

Model-Based Inference from Discrete Characters in the Formicidae

**Or: How can we use Bayesian inference to incorporate our systematic
knowledge**

April Wright, Southeastern Louisiana University

Bayesian vs. Parsimony

- A lot of ink has been spilled on this debate

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RESEARCH ARTICLE

Bayesian Analysis Using a Simple Likelihood Model Outperforms Parsimony for Estimation of Phylogeny from Discrete Morphological Data

April M. Wright , David M. Hillis

Published: October 3, 2014 • <https://doi.org/10.1371/journal.pone.0109210>

Original Article

Weighted parsimony outperforms other methods of phylogenetic inference under models appropriate for morphology

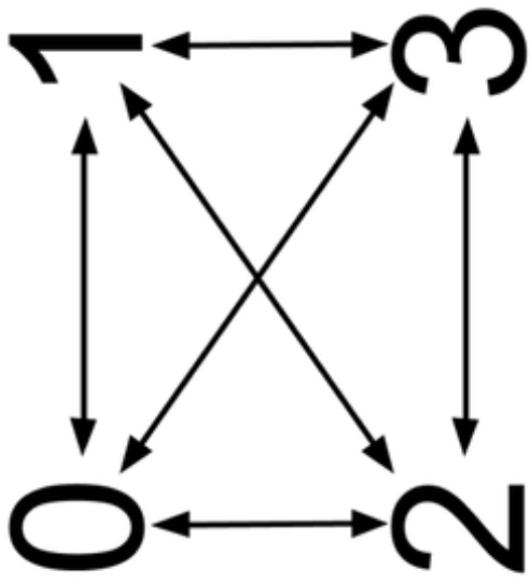
Pablo A. Goloboff , Ambrosio Torres, J. Salvador Arias

Bayesian Mk Model vs. Maximum Parsimony

- I am going to argue throughout this talk, that this is precisely the wrong question to focus on

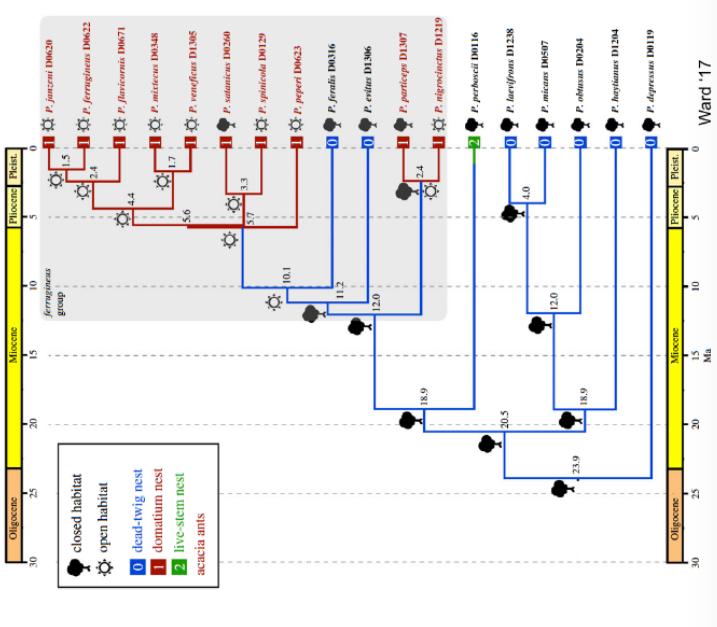
Bayesian Mk Model and Maximum Parsimony

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 - The base assumptions of these methods are not all that different



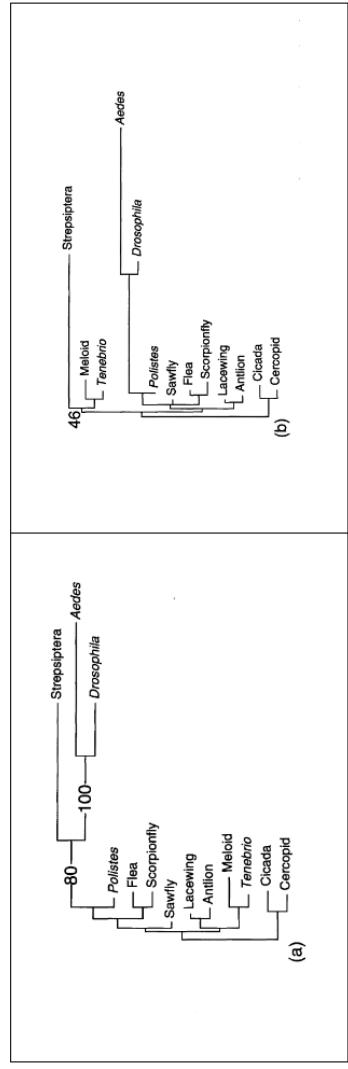
Bayesian Mk Model and Maximum Parsimony

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Huelsenbeck, 1998

Bayesian Mk Model and Maximum Parsimony

- There are differences between these methods:
 - Bayesian methods return a rate-based branch length, and can accept convergence as a solution for a character
 - Bayesian methods allow for multiple changes on a branch, and change to occur anywhere on the branch
 - Parsimony allows every character to have its own history and number of changes

The Akaike Information Criterion Will Not Choose the No Common Mechanism Model

FREE

Mark T. Holder ✉, Paul O. Lewis, David L. Swofford

Systematic Biology, Volume 59, Issue 4, 1 July 2010, Pages 477–485,
<https://doi.org/10.1093/sysbio/syq028>

Published: 31 May 2010 Article history ▾

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Bayesian Mk Model and Maximum Parsimony

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 - Which model do we believe?
 - Which model can we improve?
 - Extensions to parsimony have been implemented, but there remains no rigorous statistical method for evaluating which type of parsimony is best

Extending the Mk model

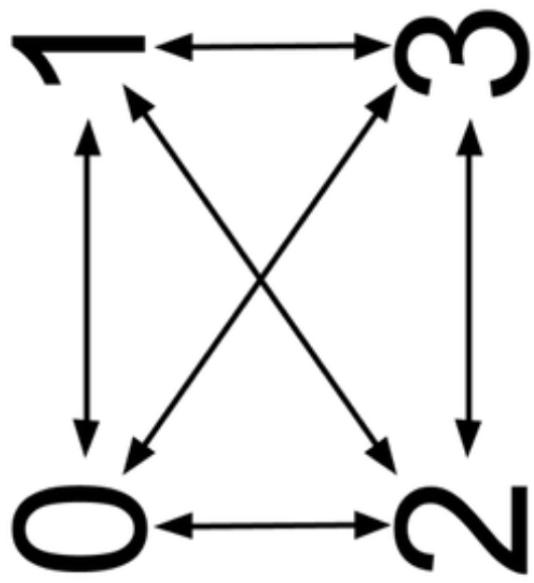
- Wright, Lloyd and Hillis 2016, adapting Mr. Bayes

Modeling Character Change Heterogeneity in Phylogenetic Analyses of Morphology
through the Use of Priors

APRIL M. WRIGHT^{1,*}, GRAEME T. LLOYD², AND DAVID M. HILLIS¹

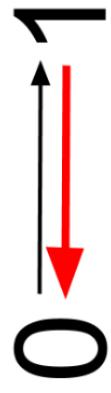
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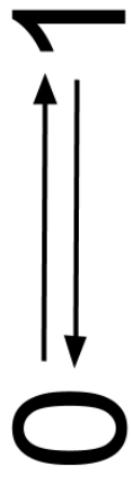
Presence of stem ants

- "... morphologically plesiomorphic and generalized with affinities to both modern ants and wasps..." - Barden and Grimaldi (2016)



Extending the Mk model

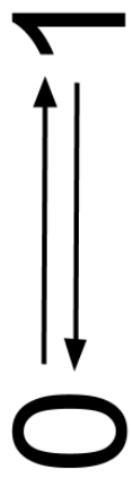
- Wright, Lloyd and Hillis 2016, adapting Mr. Bayes



A priori, we likely know very little about the actual transition rate (represented by the arrow)

Extending the Mk model

- Wright, Lloyd and Hillis 2016, adapting Mr. Bayes



But equilibrium character frequencies are a common facet in phylogenetic models.

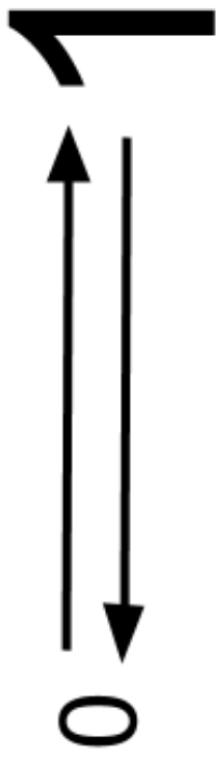
Extending the Mk model

- In most Bayesian models, the probability of observing a transition between state 0 and state 1 depends not only on the transition rate, but how common state zero is

Observed = (probability of transition) * (frequency of starting state)

Extending the Mk model

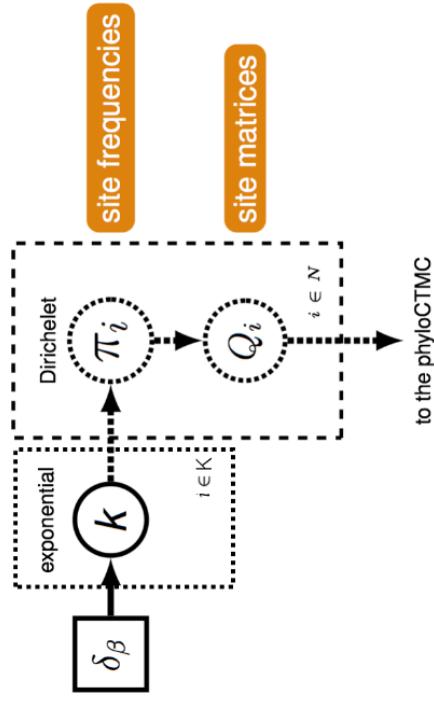
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Equilibrium character frequencies are a common facet in phylogenetic models.

Extending the Mk model

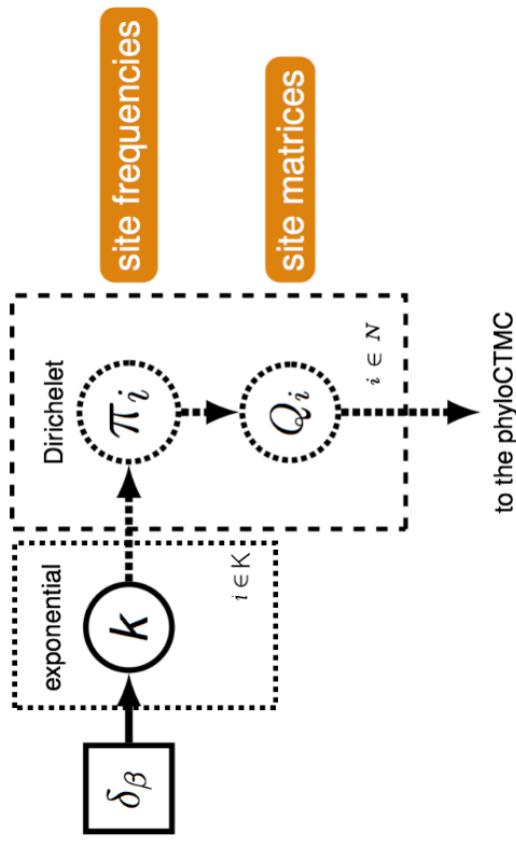
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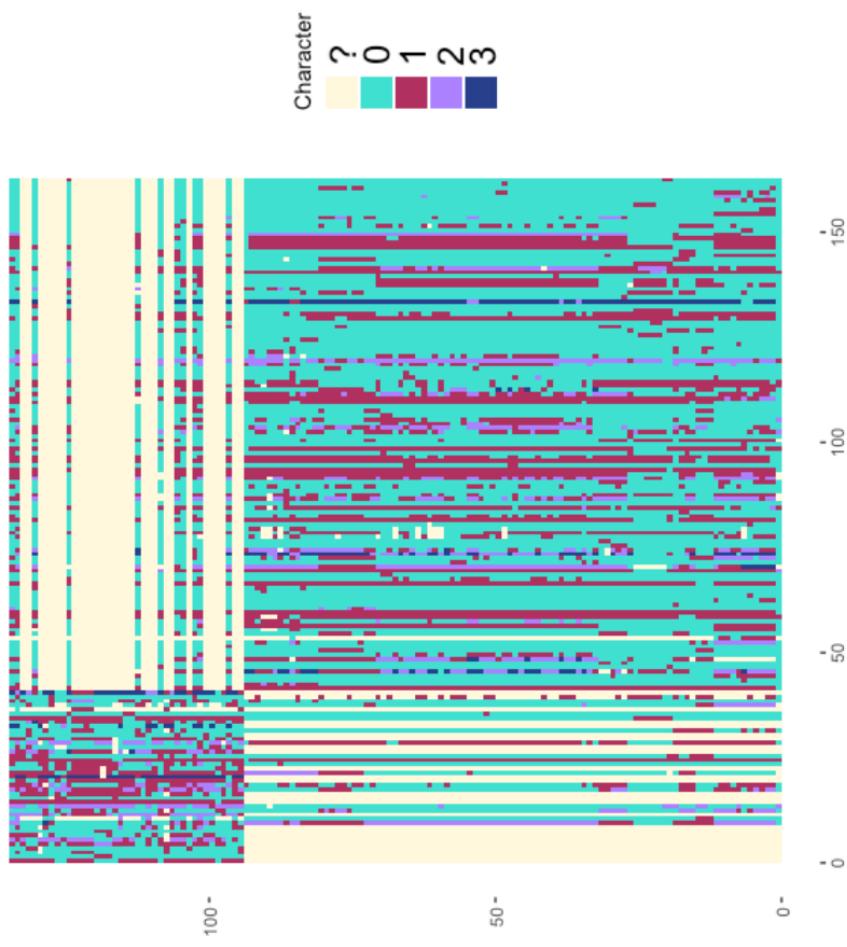
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Extending the Mk model

- Wright, Pett, Jenkins, Johnson, Mendoza, and Heath, in prep, new methods in RevBayes for modeling characters
- This model allows a straight-forward extension to multistate characters



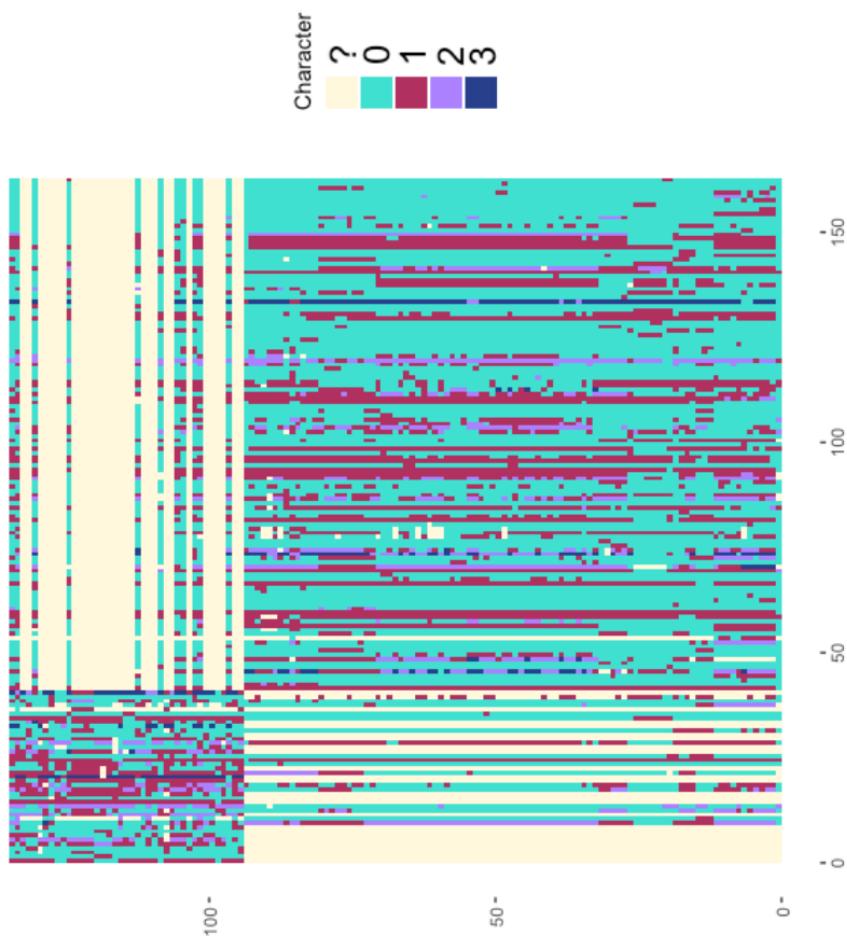
Why extend the model



Dataset

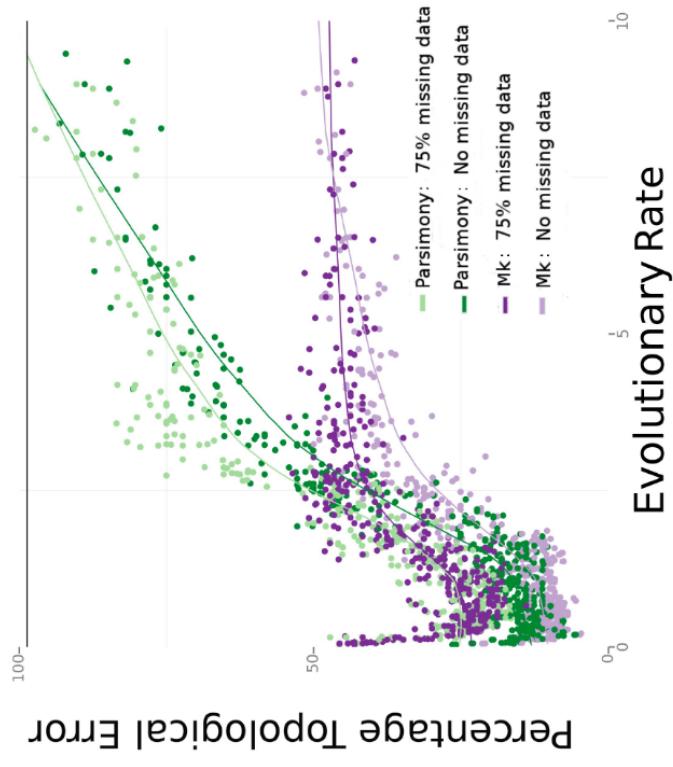
- Multistate dataset of fossil ants from Barden (2016)
- Combined with extant ants Keller (2011)
- Estimated phylogeny from:
 - Each dataset individually
 - Each dataset individually, pared down to binary characters
 - Combined dataset
 - Combined dataset, pared down to binary characters

Why extend the model



Why extend the model

Models matter more when the problem is hard

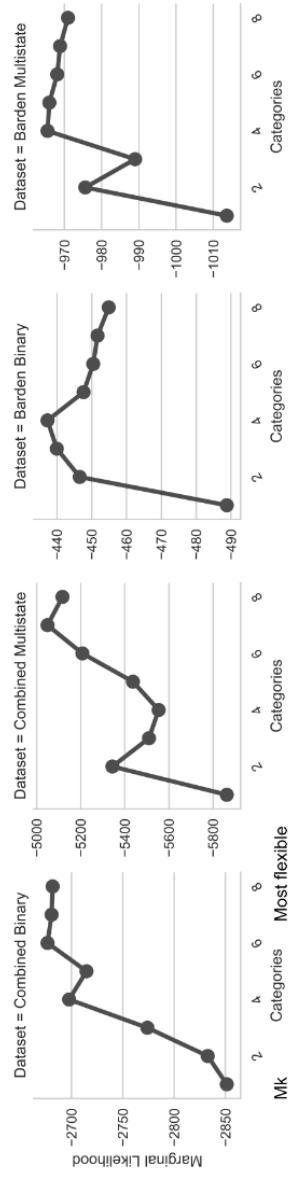


Why extend the model

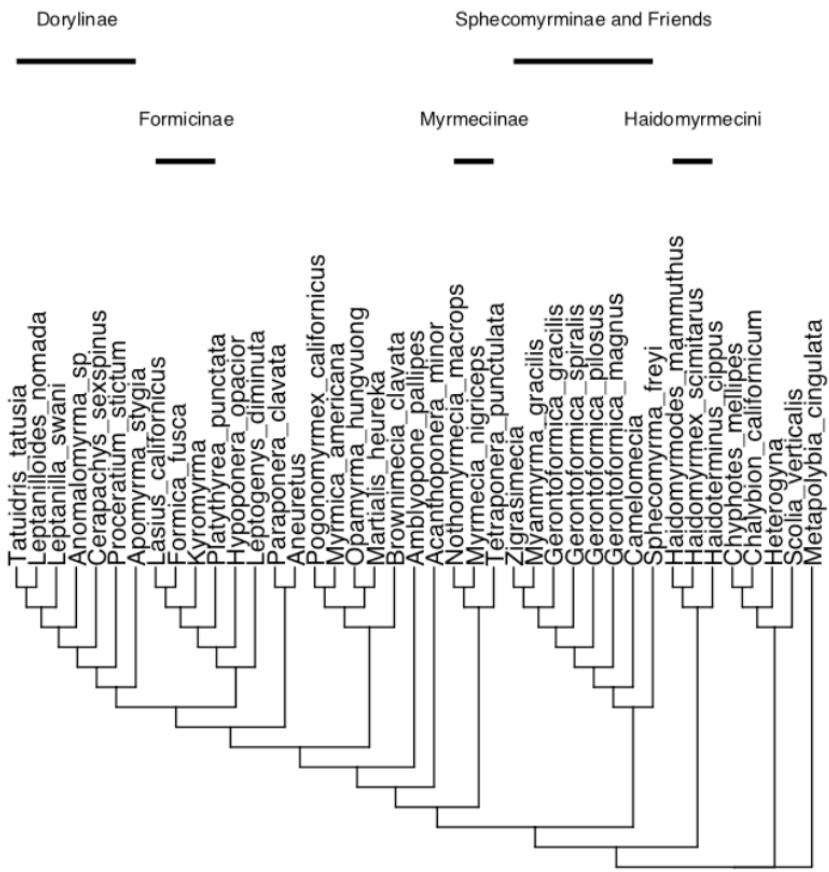
- Testability
 - Bayesian methods have a rich and flexible literature on testing to check goodness of model fit, and to compete models against one another

Model Fit

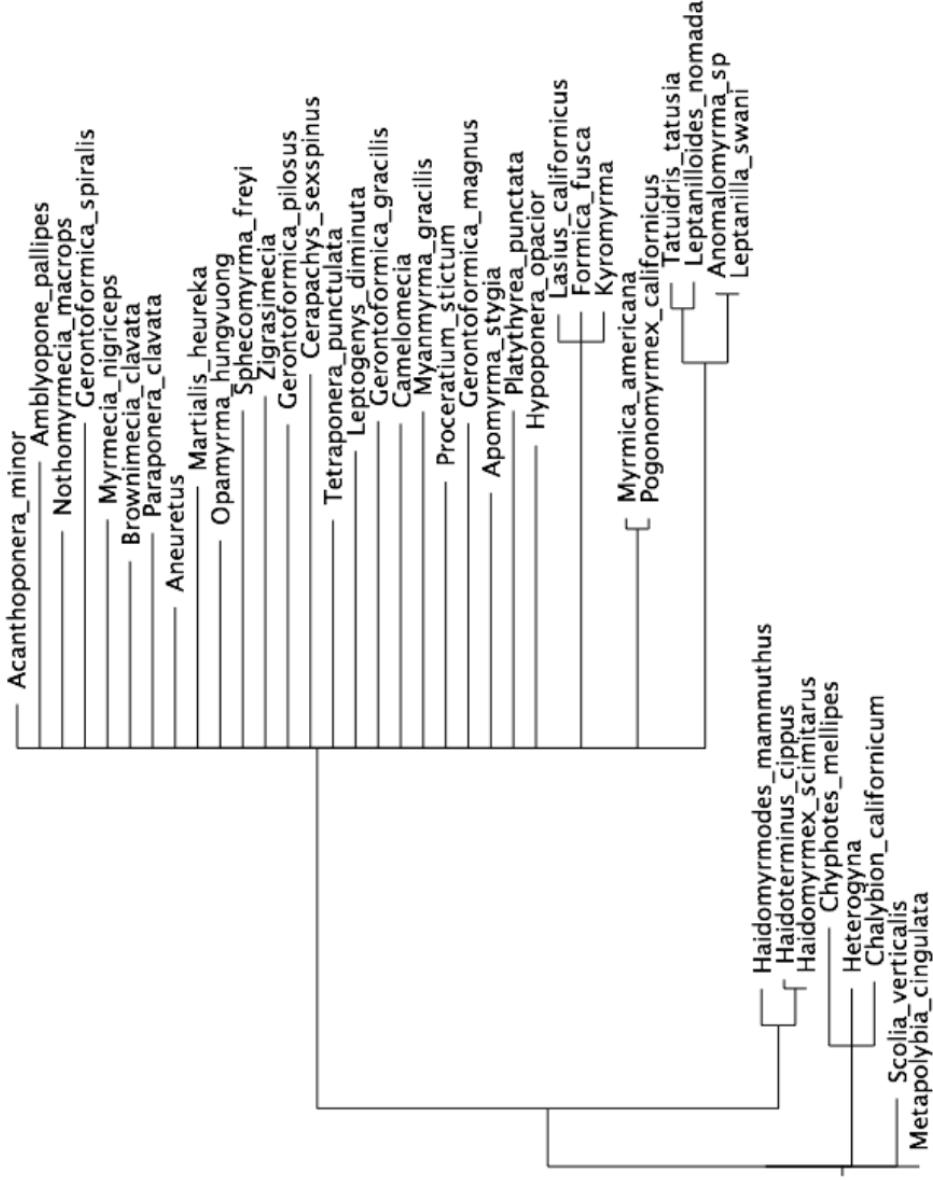
- Our flexible model fits the data better than the unexpanded Mk model



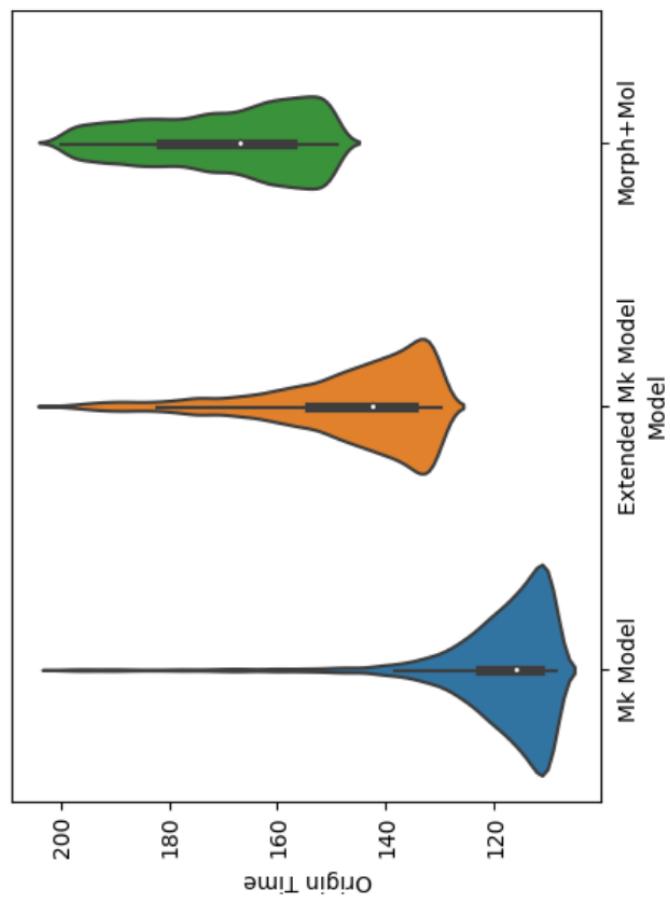
Maximum Clade Credibility Tree



Consensus tree considerably unresolved



An improved model of morphology brings molecular and morphological estimates of the age of ants closer together



Conclusions

- Parsimony vs. Bayesian is the wrong question
- The real question is "How can I incorporate my knowledge as a systematist into my mathematical models?"

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- Parsimony vs. Bayesian is the wrong question
- The real question is "How can I incorporate my knowledge as a systematist into my mathematical models?"
- When we do this, we are less certain of the answer
 - Probably, we can't resolve the ant phylogeny from morphology alone
 - But the model shows promise for jointly analysing molecules and fossils together
 - This model shows promise for integrating the whole of the knowledge from careful morphological systematics with the sampling effort and knowledge of molecular systematics

Thank you!

- Walker Pett, Tracy Heath, Rachael Johnson, Katharyn Jenkins, Patrick Mendoza
- Moreau Lab
- Brendon E. Boudinot

