


# 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**

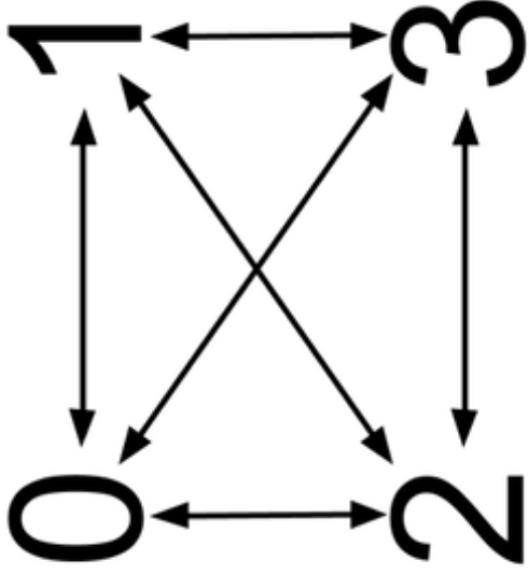
Pablo A. Goloboff , Ambrosio Torres, J. Salvador Arias

## **Bayesian Mk Model vs. Maximum Parsimony**

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

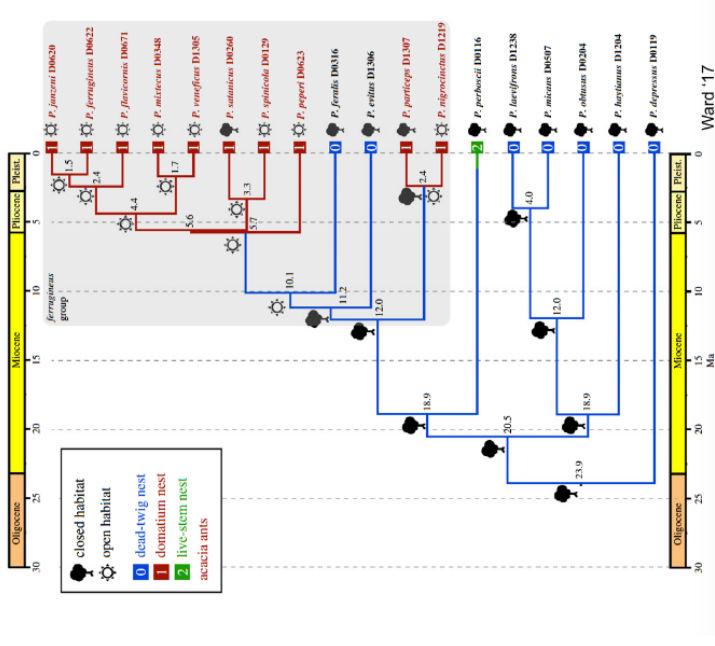
# Bayesian Mk Model and Maximum Parsimony

- I am going to argue throughout this talk, that this is precisely the wrong question to focus on
  - The base assumptions of these methods are not all that different



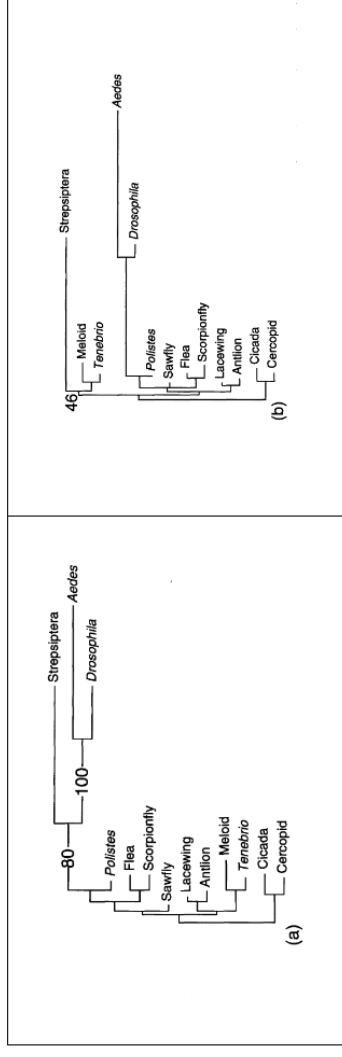
# Bayesian Mk Model and Maximum Parsimony

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Huelsenbeck, 1998

# Bayesian Mk Model and Maximum Parsimony

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  - 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** ▼

# Bayesian Mk Model and Maximum Parsimony

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## **Bayesian Mk Model and Maximum Parsimony**

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  - Which model do we believe?
  - Which model can we improve?

# Bayesian Mk Model and Maximum Parsimony

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

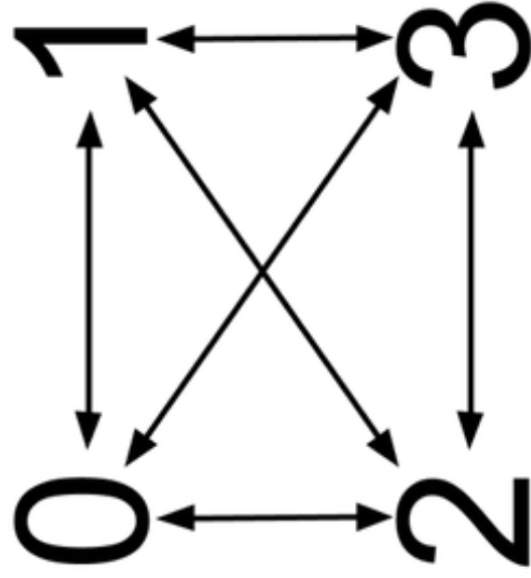
- Wright, Lloyd and Hillis 2016, adapting Mr. Bayes

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

APRIL M. WRIGHT<sup>1,\*</sup>, GRAEME T. LLOYD<sup>2</sup>, AND DAVID M. HILLIS<sup>1</sup>

## Extending the Mk model

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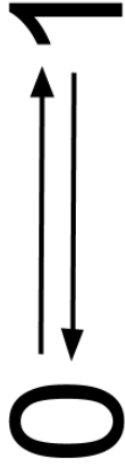
## Presence of stem ants

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



## Extending the Mk model

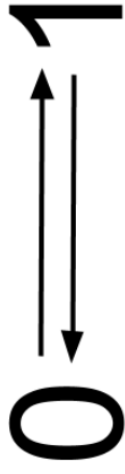
- Wright, Lloyd and Hillis 2016, adapting Mr. Bayes



*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.



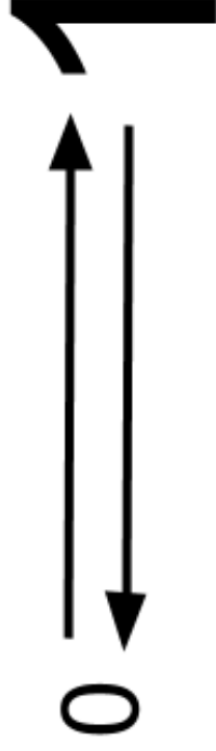
## Extending the Mk model

- 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

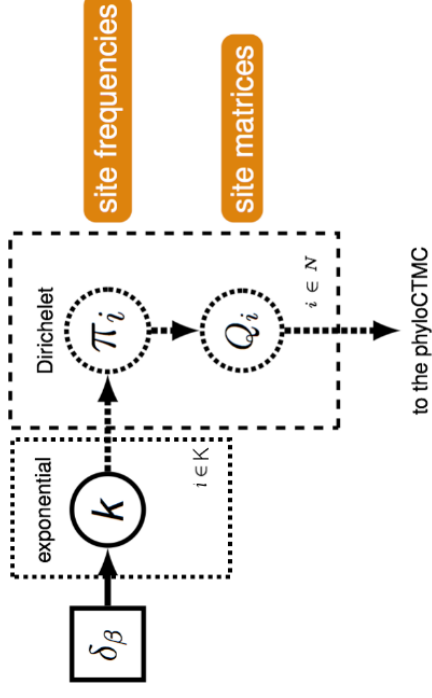
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## Extending the Mk model

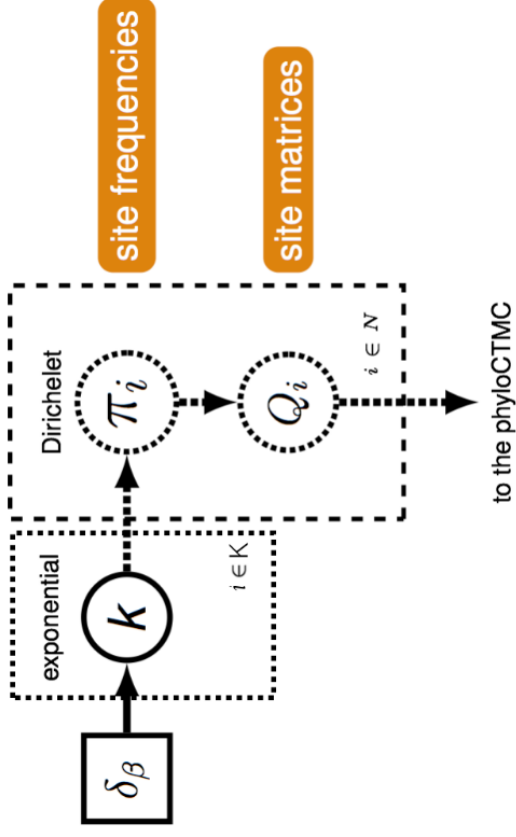
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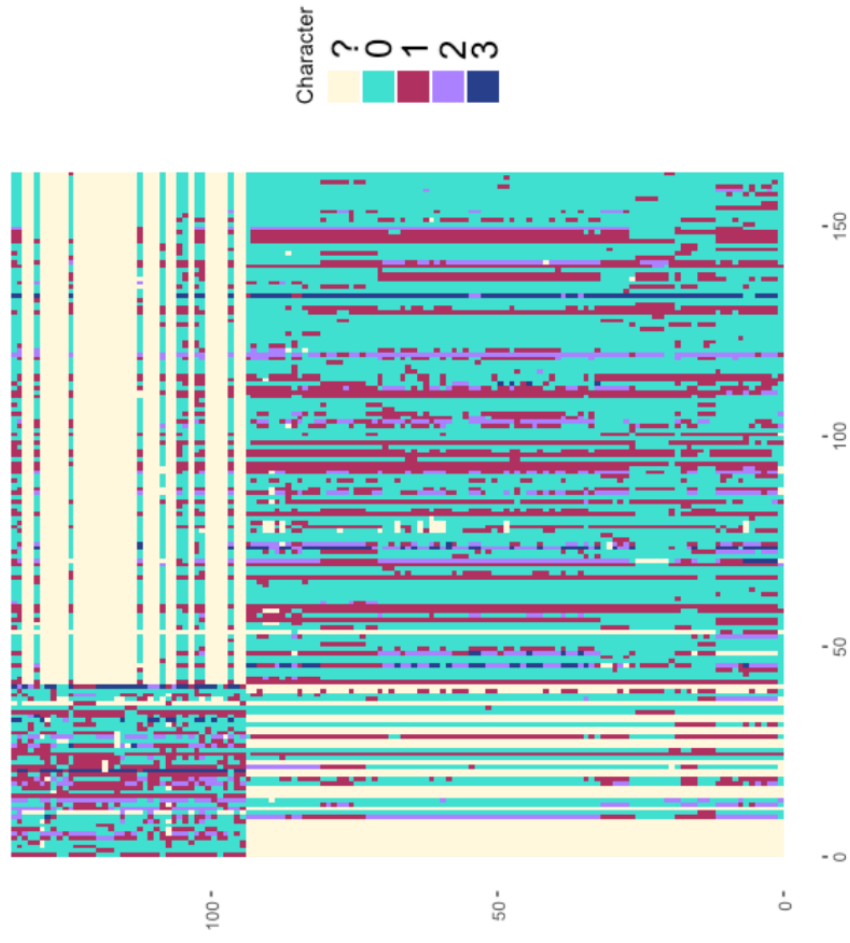
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# Extending the Mk model

- 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



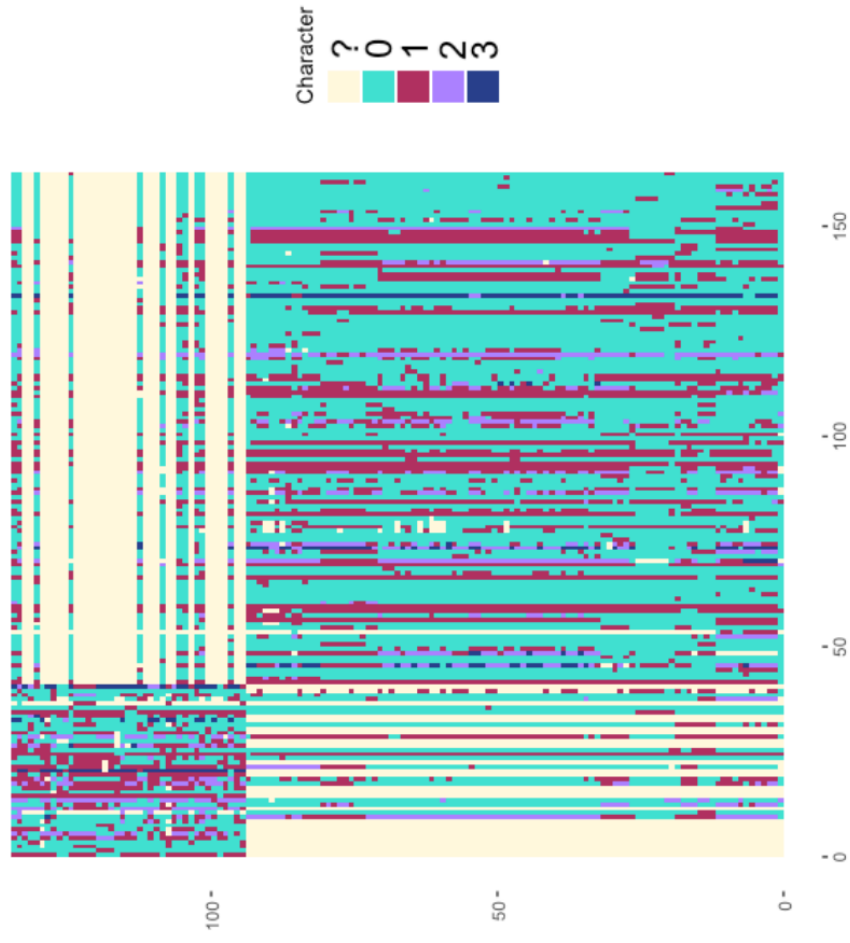
# Why extend the model



# Dataset

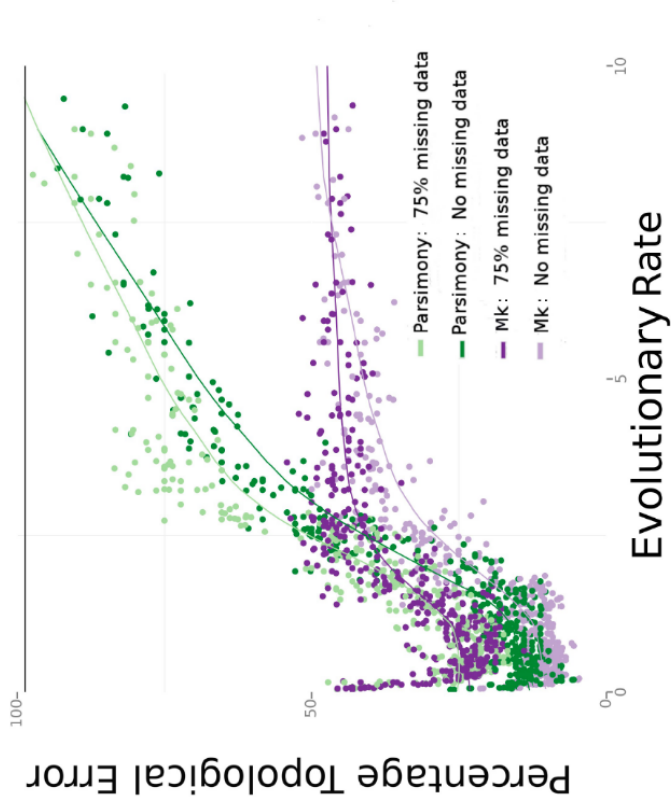
- Multistate dataset of fossil ants from Barden (2016)
- Combined with extant ants Keller (2011)
- Estimated phylogeny from:
  - Each dataset individually
  - Each dataset individually, pared down to binary characters
  - Combined dataset
  - Combined dataset, pared down to binary characters

# Why extend the model



# Why extend the model

Models matter more when the problem is hard



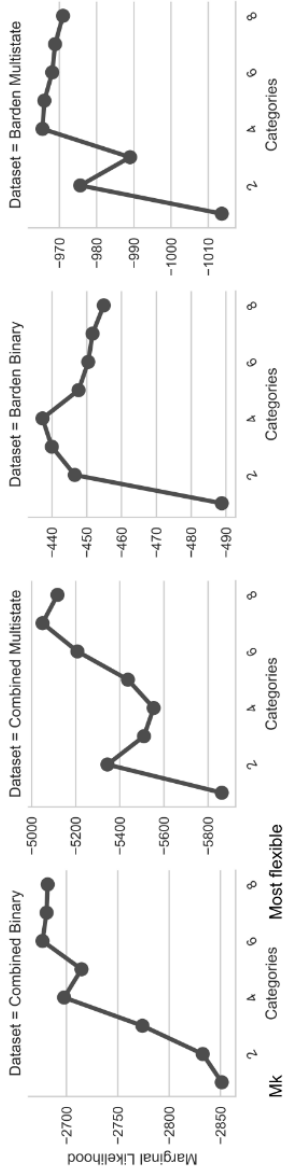


## Why extend the model

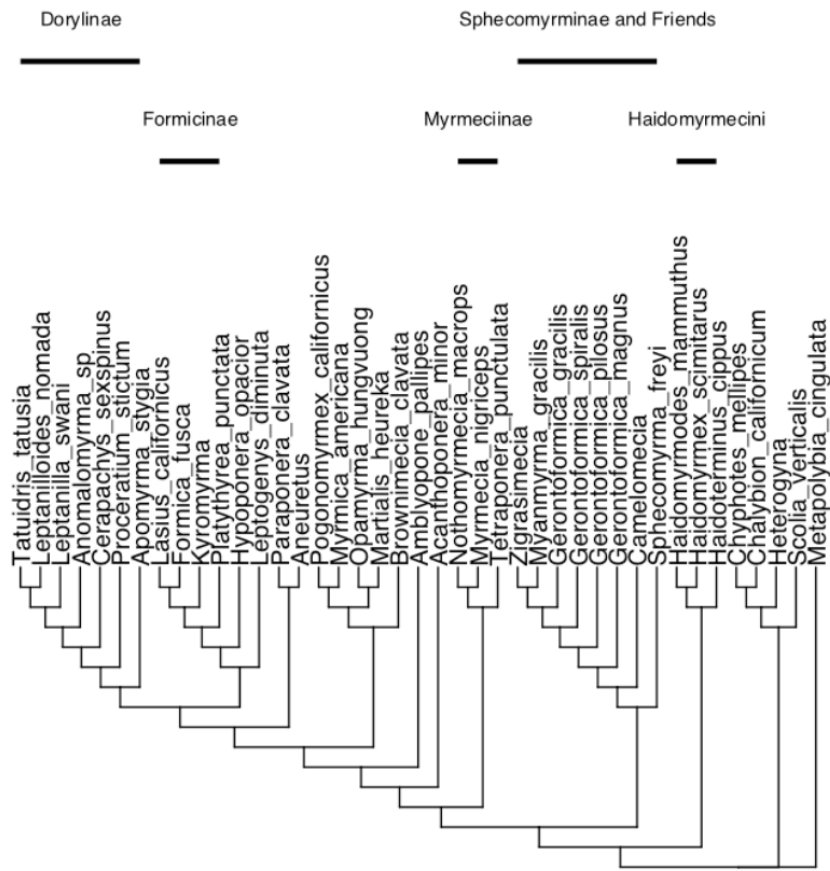
- Testability
  - Bayesian methods have a rich and flexible literature on testing to check goodness of model fit, and to compete models against one another

# Model Fit

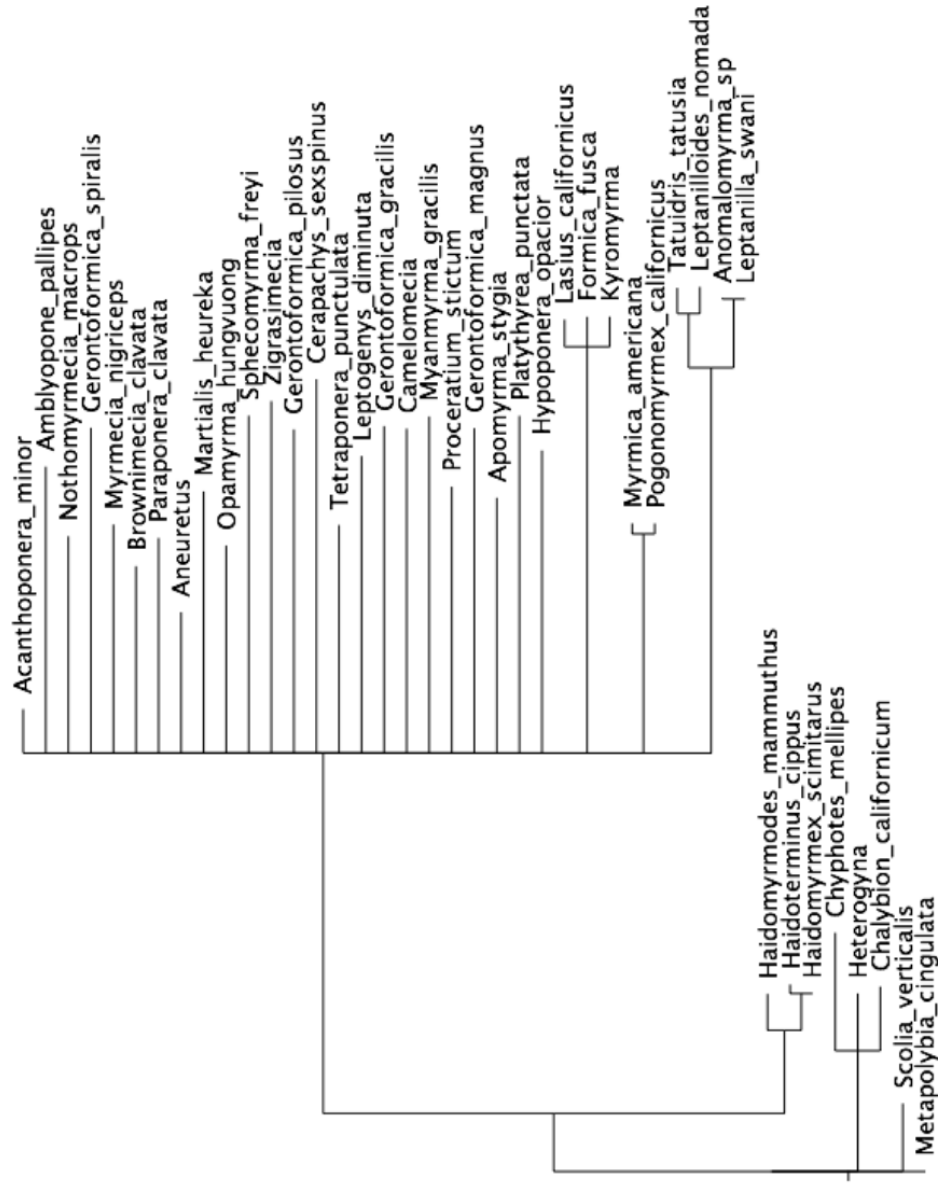
- Our flexible model fits the data better than the unexpanded Mk model



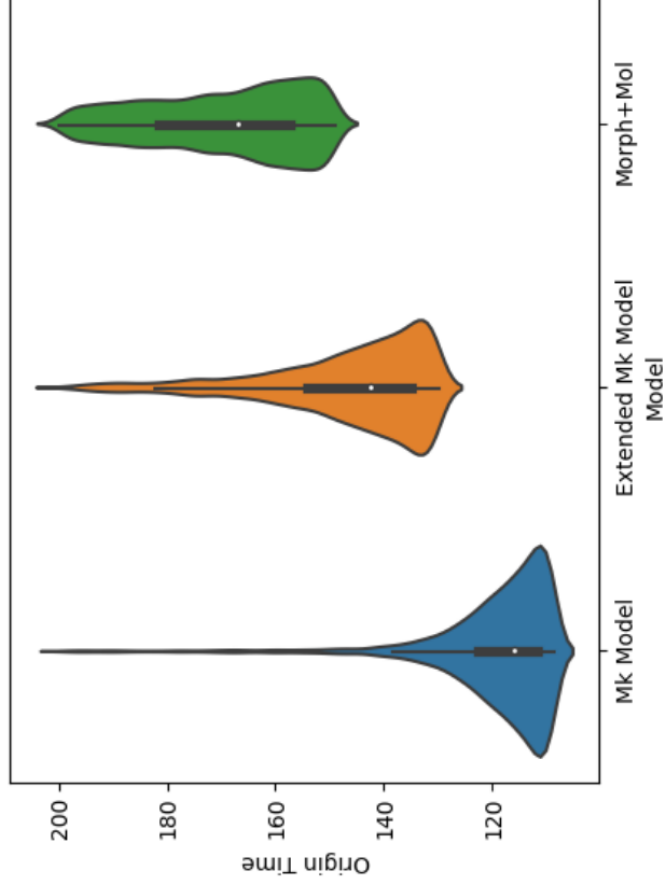
# Maximum Clade Credibility Tree



# 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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# 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?"
- 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

