

MODELING AVIAN RESPONSES TO CLIMATE CHANGE USING EVOLVING OCCURRENCE MODELS

Randall B. Boone^{a,b}, Jared A. Stabach^a, and Sunil Kumar^a

^aNatural Resource Ecology Laboratory and the

^bDepartment of Ecosystem Science and Sustainability, Colorado State University, Fort Collins, Colorado

Introduction

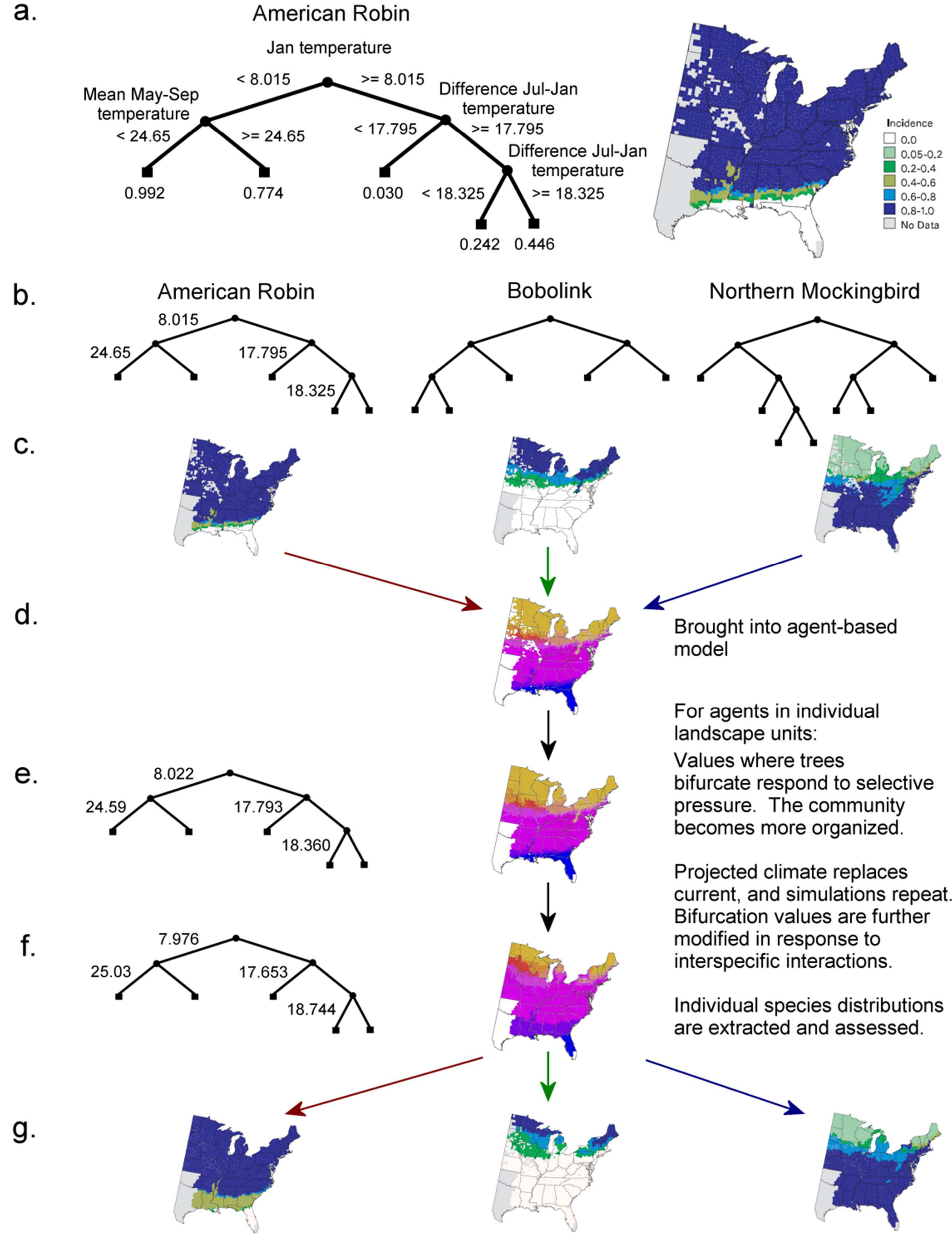
The geographic distributions of species are limited by environmental constraints, some of which are influenced by a changing climate. As climate warms, species are shifting their ranges toward the poles or to higher elevations. Numerous teams predict future ranges of species given current occurrence 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. Our methods: 1) incorporate intra- and interspecific interactions, 2) allow species involved to subtly alter their niches, and 3) adopt a localized view of the environment that prevents unrealistic dispersal distances. 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. Climate change responses will thus be projected in a dynamic way.

Methods

We are constructing regression trees for 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 boosted regression trees for species. Raster layers and bird data are being generalized to EPA EMAP hexagons, which are a statistically rigorous tessellation of the US with hexagons ca. 640 km². We anticipate between 100 and 150 species yielding regression trees with usable explanatory power.

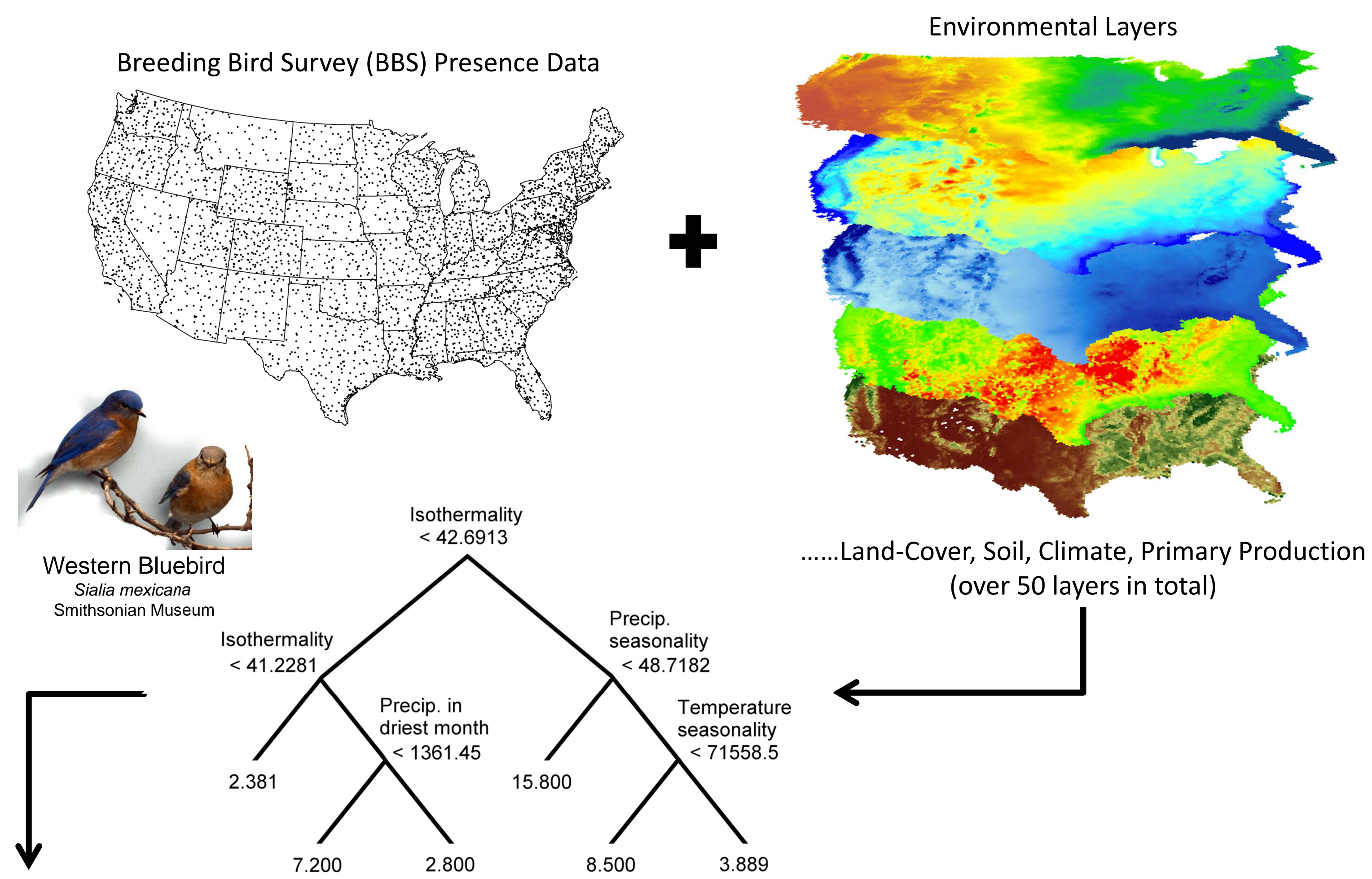
The distributions of each species will be recreated in an agent-based model using the trees and spatial data. The capacity of hexagons to host bird species will be set based on biogeographic theory (e.g., Hansen et al. 2011). Individual species will be allowed to disperse and occupy hexagons to which 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.

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 Boosted Regression Trees

To model avian species distribution, a series of raster layers from various sources (e.g., MODIS Vegetation Continuous Fields, PRISM climate data, and MRLC land-cover) are being amassed to associate with bird species presence locations identified from the Breeding Bird Survey 50-stop data. Boosted Regression Trees (BRTs) (De'ath 2007; Elith et al. 2008) will then be used to construct statistical models to predict bird species relative abundance in the U.S. BRTs are an improvement to single regression trees (Breiman et al., 1984), by predicting the response of a dependent variable through a series of additive regression analyses. This technique recursively partitions the dependent data into two homogeneous groups at an optimal independent variable value, improving model accuracy. The resulting best fit 'tree' will act to parameterize agent-based models and evolve changing species distributions over time.



Agent-based Modeling

The agent-based model will implement the evolutionary programming algorithm that allows competing species to shift their distributions in response to changing climate.

To-date, we have brought EMAP hexagons into the NetLogo modeling environment. Hexagons have been identified to state, selected explanatory variables have been mapped, and with those and the regression tree shown above, the relative abundance of Western Bluebirds was mapped, as shown.

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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