Branch Lengths and Diversification

Lecture 3 March 24, 2009

Outline

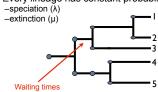
- How do lineages accumulate under the birth-death model?
- Estimating speciation and extinction rates from trees
- Testing hypotheses about diversification

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- Estimating speciation and extinction rates
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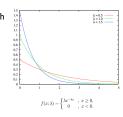
Diversification Model

- · Model: birth-death
- Every lineage has constant probability of:



Waiting times

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

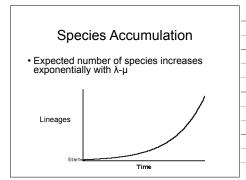


Expected species diversity under a birth-death model: $E[N_t] = N_o e^{(b \cdot d)t} \label{eq:energy}$

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

d = death rate

t = time



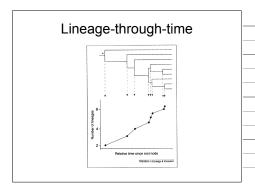
Diversification Model • Expected number of species increases exponentially with $\lambda\text{-}\mu$ What if we just have the In(Lineages) phylogeny?

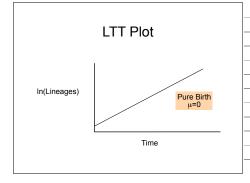
Lineage-through-time plots

Time

- Plot cumulative number of lineages through time
- Compare to expectations under null model
 Related to Van Valen's taxonomic survivorship curves

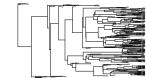


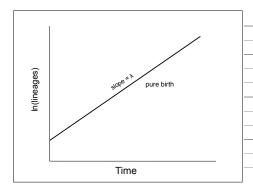


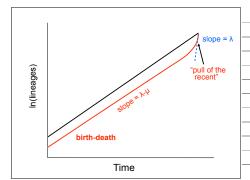


Extinction

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





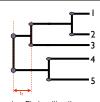


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Pure Birth

- Can use maximum likelihood to estimate parameters
- L = $Pr[tree | \lambda]$



 t_1 = First waiting time Drawn from exponential distribution with parameter 2λ

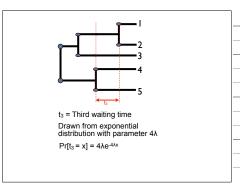
 $\Pr[t_1=x]=2\lambda e^{-2\lambda x}$

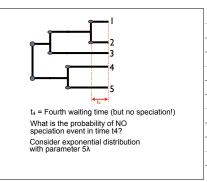


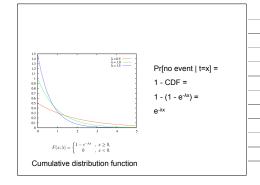
t₂ = Second waiting time

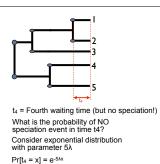
Drawn from exponential distribution with parameter 3λ

 $Pr[t_2 = x] = 3\lambda e^{-3\lambda x}$









$$\begin{split} \Pr[t_1 = x] &= 2\lambda e^{-2\lambda x} \\ \Pr[t_2 = x] &= 3\lambda e^{-3\lambda x} \\ \Pr[t_3 = x] &= 4\lambda e^{-4\lambda x} \\ \Pr[t_4 = x] &= e^{-5\lambda x} \\ \\ \text{likelihood} &= \Pr[\text{tree} \mid \lambda] = 2\lambda e^{-2\lambda t 1} \ 3\lambda e^{-3\lambda t 2} \ 4\lambda e^{-4\lambda t 3} \ e^{-5\lambda t 4} \\ \\ \text{ln general,} \\ \\ \text{likelihood} &= \Pr[\text{tree} \mid \lambda] = e^{-n\lambda x} \int_{i-1}^{n-1} i\lambda e^{-i\lambda x_i} = (n-1)! \lambda^{n-2} e^{-\lambda x} \\ \\ s &= \sum_{i=2}^{n-1} ix_i \end{split}$$

Likelihood for a tree under a Pure-birth model

L = Pr[tree | λ] = (n-1)! λ ⁿ⁻²e^{- λ s}

 $n = number of taxa \\ \lambda = speciation rate \\ s = sum of all branch lengths in the tree$



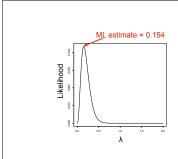
L = Pr[tree | λ] = (n-1)! $\lambda^{n-2}e^{-\lambda s}$

For $\lambda = 1$,

L = (5-1)!13e-19.5

n = 5 s = 19.5

 $L = 8.16 \times 10^{-8}$



Analytic solution

$$\hat{\lambda} = \frac{n-2}{2}$$

$$SE_{\lambda} = \frac{\lambda^2}{n-2}$$

Maximum likelihood estimate of λ under PB model



$$\hat{\lambda} = \frac{n-2}{s} = 0.154$$

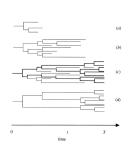
0.154 ± 0.0079

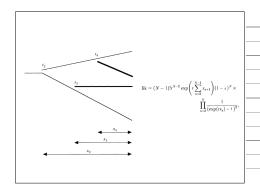
$$SE_{\hat{\lambda}} = \frac{\hat{\lambda}^2}{n-2} = 0.0079$$

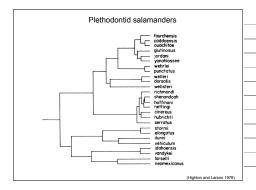
Birth-death models

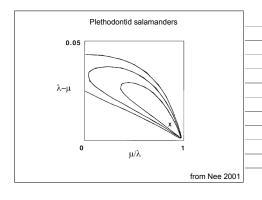
- Can use maximum likelihood to estimate parameters of a birth-death process
- L = Pr[tree | λ, μ]
 Can be difficult to estimate λ and μ
- Easier to estimate composite parameters

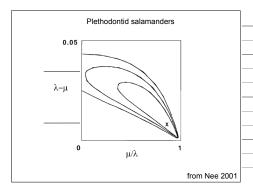
$$r = \lambda - \mu$$
 $\epsilon = \mu / 2$











PB vs. BD

- Two simple ways to test for extinction in a tree
- Likelihood Ratio Test

$$\Delta = 2(InL_2-InL_1)$$

Under model 1, Δ should follow a χ^2 distribution with df equal to the difference in parameters

PB vs. BD

- Two simple ways to test for extinction in a tree
- Akaike Information Criterion (AIC)

AIC = 2 k - 2 ln L
$$AICc = AIC + \frac{2k(k+1)}{n-k-1}$$
.

Choose the model with the lowest AIC score

Can also	gauge support
by the di	gauge support ference in AIC
scores	

Δ_{AIC}	Interpretation
0-3	no support

3-7 weak 7-10 intermediate >10 strong