

Modeling bumble bee (Hymenoptera: Apidae) spatial distributions in Texas

Final Report, TPWD Contract Number 471871

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Abstract:

The state of Texas is inhabited by at least nine different bumble bee species, six of which have experienced losses in the form of range reductions and local extirpations in other parts of the United States. However, knowledge of bumble bee distributions in Texas is limited to data compiled from natural history collections and recent surveys in the northeastern portion of the state. In order to identify target areas for conservation actions this study (1) updated existing Texas bumble bee databases to include recent (2007-2016) data from citizen science repositories, and (2) modeled statewide species distributions of bumble bees using MaxEnt. The results of this study include updated maps and species distribution models for three declining bumble bee species: *B. fraternus* (Smith, 1854), *B. pensylvanicus* (DeGeer, 1773) and *B. sonorus* Say, 1837. Based on these results the following target areas for conservation are recommended: the Trans-Pecos and Edwards Plateau ecoregions of Texas for *B. sonorus*; the Post Oak Savannah, Blackland Prairie, Cross Timbers, Piney Woods and Gulf Prairies for *B. pensylvanicus*; and the Cross-Timbers, Post Oak Savannah and Blackland Prairie for *B. fraternus*.

Introduction:

Bumble bee declines have been noted across Europe (Carvell, 2002; Fitzpatrick et al., 2007; Goulson, 2010; Goulson et al., 2006; Goulson et al., 2008; Kosior et al., 2007; Sarospataki et al., 2005), Asia (Inoue et al., 2008; Matsumura et al., 2004; Xie et al., 2008; Yang, 1999) and North America (Cameron et al., 2011; Colla et al., 2012; Colla and Packer, 2008; Colla and Ratti, 2010; Grixti et al., 2009). Moreover, Bartomeus et al. (2013) demonstrated that, while other bee taxa have shown modest, statistically insignificant declines in the northeastern United States, *Bombus* species richness declined by a statistically significant 30% over the study period.

The loss of native bumble bee pollinators may harm both native and agricultural systems. Simulations by Memmott et al. (2004) suggested that the removal of bumble bees from ecosystems would result in pronounced declines in plant diversity. In field studies Brosi and Briggs (2013) showed that the removal of the most common bumble bee species from study plots was associated with less effective pollination by other pollinators and limited seed production by native plants. Additionally, bumble bees are second only to honey bees (*Apis mellifera*, Linnaeus, 1758) in their importance in agriculture, pollinating blueberries, cranberries, tomatoes, and peppers, among other crops (Goulson, 2010; Hatfield et al., 2012; Shipp et al., 1994; Whittington and Winston, 2004).

Of the historically known species in Texas, *B. auricomus* (Robertson, 1903), *B. fervidus* Fabricius, 1798, *B. fraternus*, *B. pensylvanicus*, *B. sonorus* and *B. variabilis* (Cresson, 1872) have experienced range reductions or local extirpations in other parts of North America (Berenbaum et al., 2007; Cameron et al., 2011; Colla and Packer, 2008; Colla et al., 2012; Colla et al., 2011; Grixti et al., 2009). Such losses have raised awareness of the need for conservation measures in Texas and have led three of these species (*B. pensylvanicus*, *B. sonorus*, and *B.*

variabilis) to be designated as species of greatest conservation need in the Texas Conservation Action Plan.

Species distribution models (SDMs) estimate the geographic distribution of a species using field observations and associated environmental predictor variables. Over the last few decades, SDMs have become increasingly useful tools for conservation planning (Guisan and Thuiller, 2005). The Maximum Entropy (MaxEnt) algorithm is attractive because it is easy to implement and uses presence-only data, along with environmental variables associated with presence localities, to produce robust distribution models (Phillips et al., 2004; Phillips et al., 2006).

The current understanding of Texas bumble bee distributions is based largely on locality data gleaned from natural history collections that were compiled and mapped by Warriner (2012). Additional Texas records were included in Williams et al. (2014), wherein MaxEnt was implemented to estimate the continental ranges of all species found in North America. The only recent study to assess the status of Texas populations was limited to the northeastern portion of the state (Beckham et al., in press).

In an effort to update and increase the understanding of known and probable statewide bumble bee species presence in Texas, and aid the planning and implementation of conservation actions, this study addressed two objectives: 1) Compile statewide occurrence records from citizen science repositories, natural history collections and field studies to produce updated maps of known bumble bee presence in Texas, and 2) Create species distribution models that will illustrate the potential ranges of bumble bee species in Texas in order to aid planning of conservation actions.

Methods:*Presence Data—*

Bumble bee presence data were gathered from natural history museum collections, citizen science repositories and recent field collection data. These were compiled into one database for mapping and species distribution modeling purposes.

Museum databases previously compiled by Michael Warriner and Leif Richardson provided occurrence records from the following institutions: Texas A&M University Insect Collection, Texas Memorial Museum, Illinois Natural History Survey Insect Collection, Cornell University Insect Collection, Florida State University Collection of Arthropods, Mississippi State University Entomological Museum, K.C. Emerson Entomology Museum (Oklahoma State University), Purdue Entomological Research Collection, Smithsonian Natural History Museum, University of Arkansas Arthropod Museum, University of Georgia Collection of Arthropods, University of Michigan Museum of Zoology, University of Minnesota Insect Collection, American Museum of Natural History, Canadian National Collection, Essig Museum of Entomology, Los Angeles County Museum, Ohio State University, U.C. Davis Bohart Museum, and the Yale Peabody Museum. Additionally, Jessica Beckham provided records previously identified from the Elm Fork Natural Heritage Museum (University of North Texas). These records were georeferenced by Leif Richardson and Jessica Beckham using Google Earth.

Two citizen scientist repositories, iNaturalist and the Texas Bumblebees Facebook page (hereafter referred to as “Texas Bumblebees”), were also mined for presence records. Only records which included photographs that could be identified to species, as well as location data, were incorporated into the modeling database. The iNaturalist platform allows contributors to include locality coordinates with their submissions; when available, these coordinates were

included in the presence database. Records lacking coordinates, as well as all submissions from Texas Bumblebees, were georeferenced based on locality information provided by the observer using Google Earth.

Field collection data from northeast Texas were also included from recent research projects performed by Jessica Beckham and Michael Warriner in 2010-2014. Additional records, verified by photograph, were directly submitted to Jessica Beckham by citizen scientists (2014-2015). Geographic coordinates for all of these data were recorded in the field by the observer using GPS devices.

Environmental Variables—

Environmental layers of 19 derived bioclimatic variables (Table 1) were downloaded the WorldClim global climate database (www.worldclim.org) at a resolution of 30 arc-seconds (~1-km). In addition, the 2011 national landcover dataset (NLCD) was also downloaded from the Multi-Resolution Land Characteristics Consortium (<http://www.mrlc.gov/nlcd2011.php>) at 30-m resolution.

The NLCD consists of pixels classified into 16 different classes; in order to simplify the dataset these were recoded into eight classes using ERDAS IMAGINE 2015. The resulting land classes were: water, developed, barren, forest, shrubland, herbaceous, planted/cultivated, and wetlands. Because MaxEnt requires that all environmental raster layers have identical cell sizes and projections, the recoded NLCD raster was rescaled and reprojected in ArcMap 10.2.2 to match WorldClim layer resolution (30 arc-seconds) and projection (WGS 1984).

Table 1: Derived WorldClim bioclimatic variables used for species distribution modeling.

Code	Derived Variable
BIO1	Annual Mean Temperature
BIO2	Mean Diurnal Range (Mean of monthly (max temp - min temp))
BIO3	Isothermality (BIO2/BIO7) (* 100)
BIO4	Temperature Seasonality (standard deviation *100)
BIO5	Max Temperature of Warmest Month
BIO6	Min Temperature of Coldest Month
BIO7	Temperature Annual Range (BIO5-BIO6)
BIO8	Mean Temperature of Wettest Quarter
BIO9	Mean Temperature of Driest Quarter
BIO10	Mean Temperature of Warmest Quarter
BIO11	Mean Temperature of Coldest Quarter
BIO12	Annual Precipitation
BIO13	Precipitation of Wettest Month
BIO14	Precipitation of Driest Month
BIO15	Precipitation Seasonality (Coefficient of Variation)
BIO16	Precipitation of Wettest Quarter
BIO17	Precipitation of Driest Quarter
BIO18	Precipitation of Warmest Quarter
BIO19	Precipitation of Coldest Quarter

All rasters were then clipped to match the boundaries of the state of Texas using the *extract by mask* tool in ArcMap. The cartographic boundary file for the mask was downloaded from <https://www.census.gov/geo/maps-data/data/tiger-cart-boundary.html> and a shapefile of Texas was produced and projected to WGS_1984. Once all environmental layers had been processed, they were converted to ASCII files for use in MaxEnt.

Correcting for Sampling Bias—

The MaxEnt algorithm assumes that presence data upon which models are built have been acquired from systematic or random sampling of the study area. However, Texas *Bombus* presence data were heavily biased towards heavily populated areas, especially DFW, Houston,

and Austin. Running MaxEnt without correcting for this sampling bias would result in overfitting of models that reflects a model of survey effort rather than actual species distribution. Two tools from the SDMtoolbox (Brown, 2014) were implemented in ArcMap to address this bias: spatial filtering of presence data and selection of background points using a bias file.

When sample size is sufficient, spatial filtering is recommended to minimize errors of omission and commission (Kramer-Schadt et al., 2013). Presence data were spatially filtered using the SDMtoolbox *rarefy occurrence data for SDMs* tool that reduces spatial autocorrelation. This tool removes duplicate occurrence points and reduces occurrence records to a single point within a specified area; in the case of our data we used a 15-km² resolution.

Because MaxEnt uses presence-only data to produce species distribution models, “background pixels” are randomly selected from the study area to be used as “pseudo- absence” points. Selecting background points so that they carry the same bias as presence data aids in the production of more accurate distribution models (Phillips et al., 2009). A bias grid was produced using the SDMtoolbox *Gaussian kernel density of sampling localities* tool with a sampling bias distance of 30 km. This was implemented in MaxEnt to manipulate the selection of background points to reflect sampling bias.

Production of Species Distribution Models in MaxEnt—

Input data for species distribution modeling in MaxEnt consisted of the aforementioned spatially filtered presence data (occurrence records) and the 20 environmental layers. The Gaussian kernel density bias file was also loaded to limit selection of background points. The program was run for 50 replicates for each species with default settings, except as follows: jackknifing was selected to measure variable importance, 40% test (training) percentage was

implemented, and 5000 max iterations. The resulting species distribution models (in Results) were the average models over the 50 runs.

Results:

A total of 2,906 Texas records spanning 1897-2016 were compiled from museum collections, citizen science repositories and recent fieldwork (Table 2). This included 11 species, as follows: *B. appositus* (n=1), *B. auricomus* (n=13), *B. bimaculatus* (n=6), *B. fervidus* (n=3), *B. fraternus* (n= 157), *B. griseocollis* (n=110), *B. impatiens* (n=177), *B. morrisoni* (n=2), *B. pennsylvanicus* (n=2153), *B. sonorus* (n=273), and *B. variabilis* (n=11). These data included 747 new records from the past ten years that were present in citizen science repositories (iNaturalist and Texas Bumblebees) and have not been previously published or included as presence data for species distribution models (Figure 1).

Table 2: Sources of bumble bee presence data.

Data Source (Time Period)	Number of Records
Museum Collections (1897-2012)	2022
iNaturalist (2007-2016)	377
Texas Bumble Bees Facebook (2007-2016)	370
Field Data (2010-2015)	137
<i>Total</i>	2906

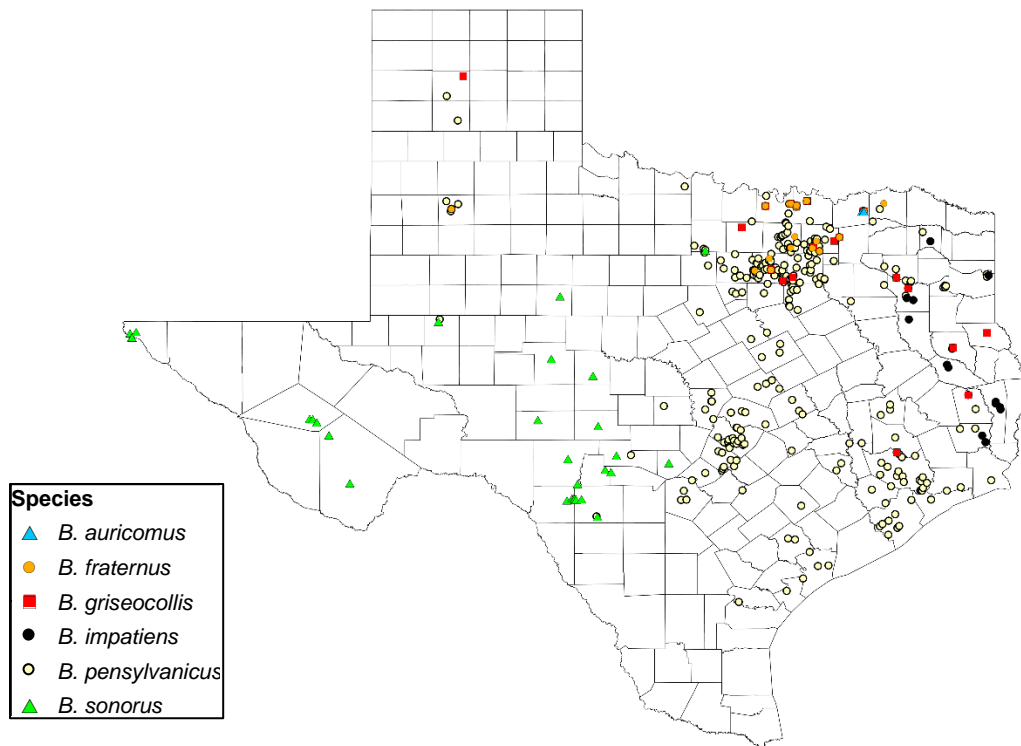
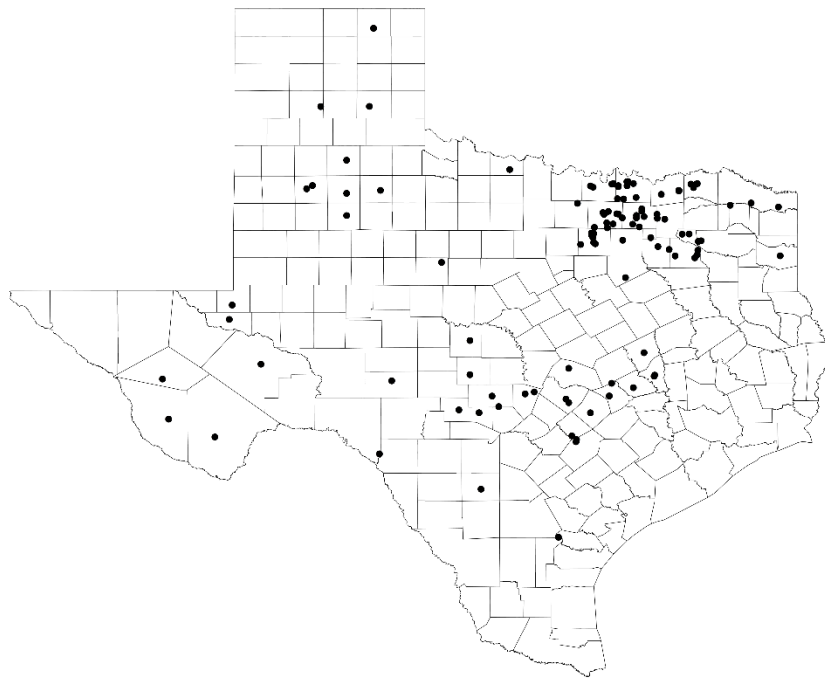


Figure 1: Novel presence data ($n=747$) compiled from the citizen science repositories iNaturalist and Texas Bumblebees Facebook page. These included six species: *B. auricomus* ($n=11$), *B. fraternus* ($n=48$), *B. griseocollis* ($n=60$), *B. impatiens* ($n=29$), *B. pensylvanicus* ($n=557$), and *B. sonorus* ($n=42$).

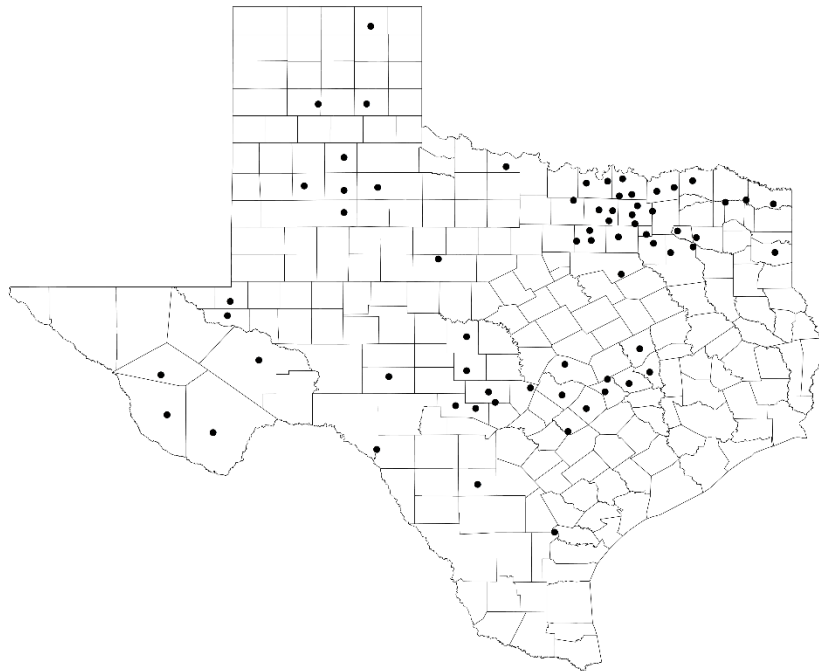
Though data were available on eleven different species, we only modeled the distributions of the five most abundant species in the state: *B. fraternus*, *B. griseocollis*, *B. impatiens*, *B. pensylvanicus* and *B. sonorus*. Of these, *B. fraternus*, *B. pensylvanicus*, and *B. sonorus* are considered declining. At least 110 presence records were compiled for each of these species; sample sizes for other species known from Texas were deemed insufficient for spatial filtering and modeling purposes. Numbers of occurrence records for each species before and after spatial filtering are shown in Table 3, and maps of these records are shown in Figures 2-6.

Table 3: Numbers of occurrence records before and after spatial filtering at 15-km². Filtered results were used for MaxEnt models.

Species	Number of Occurrence Records	Number Occurrence Records after Spatial Filtering
<i>B. fraternus</i>	157	67
<i>B. griseocollis</i>	110	41
<i>B. impatiens</i>	177	26
<i>B. pennsylvanicus</i>	2153	271
<i>B. sonorus</i>	273	66

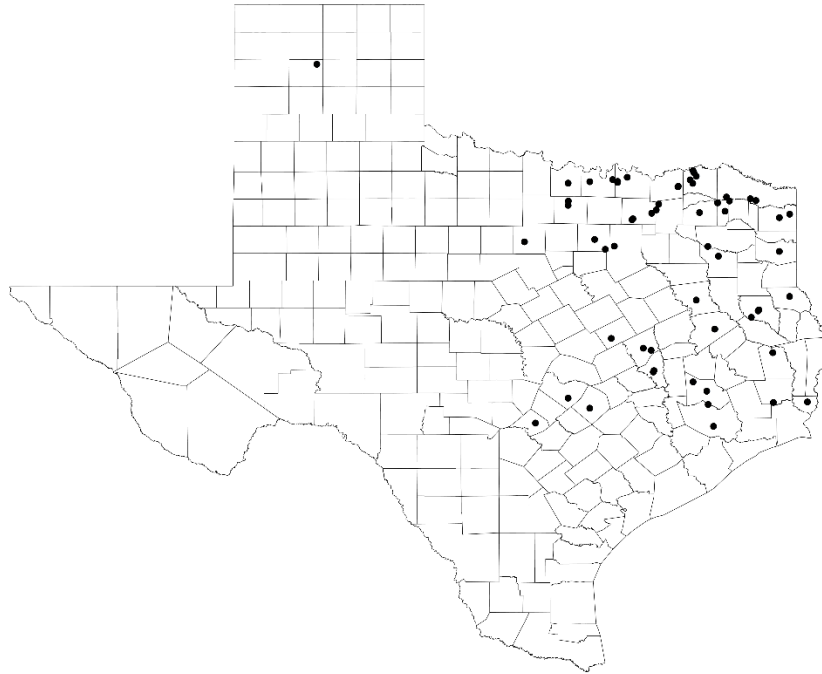


a)

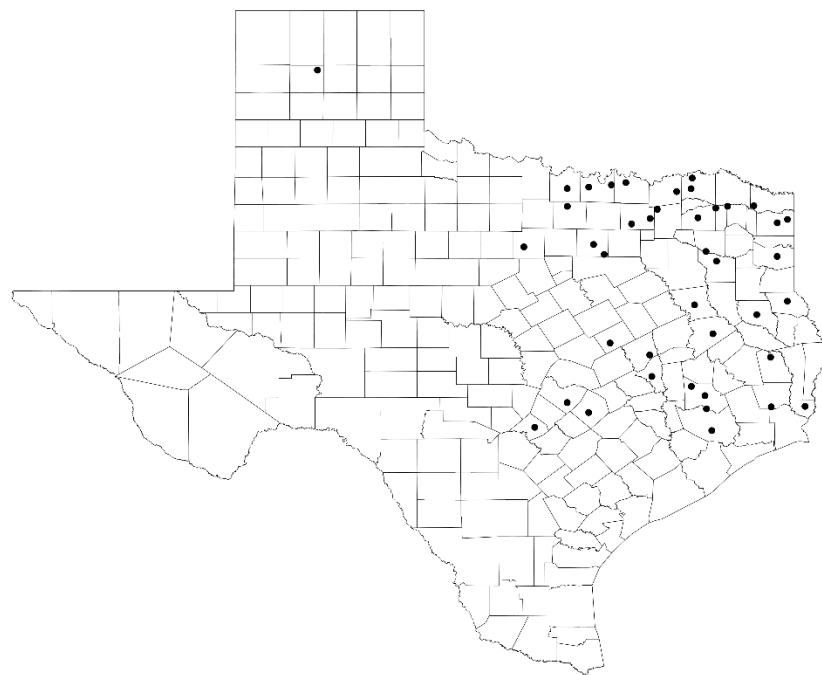


b)

Figure 2: Locations of presence points used for modeling species distribution of *B. fraternus* (a) prior to spatial filtering ($n=157$), and (b) after spatial filtering at 15-km resolution ($n=67$).

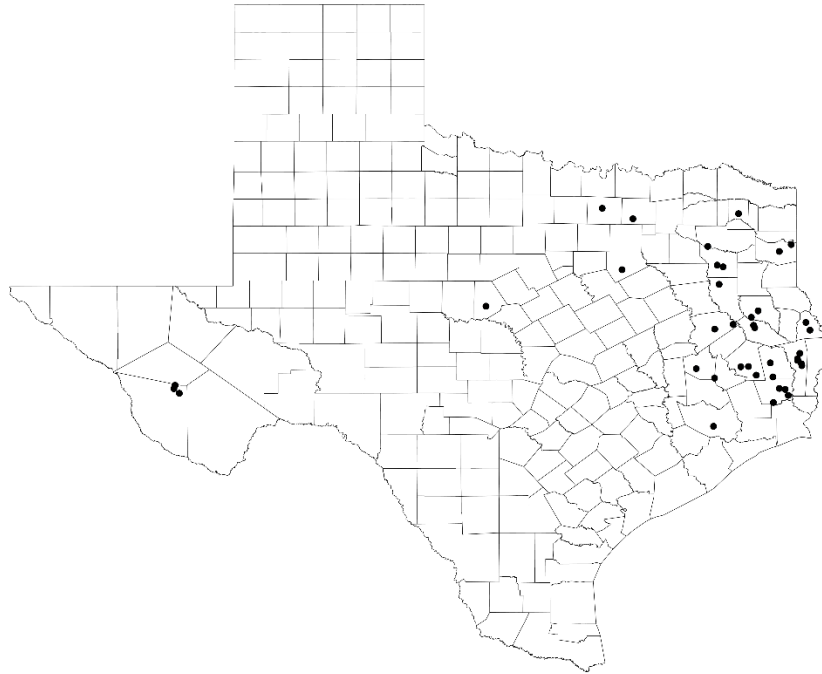


a)

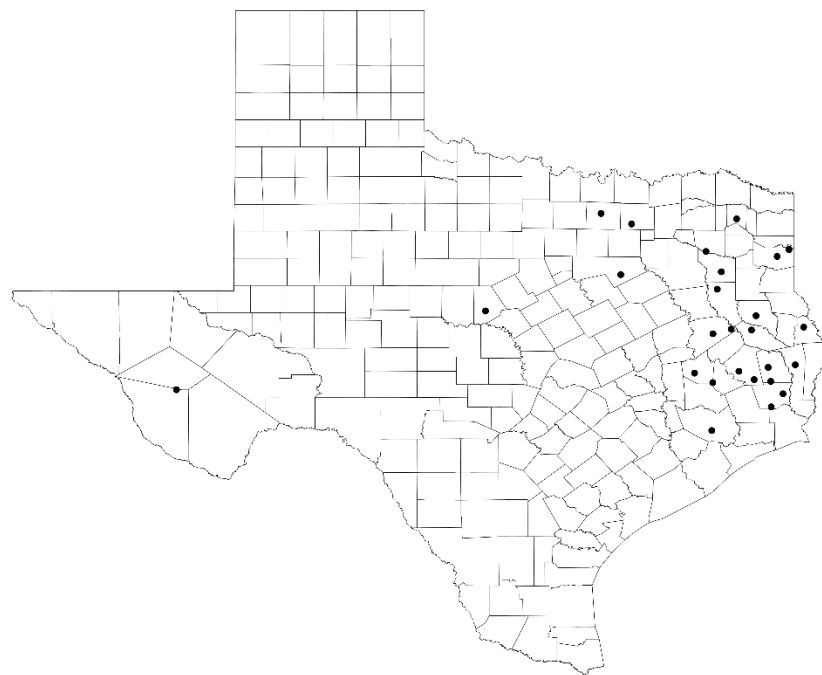


b)

*Figure 3: Locations of presence points used for modeling species distribution of *B. griseocollis* (a) prior to spatial filtering (n=110), and (b) after spatial filtering at 15-km resolution (n=41).*

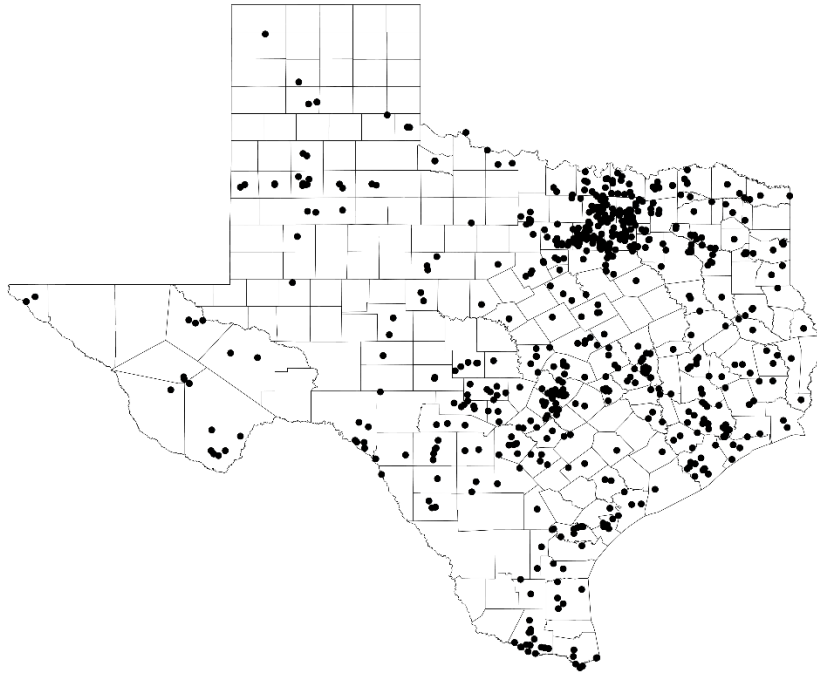


a)

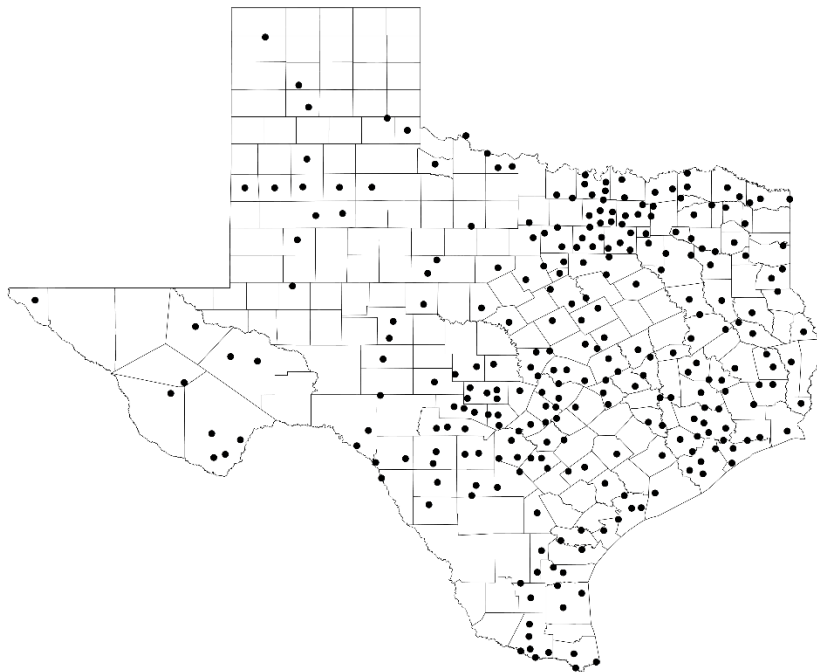


b)

Figure 4: Locations of presence points used for modeling species distribution of *B. impatiens* (a) prior to spatial filtering ($n=177$), and (b) after spatial filtering at 15-km resolution ($n=26$).

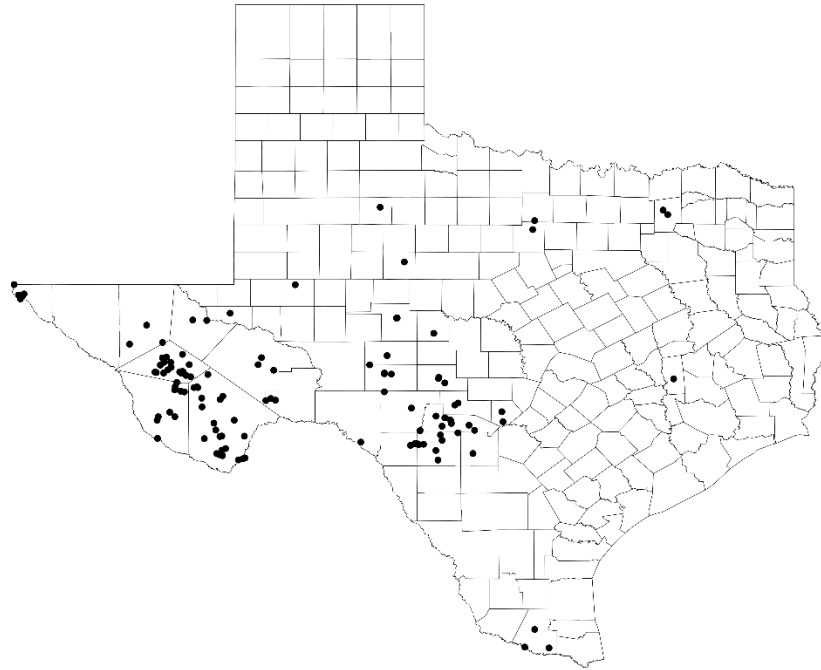


a)

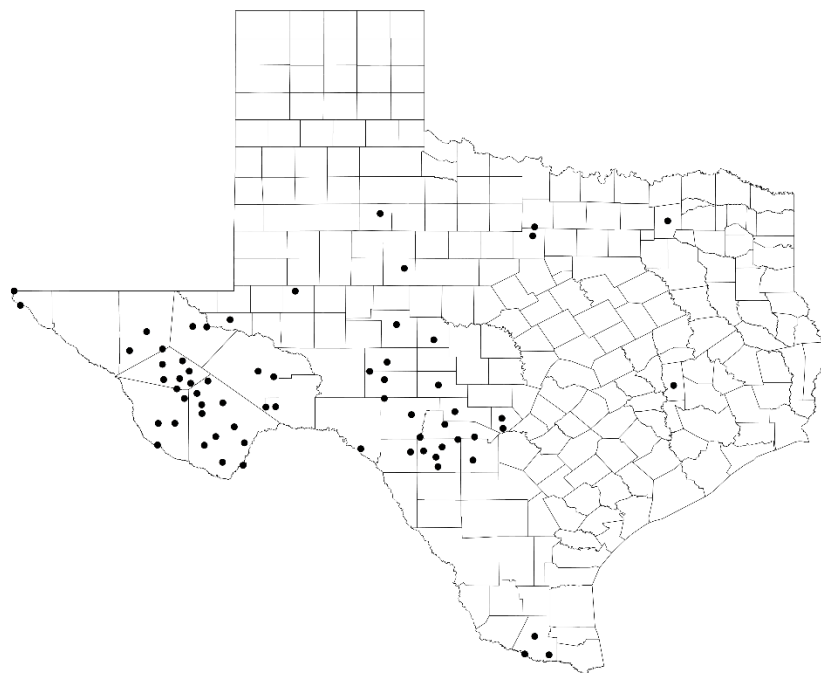


b)

*Figure 5: Locations of presence points used for modeling species distribution of *B. pensylvanicus* (a) prior to spatial filtering ($n=2153$), and (b) after spatial filtering at 15-km resolution ($n=271$).*



a)



b)

Figure 6: Locations of presence points used for modeling species distribution of *B. sonorus* (a) prior to spatial filtering ($n=273$), and (b) after spatial filtering at 15-km resolution ($n=66$).

The logistic outputs of species distribution models produced in MaxEnt for *B. fraternus*, *B. griseocollis*, *B. impatiens*, *B. pensylvanicus* and *B. sonorus* are shown in Figures 7-11, respectively. Each pixel was given a value between 0 and 1, which represents the probability of presence at sites with typical conditions for the species (see Elith et al., 2010, for a further explanation of the logistic output of MaxEnt). The accuracy of each model was evaluated by looking at the area under the Receiver Operating Characteristic (ROC) curve, or AUC value, plotted and calculated in MaxEnt based on the training data. This plot shows the predictive performance of the model as compared to a selection of random points. An AUC value of 0.5 reflects a model that is no better than random, while an AUC of 1 would be a “perfect” model. These plots are also included in Figures 7-11. All models carried AUC values above 0.85 (Table 4) and so were considered to have strong predictive power.

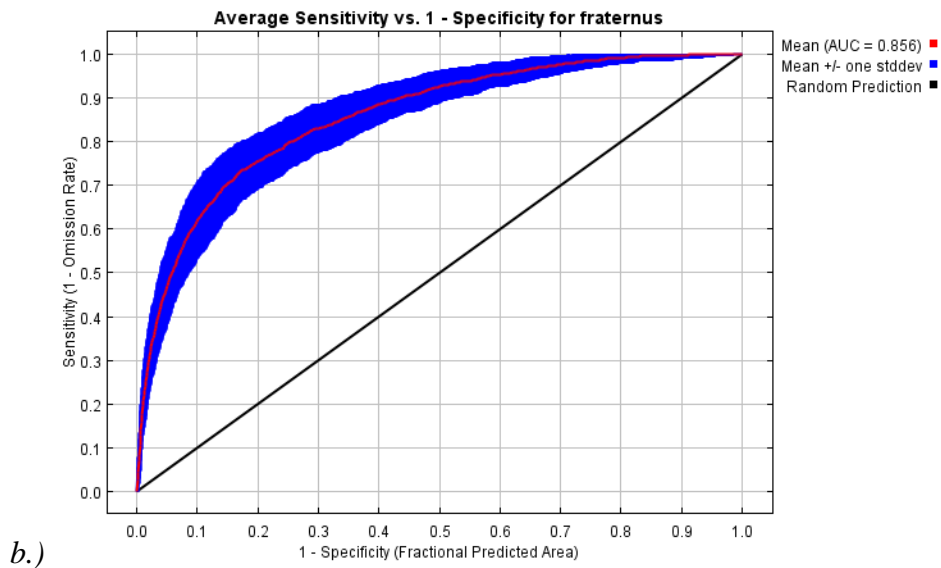
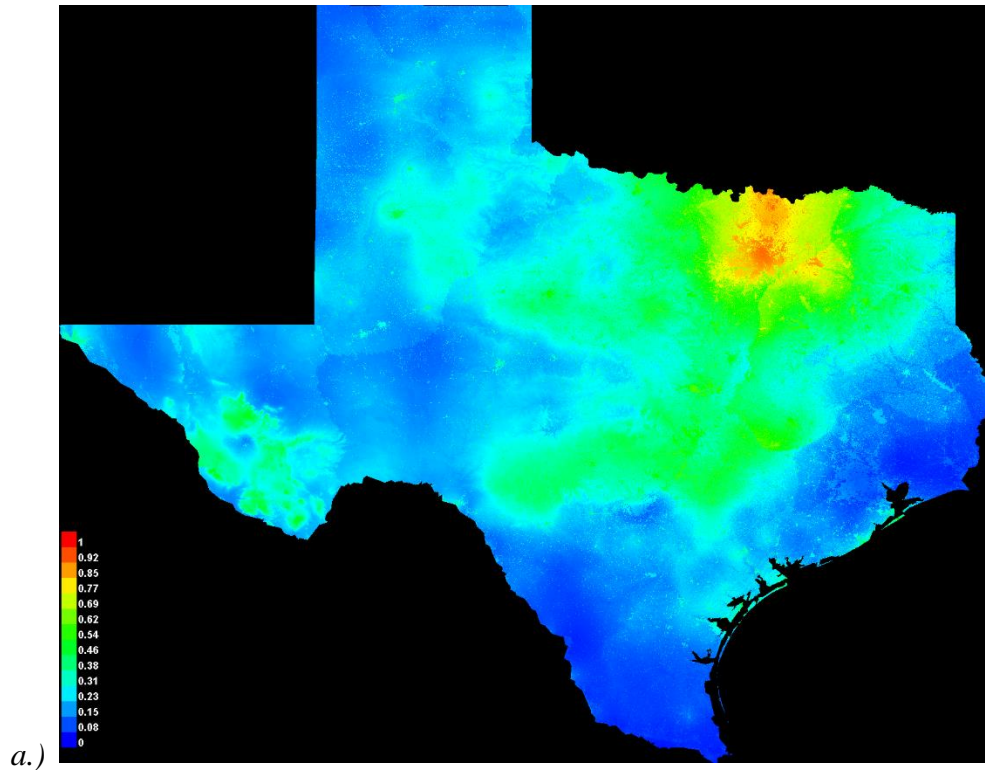


Figure 7: (a) Predicted distributions, represented by calculated probability of presence at sites with typical conditions for the species within each image pixel, of *B. fraternus* in Texas based on mean MaxEnt logistic output averaged over 50 replicates, and (b) receiver operating characteristic curve for model evaluation (average AUC over 50 runs = 0.856 ± 0.028).

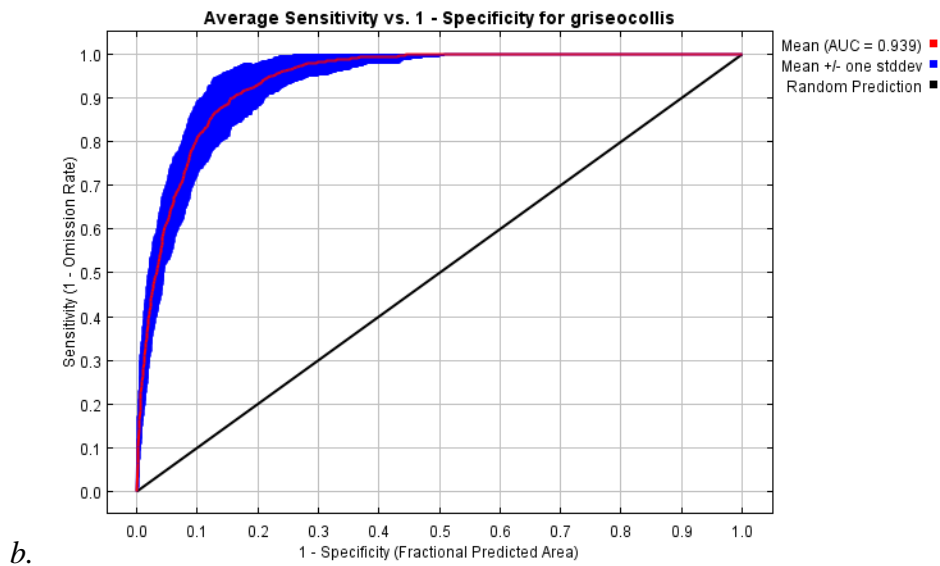
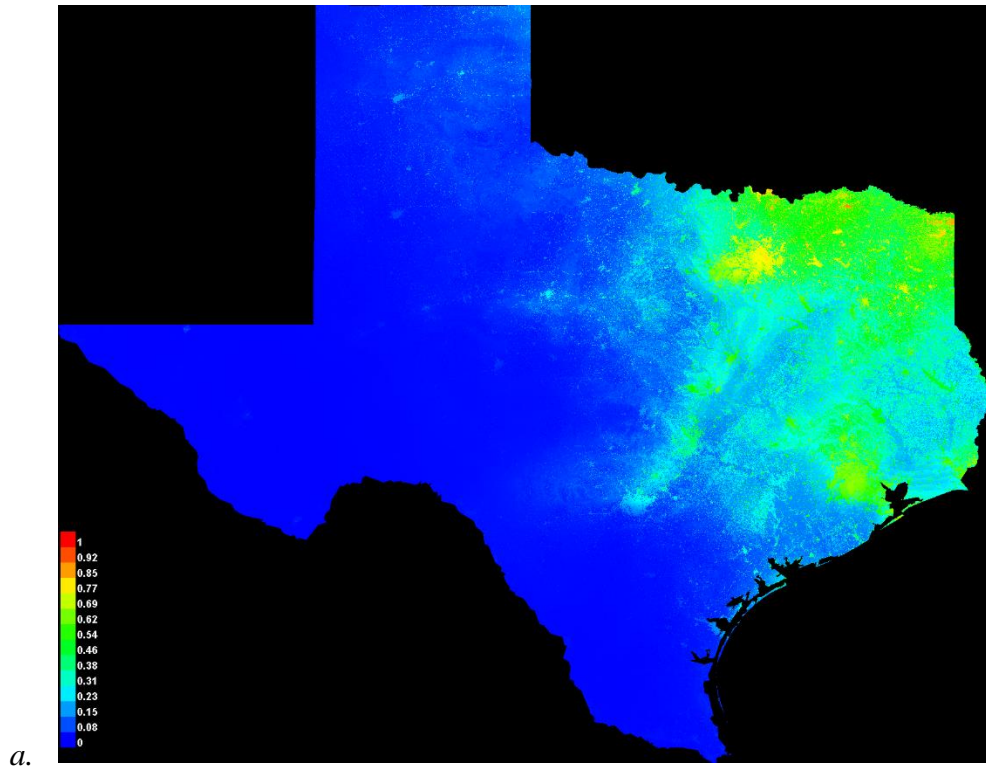


Figure 8: (a) Predicted distributions, represented by calculated probability of presence at sites with typical conditions for the species within each image pixel of *B. griseocollis* in Texas based on mean MaxEnt logistic output averaged over 50 replicates, and (b) receiver operating characteristic curve for model evaluation (average AUC over 50 runs = 0.939 ± 0.016).

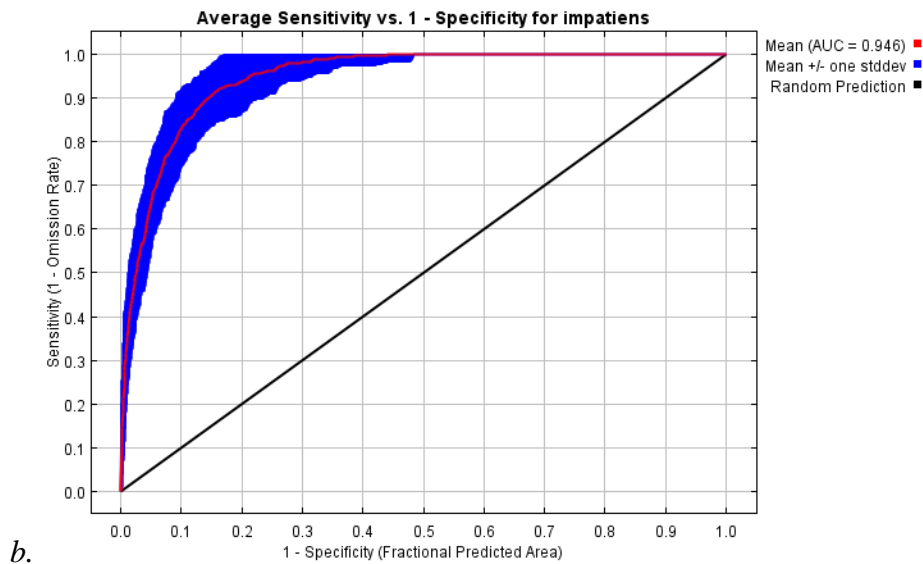
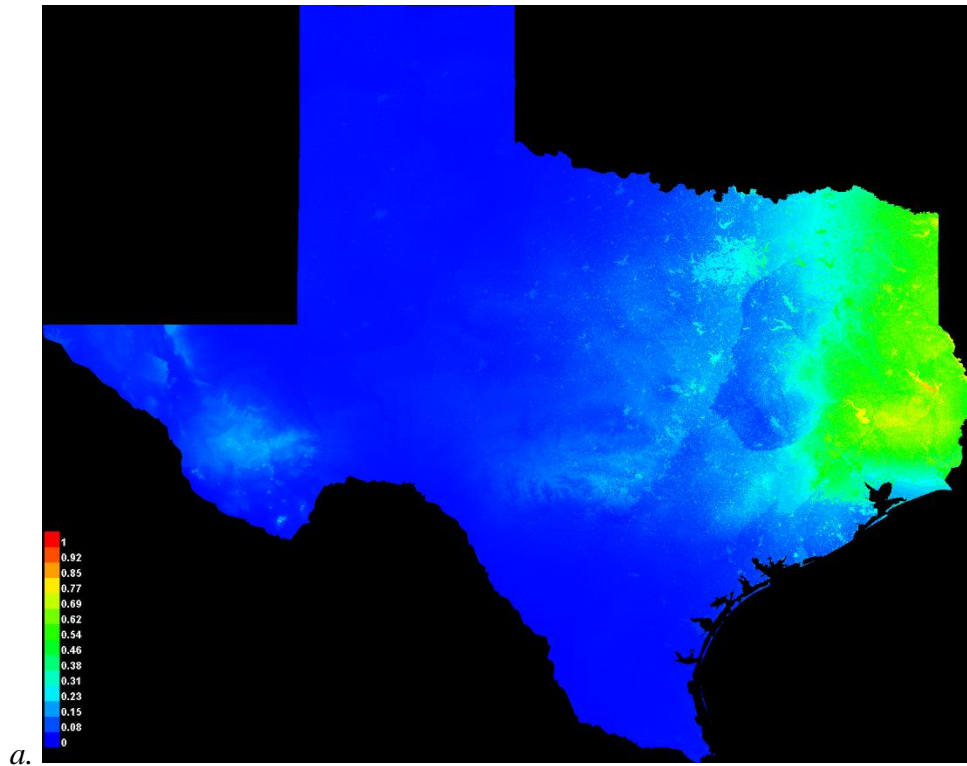


Figure 9: (a) Predicted distributions, represented by calculated probability of presence at sites with typical conditions for the species within each image pixel, of *B. impatiens* in Texas based on mean MaxEnt logistic output averaged over 50 replicates, and (b) receiver operating characteristic curve for model evaluation (average AUC over 50 runs = 0.946 ± 0.017).

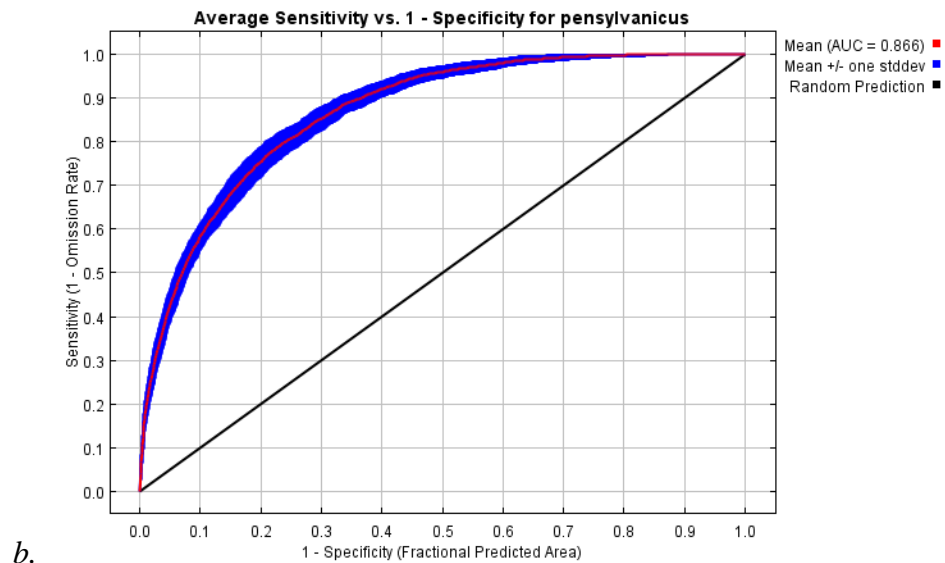
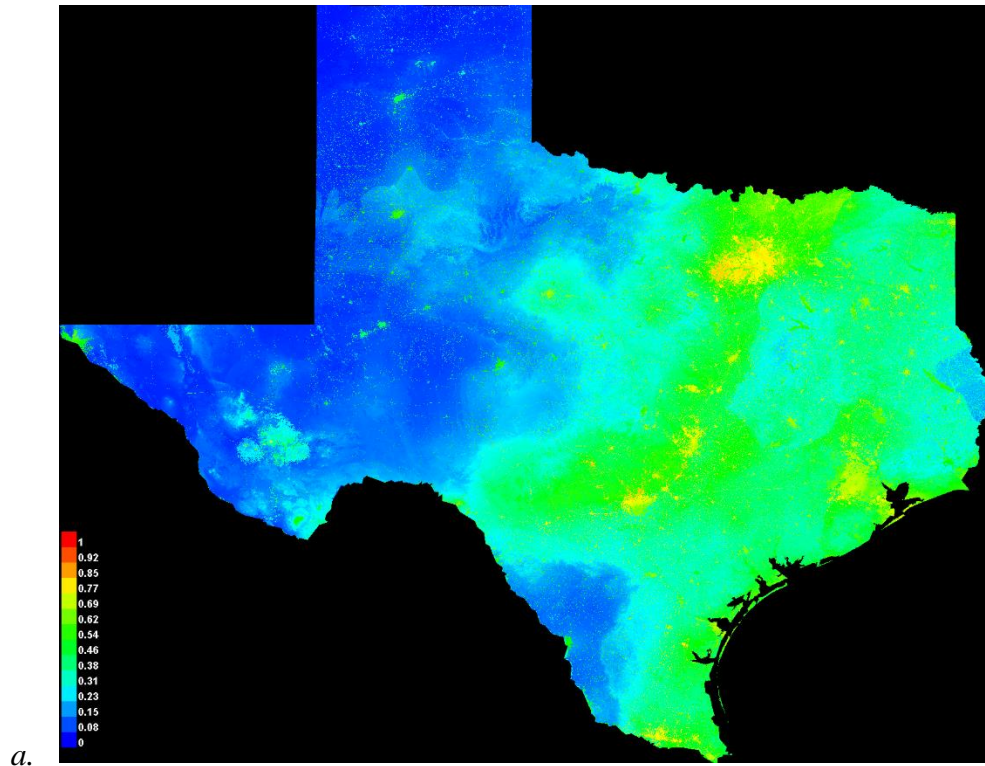


Figure 10: (a) Predicted distributions, represented by calculated probability of presence at sites with typical conditions for the species within each image pixel, of *B. pennsylvanicus* in Texas based on mean MaxEnt logistic output averaged over 50 replicates, and (b) receiver operating characteristic curve for model evaluation (average AUC over 50 runs = 0.866 ± 0.010).

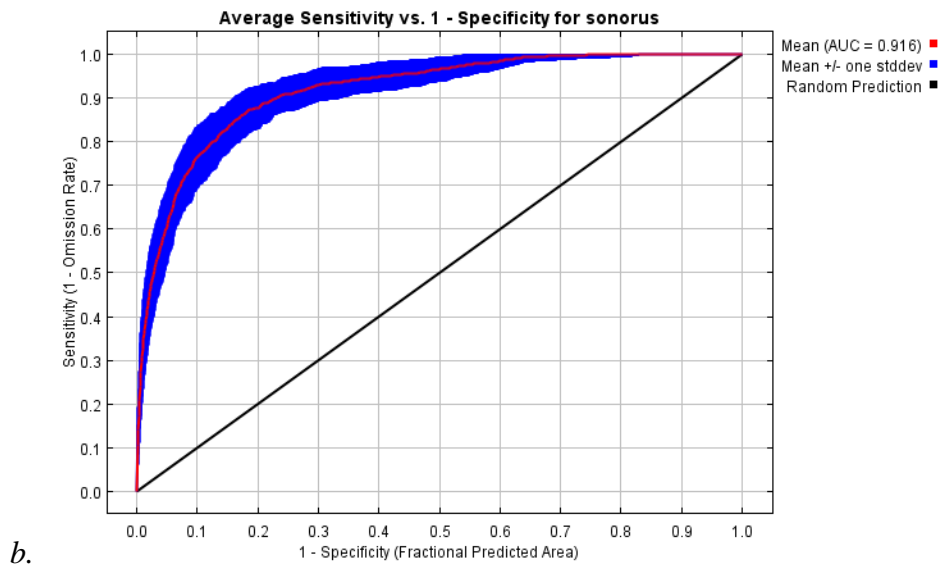
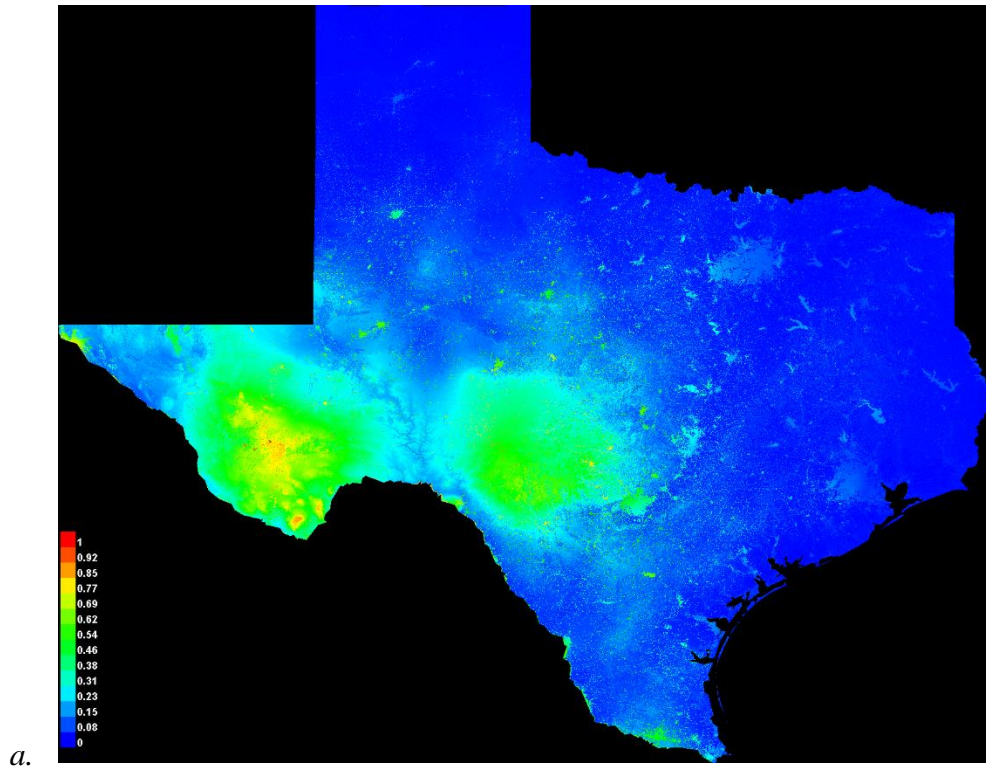


Figure 11: (a) Predicted distributions, represented by calculated probability of presence at sites with typical conditions for the species within each image pixel, of *B. sonorus* in Texas based on mean MaxEnt logistic output averaged over 50 replicates, and (b) receiver operating characteristic curve for model evaluation average (AUC over 50 runs = 0.916 ± 0.018).

Table 4: Training and test AUCs and top variables contributing to bumble bee species distribution models.

Species	Average Training AUC \pm S.D. over 50 replicates (number of training points in each replicate)	Average Test AUC \pm S.D. over 50 replicates (number of test points in each replicate)	Top variables contributing to model (percent contribution)
<i>B. fraternus</i>	0.856 \pm 0.028 (41)	0.7724 \pm 0.0512 (26)	bio03 (39.2%); NLCD (10.2%); bio18 (7.5%); bio06 (7.1%); bio15 (6.3%)
<i>B. griseocollis</i>	0.939 \pm 0.016 (25)	0.9006 \pm 0.0249 (16)	bio14 (27.1%); NLCD (20%); bio19 (18.7%); bio17 (7.8%); bio03 (7.1%)
<i>B. impatiens</i>	0.946 \pm 0.017 (16)	0.896 \pm 0.0392 (10)	bio15 (58.9%); bio19 (12.5%); NLCD (6.8%); bio17 (6.3%); bio14 (4.9%)
<i>B. pensylvanicus</i>	0.866 \pm 0.010 (160)	0.7801 \pm 0.0213 (106)	NLCD (30.8%); bio02 (16.6%); bio19 (10.8%); bio03 (3.7%); bio17 (3.6%); bio18 (3.6%)
<i>B. sonorus</i>	0.916 \pm 0.018 (39)	0.8636 \pm 0.0374 (25)	bio03 (31.7%); NLCD (18%); bio06 (7.9%); bio04 (7.7%); bio09 (5.4%)

Discussion

This study has resulted in a broader understanding of bumble bee presence in Texas, including that of three declining species: *B. fraternus*, *B. pensylvanicus* and *B. sonorus*. The vetting and compilation of citizen science records that were reported over the last ten years has helped to elucidate current (i.e., 2007-2016) presence across the state. Additionally, while continental species distribution models have previously been produced for bumble bee species found in Texas, we have modeled finer scale (Texas only) species distributions for five species

using MaxEnt. Based on these maps and models, we recommend the following target areas for bumble bee conservation efforts: the Trans-Pecos and Edwards Plateau ecoregions of Texas for *B. sonorus*; the Post Oak Savannah, Blackland Prairie, Cross Timbers, Piney Woods and Gulf Prairies for *B. pensylvanicus*; and the Cross-Timbers, Post Oak Savannah and Blackland Prairie for *B. fraternus*. Additionally, it is recommended that future survey efforts be carried out in the Panhandle and west Texas in order to fill in gaps in data in those regions.

Acknowledgments

Thank you to Leif Richardson and Michael Warriner, who provided extensive historical bumble bee databases from the state of Texas. And thank you to the many citizen scientists who contributed bumble bee records to iNaturalist and Texas Bumblebees.

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