1   **APPLICATION**

2   **geohabnet: An R package for mapping habitat connectivity for ecosystem health**

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22

23

Abstract

24

25   1. Mapping habitat quality, in terms of factors like host availability and environmental

26   suitability, is a common approach to determining which locations are important for the

27   spread of a species. Mapping habitat connectivity takes geographic analyses a step

28   further, evaluating the potential roles of locations in epidemics, invasions, or species

29   conservation. Locations with high habitat quality may play a minor role in species spread

30   if they are geographically isolated. Yet, a location with lower habitat quality may play a

31   major role in a species' spread if it acts as a bridge between regions that would otherwise

32   be physically fragmented.

33   2. Here we introduce the geohabnet R package, which evaluates the likely importance of

34   locations for the spread of species through habitat landscapes. Unlike most software

35   analyzing landscape connectivity, geohabnet incorporates key factors such as dispersal

36   probability and habitat availability in a network framework. These factors are often

37   needed to better understand habitat connectivity for host-dependent species, such as

38   pathogens, arthropod pests, or pollinators.

39   3. geohabnet uses publicly available or user-provided datasets, six network centrality

40   metrics, and a user-selected geographic scale (global, national, or regional). We provide

41   examples using geohabnet for surveillance prioritization of emerging plant pests in Africa

42   and the Americas. These examples illustrate how users can apply geohabnet for their

43   species of interest and generate maps of the estimated importance of geographic locations

44   during a species' spread.

45   4. geohabnet provides a quick, open-source, and reproducible baseline to quantify a species'

46   habitat connectivity across a wide range of geographic scales and evaluates potential

47   scenarios for the expansion of a species through habitat landscapes. Ultimately,

48   geohabnet could support biosecurity programs, invasion science, and conservation

49   biology in prioritizing management efforts for transboundary pathogens, pests, or

50   endangered species.

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INTRODUCTION

Understanding the geographic structure of habitat networks, shaped by landscape patterns of host availability and abiotic factors, supports the conservation of endangered species. The study of habitat networks also provides useful information for invasion biology, identifying locations important for programs protecting ecosystems from the harmful effects of invasive species. Species distribution models (SDMs) are widely used in ecology to map a species' potential geographic range, but few explicitly incorporate dispersal when quantifying habitat suitability for host-dependent species such as invasive arthropod herbivores, plant pathogens, or endangered pollinators (Schmitt *et al.*, 2017, Naimi & Araújo, 2016, Velazco *et al.*, 2022). Numerous algorithms exist for estimating landscape connectivity, which are commonly incorporated into biodiversity conservation planning (Brennan *et al.*, 2022, Drielsma *et al.*, 2022, Fletcher *et al.*, 2011). In landscape epidemiology and invasion science, quantifying habitat connectivity is a component to prioritize surveillance and mitigation efforts by identifying vulnerable areas with high epidemic or invasion potential (Radici *et al.*, 2023, Jousimo *et al.*, 2014, Margosian *et al.*, 2009, Meentemeyer *et al.*, 2012). However, there are few options in R for calculating habitat or landscape connectivity that consider potential species dispersal and geographic host distribution simultaneously (Rimbaud *et al.*, 2024, Jones *et al.*, 2021). Both components are key to mapping the spatial spread and potential distribution of host-dependent species, particularly plant pathogens, arthropod parasites (Xing *et al.*, 2020, Cunniffe *et al.*, 2015), endophytes, and pollinators (Bishop, 2025).

Over 100 metrics have been proposed to measure habitat or landscape connectivity (Rayfield *et al.*, 2011, Kindlmann & Burel, 2008, Keeley *et al.*, 2021). However, few open-source resources are available for applying most of these metrics. In landscape ecology, connectivity

75   metrics are generally based on three widely-used approaches: least-cost corridor analysis

76   (McRae, 2006, Lewis, 2025), resistance surface modeling or electrical circuit theory (McRae *et*

77   *al.*, 2008), and network-based landscape connectivity (Urban & Keitt, 2001). Over the past two

78   decades, interest in applying network theory to invasion ecology and landscape epidemiology

79   has been growing (Mestre & Silva, 2023, Frost *et al.*, 2019). However, there are few flexible

80   tools that readily harness the benefits of a network-based approach and geographic information

81   systems for landscape connectivity. Existing network-based tools often assess landscape

82   connectivity at the patch level (Chubaty *et al.*, 2020, Mestre & Silva, 2023, Hesselbarth *et al.*,

83   2019), which may underrepresent habitat heterogeneity of realistic landscapes (Spanowicz &

84   Jaeger, 2019).

85   To address this gap, we introduce the geohabnet R package, a geographically explicit

86   network-based tool that maps landscape or habitat connectivity of both host-dependent and host-

87   independent species. Habitat connectivity for host-dependent species often depends on the spatial

88   distribution of suitable abiotic factors (widely addressed by SDMs), compatible host species (and

89   other biotic factors), and natural or human-mediated opportunities for dispersal. To calculate

90   habitat connectivity in geohabnet, a habitat network represents a set of geographic locations in a

91   habitat landscape (nodes), and weights of connections between nodes are proportional to the

92   probability of a species' movement between habitat locations (Fig. 2). The probability of species

93   movement in geohabnet depends on habitat availability, which can be determined with SDMs

94   based on biotic or abiotic suitability, as well as dispersal ability. A network-based approach

95   offers powerful perspectives for movement ecology in complex, real-world landscapes, ranging

96   from identifying nearest neighbors to determining shortest paths between physically distant

97   regions (Garrett *et al.*, 2018, Moslonka-Lefebvre *et al.*, 2011). SDMs have been applied widely

98   to predict species' potential distributions based on abiotic factors. The case studies provided

99   below focus on habitat quality defined in terms of host availability and incorporate dispersal,

100   providing a first approximation for habitat connectivity. Inputs in geohabnet can also be coupled

101   with SDMs to provide an integrated perspective on habitat connectivity.

102   Applying this network perspective on habitat connectivity, geohabnet allows users to ask

103   fundamental questions like: once an invasive species has reached a targeted location, how easily

104   may the invasive species spread from the focus location to other areas in a landscape? We

105   illustrate the use of geohabnet with three case studies. These examples focus on habitat

106   connectivity for invasive, re-emerging, or new pathogens or pests because of their increasing

107   local and global relevance to natural plant ecosystem health (Savary *et al.*, 2019, Diagne *et al.*,

108   2021, MacLachlan *et al.*, 2021). In these examples, geohabnet harnesses publicly available or

109   user-supplied data for host distributions relevant to plant pathogens and pests [e.g., (Tang *et al.*,

110   2024)], evaluates potential scenarios for pathogen or pest dispersal, and generates regional maps

111   of habitat landscape connectivity for surveillance prioritization.

112

113   **FUNCTIONALITY**

114   **Implementation.** geohabnet 2.2 provides R users with two main functions,

115   sensitivity_analysis() and msean(), to calculate the habitat connectivity of locations in a

116   landscape. These functions allow evaluation of habitat connectivity across a set of specified

117   habitat, dispersal, and geographic parameters, and commonly used network metrics (Fig. 1).

118   Users can install geohabnet with the following code: install.packages("geohabnet") for the stable

119   version in CRAN (https://cran.r-project.org/web/packages/geohabnet/index.html) or

120   devtools::install_github("GarrettLab/HabitatConnectivity", subdir = "geohabnet") for the

121 development version in GitHub (https://github.com/GarrettLab/HabitatConnectivity). Installation

122 and functions of geohabnet have been successfully tested in R version 4.3.0-4.3.3 on Windows,

123 MacOS, and Linux operating systems, as well as High-Performance Computing settings (like the

124 University of Florida HiPerGator).

125   Once installed, users are required to download the parameters.yaml file in their working

126 directory with commands: library(geohabnet) and get_parameters(). Users can manually change

127 the values of each parameter in this file, set the newly specified values in R with

128 set_parameters(), and run sensitivity_analysis(). In the parameters.yaml file, users can provide

129 the directory location of the habitat availability map, which is assumed to be in raster format.

130   Alternatively, msean() users provide a SpatRaster object as input and modify parameter

131 values directly in the function. These functions have been successfully tested using maps of

132 habitat quality in the form of host availability from publicly available databases like

133 EARTHSTAT (Monfreda *et al.*, 2008), MAPSPAM (IFPRI, 2019), CROPGRIDS (Tang et al.,

134 2024), CroplandCROS (vignette 1), GBIF (vignette2), as well as custom-built by the user. The

135 types of data for habitat quality supported by geohabnet should preferably range from 0 (lowest

136 habitat quality) to 1 (highest habitat quality), representing host availability, environmental

137 suitability, or a combination of habitat factors.

138   A third way of customizing parameters in geohabnet is through the GHN app. The GHN

139 package boosts the geohabnet functionality into a straightforward interactive dashboard for

140 habitat connectivity (Fig. 1). This user-friendly graphical interface (i) allows easy customizations

141 of all parameters and sub-parameters in the 'Customize Input Tab', (ii) executes the habitat

142 connectivity analysis, and (iii) generates downloadable visualizations and outcomes in the 'View

143 Outputs Tab'. To use the GHN app, users must install and load the GHN package and run the

144 'run_app()' function in RStudio. Upon successful execution, a new web window will launch,

145 presenting the user with access to the interface.

```
 1  default:
 2    HCI parameters:
 3      Habitat: [C:/Users/Documents/Habitat-map-example.tif] # Insert here location of a raster file
 4      HabitatDensityThreshold: [0.00015]
 5      AggregationStrategy: [sum, mean]
 6      DistanceStrategy: "geodesic"
 7      Resolution: 12
 8      GeoExtent:
 9        global: TRUE
10        customExt: [-115, -75, 5, 32] # Ignored, when global = TRUE
11      LinkThreshold: [0.0001]
12      DispersalKernelModels:
13        InversePowerLaw:
14          beta: [0.5, 1, 1.5]
15        NegativeExponential:
16          gamma: [0.05, 1, 0.2, 0.3]
17      NetworkMetrics:
18        InversePowerLaw:
19          metrics: ["betweeness", "NODE_STRENGTH", "Sum_of_nearest_neighbors", "eigenVector_centrAlitY"]
20          weights: [50, 15, 15, 20]
21          cutoff: -1
22        NegativeExponential:
23          metrics: ["betweeness", "NODE_STRENGTH", "Sum_of_nearest_neighbors", "eigenVector_centrAlitY"]
24          weights: [50, 15, 15, 20]
25          cutoff: -1
26    PriorityMaps:
27      OutDir:
28      MeanCC: TRUE
29      Difference: TRUE
30      Variance: TRUE
```

146

147 **Fig. 1.** A) Default values of ten parameters for the sensitivity_analysis() function in

148 parameters.yaml. HCI refers to the habitat connectivity index, adapted from Xing et al. (2020).

149 **Outcomes.** Either sensitivity_analysis() or msean() will produce a map for each of the three

150 main outcomes of a habitat connectivity analysis. Both functions perform a sensitivity analysis

151 by supporting the evaluation of different combinations of up to 10 parameters and 24 sub-

152 parameters (Fig. 1) in each main outcome map. The first map represents the mean habitat

153 connectivity calculated across every combination of parameters specified by the user. This map

154 indicates the importance of locations in the potential spread of a species in a landscape,

155 considering the geographic pattern in habitat quality and dispersal probabilities of the target

156 species. The second map summarizes the variance in habitat connectivity across the same

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157   combination of specified parameters. This map helps to evaluate how habitat connectivity of a

158   location remains consistent (no variance) or changes with different values of the model

159   parameters. The third map indicates the difference in ranks between mean habitat connectivity

160   and habitat quality. This map helps identify which locations could allow a species to spread more

161   readily (positive values) or not (negative values), compared to an analysis relying solely on

162   habitat quality. Note that users can choose which of these three maps are generated when

163   specifying so in sensitivity_analysis().

164   Additional outcomes generated by sensitivity_analysis() or msean() include a spatRaster

165   object for each outcome map and an adjacency matrix for each dispersal parameter combination.

166   The spatRaster objects can be used for integration with other geographically explicit ecological

167   analyses, customized visualization, or saving a copy of maps. Adjacency matrices can be used

168   for more detailed analyses (e.g.,

169   https://github.com/jrobledob/2024_California_Rosaseae_GBIF_and_Croplandcrops), such as

170   evaluating invasion simulations and management scenarios in the Impact Network Analysis

171   (INA) package (Garrett, 2021).

172   **Unit tests.** We used the `testthat` package to incorporate unit tests. Current test coverage at

173   the time of submission is 73.16% in geohabnet 2.1.3, including system and unit tests. We are

174   updating version 2.2 to have comparable coverage of unit tests.

175

176   **CASE STUDIES**

177   To illustrate the functionality of geohabnet, we developed three case studies evaluating the

178   potential invasion of plant pests on crop-specific landscapes. A vignette of each case study is

179   available at https://garrettlab.github.io/HabitatConnectivity/

180   **Case study 1**. In this case, we created a hypothetical habitat landscape with each grid cell

181   representing a spatial unit, geographic location, and node (Fig. 2A). Case study 1 helps users

182   better understand a habitat connectivity analysis before applying it to more complex, realistic

183   landscapes. Vignette 1 provides a simple stepwise approach to calculate the habitat connectivity

184   of locations in this hypothetical habitat landscape. Briefly, the habitat landscape is transformed

185   into a species movement network (Fig. 2B), where each node represents a habitat location and

186   link weights are proportional to the probability of a species movement between locations in the

187   landscape. The importance of each node in the likely spread of a species across the network is

188   measured using a network metric (Fig. 2C). The importance of each node across a selected set of

189   network metrics is then used to map the mean habitat connectivity in the landscape (Fig. 2D-G).

190   We used the msean() function in geohabnet to easily reproduce this habitat connectivity analysis.

191   This example visually illustrates how four network metrics provide different perspectives on the

192   potential roles of locations during a species spread in a hypothetical habitat landscape (Fig. 2D-

193   G). Note that a location with high habitat quality will tend to rank among the most important

194   locations in the landscape across different network metrics. The importance of most locations

195   with low habitat quality largely increased or decreased depending on the network metric used.

196   We also generated an ensemble of possible spread scenarios based on a range of dispersal

197   parameters and four network metrics, generating a mean habitat connectivity map (Fig. 2H).
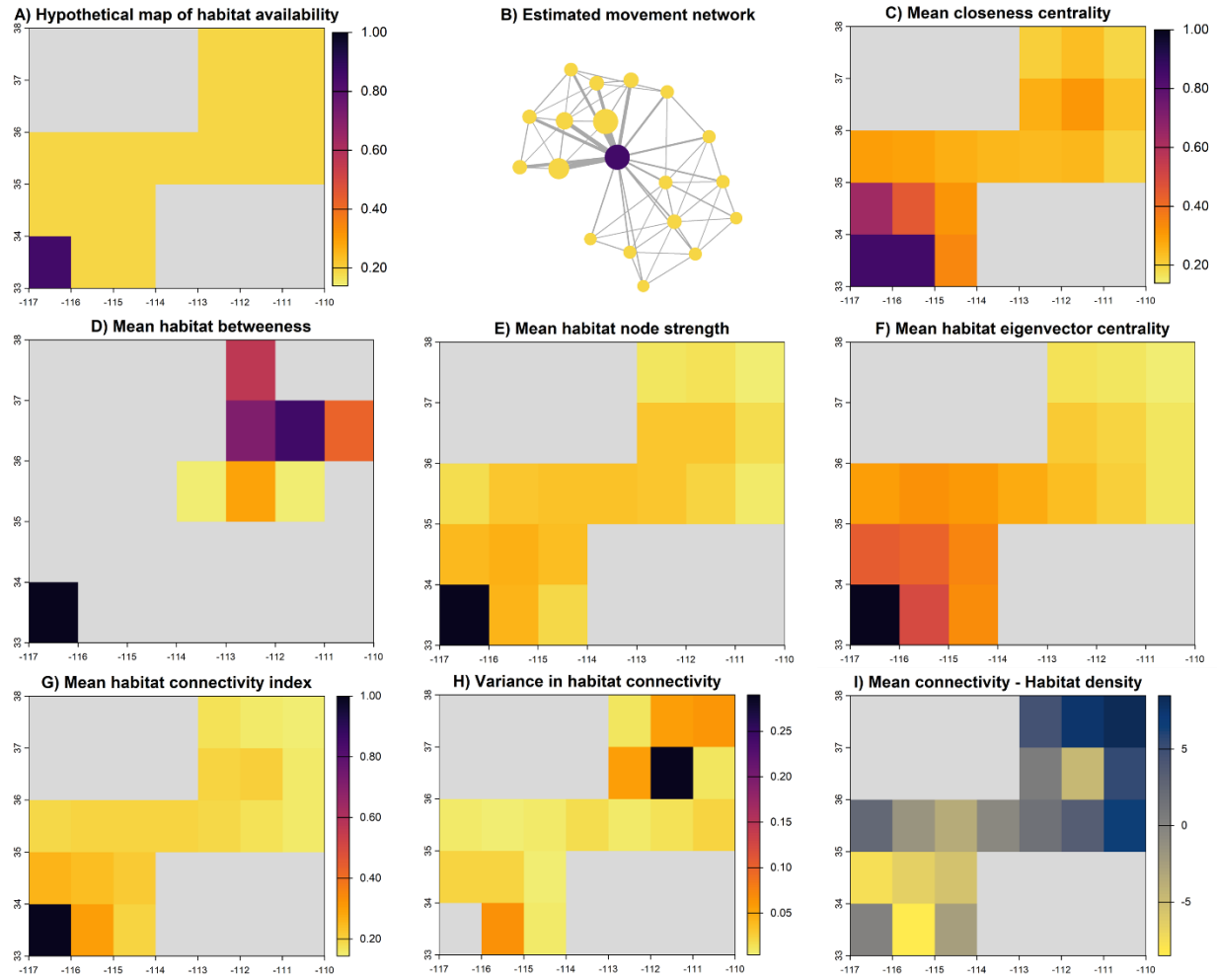
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Fig. 2. General components of a habitat connectivity analysis in a hypothetical landscape using

geohabnet 2.2. Panel A shows the hypothetical distribution of habitat availability for a species,

considering both biotic and abiotic suitability. Panel B illustrates movement probability (link

width) between habitat locations (nodes). Panels C to F show the importance of habitat locations

based on individual network metrics. Panel G shows the mean habitat connectivity across

network metrics and dispersal parameters. Panel H is the variance in habitat connectivity across

network metrics and dispersal parameters. Panel I is the difference in ranks between mean

habitat connectivity (G) and habitat availability (A).

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208   **Case study 2.** This case study aims to illustrate the use of geohabnet for mapping habitat

209   connectivity at a national, regional, or continental scale. For the threats posed by emerging crop

210   pathogens and pests, host availability is an important risk factor. Cropland connectivity can be

211   used as an approximation for understanding potential invasive spread of host-specific pathogens

212   and pests in a realistic landscape. Here, geohabnet helped us identify candidate priority locations

213   for regional surveillance of potential invasions of pathogens and pests affecting sorghum in sub-

214   Saharan Africa and yam in West Africa (Vignette 2).

215   We first downloaded geographic data on cropland harvested area for sorghum and yam in

216   sub-Saharan Africa from MAPSPAM 2017 (IFPRI, 2019), using the crop_spam() function in the

217   geodata package. We used the resulting cropland density map in the msean() function in

218   geohabnet to perform a sensitivity analysis based on cropland connectivity. We set

219   link_threshold = 0.00001 and hd_threshold = 0.0025 (Xing et al., 2020). We customized the

220   default weights of the four network centrality metrics in Fig. 1A: betweenness centrality

221   (weighted at 50%), node strength (weighted at 15%), sum of nearest neighbors (weighted at

222   15%), and eigenvector centrality (weighted at 20%).

223   For sorghum in Africa, high cropland connectivity was identified in southern Niger, northern

224   Nigeria, and northern Cameroon. For yam in West Africa, the analysis identifies south-eastern

225   Nigeria and locations near Lake Kossou (Ivory Coast) as highly connected locations.

226   Along with information on pests and pathogens in these locations, this analysis can also help

227   pathogen and pest surveillance in a region. For example, the spotted stem borer (*Chilo partellus*),

228   a damaging pest of sorghum, is now present in Cameroon and prevalent in several countries in

229   East and South Africa (van den Berge, 2023). Frequent monitoring of the landscape along the

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230   border between northern Cameroon and Nigeria could be implemented to prevent the

231   introduction of this pest into sorghum and other cereal production in West Africa.
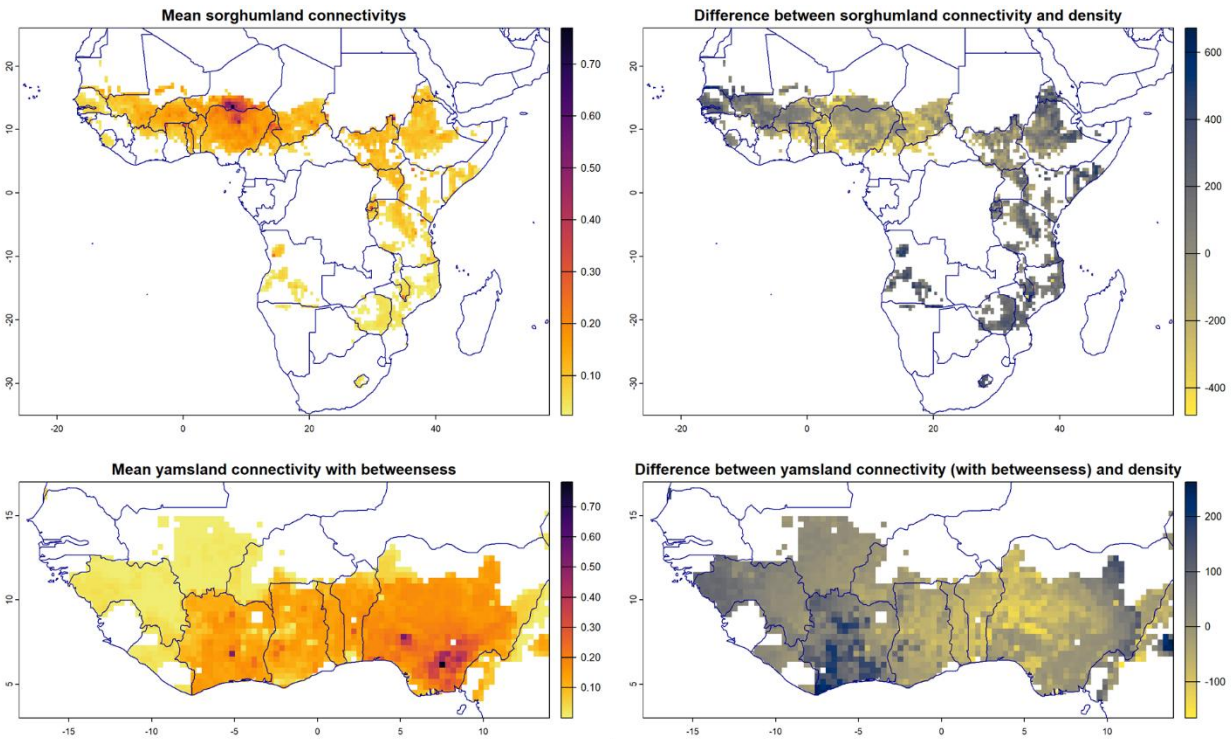

233   **Fig. 3.** Habitat connectivity analysis in terms of host availability for sorghum in sub-Saharan

234   Africa (A, B) and yam in West Africa (C, D).

235   **Case study 3.** This case study aims to illustrate habitat connectivity analysis where habitat is

236   widely available across a region, specifically maize (*Zea mays*) in the Americas (Vignette 3). We

237   downloaded global maps of maize forage and maize from CROPGRIDS (Tang et al., 2024) and

238   combined these layers to produce a cumulative map of host availability. We provided this global

239   map of maize availability in the parameters.yaml for sensitivity_analysis(). We set the host

240   density threshold to 0.25%, link weight threshold to 0.000001, and spatial resolution to 12

241   degrees. To illustrate cropland connectivity resulting from potential long-distance dispersal, we

242   estimated dispersal probabilities between locations using the inverse power law model. In a

243   sensitivity analysis, we assessed three values of the dispersal parameter (β = 0.5, 1, and 1.5).

244   There is a high mean wheat cropland connectivity in major production areas where maize is

245   densely cultivated, including the northern United States, central Mexico and southwestern Brazil

246   (Fig. 4A). Despite maize being less densely cultivated in the Andes in Peru, Ecuador and

247   Colombia, these areas were more important based on cropland connectivity than when

248   considering maize cropland availability alone (Fig. 4B). A region from Mesoamerica to Panama

249   and the Andes may serve as a bridge connecting major production areas in the mainland

250   Americas and potentially facilitating the spread of maize-specific diseases.

251   This map of maize connectivity in the Americas can help in monitoring the gradual spread of

252   invasive or emerging maize-specific pests if they are introduced to the continental mainland

253   Americas from other areas. An example of emerging diseases is maize lethal necrosis (MLN),

254   caused by a co-infection of maize by *Maize chlorotic mottle virus* and Potyviruses. MLN has

255   been reported with scattered occurrences in the Americas since 1974, but its recent emergence in

256   Africa and Asia in 2011 makes this disease a global risk concern for maize production

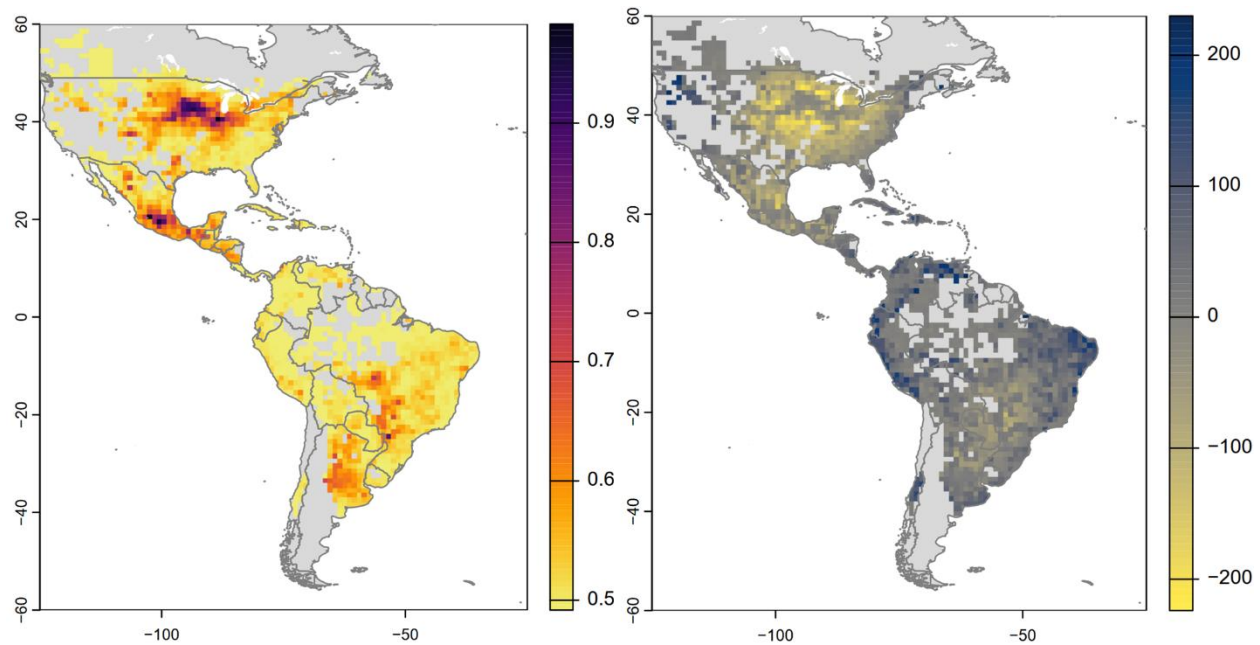257   (Boddupalli *et al.*, 2020).

Fig. 4. Panel A shows the mean maize cropland connectivity in the Americas across parameter values for long-distance dispersal. Panel B shows the difference in ranks between mean maize cropland connectivity and cropland availability.

DISCUSSION

The geohabnet package is a component of the R2M Plant Health Toolbox (https://www.garrettlab.com/r2m/), which aims to provide rapid geographic risk assessments for surveillance and mitigation of plant pathogen and pest impacts.

As part of an open-source ecosystem, authors welcome suggestions and contributions to add new functionalities to make geohabnet more general.

Case studies 2-3 illustrate how agricultural connectivity may be important in the context of emerging epidemics or invasive spread of crop-specific pests. In these case studies, host connectivity is not specific to a pest species because estimates of dispersal parameters are often unavailable. Host connectivity is thus a first approximation to understanding the potential spread

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273   of new pests. When estimates of the dispersal parameters of a target species are unknown,

274   stakeholders can evaluate a range of possible scenarios for dispersal parameters in a sensitivity

275   analysis, as in case studies 2 and 3.

276   A more complete analysis of habitat connectivity can be constructed by incorporating, for

277   example, geographic information of wild hosts, abiotic factors, and management interventions in

278   the landscape. Prospectively, geohabnet can be integrated with a wide range of available SDMs

279   (Velazco et al., 2022, Schmitt et al., 2017). More realistic analyses could include stochasticity as

280   a component of habitat connectivity. Effective strategies for species management would benefit

281   from time series analysis of how habitat connectivity changes in a year or over decades,

282   harnessing the growing availability of geographic biodiversity information (Meyer *et al.*, 2015).

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

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DATA AVAILABILITY STATEMENT

geohabnet is available in CRAN at https://cran.r-project.org/web/packages/geohabnet/index.html

and GitHub at https://github.com/GarrettLab/HabitatConnectivity

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