

Imputation of demographic traits using phylogenetic and functional trait information

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1. Introduction

Threats such as habitat loss and degradation, climate change and overexploitation impact populations by influencing vital rates. Understanding population responses to these pressures is vital for identifying at-risk species and to guide conservation interventions.

Demographic models parameterised with estimates of population vital rates are used to explore such responses by projecting a population's performance under different threats. However, obtaining estimates of vital rates requires investment of resources and time which may be lacking in a critical conservation setting. Moreover, the most at-risk species may be those for which data is lacking due to biases in recording or logistical barriers to collecting life history data.

3. Results

The accuracy of imputed vital rates depended on which vital rate was imputed, with greatest accuracy for adult survival rate and the least accuracy for fecundity. Imputation accuracy tended to decrease as the number of missing vital rates increased and was influenced by the combination of vital rates being imputed. The inclusion of body mass improved the accuracy of imputed adult survival rates when several vital rates were missing (Figure 2).



Challenges

- Vital rate information is available only for a small and biased subset of species
- Vital rate information is partially complete, with certain vital rate or stages not represented

We use a phylogenetically informed approach to assess the feasibility of filling knowledge gaps in demographic data using estimates for related species. Demographic traits, which are constrained by shared evolutionary history and trade-offs between vital rates, may be good targets for phylogenetic imputation methods.

Fig. 2: Imputed vs observed mean vital rates

Population growth rates derived from imputed values were a good match for the original value when only survival and growth rates were missing. When fecundity was imputed, the accuracy of population growth rates decreased (Figure 3).



2. Methods

We extracted demographic data for 36 species of birds from the COMADRE database of matrix population models and calculated standardised vital rates corresponding to survival of adult and juvenile stages, fecundity and maturation. In addition, we gathered morphometric, life history and ecological trait data and constructed a phylogeny for the species.

We performed cross-validation by excluding one or more vital rate estimate for a species at a time and using phylogenetic imputation to obtain imputed values for each vital rate. We compared the accuracy of phylogenetic imputation of demographic data over different numbers and combinations of missing vital rates. Further, we assessed the impact of incorporating body mass by carrying out imputation over an extended trait data set (Figure 1).

Vital rates	Body mass	Life history	Ecology
\checkmark			

Fig. 3: Population growth rate derived from imputed vs original mean vital rates

4. Conclusion

We have shown that the accuracy of vital rates obtained using phylogenetic imputation is influenced by constraints on individual vital rates and that demographic rates derived from imputed values are affected by the number and combination of vital rates estimated. Phylogenetic imputation is most successful for survival rates, suggesting that research efforts should focus on gathering accurate information about fecundity and growth. Further work will determine whether including additional functional trait data can improve the accuracy of vital rate imputation.



Fig. 1: Proposed trait sets for phylogenetic imputation incorporating standardised vital rates, body mass, life history and ecological traits

We compared the imputed and original values to allow us to determine the accuracy of imputation among the standardised vital rates. We reconstructed matrix models using the imputed values and calculated a derived metric, population growth rate, for comparison with rates calculated from the original matrix models to identify biases arising from the use of imputed values.

