Global conservation prioritization approach provides credible results at a regional scale

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Abstract

Aim Conservationists and managers must direct resources and enact measures to protect species, despite uncertainty about their present statuses. One approach to covering the data gap is borrowing information from data-rich species or populations to guide decisions about data-poor ones, via machine learning. Recent efforts demonstrated proof-of-concept at the global scale, leaving unclear whether similar approaches are feasible at the local and regional scales at which conservation actions most typically occur. To address this gap, we tested a global-scale predictive approach at a regional scale, using two groups of taxa.

Location Maryland, USA.

Taxa Vascular land plants and lepidopterans.

Methods Using publicly available occurrence and biogeographic data, we trained random forest classifiers to predict the state-level conservation status of species in each of the two focal taxa. We assessed model performance with cross-validation, and explored trends in the predictions.

Results Our models had strong discriminatory ability, accurately predicting status for species with existing status assessments. They predict that the northwestern part of Maryland, USA, which overlaps the Appalachian Mountains, harbors a higher concentration of unassessed, but threatened plants and lepidopterans. Our predictions track known biogeographic patterns, and unassessed species predicted as most likely threatened in Maryland were often recognized as also needing conservation in nearby jurisdictions, providing external validation to our results.

Main Conclusions We demonstrate that a modelling approach developed for global analysis can be downscaled and credible when applied at a regional scale that is smaller than typical species ranges. We identified select unassessed plant and lepidopteran species, and the western, montane region of Maryland as priority targets for additional monitoring, assessment, and conservation. By rapidly aggregating disparate data and integrating information across taxa, models like those we used can complement traditional assessment tools and assist in prioritization for formal assessments, as well as protection.

Key words

Predictive modelling, conservation status, random forest, lepidopterans, plants, downscaling, prioritization, multi-taxon

Introduction

Conservationists and natural resource managers cannot wait until all the data are in, and must direct resources and enact measures to assess – and ultimately protect – species and populations, despite uncertainty about their present status. One stepping-stone approach to bridging the data gap is borrowing information from data-rich species or populations to guide decision making about data-poor ones (Callaghan, Nakagawa, & Cornwell, 2021; Free et al., 2020; Pelletier, Carstens, Tank, Sullivan, & Espíndola, 2018; Zizka, Andermann, & Silvestro, 2022), using predictive modelling frameworks. Increasingly, publicly available datasets that aggregate observations (Heberling, Miller, Noesgaard, Weingart, & Schigel, 2021) enable formulating and fitting predictive models to guide conservation and natural resource management (Bastin et al., 2019; Caetano et al., 2022; Callaghan et al., 2021; Panter et al., 2020; Pelletier et al., 2018; Zizka et al., 2022). The predictions from such models might be used to support conservation actions, and guide prioritization for resource-intensive status assessments (Pelletier et al., 2018). On the latter, national and subnational jurisdictions generate taxon-specific management plans triggered by formal status assessments (e.g., via National and State-level Endangered Species Acts in the United States (Department of the Interior, 1973; Nongame and endangered species conservation act, 2022)). In this context, status predictions from predictive models such as those mentioned above are not sufficient to trigger protections, but might undergird the listing process, by assisting with monitoring and assessment prioritization in a resource-limited

world.

Several knowledge gaps or “shortfalls” prevent strategic species protection (Cardoso, Erwin, Borges, & New, 2011b; Mokany & Ferrier, 2011). Here, we focus on the “Rabinowitzian” shortfall, i.e., the gap between knowing species’ occurrence patterns and using that information directly for evaluating their conservation risks (Cardoso, Erwin, Borges, & New, 2011a; Crisfield, Blanchet, & Gravel, 2022; Isbell et al., 2023; Rabinowitz, 1981). Models that use existing data efficiently can identify under-recognized patterns of threat and endangerment (Regan et al., 2008), and enable efficient allocation of monitoring, assessment, and protection resources (Hochkirch et al., 2021). For these goals, statistical learning tools that aggregate disparate data streams can recognize meaningful patterns that might escape notice in more granular analyses. These types of tools were used by Pelletier et al. (2018), who used only a handful of spatial and climatic covariates, and were able to predict the conservation status of unassessed land plants. They identified taxa likely to meet IUCN red list criteria, as well as previously unrecognized hotspot regions that likely harbor high concentrations of threatened but unassessed taxa. The authors anticipated that their approach could easily serve conservation needs at smaller spatial scales, which would make their method directly applicable at the scales at which most conservation actions take place.

Although the approach Pelletier et al. (2018) used can be technically readily implemented at nearly any scale, downscaling entails radical shifts in data availability, quality, and biogeographic representation that could improve or erode the utility of the approach. At smaller, regional scales, data quality may be more similar between assessed and un-assessed taxa, which should improve predictions. Additionally, at smaller scales, complete datasets containing a wider variety of potentially appropriate covariates (e.g., land use and its history) may be available. Nevertheless, at smaller spatial scales, records of species’ occurrences are unlikely to cover species’ whole ranges, and the number of species in a smaller region is also likely to be smaller, potentially limiting statistical power. Additionally, it is unknown whether the approach is extensible to other taxa beyond plants with little modification. If the same suites of geographic covariates can predict conservation status of disparate taxa, this predictive approach has high promise to assist in a variety of conservation contexts.

Here, we downscale the approach Pelletier et al. (2018) took to predict conservation statuses, applying similar methods to vascular land plants (the focal higher taxon in Pelletier et al. (2018), hereafter “plants”) and lepidopterans (a new focal group) within a sub-national management region (the state of Maryland, USA). We selected these two taxa because the state of Maryland maintains a rare, threatened, and endangered list for each (Maryland Natural Heritage Program, 2021a, 2021b)and the conservation biology of these two taxa differ (Isbell et al., 2023; Wagner, Fox, Salcido, & Dyer, 2021). We asked whether, despite differences in the quality and quantity of data available, as well as the ecology of the taxa upon which predictions are made, these highly general predictive modelling tools can help cover the Rabinowitzian shortfall, and guide conservation decisions at smaller, sub-national scales. In discussing our results, we evaluate model performance and prediction credibility, and then explore our predictions. We identify species that are likely threatened in the state of Maryland, USA, and regions within the state that are likely to harbor a high density of threatened, unassessed species. Finally, we use our case studies to discuss the promises and potential pitfalls of using similar predictive modelling tools for conservation prioritization at regional and local scales.

Materials and Methods

Method Overview

To predict the conservation status of lepidopterans and plants in the state of Maryland, we obtained publicly available species occurrence and spatial data. We used data for all assessed species to build random forest classifiers, tuning hyperparameters and evaluating model discriminatory ability, and expected generalization error, through nested cross-validation. Then, for each taxon group (i.e., lepidopterans and plants), we fit a final model that was trained on all assessed species, and uses these to predict conservation status for all unassessed species known to occur within the state. We mapped predictions to visually screen for spatial patterns, and then conducted a limited literature search to contextualize status predictions with independent lines of evidence. In the following sections, we provide details on the data we used, how we constructed and assessed models, the ways we generated and visualized predictions, and how we used independent lines of evidence to corroborate predictions.

Data

Plant and Lepidopteran Records

We obtained observations of plants and lepidopterans from the state of Maryland between 1989-2021 from GBIF (Appendix S2), irrespective of life stage. We filtered this dataset to include only records associated with valid species observed in the wild. We assigned each species to a conservation status category, based on Maryland's state-level rankings, as recorded in NatureServe (NatureServe, 2023). In order to do this, we first harmonized the taxonomies used by NatureServe and GBIF with programmatic tools from the R Packages *rgbif, natserv,* and *taxize* (Chamberlain, 2020; Chamberlain, Oldoni, et al., 2022; Chamberlain, Szoecs, et al., 2022), and some manual curation (Appendix S1), and then merged the NatureServe conservation status ranks with the occurrence data based on the consensus species identification. Because relatively few plants, butterflies, or moths had state conservation statuses in Maryland, we grouped their state conservation categories into three groups as follows: "secure" taxa were all those categorized as S4 or S5, "threatened" taxa were all those categorized as S1, S2, S3, SH, or SX; all other taxa were considered unranked. To restrict our analysis to only species considered native to the state, we first filtered records based on the national and subnational exotic/native fields from NatureServe, and subsequently, for plants, also filtered them based on a recent Maryland flora (Knapp & Naczi, 2020). Six threatened, one secure, and 331 unranked lepidopteran species, and 84 threatened, 20 secure, and 306 unranked plant species were dropped from future analyses because they were represented by only a single occurrence location. Overall, our filtered dataset contained records for, respectively, 29, 77 and 1269 threatened, secure and unranked lepidopterans, and 261, 123 and 940 threatened, secure and unranked plant species. The 1375 lepidopteran species were represented by a total of 78,184 records; 1324 plant species were represented by 110,232 records.

Environmental Variables

For each location record of a valid native species, we extracted latitude, longitude, and a suite of associated spatial variables. We extracted current and historic landcover, and indices of landcover change, from the National Land Cover Dataset (J. Wickham, Stehman, Sorenson, Gass, & Dewitz, 2021), which includes 30m x 30m landcover data at 5-year intervals from 2001 to 2016. We also extracted interpolated climate data from the expanded CHELSA dataset, which includes 19 variables that summarize estimated daily, monthly, and annual temperature and precipitation (bioclim), and an additional 50 variables derived from physical data such irradiance, pressure, and humidity, as well as

their relationships to biological tolerance ranges (e.g., growing season length estimates) at the resolution of 30 x 30 arc-seconds (Brun, Zimmermann, Hari, Pellissier, & Karger, 2022). Additionally, for each occurrence record, we extracted the estimated slope (at roughly 100m x 100m resolution) from the 1-m Statewide Slope layer (Eastern Shore Regional GIS Cooperative, 2021). In total, this included 69 spatial variables.

Although we gathered spatial data at the occurrence level, we fit models at the species level. To create the species-level datasets, we summarized each environmental variable across all occurrences of a species to a pair of summary statistics: for continuous variables we recorded the mean and standard deviation, and for categorical variables we recorded the modal value and the number of unique levels observed for the given species. In addition, for each species, we recorded the minimum and maximum latitude and longitude of their records. Variables with only a single value or missing values prevented model fitting and were thus dropped from the datasets for both groups of organisms. To serve as a sort of null model for variable importance, we also included a random continuous variable as a predictor in each model. Models were built using these 133 summarized species-level predictors.

Model Construction and Evaluation

We divided the dataset into a training dataset, comprised of all species within the categories "threatened" or "secure," and a prediction dataset, comprised of all unranked species. In order to tune hyperparameters and evaluate model performance, while retaining as much training data as possible, we used nested repeated 10 x 10-fold cross-validation. To do this, we created 10 x 10 outer folds of the training dataset, and on each outer fold, trained a random forest classifier using 10 x 10-fold cross-validation, using the R packages *caret* and *randomForest* (Kuhn et al., 2022; Liaw, Wiener, Breiman, & Cutler, 2022). On the inner folds, we conducted a grid search over the hyperparameter "mtry," which controls the number of features available to use for splitting the data at each node, and has been shown among the random forest hyperparameters to substantively affect model performance (Hastie, Tibshirani, & Friedman, 2017; Probst, Wright, & Boulesteix, 2019). We left the other hyperparameters at their default values, as these are typically considered adequate for model construction (Probst et al., 2019). We used the area under the receiver-operating characteristic curve (AUROC) as our measure of performance in parameter tuning, as this measure emphasizes model discriminatory ability (Ling, Huang, & Zhang, 2003). Although the Random Forest algorithm enables

less computationally intensive model assessment using out-of-bag errors, here we used traditional cross-validation, which would be applicable to any model fitting algorithm (Kuhn et al., 2022).

For each of the 100 outer folds, we fit a “final model” with the entire dataset, save the held-out fold, based on the selected hyperparameters, and used this model to make predictions on the held-out fold. Using random forest votes as a measure of class probability, we computed AUROC, and to evaluate model performance on unseen data, we computed the mean and standard deviation of the 100 AUROC values computed on these 100 outer folds. In addition, we recorded the mean and standard deviation in AUROC from the inner, tuning folds, as large differences between AUROC from the inner and outer folds could indicate a lack of stability in model performance, or a tendency to overfit the training data.

After the extensive cross-validation described above, we re-trained each model (i.e., one for plants and one for lepidopterans) on the entire training dataset, again tuning the hyper-parameter “mtry” with 10x repeated 10-fold cross-validation. We used the “final model” for each taxon group from this step to make all predictions on unclassified species. The performance estimates we obtained from previous cross-validation provide the expected performance of these final models on unseen data, with two major caveats. First, additional data were used to train the final models, which are therefore not exactly equivalent to the models built on subsets of the same data. Second, we use these final models for predicting conservation status for unassessed, rather than assessed species. For unassessed species, we can only evaluate model performance indirectly, by comparing predictions with non-definitive external data (see below).

Optimal Threshold

Depending on the application, greater precaution may be warranted for misclassification errors for either threatened or relatively secure species, implying different ideal thresholds for the share of random forest “votes” required to classify a species into a certain category. As the threshold for classifying a species as threatened increases, fewer species will be classified as threatened, and the chance of mis-classifying a species that is, in fact, relatively secure as “threatened” falls, while the chance of mis-classifying a threatened species as “secure” rises. In evaluating model performance, we focused on discriminatory ability (using AUROC, which effectively considers all possible dichotomous

thresholds (Hand, 2009)), and did not assess accuracy (i.e., the average rate of prediction errors) (Ling et al., 2003). However, in order to visualize predictions, we selected a binary classification threshold, acknowledging that across different applications, other thresholds might be preferable (Walker, Leão, Bachman, Bolam, & Nic Lughadha, 2020). To set a threshold, we assumed equal costs of misclassification for threatened and secure species. For each taxon group, we selected the threshold that maximized summed sensitivity and specificity on out-of-fold training data using the function *performance* from the R package *ROCR* (Tobias, Sander, & Beerenwinkel, 2022).

Visualizing Predictions

We created state maps using the R packages *raster, tigris, sf, rnaturalearth,* and *ggplot2* (Etten et al., 2023; Massicotte, South, Hufkens, & Philippe, 2023; Pebesma et al., 2023; H. Wickham et al., 2022) to visualize areas in which many records of putatively threatened species were found. We divided the study region into 8km x 8km grid cells, and each cell value represented the number of species classified as threatened according to the threshold for each higher taxon (see above). Such maps can be used to prioritize locations for additional survey and assessment resources, or to prioritize locations for conservation funding, as locations with a high concentration of putatively threatened species may both yield valuable data for evaluating species' conservation statuses, and warrant precautionary protection.

Assessing Predictors

Random forest models are poorly suited to inference on causal relationships, but it is possible to diagnose which predictors most strongly drive model predictions. Towards this end, we measured "MDA" using the R package r*andomForest* (Bénard, Da Veiga, & Scornet, 2022; Breiman, 2001; Ishwaran, 2007; Liaw et al., 2022). MDA approximates the degree to which each variable improves the predictive accuracy of trees within the random forest. We ranked all variables based on their MDA scores within each cross-validation run such that the variable with the greatest MDA score in a particular run would be ranked first. We then plotted the distribution of MDA ranks across cross-validation runs for the top five predictors for each taxon group. Variables exhibiting consistent, low MDA ranks had relatively strong and/or clear associations with conservation status.

Literature Search

Although we cannot directly test whether predictions on unassessed species are correct without formal status assessments, we can use external data sources as additional lines of evidence to corroborate or challenge our predictions. To do this, we gathered external data for the ten species for each taxon group that received the most and fewest votes for the category “threatened”. For each of these species, we first asked if the species had been recognized as threatened in nearby jurisdictions by querying the species name on NatureServe (NatureServe, 2023)(Appendix S2). If we found that a conservation status had been assigned elsewhere in Eastern North America (i.e., the continental USA east of the Mississippi, and the Canadian provinces of Ontario, Québec, Nova Scotia, New Brunswick, Newfoundland and Labrador, Prince Edward’s Island, and tribal/first nations lands within this region), we attempted to recover documentation of a previous status assessment. A match between our status prediction and the recorded statuses in neighboring locations supports our prediction. Second, we also examined contemporary geographic range data for the same top species. To do this, we visualized recent occurrence records for each species using iNaturalist (iNaturalist Network, 2022). For species predicted as “threatened” (and the opposite for species predicted as “secure”), if it appeared that species current range limits may be in or near Maryland, we considered our predictions further supported.

Results

Model Construction and Performance

On average, the discriminatory abilities were considerable for models for both taxon groups (mean AUROC plants = 0.720, sd = 0.091; lepidopterans = 0.846, sd = 0.134; Fig. 1), with both models generally outputting higher “threatened” probabilities to threatened species than to secure ones (Fig. 2). We did not detect large differences in AUROC between the inner and outer folds, which would have indicated unstable models. Hyperparameter selection was highly variable for lepidopteran and more consistent for plant models (mean mtry for plant models = 2.1, sd = 0.4; lepidopterans = 16.5, sd = 28). Assuming equal cost to misclassification for both threatened and secure species, the optimal fraction of random forest votes to consider a species “threatened” (vs. “secure”) for binary classification differed between the two taxon groups: 0.606 for plants and 0.348 for lepidopterans. At these thresholds, both models accurately classify previously assessed species.

Predictions for unassessed species

At the selected vote thresholds, our classifiers predicted 53% (502/940) of unassessed plant species and 63% (798/1269) of unassessed lepidopteran species as threatened in Maryland (Table S1). The most predictive variables differed between plants and lepidopterans (Fig. 3). For lepidopterans, variables related to coldest temperatures tended to place among the top variables. These included the mean last and first days of year above critical temperatures (5° and 10° C), the mean daily minimum temperature in the coldest month, and the latitude of the northernmost Maryland record. For plants, the top variables were often associated with variability, such as that measured in daily mean air temperature during the coldest month, and in daily and annual temperature ranges. The mean maximum relative humidity and maximum Maryland latitude were also important predictors for plant conservation status.

Model predictions highlighted the northwesternmost part of the state as a possible conservation hotspot for both plants and lepidopterans (Fig. 4). Although unassessed species predicted as "threatened" were found throughout the state, their occurrence records appear concentrated in the northwestern half of Maryland (Fig. 4). Furthermore, the mean per-cell predicted threat probabilities showed a strong east-west gradient, with the highest mean threat probabilities in the westernmost parts of Maryland (Fig. S1). In the case of plants, a higher number, but not high proportion, of species were predicted as "threatened" in the Piedmont region in the center of the state (Figs. 4, S1).

When corroborating predictions with external data, we found that species with high "threatened" probabilities were either unassessed in Eastern North America (5/20) or had been identified as Vulnerable or Imperiled in at least one nearby jurisdiction (15/20). Recent occurrence patterns for many of the species strongly predicted as "threatened" suggest they have a range primarily north of Maryland, often with southern range extensions along the Appalachian Mountains (Table 1). Lepidopterans receiving the highest "secure" probabilities were rarely listed as Vulnerable or Imperiled in nearby jurisdictions (1/10). The case was different for plants, where 9/10 species had been assessed as Vulnerable or Imperiled elsewhere in Eastern North America; primarily to the west and north of Maryland. We note that many of these plant species had also been assessed as relatively secure in coastal states from Delaware southwards, where climates tend to be warmer and where their ranges primarily extend. These patterns also support, to some degree, our predictions.

Discussion

Here, we showed that random forest models can help cover the Rabinowitzian shortfall, using the biogeographic information about species contained in their occurrence records to evaluate conservation status. We showed that this machine learning method, originally developed for global analysis, applies at regional scales (here, the state of Maryland) and to a variety of taxa. We identified unassessed plant and lepidopteran species that are likely to be threatened and thus can be considered as having high conservation priorities. Our prediction mapping highlighted the western, montane section of the state as a potential hotspot for species monitoring, assessment, and protection. In the following sections, we discuss the implications of our results, explore the biogeographic trends recognized by our models, and describe how our study supports the use of similar methods to cover Rabinowitzian shortfalls in additional contexts.

Publicly Available Data and Simple Predictive Models Identify Regional-Scale Conservation Priorities

Several studies have demonstrated proof-of-concept for predictive modelling approaches for monitoring or conservation prioritization for plant and animal groups, but at continental or global scales (Bastin et al., 2019; Parsons, Pelletier, Wieringa, Duckett, & Carstens, 2022; Pelletier et al., 2018; Wieringa, 2022; Zhang, Campomizzi, & Lebrun-Southcott, 2022; Zizka et al., 2022). Because decisions about monitoring, research, and protection are often made at smaller spatial scales, before recommending adoption of these tools for conservation practice, it is crucial to determine if they still provide useful predictions at those scales (Meyer & Pebesma, 2021; Wyborn & Evans, 2021), as we have done here.

We anticipated several obstacles to prediction would be larger at the smaller geographical scale considered here, but also recognized mitigating advantages. Formally similar models trained on global vs. regional datasets may reflect fundamentally different biogeographic processes (e.g., continental vs. local), and are built on data of different quality and quantity. Disadvantages at regional scales include the fact that occurrence records are unlikely to cover complete species' ranges, thereby obscuring their ecological preferences (A. Lee-Yaw, L. McCune, Pironon, & N. Sheth, 2022; Phillips et al., 2009). Another limitation is that the variation of environmental covariates used is likely smaller, theoretically limiting the strength of any ecological signals and increasing the chance that model

predictions would be based on noise (Garcia-Rosello, Gonzalez-Dacosta, Guisande, & Lobo, 2023; Hughes et al., 2021). Finally, and most simply, the number of taxa available on which to train models at regional scales is likely to be much smaller, further reducing the chance that predictive models reflect generally applicable trends.

Mitigating some of these concerns, at smaller scales, geographic datasets may have higher resolution and higher quality, or be more consistently available across species or space, which should improve the performance of resulting models. In this vein, we used complete, publicly-accessible, high-resolution covariates at the regional scale, such as land use, land cover, and their history, as well as slope – information that may be less readily available at much larger scales (Gogol-Prokurat, 2011). Though subject to many of the environmental and spatial gaps and biases typical among large biodiversity data (Bachman, Nic Lughadha, & Rivers, 2018; Gallagher et al., 2023; Kitzes & Shirley, 2016; Newbold, 2010), occurrence datasets from our study region benefit from high densities of monetary wealth, human population, and roads, as well as proximity to flagship natural history collections and older research universities. These advantages may, in this study, have counterbalanced the limitations of the smaller spatial scale discussed above.

Overall, even as our regional datasets differ from those used in larger scale predictive models, they appear to contain sufficient information to generate credible predictions. First, we found evidence that the models were using stable – and perhaps robust – signals to generate predictions. Across cross-validation runs of models for the same higher taxon, the same top predictors were frequently identified, implying sample sizes and signal strengths were adequate within our regional-scale data. Furthermore, the resulting models discriminated well between previously assessed threatened and relatively secure species. We found binary thresholds for each higher taxon at which all previously assessed species were classified accurately (albeit at quite different vote counts; 39% for lepidopterans and 61% for plants). Relatively low representation of threatened species among assessed lepidopterans (29%) versus plants (68%) may partly explain differences in the selected thresholds (Peirce, 1884).

Our models showed strong performance on unseen data via cross-validation. Nevertheless, because we do not suspect that the training data (assessed species) are a representative sample of all species,

we remain cautious in our claims of success. We know *a priori* that species have historically been prioritized for assessment based on a variety of social and ecological factors that, while potentially shared among assessed species, may not predict threat across other species that have not been historical priorities for monitoring or protection (Bachman et al., 2019; Brummitt et al., 2015; Di Marco et al., 2017; Fraixedas, Roslin, Antão, Poyry, & Laine, 2022; Ricketts, Daily, & Ehrlich, 2002). A strong test of our predictions would require performing formal status assessments across a large, representative subsample of previously unassessed species, which is beyond the scope of the present study. Here, we informally validated selected predictions using external data, which were largely corroboratory and supports the use of this predictive approach at such a regional scale.

Predicted Conservation Needs Reflects Biogeographic Trends

Generally, our predictions received support from the external data sources, with some caveats. Among the 10 species per group that received the strongest predictions of threat from our models, all had either previously been recognized as threatened in nearby jurisdictions or were unassessed. These findings are compatible with elevated threat in Maryland, as well. Without exception, plant and lepidopteran species that we predicted with high probability as “secure” in Maryland that had also been assessed nearby were found to be secure in at least one jurisdiction in Eastern North America as well, supporting our predictions. We note that among the unassessed plants predicted as most likely to be secure, most were assessed as threatened elsewhere in the wider region, which does not support our predictions. However, apparent trends in recent occurrences of species predicted as “threatened” and “secure” with high probabilities may partly explain the latter result, and provide biogeographic context and support to our predictions.

Our models predicted the likely statuses of species, but their occurrences point to spatial patterns relevant in the context of regional conservation and climate change. First, we found that the species our models predicted as “threatened” were concentrated in the northwestern part of the state, which includes a central portion of the Appalachian Mountains. Second, our models predicted threat in both taxon groups for northern-ranged, likely cold-adapted species, and relative security for southern-ranged, likely warmer-adapted species. Montane habitats harbor a high proportion of total, rare, and threatened species (Körner, 2004) and the Appalachians are no exception (Jenkins, Van Houtan, Pimm, & Sexton, 2015). The Appalachian Mountains are home to species considered relicts from

glacial periods (Pickering, Kays, Meier, Andrew, & Yatskievych, 2003) that face increasing threats from climate warming (La Sorte & Jetz, 2010; Zhu, Papeş, Armsworth, & Giam, 2022). It is thus expected that our predictions would also highlight montane regions of Maryland as potential conservation hotspots. Furthermore, the northwestern half of Maryland contains many habitats recognized as key for wildlife conservation (Maryland Department of Natural Resources, 2015b), as well as priority areas for conservation and monitoring (Maryland Department of Natural Resources, 2015a), constituting a compelling stage for long-range conservation (Lawler et al., 2015). Beyond the Appalachian region, our results recovered a large number (but not proportion) of plant species predicted as threatened in the Piedmont region of the state, which has seen rapid development over the past 50 years (Maryland Department of Planning, 2010). Sheer densities of roads, institutions, money, and people in the center of the state may explain this result. However, that section of Maryland is experiencing stark habitat loss and fragmentation, and may also be an emerging priority for monitoring, status assessment, and conservation.

Even as they are not designed for inference, our models recovered ecological signals both within (and between) the plant and lepidopteran models in measures of variable importance. These signals point towards mechanisms that drive threat for some species and relative security for others. The latitude of the northernmost Maryland occurrence was a top predictor variable for both lepidopteran and plant status, with species with occurrences at higher latitudes being predicted as “threatened” with higher probabilities. Otherwise, top predictor variables differed between the taxon groups, and likely reflect the ecology of each group. For plants, variables associated with niche breadth were important, along with latitude and humidity. Niche breadth has long been associated with vulnerability (Slatyer, Hirst, & Sexton, 2013), and plants restricted to microclimates or habitat types that are rare in Maryland are likely under threat from anthropogenic change. For lepidopterans, the top variables reflected low-temperature tolerance, which we interpret to mean that more cold-associated lepidopterans tend to be more threatened in Maryland. Abundance and range shifts and declines in response to changing climate are well-documented in lepidopterans (Crossley et al., 2022; Hill, Kawahara, Daniels, Bateman, & Scheffers, 2021), and it is likely that some of Maryland’s most threatened insect fauna are retreating to relatively cool and high-elevation refugia.

Applications

Our methodology is not intended to replace species conservation assessments (Zizka et al., 2022) nor to stand in for highly contextual, place-based ecological knowledge (Wyborn & Evans, 2021), but rather as a tool that can inform prioritization in a resource-limited conservation world (Sinclair et al., 2018). As resources for protection are already biased towards monitoring and research, approaches like ours can use existing data to accelerate movement of conservation resources towards active conservation work (Buxton et al., 2020). Maryland's 2015-2025 State Wildlife Action Plan calls for greater coherence in monitoring efforts, especially for species that have yet to be recognized as "of greatest conservation need" (Maryland Department of Natural Resources, 2015c). Towards these ends, first, our models provide guidance about assessed and unassessed plant and lepidopteran species (table S1) in a coherent, quantitative framework that can immediately integrate new data as they become available. Second, beyond individual species predictions, we also produce regional maps (Fig. 3, S1), that highlight priority areas where conservation needs likely intersect; these maps can support proactive, place-based conservation (Cardillo & Meijaard, 2012). Third, we tentatively identify ecological features of threatened and relatively secure plants and lepidopterans, which warrant further investigation and may be applicable in other regions or to other taxa as well. Our results echo calls to protect climate refugia and unique habitat types within Maryland, and perhaps to assist climate-driven migration (Maryland Department of Natural Resources, 2015a). Finally, as the data inputs for the approach we used are publicly available, and we have made scripts containing our workflows open (CITE CODE REPOSITORY), any interested party can easily reproduce our analysis, update our predictions with new data, or extend our method to additional taxa and locations.

Future applications of our approach would ideally involve stakeholders (Knight et al., 2008). In our study, direct decision-maker input during model construction might have altered which data sources were used or how species were grouped into individual models (here, we generated separate models for plants and lepidopterans), and would also have affected how the models were trained on those data. Decision-makers, uniquely positioned to name the problems associated with different types of misclassification errors, could help translate these problems into loss functions and classifier training criteria (Hand, 2009; Walker et al., 2020). These criteria help tune the model to a specific application (e.g., by avoiding predicting that species are threatened when they are not, or the opposite), via hyperparameter values and vote threshold selections. This approach is fit for stakeholder-driven

model construction: models were fit on a personal laptop; the decision trees at the heart of random forests are concrete, easily apprehended, and thus accessible; the data we used are publicly available and well-documented. Overall, this modelling approach is well-suited to use by local and regional conservation planners and decision-makers.

Conclusion

Predictive methods cannot replace localized knowledge systems nor systematic species assessments (Betts et al., 2020). Instead, in a fast-changing world in which most species, including threatened species, remain unassessed and data-deficient, they extend the conservation utility of existing data. Here, we showed that a predictive method for prioritizing unassessed species, originally developed for global applications, can be flexibly applied at smaller, regional scales and to a variety of taxa. We show how using occurrence records as input data enables spatially explicit predictions, which can highlight priority locations, and could facilitate place-based or ecosystem-level conservation. We highlighted Maryland (USA) unassessed plant and lepidopteran species likely to be threatened, and identified the western part of the state and Appalachian Mountains as hotspots for such likely-threatened species. Such emergent results can help resolve a central conservation mystery: which taxa are most vulnerable to which drivers (Isbell et al., 2023; Sánchez-Bayo & Wyckhuys, 2019). The random forests we used “learn” from existing, publicly accessible datasets using simple decision trees, require relatively little computational resources or natural history expertise to implement, and can be used “in house” by researchers, planners, or managers at regional scales. As a result of the immediacy of our method, as well as the encouraging results from the plant and lepidopteran case studies we present here, we advocate for regional applications of similar predictive tools to better identify conservation priorities. Finally, future applications of these methods could more explicitly integrate stakeholders, as well as consider other niche (e.g., species interactions or co-occurrences) into both threat assessment and conservation prioritization.

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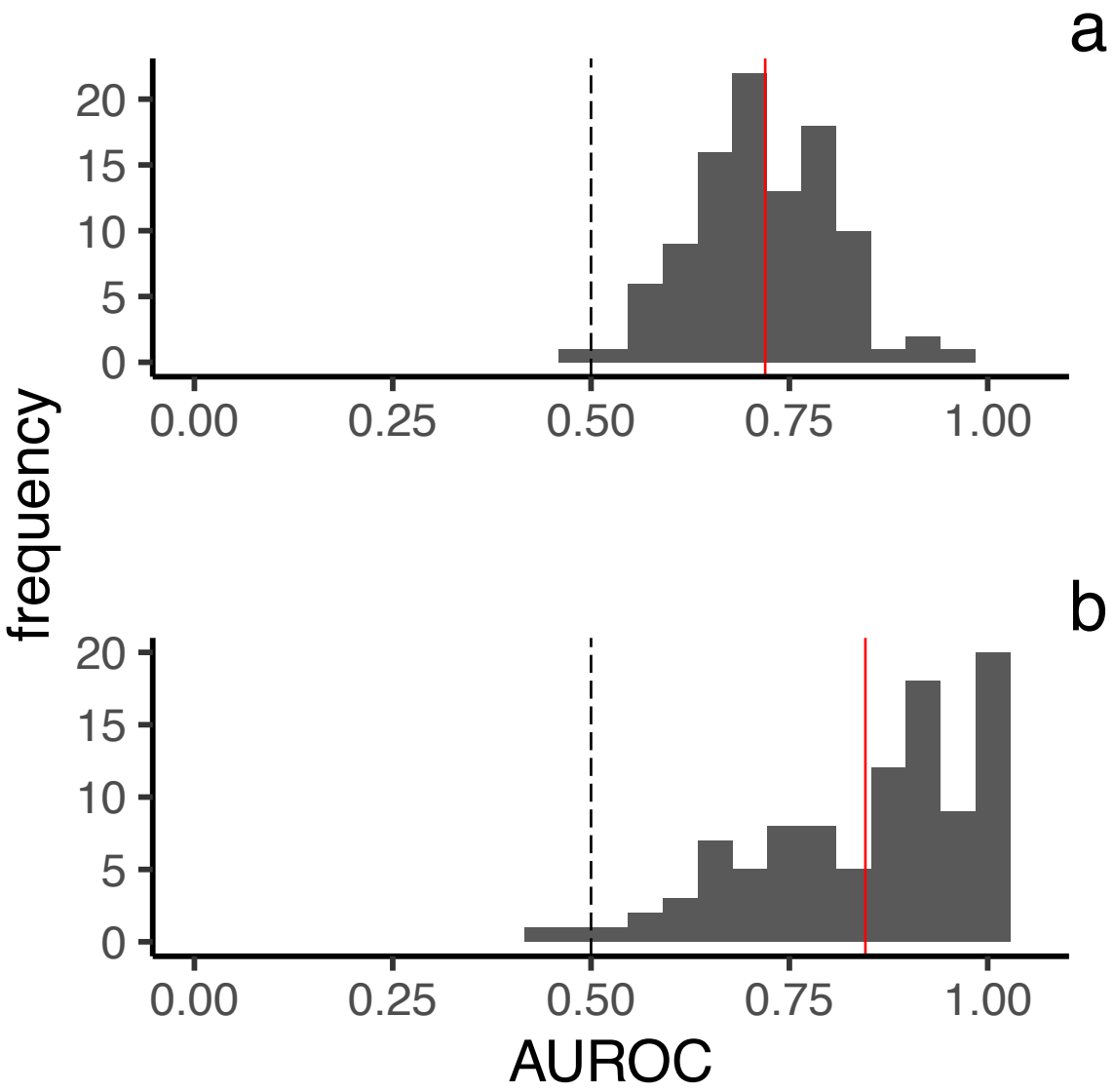
725 **Tables and figures**



726

727 **Figure 1**. Distribution of area under the receiver operating curve (AUROC) values on unseen data in
728 10x repeated 10-fold cross-validation. For plants (a) mean AUROC was moderate (mean = 0.72; sd =
729 0.09). For lepidopterans (b), model performance was stronger but more variable (AUROC mean = 0.84,
730 sd = 0.13). In each panel, mean AUROC is shown with a red vertical line; dashed vertical line indicates
731 the expected performance of a model making random guesses (AUROC of 0.50).

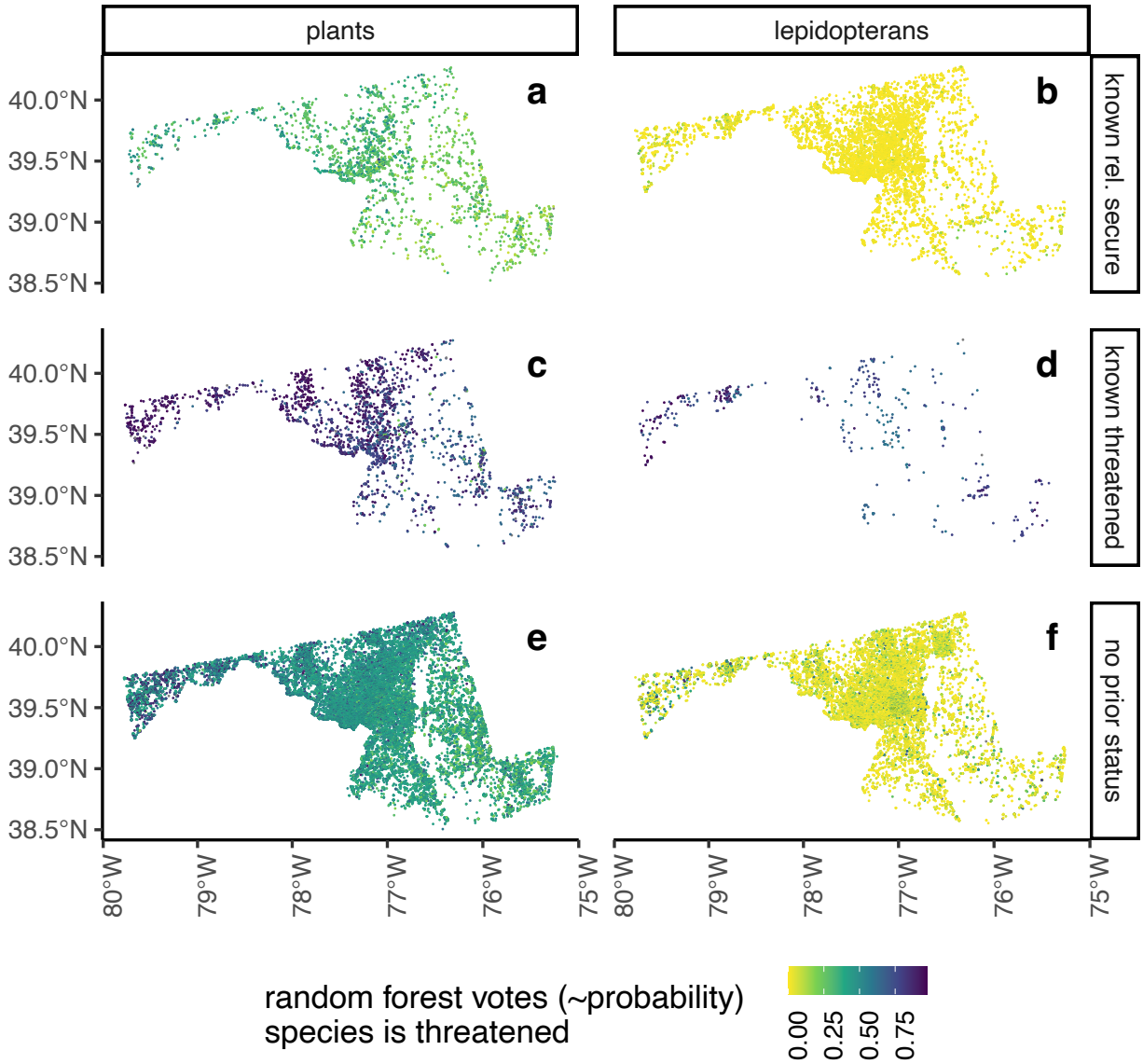


Figure 2. Random forest predictions from final models on occurrence records of assessed (a-d) and unassessed (e, f) species. Models distinguished threatened and relatively secure species in the training dataset (lighter points in panels a and b, darker in c and d), and identify a concentration of putatively threatened, unassessed species in Western Maryland (trend towards darker points in western portion of maps in e, f).

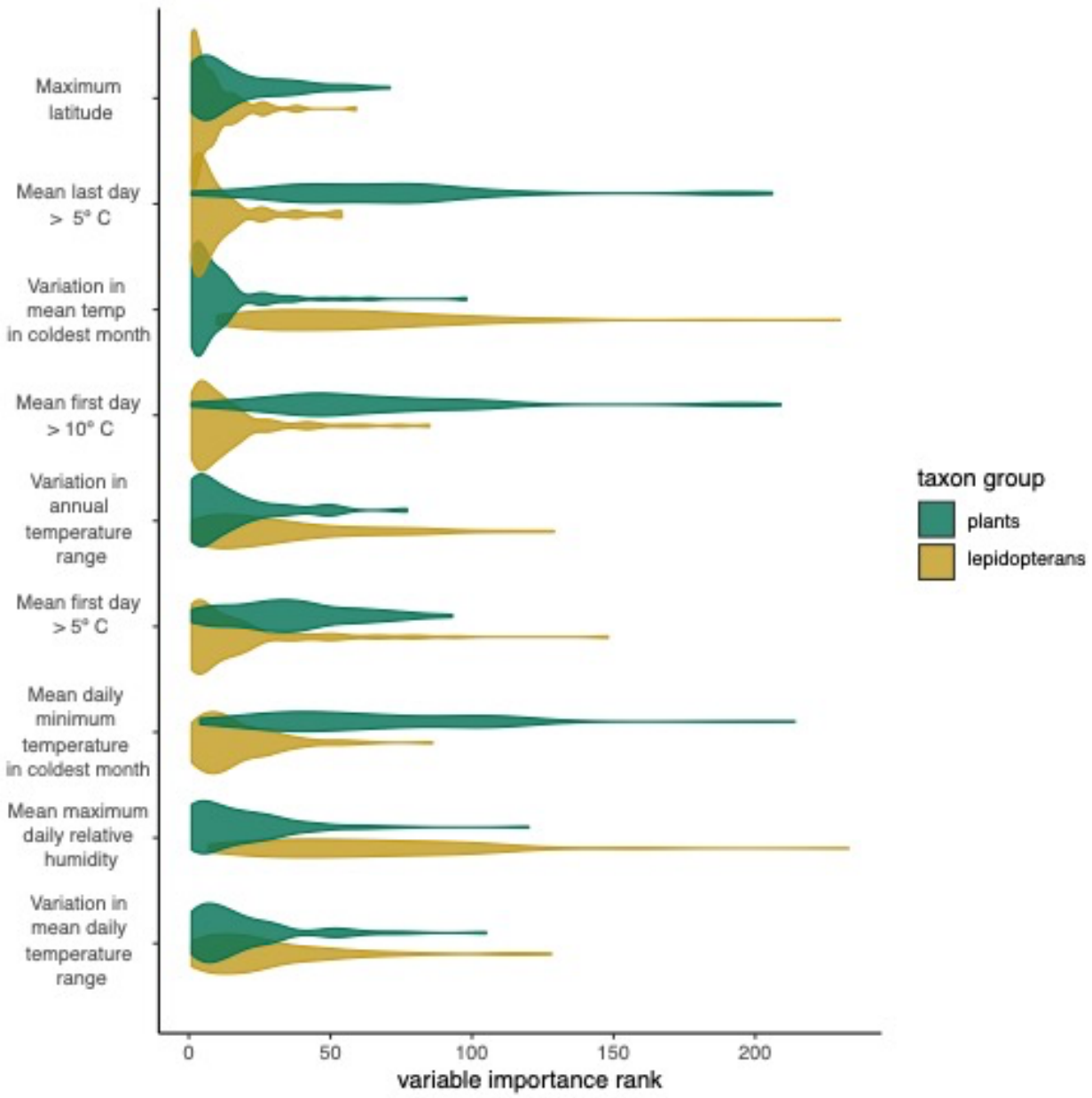


Figure 3. Distribution of variable importance ranks for the five predictors with the lowest mean MDA ranks (i.e., those with higher importance across cross-validation runs) for plants (green) and lepidopterans (yellow). Maximum ranks exceed the total number of variables because each level of categorical variables receives its own MDA measure.

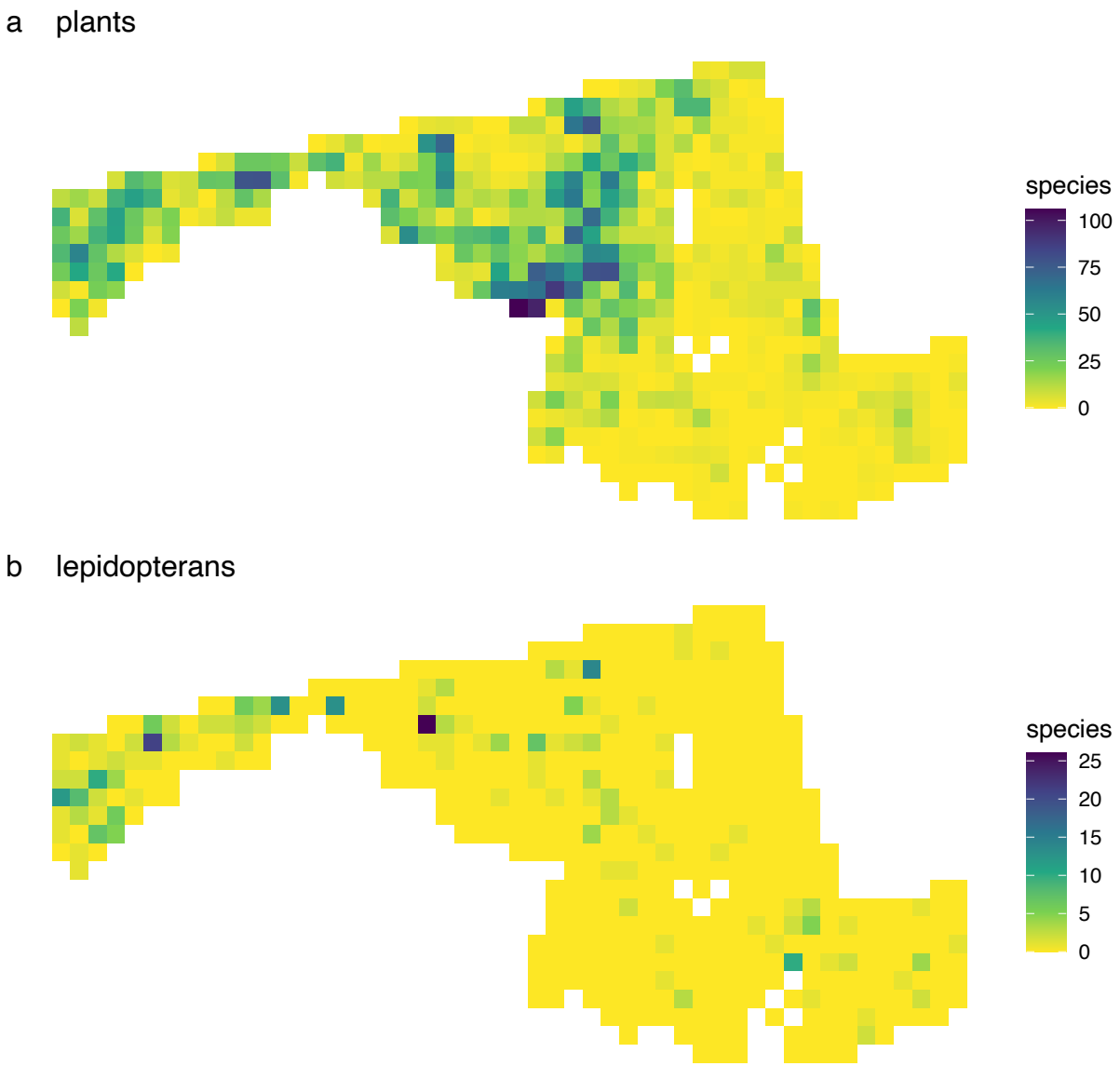


Figure 4. Number of species classified as threatened by the final models using the taxon group-specific probability thresholds (0.614 for plants, 0.39 for lepidoptera), per 8km x 8km grid cell across the state of Maryland. Colors represent number of species (see figure scales).

Table 1. Top and bottom ten species per taxon group, based on the predicted probability of being threatened. Known conservation status from other jurisdictions in Eastern North America is shown, if available. Codes indicate state/province conservation status and the state/province in question. Row coloring indicates species range type. Orange: iNaturalist occurrence records appeared concentrated north of Maryland, with a southward extension along the Appalachian Mountains; blue: occurrences concentrated north of Maryland, without an Appalachian extension; green: occurrences neither concentrated to the north of Maryland nor clustered along the Appalachian Mountains.

taxon group	genus	species	predicted status	vote fraction (threatened)	Status elsewhere	notes
plants	*Pyrola*	*elliptica*	threatened	0.95	S1 VA, NC; S2 DE, S4 WV, NJ	
	Poa	*autumnalis*	threatened	0.94	SX MI, IL, SH NJ, S1 PA, S3 DE, S4 NC, S5 SC, VA, KY	
	Pyrola	*americana*	threatened	0.94	SX KY, IL, S2 NJ, NC, TN, IN; S4 NJ, VT; S5 VA, WV	
	Eragrostis	*hypnoides*	threatened	0.938	SH ME, NH; S2 NC, DE; S3 NJ, VT, S4 NY, VA, WV, KY	
	Bidens	*connata*	threatened	0.936	S1 RI; SH WV; S4 VA; QE; S5 NJ, NY, KY	
	Viola	*macloskeyi*	threatened	0.932	S1 DE; S3 GA, NC; S4 VA, WV; S5 NY, QE, ON	
	Dichanthelium	*longiligulatum*	threatened	0.928	S1 Nj, S3 NC; S4 VA, KY	
	Carex	*gynandra*	threatened	0.926	S1 OH; S2 De; S4 Nj, NC; S5 VA, WV, NY, ON, KY	
	Gentiana	*clausa*	threatened	0.926	S2 QE, RI; S3 NC, OH; S4VA, WV, NY, NJ	
	Selaginella	*rupestris*	threatened	0.926	S1 OH, NB, NS; S2 IA, NJ; S3 WV, VT, NC, IL, MA; S4 NY; S5 ON, QE, GA	
	Elymus	*virginicus*	secure	0.134	S4 WV, S5 ON, NC, IL, IN, KY	
	Juncus	*dichotomus*	secure	0.14	S1 PA, WV, OH; S2 NY, S4 DE, GA, S5 NC, VA, NJ	
	Carex	*longii*	secure	0.144	S1 OH, WV, S2 KY, PA; S3 NY; S4 NJ, DE; S5 VA	
	Cyperus	*retrorsus*	secure	0.15	S1 MA, NY; S2 KY; S4 NJ; S5 GA, NC, VA	
	Polygala	*mariana*	secure	0.154	S1 TN, S2 NJ, S4 DE, NC; S5 KY, VA	
	Eupatorium	*album*	secure	0.16	S1 CT, OH, S3 IN, WV; S4 DE; S5 NC, VA, KY	
	Lobelia	*puberula*	secure	0.162	S1 PA; S4 KY; S5 NC, WV, VA	

	Panicum	*virgatum*	secure	0.162	S2 QE; S3 VT; S4 ON, KY; S5 IL, NC, VA, NC	
	Fimbristylis	*autumnalis*	secure	0.166	S1 VT; S2 ME; S3 IL; S4 NC, ON, QE; S5 KY, VA, WV, NJ, NY	
	Dichanthelium	*scoparium*	secure	0.168	SH WV, MA; S1 IL, IN, OH, PA, NY; S4 NJ; S5 NC, VA, DE	
lepidopterans	*Olethreutes*	*bipartitana*	threatened	0.936		
	Scoparia	*cinereomedia*	threatened	0.93		
	Euphyia	*intermediata*	threatened	0.928		
	Haploa	*confusa*	threatened	0.926		
	Catocala	*blandula*	threatened	0.916	S1 KY, IN; S4 PA	
	Panthea	*acronyctoides*	threatened	0.916	S3 VA; S4 NB, ON	
	Argyresthia	*calliphanes*	threatened	0.898	S1 CT; S2 MA; S4 NH, NB; S5 ON	
	Cingilia	*catenaria*	threatened	0.898		
	Chrysanympha	*formosa*	threatened	0.896	S1 IN; S3 NC; S4 NY, PA, NB; S5 ON	
	Idia	*diminuendis*	threatened	0.894	S2 QE; S3 NH; S4 PA	
	Hyphantria	*cunea*	secure	0	S5 ON; ID, PA	
	Marimatha	*nigrofimbria*	secure	0	S1 NY, S4 PA	
	Nomophila	*nearctica*	secure	0	S5 PA	
	Palthis	*asopialis*	secure	0	S3 ON, S4 NY	
	Hemaris	*diffinis*	secure	0.002	S4 ON, S5 PA, KY	
	Atteva	*punctella*	secure	0.004	S4 ON, S5 PA	
	Hylephila	*phyleus*	secure	0.004	S4 KY, WV; S5 IN, MS, AL, FL, GA, SC, NC, VA, **MD (See appendix S1)**	Syn. *Papilio phyleus*
	Malacosoma	*americana*	secure	0.004	S5 ON, PA	
	Pyrrharctia	*isabella*	secure	0.004	S4 ID, S5 ON, PA	
	Actias	*luna*	secure	0.006	S4 QE, S5 ON, PA, VT	

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