

Diversification models

Birth-death model

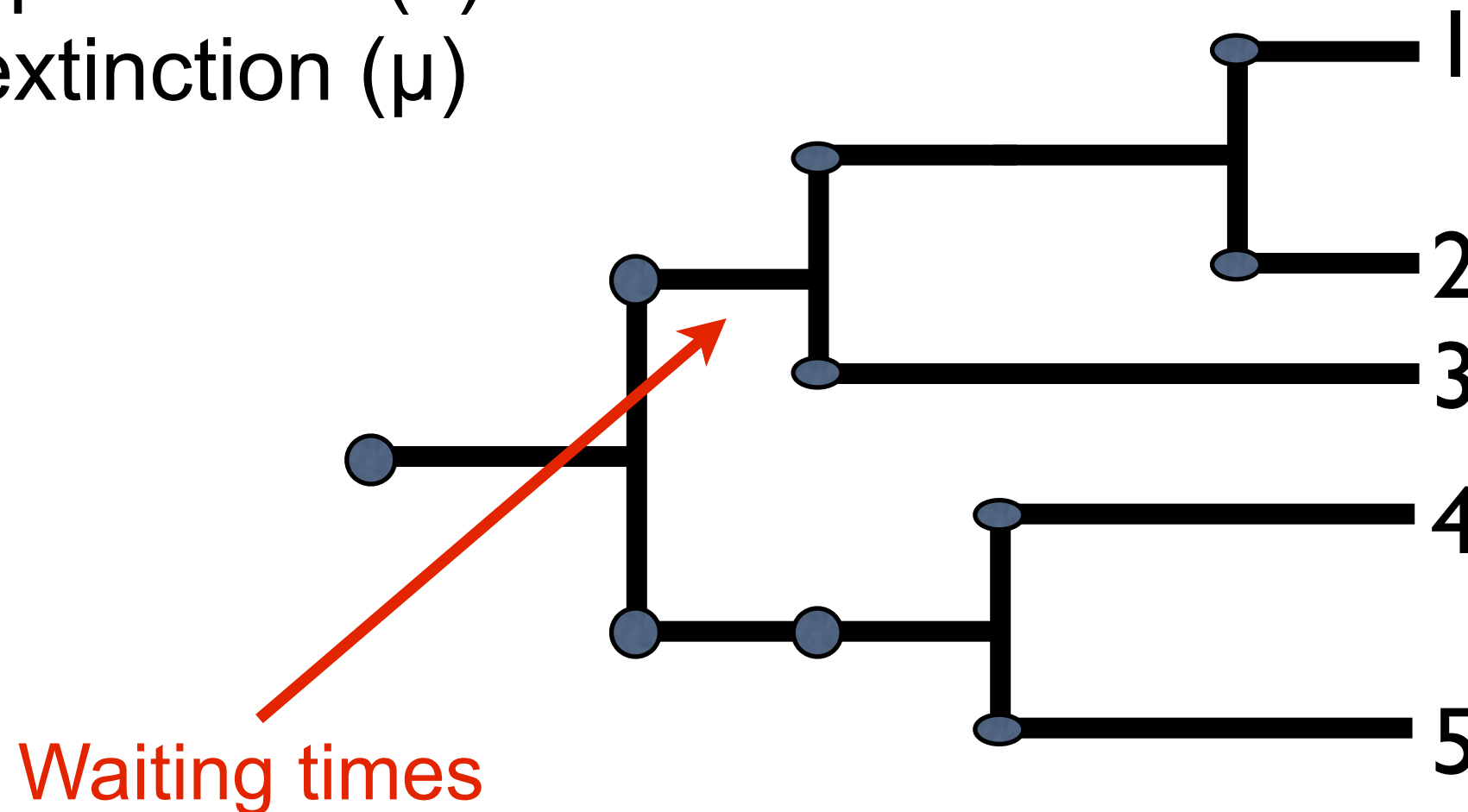
- Assumptions:
 - Speciation and extinction occur randomly
 - Each lineage has an equal and constant rate of speciation, b , and extinction, d

ERM Model

- BD is a special case of the Equal Rates Markov model (ERM)
- ERM Model assumptions
 - Markov model: next step depends only on current state
 - Equal rates: b and d are constant across lineages at any given time
 - b and/or d might change through time

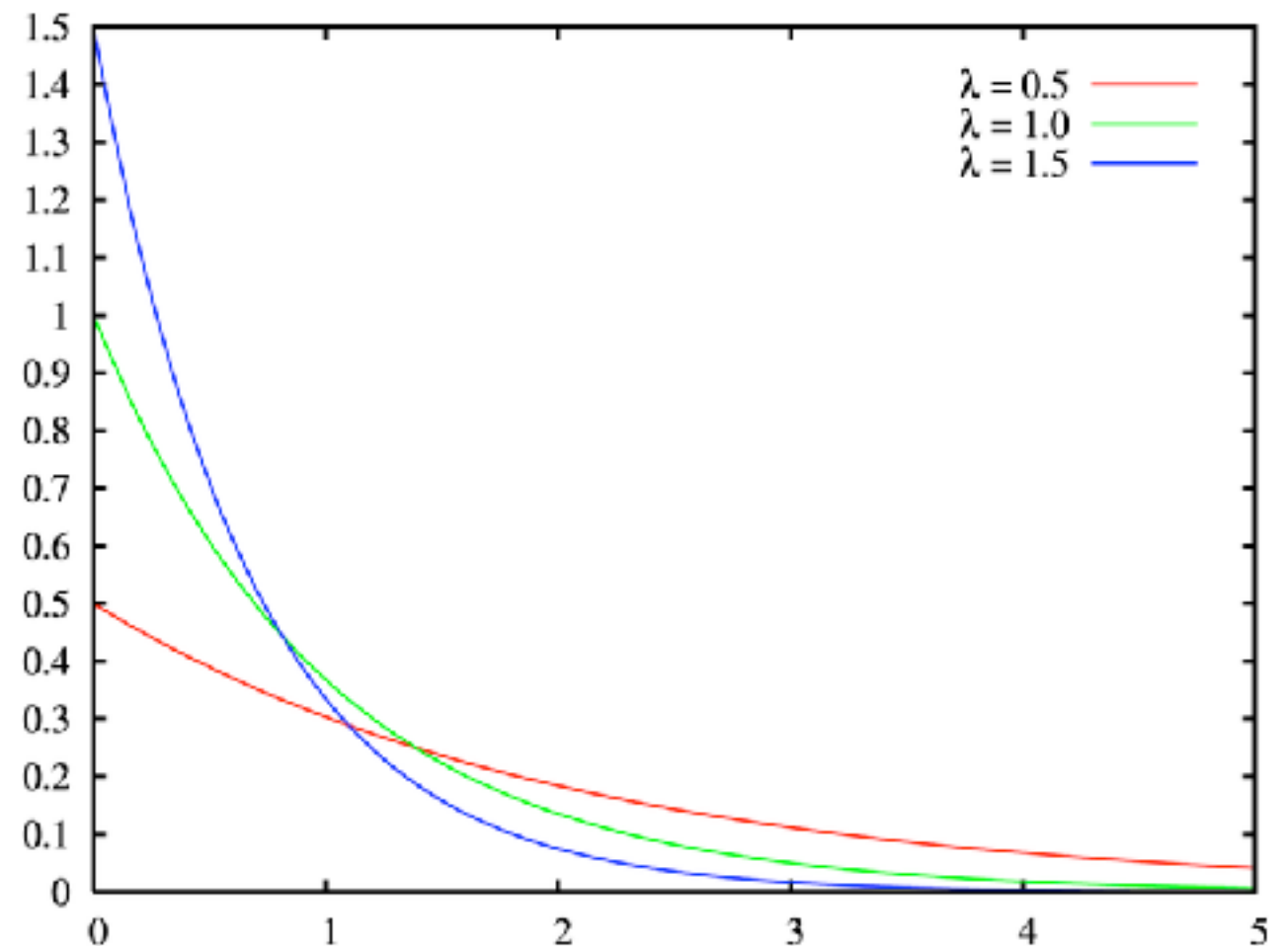
Diversification Model

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



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

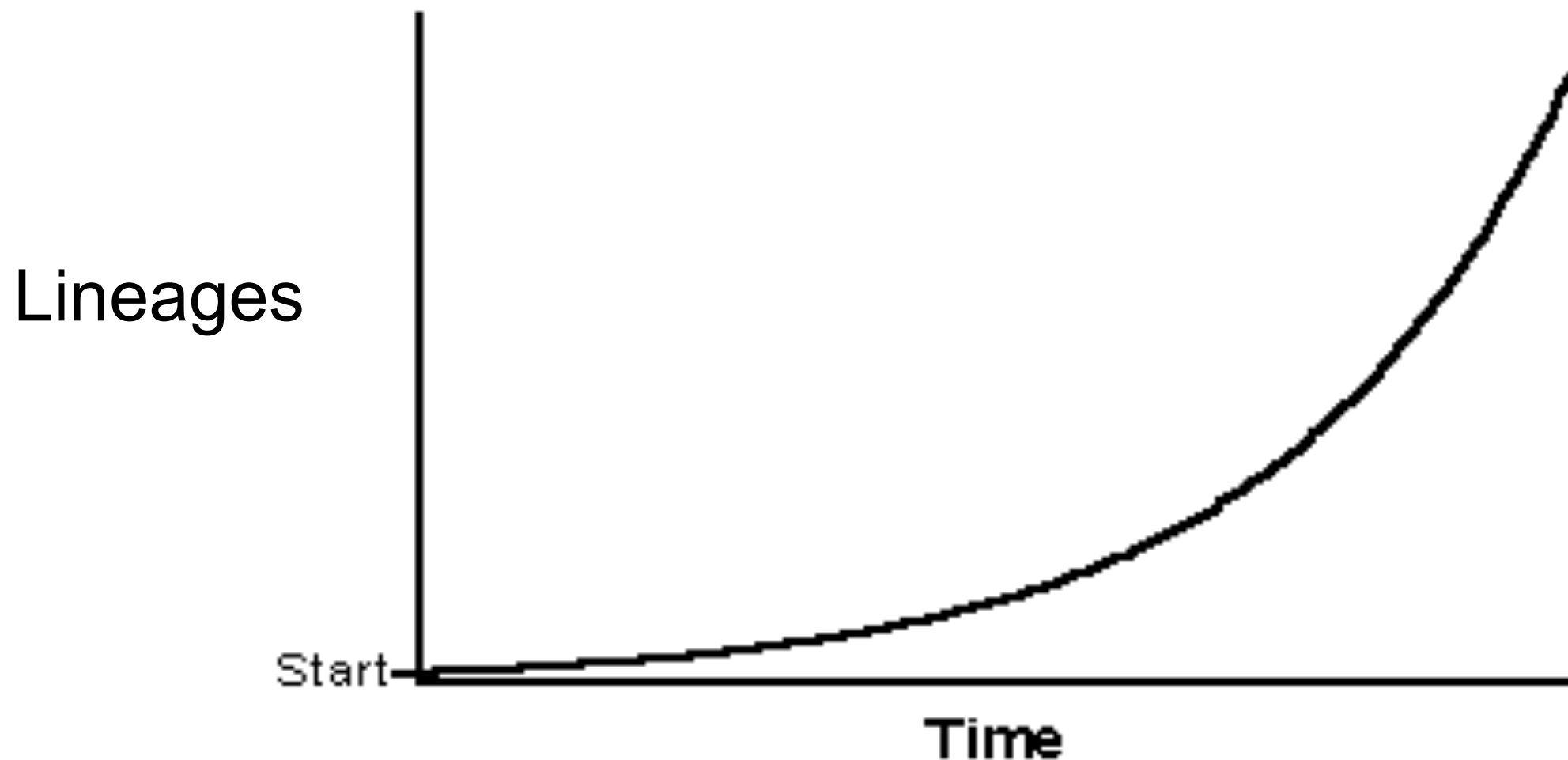
b = birth rate

d = death rate

t = time

Species Accumulation

- Expected number of species increases exponentially with $\lambda - \mu$



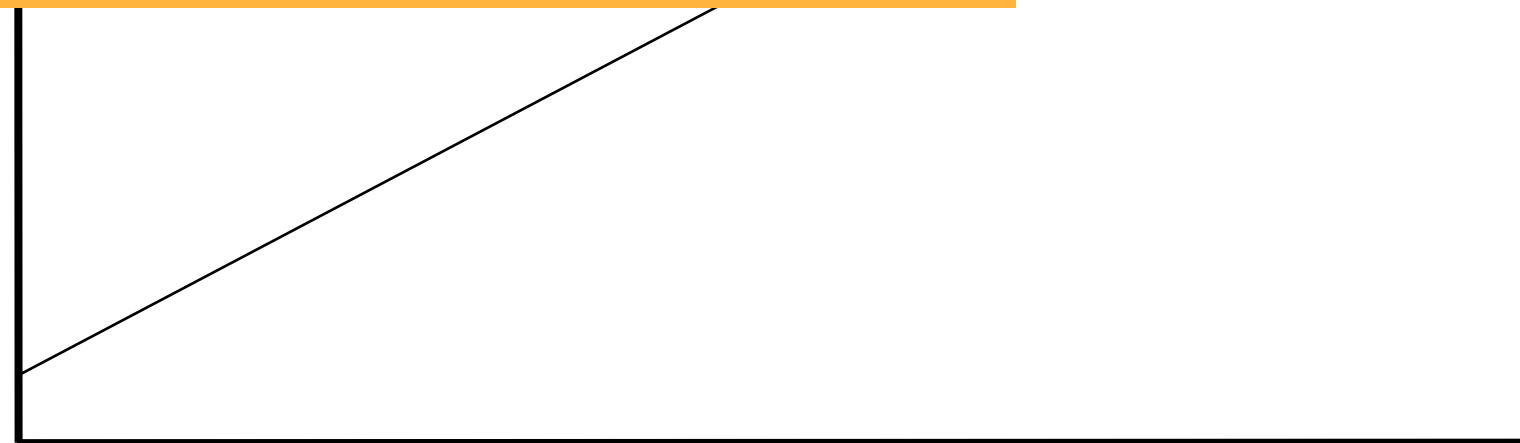
Diversification Model

- Expected number of species increases exponentially with $\lambda - \mu$

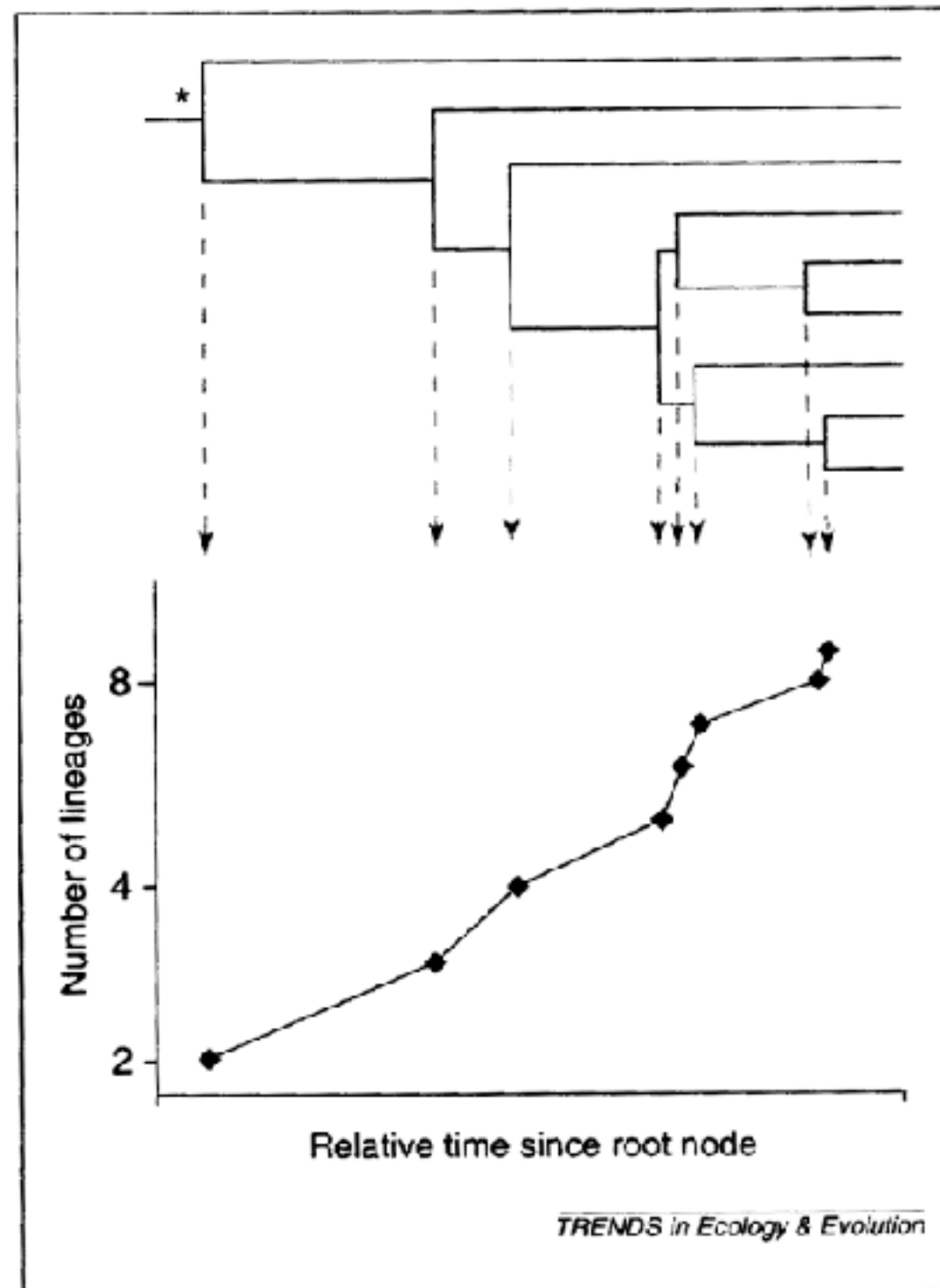
What if we just
have the
phylogeny?

$\ln(\text{Lineages})$

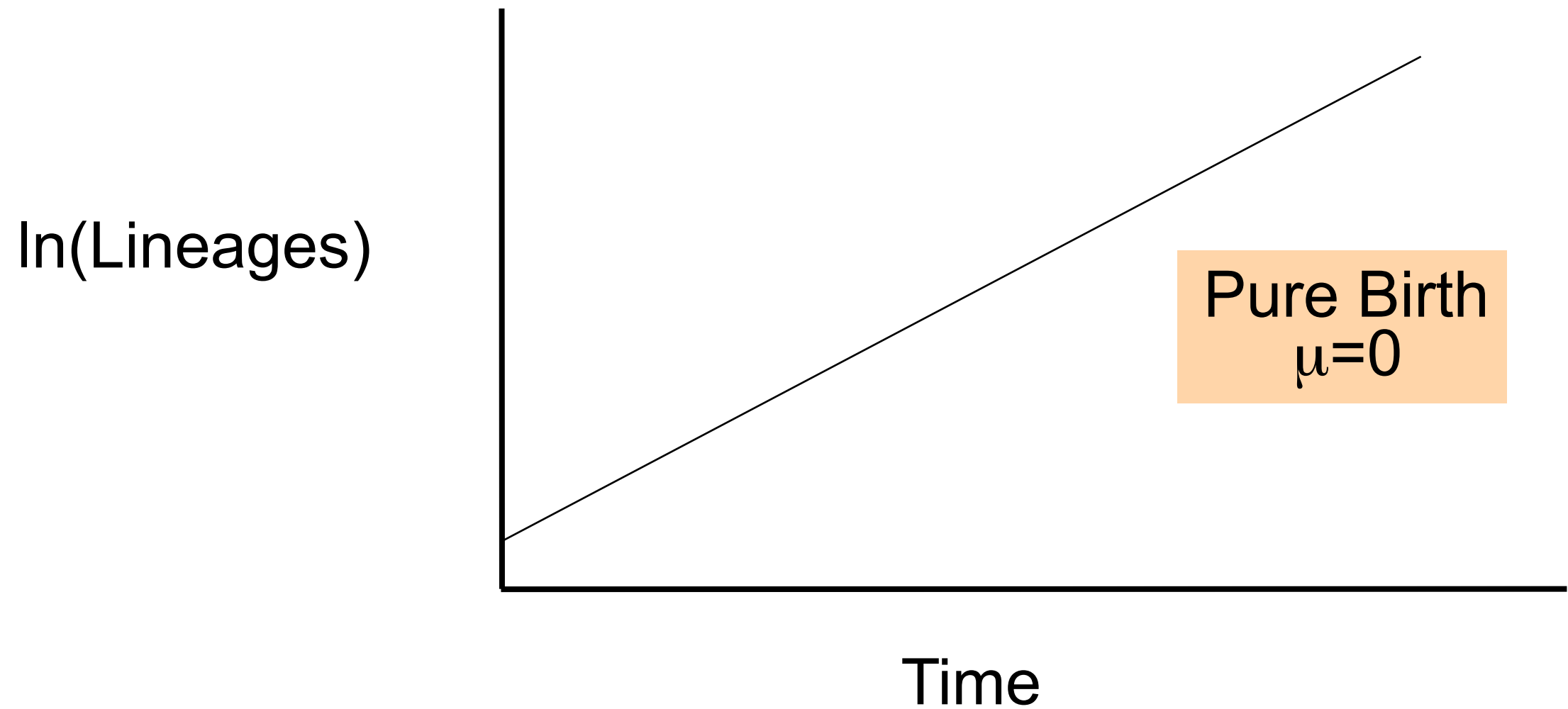
Time



Lineage-through-time

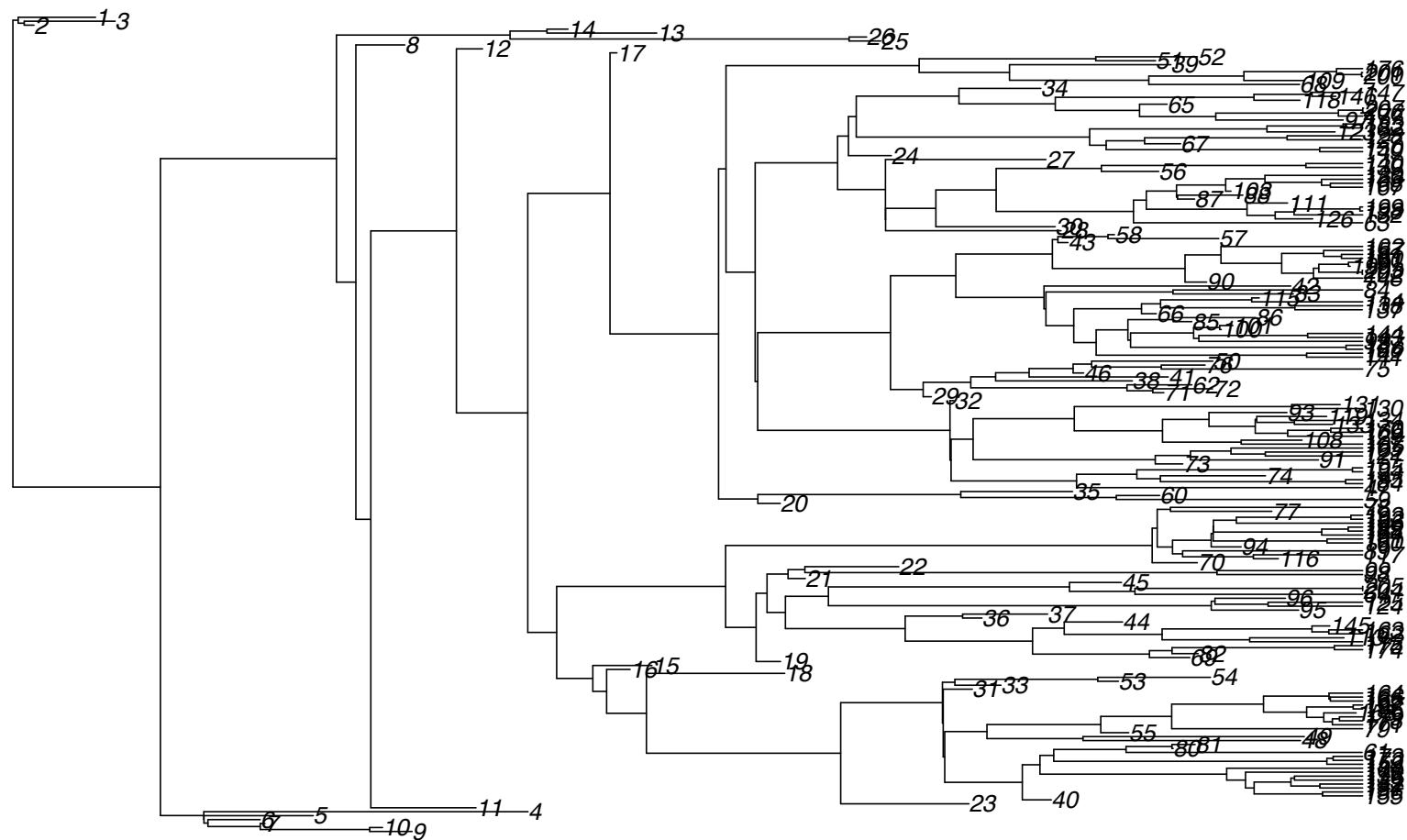


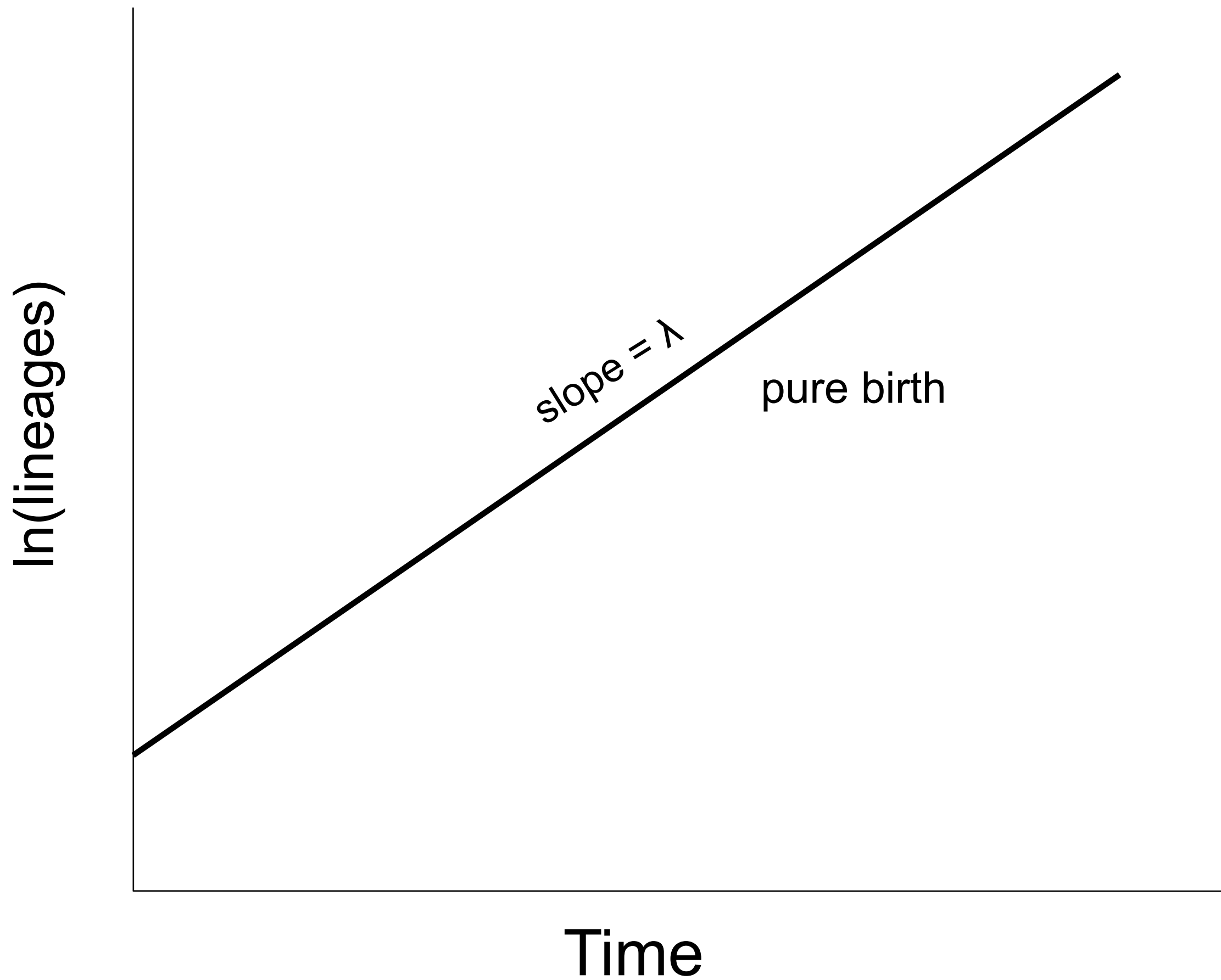
LTT Plot

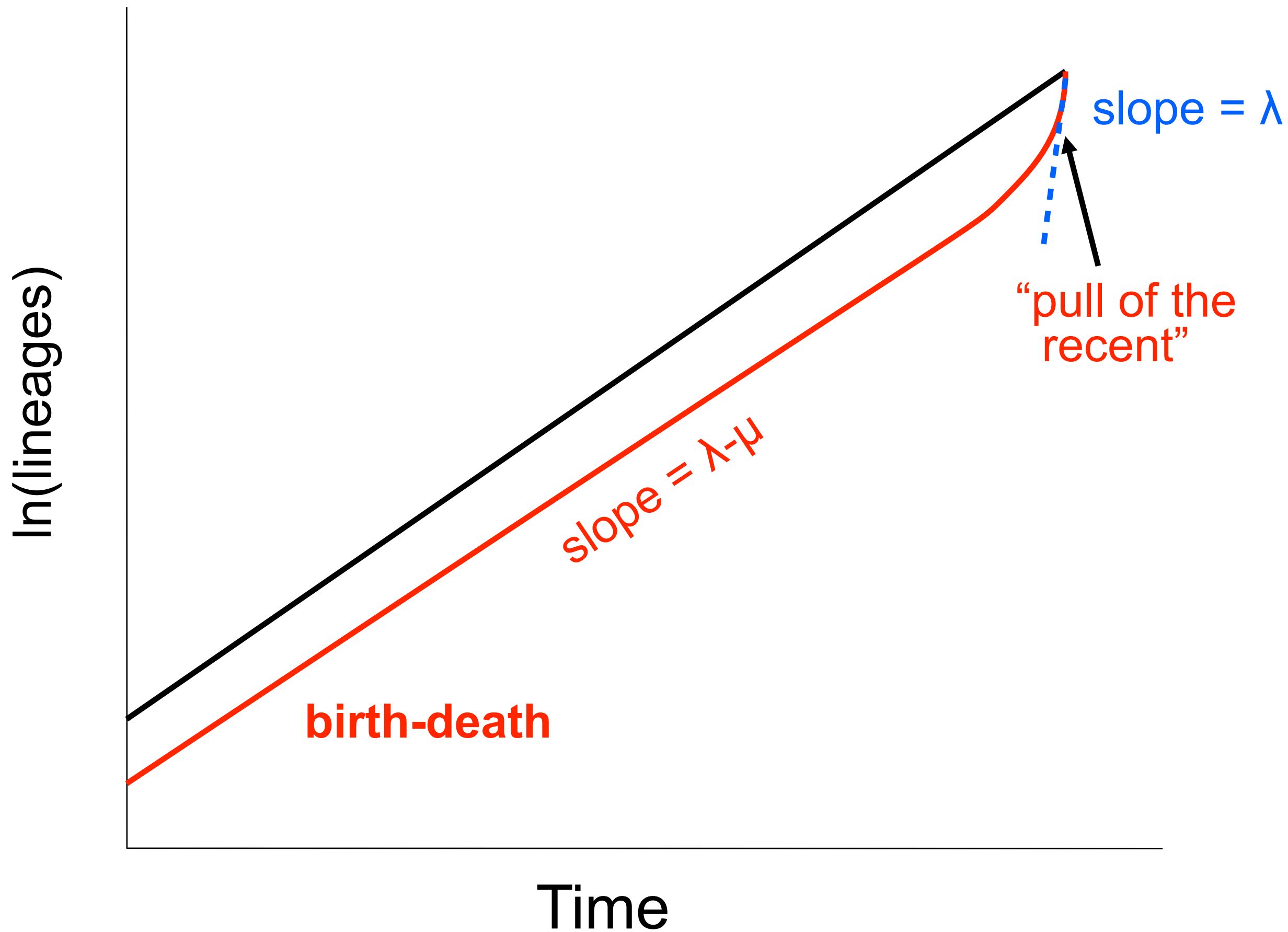


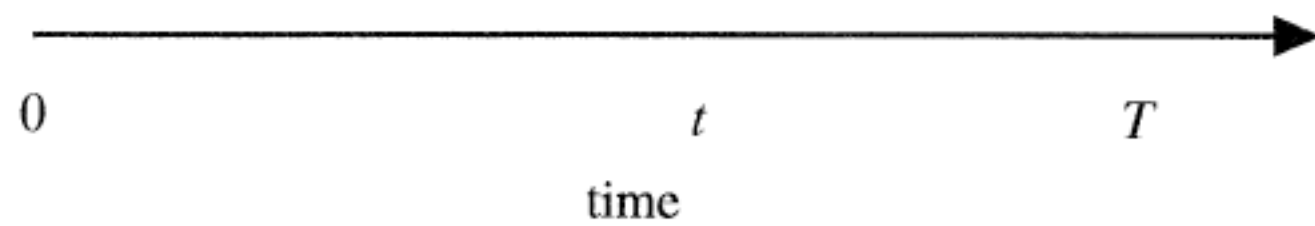
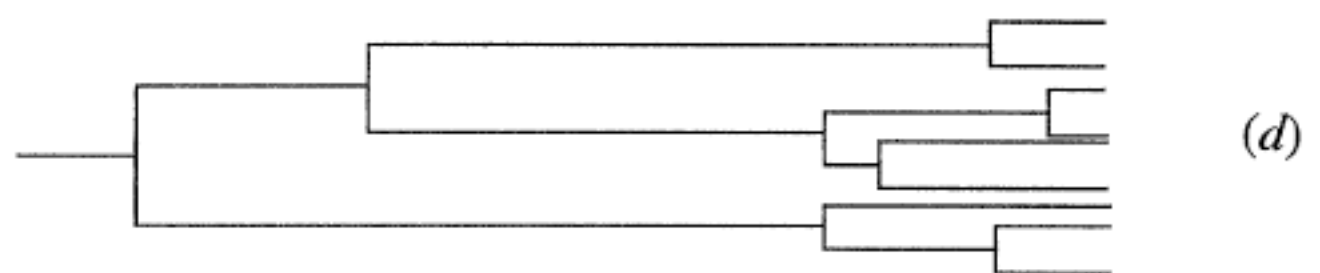
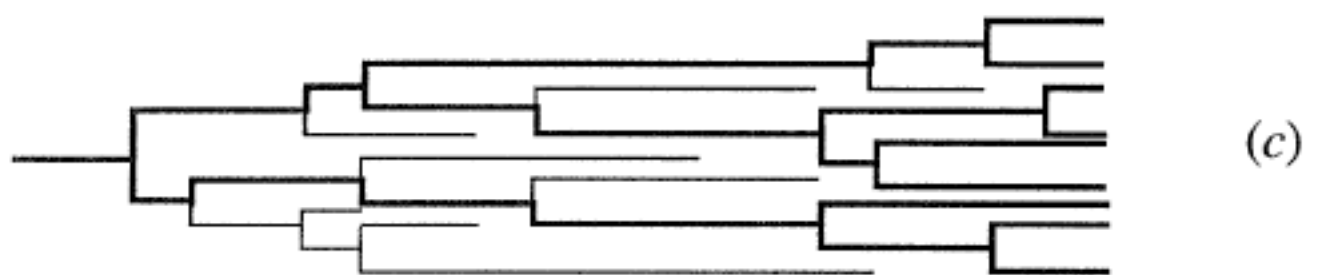
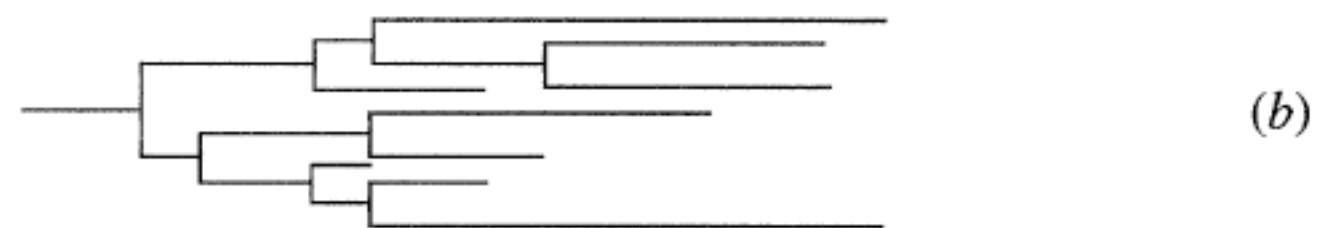
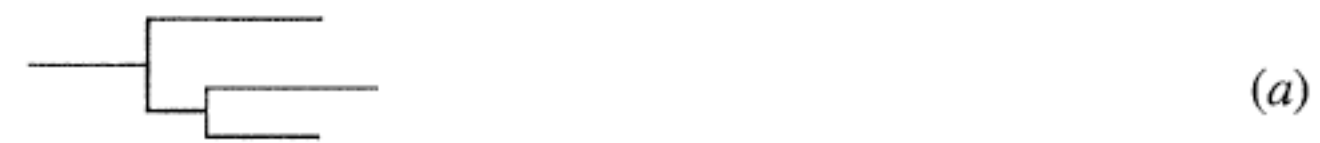
Extinction

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

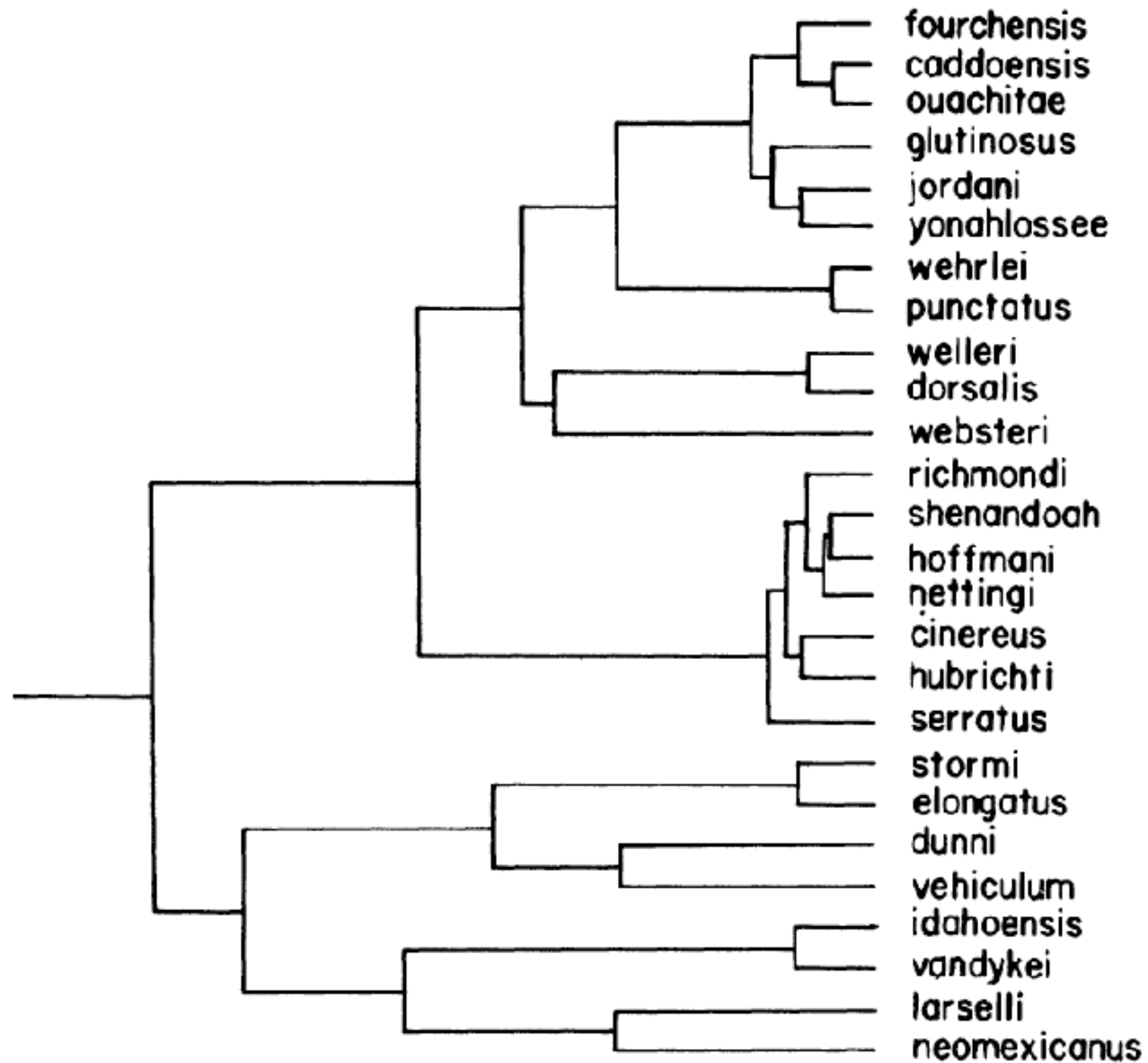






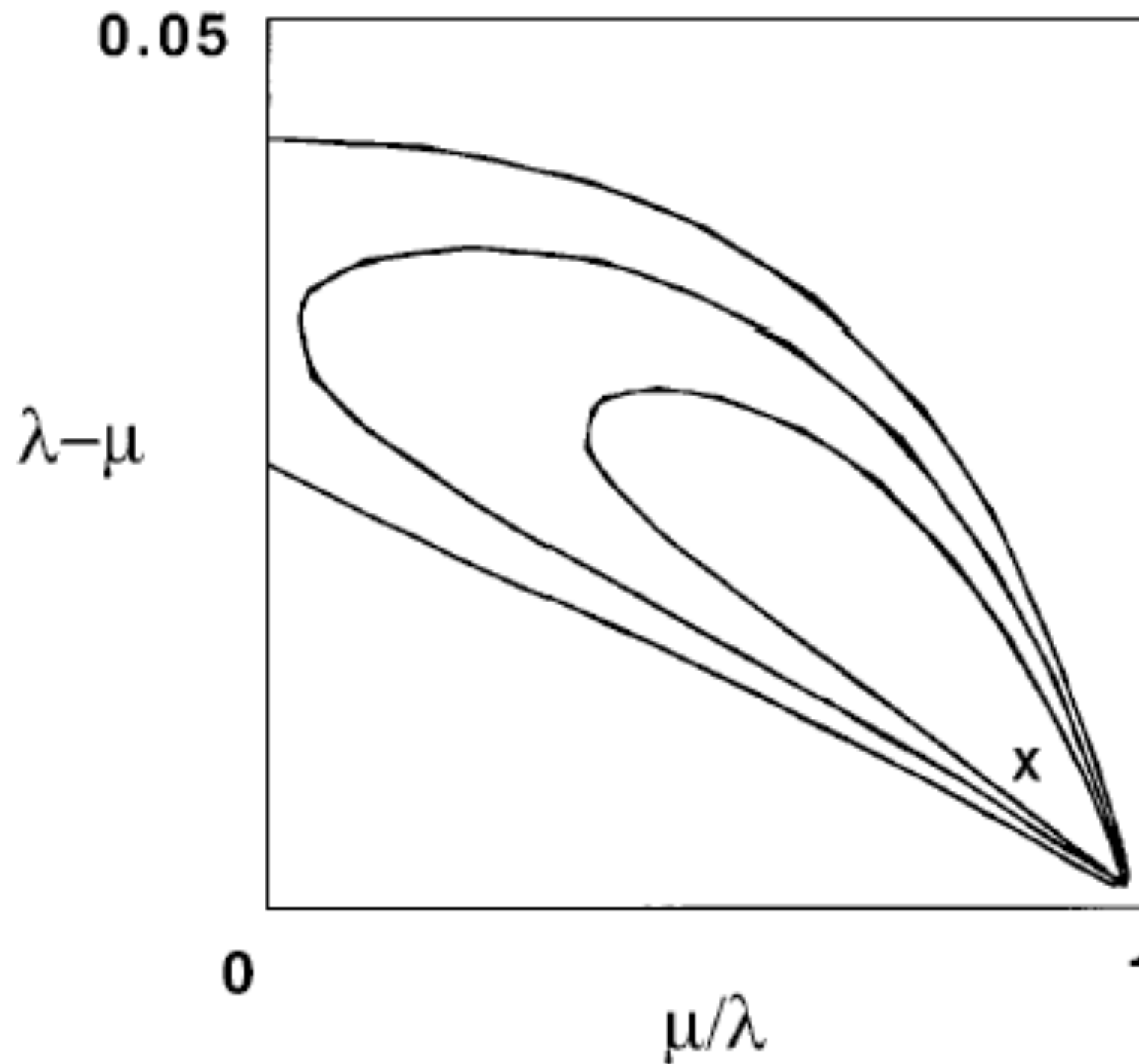


Plethodontid salamanders

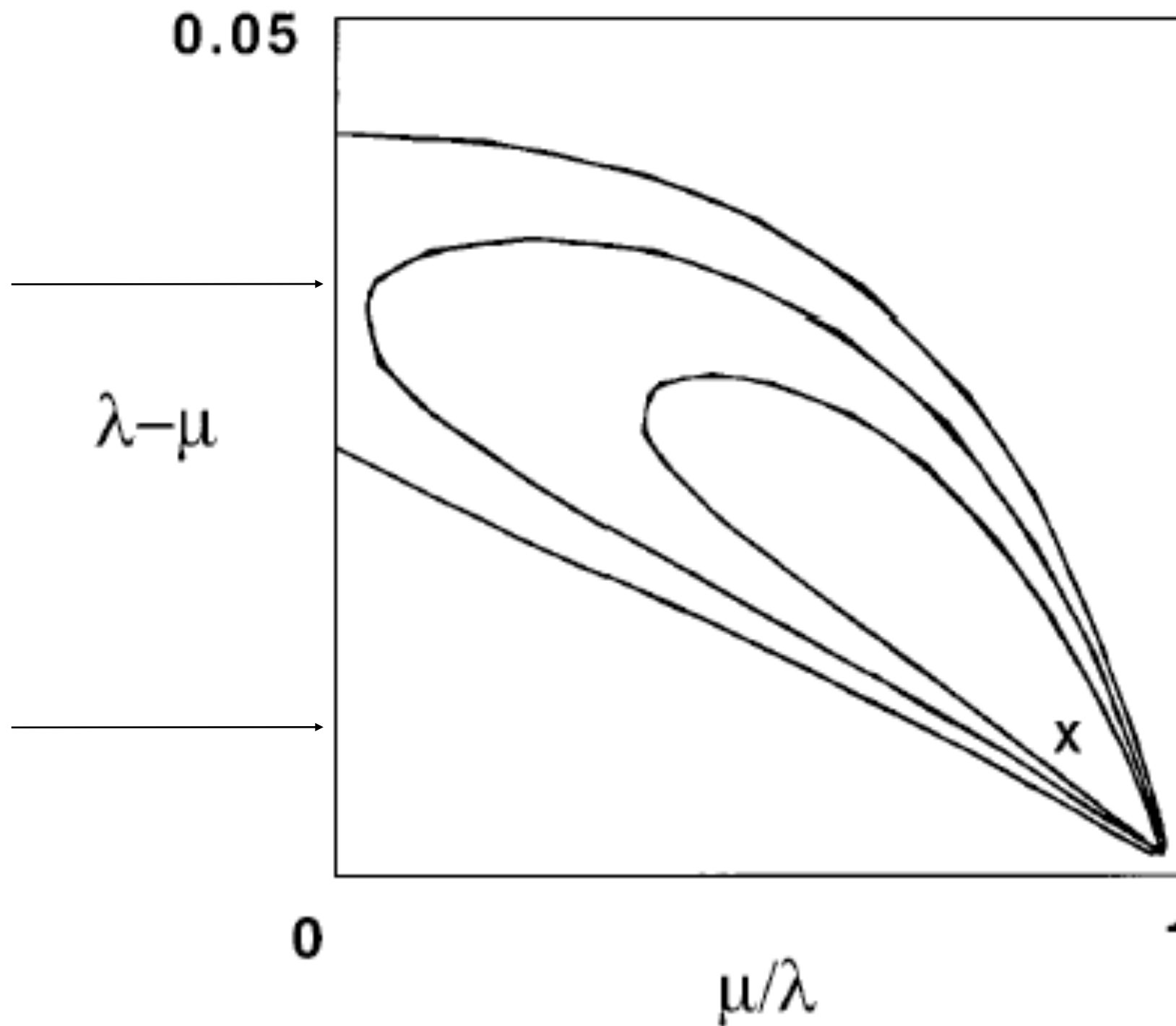


(Highton and Larson 1979)

Plethodontid salamanders



Plethodontid salamanders



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

Testing for slowdowns

- Pybus and Harvey gamma statistic
- Rabosky DDX/DDDL models

Trait-dependent diversification models

- We can use BiSSE (and related) models to test for a relationship between traits and diversification rates
- For example, do speciation rates depend on character state?

Character-independent model

vs.

Character-dependent model

Diversification rate

λ

μ

0



1



Character State

Diversification rate

λ

μ

0



1



Character State

BiSSE Family

- BiSSE - binary character
- MuSSE - multi-state character
- ClaSSE - cladogenesis
- GeoSSE - geography
- QuaSSE - quantitative character