Wainwright Review

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1 Diversification Rates: Tree Evolution

Branching process of creating a tree. YULE (pure-birth) model: Speciation rate b is

$$b = \frac{\ln(n/2)}{t} \tag{1}$$

Nee (2006) Baldwin & Sanderson (1998) Silverswords, Fig 1.

1.1 Time calibration

Phylogeny adjusted by molecular clock, or `BEAST` for Bayesian variable rates, ULTRAMETRIC TREES time calibrated into CHRONOGRAMS using fossils, i.e. Near & Shaffer method, removes fossils with greatest disagreement (sum of squares). Ways to be wrong: wrong phylogeny, wrong fossil date, fossil age is *minimum* age of node only.

With a time calibrated tree and estimate of diversification rate:

1. Tests for an ADAPTIVE RADIATION
2. Geography of diversification rate
3. Tests for a KEY INNOVATION: Moore et al. (2004) Compute the likelihood ratio for differing diversification rates somewhere on the tree. In an equal rates Markov branching process model, the cumulative probability of an L, R partition of N species across any node is given by

$$\frac{2L}{N-1}, \quad L < \frac{N}{2} \tag{2}$$

Hodges & Arnold (1995), nectar spurs, Farrell (1998) angiosperm feeding in phytophagous beetles.

Factors affecting diversification rates Coyne & Orr (2004) Creating correlation between traits and diversification rate $b - d$.

1. Properties facilitate speciation: sexual selection (dichromatism in fish), pollinator isolation (Nectar spurs)

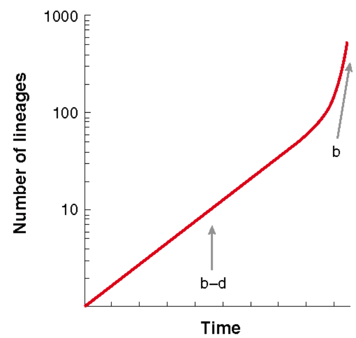

Figure 1: Diversification rates

2. Reduce extinction rate (range size or population size increases).

3. Properties opening new adaptive zones, (angiosperm feeding in beatles)

McPeek & Brown (2007) Consider huge number of published trees. No correlation between number of species and diversification rates. Strong negative correlation between rate and estimated clade age – old clades have small diversification rates. Why? Selection bias, because old clades with high rates would be much too big!

2 Phenotypic Diversity: Trait Evolution

Given a tree, what can we conclude about traits? Entering the realm of comparative phylogenetic methods, independent contrasts and Brownian motion. Just as diversification *rate* replaced old metric of *diversity*, we'll replace DISPARITY (trait variance within a clade) vs DISPARITY RATE: the rate at which we accumulate trait differences along a phylogeny.

What causes the rate of trait evolution to change?

- EXTRINSIC causes geography, community, or adaptive landscape change.
- INTRINSIC causes: functional innovation, decoupling, increased complexity.

Methods to detect a change in rates:

- Between lineages (separate branches) Brian O'Meara, `Brownie` likelihood ratio test for different Brownian trait evolution rates (or O-U parameter) between lineages.
- Change in time along a single lineage: `Geiger` Can only show deceleration.

2.1 Radiations

Streelman & Danley (2003) 3 stages of radiation: habitat, morphology, communication. Ricklefs (2006) Variance independent of number of lineages, but topology matter: star phylogeny highest, then asymmetric, then symmetric (maximize shared history minimizes variance)..

3 Allometry

ISOMETRY is expected scaling, i.e. $L^3 \sim M$, while ALLOMETRY is a deviation from that scaling due to functional constraint, i.e. $L^2 \sim M$ because force is proportional to the mass $F \sim M$ and strength to support it proportional to the area, $F \sim L^2$. A log-log plot of M vs L would have a slope of 2 instead of 3, which we call NEGATIVE ALLOMETRY.

4 Functional Morphology

MANY-TO-ONE MAPPINGS

5 Community Phylogenetics

See Jay's section notes.

6 Misc

6.1 Phylogenetic Niche Conservatism

Kozak & Wiens (2006) both species groups occupy same position along principle component, while absent area separating them is at a very different location along the axis.

6.2 Latitudinal Gradients & Phylogeny

- Weir & Schluter (2007)
- Wiens & Donoghue

See Jay's section notes.