# MODELING AVIAN RESPONSES TO CLIMATE CHANGE USING EVOLVING OCCURRENCE MODELS

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# Introduction

The geographic distributions of species are limited by environmental constraints, some of which are influenced by a changing climate. As climate warms, species are shifting their ranges toward the poles or to higher elevations. Numerous teams predict future ranges of species given current occurrence data and projections of climate change using niche envelop modeling. The method has been criticized because: 1) interspecific interactions are ignored, 2) species are static in their genotypes and niche dimensions, and 3) individuals are unlimited in their dispersal abilities. We have devised a novel approach that addresses these concerns. We are representing species and their niche dimensions in an agent-based context, with those niches defined using regression trees with splitting values that will evolve under selective pressure. Spatial surfaces reflecting projected climate change will be substituted for observed climate data. Simulations will continue, with the ranges and incidences of avian species changing in response to the projected change in climate plus the myriad biotic interactions represented in the simulations.

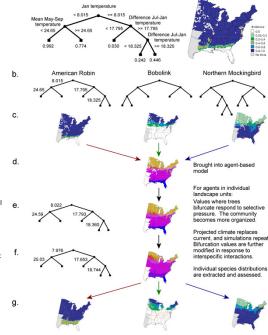
# Methods

We constructed regression trees for 251 bird species of the coterminous US. Species data are drawn from the USGS Breeding Bird Survey. For more than 40 years thousands of routes have been surveyed annually. We are using a suite of spatial layers (e.g., climate and weather, productivity, land cover, phenology) as explanatory data to create trees for species. Raster layers and bird data were generalized to EPA EMAP hexagons, which are a statistically rigorous tessellation of the US with hexagons ca. 640 km<sup>2</sup>.

The distributions of each species was recreated in an agent-based model using the trees and spatial data. The capacity of hexagons to host bird species may be set based on biogeographic theory (e.g., Hansen et al. 2011) or the observed richness. Individual species will be allowed to disperse and occupy hexagons to which they are well adapted. An evolutionary programming approach will be used to allow subtle changes in the splitting values in each species' regression tree, enabling niche packing. Surfaces that will change in response to a changing climate will be replaced in the model. Species will then be allowed to compete and shift their distributions and relative abundances. When distributions reach stability, those distributions will be compared to those from more traditional methods.

American Robin

A pictorial representation of our methods, drawing on products from Matthews et al. (2004) for bird information. Regression trees (a) for bird species will describe the incidence of species across the US. These trees (b, c) will be used in an agent-based model (d), where species will compete to occupy landscape units. Points of bifurcation in trees will slowly evolve (e) through simulation cycles, with each agent able to have unique but related values. The simulation will stop when distributions are stable. Current climate data will be replaced with projected climate data in the application (f) and simulations will continue, with agents producing mutated offspring that may occupy nearby landscape units and bifurcations continuing to slowly evolve in response to changing climate and interspecific interactions. Resulting incidences (g) will be the result of both climate change and intra and interspecific interactions.



#### **Creating Regression Trees**

The utility of boosted regression trees (De'ath 2007; Elith et al. 2008) as full models and using only the single best-fitted tree was assessed (Table), and the method was unsuitable for modeling four selected species. Trees were created using a series of raster explanatory layers (e.g., MODIS Vegetation Continuous Fields, PRISM climate data, MRLC land cover) and BBS observations. Boosted regression tress described the 90% training data well, but when compared to a 10% test set, fits were poor. Further, using the single best-fitted tree, which is required for the agent-based approach we are using, led to poor fitting trees. CART single regression trees (Breiman et al. 1994) yielded trees that had lower fit than boosted regression trees, but they were robust when tested with novel data. We are therefore using CART trees in agent-based modeling.

Table. Model comparison for avian species abundance prediction in the continental United States

	Boosted Full Model		Boosted Main Tree		CART Tree	
	Train R <sup>2</sup>	Test R <sup>2</sup>	Train R <sup>2</sup>	Test R <sup>2</sup>	Train R <sup>2</sup>	Test R <sup>2</sup>
Eastern Bluebird (n = 1922)	0.692	0.419	0.314	0.273	0.418	0.549
Canada Goose (n = 1697)	0.631	0.034	0.130	0.008	0.306	0.315
Bald Eagle $(n = 457)$	0.572	0.060	0.070	0.002	0.267	0.312
Greater Sage Grouse (n = 95)	0.812	0.007	0.032	0.000	0.255	0.209

Note: Data for all species were split into Training (90%) and Test (10%) datasets

### Agent-based Modeling

A draft of the agent-based model is complete, and is being tested. Six parameters control model operation, including the rate of mutation and weightings that reflect the importance of relative abundance, occupancy, and depth in tree as species compete for space. As species



compete, more abundant species may be favored, those occupying a hexagon in the previous time step may be favored, and those with leaves deeper in a binary tree may be considered more specialized and better adapted for the areas in which they may occur than generalists, and favored.

The performance of the agent-based model must be assessed, and the model adjusted and run until the distributions of species are stable and similar to observed patterns. Then we will replace explanatory climate surfaces with those portraying a changing climate, repeat simulations, and compare the distributions of species before and after climate change.

#### Merit

Agent-based modeling approaches are rare in macro-biological analyses. Rarer still are applications that include evolvable agents. And the inclusion of regression trees – a widely used approach in macro-biological analyses – that can evolve through time is a unique contribution. Straightforward modifications to a popular method may allow analyses to 'come to life,' and provide the potential for dynamic solutions to scenarios. An agent-based application representing evolving niche dimensions of species may be used to address questions of island biogeography, evolution and cladistics, fundamental versus realized niches, path dependence, community structure, the neutral niche paradigm, invasion, and other aspects of climate change.

# **Citations and Acknowledgements**

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