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Open-Source Software Integration: A Tutorial on Species Distribution Mapping and Ecological Niche Modelling

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Open-Source Software Integration: A Tutorial on Species Distribution Mapping and Ecological Niche Modelling

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Abstract

Over the last decade, access to global data has become increasingly critical for research, allowing insights into diverse biological, environmental, and societal questions at a macro scale. Digitization has greatly enhanced the use of herbarium data in the analysis of species distribution data and ecological niche modeling. Yet, sources on modeling and mapping methodology using open source software is greatly lacking for beginners. We have created a replicable and thorough tutorial to visualize species occurrence data and exploratory analysis that was developed by undergraduates with broad backgrounds and levels of experience. This tutorial integrates the open-source programs QGIS, MaxEnt, and R to develop distribution maps, using bryophytes as a case study, to promote the accessibility of open source software and remote access learning. This tutorial has already set the foundation for further research into distribution modeling of rare Illinois bryophytes to better understand the potential impact of climate change.

Keywords

Bryophytes, QGIS, MaxEnt, R, Rstudio, tutorial, open source, ecological niche modeling, species distribution maps

Introduction

Digitization and Natural History Collections

Globally, thousands of institutions house nearly three billion scientific collections containing multiple layers of associated metadata (Holmes et al. 2016, Sweeney et al. 2018). Extensive, professionally managed natural history collections, with their broad taxonomic, geographic, and temporal scope, offer unparalleled resources that contribute to science, society and their community (e.g., Saxena and Harinder 2004, Berendsohn and Seltmann 2010, Hedrick et al. 2019). Digitization has greatly enhanced the use of herbarium data in scientific research, impacting diverse research areas, ranging from biodiversity informatics, conservation biology to global change biology (Bebber et al. 2010, Soltis et al. 2018). Nualart et al. 2017 reviewed the potential use of herbarium specimens and categorized them based on:

1. occurrence data, such as studies about plant extinction or introduction, or those focused on modeling their ecological niche;
2. the specimens themselves, such as morphological or phenological studies to evaluate the impact of climate change;
3. genetic data, such as phylogeographic or taxonomical studies; and
4. other applied studies.

Despite the scientific, educational, and societal relevance (Heberling et al. 2019) of museum specimens, they remain underused particularly in ecological studies. Yet, the wealth of hidden biodiversity may reveal global patterns that are not observable from other data sources (Meineke et al. 2018). Herbarium specimens, in particular, offer a great resource for research projects to involve the public, high school interns and university students, allowing for the entire community to create scientific discoveries (Pivarski et al. 2022).

Modeling and Mapping

The geographic range a species can exist in is defined by three boundaries: biotic, abiotic, and mobility factors, also called the BAM framework (Peterson and Soberón 2012, Melo-Merino et al. 2020). Models can be created with any number of these factors to describe species distributions (species distribution model [SDM]), or niches (ecological niche model [ENM]). A model can be an SDM and/or an EDM depending on desired goal, which should inform a researcher's prioritization and selection of BAM factor data (Melo-Merino et al. 2020, Barve et al. 2011).

This paper outlines a beginner-friendly SDM/ENM modeling tutorial using Illinois bryophytes as a case study. Bryophytes lend themselves well to such methods due to their broad distribution and important ecological role, but this tutorial can be followed with any organism. The project aims to explore the potential range of bryophytes based on climate variables while utilizing open-source data and programs. A more detailed set of instructions can be found in the supplementary materials.

Bryophytes and Ecological Significance

Bryophytes, including mosses, liverworts, and hornworts, are the second largest group of land plants after flowering plants and are pivotal in our understanding of early land plant

evolution (Leebens-Mack et al. 2019, Zhang et al. 2020). Fig. 1 and Fig. 2 illustrates some common bryophytes demonstrating the salient morphological characters used to distinguish between them, e.g., a common liverwort, *Frullania*, (Fig. 1a,d) and some common mosses, e.g., *Plagiomnium* (Fig. 1 b,e), *Polytrichum* (Fig. 1c,f) and *Entodon* (Fig. 2). Bryophytes are of great ecological and environmental significance, playing an important role as possible indicators of climate change (e.g., Lindo and Gonzalez 2010, Ruklani et al. 2021), air pollution (Zechmeister et al. 2003, Dymytrova 2009), in nutrient cycling (Rieley et al. 1979) and through their water retention - reducing soil nutrient loss and flooding risk (Anderson et al. 2010). Bryophytes have been recently utilized as climate change indicators in many studies due to their small size, broad distribution, and environmental sensitivity (Hespanhol et al. 2022, Mallen-Cooper et al. 2022, Zanatta et al. 2020).

Aims

Alban (2017) created a short tutorial utilizing QGIS, R and MaxEnt. This provided a foundation for creating a project in these programs, but lacked detail outlining the MaxEnt modeling process, MaxEnt statistics, and map formatting options in QGIS a beginner would need. Additionally, our tutorial provides an account of how to collect distribution data, as well as highlighting the bioclim variables as environmental layers. Therefore, a comprehensive tutorial and supplementary guides have been developed that aim to be beginner-friendly and use open-source software that is free and easily accessible. It has been designed to be easily replicable for other studies using QGIS. We outline this using bryophytes as case studies investigating distribution patterns regionally in Illinois and on a broader continental scale using United States.

Description

Data Resources

The process of producing maps and modeling requires many resources, e.g., online data aggregators (e.g., Consortium of Bryophyte Herbaria (Consortium of Bryophyte Herbaria 2024), GADM (GADM 2018,) WorldClim (Fick and Hijmans 2017), QGIS (QGIS.org 2021), R (R Core Team 2022), and MaxEnt (Phillips et al. 2024). All of these resources are open access.

Distribution Data

Occurrence datasets of *Entodon seductrix*, *Dicranella heteromalla*, *Plagiomnium cuspidatum*, *Frullania eboracensis*, and *Polytrichum commune* were downloaded from CNABH and used to construct the models outlined below.

QGIS

QGIS is an open-source GIS software (Geographical Information System) that was used to visualize occurrence and environmental data. It is a user-friendly tool used for mapping

points with longitude and latitude, shapefiles, and pixelated raster data. QGIS can accommodate a variety of data types in order to create a cohesive visualization of the information being used.

R and Rstudio

Rstudio is an integrated development environment (IDE) that runs the programming language R and is commonly used for statistical analysis and bioinformatics. We used a brief script to clean our data of occurrences lacking longitude and latitude that generates a new CSV file containing only the georeferenced occurrences.

MaxEnt

MaxEnt is an open-source software which creates a heat map of potential habitats for the modeled species within the study area. These areas are identified with varying probabilities using correlations between occurrence points and environmental data. The heat map generated by MaxEnt can be input into QGIS for further visualization. MaxEnt also generates model statistics, such as a jackknife plot indicating the relevancy of each environmental variable to constructing the model.

Implementation

A brief summary of the methodology is provided below, to serve as introductory steps into distribution modeling. Supplementary materials provide detailed and step-by-step instructions and information.

Suppl. material 1 : A full tutorial with reference images and text-focused steps of QGIS and MaxEnt.

Suppl. material 2 : For more advanced users that have some background, and some steps and details lacking.

Suppl. material 3: A tutorial on how collect and plot occurrence data in QGIS.

Suppl. material 4 : For more advanced users - a QGIS Quick Steps guide.

Suppl. material 5 : A downloadable template for QGIS map outputs and associated information.

Methodology

Occurrence Map

This occurrence data from CNABH is entered into QGIS in order to create a distribution map of the species. For Illinois focused maps, a shapefile was freely downloaded from GADM (2018) to cut out occurrences outside the state boundaries. In the first tutorial we

used Suppl. material 3 and Suppl. material 4 culminated in a species distribution map showing occurrences. These maps are seen in Figs 3, 4, 5 .

Environmental Layers

Bioclim historical climate variables were downloaded from WorldClim to act as the environmental layers for the model (Fick and Hijmans 2017). This data was free for download and provided worldwide climate information in the form of a TIFF file. To make the environmental data specific to the study area, the layers were clipped using the Illinois Mask Layer file and Extraction Raster tool. More types of environmental layers, such as those provided by US National Land Cover Database (Dewitz and U.S. Geological Survey 2021) can be explored as additional modeling parameters (e.g., Figs 7, 8).

Using R and MaxEnt

The R script was run to remove bryophyte occurrences where georeferenced data was lacking. The cleaned CSV file was put into the MaxEnt program as the “Samples” and the clipped WorldClim data which was put in as “Environmental Layers”. Running MaxEnt results in a comprehensive distribution map that takes a set of chosen environmental factors into account in reference to occurrence data. MaxEnt results can be put into QGIS, which allows us to visualize the distribution of a species in relation to where they are predicted to be seen. These distributions can be seen in figures Figs 6, 9, 10. This visualization was then placed into a template that was created so that it is represented in a cohesive format that can be easily replicated with different species. The template is found here Suppl. material 5. Examples of maps displayed using this template can be seen in figures Figs 11, 12.

Troubleshooting

Some common issues:

- The MaxEnt program can have difficulties running on the MacOS 11.4 Big Sur operating system. The MaxEnt team recommend using MacOS 10 to resolve this. The stand-alone MaxEnt program has not been tested on more updated MacOS operating systems.
- If QGIS stops working after a long period of use, saving your work and restarting the program often resolves this.
- It is recommended that you run the R code in a script in Rstudio, otherwise editing the code after running it can be difficult; taking this extra step makes the data cleaning process run more smoothly.

Conclusions

A detailed step-by-step guide to develop species distribution maps and preliminary ecological niche modeling using the open source software - QGIS, Rstudio, and MaxEnt - is provided. The tutorial uses selected moss and liverwort species as a case study

mapping occurrences in Illinois compared to climatic variables, demonstrating the potential capacity of mosses as climate change indicators (e.g., Gignac 2001). The tutorial has been designed to be versatile and be adapted to projects that use QGIS for distribution mapping. Significantly, the guide highlights the importance of open-source resources to help accelerate our understanding of biodiversity patterns, making this field more accessible and equitable through both location and cost. The guide and tutorial especially serves the intended audience of those who are beginners or first time investigators navigating QGIS, MaxEnt, and Rstudio mapping.

Next Steps: Increasing Model Precision, Accuracy, and Specific Niche Analysis

Starting with open-source materials and simple methodology provides the foundation for building more complex and accurate models. All of the data editing and modeling completed in this tutorial can be done entirely in R for a more seamless and customizable experience. Fig. 13 shows the predictive distribution for *E. seductrix* based on non-correlated Bioclim variables, and NLCD variables for land cover and percentage tree canopy cover. The jackknife plot accompanying the map indicates relevance and importance of each variable to the model, which is relevant for describing the species niche and comparing it to other bryophyte species.

The creation of accurate and useful distribution and niche models is a challenging process, and can be overwhelming for beginners to rebuild their work over and over to reach this point. We hope this tutorial demystifies modeling methodology for researchers, students, and citizen scientists and allows for a cost-free starting point into learning what creates a useful model.

Acknowledgements

This project would not have been possible without the hard work of many people. We would like to acknowledge Don De Alban from the National University of Singapore, who made the first tutorial for using these three programs to create distribution maps which we then expanded upon to develop our own case study. The Student Center for Science Engagement at Northeastern Illinois University, the Dean's Undergraduate Fellowship, College of Science and Health, DePaul University, the Field Museums Women's Board helped provide funding for student interns. Financial support was provided by the National Science Foundation (Award No. 0949136, 1145898, 1458300, 1541545, 2001509) and the Friends of Nachusa Grasslands Scientific Research Grant. We also thank Jerry Jenkins for permission to use his images and Daniel Le and Chris Maves for their macro-photography.

Hosting institution

The Field Museum of Natural History

Conflicts of interest

The authors have declared that no competing interests exist.

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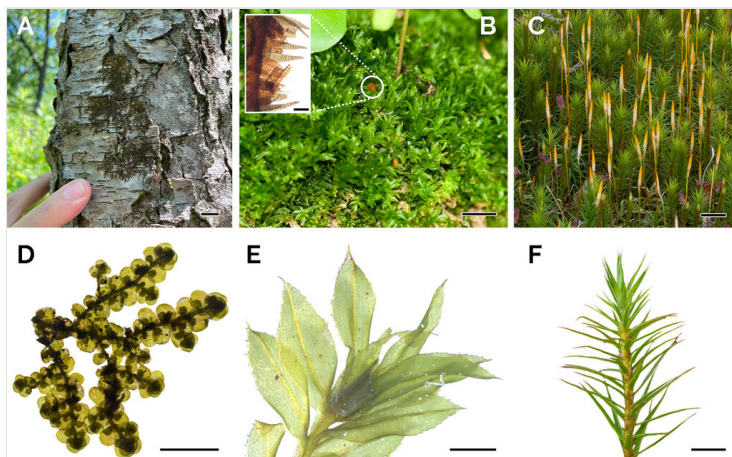


Figure 1.

A, D) The liverwort, *Frullania*. A) Growing on bark, D) Ventral view of the stem under the microscope; B, E) *Plagiomnium*. B) Mat with sporophytes, inset, magnification on peristome teeth, E) Shoot with leaves illustrating a mid-rib; C, F) *Polytrichum commune*. C) Erect stems with sporophytes, F) Close up of stem showing the spiral leaf arrangement (courtesy of Jerry Jenkins). Scale bars: A, B, C=1cm (B inset=20um); D, E=1mm; F=500mm.



Figure 2.

Entodon seductrix. A) Growing on bark, showing mat-like growth, B) Close-up with sporophytes, C) Whole leaf, D) Leaf cells. Scale bars: A, B=1cm; C=100um; D=20um.

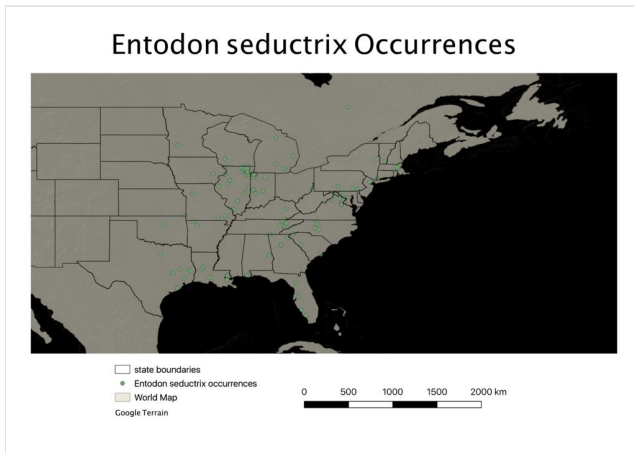


Figure 3.

Eastern United States map of *Entodon seductrix*, with green points representing each occurrence.

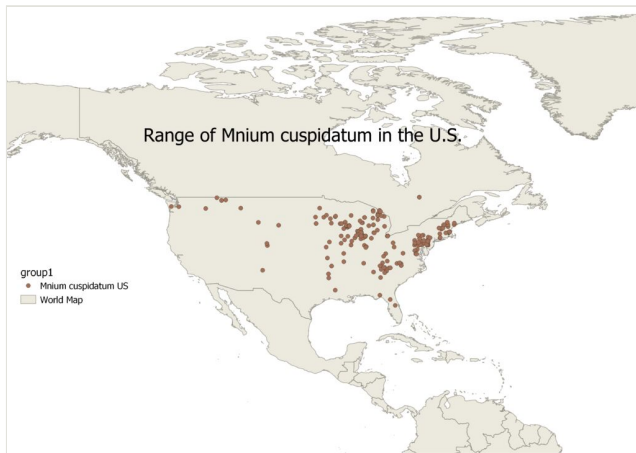


Figure 4.
United States distribution of *Plagiomnium cuspidatum*.

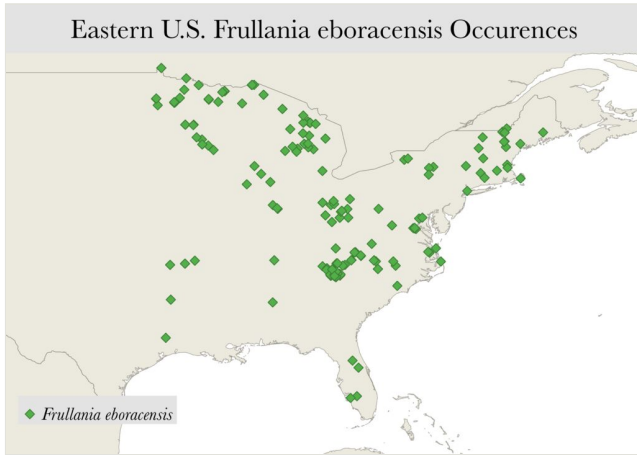


Figure 5.
Eastern US distribution of *Frullania eboracensis*.

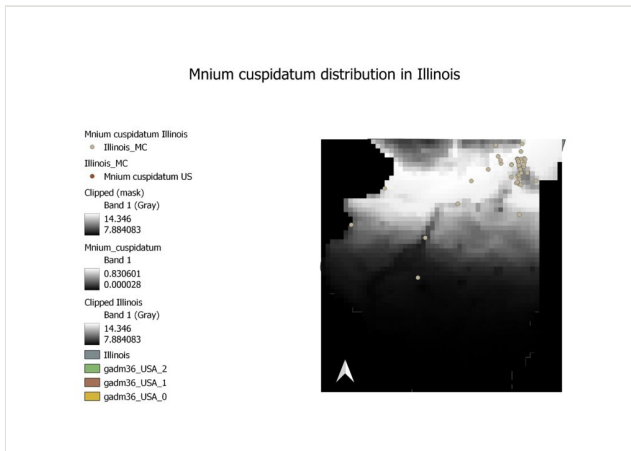


Figure 6.

Predictive distribution of *Plagiomnium cuspidatum* in Illinois, represented by tan points. The white of the predictive gradient indicated a location where the bryophyte is likely to be found.

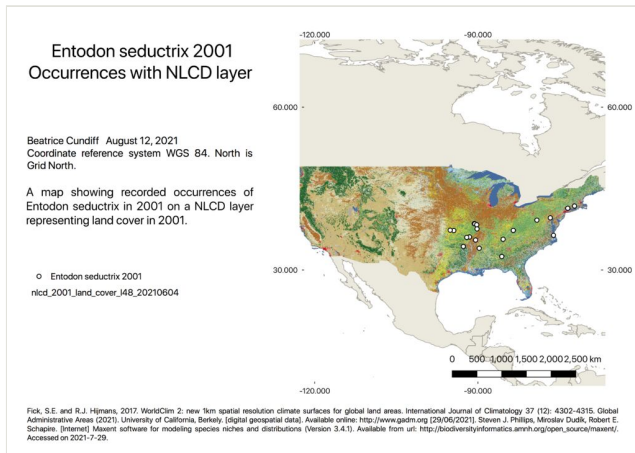


Figure 7.

Entodon seductrix occurrences overlaid on the 2001 U.S. National Land Cover Data layer. Prepared from the supplementary template.

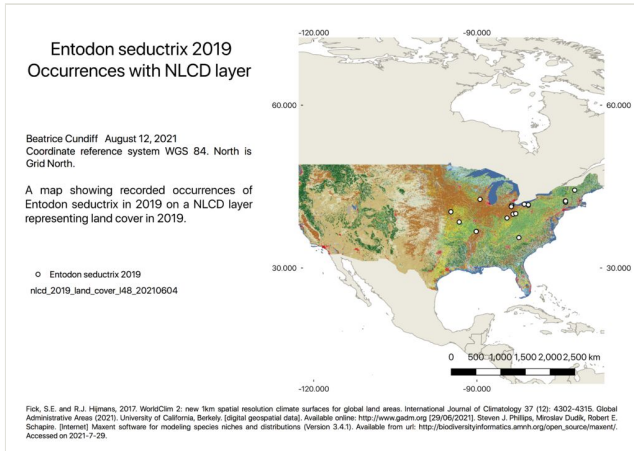


Figure 8.

Entodon seductrix occurrences overlaid on the 2019 U.S. National Land Cover Data layer. Prepared from the supplementary template.

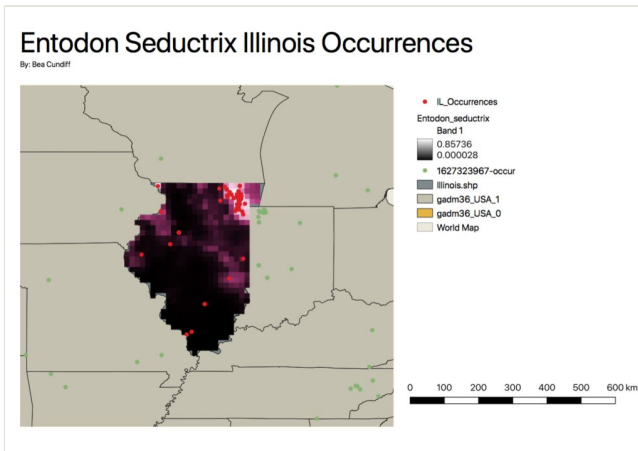


Figure 9.

Entodon seductrix occurrences in Illinois, represented by red points. The light end of the gradient represents a location where the species is likely to be found.

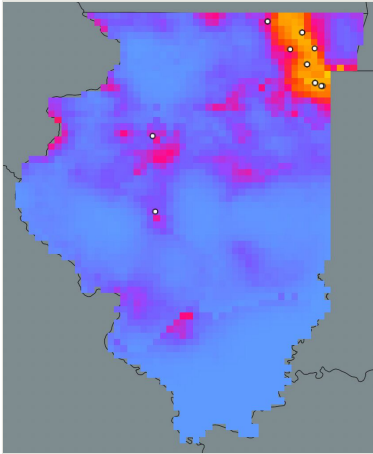


Figure 10.

Predictive distribution of *Polytrichum commune* in Illinois. The occurrences are represented by white points, with the yellow end of the gradient representing a location the bryophyte is likely to be found. The color gradient can be altered to be colorblind-friendly, such as the IBM palette as depicted here.

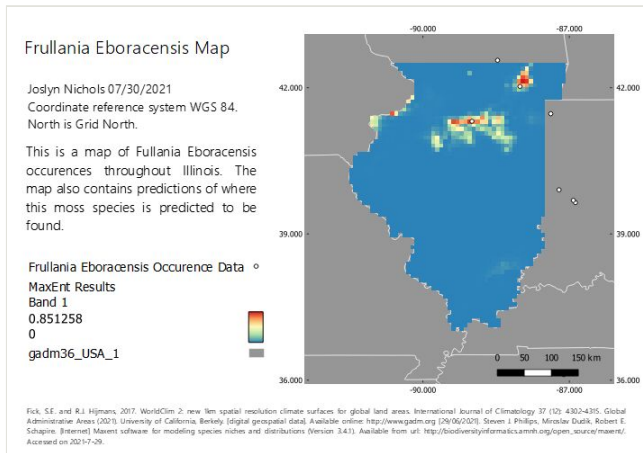


Figure 11.

Predictive distribution of *Frullania eboracensis*, using the created template for presentation. The white points represent the occurrences of the bryophyte, with the red end of the gradient representing an area the species is likely to be found.

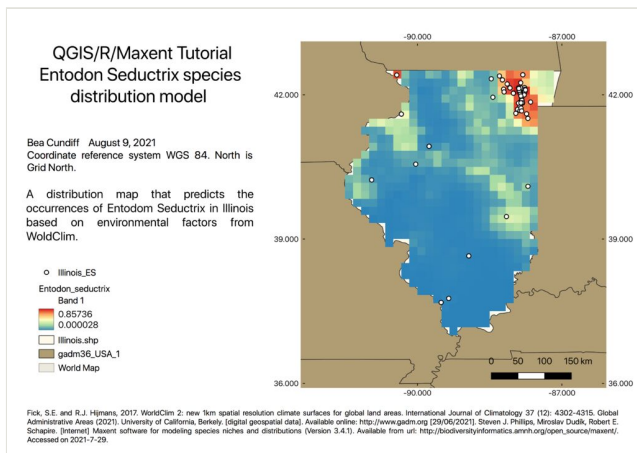


Figure 12.

Predictive distribution of *Entodon seductrix*, using template for presentation. The white points represent recorded occurrences for the bryophyte, and the red end of the spectrum indicates a location the species is likely to be found.

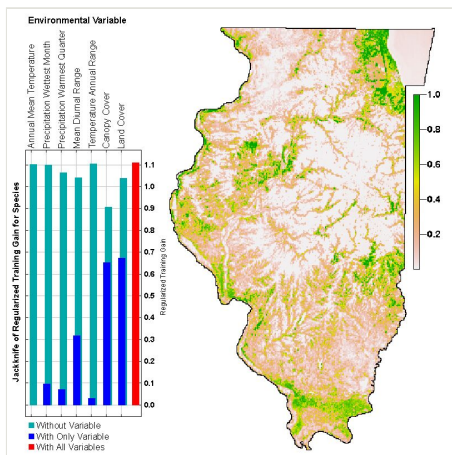


Figure 13. Predictive distribution model of *Entodon seductrix* and jackknife plot of environmental variables.

Supplementary materials

Suppl. material 1: Full QGIS MaxEnt Tutorial

Authors: Emily Clark

Data type: pdf

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Suppl. material 2: Quick Step QGIS MaxEnt Tutorial

Authors: Emily Clark

Data type: pdf

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Suppl. material 3: QGIS Intro and Instructions for Mapping Species Occurrences

Authors: Zoe Ryan

Data type: pdf

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Suppl. material 4: Quick Guide to Mapping Occurrences in QGIS

Authors: Zoe Ryan

Data type: pdf

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Suppl. material 5: QGIS Map Output Template

Authors: Emily Clark

Data type: qpt

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