Predicting Missing Values in Biodiversity Datasets Using Phylogenetics and Spatial Mapping

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Introduction

- Large biodiversity datasets with many missing values have become common in ecology.
- Filling in missing values is critical to understanding biodiversity in the age of climate change.
- Models based on both phylogenetic and spatial factors can be used to predict missing trait values.
- Such models use the Monte Carlo method to solve multi-dimensional integrals

Objective

- To demonstrate that a Bayesian method of imputation that combines phylogenetic and spatial methods will outperform existing imputation methods.

Methods

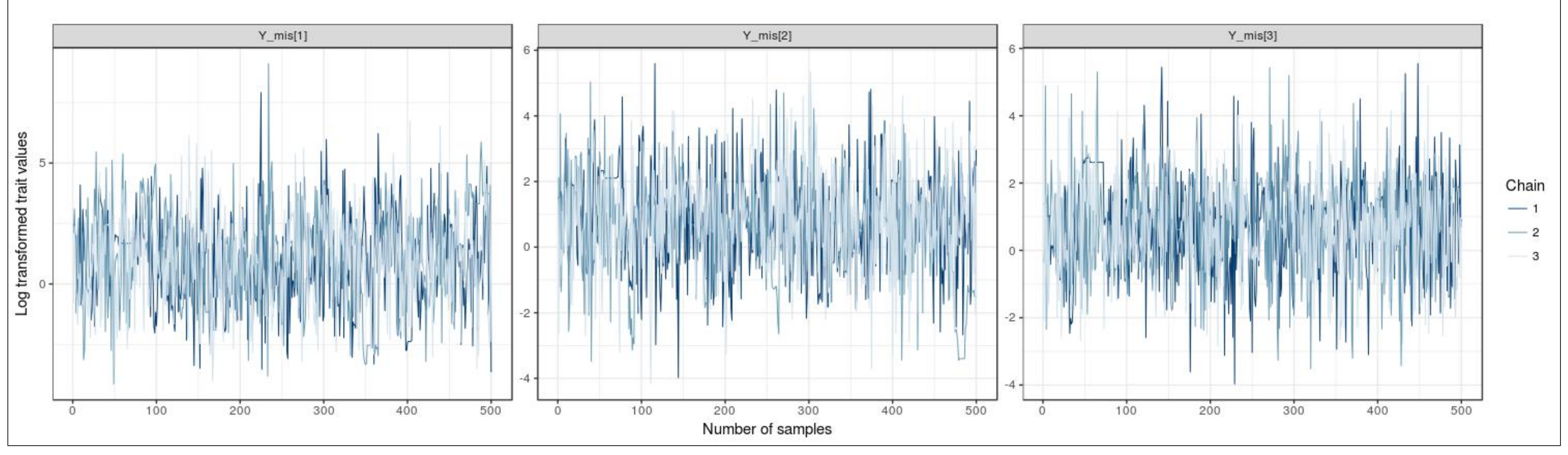
- Data was removed at random from a North American forest tree species dataset.
- Trait values were imputed using packages available in the R programming languages.
- The imputed values were compared to the known values with 95% confidence intervals.
- The combined model was developed using STAN, a programming language for statistical inference written in C++ .

$$y \sim X\beta + Z\alpha + \varepsilon$$

y = imputed traits
Z = identity matrix
X = predictor matrix
α = phylogenetic random effects
β = fixed effects/slope
ε = residuals

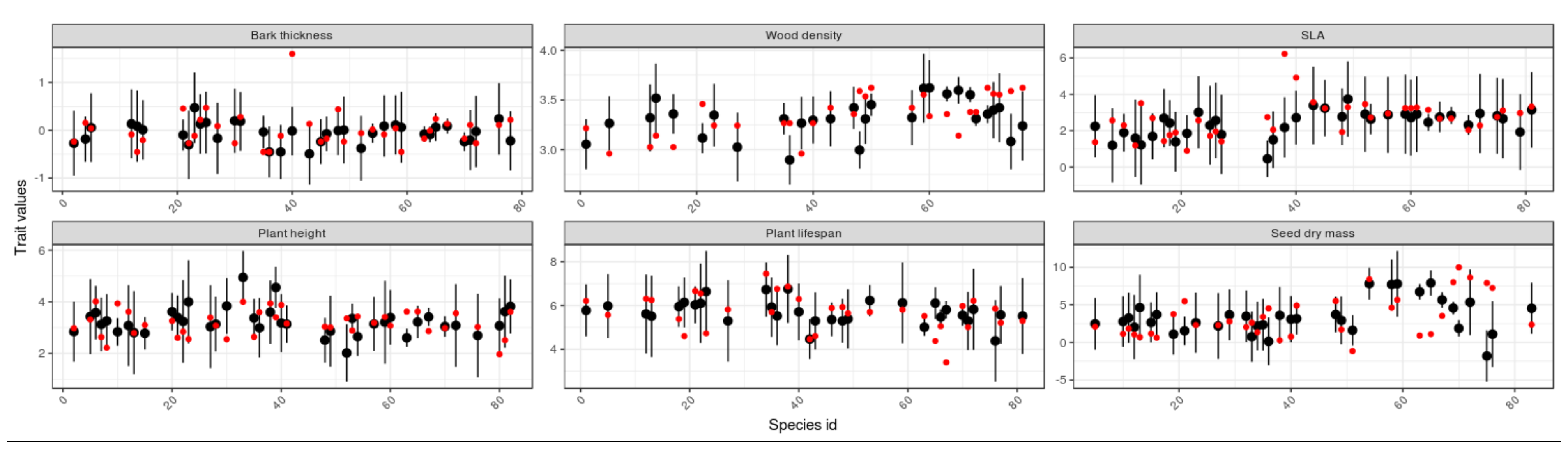
- The Ornstein-Uhlenbeck process was used to model the phylogenetic tree reconstruction.

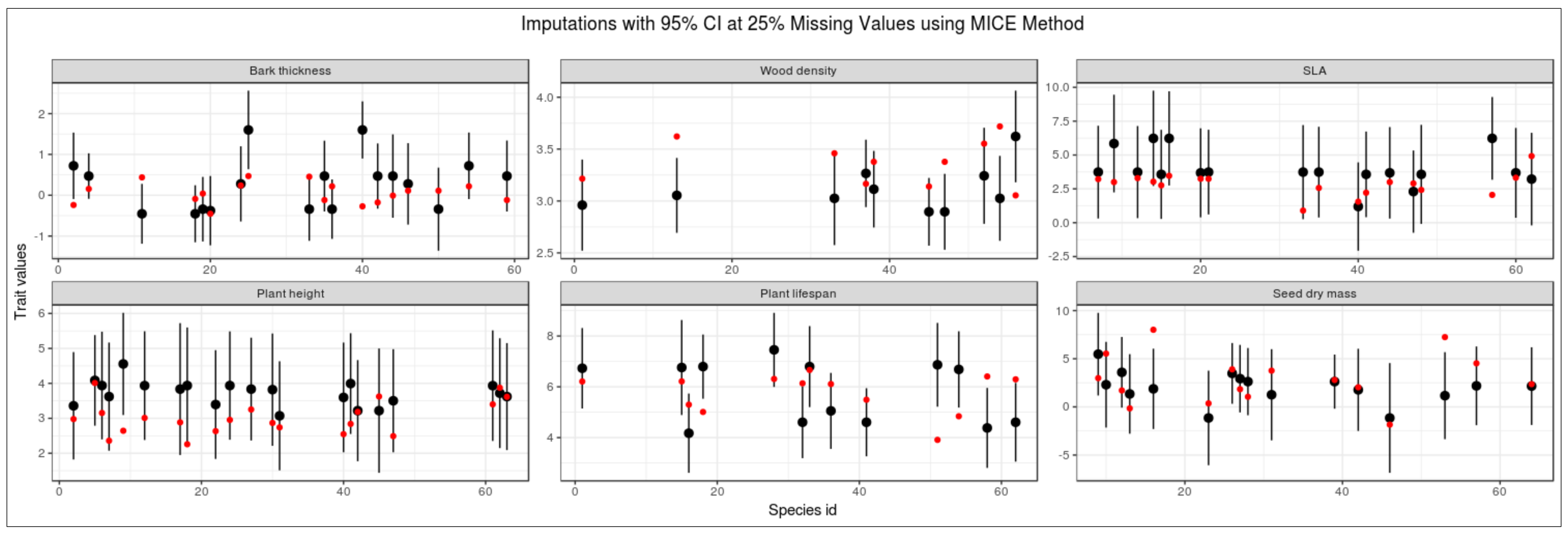
Monte Carlo Method Convergence



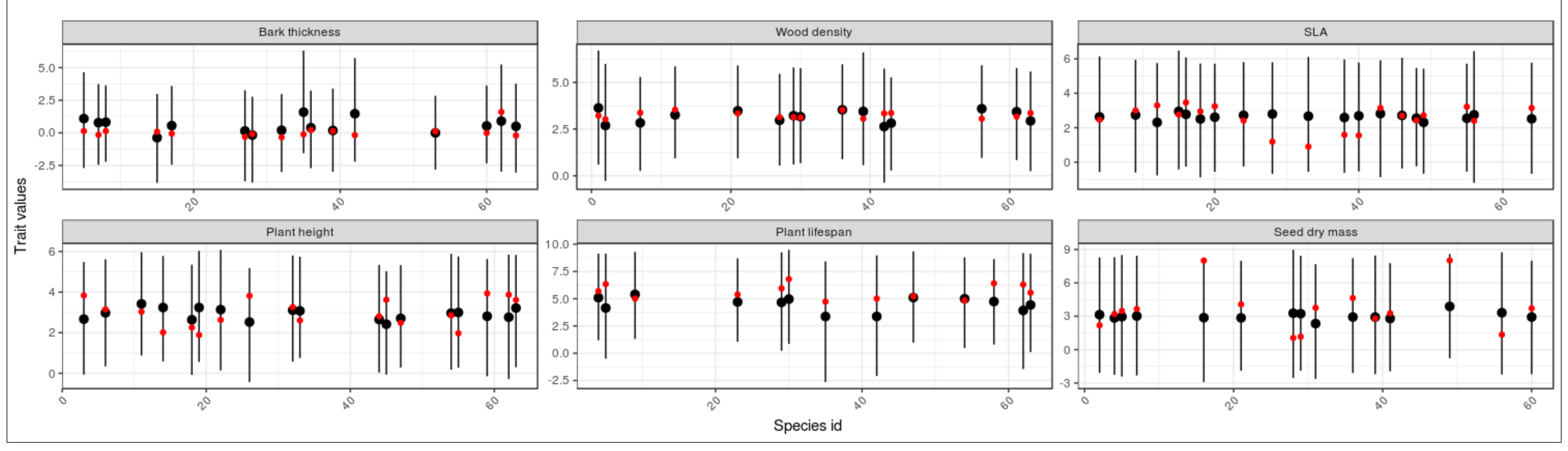
Results

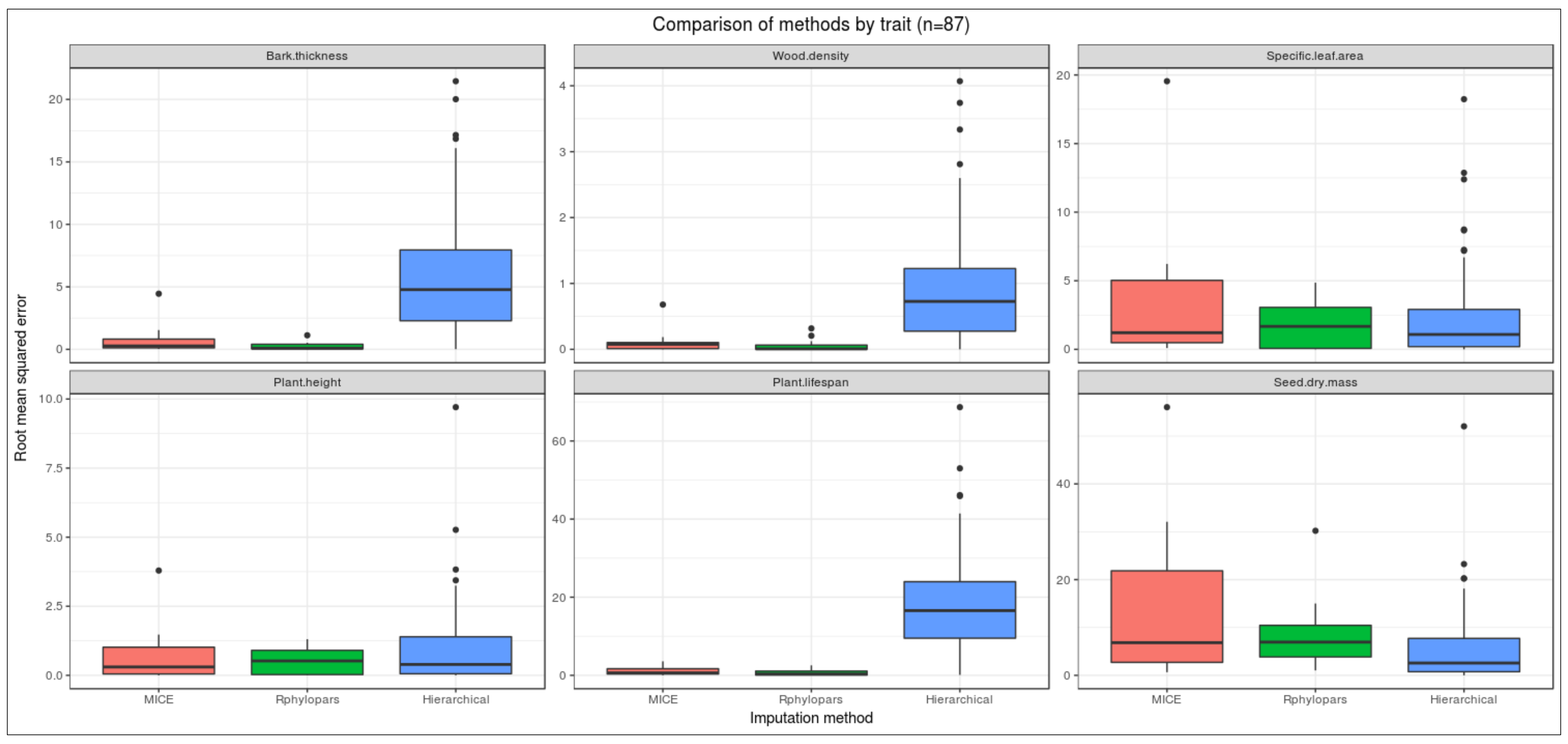
Imputations with 95% CI at 25% Missing Values using Phylogenetic Method





Imputations with 95% CI at 25% Missing Values using Hierarchical Model





Conclusions & Future Work

- The proposed Bayesian model imputed values better for some traits than others compared to phylogenetic and multivariate imputation.
- Continue to test the model at varying rates of missing data while using different phylogenetic and spatial parameters.

Acknowledgements

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