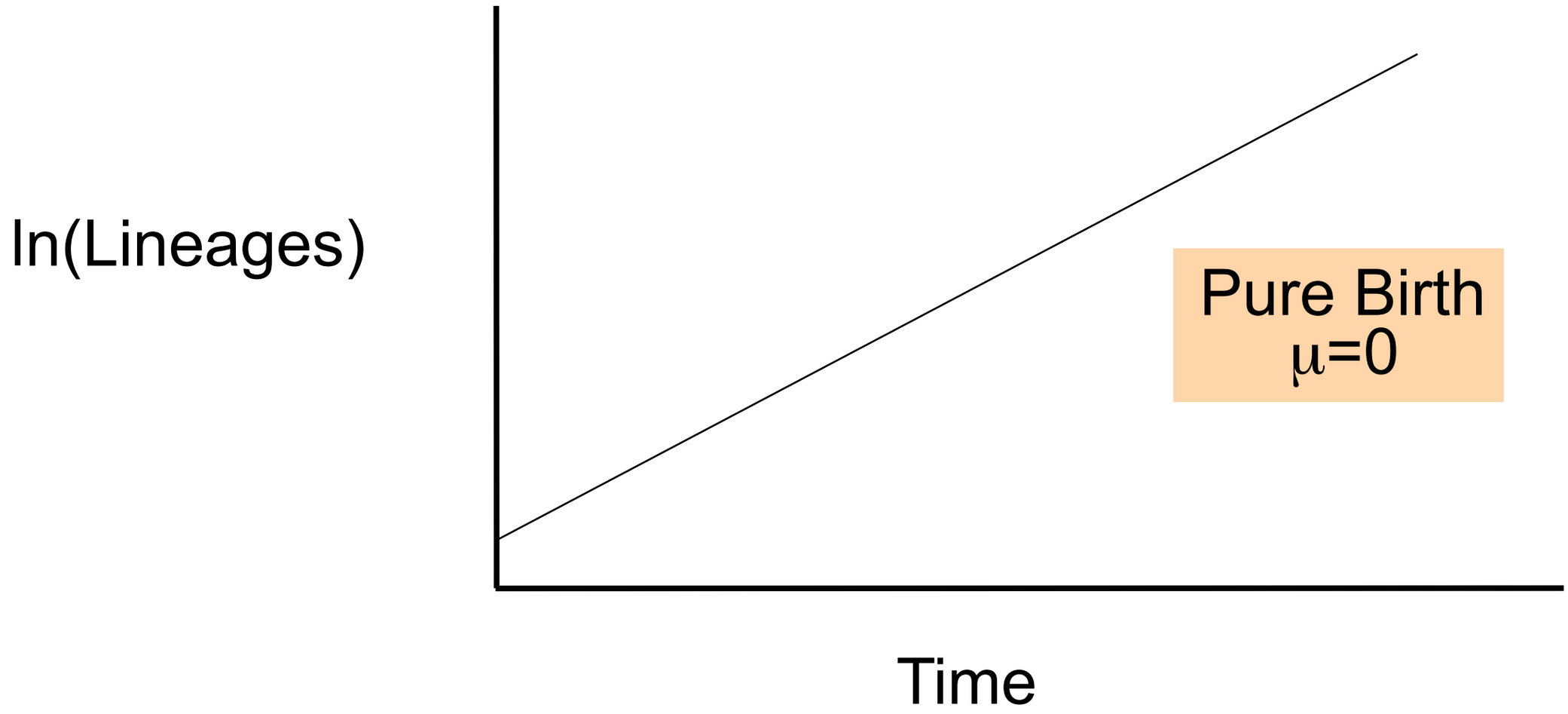


Lineage-through-time



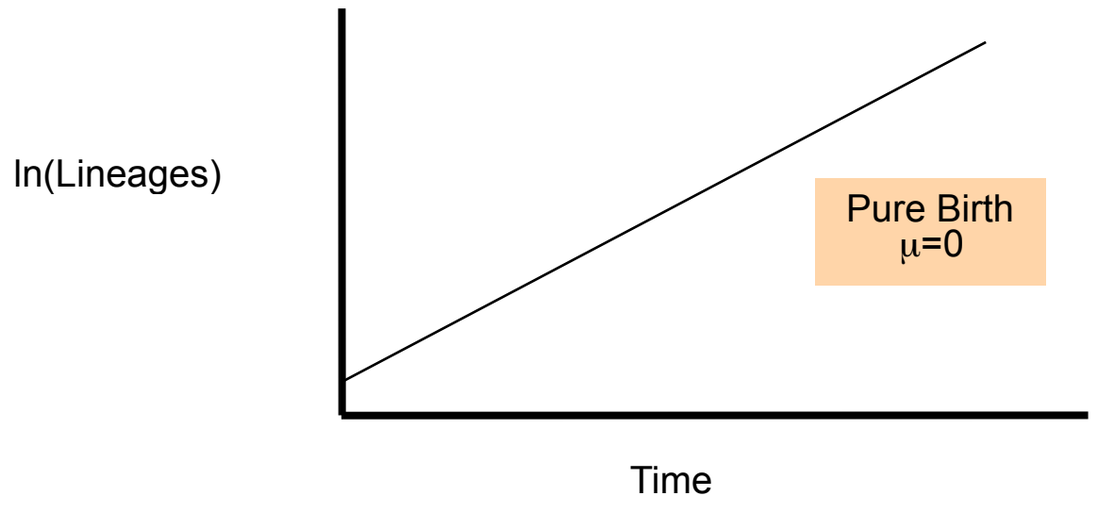
Barraclough T.G., Nee S. 2001. Phylogenetics and speciation. Trends Ecol. Evol. 16:391–399.

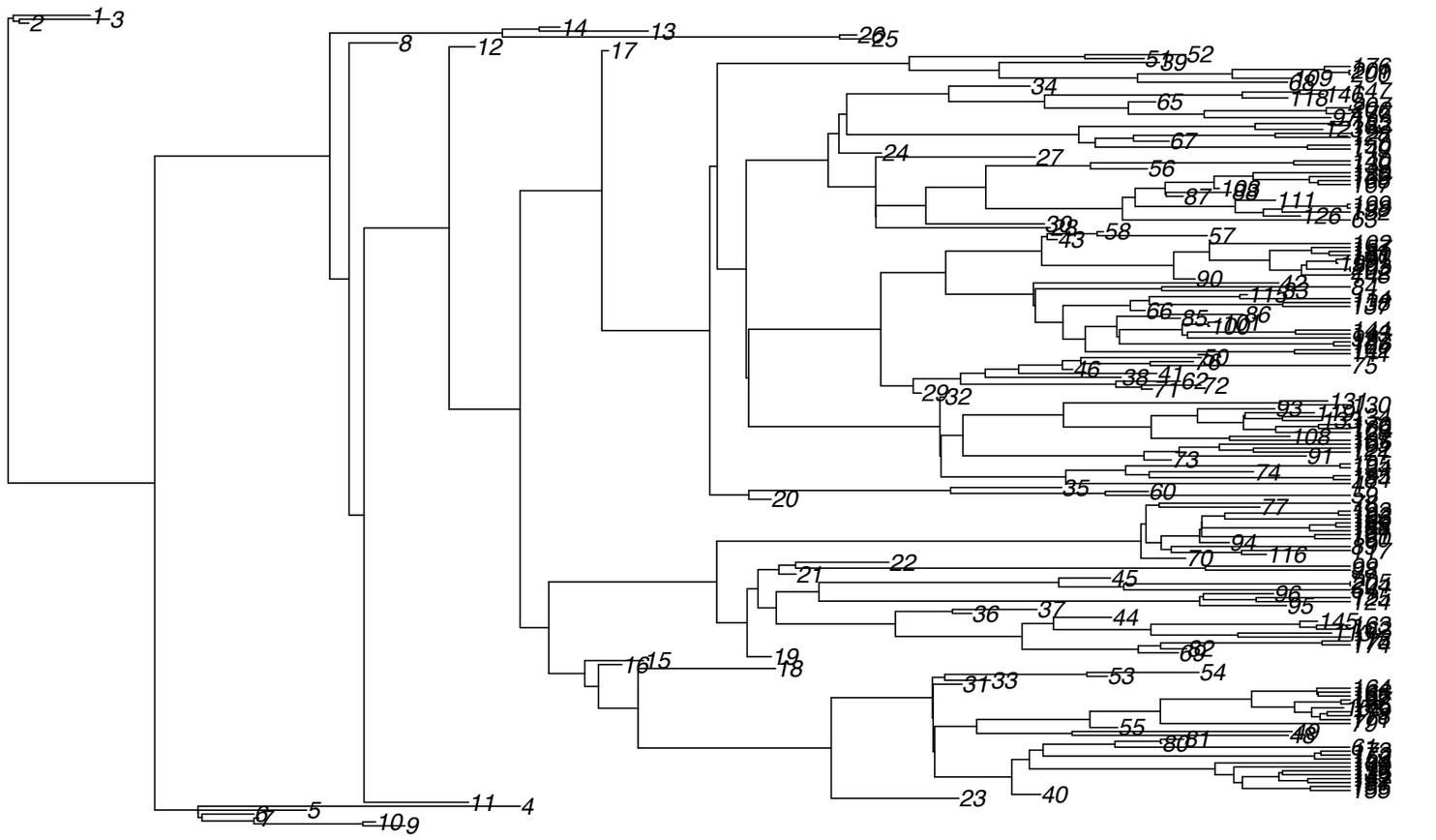
LTT Plot



Think about extinction

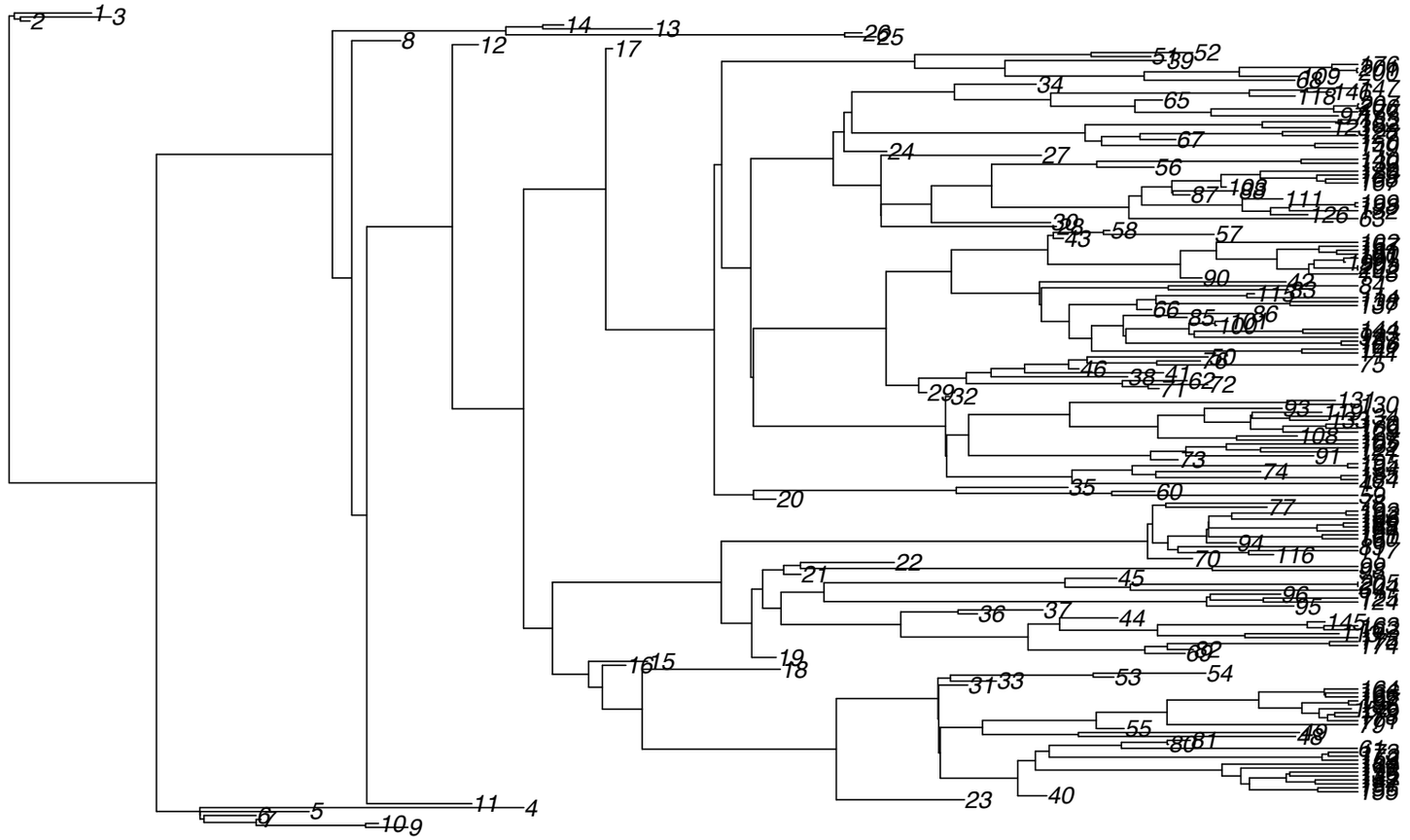
- how should extinction affect the rate of species accumulation in a phylogeny? why?
- can we infer extinction from phylogenetic data?

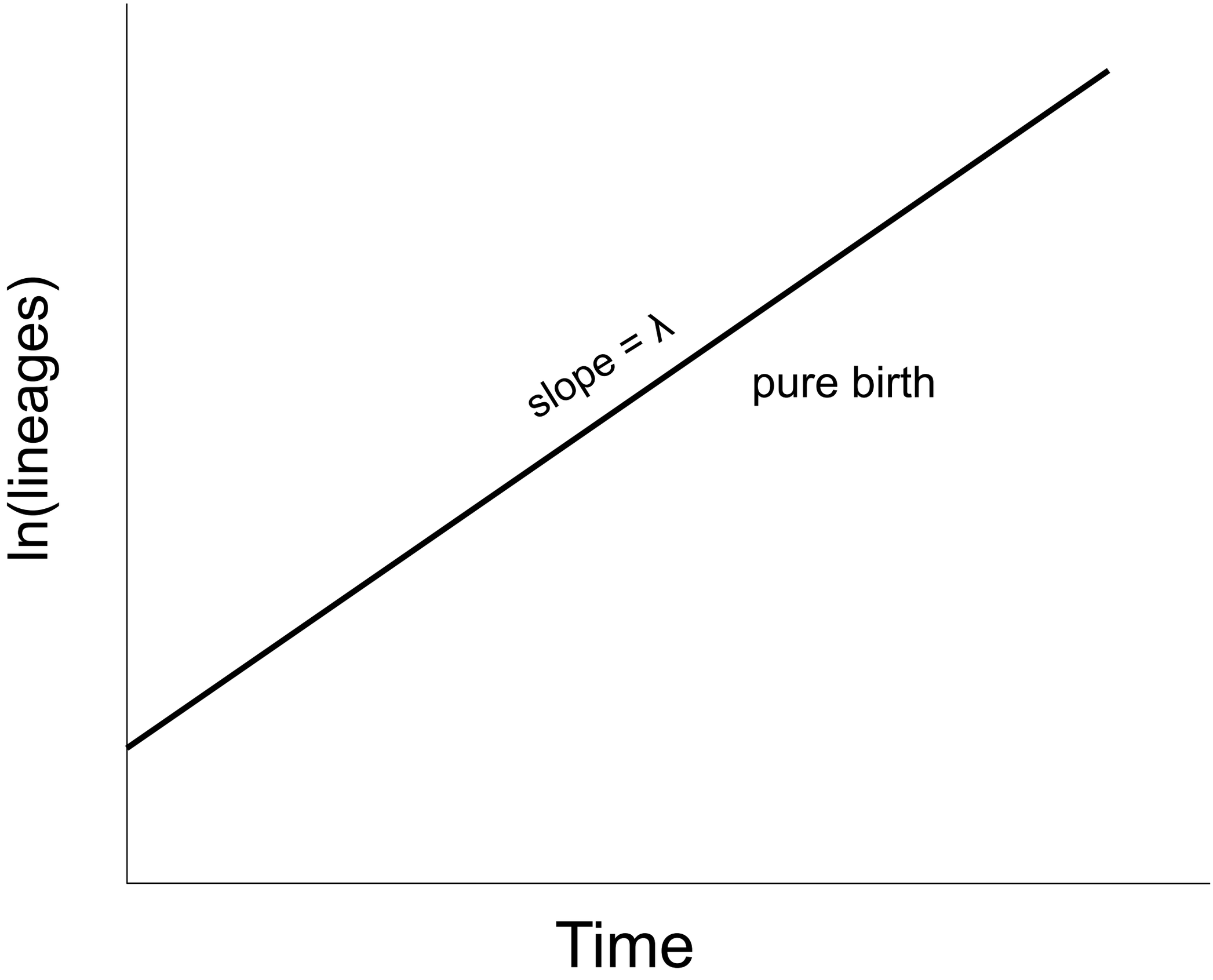


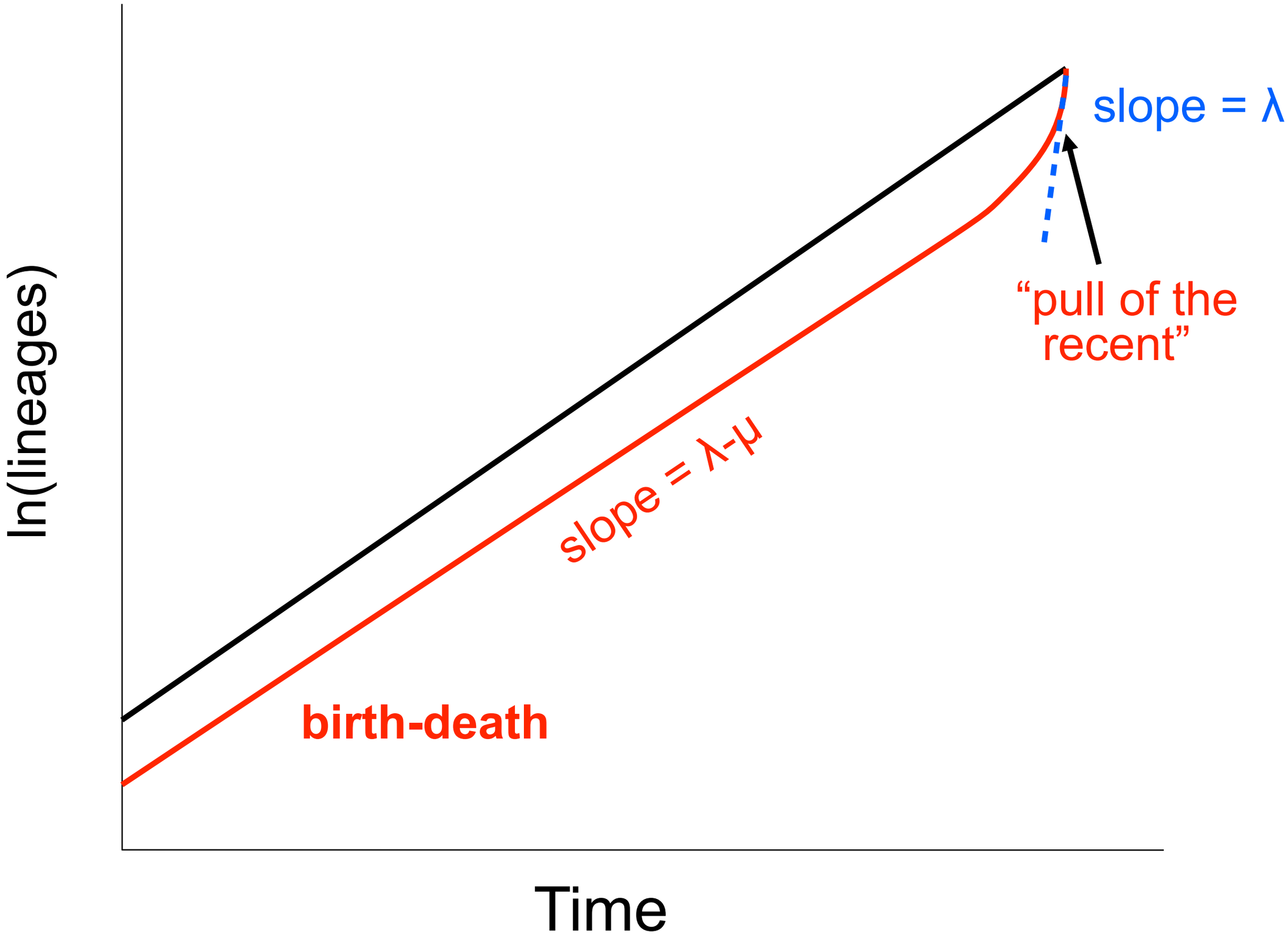


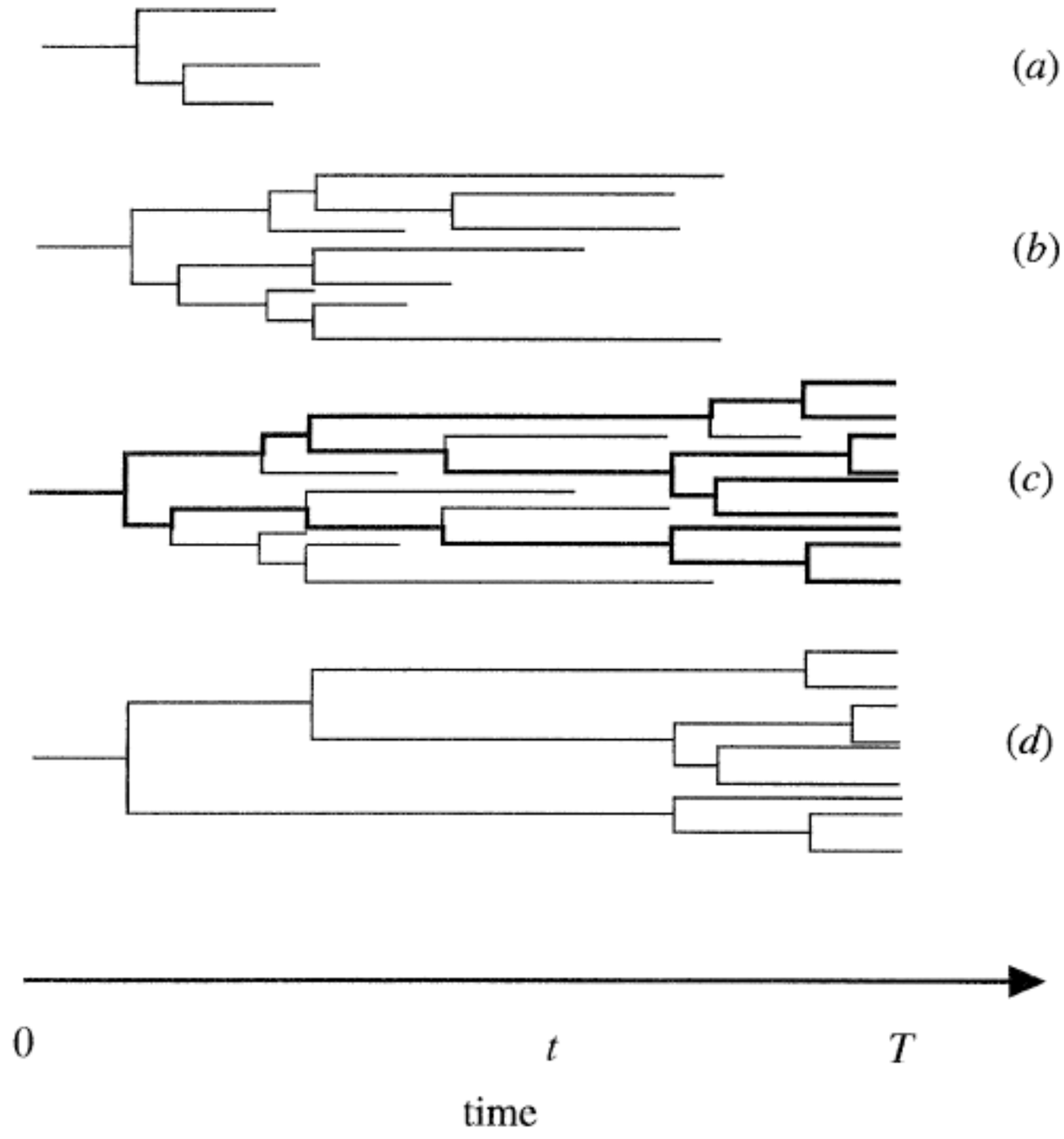
Extinction

- Can leave an imprint on present-day phylogenies
- Older lineages are more likely to have gone extinct than younger ones



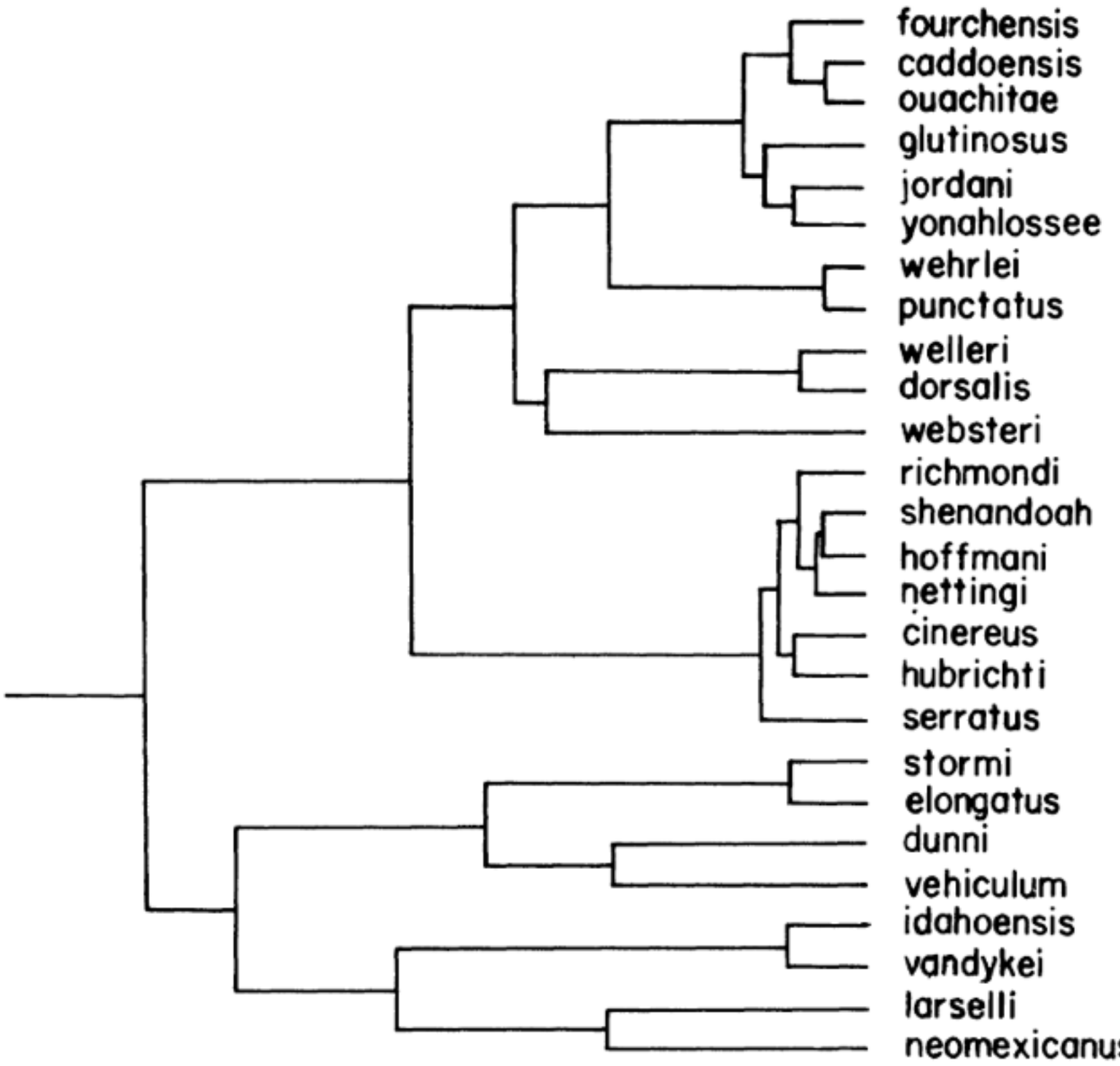

ln(lineages)
slope = λ
pure birth
Time


ln(lineages)
slope = λ
“pull of the recent”
slope = λ-μ
birth-death
Time



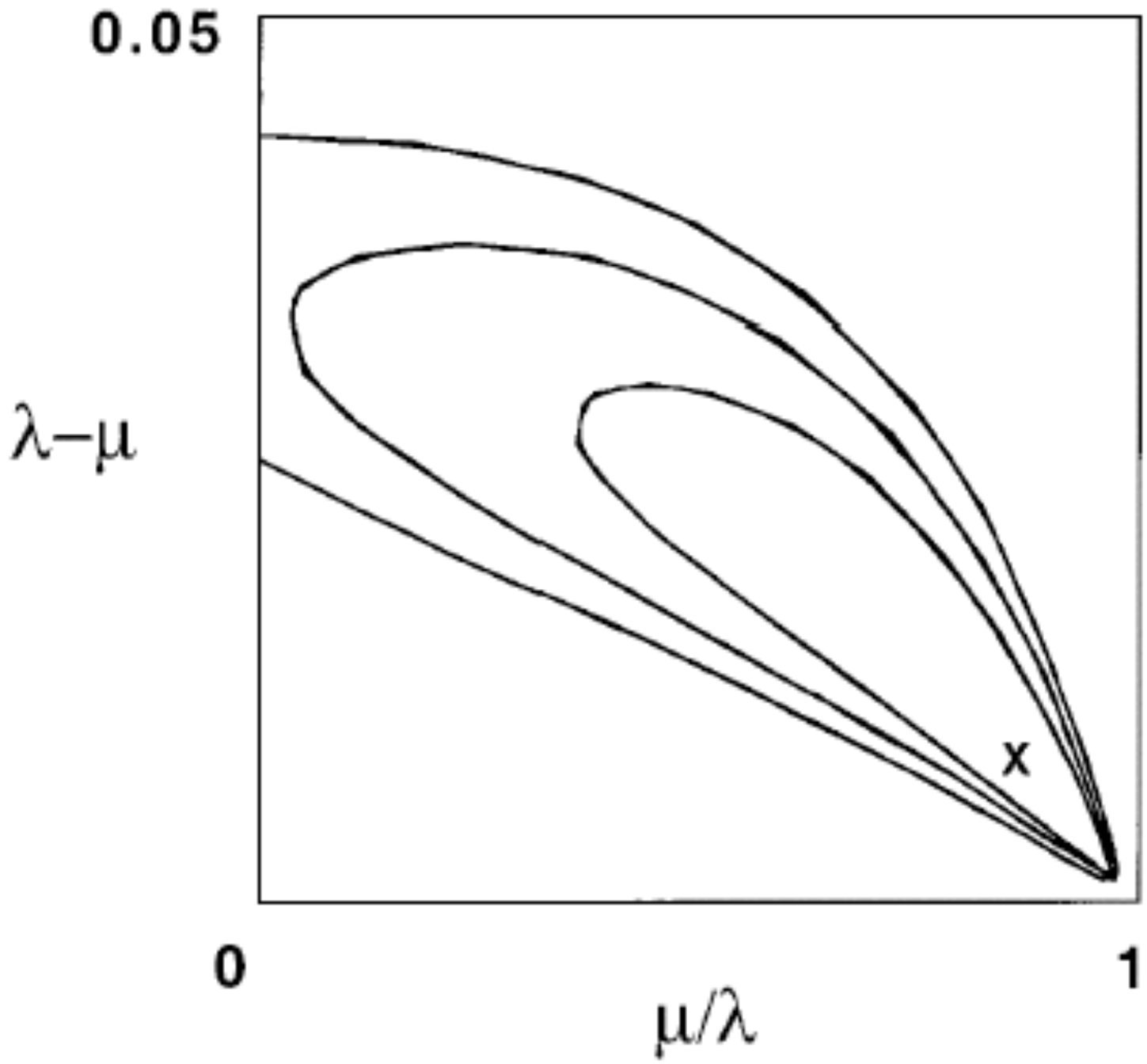
Nee S., May R.M., Harvey P.H. 1994. The reconstructed evolutionary process. Philos. Trans. R. Soc. Lond. B Biol. Sci. 344:305–311.

Plethodontid salamanders



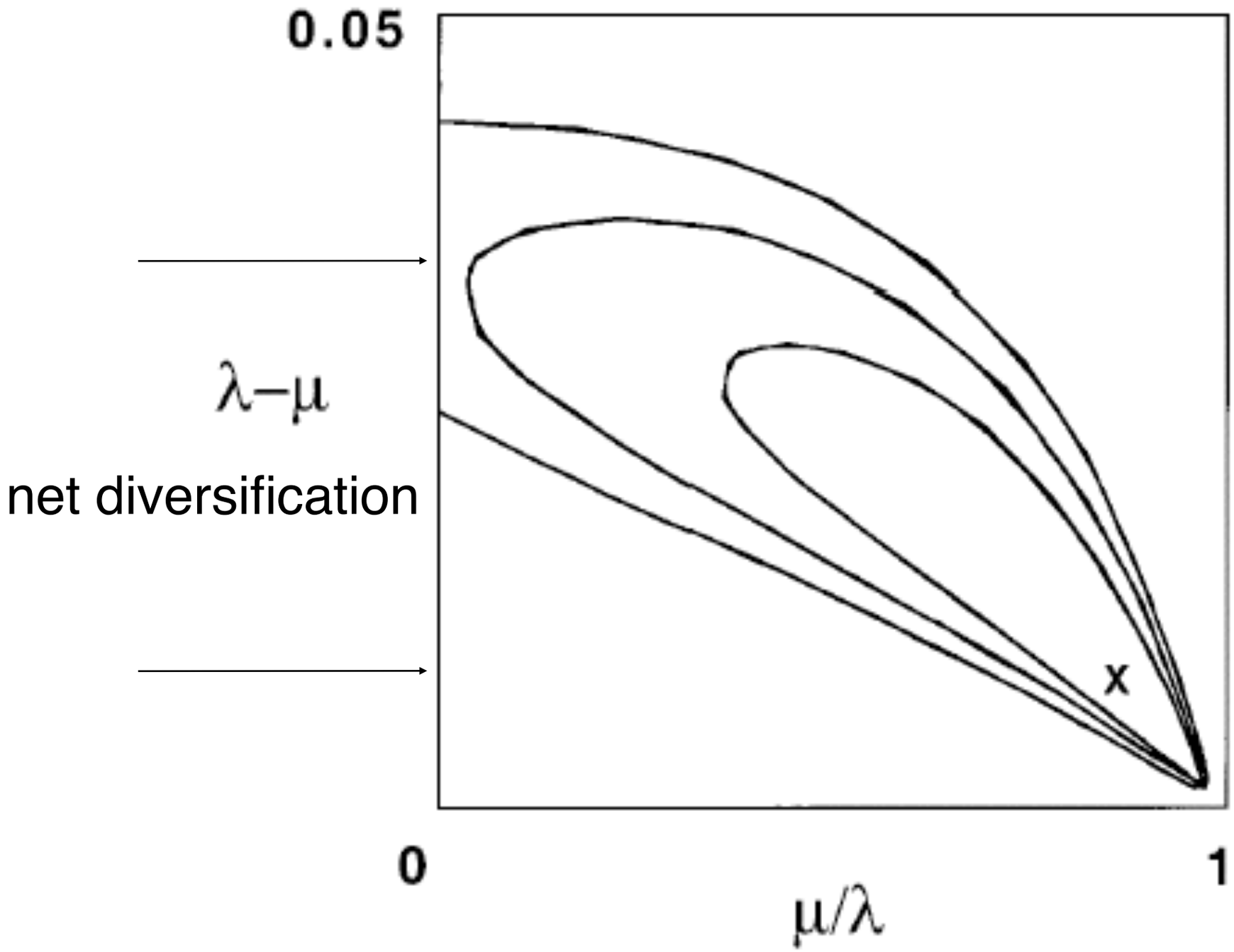
(Highton and Larson 1979)

Plethodontid salamanders



Nee S. 2001. Inferring speciation rates from phylogenies. Evolution. 55:661–668.

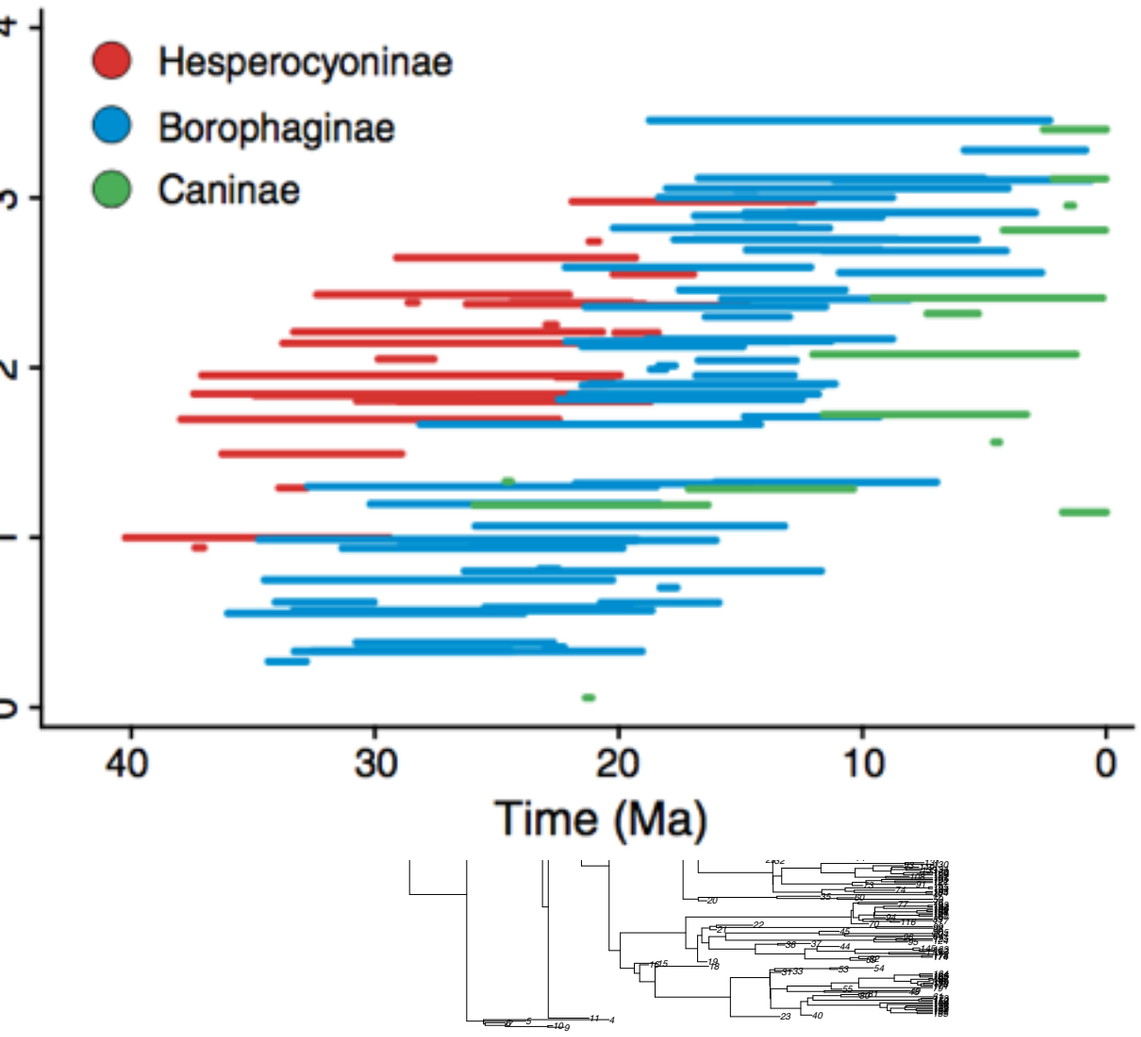
Plethodontid salamanders

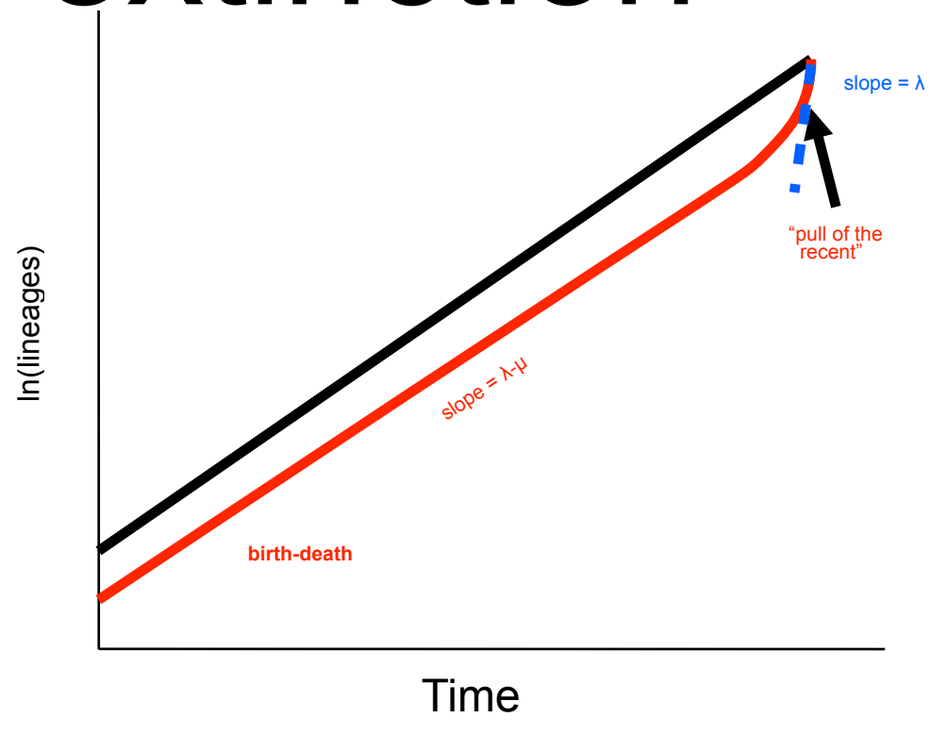


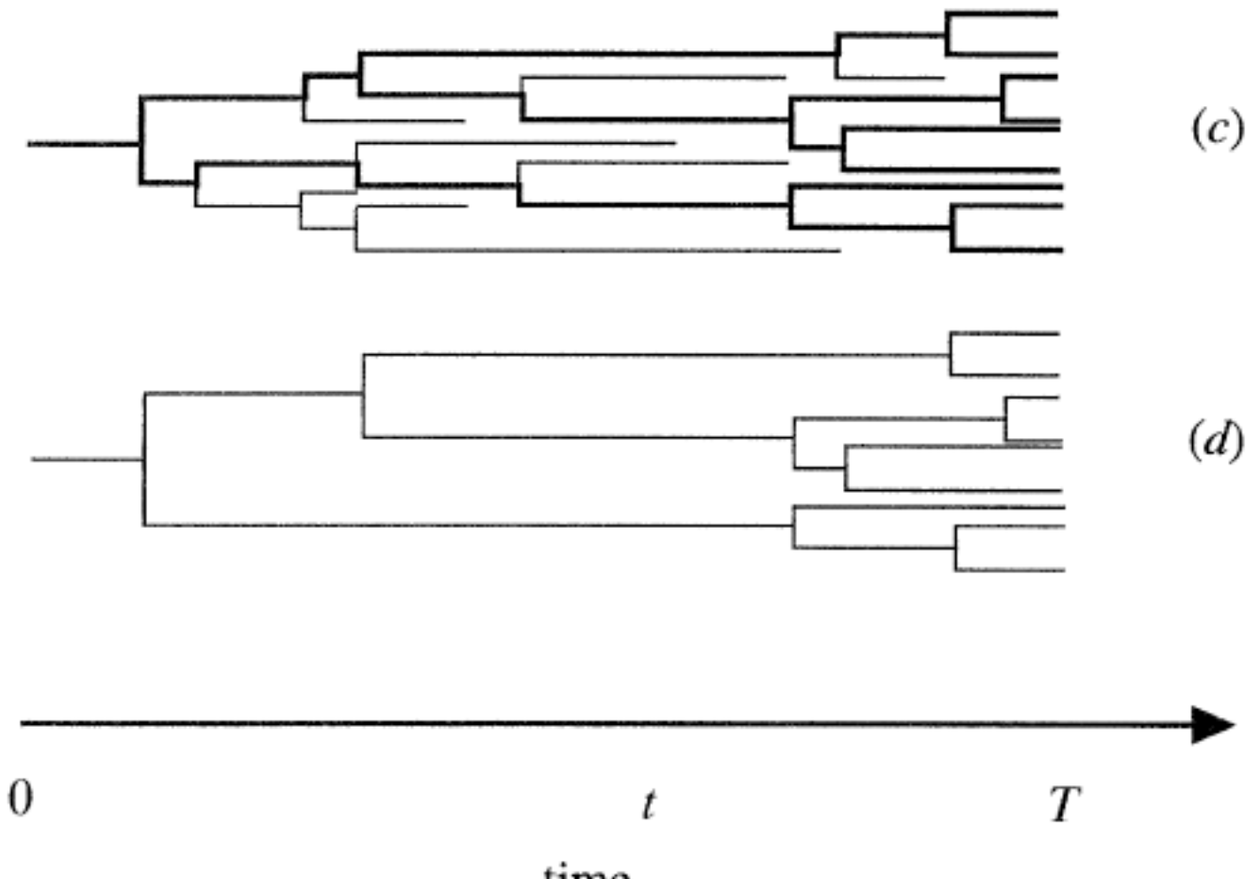
Nee S. 2001. Inferring speciation rates from phylogenies. Evolution. 55:661–668.

We can use ML or Bayesian methods to analyze data, estimate parameters, and carry out model selection

fossil versus molecular signature of extinction







Silvestro D., Antonelli A., Salamin N., Quental T.B. 2015. The role of clade competition in the diversification of North American canids. Proc. Natl. Acad. Sci. U. S. A. 112:8684–8689.

Models have grown in sophistication since Nee 2001