Documentation

Reconnect approach

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The "Rapid Evaluation of Multispecies Connectivity" (Reconnect) approach, is a scalable and generalizable workflow to rapidly generate and evaluate ensemble connectivity maps for a range of species with different habitat needs, in order to support spatial prioritization for connectivity conservation management.

Approach Overview

The Reconnect approach (Figure 1) allows for the simultaneous computation of connectivity indicators (Table 1) for multiple species based on simple habitat distribution maps and a parallel implementation of moving windows. Connectivity results in moving windows can be aggregated to generate ensemble connectivity maps at pixel-, patch-, or landscape-level. Finally, connectivity results for multiple species can be evaluated by ranking connectivity values for each species in any region of interest and comparison with a target connectivity value ("Conservation target" in Figure 1).
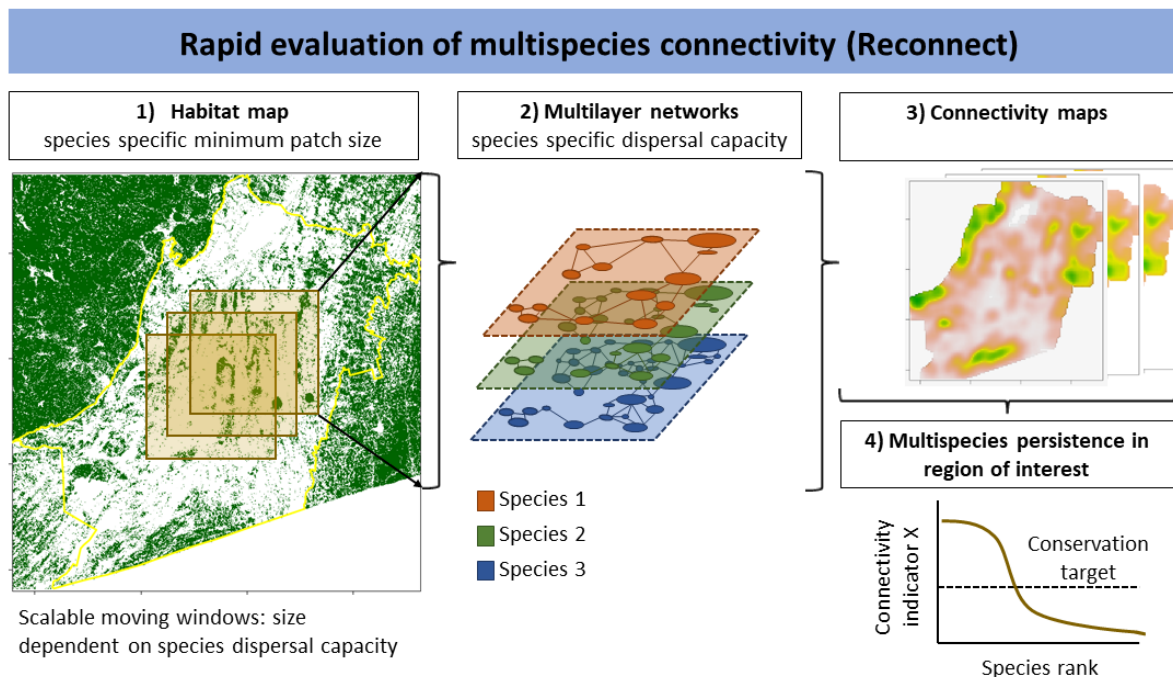
Figure 1. Rapid Evaluation of Multispecies Connectivity (Reconnect) approach. 1) The basic data input for the Reconnect approach is a species (or ecoprofile) specific, binary habitat map that can be determined *a priori*[1–4] or *a posteriori* from species distribution models[5–9]. Note that maps of protected areas or other effective area-based conservation measures (OECMs) could be used as well[10,11]. **2)** Multiple habitat maps can be "stacked" and multilayer habitat networks[10,12,13] can be extracted, in which links between habitat patches are determined using estimates of species-specific dispersal capacities[10]. These multilayer habitat networks can be computed in moving windows of relevant size[14] and variable

spatial overlap[15]. **3)** Multiple connectivity functions can be defined in a simple inifile and computed simultaneously for multiple species in the moving windows. Moving window results can then be aggregated into mosaics, i.e. coherent maps of connectivity at pixel-level, patch-level or landscape-level[16] for the species of interest. **4)** The resulting maps can be used to evaluate multiple connectivity indicators for the multiple species, for example by ranking species connectivity values and comparing them with *a priori* definitions of a target connectivity value ("Conservation target" in Figure 1). This approach allows to summarize the number or fraction of species deviating from target connectivity values and allows the identification of vulnerable species with critically low connectivity values in any region of interest.

Reconnect R-tool

The Reconnect approach is implemented in the **Reconnect R-tool**, which works with one inifile and four sets of functions:

1. inifile (Reconnect_inifile.xlsx): where connectivity functions, dispersal capacities and habitat needs can be specified. Any function that takes either a binary habitat raster and optionally, resistance surface (e.g. ".tif"), shapefile (e.g. ".shp"), vector of patch areas and distance matrices as input (e.g. ".csv") can be specified.

2. Reconnect_functions
   Reconnect - core, wrapper and summary functions, as well as general functions for processing geographic data.
   - wrapper function (Reconnect_wrap): specifies scale (window size), resolution in and increment of moving windows, which are computed with a parallel implementation[17]. The defined spatial grain and extent in any connectivity assessment should match the species and conservation needs of interest[14,16]. For example, the side length of square moving windows could be set to 8,700 m (radius = 4,350 m), which results in landscape areas of ~75 km^2, similar to what has been used in previous research[14,18,19]. A window overlap of 1,500 m allows for landscape-level connectivity maps at an effective resolution of 1.5 km. Dividing the study area into non-overlapping spatial planning units[19] is also possible and less computationally demanding.
   - core function (Reconnect_core): applying connectivity functions (inifile) in moving windows. **Within moving windows, multilayer habitat networks[10,20]** can be extracted based on species-specific habitat needs and dispersal capacities. Hence, in one run, connectivity values for multiple species can be generated simultaneously.
   - summary function (Reconnect_summary): aggregating moving window results into a coherent raster or shapefile. **Output can be generated at the pixel-level, patch-level or landscape-level,** depending on the connectivity function (see below).

3. CONN_functions
   Functions for calculating a set of connectivity indicators (Table 1). **Distances** can be calculated from edge to edge or centroid to centroid, and can be measured as Euclidean or resistance (if a resistance layer is provided). **Dispersal probabilities**

depend on a distance (d) and a dispersal capacity (α) in one of three common dispersal probability functions:

- negative exponential[10,19,21]

$$p_{ij} = exp(-(\tfrac{1}{\alpha})d_{ij}) \tag{1}$$

, where p_{ij} describes the probability of dispersing between patch i and j, α is usually the species-specific mean gap crossing distance[10,21,22] and *dij* is the distance between patch *i* and patch *j* in the habitat network.

- linear decay[19]

$$p_{ij} = 1 - (\tfrac{d_{ij}}{\alpha}) \; for \; d_{ij} < \alpha \; and \; p_{ij} = 0 \; for \; d_{ij} \geq \alpha \tag{2}$$

, where p_{ij} describes the probability of dispersing between patch i and j, α is usually the species-specific maximum gap crossing distance[10,21,22] and *dij* is the distance between patch *i* and patch *j* in the habitat network.

- log-sech[18,23]

$$p_{ij} = \tfrac{2}{\pi} arctan\left[(\alpha/d_{ij})^{1/(\frac{1}{\beta-1})} \right] \; for \; d_{ij} \geq 0 \tag{3}$$

where p_{ij} describes the probability of dispersing between patch i and j, α is usually the species-specific mean gap crossing distance[10,21,22], β describes the tail of the dispersal kernel (by default set to 1.77)[23] and *dij* is the distance between patch *i* and patch *j* in the habitat network.

- quantile[1,24,25]

$$p_{ij} = exp((\tfrac{log(q)}{\alpha})d_{ij}) \; for \; q > 0 \; and \; \leq 1 \tag{4}$$

, where p_{ij} describes the probability of dispersing between patch i and j, *dij* is the distance between patch *i* and patch *j* in the habitat network and α is usually the species-specific median or maximum gap crossing distance, associated with a median or maximum quantile q (e.g. 0.5 and 0.1, respectively). The quantile value describes the probability covered by the "tail-distance" on the flat tail of the dispersal-distance function[1,24,25].

4. MPC_functions
   Functions for calculating metapopulation capacity (MPC) and -related indices from binary habitat distribution maps (Table 1). Distances and dispersal probabilities can be calculated as in "CONN_functions". A detailed report on the metapopulation capacity indicator and related indices can be accessed here: https://oehrij.shinyapps.io/MPC_report/

5. NLMC_functions
   Functions for generating simulated and neutral landscapes that are based on the algorithm by Saura and Martinez-Millan 2000[26] implemented in the R-package NLMR[27].

Connectivity Indicators

This set of connectivity indicators can be calculated by using the "CONN_functions" and "MPC_functions" in the Reconnect R-tool, on the basis of habitat or protected area distribution maps, species-specific habitat needs and dispersal capacities.

Table 1. Selected key-set of connectivity indicators. Distance type: can be Euclidean or scaled by a resistance surface[1,28,5]. Scale: the scale at which indicator is typically calculated (pixel-, patch-, or landscape-level). Landscape-level indicators can also be calculated at patch level using the "general patch importance" computation (I_{pi}), or in the case of metapopulation capacity, the dominant eigenvector value for patch i (λ_i). Note that patch-level indicators can usually be aggregated at the landscape-level, using any aggregation function of interest (e.g. mean, range, variation). Note that the Reconnect approach (Figure 1) is not limited to these indicators but can be implemented with any connectivity indicator that is computable on the basis of habitat, protected area or resistance surface maps.

Nr	Abbre-viation	Description	Formula	Unit [value range]	Interpretation	Scale and distance type
1	**MPC**	Metapopulation Capacity[22,29,30]	$$MPC = \lambda_m$$ $$m_{ij} = \begin{cases} f(d_{ij})a_j a_i^x & i \neq j \\ a_j a_i^x & i = j \end{cases}$$, where λ_m is the leading eigenvalue of a square 'landscape matrix' m, in which elements m_{ij} reflect rates of change for the occupancy of patches i (p_i) as a function of patch attributes (often patch area in m², a_i and a_j), a dispersal probability function of interpatch distance $f(d_{ij})$ and an extinction probability constant x (commonly set to 0.5).	no unit $[0,\lambda_{max}]$, where λ_{max} corresponds to the leading eigenvalue of the maximum landscape matrix, i.e. where the rates of change of patch occupancy is 1 for all patches.	-metapopulation carrying capacity, based on area and connectance of habitat -focus on potential long-term species persistence[22,29,30]	- landscape - Euclidean and resistance

2	**ECA**	Equivalent Connected Area index[31], based on the probability of connectivity index (PC[32])	$$ECA = \sqrt{\sum_{i=1}^{n}\sum_{j=1}^{n} a_i a_j p_{ij}^*}$$, where n is the total number of habitat patches in the landscape, ai and aj are attributes of habitat patches i and j (commonly area) and pij* is the maximum product probability of dispersal between patches i and j.	unit of a (e.g. area) [0,Al] , where Al is the attribute (e.g. area) of the entire landscape.	- the size of a single habitat patch that would provide the same probability of connectivity than the actual habitat pattern in the landscape[31] - focus on connectivity of habitat, and potential species dispersal	- landscape - Euclidean and resistance
3	**ECA$_{Ap}$**	Fraction of habitat that is connected (ECA divided by the total habitat area)	$$ECA_{Ap} = \frac{ECA}{Ap}$$, where Ap is the total area of habitat in a given landscape.	no unit [0,1]	- size of equivalent connected area (ECA) relative to maximum possible with a given habitat area - focus on underused connectivity potential	- landscape - Euclidean and resistance
4	**ECA$_{Al}$**	Fraction of habitat that is connected (ECA divided by the total landscape area, cf. ProtConn[33] index)	$$ECA_{Al} = \frac{ECA}{Al}$$, where Al is the total area of a given landscape.	no unit [0,1]	-size of equivalent connected area (ECA) relative to maximum possible in a landscape -focus on underused connectivity potential	- landscape - Euclidean and resistance
5	**BC**	Betweenness centrality[1,34,35]	$$BC_v = \sum_{i \neq j, i \neq v, j \neq v} \frac{g_{ivj}}{g_{ij}}$$, where givj is the total number of shortest paths between each pair of habitat patches ij going through a focal patch v in the habitat network. gij, is the total number of all the shortest paths between each pair of habitat patches ij in the habitat network.	no unit $[0, \frac{(n-1)(n-2)}{2}]$, where n corresponds to the number of patches in the landscape.	-number of shortest paths between each pair of habitat patches passing through a focal patch -focus on the degree to which a habitat patch is a stepping stone at short and long distances in the habitat network[36]	- patch - Euclidean and resistance
6	**ND**	Node Degree[37]	$$ND_v = \sum_{j \neq v} e_{vj}$$ $$e_{vj} = \begin{cases} 1 & p_{vj}^* > c \\ 0 & p_{vj}^* \leq c \end{cases}$$, where evj denotes a habitat patch j connected to the	no unit [0,n-1] , where n corresponds to the number of patches in the landscape.	-number of other habitat patches connected to a focal patch -focus on the number of patches reachable within a given distance[37], the degree to which a patch is a stepping stone at short distances in the habitat network	- patch - Euclidean and resistance

			focal patch v. A habitat patch can be considered connected (evj = 1) if pij*, the maximum product probability of dispersal between patches j and v is greater than a threshold probability c.			
7	**invCR**	Omnidirectional inverse cumulative resistance[1]	$$\frac{1}{CR} = \frac{n}{\sum_{k=1}^{n} CR_k}$$, where n is the number of pairs of locations selected in a given landscape and CR_k is the cumulative resistance of the shortest paths between each pair of locations k.	variable unit $(0,+\infty)$	-ease of traversability of the landscape -focus on contribution to global, omnidirectional connectivity	- pixel and landscape - resistance
8	**I_rel**	Indicator value relative to minimum threshold[14,30,38]	$$I_{rel} = \frac{I}{I_{min}}$$, where I is the indicator value of the entire habitat network in a landscape and Imin is the estimated minimum value required for species persistence.	no unit $[0,+\infty)$	-indicator value, relative to an estimated minimum for species persistence -focus on potential species persistence[22,29,30]	- landscape - Euclidean and resistance
9	**I_v**	General estimate of patch importance[32]	$$I_v = \frac{I - I'}{I} \times 100$$, where I is an index value when habitat patch v is present and I' is the same index value when patch v is not present in the landscape.	no unit $[0,100]$	-the degree to which a patch contributes to the connectivity value of the habitat network	- patch - Euclidean and resistance
10	**MPC_i**	Patch importance: leading eigenvector at position i[22]	$$MPC_i = \lambda_{mi}$$ $$m_{ij} = \begin{cases} f(d_{ij})a_j a_i^x & i \neq j \\ a_j a_i^x & i = j \end{cases}$$, where λ_{mi} is the leading eigenvector at position i, for patch i of a square 'landscape matrix' m, in which elements mij reflect rates of change for the occupancy of patches i (pi). ai and aj are patch attributes (often patch area in m^2), f(dij) is a dispersal probability function of interpatch distance x denotes an extinction probability constant (commonly set to 0.5).	no unit $[0,\lambda_{max}]$, where λ_{max} corresponds to the leading eigenvalue of the maximum landscape matrix, i.e. where the rates of change of patch occupancy is 1 for all patches.	-the degree to which a patch contributes to the metapopulation capacity value of the habitat network	- patch - Euclidean and resistance

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