

APPLICATION

geohabnet: An R package for mapping habitat connectivity for biosecurity and conservation

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AUTHOR CONTRIBUTIONS STATEMENT

Aaron I. Plex Sulá and Karen A. Garrett developed the initial concepts. Aaron I. Plex Sulá, Krishna Keshav, and Stavan Nikhilchandra Shah developed the initial version of the R package. All authors contributed to refining the R package. All authors contributed to the development of the main text and case studies.

ACKNOWLEDGEMENTS

We appreciate support from the USDA Animal and Plant Health Inspection Service Cooperative Agreements AP21PPQS&T00C195 and AP22PPQS&T00C133 and the USDA Specialty Crop Research Initiative, project award nos. 2020-51181-32198, 2022-51181-38242 and 2024-51181-43302, from the USDA National Institute of Food and Agriculture. We also appreciate support from the CGIAR Seed Equal Research Initiative, USAID Bureau of Humanitarian Assistance award number 720BHA22IO00136, and the CGIAR Trust Fund. We thank all donors and organizations that globally support the work of CGIAR through their contributions to the CGIAR Trust Fund. The opinions expressed in this article are those of the authors and do not necessarily reflect the views of USAID or USDA. We appreciate helpful input from Yanru Xing.

DATA AVAILABILITY STATEMENT

The stable version of geohabnet is available in CRAN at <https://cran.r-project.org/web/packages/geohabnet/index.html> (Keshav et al., 2026). The development version of geohabnet is available in GitHub at <https://github.com/GarrettLab/HabitatConnectivity>. Instructions for reproducing the analyses developed in this application are available in the Supporting Information on figshare at <https://doi.org/10.6084/m9.figshare.32927366> (Plex Sulá et al., 2026), with any updates online at <https://garrettlab.github.io/HabitatConnectivity/articles/>. The latest version of the user guide for geohabnet is available at https://garrettlab.github.io/HabitatConnectivity/articles/user_guide.html. All data used in this article are publicly available in MAPSPAM at <https://doi.org/10.7910/DVN/SWPENT> (International Food Policy Research Institute, 2026) and CROPGRIDS at <https://doi.org/10.1038/s41597-024-03247-7> (Tang et al., 2024).

ABSTRACT

1. Habitat connectivity is critical for conservation of endangered and endemic species, and conversely, it can hinder efforts to contain the spread of harmful biological agents.
2. Here, we introduce geohabnet: a general, spatially explicit, network-based R package for evaluating, estimating and mapping landscape connectivity from continuous habitat surfaces. The package integrates habitat suitability maps with commonly used dispersal models to evaluate the relative importance of habitat locations to the potential spread of an organism.
3. By incorporating a range of geographic parameters, geohabnet offers a scalable approach to assessing multi-scale habitat connectivity. Furthermore, geohabnet enables sensitivity analysis across geographic, habitat, and network-metric parameters to quantify uncertainty in habitat connectivity when information about an organism is incomplete, as for emerging diseases or invasive species.
4. To demonstrate geohabnet's functionality, we use publicly accessible plant data to assess habitat connectivity for species that depend on plant hosts, such as plant pathogens, pests, and pollinators, across Africa and the Americas.
5. geohabnet provides a quick, open-source, reproducible, and generalizable approach to evaluating potential scenarios for the spread of a species through habitat landscapes. By mapping habitat connectivity, geohabnet can support biosecurity and conservation programs, including the design of surveillance strategies for transboundary pathogens, biological invasions, and endangered species.

RESUMEN

1. La conectividad del hábitat es fundamental para la conservación de especies endémicas y en peligro de extinción, pero también puede obstaculizar los esfuerzos de contener la propagación de agentes biológicos nocivos.
2. En este estudio se presenta geohabnet: un paquete en el programa R para evaluar, estimar y cartografiar la conectividad de las especies a partir de superficies continuas de hábitat, basado en un modelo general de redes geográficas. El paquete integra mapas de idoneidad del hábitat con modelos de dispersión de uso común para evaluar la importancia de distintas áreas de hábitat en la propagación potencial de un organismo.
3. Al incorporar una amplia gama de parámetros geográficos, geohabnet ofrece un enfoque escalable para evaluar la conectividad de las especies a múltiples escalas. Además, geohabnet permite realizar análisis de sensibilidad de parámetros geográficos, de hábitat y de métricas de red para cuantificar la incertidumbre en las estimaciones de conectividad cuando la información sobre un organismo es incompleta, como ocurre con las enfermedades emergentes o las especies invasoras.
4. Para demostrar la funcionalidad de geohabnet, se utilizaron datos públicos sobre cultivos en África y el continente americano, evaluando así la conectividad para especies que dependen de hospedantes vegetales, tales como plagas, enfermedades y polinizadores.
5. geohabnet proporciona un enfoque rápido, de código abierto, reproducible y generalizable para evaluar escenarios potenciales de propagación de una

especie a través de áreas con hábitat. Mediante el mapeo de la conectividad del hábitat, geohabnet puede ser de apoyo para los programas de bioseguridad y conservación, incluyendo el diseño de estrategias de vigilancia para plagas transfronterizas, especies invasoras y en peligro de extinción.

INTRODUCTION

Understanding landscape or habitat connectivity supports area-wide species management and the protection of natural or managed ecosystems. Maintaining or enhancing habitat connectivity for endemic, endangered, or beneficial organisms (e.g., pollinators, mycorrhizal fungi, or biocontrol agents) is key to biodiversity conservation planning (Brennan *et al.*, 2022, Drielsma *et al.*, 2022, Fletcher *et al.*, 2011). Conversely, reducing habitat connectivity is a common goal of biosecurity, invasion science, and landscape epidemiology to limit the spread of harmful biological agents [e.g., invasive species, emerging infectious diseases, and plant pests] (Radici *et al.*, 2023, Jousimo *et al.*, 2014, Margosian *et al.*, 2009, Meentemeyer *et al.*, 2012).

Species distribution models (SDMs) are widely used in ecology to inform area-wide species management by mapping a species' potential geographic range or environmentally suitable hotspots. However, SDMs often ignore how a species is likely to move through a heterogeneous region and how landscape features may regulate dispersal (Schmitt *et al.*, 2017, Naimi & Araújo, 2016, Velazco *et al.*, 2022). For example, host distribution is a landscape feature constraining the spread of obligate plant pathogens or endangered pollinators. Dispersal processes determine the connectivity of a landscape, and which locations in a landscape of suitable habitats are most important for a species' spread. Here, habitat suitability refers to the quantity and

quality of suitable environments (e.g., climate or soil conditions) and biotic resources (e.g., host abundance) for a target organism at a given location (Guisan *et al.*, 2017).

Over 100 metrics have been proposed to measure habitat or landscape connectivity (Rayfield *et al.*, 2011, Kindlmann & Burel, 2008, Keeley *et al.*, 2021). Many of these metrics are available as custom code, potentially lacking alignment with the FAIR principles for research software (Barker *et al.*, 2022). Few open-source resources are available that apply most of these connectivity metrics. Available software tools estimate landscape connectivity based on graph theory (e.g., Makurhini, graph4lg, or grainscape in R, coneфор in Fortran, graphab in Java) or using resistance surfaces via circuit theory (e.g., Circuitscape or Omniscape) [Supplementary Table in Plex Sulá *et al.* (2026b)].

Alongside least-cost corridor analysis, circuit and graph theory are widely used to evaluate species movement in landscape ecology (McRae, 2006, Lewis, 2025, McRae *et al.*, 2008, Urban & Keitt, 2001). Existing network-based tools assess landscape connectivity only at the patch level (Chubaty *et al.*, 2020, Mestre & Silva, 2023, Hesselbarth *et al.*, 2019), potentially underrepresenting the spatial habitat heterogeneity of many realistic landscapes (Spanowicz & Jaeger, 2019). To our knowledge, network-based software for measuring landscape connectivity across continuous yet heterogeneous habitat surfaces is not available. This gap exists despite the growing interest over the past two decades in applying network science to movement ecology, landscape epidemiology, ecology and evolution, and invasion ecology (Mestre & Silva, 2023, Frost *et al.*, 2019).

To address this gap, we introduce geohabnet: an R package for mapping habitat connectivity for terrestrial species. Complementing existing tools, geohabnet is a new

analytical tool for habitat connectivity to the growing R user community of landscape ecologists. It draws on a network-based landscape connectivity framework and operates directly on continuously distributed habitat data. geohabnet provides connectivity analysis for spatially explicit real-world habitat gradients, preserving contiguous habitat heterogeneity while avoiding the need for discrete patch delineation.

As continuous spatial data from satellite imagery, remote sensing, and surface modeling are increasingly available, geohabnet can serve as a general, reproducible, and stable framework for evaluating continuous habitat connectivity in biosecurity and biodiversity conservation planning. This method expands the toolbox for landscape connectivity to biosecurity applications; resistance surfaces and patch delineation have rarely been applied to non-native species, such as invasive pathogens or arthropod pests. Some organisms, though, are restricted to structurally discrete or isolated resource patches (Chubaty et al., 2020). Compared with patch-level data, geospatial information on habitat suitability surfaces is often readily available (Guisan et al., 2017).

We illustrate the use of geohabnet with three case studies, focusing on habitat connectivity for invasive, re-emerging, or new plant pests. These case studies exemplify the generalizability of geohabnet for analyzing the landscape connectivity of host-dependent organisms such as plant parasites, endophytes, and pollinators (Bishop, 2025, Cunniffe *et al.*, 2015, Rimbaud *et al.*, 2024). They also illustrate the potentially devastating effects of plant pests on natural and managed ecosystems (Savary *et al.*, 2019, Diagne *et al.*, 2021, MacLachlan *et al.*, 2021). Despite the wide range of microbial organisms and arthropods (including host-dependent species), few studies have examined their habitat connectivity using existing connectivity tools. Quantifying habitat

connectivity can inform surveillance and mitigation placement by identifying vulnerable areas with high potential for epidemics or invasions. geohabnet is applicable to a wide range of taxa, including organisms that depend on compatible hosts as their habitat.

CONCEPTUAL FRAMEWORK

In geohabnet, habitat networks are spatial representations of the potential paths of spread of an organism through a suitable habitat landscape. In a habitat network, nodes represent geographic locations that are denoted as grid cells of nearly equal area, have specific levels of suitable habitat, and are spatially distributed across a raster layer of regular tessellation (hereafter, habitat surface or landscape). The surface of habitat suitability serves as an input to geohabnet and is produced by the user either through direct observation or by calculating an index from factors that may facilitate the establishment of a target organism, for example, using SDMs.

Undirected links indicate the potential for the organism to move between two locations. Generalized gravity models are used to calculate link weights, which are proportional to the probability of a species' movement between habitat locations (Fig. 2). In general, gravity models estimate the probability of dispersal using functions that describe the characteristics of locations where organisms can disperse (e.g., habitat suitability) and the relocation process (Jongejans *et al.*, 2014). In geohabnet, gravity models combine dispersal kernels modeling the relocation process with the likely influence of habitat suitability across a landscape. Dispersal kernels are probability density functions that describe the inverse relationships between dispersal probability and geographic distance (Nathan *et al.*, 2012). The probability of species movement also depends directly on the habitat suitability of connected sites. Source locations with

higher suitability are likely to generate more dispersing units (such as spores or seeds), while destination sites with higher suitability can support a greater influx of dispersing units (Margosian et al., 2009).

Network theory offers powerful perspectives for movement ecology in complex, real-world landscapes, ranging from identifying closest neighbors to determining shortest paths between physically distant regions [e.g., (Moslonka-Lefebvre *et al.*, 2011)]. geohabnet harnesses the flexibility of network theory by incorporating seven node-level network metrics to quantify habitat connectivity. In geohabnet, habitat connectivity indicates the extent to which a geographic location facilitates an organism's mobility through the habitat network. Each measure of node centrality evaluates a specific role within the landscape, ranging from the local spread of an organism to the nearest neighbors reachable in a single step (e.g., node strength or node degree), as well as spread over multiple steps through the shortest paths (e.g., betweenness or closeness centrality). When multiple network metrics are selected, geohabnet calculates a weighted mean of habitat connectivity based on user-assigned weights (in percentages) that represent the relative importance of each metric.

Users can apply geohabnet to answer key questions in movement ecology, such as: What is the relative importance of specific locations in the potential spread of an organism through a habitat landscape? Which locations are more likely to serve as bridges for organismal movement in the landscape, defined as nodes having above-average betweenness or closeness centrality? Which locations are more likely to act as hubs, defined as nodes with above-average connections in the habitat network? Which

locations should be area-wide priorities for monitoring the spread of an invasive or endangered species, given their habitat connectivity?

FUNCTIONALITY

Implementation. geohabnet 2.3 provides R users with two core functions, `msean()` and `sensitivity_analysis()`, to evaluate the habitat connectivity of locations in a landscape. (A complete summary of all geohabnet functions is available in the package reference manual on CRAN at <https://cran.r-project.org/web/packages/geohabnet/geohabnet.pdf>). These functions allow calculation of habitat connectivity across a set of user-specified habitat, dispersal, and geographic parameters, and commonly used network metrics. The user guide provides a rationale to guide selection of values of each parameter (Plex Sulá et al., 2026b). Users can install the stable version of geohabnet from CRAN by running `install.packages("geohabnet")` in RStudio. Users are recommended to install dependencies as needed. geohabnet 2.3 is compatible with R versions 4.3.0-4.5.2 and has been validated on Windows, MacOS, and Linux.

If using `msean()`, users should provide a `SpatRaster` object as input and can modify parameter values directly in the function. If using `sensitivity_analysis()`, users need to download the `parameters.yaml` file in their working directory by running `library(geohabnet)` and `get_parameters()`. Users can manually change the values of each parameter in `parameters.yaml`, set the newly specified values in R with `set_parameters()`, and perform the connectivity analysis with `sensitivity_analysis()`. In `parameters.yaml`, users can specify the directory path to the habitat suitability map.

`msean()` provides an R interface in which parameter values are specified directly in the function. This script-based approach is consistent with standard R workflows and facilitates exploratory analyses, rapid testing, or incremental parameter adjustments. In contrast, `sensitivity_analysis()` is designed for structured, large-scale analyses involving multiple values for each parameter or sub-parameter (see user guide). By centralizing inputs in `parameters.yaml` outside R, users can efficiently manage complex parameter sets across scenarios or computing environments. This design is particularly suited for automated workflows, where configurations can be saved, shared, and reloaded using `set_parameters()`. This avoids the need to manually list all parameters in the R console each time the function is called. Both functions rely on the same underlying process and exhibit equivalent performance. They are complementary, allowing users to choose between configuration-driven and script-based workflows depending on their preference.

A third way of customizing parameters is through the geohabnet app (<https://geohabnet.rc.ufl.edu/>). This app makes geohabnet functionality available to non-R users through a straightforward, interactive dashboard for habitat connectivity. The user-friendly graphical interface (i) allows easy customizations of all parameters and sub-parameters, (ii) executes the habitat connectivity analysis using one Central Processing Unit (1 CPU), and (iii) generates downloadable graphical visualizations and outputs (see below).

Inputs. Two inputs are required to run `msean()` or `sensitivity_analysis()`: (i) a raster layer of habitat suitability in the standard coordinate reference system (World Geodetic System 1984 or WGS 84), and (ii) a set of selected parameters (specified in R or in

`parameters.yaml`). Entries in the habitat suitability layer should range from 0 (no habitat suitability) to 1 (highest habitat suitability). Both `msean()` and `sensitivity_analysis()` have been tested using maps of habitat suitability in the form of host abundance, from MAPSPAM (IFPRI, 2026), CROPGRIDS (Tang *et al.*, 2024), EARTHSTAT (Monfreda *et al.*, 2008), CroplandCROS (<https://croplandcros.scinet.usda.gov/>), GBIF (<https://www.gbif.org/>), and user-built maps (Plex Sulá *et al.*, 2026a, Mouafo-Tchinda *et al.*, 2026).

Outputs. Both `sensitivity_analysis()` and `msean()` produce three types of maps from a habitat connectivity analysis. Each map is produced as a `spatRaster` object and/or an automated graphical visualization.

- i) The first map indicates the habitat connectivity averaged across all parameter combinations chosen by the user, with unitless values scaled between 0 and 1. The mean habitat connectivity indicates the relative importance of locations for the potential spread of an organism across the landscape. This map is the primary output from geohabnet for identifying candidate connectivity hotspots in conservation or biosecurity applications.
- ii) The second map measures the variance in habitat connectivity across all combinations of the specified parameters, functioning as a tool for uncertainty quantification. This map indicates whether a location's importance remains the same across model parameter values (no variance in habitat connectivity) or varies across them. Low variance at a location indicates low uncertainty in habitat connectivity, particularly when evaluating different parameter values. Conversely, high variance at a location indicates that habitat connectivity is highly sensitive to parameter choices,

so more information is needed to be confident about a location's role. Quantifying uncertainty is particularly important for biosecurity applications of habitat connectivity, where time-sensitive decision-making often relies on incomplete information about parameter values for a newly identified harmful biological agent.

- iii) The third map indicates the difference in ranks between mean habitat connectivity and habitat suitability. This map is a quantitative assessment of the information gained from the habitat connectivity analysis compared with an analysis that considers habitat suitability alone. Positive values on this map indicate potentially greater importance based on habitat connectivity than habitat suitability and identify locations likely to play important roles in organismal spread that analyses of habitat suitability alone would not identify. Negative values on this map indicate lower habitat connectivity than habitat suitability and identify locations where an organism would spread less readily than indicated by an analysis based solely on habitat suitability.

By allowing assessment of a range of parameter values, geohabnet provides a flexible framework for sensitivity analysis, that is, measuring how variations in inputs (e.g., dispersal kernels, network metrics) affect habitat connectivity outcomes (e.g., mean or variance maps).

Competitive Advantage. The package integrates graph theory, a general dispersal framework, and geospatial analyses to evaluate, quantify, and map landscape connectivity across spatial scales. Compared to other software tools, the package offers a generalizable framework to build habitat networks from a given continuous yet heterogeneous surface of habitat suitability. Another difference compared to previous

network-based packages is that geohabnet estimates link weights incorporating dispersal kernels that are widely used and validated across taxonomic groups (Nathan et al., 2012). Furthermore, for link estimation, geohabnet supports two robust methods for geographic distance calculations: the geodesic method, which is most computationally efficient, and the Vincenty ellipsoid method, which is the most geographically accurate. Unlike Euclidean distances used in other packages, these spatially explicit methods account for the Earth's curvature and elliptical shape, ensuring high accuracy in large-scale or long-distance connectivity analysis. Another feature of geohabnet is the spatial aggregation methods, which enable multi-scale and scale-dependent connectivity analyses for high- or ultra-high-resolution habitat data.

Limitations. geohabnet assumes balanced or undirected dispersal and ignores other geographic factors that directly affect habitat connectivity (e.g., wind, human-mediated movement, or physical barriers like mountains or deserts). Another limitation is the computational cost of global analysis of high-resolution habitat data, but high-performance computing resources are increasingly available.

CASE STUDIES

We present three examples to illustrate the functionality of geohabnet across different scenarios. Case Study 1 is a hypothetical illustration of how habitat connectivity in a region varies across network metrics. In the other examples, an applied researcher aims to identify habitat connectivity hotspots in regions where habitat for plant pathogens and pests is moderate (case 2) or abundant (case 3). A vignette to run each example is available in Plex Sulá et al. (2026b).

In Case Studies 2 and 3, habitat suitability is defined in terms of host availability, namely, the fraction of an area with plants susceptible to a pathogen or pest. Dispersal parameter values are not available for many plant pathogens and pests, including those in the case studies. We thus include a range of possible parameter values in the connectivity analyses below to explicitly account for uncertainty. These examples provide a first approximation of habitat connectivity and potential dispersal scenarios for the target species; further assessments can incorporate the influence of climate factors with host availability to generate more integrated maps of habitat suitability (Plex Sulá et al., 2026a).

Case Study 1. This example is the analysis of a hypothetical habitat landscape in which each grid cell represents a geographic location and node (Fig. 2A). This example helps users better understand habitat connectivity analysis before analyzing more complex, realistic landscapes. It illustrates a simple stepwise approach to calculating habitat connectivity among locations. Briefly, the habitat landscape is transformed into a habitat network (Fig. 2B), where each node represents a habitat location. Link weights are proportional to the probability of an organism moving between locations in the landscape, calculated as the product of the habitat availability of the connecting locations and the dispersal probabilities derived from the negative exponential kernel and the inverse power-law model. The importance of each node to the spread across the network is measured using a set of node centrality metrics, such as closeness centrality (Fig. 2C). The overall importance of each node is computed as a weighted mean of a user-selected set of network metrics (see the user guide for all metrics available in geohabnet). To allow comparative analysis, geohabnet scales each network

metric (e.g., Fig. 2C-F) before calculating the weighted mean across these metrics. Then, the mean across dispersal parameters is used to map the mean habitat connectivity across the landscape (Fig. 2D-G). We used the `msean()` function in `geohabnet` to implement this habitat connectivity analysis (see Plex Sulá et al. (2026b) for the full list of parameters used in this case study). This example illustrates how four network metrics provide different perspectives on the potential roles of locations when an organism spreads in a hypothetical habitat landscape (Fig. 2D-G). Note that a location with high habitat suitability will tend to rank among the most important locations in the landscape across different network metrics. The importance of low-habitat-suitability locations varied depending on the network metric used, where each metric measures a different potential role for a node in the network. The analysis includes a sensitivity analysis for a range of dispersal parameters and four network metrics, generating a mean habitat connectivity map (Fig. 2H).

Case Study 2. This example illustrates the use of `geohabnet` for mapping habitat connectivity across realistic national, regional, or continental landscapes. Here, cropland connectivity can serve as a proxy for habitat connectivity of host-specific plant pests, with cropland area representing host abundance. In this example, `geohabnet` generates maps of habitat landscape connectivity of emerging or potentially invasive pathogens or pests affecting sorghum in sub-Saharan Africa and yam in West Africa.

The geographic data was cropland harvested area for sorghum and yam in Africa from MAPSPAM 2017 (IFPRI, 2026), using the `crop_spam()` function from the `geodata` package. Each cropland map was used in the `msean()` function in `geohabnet` to perform a sensitivity analysis based on cropland connectivity. The user set a link threshold

(`link_threshold = 0.00001`) to consider only links that have a probability of movement greater than 0.001% (once every one hundred thousand events) and a habitat threshold (`hd_threshold = 0.0025`) to consider locations where habitat is available in at least 0.25% (Xing *et al.*, 2020). The user customized the default weights for four network centrality metrics: betweenness centrality (weighted 50%), node strength (weighted 15%), sum of nearest neighbors (weighted 15%), and eigenvector centrality (weighted 20%). All other parameters were kept at their default values in `msean()`.

For sorghum in Africa, high cropland connectivity was identified in locations in southern Niger, northern Nigeria, and northern Cameroon (Fig. 3A). For yam in West Africa, the analysis identifies locations in south-eastern Nigeria and near Lake Kossou (Ivory Coast) as highly connected (Fig. 3C). Along with information on pests and pathogens in these locations, these maps of cropland connectivity can inform strategies for prioritizing regional surveillance. For example, the spotted stem borer (*Chilo partellus*), a damaging pest of sorghum, is now present in Cameroon and prevalent in several countries in East and South Africa (van den Berge, 2023). The analysis identifies locations along the border between northern Cameroon and Nigeria as candidate priority areas to prevent the introduction of this pest into sorghum and other cereal crops in West Africa.

Case Study 3. This example illustrates habitat connectivity analysis where habitat is widely available across a region, specifically maize as a host of pathogens in the Americas. Global maps of “maize” and “maize forage” from CROPGRIDS (Tang *et al.*, 2024) were combined to produce a cumulative map of host availability. We used this global map of host availability in the `parameters.yaml` for `sensitivity_analysis()`. The user

set the following parameters: the spatial resolution factor to 24 (so each grid cell represents 2° or ~222×222 km² at the Equator), the habitat threshold to 0.25% (so only grid cells having over 12,000 hectares of maize are retained in the analysis), and the threshold for link weight to 1×10^{-6} (so only links with a probability of movement above this value are considered). To assess habitat connectivity resulting from potential long-distance dispersal, the user estimated dispersal probabilities between locations using the inverse power law (IPL) model. In a sensitivity analysis, we assessed three values of the dispersal parameter ($\beta = 0.5, 1, \text{ and } 1.5$), the exponent in the IPL model, where the probability of dispersal decreases as the dispersal parameter increases (Xing et al., 2020).

There is high mean cropland connectivity in major production areas where maize is densely cultivated, including the northern United States, central Mexico and southwestern Brazil (Fig. 4A). Maize is less densely cultivated in the Andes, but cropland connectivity analyses indicated locations in the Andes that were relatively more important than solely considering maize cropland availability (Fig. 4B). A region from Mesoamerica to Panama and the Andes may serve as a bridge connecting major production areas in the mainland Americas and potentially facilitating the spread of maize-specific diseases.

This map of maize connectivity in the Americas can help in monitoring the spread of invasive pests or emerging maize-specific diseases, such as maize lethal necrosis (MLN), caused by a co-infection of *Maize chlorotic mottle virus* and Potyviruses. MLN has been reported with scattered occurrences in the Americas since 1974, but its recent

emergence in Africa and Asia in 2011 makes this disease a global concern for maize production (Boddupalli *et al.*, 2020).

DISCUSSION

The case studies in Plex Sulá *et al.* (2026b) illustrate how geohabnet can provide analyses of habitat connectivity relevant to surveillance, emerging epidemics, and invasive spread of crop-specific pests and pathogens. When dispersal parameters for a target species are uncertain, geohabnet allows users to evaluate alternative scenarios through sensitivity analyses, as demonstrated in case studies 2 and 3. In addition to standalone analyses, geohabnet outputs can be used in broader network-based analyses and decision-support frameworks, such as impact network analysis (Garrett, 2021). For such applications, geohabnet is integrated in the R2M Plant Health Toolbox (<https://www.garrettlab.com/r2m/>), designed to provide rapid geographic risk assessments for surveillance and mitigation of plant pathogen and pest impacts.

geohabnet is intended as a flexible and computationally accessible framework for raster-based habitat connectivity analysis that can be integrated with a broad range of additional ecological or epidemiological information. A more complete analysis of habitat connectivity may incorporate information about wild hosts, management interventions or outputs from SDMs (Velazco *et al.*, 2022, Schmitt *et al.*, 2017). The package is designed to operate across a range of spatial resolutions, although analyses using high-resolution data may substantially increase computational requirements as network size and pairwise calculations would scale rapidly with the number of habitat cells. Users should balance spatial detail with computational resources, depending on their study's objectives. Compared with general-purpose geographic or network-analysis tools,

geohabnet offers a unified workflow to habitat connectivity analysis for rasterized spatial data within the R environment. Future developments may incorporate dynamic habitat variability through time, harnessing the growing availability of geographic biodiversity information (Meyer *et al.*, 2015). Additional methods for representing heterogeneous landscapes and dispersal processes will also broaden the functionality of geohabnet.

CONFLICT OF INTEREST STATEMENT

The authors declare that they have no conflicts of interest.

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Figures

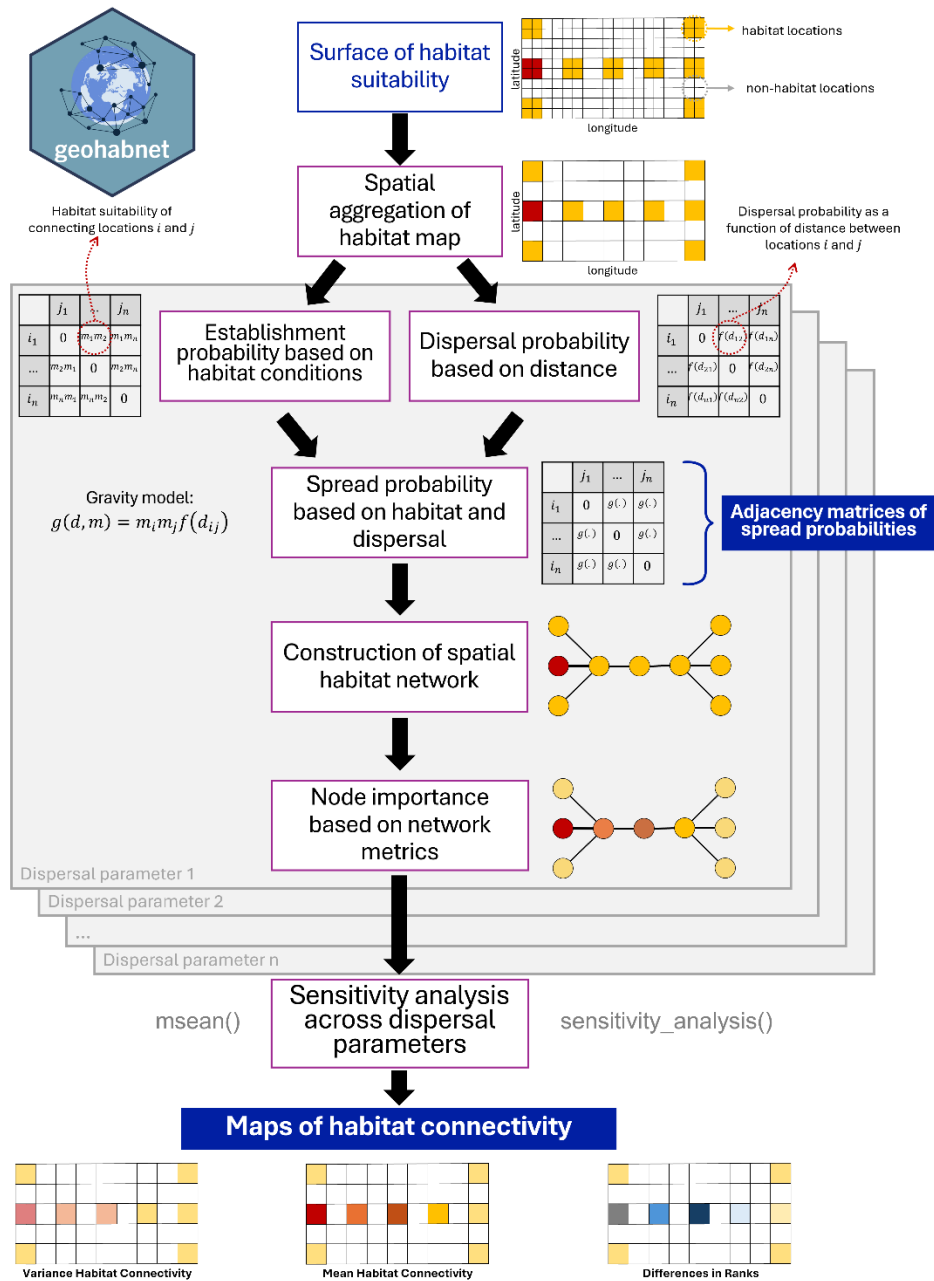


Fig. 1. Conceptual framework for evaluating habitat connectivity in geohabnet.

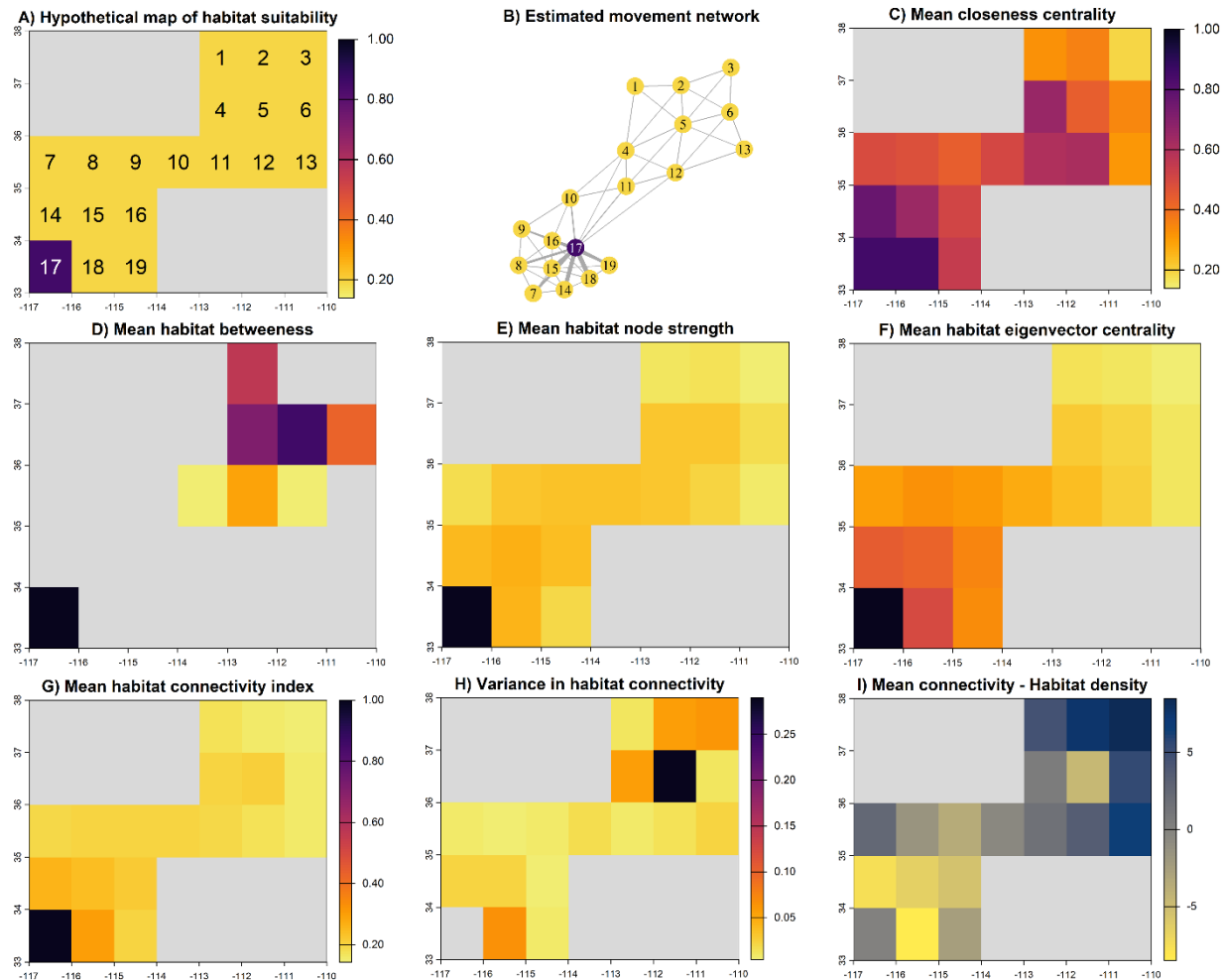


Fig. 1. Components of a habitat connectivity analysis in a hypothetical landscape using geohabnet. A) The hypothetical distribution of habitat suitability for an organism, where cell 17 has unusually high suitability. B) The corresponding network of potential movement between habitat locations (nodes), with link width proportional to movement probability. C) to F) The importance of habitat locations based on individual network metrics. G) The mean habitat connectivity across these network metrics and dispersal parameters. H) The variance in habitat connectivity across network metrics and dispersal parameters. I) The difference in ranks between mean habitat connectivity (G) and habitat suitability (A).

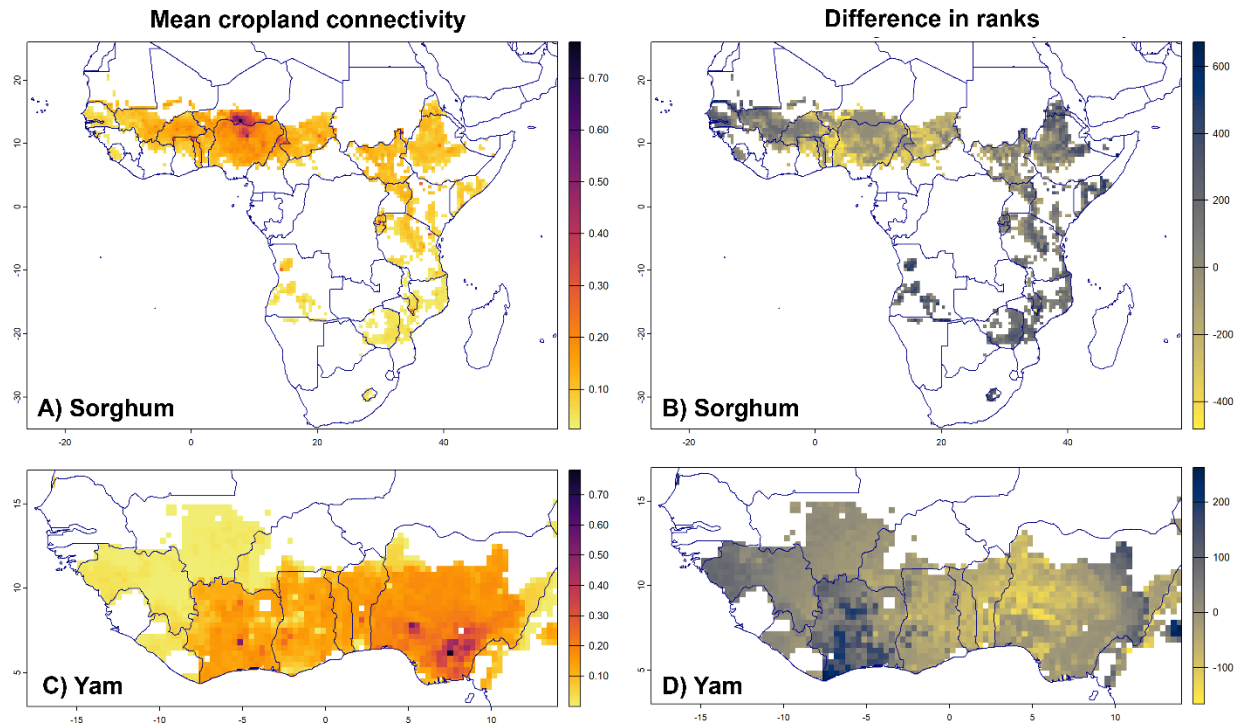


Fig. 2. Habitat connectivity analyses from geohabnet for pests of sorghum in sub-Saharan Africa (A, B) and of yam in West Africa (C, D). Mean cropland connectivity is a relative index for habitat connectivity of host-specific pests calculated across a range of dispersal parameters and network metrics. In A) and C), locations with higher cropland connectivity (dark grid cells) are likely to support pathogen or pest movement more than other locations (light grid cells). In B) and D), the difference in ranks between cropland connectivity and cropland availability indicates where the connectivity analysis estimates a higher (dark grid cells) or lower (light grid cells) probability of movement compared with simply identifying locations with high cropland availability.

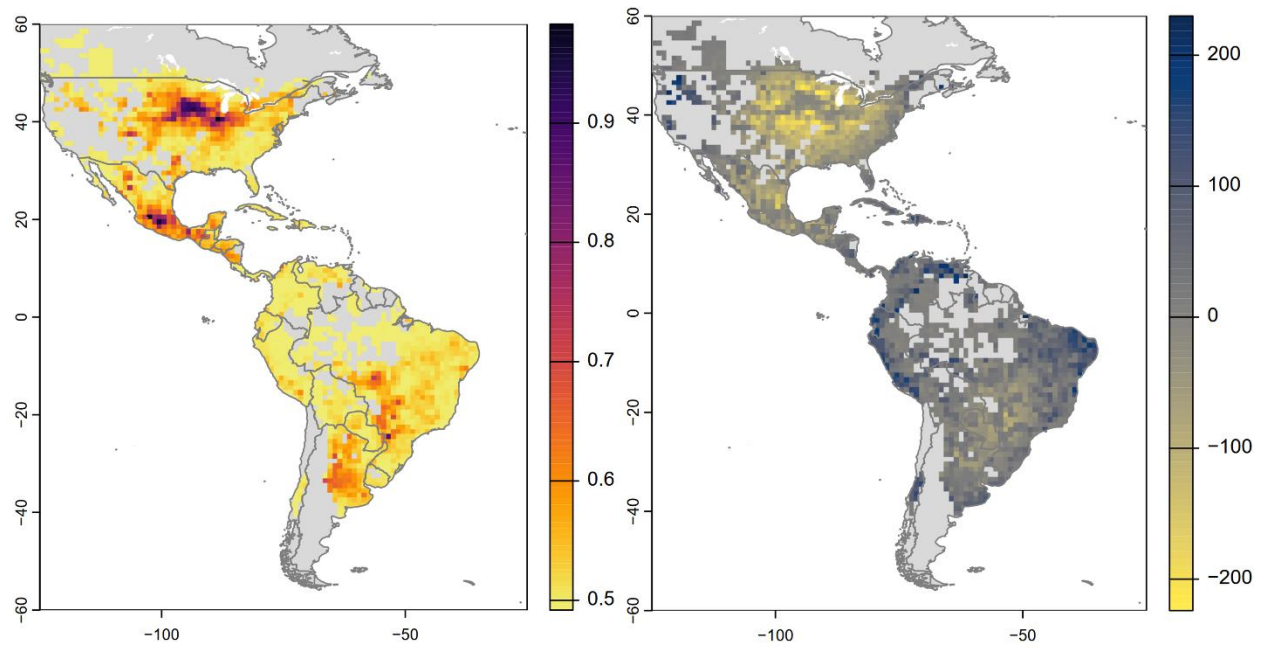


Fig. 4. (A) Mean maize cropland connectivity analyses from geohabnet for the Americas, across a range of dispersal parameter values. (B) The difference in ranks between mean cropland connectivity and cropland connectivity for maize-specific pests.