# Increasing the tractability of occupancy models

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## Abstract

place holder

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# Introduction

Estimating the proportion of sites occupied by a species is common challange for many subdisciplines ecology and evolution including metapopulation, engangered and invasion biology. Greater acceptance of the biases of imperfect detection has lead to the development and proliferation of occupancy models, which model the occurrence of a species at a site as a latent state layered underneath a detection process (e.g., MacKenzie *et al.*, 2006; Royle & Kéry, 2007). Now only a little over a decade after occupancy models were introduced to ecology, they are being used to model the occurence of everything from bees (M'Gonigle *et al.*, 2015) to tigers (Hines *et al.*, 2010) in an endless variety of complexity.

Occupancy models are part of a larger class of models known as Hidden Markov Models. For discrete Hidden Markov Models like occupancy models where a species is either present or absent from a site, likelihood calculation involves summing over the distribution of latent states. Because estimating the effect of explanatory variables on site occupancy or shared variation of in occupancy across species is often of greatest interest to ecologsits (e.g., Iknayan *et al.*, 2014), the Hidden Markov Models are embedded in a larger hierarchical model. In such cases, practitioners may rely on Markov chain Monte Carlo (MCMC) to perform a Bayesian analysis. Such models are computationally intensive, and large models requiring hundreds or thousands of dimensions which require MCMC can be computationally impractical. To ensure occupancy models are accessible to practitioners, more efficient methods for estimating these models are necessary.

# Materials & Methods

# Results

# Discussion

# Acknowledgments

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