



Maximizing Ecological and Social Co-benefits of Green Spaces by Enhancing Urban Pollinator Habitat Connectivity in Boston, MA

Introduction

Background and Significance

Pollinator species are critical components of functioning ecosystems, yet they have been declining worldwide due to a variety of threats, including habitat loss and fragmentation¹. In particular, urban development impacts pollinator habitat in a variety of ways. Urban areas contain patches of green space that can serve as suitable habitats, but they are embedded in a matrix of buildings, roads, and concrete surfaces which may be difficult for pollinators to move through. Pollinator species face many threats when straying outside of suitable habitats, including but not limited to collisions with buildings and vehicles². Additionally, urban green spaces are not always representative of pollinators' habitat needs. Depending on how they are designed and for what purpose, green spaces may vary in size, location, vegetation composition, and species richness³. Pollinator-plant interactions are categorized along a continuum, from specialists (one-to-one pollinator-to-plant relationship) to generalists (one pollinator to many plants)⁴. A lack of specialized habitat for pollination specialists will likely result in a decline in their populations. As a result of so many interacting factors, the abundance and diversity of pollinators are often lower in cities than in natural or semi-natural areas⁵.

As climate change projections show increased temperatures in the northeastern U.S., decreasing the urban heat island effect becomes increasingly important for urban resilience⁶. Green spaces, including those suitable for pollinator's needs, can be strategically designed and used for such purposes, aiding cities in preparing for these natural hazards^{6,7}. In addition to these physical co-benefits, studies have shown mental health improvements in people who can access green spaces⁸. Studies show that access to green space also plays a role in an individual's connection with the environment, serving as a gateway to environmental values and advocacy^{9,10}. Unfortunately, green spaces tend to be distributed inequitably, with more green spaces in wealthier and whiter neighborhoods¹¹. It is important to incorporate environmental justice and equity in green space additions so that more people can reap the myriad benefits of equitable dispersed green spaces, such as reduced heat intensity, improved mental health, and a greater connection to the outdoors¹¹.

Preserving and enhancing the benefits of urban green spaces requires ensuring these spaces are ecologically functional and resilient. In effect, maintaining healthy pollinator communities is paramount, which can be partially achieved by ensuring and bolstering habitat connectivity throughout a city¹². With this in mind, this conservation plan focuses on three pollinator species found in the northeastern U.S.: the brown-belted bumblebee (*Bombus griseocollis*), the ruby-throated hummingbird (*Archilochus colubris*), and the monarch butterfly (*Danaus plexippus*). We selected these urban pollinator species for a variety of reasons, including their representation of different pollinator taxa, various habitat needs, as well as charisma and broad appeal. We will map their areas of suitable habitat and their habitat connectivity in the city of Boston, Massachusetts. We close by presenting spatially-explicit recommendations for pollinator habitat creation that enhance habitat connectivity and provide social co-benefits.

Objectives

1. Model species distribution across the city of Boston for three species of pollinators.
 - a. *Goal: Identify areas of suitable habitat for each species.*
2. Analyze connectivity pathways and movement pinch points in between green spaces in Boston for the three species of pollinators.
 - a. *Goal: Visualize likely movement pathways for each species and pinch points (areas especially crucial for preserving connectivity).*
3. Identify priority areas for improving habitat connectivity that could provide co-benefits for heat mitigation and equitable green space access.
 - a. *Goal: Find locations in the city to recommend pollinator habitat creation that provides for both social and ecological benefits.*

Methods

Study Area Selection

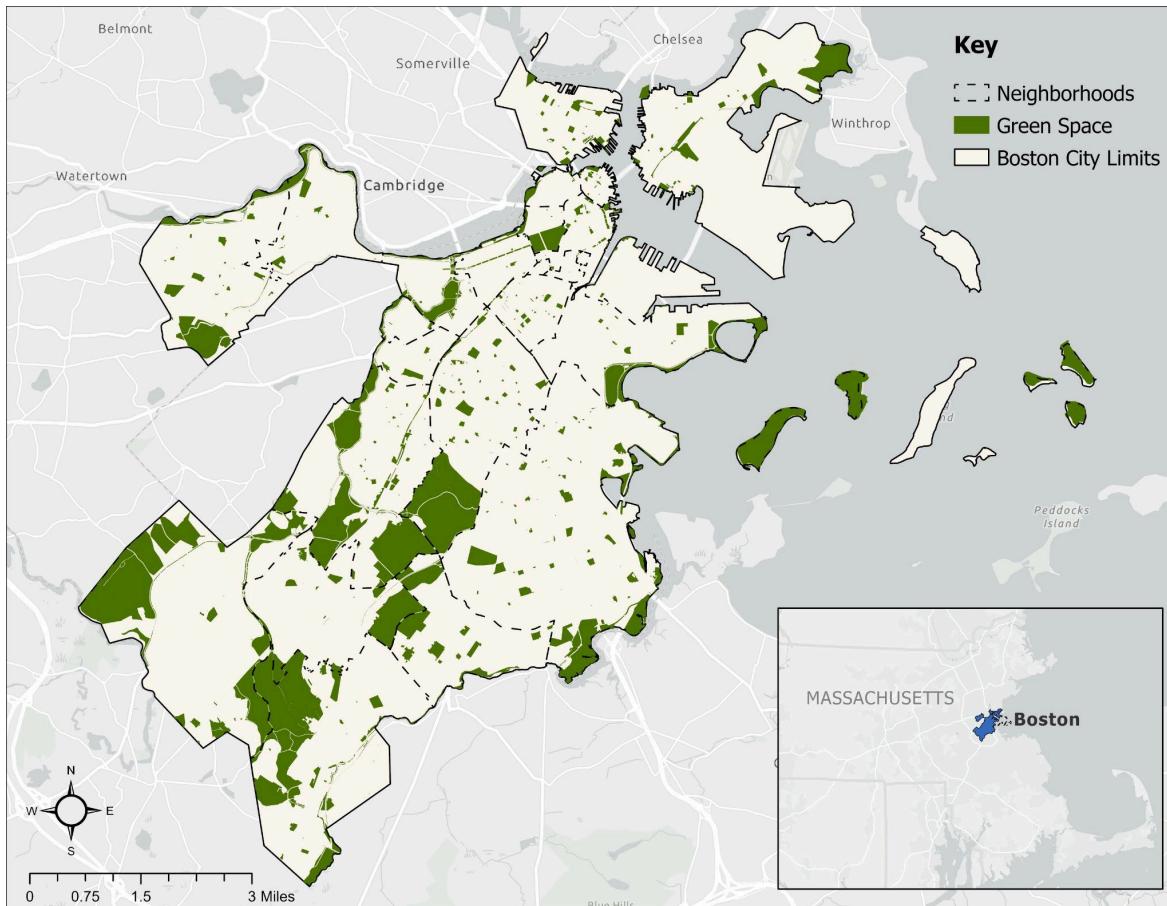


Figure 1. Study area of the city of Boston with city boundaries, neighborhood boundaries, and existing green spaces identified.

Our project location is the city of Boston, Massachusetts (Figure 1). Boston is a major metropolitan area with a large population, significant urban development, and a variety of parks and green spaces. While there are several green spaces and small-scale gardens throughout the city, these spaces were not planned with pollinator connectivity in mind and are not necessarily well-connected. Additionally, its green spaces, while numerous, tend to be clustered in wealthier, whiter areas (Figures 1 and 2), which indicates the need to explore the strategic addition of pollinator habitat in disadvantaged communities.

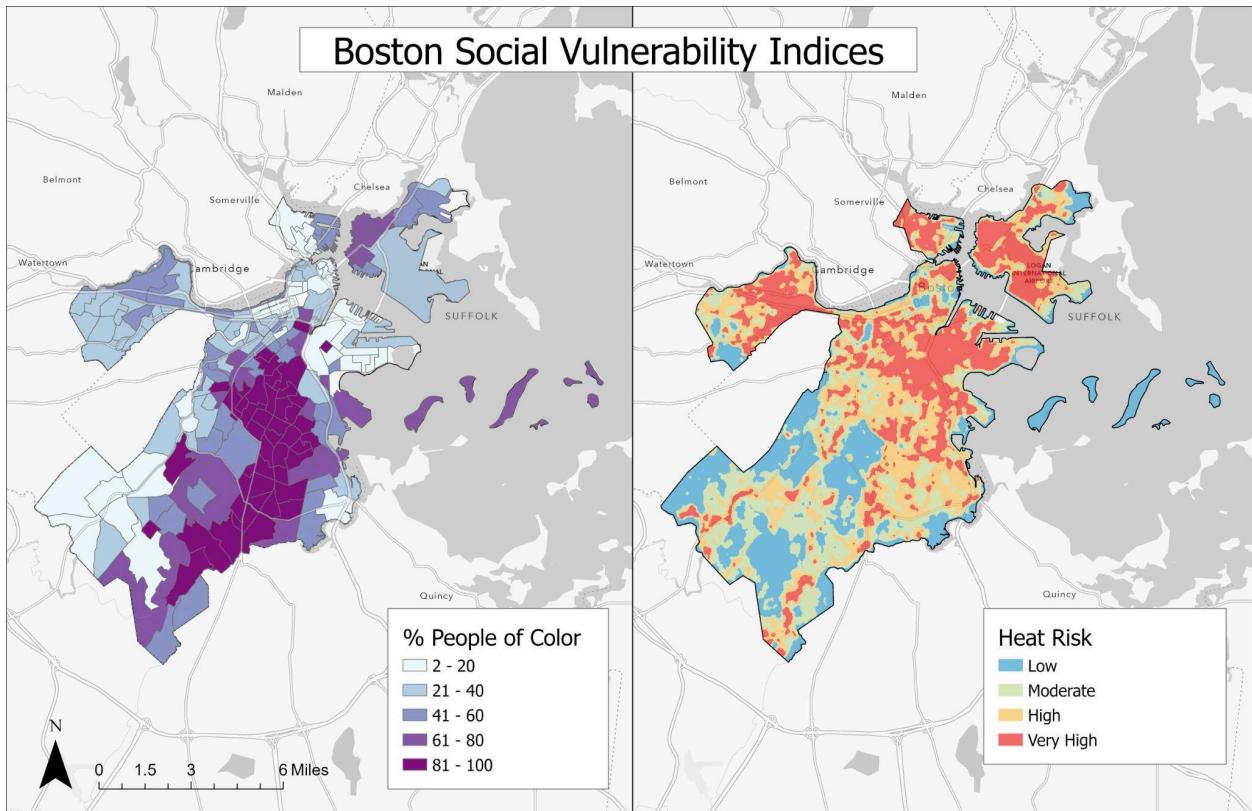


Figure 2. Indices of social vulnerability for census tracts within Boston, Massachusetts. The percent of the population identifying as people of color is shown on the left and the relative heat exposure risk is on the right.

Species Selection

We selected three pollinator species to focus our analysis. The brown-belted bumblebee (*Bombus griseocollis*), ruby-throated hummingbird (*Archilochus colubris*), and monarch butterfly (*Danaus plexippus*) for the following reasons.

1. They represent a diversity of taxa (bee, butterfly, and bird),
2. They are present in the city of Boston (all overlap during the summer months),
3. They represent the continuum of pollinator-to-plant relationships, with brown-belted bumblebees¹³ and hummingbirds¹⁴ as generalists and monarch butterflies¹⁵ as specialists, and
4. They are charismatic species, which provides the potential for broad public support of conservation actions.

Data Acquisition

Data was acquired freely from open-source locations on the web. All datasets used in this analysis are listed in raw form in Table 1, Appendix A, and in the linked metadata table, which is accessible in viewer mode to anyone with the link: [PP_DataMetadata](#).

Data Processing

To process our data, we followed a series of steps to ensure everything was properly projected, aligned, and clipped. All data layers are projected into the same coordinate system for processing: WGS 1984 Web Mercator (auxiliary sphere), with the geographic coordinate system being WGS 1984. The species occurrence points were filtered to include only those observations from the past ~20 years (the exact time span varied with the dataset, as not all datasets had observations every year). To calculate the NDVI values from the Landsat imagery, we used Band 4 (red) and Band 5 (infrared) and the following equation: $NDVI = 100 + ((IR - R)/(IR + R)) * 100$. The open space polygons and garden location points were both used to generate “distance from” raster layers, with each pixel value representing the distance to the closest open space or garden location. All rasters were processed into the same resolution (30 m) using bilinear interpolation. All the rasters that needed resampling were numerical data, none were categorical, so bilinear interpolation was an appropriate method. All final data layers were clipped to the city of Boston polygon and all pixels were aligned using the same snap raster and the same raster extent. Post-processing, all data was projected into the WGS 1984 geographic coordinate system using the R script in Appendix B for final use in *Wallace*.

Species Distribution Modeling

Using the R package *Wallace* we ran Maxent models for our three focal species (brown-belted bumblebees, ruby-throated hummingbirds, and monarch butterflies) to generate localized species distribution models (SDMs). SDMs provide a way of modeling the relationship between species occurrence points and background environmental variables, which can then be used to predict areas of greatest habitat suitability in a given landscape. We input our own species occurrence data, obtained from GBIF (see Table 1 in Appendix A). We also provided our own environmental data inputs to the Maxent models, instead of the typical bioclimatic variables, due to the highly localized nature of this project and the need for finer-resolution data. Our variables include six raster layers: 1) land cover, 2) elevation, 3) NDVI, 4) distance to open space, 5) distance to gardens, and 6) surface temperature index (see Table 1 in Appendix A). This approach is supported by the literature, as we found several papers that focus on SDMs in urban areas incorporate variables such as land cover class, proximity to different land cover classes, population density, elevation, slope, and NDVI¹⁶⁻¹⁸. We used the city of Boston as the background extent and sampled 10,000 background points for each species. For bumblebees and monarch butterflies, a total of ten models were generated via Maxent with a range of regularization parameters (1-5, in increments of 1) and feature sets (linear [L] and linear+quadratic [LQ]). For hummingbirds, a total of five models were generated, using a range of regularization parameters (1-5, in increments of 1). However, hummingbird models only utilized one feature set (linear [L]) due to data limitations, which created errors in any LQ model runs. For each species, the selection of the best model was done by selecting the maximum AUC value and the minimum average AUC difference value. Finally, to ensure accuracy, each model was also visualized and its response curves were inspected. See Appendices C, D, and E for the R script detailing the creation of each SDM.

Connectivity Analysis

We analyzed connectivity for the three species between five core areas in Boston using the ArcGIS Pro Linkage Mapper toolbox in ArcGIS Pro, connected to Circuitscape 4.0.7. Resistance layers for each species informed the generation of least-cost pathways (LCPs), connectivity visualizations, and pinch points—critical areas for movement—using the same inputs.

The five core areas were selected for their size (see Appendix A Table 3) and representation of Boston neighborhoods. Larger open spaces were selected as core areas due to their ability to support the connectivity and habitat needs of multiple species and provide more impactful climate benefits¹⁹. Neighborhood representation was used to address low levels of species occurrence data and green space prevalence in lower-income and racially diverse communities. Resistance layers were created by transforming the SDMs through this formula developed by Keeley, 2016: $R = 100 - 99 * ((1 - \exp(-c * h)) / (1 - \exp(-c)))^{20}$. For each resistance layer, h was one of the three SDMs, and we used a c value equal to 1 to balance resistance layer sensitivity (see Appendix F for R script). Lastly, we explored how connectivity and flow (e.g., LCPs and pinch points) shifted under no cost-weight and 10k cost-weighted distance (CWD) to represent varying movement and constraints across our study area ¹⁶⁻¹⁸.

Social Co-benefit Hotspots

As noted early in our report, we were interested in identifying co-benefits for improved pollinator connectivity. The literature finds there are fewer green spaces – also where pollinator habitats exist – accessible to communities of color and lower-income communities¹¹. The literature also finds that green spaces, or green infrastructure, can reduce the urban heat island effect and overall heat intensity in urban areas. We used a hotspot-esque approach to identify where pollinator habitat connectivity (corridor areas from the connectivity analysis) overlaps with socio-economically vulnerable areas (the highest quantile of communities designated as minority communities) and high heat risk areas (the highest quantile of urban heat island effect). Overlapping these datasets allowed us to identify areas for future green space investment that also produce social co-benefits.

To identify socio-economically vulnerable areas more exposed to heat, we overlaid environmental justice (EJ) communities (as designated by the Commonwealth of Massachusetts) with high heat risk areas (land surface temperature index top quantile: 0.685 to 1). Heat risk is concentrated throughout portions of Boston with low green space, high development, and higher percentages of communities of color (Figures 1 and 2). We then overlaid pinch points with these vulnerable areas to find locations for potential investment using a simple calculation in ArcGIS Pro (see Appendix G, Figure 1 for full outline of methodology). Our final recommendations will specifically prioritize pollinator habitat creation in areas with higher social vulnerability and areas at higher risk of extreme heat exposure that also support pollinator connectivity across the cityscape.

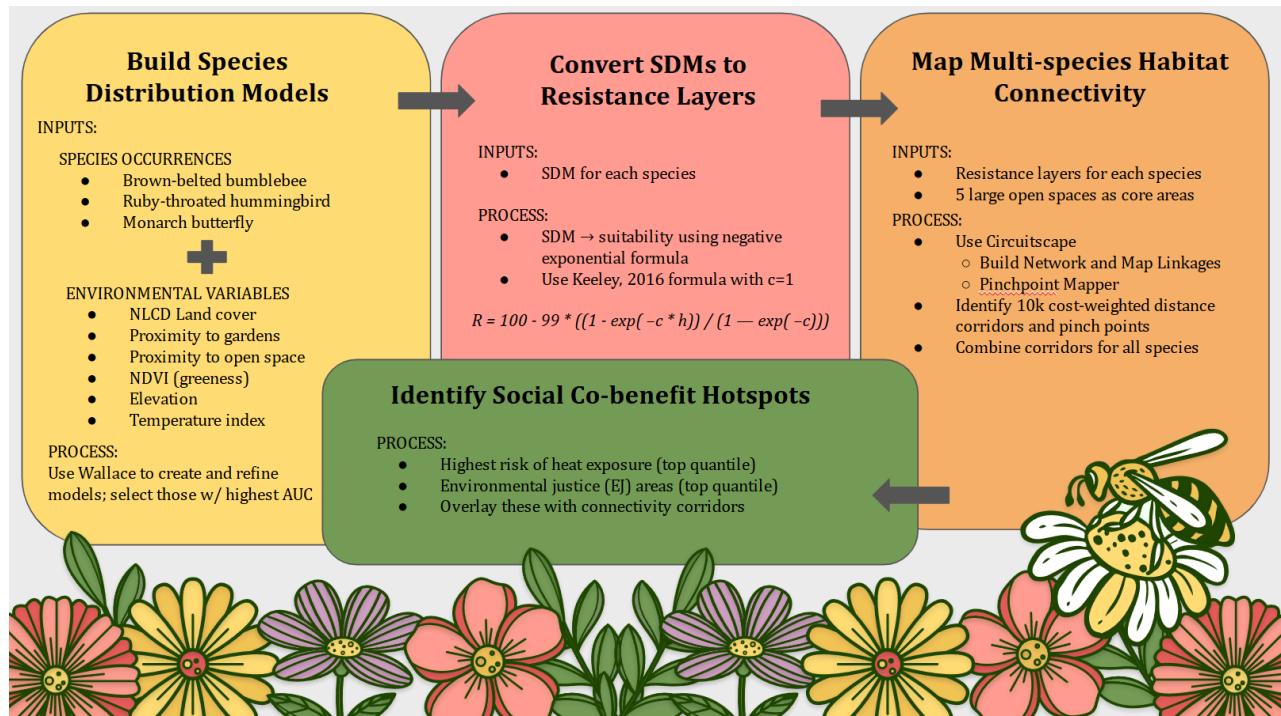


Figure 3. Conceptual diagram of methods: In the diagram above, the yellow box outlines the inputs and processes for building the SDM. The pink box outlines the inputs and processes for converting the SDMs to resistance layers. The orange box outlines the inputs and process for the connectivity analysis. Lastly, the green box includes the process for the social co-benefit component of the project.

Results

Species Distribution Modeling

Three species distribution models were built, one for each focal species. All selected models had high performance metrics ($AUC > 0.89$, see Appendix A Table 2). The brown-belted bumblebee has a fairly extensive amount of low- to moderate- habitat suitability throughout Boston, with very few areas above 0.6 for predicted suitability (Figure 4). For the ruby-throated hummingbird, suitable habitat is found in much larger patches and is mostly above 0.4 for predicted suitability. These areas tend to be within large parks and near inland water bodies in the city (Figure 5). Finally, for the monarch butterfly, suitable habitat is again fairly extensive and of only low- to moderate- suitability, similar to the brown-belted bumblebee (Figure 6). Upon comparing areas of moderate- to high-habitat suitability (predicted suitability >0.4) across the three species, only a few small patches of habitat are suitable for all three species (shown in orange in Figure 7). A larger amount of area is suitable for two out of three species (blue in Figure 7).

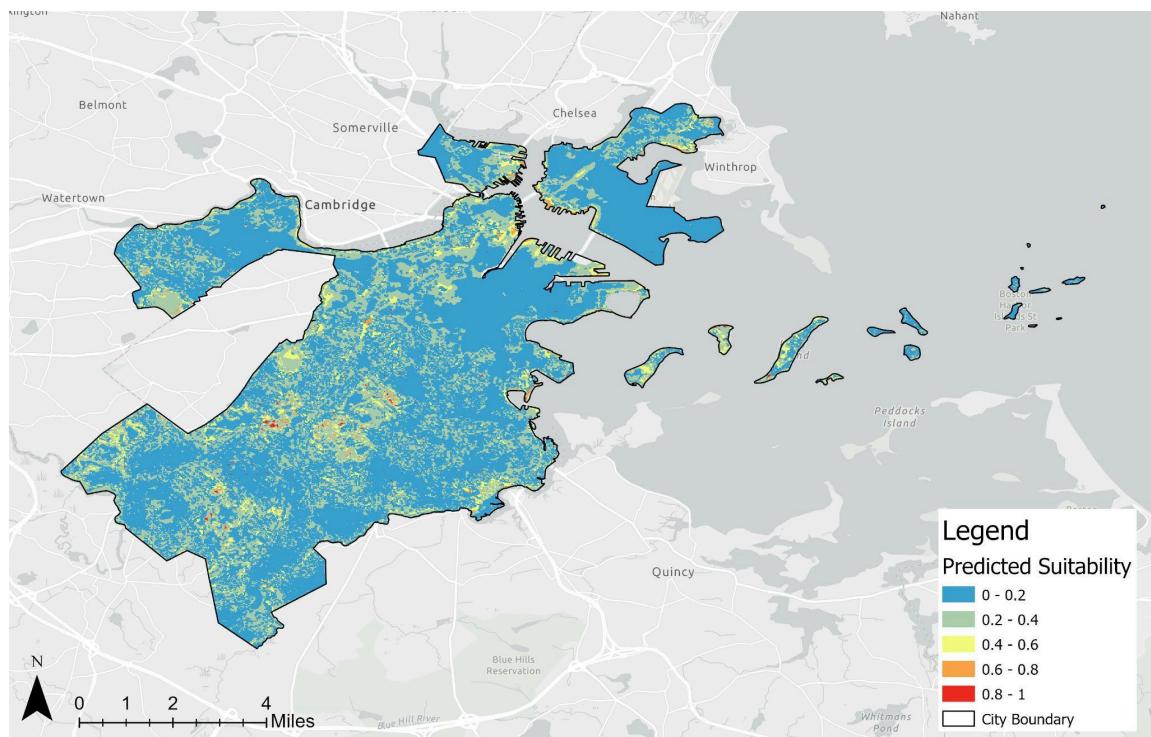


Figure 4. Species distribution model for brown-belted bumblebee within Boston. Predicted habitat suitability shown on a scale from 0 (not suitable) to 1 (highly suitable). Visualized best model (LQ rm 1) as described in Appendix A, Table 2.

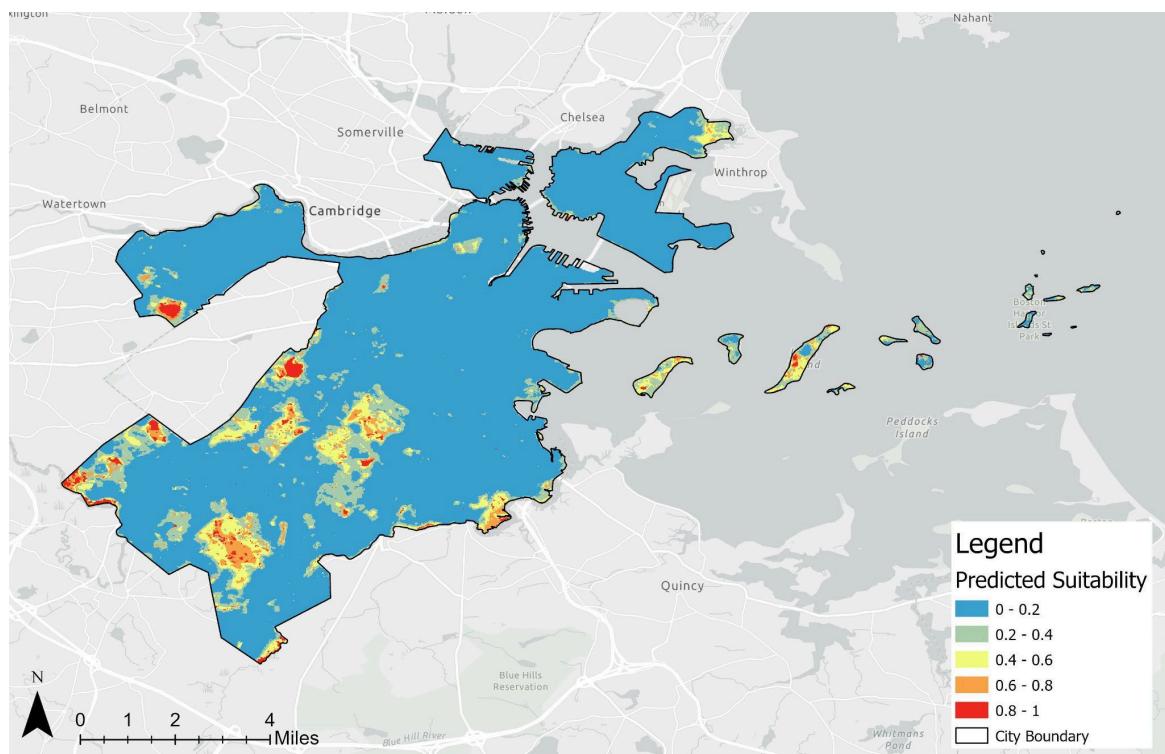


Figure 5. Species distribution model for ruby-throated hummingbird within Boston. Predicted habitat suitability shown on a scale from 0 (not suitable) to 1 (highly suitable). Visualized best model (L rm 2) as described in Appendix A, Table 2.

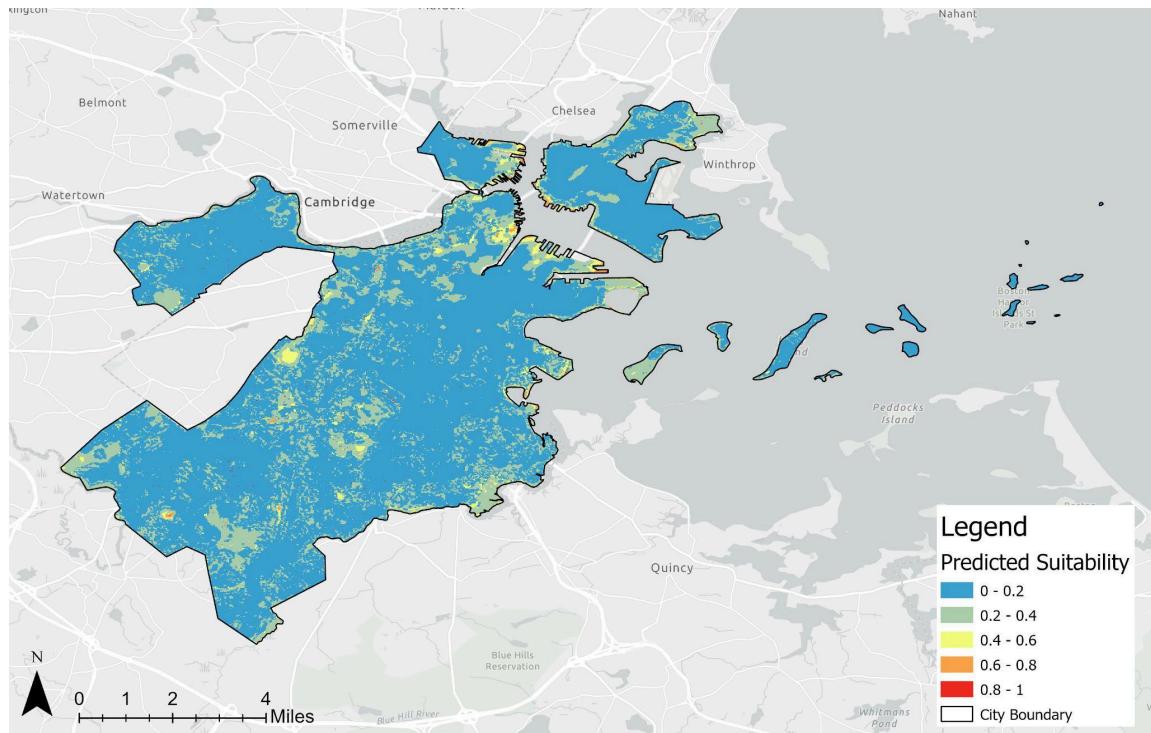


Figure 6. Species distribution model for monarch butterfly within Boston. Predicted habitat suitability shown on a scale from 0 (not suitable) to 1 (highly suitable). Visualized best model (LQ rm 1) as described in Appendix A, Table 2.

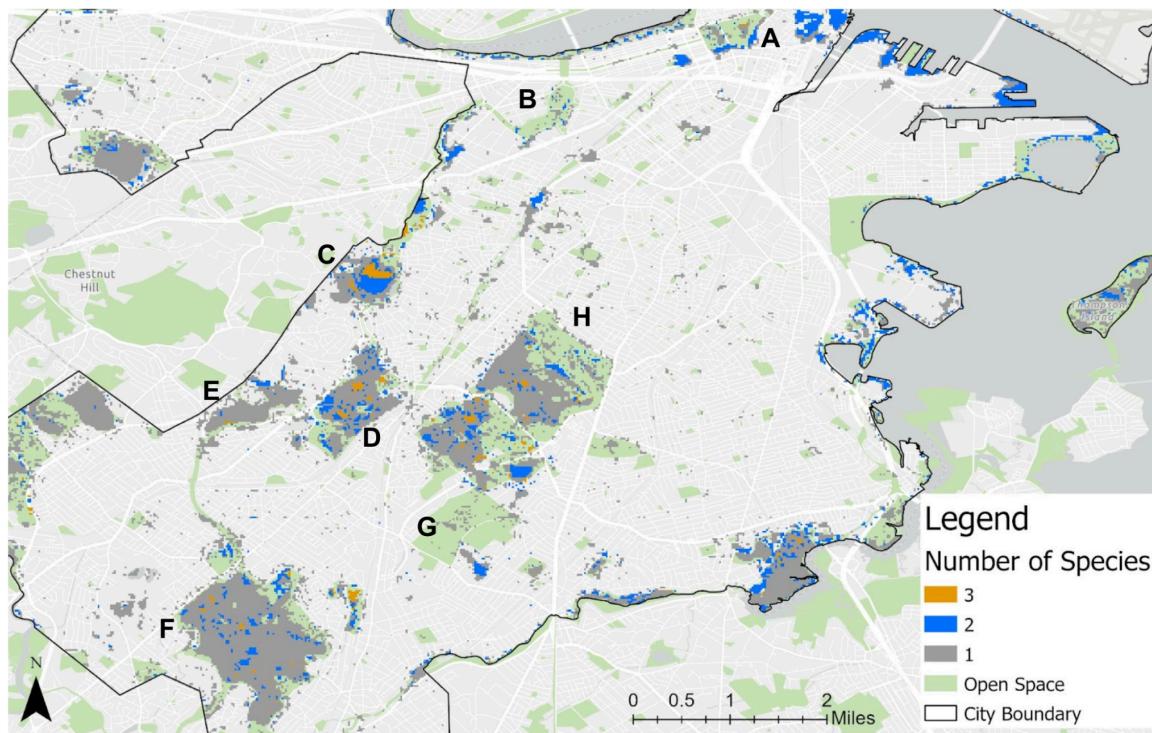


Figure 7. Multi-species habitat suitability across central Boston. Areas of suitable habitat (predicted suitability >0.4) for one, two, or all three species are colored gray, blue, and orange, respectively. Open spaces are shown in green (A = Boston Common, B = Back Bay Fens, C = Jamaica Pond, D = Arnold Arboretum, E = Allandale Woods, F = Stony Brook Park, G = Mount Hope Cemetery, H = Franklin Park & Franklin Park Zoo).

Connectivity Analysis

The connectivity analyses, one for each species, were generated across five core areas – Arnold Arboretum, Boston Common, Stony Brook Park, Moakley Park, and Pope John Paul II Park – throughout the City of Boston. The brown-belted bumblebee has relatively narrow corridors between core areas throughout the cityscape. Segments of corridors that are most critical connectivity are depicted in brown (Figure 8) and fall along some existing green spaces like the South West Corridor Park, a linear park that connects Back Bay to Forest Hills and the Harbor Walk or where skyscrapers are replaced with land cover like train tracks and along bodies of water. For ruby-throated hummingbirds, connectivity corridors are slightly broader, likely due to hummingbirds being larger in size compared to brown-belted bumblebees and monarch butterflies, with more options for dispersal across the cityscape. Segments of corridors that are most critical connectivity are depicted in pink (Figure 9). Interestingly, critical connectivity segments congregate along the southwestern portions of the city. For monarch butterflies, we see similar trends with narrow corridors but more path options between core areas. Segments of corridors that are most critical connectivity are depicted in orange (Figure 10) and fall along areas like the Harbor Walk, similar to the brown-belted bumblebees. Lastly, connectivity for all species, with critical connectivity in brown, pink, and orange, respectively is depicted in Figure 11.

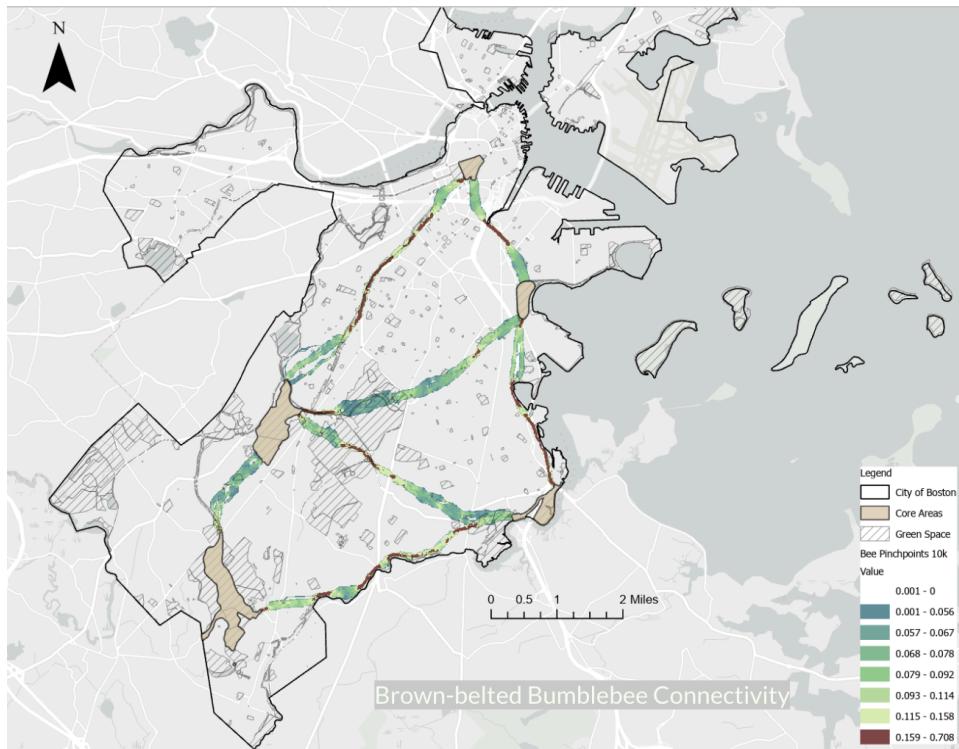


Figure 8. Connectivity analysis with pinch points highlighted for brown-belted Bumblebee within Boston. Essential segments of corridors shown on a scale of 0 (diffuse connectivity) to 0.708 in brown (critical connectivity). Patches of land with gray hatch marks represent open spaces.

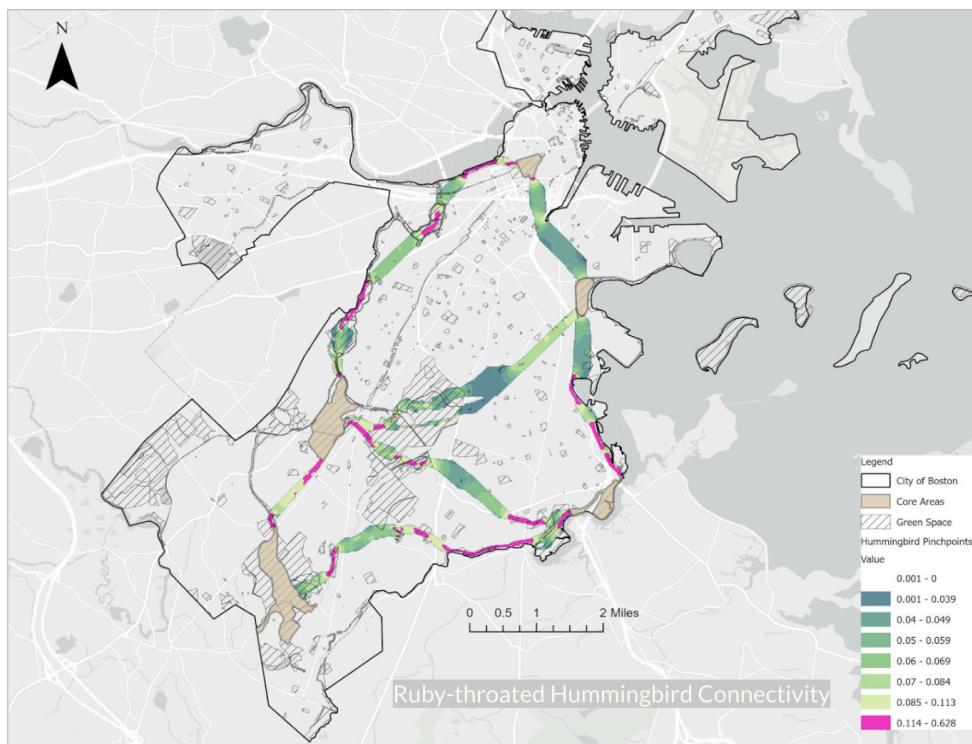


Figure 9. Connectivity analysis with pinch points highlighted for ruby-throated hummingbirds within Boston. Essential segments of corridors shown on a scale of 0 (diffuse connectivity) to 0.687 in pink (critical connectivity). Patches of land with gray hatch marks represent open spaces.

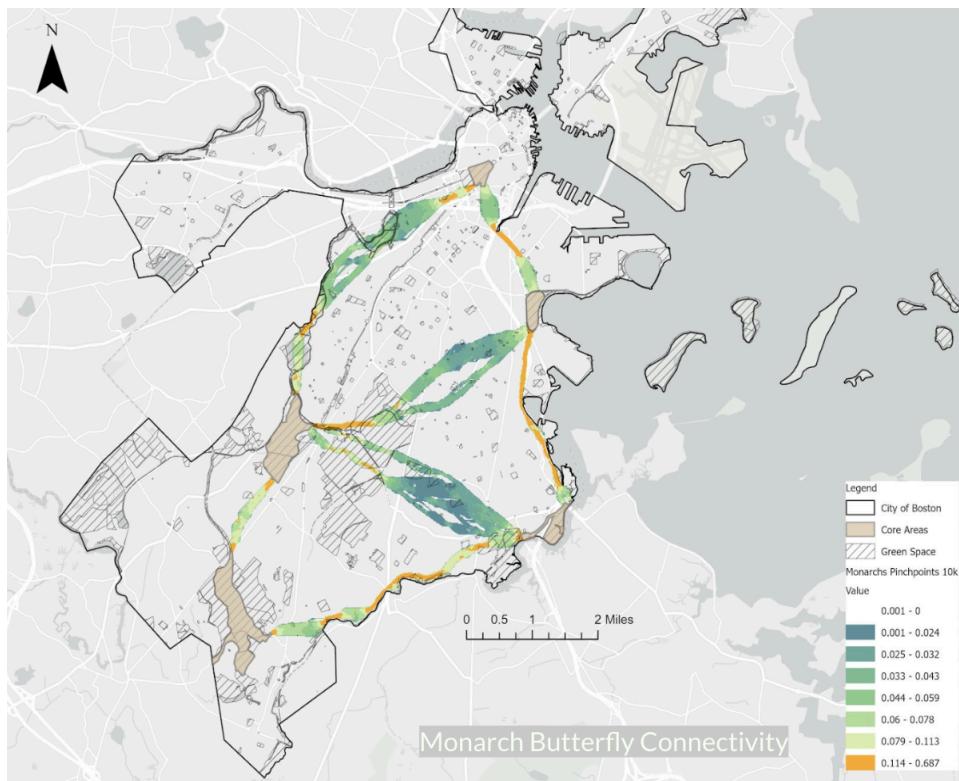


Figure 10. Connectivity analysis with pinch points highlighted for monarch butterflies within Boston. Essential segments of corridor shown on a scale of 0 (diffuse connectivity) to 0.687 in orange (critical connectivity) for habitat connectivity. Patches of land with gray hatch marks represent open spaces.

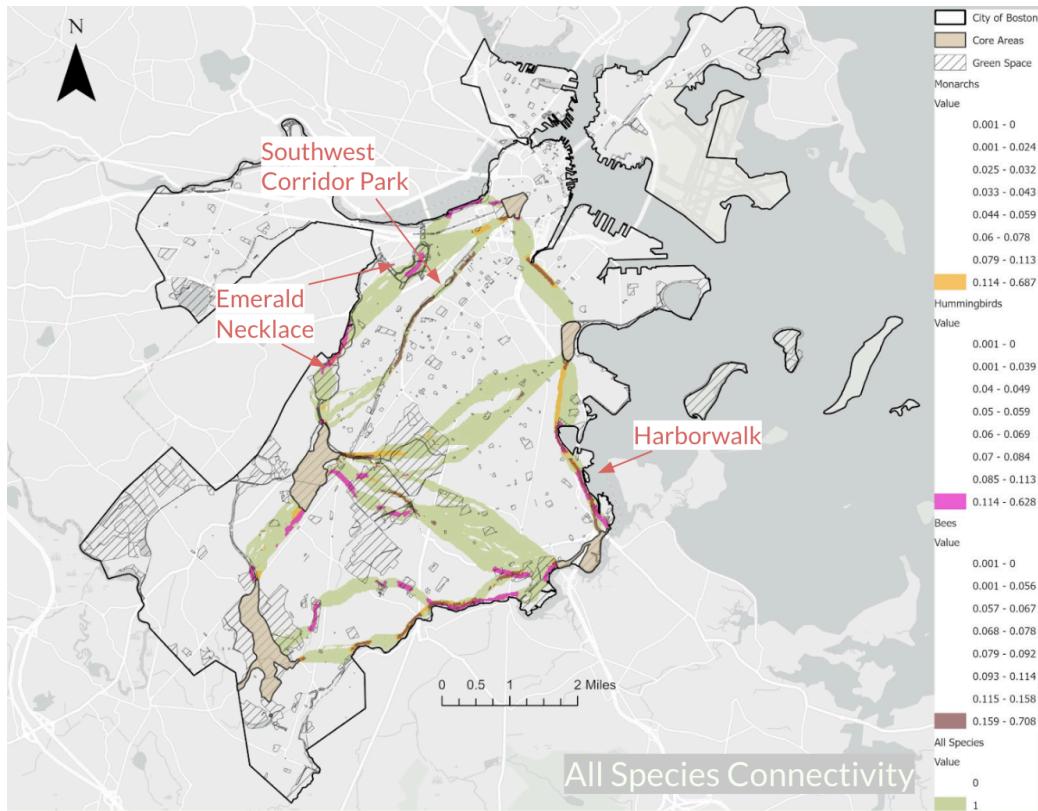


Figure 11. Connectivity analysis with pinch points highlighted for all species within Boston shown in light green, all diffuse connectivity segments. Orange, pink, and brown indicate critical connectivity segments. Patches of land with gray hatch marks represent open spaces.

Social Co-benefit Hotspots

The social co-benefit hotspots analysis identified a few small regions of the city in which pollinator habitat creation could support connectivity, provide equitable green space access, and mitigate the urban heat island effect. As indicated in Figure 12, one of these areas is in the South End of Boston, by the I-90 interstate highway as it passes through the city. Many more co-benefit hotspots are located in Dorchester, some in more northern areas along portions of Columbia Road and some in more southern areas near Talbot Ave and Gallivan Blvd (Figure 12). No co-benefit hotspots were identified in the more western neighborhoods of the city.

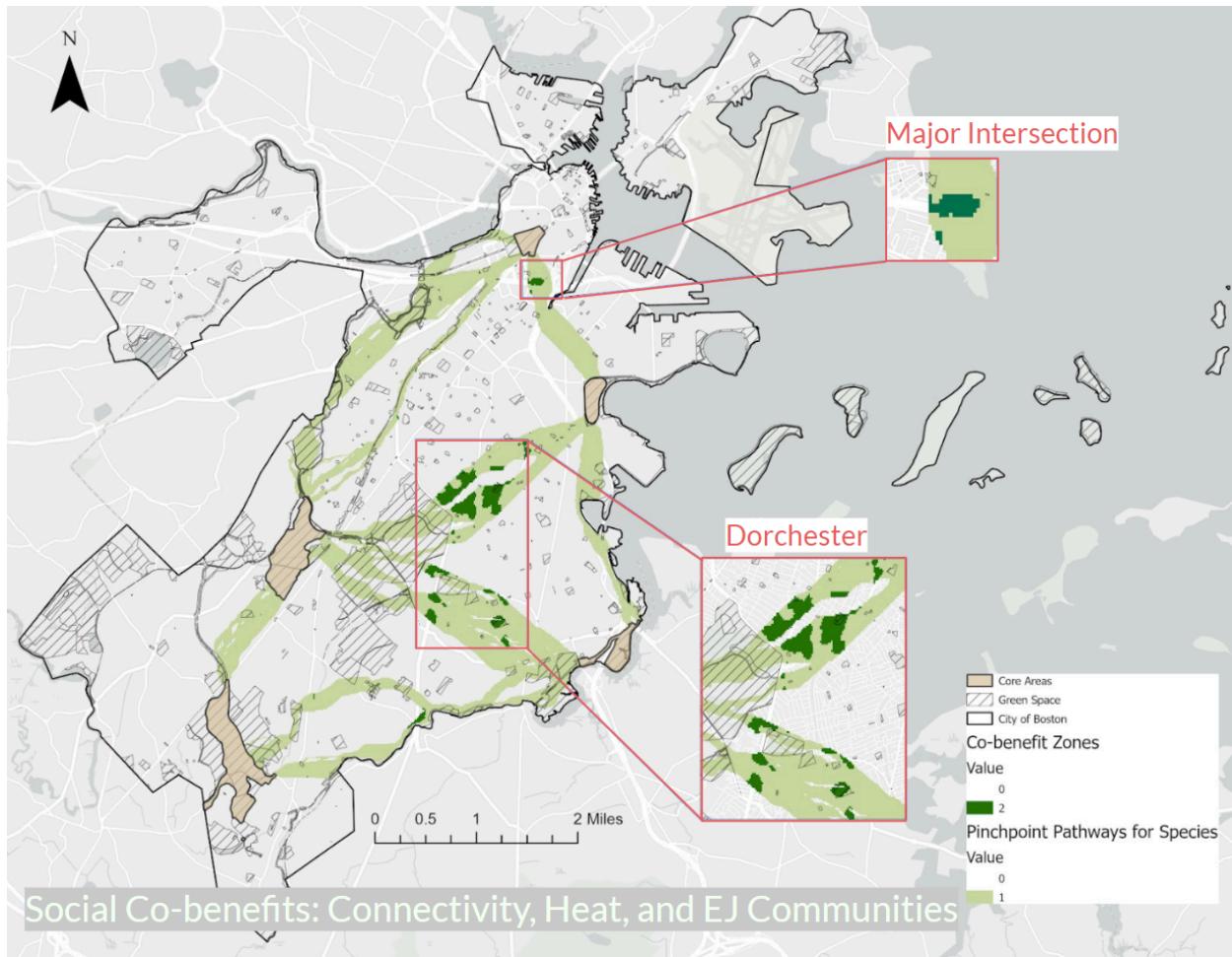


Figure 12. Multi-species corridors and social co-benefit hotspots. Combined movement corridors for the three focal species are shown in light green. Social co-benefit hotspots, defined as areas with high heat risk and high EJ priority, are shown in dark green.

Conclusions & Implications

Species Distribution Modeling

Suitable pollinator habitat is not widespread across Boston. Suitable habitat is fragmented and generally found within existing large open spaces, along greenways, along coastlines, and near inland water bodies (Figure 7). While most suitable habitat is found within parks, not all parks provide pollinator habitat. Jamaica Pond, the Arnold Arboretum, Allandale Woods, and Stony Brook Park (C, D, E, & F in Figure 7) are examples of open spaces that are almost completely covered by suitable habitat. This could be due to the large amount of forest cover and non-grassy vegetation in these areas. Conversely, the Boston Common, Mount Hope Cemetery, Back Bay Fens, and the Franklin Park Zoo (A, B, G, & H in Figure 7) are all open spaces with large amounts of unsuitable habitat. These spaces consist mainly of lawns and managed pathways, with less natural habitat present. These results align with other studies that have found greatest pollinator abundance in gardens and lower pollinator abundance in cemeteries, public parks, and other greenspaces such as sports fields and schoolyards²¹.

Very little land area in Boston is suitable for all three focal species of pollinators, and habitat that is suitable for just two out of three species is still fairly sparse (Figure 7). This is not necessarily surprising, as the three pollinator species represent different taxa with varying ecological needs and thus different areas of suitable habitat. However, due to the space limitations inherent in developed areas, urban ecologists should consider strategies that can better support a diversity of pollinator species within existing open spaces that have low habitat suitability. This may include increasing the diversity and abundance of flowering plants in these spaces and creating additional community gardens near housing developments that lack them.

Connectivity Analysis

Similar to the findings from the species distribution modeling component of our study, connectivity is not widespread throughout Boston. Instead, it is concentrated along the edges of the city boundary, taking advantage of coastlines, bodies of water, and the less developed and dense neighborhoods surrounding Boston. Considering how to replicate these habitat characteristics throughout the city could improve connectivity and support pollinator populations. Connectivity only appears in the center where existing green spaces and greenways exist, like Franklin Park and Zoo or the South West Corridor Park. These findings suggest the importance of green spaces in connectivity for pollinators.

Overall, pinch point values were relatively low across all species, ranging from 0.0 to 0.708 (Figure 8) for brown-belted bumblebees, 0.0 to 0.628 (Figure 9) for ruby-throated hummingbirds, and 0.0 to 0.687 (Figure 10) for monarch butterflies. The general low values indicate that resistance could be uniform throughout the city, making connectivity challenging for pollinators. Future analyses could adjust CWD to lower values to produce finer results. Based on the results of the analysis, we recommend conserving the areas of critical connectivity and improving areas of diffuse connectivity. Preserving current critical connectivity will strengthen these corridor segments. Investing in diffuse connectivity segments will provide long-term resilience and network expansion, providing pollinators with alternative pathways across the landscape.

Social Co-benefit Hotspots

The social co-benefit hotspot analyses pull our work together. Areas for investment in green space that will bolster existing pollinator connectivity, increase access to green spaces in communities with higher percentages of people of color, and reduce the impacts of the urban heat island effect were mostly identified in Dorchester. Dorchester is a residential neighborhood within the city of Boston, providing several opportunities for green space investment. This is especially important as the other location that our analysis identified was a major intersection (Figure 12), which is a far more challenging location for green space investment and would not necessarily provide the co-benefits of equitable green space access or reduced heat intensity.

The co-benefit zones overlap with the proposed Emerald Necklace expansion along Columbia Road, known as the Columbia Road Transportation Action Plan (Action Plan), traveling through Dorchester. Serendipitously, the Action Plan's main objective is to connect Franklin Park, an area of

high habitat suitability, to Moakley Park, one of our designated core areas, and the waterfront, where the Harbor Walk is located^{22,23}. The Action Plan includes “a green experience,” as one of its three goals, highlighting tree planting to reduce the intensity of summer heat²². The vision and design process for the Action Plan is not yet complete, so there are opportunities for the public and decision-makers to advocate for pollinator habitat investment in these social co-benefit zones²².

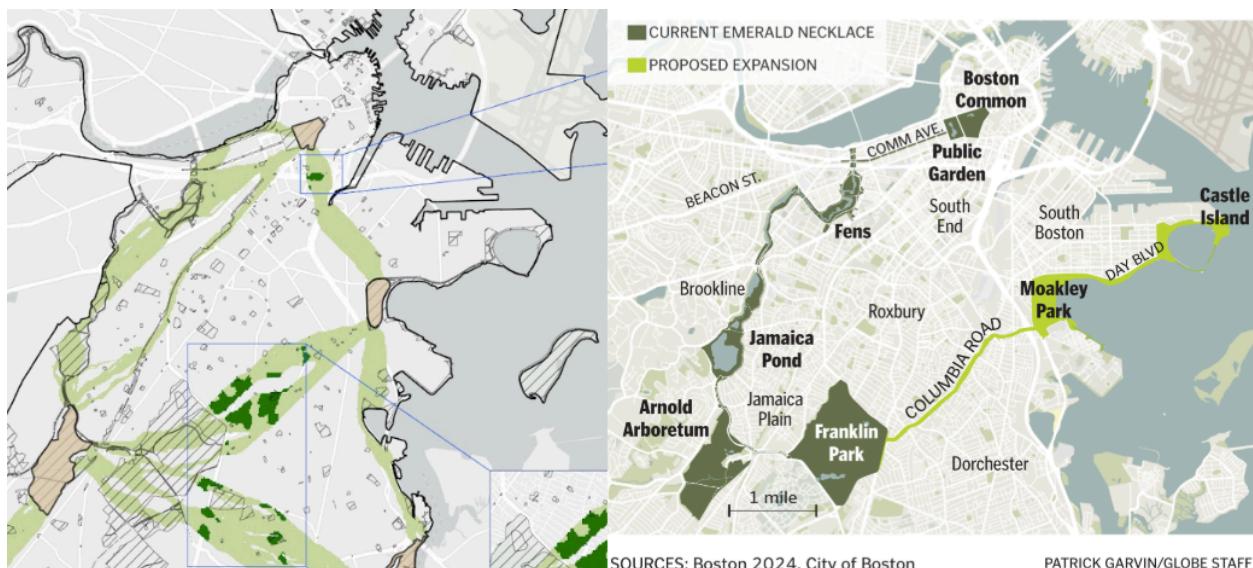


Figure 13. Corridors with social co-benefit hotspots (left) and proposed Emerald Necklace expansion plans (right, source: *Boston Globe*)²⁴.

Limitations of the Analyses

This analysis has a few limitations. First, the shape and size of the city of Boston presented a few challenges: obtaining data at a small enough scale to be relevant, processing data to exactly capture the irregular shape of the city, and accounting for rivers and other water bodies that separate parts of the city from each other. Another limitation is the fact that the species occurrence data used was based on individual sightings rather than more comprehensive tracking data. This may reflect biases in terms of who recorded the data, what locations they recorded data in, and what species they noticed and recorded. Finally, we acknowledge that, given their ecology, pollinators are often highly dependent on the abundance of specific flowering plant species. We did not have this data available to inform our species distribution modeling and instead used NDVI, greenspaces, and gardens as proxies for suitable habitat metrics. However, plant diversity and abundance data could yield more informed habitat suitability results for future studies.

Future analyses focused on pollinator species distribution modeling and connectivity in Boston, and urban areas in general, should consider the following:

1. Include more robust environmental variables when completing species distribution modeling, including flowering plant diversity and seasonality, and
2. Adjust cost-weighted distance to lower values for smaller study areas like the city of Boston, in order to construct movement corridors.

RECOMMENDATIONS

While there are not many areas throughout Boston that are suitable for the pollinators we considered in this report, there are essential areas that can provide important co-benefits. Additionally, not all green and open spaces provide the habitat needs of pollinators. For example, cemeteries and grassy fields are not as beneficial as parks with greater plant diversity. Furthermore, existing greenways prove to be vital to current pollinator connectivity. Finally, social co-benefits, at least when considering communities with high percentages of people of color and heat intensity, are not found throughout the city.

Considering these key takeaways, we propose the following recommendations to maximize pollinator connectivity enhancement with ecological and social co-benefits:

1. **Transition Grassy Areas:** Increase diversity and abundance of flowering plants in existing grass-dominated parks to provide additional habitat and food sources for pollinators.
2. **Enhance Current Connectivity:** Strategically select additional habitats within corridors to enhance current connectivity. This includes investments in green spaces in critical connectivity segments as well as in diffuse connectivity segments.
3. **Advocate for Social Co-benefits:** Prioritize pollinator habitat creation in social co-benefit hotspots. Options for habitat creation include small parks, community gardens, schoolyard gardens, planters, rain gardens, and green roofs. Community engagement and support for these projects, as well as funding opportunities for homeowners, renters, and schools to support investments in private land, is essential.
4. **Relate Findings to Current Planning Efforts:** Incorporate pollinator and environmental justice efforts into Emerald Necklace expansion and Columbia Road Transportation Action Plan.

Literature Cited

1. Dicks, L. V. *et al.* A global-scale expert assessment of drivers and risks associated with pollinator decline. *Nat. Ecol. Evol.* **5**, 1453–1461 (2021).
2. Van Doren, B. M. *et al.* Drivers of fatal bird collisions in an urban center. *Proc. Natl. Acad. Sci.* **118**, e2101666118 (2021).
3. Skaldina, O., Nylund, A. & Ramula, S. Neglected puzzle pieces of urban green infrastructure: richness, cover, and composition of insect-pollinated plants in traffic-related green spaces. *Landsc. Ecol.* **39**, 80 (2024).
4. Ollerton, J. Pollinator Diversity: Distribution, Ecological Function, and Conservation. *Annu. Rev. Ecol. Evol. Syst.* **48**, 353–376 (2017).

5. Wenzel, A., Grass, I., Belavadi, V. V. & Tscharntke, T. How urbanization is driving pollinator diversity and pollination – A systematic review. *Biol. Conserv.* **241**, 108321 (2020).
6. Cheng, C., Yang, Y. C. E., Ryan, R., Yu, Q. & Brabec, E. Assessing climate change-induced flooding mitigation for adaptation in Boston's Charles River watershed, USA. *Landsc. Urban Plan.* **167**, 25–36 (2017).
7. Cheng, C. Spatial Climate Justice and Green Infrastructure Assessment: A Case Study for the Huron River Watershed, Michigan, USA. <https://keep.lib.asu.edu/items/127813> (2016).
8. Nutsford, D., Pearson, A. L. & Kingham, S. An ecological study investigating the association between access to urban green space and mental health. *Public Health* **127**, 1005–1011 (2013).
9. Martin, L. *et al.* Nature contact, nature connectedness and associations with health, wellbeing and pro-environmental behaviours. *J. Environ. Psychol.* **68**, 101389 (2020).
10. Whitburn, J., Linklater, W. & Abrahamse, W. Meta-analysis of human connection to nature and proenvironmental behavior. *Conserv. Biol.* **34**, 180–193 (2020).
11. Wolch, J. R., Byrne, J. & Newell, J. P. Urban green space, public health, and environmental justice: The challenge of making cities 'just green enough'. *Landsc. Urban Plan.* **125**, 234–244 (2014).
12. Graffigna, S., González-Vaquero, R. A., Torretta, J. P. & Marrero, H. J. Importance of urban green areas' connectivity for the conservation of pollinators. *Urban Ecosyst.* **27**, 417–426 (2024).
13. Feuerborn, C. Brown-belted Bumble Bee Hymenoptera: Apidae *Bobmus griseocollis*. <https://pollinators.psu.edu/assets/uploads/documents/Bug-of-the-Month-2.pdf>.
14. Rodríguez-Flores, C. I., Ornelas, J. F., Wethington, S. & Arizmendi, M. del C. Are hummingbirds generalists or specialists? Using network analysis to explore the mechanisms influencing their interaction with nectar resources. *PLoS ONE* **14**, e0211855 (2019).
15. Tan, W.-H. *et al.* Transcriptomics of monarch butterflies (*Danaus plexippus*) reveals that toxic host plants alter expression of detoxification genes and down-regulate a small number of immune genes. *Mol. Ecol.* **28**, 4845–4863 (2019).

16. McCluskey, E. M. *et al.* Assessing habitat connectivity of rare species to inform urban conservation planning. *Ecol. Evol.* **14**, e11105 (2024).
17. Yu, H., Xiao, H. & Gu, X. Integrating species distribution and piecewise linear regression model to identify functional connectivity thresholds to delimit urban ecological corridors. *Comput. Environ. Urban Syst.* **113**, 102177 (2024).
18. Serret, H. *et al.* Towards Ecological Management and Sustainable Urban Planning in Seoul, South Korea: Mapping Wild Pollinator Habitat Preferences and Corridors Using Citizen Science Data. *Anim. Open Access J. MDPI* **12**, 1469 (2022).
19. Liu, C., Newell, G., White, M. & Bennett, A. F. Identifying wildlife corridors for the restoration of regional habitat connectivity: A multispecies approach and comparison of resistance surfaces. *PLOS ONE* **13**, e0206071 (2018).
20. Keeley, A. T. H., Beier, P. & Gagnon, J. W. Estimating landscape resistance from habitat suitability: effects of data source and nonlinearities. *Landsc. Ecol.* **31**, 2151–2162 (2016).
21. Baldock, K. C. R. *et al.* A systems approach reveals urban pollinator hotspots and conservation opportunities. *Nat. Ecol. Evol.* **3**, 363–373 (2019).
22. Columbia Road Transportation Action Plan | Boston.gov.
<https://www.boston.gov/departments/transportation/columbia-road-transportation-action-plan> (2023).
23. Boston Kicks Off Planning to Redesign Columbia Road, A Lost Link In Its Emerald Necklace - Streetsblog Massachusetts.
<https://mass.streetsblog.org/2024/04/25/boston-kicks-off-planning-to-redesign-columbia-road-a-lost-link-in-its-emerald-necklace> (2024).
24. Boston 2024 sees Columbia Road as Olmsted jewel - The Boston Globe.
<https://www.bostonglobe.com/metro/2015/07/19/boston-pledges-complete-olmsted-vision-columbia-road/VdXZpgM6VKdT3JJeDsbjIP/story.html>.

Appendix

Appendix A:

Table 1. Data Layers, Uses, Descriptions, and Sources. All data are open-access and freely available for use.

Data Layer	Use	Description	Source(s)
Species occurrence data	<i>SDMs</i>	Occurrence points for: <ul style="list-style-type: none"> • Brown-belted bumble bees • Ruby-throated hummingbirds • Monarch butterflies <i>(point data)</i>	GBIF (Xerces Society Bumble Bee Watch ; Ruby-throated hummingbirds , & Monarch butterflies)
Land cover map	<i>SDMs</i>	National Land Cover Database (NLCD) 2019 land cover for the contiguous United States <i>Resolution: 30 m</i>	https://www.mrlc.gov/
NDVI	<i>SDMs</i>	Landsat NDVI data <i>Resolution: 30 m</i>	https://earthexplorer.usgs.gov/
Elevation	<i>SDMs</i>	Digital elevation model (DEM) data that can be used to map elevation <i>Resolution: 1/3 arc second (~10 m)</i>	https://apps.nationalmap.gov/d_downloader/
Garden locations	<i>SDMs</i>	Locations of existing pollinator gardens and community gardens in the Boston area. Compiled into one file with geographic coordinates <i>(point data)</i> .	https://www.pollinatornetworks.org/gardens.html#/ https://www.massaudubon.org/places-to-explore/activities/gardens-gardening https://www.pollinator-pathway.org/towns/brookline https://www.bu.edu/articles/2023/bu-creates-a-new-pollinator-garden/ https://thetrustees.org/content/list-of-boston-community-gardens/
Existing green spaces	<i>SDMs, connectivity</i>	Massachusetts open spaces (<i>polygons</i>).	https://www.mass.gov/info-details/massgis-data-protected-and-recreational-openspace
Surface temperature index	<i>SDMs, social co-benefits</i>	Land surface temperature index for the state of Massachusetts <i>Resolution: 30 m</i>	<i>Obtained through information request to MAPC</i> https://www.mapc.org/learn/data/#landsurface
Boston city boundary	<i>Study extent</i>	Boston city boundary (<i>polygons</i>)	https://data.boston.gov/dataset/city-of-boston-outline-boundary-water-included
Socioeconomic data	<i>Social co-benefits</i>	Social vulnerability map (in the context of climate resilience) (<i>polygons</i>)	https://data.boston.gov/dataset/climate-ready-boston-social-vulnerability

Environmental justice	<i>Social co-benefits</i>	Census block groups designated as environmental justice communities by the Commonwealth of Massachusetts (<i>polygons</i>)	https://mass-eoeea.maps.arcgis.com/home/item.html?id=015d4db1ed4b4816a456198c0c3d63ee#overview
------------------------------	---------------------------	--	---

Table 2. Selected best models for each species. Model selection was based upon maximizing AUC value and minimizing average AUC difference.

Species	Selected Model	Variables Included	AUC	Average AUC Difference
Brown-belted bumblebee	LQ Rm 1 cloglog	land cover, NDVI, distance to open space, distance to gardens, surface temperature index (n = 5)	0.897	0.25
Ruby-throated hummingbird	L Rm 2 cloglog	land cover, elevation, NDVI, distance to open space, distance to gardens, surface temperature index (n = 6)	0.914	0.073
Monarch butterfly	LQ Rm 1 cloglog	land cover, elevation, NDVI, distance to open space, distance to gardens, surface temperature index (n = 6)	0.899	0.273

Table 3. Selected core areas for all species.

Site Name	Core Area Number	Acres	Shape Area (rounded)	Type	Ownership & Jurisdiction
Boston Common	1	45.74	2,419,320.8	Parks, Playgrounds & Athletic Fields	City of Boston; BPRD
Stony Brook Park	2	285.44	14,657,574.8	Parkways, Reservations & Beaches	Commonwealth of Massachusetts; DCR
Moakley Park	3	58.78	3,044,524.2	Parks, Playgrounds & Athletic Fields	City of Boston;
Arnold Arboretum	4	224.27	11,061,724.0	Parks, Playgrounds & Athletic Fields	City of Boston; BPRD
Pope John Paul II Park I	5	70.01	4,273,169.5	Parkways, Reservations & Beaches	Commonwealth of Massachusetts; DCR

Appendix B:

R code for the final step of data processing.

```

# load required libraries
library(raster)
library(here)

# read in and define projection for each file
openspace <- raster(here("ESM270P", "Wallace_Testing", "Final Rasters", "os_dist_final.tif"))
crs(openspace) <- crs("+proj=merc +a=6378137 +b=6378137 +lat_ts=0 +lon_0=0 +x_0=0 +y_0=0 +k=1
+units=m +nadgrids=@null +wktext +no_defs +type=crs")

dem <- raster(here("ESM270P", "Wallace_Testing", "Final Rasters", "dem_final.tif"))
crs(dem) <- crs("+proj=merc +a=6378137 +b=6378137 +lat_ts=0 +lon_0=0 +x_0=0 +y_0=0 +k=1 +units=m
+nadgrids=@null +wktext +no_defs +type=crs")

lst <- raster(here("ESM270P", "Wallace_Testing", "Final Rasters", "LST_index_proj_clip.tif"))
crs(lst) <- crs("+proj=merc +a=6378137 +b=6378137 +lat_ts=0 +lon_0=0 +x_0=0 +y_0=0 +k=1 +units=m
+nadgrids=@null +wktext +no_defs +type=crs")

nlcd <- raster(here("ESM270P", "Wallace_Testing", "Final Rasters", "nlcd_final.tif"))
crs(nlcd) <- crs("+proj=merc +a=6378137 +b=6378137 +lat_ts=0 +lon_0=0 +x_0=0 +y_0=0 +k=1 +units=m
+nadgrids=@null +wktext +no_defs +type=crs")

ndvi <- raster(here("ESM270P", "Wallace_Testing", "Izzy_11_12_24", "ndvi_final.tif"))
# izzy processed this, so no need to do the set CRS and reproject steps. just save it to the final rasters folder

garden <- raster(here("ESM270P", "Wallace_Testing", "Izzy_11_12_24", "garden_distance_final.tif"))
crs(garden) <- crs("+proj=merc +a=6378137 +b=6378137 +lat_ts=0 +lon_0=0 +x_0=0 +y_0=0 +k=1 +units=m
+nadgrids=@null +wktext +no_defs +type=crs")

# project
# define WGS84 projection
wgs84 <- "+proj=longlat +datum=WGS84 +no_defs +type=crs"
# assign to each raster
openspace <- projectRaster(openspace, crs = wgs84)
dem <- projectRaster(dem, crs = wgs84)
lst <- projectRaster(lst, crs = wgs84)
nlcd <- projectRaster(nlcd, crs = wgs84)
garden <- projectRaster(garden, crs = wgs84)

# ndvi raster needs additional troubleshooting: different extent than the others
extent(ndvi) <- extent(lst)
ndvi <- raster::resample(ndvi, lst, method = "bilinear")

# garden raster needs additional troubleshooting: different extent than the others
extent(garden) <- extent(lst)
garden <- raster::resample(garden, lst, method = "bilinear")

```

```
# nlcd raster needed additional troubleshooting
library(terra)
lst <- rast(here("ESM270P", "Wallace_Testing", "Final Rasters", "CRS_in_R", "LST_index_final.tif"))
nlcd <- rast(here("ESM270P", "Wallace_Testing", "Final Rasters", "CRS_in_R", "nlcd_final.tif"))
# set extent to be lst extent
ext(nlcd) <- ext(lst)
# resample to get same number of rows and columns
nlcd_v2 <- terra::resample(nlcd, lst, method = "near")

# save all six files
writeRaster(openospace, here("ESM270P", "Wallace_Testing", "Final Rasters", "CRS_in_R", "os_dist_final.tif"))
writeRaster(dem, here("ESM270P", "Wallace_Testing", "Final Rasters", "CRS_in_R", "dem_final.tif"))
writeRaster(lst, here("ESM270P", "Wallace_Testing", "Final Rasters", "CRS_in_R", "LST_index_final.tif"))
# writeRaster(nlcd, here("ESM270P", "Wallace_Testing", "Final Rasters", "CRS_in_R", "nlcd_final.tif"))
writeRaster(nlcd_v2, here("ESM270P", "Wallace_Testing", "Final Rasters", "CRS_in_R", "nlcd_final_v2.tif"))
writeRaster(ndvi, here("ESM270P", "Wallace_Testing", "Final Rasters", "CRS_in_R", "ndvi_final.tif"))
writeRaster(garden, here("ESM270P", "Wallace_Testing", "Final Rasters", "CRS_in_R", "garden_dist_final.tif"))
```

Appendix C:

Wallace code for brown-belted bumblebee species distribution model.

Wallace Session 2024-11-15

Please find below the R code history from your *Wallace* v2.1.3 session.
You can reproduce your session results by running this R Markdown file
in RStudio.

Each code block is called a “chunk”, and you can run them either
one-by-one or all at once by choosing an option in the “Run” menu at the
top-right corner of the “Source” pane in RStudio.

For more detailed information see <<http://rmarkdown.rstudio.com>>).

Package installation

Wallace uses the following R packages that must be installed and loaded
before starting.

```
```{r}
library(spocc)
library(spThin)
library(dismo)
library(sf)
library(ENMeval)
library(wallace)
```
-----
```

```
## Analysis for *Bombus griseocollis* (Bg)
```

User CSV path with occurrence data. If the CSV file is not in the current workspace, change to the correct file path (e.g. "/Users/darwin/Documents/occs/").

```
```{r}
NOTE: provide the folder path of the .csv file
occs_path <- ""
occs_path <- file.path(occs_path, "bumble_points_clean.csv")
get a list of species occurrence data
userOdds_Bg <- occs_userOdds(
 txtPath = occs_path,
 txtName = "bumble_points_clean.csv",
 txtSep = ",",
 txtDec = ".")
occs_Bg <- userOdds_Bg$Bombus_griseocollis$cleaned
```

```

Obtain environmental data

Using user-specified variables.

```
```{r}
Specify the directory with the environmental variables
dir_envs_Bg <- ""
envs_path <- file.path(dir_envs_Bg, c('dem_final.tif', 'garden_dist_final.tif', 'LST_index_final.tif', 'ndvi_final.tif',
 'nlcd_final_v2.tif', 'os_dist_final.tif'))
Create environmental object
envs_Bg <- envs_userEnv(
 rasPath = envs_path,
 rasName = c('dem_final.tif', 'garden_dist_final.tif', 'LST_index_final.tif', 'ndvi_final.tif', 'nlcd_final_v2.tif',
 'os_dist_final.tif'),
 doBrick = TRUE)
occs_xy_Bg <- occs_Bg[c('longitude', 'latitude')]
occs_vals_Bg <- as.data.frame(raster::extract(envs_Bg, occs_xy_Bg, cellnumbers = TRUE))
Remove duplicated same cell values
occs_Bg <- occs_Bg[!duplicated(occs_vals_Bg[, 1])]
occs_vals_Bg <- occs_vals_Bg[!duplicated(occs_vals_Bg[, 1]), -1]
remove occurrence records with NA environmental values
occs_Bg <- occs_Bg[!(rowSums(is.na(occs_vals_Bg)) >= 1),]
also remove variable value rows with NA environmental values
occs_vals_Bg <- na.omit(occs_vals_Bg)
add columns for env variable values for each occurrence record
occs_Bg <- cbind(occs_Bg, occs_vals_Bg)
```

```

Process environmental data

Sampling of 10000 background points and corresponding environmental data using a user provided background extent with a 0 degree buffer.

```
```{r}
Load the user provided shapefile or csv file with the desired extent.
##User must input the path to shapefile or csv file and the file name
Define path
bgPath_Bg <- ""
bgExt_Bg <- penvs_userBgExtent(
 bgShp_path = paste0(bgPath_Bg, "boston_WGS84", ".shp"),
 bgShp_name = paste0("boston_WGS84", c(".shp", ".shx", ".dbf")),
 userBgBuf = 0,
 occs = occs_Bg)
Mask environmental data to provided extent
bgMask_Bg <- penvs_bgMask(
 occs = occs_Bg,
 envs = envs_Bg,
 bgExt = bgExt_Bg)
Sample background points from the provided area
bgSample_Bg <- penvs_bgSample(
 occs = occs_Bg,
 bgMask = bgMask_Bg,
 bgPtsNum = 10000)
Extract values of environmental layers for each background point
bgEnvsVals_Bg <- as.data.frame(raster::extract(bgMask_Bg, bgSample_Bg))
##Add extracted values to background points table
bgEnvsVals_Bg <- cbind(scientific_name = paste0("bg_", "Bombus griseocollis"), bgSample_Bg,
 occID = NA, year = NA, institution_code = NA, country = NA,
 state_province = NA, locality = NA, elevation = NA,
 record_type = NA, bgEnvsVals_Bg)
```
```

```

### Partition occurrence data

Partition occurrences and background points for model training and validation using “hierarchical checkerboard”, a spatial partition method with an aggregation factor of 2.

```
```{r}
# R code to get partitioned data
groups_Bg <- part_partitionOdds(
  occs = occs_Bg ,
  bg = bgSample_Bg,
  method = "cb2",
  bgMask = bgMask_Bg,
  aggFact = 2)
```

```

### ### Build and Evaluate Niche Model

Generating a species distribution model using the maxnet algorithm as implemented in ENMeval V2.0 (with clamping = TRUE). For tuning using L, LQ feature classes and regularization multipliers in the 1, 5 range increasing by 1. Using a total of 1 categorical predictor variables.

```
```{r}
# Run maxent model for the selected species
model_Bg <- model_maxent(
  occs = occs_Bg,
  bg = bgEnvsVals_Bg,
  user.grp = groups_Bg,
  bgMsk = bgMask_Bg,
  rms = c(1, 5),
  rmsStep = 1,
  fcs = c('L', 'LQ'),
  clampSel = TRUE,
  algMaxent = "maxnet",
  catEnv = "nlcd_final_v2",
  parallel = FALSE,
  numCores = 11)
```

```

### ### Visualize

Generate a map of the maxnet generated model with no threshold

```
```{r}
# Select current model and obtain raster prediction
m_Bg <- model_Bg@models[["fc.LQ_rm.2"]]
predSel_Bg <- predictMaxnet(m_Bg, bgMask_Bg,
  type = "cloglog",
  clamp = TRUE)
#Get values of prediction
mapPredVals_Bg <- getRasterVals(predSel_Bg, "cloglog")
#Define colors and legend
rasCols <- c("#2c7bb6", "#abd9e9", "#ffffbf", "#fdbe61", "#d7191c")
legendPal <- colorNumeric(rev(rasCols), mapPredVals_Bg, na.color = 'transparent')
rasPal <- colorNumeric(rasCols, mapPredVals_Bg, na.color = 'transparent')
#Generate map
m <- leaflet() %>% addProviderTiles(providers$Esri.WorldTopoMap)
m %>%
  leaflet::addLegend("bottomright", pal = legendPal,
  title = "Predicted Suitability<br>(Training)",
  values = mapPredVals_Bg, layerId = "train",
  labFormat = reverseLabel(2, reverse_order = TRUE)) %>%
```

```

```
#add occurrence data
addCircleMarkers(data = occs_Bg, lat = ~latitude, lng = ~longitude,
 radius = 5, color = 'red', fill = TRUE, fillColor = "red",
 fillOpacity = 0.2, weight = 2, popup = ~pop) %>%
##Add model prediction
addRasterImage(predSel_Bg, colors = rasPal, opacity = 0.7,
 group = 'vis', layerId = 'mapPred', method = "ngb") %>%
##add background polygons
addPolygons(data = bgExt_Bg, fill = FALSE,
 weight = 4, color = "blue", group = 'proj')
```

```

Visualize

Visualize response curves from “maxnet” model.

```
```{r}
Retrieve env variables
n <- mxNonzeroCoefs(model_Bg@models[["fc.LQ_rm.2"]], "maxnet")

Create response curves
for (i in n) {
 maxnet::response.plot(
 model_Bg@models[["fc.LQ_rm.2"]],
 v = i,
 type = "cloglog")
}
```

```

Appendix D:

Wallace code for ruby-throated hummingbird species distribution model.

Wallace Session 2024-11-17

=====

Please find below the R code history from your *Wallace* v2.1.3 session.

You can reproduce your session results by running this R Markdown file in RStudio.

Each code block is called a “chunk”, and you can run them either one-by-one or all at once by choosing an option in the “Run” menu at the top-right corner of the “Source” pane in RStudio.

For more detailed information see <<http://rmarkdown.rstudio.com>>).

Package installation

Wallace uses the following R packages that must be installed and loaded before starting.

```
```{r}
library(spocc)
library(spThin)
library(dismo)
library(sf)
library(ENMeval)
library(wallace)
```
-----
```

```
## Analysis for *Archilochus colubris* (Ac)
```

User CSV path with occurrence data. If the CSV file is not in the current workspace, change to the correct file path (e.g. "/Users/darwin/Documents/occs/").

```
```{r}
NOTE: provide the folder path of the .csv file
occs_path <- ""
occs_path <- file.path(occs_path, "hummingbird_points_boston_clean.csv")
get a list of species occurrence data
userOdds_Ac <- occs_userOdds(
 txtPath = occs_path,
 txtName = "hummingbird_points_boston_clean.csv",
 txtSep = ",",
 txtDec = ".")
occs_Ac <- userOdds_Ac$Archilochus_colubris$cleaned
```

```

```
#### Obtain environmental data
```

Using user-specified variables.

```
```{r}
Specify the directory with the environmental variables
dir_envs_Ac <- ""
envs_path <- file.path(dir_envs_Ac, c('dem_final.tif', 'garden_dist_final.tif', 'LST_index_final.tif', 'ndvi_final.tif',
'nlcd_final_v2.tif', 'os_dist_final.tif'))
Create environmental object
envs_Ac <- envs_userEnv(
 rasPath = envs_path,
 rasName = c('dem_final.tif', 'garden_dist_final.tif', 'LST_index_final.tif', 'ndvi_final.tif', 'nlcd_final_v2.tif',
'os_dist_final.tif'),
 doBrick = TRUE)
occs_xy_Ac <- occs_Ac[c('longitude', 'latitude')]
```

```

occ_vals_Ac <- as.data.frame(raster::extract(envs_Ac, occs_xy_Ac, cellnumbers = TRUE))
Remove duplicated same cell values
occs_Ac <- occs_Ac[!duplicated(occs_vals_Ac[, 1]),]
occs_vals_Ac <- occs_vals_Ac[!duplicated(occs_vals_Ac[, 1]), -1]
remove occurrence records with NA environmental values
occs_Ac <- occs_Ac[!(rowSums(is.na(occs_vals_Ac)) >= 1),]
also remove variable value rows with NA environmental values
occs_vals_Ac <- na.omit(occs_vals_Ac)
add columns for env variable values for each occurrence record
occs_Ac <- cbind(occs_Ac, occs_vals_Ac)
```

```

Process environmental data

Sampling of 10000 background points and corresponding environmental data using a user provided background extent with a 0 degree buffer.

```

``{r}
# Load the user provided shapefile or csv file with the desired extent.
##User must input the path to shapefile or csv file and the file name
# Define path
bgPath_Ac <- ""
bgExt_Ac <- penvs_userBgExtent(
  bgShp_path = paste0(bgPath_Ac, "boston_WGS84", ".shp"),
  bgShp_name = paste0("boston_WGS84", c(".shp", ".shx", ".dbf")),
  userBgBuf = 0,
  occs = occs_Ac)
# Mask environmental data to provided extent
bgMask_Ac <- penvs_bgMask(
  occs = occs_Ac,
  envs = envs_Ac,
  bgExt = bgExt_Ac)
# Sample background points from the provided area
bgSample_Ac <- penvs_bgSample(
  occs = occs_Ac,
  bgMask = bgMask_Ac,
  bgPtsNum = 10000)
# Extract values of environmental layers for each background point
bgEnvsVals_Ac <- as.data.frame(raster::extract(bgMask_Ac, bgSample_Ac))
##Add extracted values to background points table
bgEnvsVals_Ac <- cbind(scientific_name = paste0("bg_", "Archilochus colubris"), bgSample_Ac,
  occID = NA, year = NA, institution_code = NA, country = NA,
  state_province = NA, locality = NA, elevation = NA,
  record_type = NA, bgEnvsVals_Ac)
```

```

### ### Partition occurrence data

Partition occurrences and background points for model training and validation using “hierarchical checkerboard”, a spatial partition method with an aggregation factor of 2.

```
```{r}
# R code to get partitioned data
groups_Ac <- part_partitionOdds(
  occs = occs_Ac,
  bg = bgSample_Ac,
  method = "cb2",
  bgMask = bgMask_Ac,
  aggFact = 2)
```

```

### ### Build and Evaluate Niche Model

Generating a species distribution model using the maxnet algorithm as implemented in ENMeval V2.0 (with clamping = TRUE). For tuning using L feature classes and regularization multipliers in the 1, 5 range increasing by 1. Using a total of 1 categorical predictor variables.

```
```{r}
# Run maxent model for the selected species
model_Ac <- model_maxent(
  occs = occs_Ac,
  bg = bgEnvsVals_Ac,
  user.grp = groups_Ac,
  bgMsk = bgMask_Ac,
  rms = c(1, 5),
  rmsStep = 1,
  fcs = 'L',
  clampSel = TRUE,
  algMaxent = "maxnet",
  catEnvs = "nlcd_final_v2",
  parallel = FALSE,
  numCores = 15)
```

```

### ### Visualize

Generate a map of the maxnet generated model with no threshold

```
```{r}
# Select current model and obtain raster prediction
m_Ac <- model_Ac@models[["fc.L_rm.2"]]
predSel_Ac <- predictMaxnet(m_Ac, bgMask_Ac,
  type = "cloglog",
  clamp = TRUE)
```

```

```

#Get values of prediction
mapPredVals_Ac <- getRasterVals(predSel_Ac, "cloglog")
#Define colors and legend
rasCols <- c("#2c7bb6", "#abd9e9", "#ffffbf", "#fdbe61", "#d7191c")
legendPal <- colorNumeric(rev(rasCols), mapPredVals_Ac, na.color = 'transparent')
rasPal <- colorNumeric(rasCols, mapPredVals_Ac, na.color = 'transparent')
#Generate map
m <- leaflet() %>% addProviderTiles(providers$Esri.WorldTopoMap)
m %>%
 leaflet::addLegend("bottomright", pal = legendPal,
 title = "Predicted Suitability
(Training)",
 values = mapPredVals_Ac, layerId = "train",
 labFormat = reverseLabel(2, reverse_order = TRUE)) %>%
#add occurrence data
addCircleMarkers(data = occs_Ac, lat = ~latitude, lng = ~longitude,
 radius = 5, color = 'red', fill = TRUE, fillColor = "red",
 fillOpacity = 0.2, weight = 2, popup = ~pop) %>%
##Add model prediction
addRasterImage(predSel_Ac, colors = rasPal, opacity = 0.7,
 group = 'vis', layerId = 'mapPred', method = "ngb") %>%
##add background polygons
addPolygons(data = bgExt_Ac, fill = FALSE,
 weight = 4, color = "blue", group = 'proj')
```

```

Visualize

Visualize response curves from “maxnet” model.

```

```{r}
Retrieve env variables
n <- mxNonzeroCoefs(model_Ac@models[["fc.L_rm.2"]], "maxnet")

Create response curves
for (i in n) {
 maxnet::response.plot(
 model_Ac@models[["fc.L_rm.2"]],
 v = i,
 type = "cloglog")
}
```

```

Appendix E:

Wallace code for monarch butterfly species distribution model.

Wallace Session 2024-11-16

=====

Please find below the R code history from your *Wallace* v2.1.3 session.

You can reproduce your session results by running this R Markdown file in RStudio.

Each code block is called a “chunk”, and you can run them either one-by-one or all at once by choosing an option in the “Run” menu at the top-right corner of the “Source” pane in RStudio.

For more detailed information see <<http://rmarkdown.rstudio.com>>).

Package installation

Wallace uses the following R packages that must be installed and loaded before starting.

```
```{r}
library(spocc)
library(spThin)
library(dismo)
library(sf)
library(ENMeval)
library(wallace)
```
-----
```

Analysis for *Danaus plexippus* (Dp)

User CSV path with occurrence data. If the CSV file is not in the current workspace, change to the correct file path (e.g. “/Users/darwin/Documents/occs/”).

```
```{r}
NOTE: provide the folder path of the .csv file
occs_path <- ""
occs_path <- file.path(occs_path, "monarch_points_boston_clean.csv")
get a list of species occurrence data
userOdds_Dp <- occs_userOdds(
 txtPath = occs_path,
 txtName = "monarch_points_boston_clean.csv",
 txtSep = ",",
 txtDec = ".")
occs_Dp <- userOdds_Dp$Danaus_plexippus$cleaned
```

```

Obtain environmental data

Using user-specified variables.

```
```{r}
Specify the directory with the environmental variables
dir_envs_Dp <- ""
envs_path <- file.path(dir_envs_Dp, c('dem_final.tif', 'garden_dist_final.tif', 'LST_index_final.tif', 'ndvi_final.tif',
'nlcd_final_v2.tif', 'os_dist_final.tif'))
Create environmental object
envs_Dp <- envs_userEnvs(
 rasPath = envs_path,
 rasName = c('dem_final.tif', 'garden_dist_final.tif', 'LST_index_final.tif', 'ndvi_final.tif', 'nlcd_final_v2.tif',
'os_dist_final.tif'),
 doBrick = TRUE)
occ_xy_Dp <- occs_Dp[c('longitude', 'latitude')]
occs_vals_Dp <- as.data.frame(raster::extract(envs_Dp, occs_xy_Dp, cellnumbers = TRUE))
Remove duplicated same cell values
occs_Dp <- occs_Dp[!duplicated(occs_vals_Dp[, 1]),]
occs_vals_Dp <- occs_vals_Dp[!duplicated(occs_vals_Dp[, 1]), -1]
remove occurrence records with NA environmental values
occ_Dp <- occs_Dp[!(rowSums(is.na(occ_Dp)) >= 1),]
also remove variable value rows with NA environmental values
occ_vals_Dp <- na.omit(occ_Dp)
add columns for env variable values for each occurrence record
occ_Dp <- cbind(occ_Dp, occs_vals_Dp)
```

```

Process environmental data

Sampling of 10000 background points and corresponding environmental data using a user provided background extent with a 0 degree buffer.

```
```{r}
Load the user provided shapefile or csv file with the desired extent.
##User must input the path to shapefile or csv file and the file name
Define path
bgPath_Dp <- ""
bgExt_Dp <- penvs_userBgExtent(
 bgShp_path = paste0(bgPath_Dp, "boston_WGS84", ".shp"),
 bgShp_name = paste0("boston_WGS84", c(".shp", ".shx", ".dbf")),
 userBgBuf = 0,
 occs = occs_Dp)
Mask environmental data to provided extent
bgMask_Dp <- penvs_bgMask(
 occs = occs_Dp,
 envs = envs_Dp,
 bgExt = bgExt_Dp)
Sample background points from the provided area
bgSample_Dp <- penvs_bgSample(
 occs = occs_Dp,
```

```

bgMask = bgMask_Dp,
bgPtsNum = 10000)
Extract values of environmental layers for each background point
bgEnvsVals_Dp <- as.data.frame(raster::extract(bgMask_Dp, bgSample_Dp))
##Add extracted values to background points table
bgEnvsVals_Dp <- cbind(scientific_name = paste0("bg_", "Danaus plexippus"), bgSample_Dp,
 occID = NA, year = NA, institution_code = NA, country = NA,
 state_province = NA, locality = NA, elevation = NA,
 record_type = NA, bgEnvsVals_Dp)
```

```

Partition occurrence data

Partition occurrences and background points for model training and validation using “hierarchical checkerboard”, a spatial partition method with an aggregation factor of 2.

```

``{r}
# R code to get partitioned data
groups_Dp <- part_partitionOdds(
  odds = odds_Dp,
  bg = bgSample_Dp,
  method = "cb2",
  bgMask = bgMask_Dp,
  aggFact = 2)
```

```

### ### Build and Evaluate Niche Model

Generating a species distribution model using the maxnet algorithm as implemented in ENMeval V2.0 (with clamping = TRUE). For tuning using L, LQ feature classes and regularization multipliers in the 1, 5 range increasing by 1. Using a total of 1 categorical predictor variables.

```

``{r}
Run maxent model for the selected species
model_Dp <- model_maxent(
 odds = odds_Dp,
 bg = bgEnvsVals_Dp,
 user.grp = groups_Dp,
 bgMsk = bgMask_Dp,
 rms = c(1, 5),
 rmsStep = 1,
 fcs = c('L', 'LQ'),
 clampSel = TRUE,
 algMaxent = "maxnet",
 catEnvs = "nlcd_final_v2",
 parallel = FALSE,
```

```

```
numCores = 11)
````
```

```
Visualize
```

Generate a map of the maxnet generated model with no threshold

```
```{r}
# Select current model and obtain raster prediction
m_Dp <- model_Dp@models[["fc.LQ_rm.1"]]
predSel_Dp <- predictMaxnet(m_Dp, bgMask_Dp,
                             type = "cloglog",
                             clamp = TRUE)
#Get values of prediction
mapPredVals_Dp <- getRasterVals(predSel_Dp, "cloglog")
#Define colors and legend
rasCols <- c("#2c7bb6", "#abd9e9", "#ffffbf", "#fdbe61", "#d7191c")
legendPal <- colorNumeric(rev(rasCols), mapPredVals_Dp, na.color = 'transparent')
rasPal <- colorNumeric(rasCols, mapPredVals_Dp, na.color = 'transparent')
#Generate map
m <- leaflet() %>% addProviderTiles(providers$Esri.WorldTopoMap)
m %>%
  leaflet::addLegend("bottomright", pal = legendPal,
                     title = "Predicted Suitability<br>(Training)",
                     values = mapPredVals_Dp, layerId = "train",
                     labFormat = reverseLabel(2, reverse_order = TRUE)) %>%
#add occurrence data
addCircleMarkers(data = occs_Dp, lat = ~latitude, lng = ~longitude,
                  radius = 5, color = 'red', fill = TRUE, fillColor = "red",
                  fillOpacity = 0.2, weight = 2, popup = ~pop) %>%
##Add model prediction
addRasterImage(predSel_Dp, colors = rasPal, opacity = 0.7,
               group = 'vis', layerId = 'mapPred', method = "ngb") %>%
##add background polygons
addPolygons(data = bgExt_Dp, fill = FALSE,
            weight = 4, color = "blue", group = 'proj')
````
```

```
Visualize
```

Visualize response curves from “maxnet” model.

```
```{r}
# Retrieve env variables
n <- mxNonzeroCoefs(model_Dp@models[["fc.LQ_rm.1"]], "maxnet")

# Create response curves
for (i in n) {
```

```
maxnet::response.plot(
  model_Dp@models[["fc.LQ_rm.1"]],
  v = i,
  type = "cloglog")
}
```

```

## Appendix F:

**R code for creating resistance layers from the SDMs for the Circuitscape connectivity analysis:**  
`getwd()`

```
library(raster)

Load the habitat suitability raster 1
suitability_raster_1 <- raster("Sofio270/Archilochus_colubris_fc.L_rm.2_cloglog.tif")
suitability_raster_2 <- raster("Sofio270/Danaus_plexippus_fc.LQ_rm.1_cloglog.tif")
suitability_raster_3 <- raster("Sofio270/Bombus_griseocollis_fc.LQ_rm.1_cloglog.tif")

plot(suitability_raster_1)

Define the factor c
c <- 1

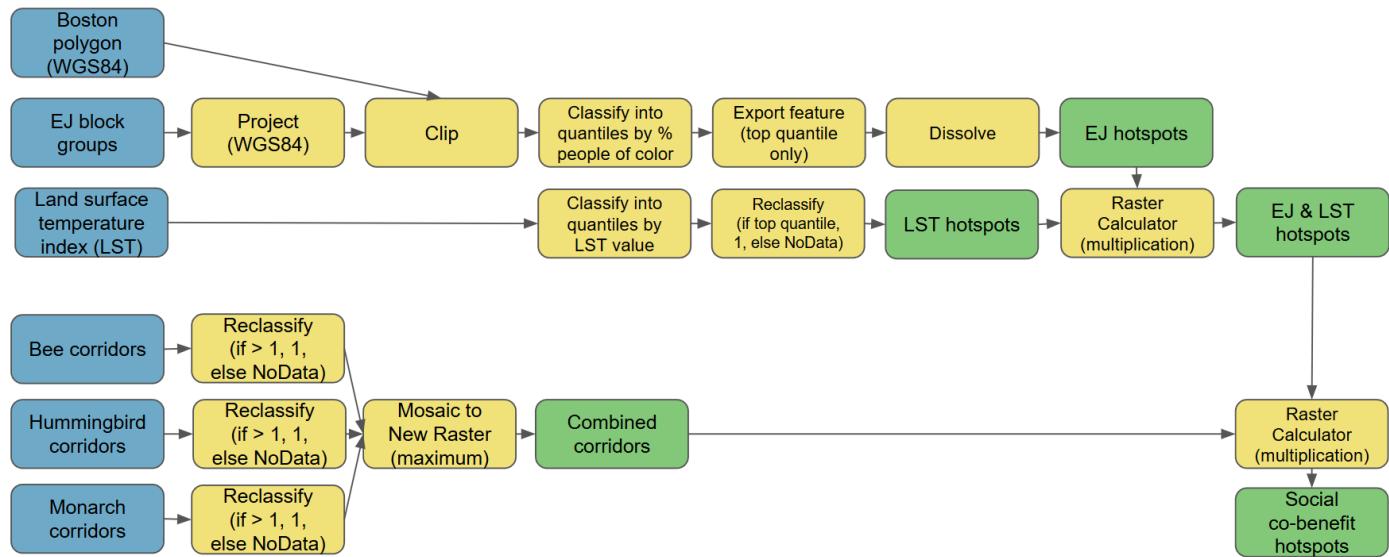
Define a function to calculate resistance from suitability
calculate_resistance <- function(H, c) {
 R <- 100 - 99 * ((1 - exp(-c * H)) / (1 - exp(-c)))
 return(R)
}

Apply the function to the raster using calc
resistance_raster_1 <- calc(suitability_raster_1, function(H) calculate_resistance(H, c))
resistance_raster_2 <- calc(suitability_raster_2, function(H) calculate_resistance(H, c))
resistance_raster_3 <- calc(suitability_raster_3, function(H) calculate_resistance(H, c))

Save the resulting resistance raster
writeRaster(resistance_raster_1, "boston_1.tif", format = "GTiff", overwrite = TRUE)
writeRaster(resistance_raster_2, "boston_2.tif", format = "GTiff", overwrite = TRUE)
writeRaster(resistance_raster_3, "boston_3.tif", format = "GTiff", overwrite = TRUE)
Plot to verify
plot(resistance_raster_1, main = "Resistance Raster")
plot(resistance_raster_2, main = "Resistance Raster")
plot(resistance_raster_3, main = "Resistance Raster")
```

## Appendix G:

### Social Co-benefit Hotspots: Methodology



**Figure 1.** Methodology for social co-benefit hotspots analysis. Input data are shown in blue, processes are shown in yellow, and output data are shown in green.

## RESPONSE TO REVIEWER

Thank you for your thoughtful feedback on the first draft of our report. We appreciate that you spent time with our work. To address your feedback, we have bolstered the sections you suggested need additional information, completed our final analysis, and included more thorough descriptions of our figures where appropriate. We hope that you find these revisions satisfactory. The rest of this document includes our initial draft as well as the feedback we received from our reviewer.