Introduction to BiSSE Annotated Bibliography

Phyloseminar 2024

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Mitter, C., Farrell, B. D., & Wiegmann, B. M.. (1988). The Phylogenetic Study of Adaptive Zones: Has Phytophagy Promoted Insect Diversification?. 132(1). https://doi.org/10.1086/284840

This paper represents one of the pioneering attempts to investigate whether phylogenetic trees can be used to demonstrate that certain characteristics of a lineage, such as ecological niche or mating system, affect the rate of speciation or extinction. This paper used sister-clade analyses to explore the relationship between phytophagy (the consumption of plant material) and insect diversification. The authors investigate whether the adaptation to feeding on plants has led to increased diversification among insects. They discuss various hypotheses and models to understand the role of phytophagy in insect evolution and propose phylogenetic approaches to study adaptive zones. Through a comprehensive review and analysis, the paper provides insights into the evolutionary mechanisms driving insect diversification and the importance of phytophagy in shaping insect ecology and biology.

Pagel, M. (1994). Detecting correlated evolution on phylogenies: A general method for the comparative analysis of discrete characters. Proceedings of the Royal Society of London. Series B: Biological Sciences, 255(1342), 37–45. https://doi.org/10.1098/rspb.1994.0006

In this paper, Pagel presents a general method for detecting correlated evolution of discrete characters on phylogenies. The method assesses whether a pattern of association across a group is evidence for correlated evolutionary change in the two characters. Pagel's method provides a rigorous approach for testing hypotheses about the evolutionary associations between different rates of character state change, offering insights into the underlying patterns of character evolution across phylogenetic trees. Through theoretical exposition and practical examples, the paper illustrates the utility of this method in comparative analyses of discrete characters, paving the way for advancements in phylogenetic comparative methods. The paper continues to be widely cited and influential in the field of evolutionary biology, serving as a foundational resource for researchers interested in understanding the evolutionary dynamics of traits across diverse taxa.

Nee, S., May, R. M., & Harvey, P. H. (1994). The reconstructed evolutionary process. Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences, 344(1309), 305–311. https://doi.org/10.1098/rstb.1994.0068

Phylogenies reconstructed from contemporary taxa do not contain information about lineages that have gone extinct. In this paper, the authors construct the likelihood function for a reconstructed

phylogeny which provides the basis for the estimation of birth and death rates. This paper shows how the theory can be generalized to phylogenies that contain only a sample of the extant members of a clade and where the phylogenies do not contain information about lineages that have gone extinct. This paper was among the early articles to describe likelihood calculations for models involving speciation and extinction rates.

Pagel, M. (1999). The Maximum Likelihood Approach to Reconstructing Ancestral Character States of Discrete Characters on Phylogenies. Systematic Biology, 48(4), 612–622. https://doi.org/10.1080/106351599260184

In this paper, Pagel introduces the maximum likelihood approach for reconstructing ancestral character states of discrete characters on phylogenies. The author provides a detailed explanation of the theoretical framework and methodology behind maximum likelihood estimation, highlighting its advantages and applications in evolutionary biology. The model introduced in this article can be used to infer ancestral character states with greater accuracy and precision compared to alternative methods at that time. This model also permits different character states to confer different rates of speciation; however, it assumes no extinction. It also assumed that ancestral states can be assessed without accounting for the effects of the character on speciation/extinction processes.

Paradis, E. (2005). Statistical analysis of diversification with species traits. Evolution, 59(1), 1–12. https://doi.org/10.1111/j.0014-3820.2005.tb00889.x

This is another seminal methods paper where Paradis presented a new method to analyze whether some traits affect diversification rate using observations of these traits on recent species and the phylogenetic tree of these species. Paradis discusses the theoretical underpinnings of trait-dependent diversification models and provides practical guidelines for implementing these models in empirical studies. Through a combination of mathematical formalism and empirical examples, the paper elucidates the methods used to quantify trait-dependent diversification rates and assess their significance. Paradis also discusses the implications of trait-based diversification analyses for understanding the mechanisms driving species evolution and diversification. Though Paradis introduced a likelihood-based method that incorporates reconstructed ancestral states to compare speciation rates between different states in this paper; however, the method fails to account for extinction, which is a limitation of the approach.

**Maddison, W. P. (2006). Confounding asymmetries in evolutionary diversification and character change. Evolution, 60(8), 1743–1746. https://doi.org/10.1111/j.0014-3820.2006.tb00517.x

This is the paper where Maddison explained that biases introduced by asymmetries in diversification and character state change can confound interpretations of evolutionary patterns

and mislead our understanding of the effect of trait evolution in diversification. The author identified two intertwined problems that could potentially result in misinterpretations. First, inferences about character state transitions based on simple transition models like Pagel, (1999) can be thrown off if the character affects rates of speciation or extinction. Second, inferences about whether a character affects lineage diversification based on sister clade comparisons like Mitter et al. (1988) can be thrown off if the transition rates are asymmetric. This paper was among the first to highlight the need for methods that consider jointly the biases in diversification and character change because these two processes cannot be teased apart.

**Maddison, W. P., Midford, P. E., & Otto, S. P. (2007). Estimating a binary character's effect on speciation and extinction. Systematic Biology, 56(5), 701. https://doi.org/10.1080/10635150701607033

This is the paper that introduced the Binary-State Speciation and Extinction (BiSSE) Model. BiSSE is a model that assesses if the states of a character are associated with different rates of speciation or extinction. So, this is the paper that introduced a method that could be used to address the two problems identified by Maddison (2006). Through theoretical modeling and statistical analyses, the authors developed the first framework that incorporate explicitly the process of character state change directly and simultaneously into the likelihood assessment of speciation and extinction rates. The paper presents a novel approach that enables researchers to calculate the probability of the tree and observed states given a basic model with six parameters. By providing this methodological tool for studying the evolutionary consequences of binary characters, Maddison et al.'s work contributes to advancing our understanding of the factors driving speciation and extinction processes.

FitzJohn, R. G., Maddison, W. P., & Otto, S. P. (2009). Estimating trait-dependent speciation and extinction rates from incompletely resolved phylogenies. Systematic Biology, 58(6), 595–611. https://doi.org/10.1093/sysbio/syp067

This is another methods paper that made an improvement to the BiSSE model introduced by Maddison et al. (2007). The BISSE method, as formulated by Maddison et al. (2007), assumes that the phylogenetic tree is complete and fully resolved; that is, the tree must include every extant species. It also assumes that all character state information is known. The authors of this paper developed 2 likelihood methods that can be used to infer the effect of a trait on speciation and extinction without complete phylogenetic information. Their approaches can be used where a phylogeny can be reasonably assumed to be a random sample of extant species or where all extant species are included, but some are assigned only to terminal unresolved clades. Through simulations and empirical analyses, they demonstrate the effectiveness of their approach in accurately estimating the impact of traits on speciation and extinction processes.

FitzJohn, R. G. (2012). Diversitree: Comparative Phylogenetic Analyses of Diversification in R. Methods in Ecology and Evolution, 3(6), 1084–1092. https://doi.org/10.1111/j.2041-210X.2012.00234.x

In this paper, FitzJohn introduces Diversitree, a software package implemented in the R programming language for conducting comparative phylogenetic analyses of diversification patterns. Key included methods are BiSSE (binary state speciation and extinction), MuSSE (a multistate extension of BiSSE), and QuaSSE (quantitative state speciation and extinction). Diversitree also includes methods for analyzing trait evolution and estimating speciation/extinction rates independently. The author demonstrates the utility of Diversitree through illustrative examples and showcases its flexibility in analyzing diverse datasets and addressing specific research questions related to speciation, extinction, and trait evolution. This paper serves as a valuable resource for researchers interested in applying phylogenetic comparative methods to investigate patterns and mechanisms of diversification.