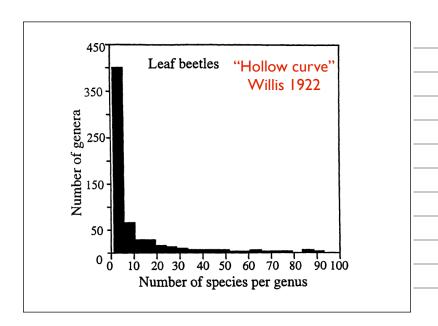
Birth-death Models and Tree Balance

Lecture 2 March 12, 2009





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Outline



- Review of BD model
- Diversity of sister clades
- Tree balance
- Newer approaches



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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

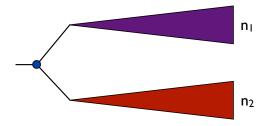


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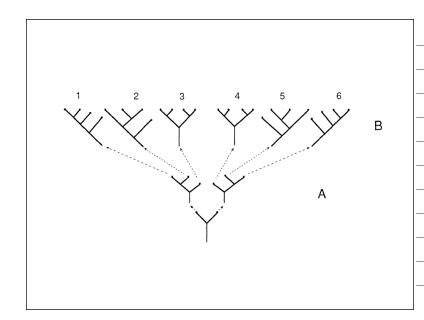


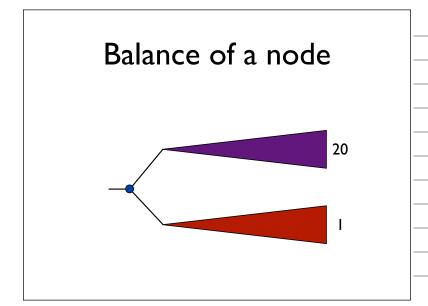
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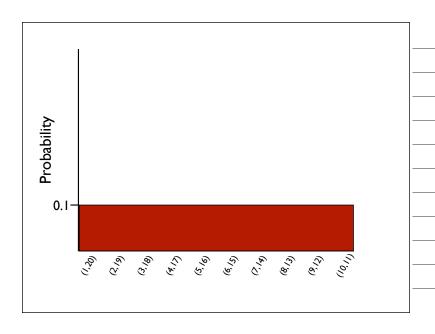
Diversity of Sister Clades



What is the expected distribution for n_1 and n_2 under BD?





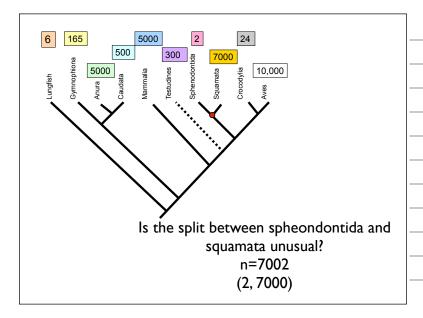


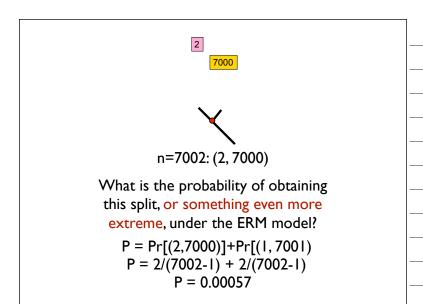
Probability of a split at one node

$$\frac{2}{n-1} \quad k \neq n-k$$

$$Pr[(k,n-k)] = \frac{1}{n-1} \quad k=n-k$$

* Under any ERM model, including BD





The Slowinski-Guyer Test

- Assumes ERM model for diversification
- Requires strikingly large differences between clades for significance
- If applied haphazardly, danger of multiple comparisons



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Tree Balance

- How do we summarize balance across a whole phylogenetic tree?
- How do we calculate the "null" expectation for this statistic?
- How do we compare this distribution to real data?

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Tree Balance

- What is the "average imbalance" of all nodes in a tree?
- There are many ways to calculate this
- I will introduce one of the first, but be aware that there are different measures with different statistical properties

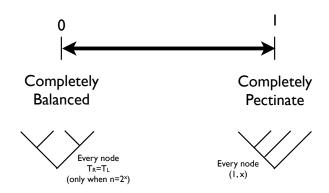
I_c (Colless 1982)

$$I_{\mathrm{c}} = rac{\sum\limits_{\mathrm{(all interior nodes)}} \mid T_{\mathrm{R}} - T_{\mathrm{L}} \mid}{\sum\limits_{\mathrm{2}} \frac{(n-1)(n-2)}{2}}$$

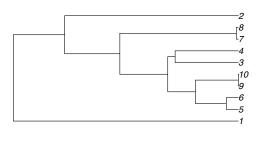
T_R,T_L = number of taxa subtended by "left" and "right" branches

Maximum possible value for I_c with a completely pectinate tree

I_c (Colless 1982)

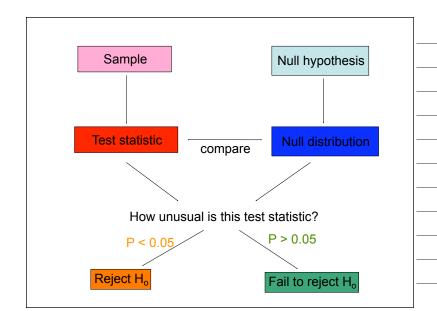


Example

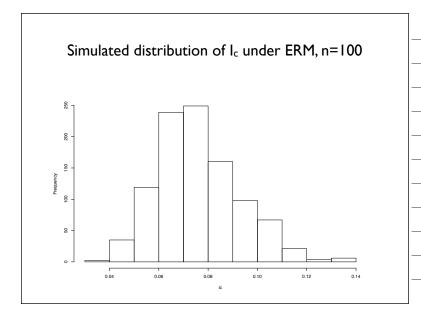


Tree Balance

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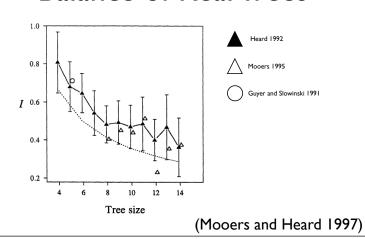
$$\mathsf{E}[\mathsf{I}_{\mathsf{c}}] = \begin{bmatrix} \frac{2n}{(n-1)(n-2)} \sum_{j=2}^{n/2} \frac{1}{j} & (n \text{ even}) \\ \frac{2n}{(n-1)(n-2)} \left[\frac{1}{n} + \sum_{j=2}^{(n-1)/2} \frac{1}{j} \right] & (n \text{ odd}) \end{bmatrix}$$
(Heard 1992)



Tree Balance

- How do we summarize balance across a whole phylogenetic tree?
- How do we calculate the "null" expectation for this statistic?
- How do we compare this distribution to real data?

Balance of Real Trees



Possible Explanations

- Methodological artifact
 - Sampling
 - Phylogenetic reconstruction methods
- Variation in speciation and/or extinction across lineages



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Sister-clade Comparisons



Does a given trait influence diversification rates?

Sister-clade Comparisons

- Compare pairs of sister clades, where one clade has the trait of interest and the other does not
- Under ERM, either clade is equally likely to be the larger of the two
- Use binomial test to evaluate significance

Binomial Probability

$$Pr(x) = \binom{n}{x} p^{x} (1-p)^{n-x}$$

x = number of "successes" n = number of trials (sister pairs) p = 0.5 (Pr[success] under H_o)

Example





zygomorphic

Example

 Zygomorphic group more diverse in 15 of 19 comparisons

$$Pr(x) = \binom{n}{x} p^{x} (1 - p)^{n - x}$$

$$Pr(x=15) = \binom{19}{15} 0.5^{15} 0.5^{4}$$

$$Pr(x=15) = 3876*0.5^{15}0.5^{4} = 0.007$$

$$Pr(x \ge 15) = 0.019$$

More developments

- Different tree balance statistics: N, σ^2_N , B_1 , B_2 , R, etc.
- Methods to identify particularly imbalanced nodes in a phylogenetic tree: SymmeTREE (Chan and Moore 2002)
- Other aspects of tree shape: number of cherries, etc.
- More analytic results