



Amphibian and Reptile Conservation

RESEARCH REPORT 18/01

Jersey multi-species distribution, habitat suitability & connectivity modelling

Appendix C

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States 
of Jersey

**amphibian and reptile
conservation**



Appendix C – Supplementary Methods

Overview

This document provides details on the selection, justification and use of methods associated to the main report. These include the following steps:

1. **Selection of species** to be used in the analysis.
2. **Species distribution modelling** to identify the suitability of Jersey's landscape for a set of selected species, investigate the parameters influencing suitability for those species and to provide the basis for a resistance surface during connectivity modelling.
3. Identification of the most important areas in Jersey for wildlife (referred to as **Habitat Concentration Areas** (HCAs)) using a binary threshold and fragmentation metrics.
4. **Connectivity modelling** to identify the most likely corridors through which species of varying dispersal abilities and ecological life-histories may move and disperse.
5. **Prioritisation** of HCAs based on their contributions to connectivity.

Software and Data

This study utilised the following software:

- MaxEnt v3.4.1 (Phillips et al. 2018) for species distribution modelling
- ENMTools v1.4.4 (Warren et al. 2010) for assessing correlations between predictor variables
- The freeware known as 'R' v.3.4.4 (R Core Team 2018) for data visualisation and statistical analyses
- ArcGIS Pro v.2.0.1. (ESRI 2017a) for compiling, editing and visualising maps
- ArcMap and ArcCatalog v.10.5.1 (ESRI 2017b) for conducting connectivity analyses
- Linkage Mapper v.1.1.1 (McRae and Kavanagh 2011) for conducting connectivity analyses
- Conefor v.2.6 (Saura and Torné 2009) for prioritising landscape components for protection

Data sources are as follows:

- GIS files have been provided by the Department of Natural Environment, Growth Housing and Environment, States of Jersey, Jersey Water and The National Trust for Jersey.
- Species occurrence data were provided by the Jersey Biodiversity Centre, Société Jersiaise Botany, Mycology, Entomology and Ornithology sections, Jersey Amphibian and Reptile Group as well as private naturalists.
- Bioclimatic data were downloaded from WorldClim (Fick and Hijmans 2017).

Throughout the document, source GIS files are displayed in *purple italics*, and tools are indicated in **UPPERCASE DARK RED TEXT**.

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Step 1: Selection of species

A preliminary selection of study species was identified through discussion with stakeholders including local species experts, applying the following criteria:

1. Species is not completely widespread throughout the island
2. Species records are
 - a. not heavily biased by survey effort, **or**
 - b. any survey biases can be accounted for
3. Sufficient records of high accuracy¹ are available to construct a species distribution model
4. Species are
 - a. of conservation concern; protected or proposed for protection under either the Conservation of Wildlife Law (Jersey) 2000 or the Conservation of Wildlife (Protected Plants) (Jersey) Order 2009, **or**
 - b. representative of the distribution of species or habitat types or conservation concern otherwise unaccounted for.

Data for those species identified were then sourced from the Jersey Biodiversity Centre (JBC) and local taxonomic specialist groups such as the Société Jersiaise sections. Data was filtered to include only those records between 2007 and 2017, those considered to have accurate identification and a geographic accuracy of ≤ 10 metres. Some species that had multiple records but that were highly clustered were removed as spatial filtering would result in very few records.

Species included plants, fungi, insects, volant and non-volant mammals, reptiles and amphibians. Birds were excluded due to a lack of data on nesting sites and their ability to traverse across the island with ease. However, we account for their needs later in this report.

As a result, 17 focal species or species groups (genera) were selected for species distribution and other modelling approaches described from here on unless stated otherwise. Many other species had limited records and / or occurred in few localities; making them unsuitable for species distribution modelling. Though there is an abundance of free-flying bat data collected through schemes such as iBats (Hawkins et al. 2016) and the use of static detectors, without capture, there was risk of species mis-identification using automated call ID (Walters et al. 2012). Furthermore, the iBats dataset is concentrated around roads due to

¹ We consider high accuracy records to be those that have been validated constituting an accurate species identification, and high geographic accuracy within 10 metres of the coordinates provided.

the car-based survey methodology used, which therefore introduces heavy spatial biases in to the dataset that we have found it difficult to overcome in preliminary tests. Therefore, only bat roost data were used in this report.

To inform steps later on in this report, we conducted a literature review of the ecology, conservation and movement and dispersal capabilities of both our focal species and other protected species in Jersey (see Appendix B).

Step 2: Species distribution modelling

Occurrence records

Occurrence records of the 17 species identified (Table 5 in main document) were restricted to those between 2007 and 2017, that had accurate identification and a geographic accuracy of ≤ 10 metres. This ensured records were spatially and temporally accurate, and reduced the risk of recently mapped predictor variables (e.g., landcover) being inaccurate in relation to old occurrences. To reduce bias in the occurrence datasets, records were spatially filtered (Kramer-Schadt et al. 2013) using the **CREATE RANDOM POINTS** tool (Data Management Tools) in ArcGis Pro ModelBuilder so that remaining occurrences were at least 100 m apart (Figure C1). This step was repeated 20 times, with the run retaining the most points used for further modelling. This method has been shown to be effective in reducing sampling bias (e.g. Ward 2017). Alternative methods for dealing with bias include a bias file, which accounts for the locations where surveys have taken place and puts a greater weight for model predictions on areas that have not been surveyed.

Predictor layers

Scientific literature and species experts were consulted to identify potential drivers of landscape suitability for each focal species and appropriately parameterise each species distribution model. Discussions with species experts were conducted via email and face-to-face in focus group sessions to identify a list of suitable predictor variables; displayed in Table 7 of the main report. To use these in the analyses, it would be necessary to map each variable across the island in ArcGIS Pro to produce a layer matching in extent and projection of a Jersey base map.

We first created a 'base' layer to which all future layers could be matched against. A shapefile depicting Jersey's terrestrial extent (*JsyDissolve.shp*) was created and could be used for the creation of future shapefiles. This layer excluded any offshore land (e.g. St Aubin's Fort), thus these offshore areas of land and any associated records will not be

included in all further analysis steps. This file was also then converted to a raster (**POLYGON TO RASTER**; Conversion Tools) with a 25 metre cell size, ETRS 1989 Jersey Transverse Mercator coordinate system (EPSG 4258) and an extent of 31300.4090999177 (west), 49073.7491000853 (east), 63058.1611000338 (south) 74134.6890999813 (north). This layer (*base*) was then used as a basis for the extent, spatial reference, cell size, snapping and clipping of all future raster layers.

Environmental variables

Environmental variables were downloaded from WorldClim (www.worldclim.org), consisting of data from WorldClim Version 2.0 (Fick and Hijmans 2017) at a resolution of 30 seconds (equivalent to ~1 km²) averaged between 1970–2000. Each of the 19 bioclimatic variables (Table C1) were clipped in ModelBuilder with the **CLIP** tool (Data Management Tools, Figure C2) to the extent of the base layer, the raster grids were converted to points (**RASTER TO POINT**; Conversion Tools) in ModelBuilder (Figure C3) and kriged (**KRIGING**; Spatial Analyst Tools) (method: ordinary, semi-variogram model: spherical, search radius: variable) to create a smooth surface at 25 metre resolution in ArcGIS Pro. Following inspection, we decided to exclude environmental variables from further analyses as they had limited variation over the island given its relatively small extent.

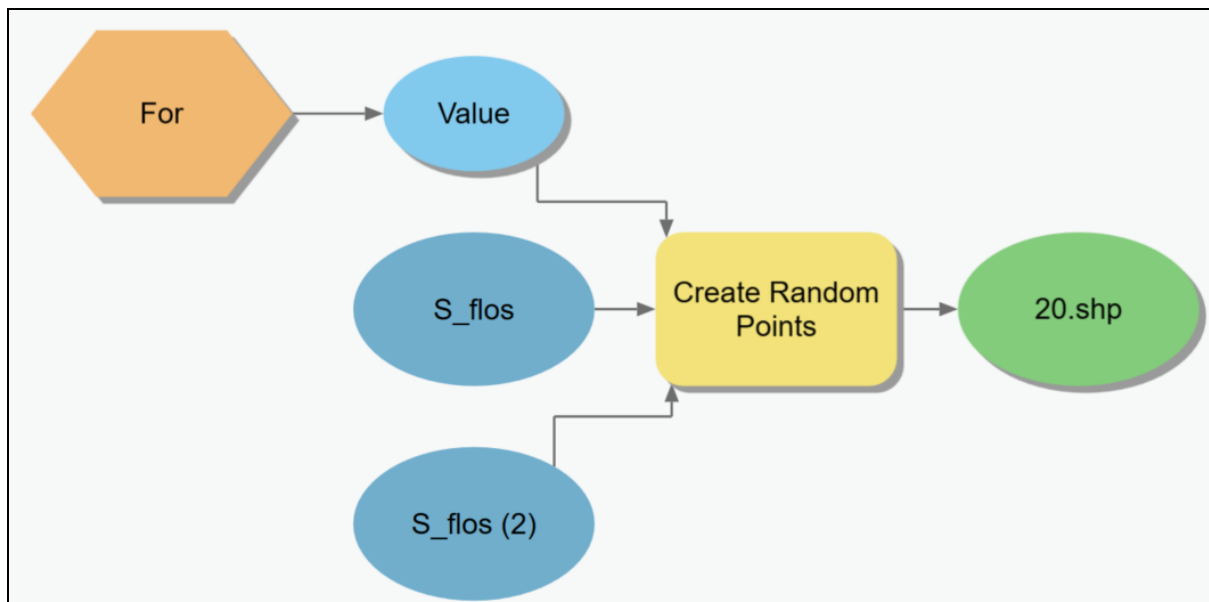


Figure C1 ModelBuilder scenario for iterating multiple runs of the **CREATE RANDOM POINTS** tool for spatial filtering of occurrence records. The 'For' iterator was set from 1 to 20, by 1. The original occurrence point layer for each species was used as the constraining feature class with a maximum of 10,000 points that could be generated and a minimum allowed distance of 100 metres between randomly created points.

Table C1 Description of bioclimatic variables sourced from WorldClim.

Variable	Description
BIO1	Annual mean temperature
BIO2	Mean diurnal range (Mean of monthly (max temp - min temp)
BIO3	Isothermality (BIO2 / BIO7)(* 100)
BIO4	Temperature seasonality (standard deviation * 100)
BIO5	Max temperature of warmest month
BIO6	Min temperature of coldest month
BIO7	Temperature annual range (BIO5 - BIO6)
BIO8	Mean temperature of wettest quarter
BIO9	Mean temperature of driest quarter
BIO10	Mean temperature of warmest quarter
BIO11	Mean temperature of coldest quarter
BIO12	Annual precipitation
BIO13	Precipitation of wettest month
BIO14	Precipitation of driest month
BIO15	Precipitation seasonality (coefficient of variation)
BIO16	Precipitation of wettest quarter
BIO17	Precipitation of driest quarter
BIO18	Precipitation of warmest quarter
BIO19	Precipitation of coldest quarter

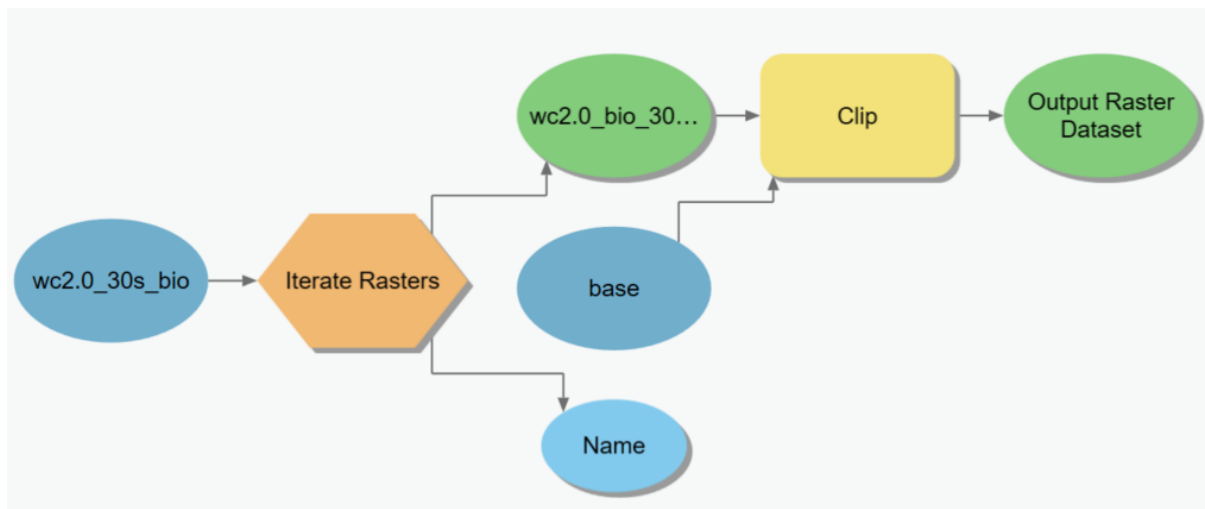


Figure C2 ModelBuilder scenario for iterating multiple runs of the CLIP tool to clip environmental variables to the extent of Jersey.

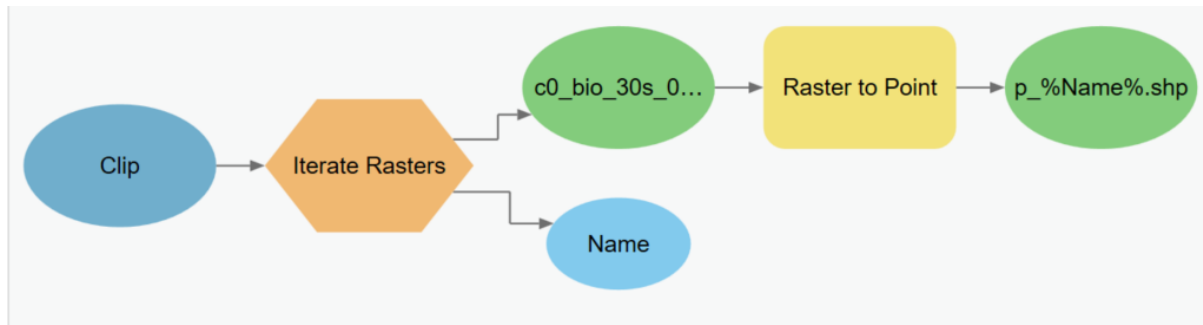


Figure C3 ModelBuilder scenario for iterating multiple runs of the **RASTER TO POINT** tool to transform environmental rasters to points.

Jersey landcover

Landcover type is often the most important variable in species distribution models as it is a fundamental driver of species occurrence. We derived a landcover layer from the Phase 1 Habitats layer (*Habitat_Vegetation.shp*) provided by the Department of Natural Environment, Growth Housing and Environment, States of Jersey. This file contained detailed descriptions of landcover types in the 'Description' field, but contained holes which would affect subsequent analysis. Therefore, we used the **UNION** tool (Analysis Tools) in ArcGIS Pro to combine it with the following layers:

1. Buildings (*Buildings.shp*)
2. Road polygons (*Roads.shp*)
3. Land parcels (*Landparcels.shp*)

A field within the resulting combination layer (*LandCombined.shp*) was then generated and reclassified in ArcGIS Pro to contain the relevant landcover description from 23 categories (Table 6 in main document). These 23 categories were selected based on the study aims and existing landcover categorisation schemes in Jersey and the UK (see Appendix A). This final shapefile was validated using close visual inspection of maps to check for gaps and inconsistencies, with high resolution aerial imaging used as a basis for visual checks. The boundaries of polygons within the same landcover class were then dissolved using the **DISSOLVE** tool (Data Management Tools), resulting in *Jersey_LandcoverDiss1.shp* which was subsequently clipped to the base shapefile described above to produce *Jersey_LandDissClip1.shp*. Following this, it was converted to a raster (**POLYGON TO RASTER**; Conversion Tools) using the *base* raster and the maximum combined area cell assignment type to produce *r_landcover1*.

This conversion can cause smaller features to be absorbed by more dominant landcover features and subsequently 'lost' during analysis. Therefore, we generated layers

representing the Euclidean (straight-line) distance to small or linear features (roads, boundaries, freshwater, amphibians as a proxy for grass snake prey) and to each landcover class. The *Jersey_LandDissClip1.shp* was split by attribute (by landcover type) (**SPLIT**; Analysis Tools) to create separate shapefiles for each landcover type. In some instances, we also created combined shapefiles for grouped landcover types (e.g. all grassland types, all bare ground types) (see Table 7 in main document). The Euclidean (straight-line) distance to features for each of these landcover files was then calculated to create rasters (**EUCLIDEAN DISTANCE**; Spatial Analyst Tools).

Similar rasters were created for the distance to buildings (*Buildings.shp*) (including separate rasters for distances to minor and major buildings), roads (using *Roadcentrelines.shp* to first create *RoadsOnly.shp* after the removal of non-road classes), built-up (urban) areas (*BuiltUp2011.shp*), five boundary feature (*Boundary.shp*) distance rasters (bank, hedge, dry stone wall, mortared wall, stream) and all boundaries (excluding fence, streams, ditches and no boundary classes), toad records (*Toads_combined.shp*) refined to ≤ 100 m accuracy and recorded from 2007 onwards (*Toads_new_100m.shp*) and finally to ponds and reservoirs (*Water.shp*).

We also calculated density layers within a within a 250 m radius with the **KERNEL DENSITY** tool (Spatial Analyst Tools) for permanent anthropogenic structures (buildings, roads and street lighting) and human population. Building density was calculated by first generating a single point feature per major building (*build_pts.shp*, 'Feature' = Major Building or MultiProperty) (**FEATURE TO POINT**; Data Management Tools), clipping (**CLIP**; Analysis Tools) those points to Jersey's extent (*JsyDissolve.shp*) and then applying the **KERNEL DENSITY** tool (Spatial Analyst Tools) to those remaining points with density cell values, the planar method and an output of density per square metre. Road density was also created in a similar way (based on *RoadsOnly.shp*), population density from the *EnumerationDistricts.shp* file (based on the 'MedPopDen' field) and finally street lighting density from *S_Lighting2011.shp*.

Lastly, a digital elevation model (DEM) was calculated based on a pre-existing file (*DEMTrimmed.tif*). This was resampled (**RESAMPLE**; Data Management Tools) with bilinear sampling, and gaps filled using a conditional Focal Statistics python argument:

```
fillDEM = arcpy.sa.Con (arcpy.sa.IsNull ('DEM_25m'), arcpy.sa.FocalStatistics ('DEM_25m', arcpy.sa.NbrCircle (2, 'CELL'),' MEAN'), 'DEM_25m')
```

The **EXTRACT BY MASK** tool (Spatial Analyst Tools) was then used to create the final DEM layer at a 25 metre resolution, using the *base* raster as a template. A similar process was used to create an aspect layer.

Prior to modelling, all predictor layers were in ASCII format and checked to ensure they matched in extent, resolution and coordinate system.

Modelling

Collinearity

Correlations between variables in each species' variable set were tested in ENMTools v1.4.4 (Warren et al. 2010). Where two variables had Pearson's $R^2 \geq 0.7$, the variable considered to have the most ecological relevance was retained and the other removed (Table C2). The Variance Inflation Factor (VIF) for each remaining variable in each species variable set was then calculated in R (R Core Team 2018) using the **VIFCOR** and **VIFSTEP** functions in the package *usdm* (Naimi 2015). All VIF values were < 3 (Zuur et al. 2010), and so no further variables were removed. The final set of predictor variables are listed for each species in Appendix D. A layer for each of these predictive variables was included in the MaxEnt analysis in order to predict suitability across the island and identify the most likely drivers of species distribution.

Model settings

Species distribution modelling approaches can make use of presence-absence data, or more commonly, presence-background data (also known as presence-only data) where true absences are unknown or uncertain. In this study we take a presence-background approach due to the data available, running all models in Maxent V.3.4.1 (available from https://biodiversityinformatics.amnh.org/open_source/maxent/) (Phillips et al. 2018). This programme uses machine learning and Maximum Entropy to make species distribution predictions (Phillips et al. 2006). This software is widely used, and has been shown to be suitable even with small sample sizes (Wisz et al. 2008).

We used the ClogLog transform output, which can be interpreted as predicted probability of presence. However here, we consider it predicted probability of suitability due to the inherent detectability issues of many species. Due to small sample size, k-fold cross-validation was used to generate test and training datasets; whereby the data is partitioned and tested and trained using each partition. Each model was run up to 20 times (less for species with small numbers of occurrence records), with a maximum of 5,000 iterations and no more than

10,000 background points. All other settings were left as the defaults, and the average of the runs was used for model selection steps and interpretation.

Model selection

Models were assessed using threshold-independent measures and inspection of jackknife responses. Threshold-independent measures were based on the receiving operating characteristics (ROC) under the curve (AUC). Models can be ranked by these threshold-independent measures by assessing how well the models discriminate between presences and the background (Phillips et al. 2006). The measures used consisted of the area under the curve of the test data (AUC_{test}) (Phillips et al. 2006), and the difference (AUC_{diff}) between training AUC (AUC_{train}) and testing AUC (AUC_{test}) values (Warren and Seifert 2011), calculated as $AUC_{diff} = AUC_{train} - AUC_{test}$.

Higher AUC_{test} values indicate better performing models, with values > 0.7 considered to indicate good model performance. However, this approach does not assess overfitting (Radosavljevic and Anderson 2014), which is better measured by AUC_{diff} . Lower AUC_{diff} values are expected to indicate more reliable models (Warren and Seifert 2011). Therefore, the optimum model was that which had the highest AUC_{test} and lowest AUC_{diff} values whilst producing biologically plausible outputs.

After identifying the optimum model, we tested the effects of different regularisation values on each species' optimum model to identify the value where the risks of over-fitting and unnecessary model complexity were minimised (Merow et al. 2013), using the same threshold-independent and jackknife measures to assess their performance. Briefly, higher regularisation values increase smoothing of the response curves and therefore produce a more 'regular' model output which may be more suitable for generalising to wider areas. The default value of one was calculated by (Phillips and Dudík 2008) using a variety of test species, but may not be applicable to all species or situations. The regularisation values tested here therefore were 0.1, 0.5, and upwards to the 10.0 at 0.5 intervals which alter the default value by multiplying it by our given test values (Pearson et al. 2007; Merow et al. 2013; Boria et al. 2014; Radosavljevic and Anderson 2014). Visual inspection of the maps produced was also used to ensure biological plausibility. The model showing the best overall performance and with the most suitable regularisation value was then selected as the final model for that species, from which the influence of predictor variables was assessed from permutation importance and by inspecting the outputs from jackknife tests; whereby variables with a strong influence on the training gain (increasing when present and decreasing when absent) had the greatest influence.

Table C2 Predictor variables with a Pearson's correlation (R^2) ≥ 0.7 for each species. The variables with the most ecological relevance were retained (shown in **bold**) and the others discarded. Where no predictor variables were highly correlated, rows are shown with '-'. Full explanations of the variables are shown in Table 7 of the main document.

Species	Variable 1	Variable 2	Correlation (R^2)
Western toad	distance to gardens	distance to (all) buildings	0.770
	distance to hedges	distance to (all) boundary features	0.921
	distance to wetlands	distance to ponds and reservoirs	0.727
	building density	population density	0.742
	building density	road density	0.807
Grass snake	distance to (all) boundary features	distance to banks	0.892
	distance to dune heathland	distance to dune grassland	0.894
	distance to dune marram	distance to dune grassland	0.906
	distance to dune marram	distance to dune heathland	0.980
	distance to hedges	distance to banks	0.815
	distance to hedges	distance to (all) boundary features	0.921
	distance to wetlands	distance to ponds and reservoirs	0.727
	building density	road density	0.807
Bank vole	distance to (all) scrub	distance to scrub	0.893
	distance to (all) boundary features	distance to banks	0.892
	distance to hedges	distance to banks	0.815
	distance to hedges	distance to (all) boundary features	0.921
	distance to treelines	distance to banks	0.878
	distance to treelines	distance to (all) boundary features	0.804

Table C2 continued

Species	Variable 1	Variable 2	Correlation (R ²)
	distance to treelines	distance to hedges	0.718
Common pipistrelle bat	distance to (all) boundary features	distance to banks	0.892
	distance to hedges	distance to banks	0.815
	distance to hedges	distance to (all) boundary features	0.921
	distance to historic farmsteads	distance to historic buildings	0.745
	distance to treelines	distance to banks	0.878
	distance to treelines	distance to (all) boundary features	0.804
	distance to treelines	distance to hedges	0.718
	street lighting density	population density	0.731
	building density	population density	0.742
	building density	road density	0.807
	building density	street lighting density	0.719
Long-eared bats	distance to hedges	distance to (all) boundary features	0.921
	distance to historic farmsteads	distance to historic buildings	0.745
	distance to gardens	distance to historic buildings	0.748
	distance to gardens	distance to major buildings	0.815
	distance to treelines	distance to (all) boundary features	0.804
	distance to treelines	distance to hedges	0.718
	building density	road density	0.807
	building density	street lighting density	0.719

Table C2 continued

Species	Variable 1	Variable 2	Correlation (R ²)
Red squirrel	distance to (all) boundary features	distance to banks	0.892
	distance to hedges	distance to banks	0.815
	distance to hedges	distance to (all) boundary features	0.921
	distance to treelines	distance to banks	0.878
	distance to treelines	distance to (all) boundary features	0.804
	distance to treelines	distance to hedges	0.718
	distance to broadleaved woodland	distance to (all) woodland	0.841
	distance to gardens	distance to major buildings	0.815
	building density	road density	0.807
	building density	population density	0.742
Field cricket	–	–	–
Waxcap fungi	–	–	–
Scaly stalkball	distance to (all) boundary features	distance to banks	0.892
	distance to dune marram	distance to dune grassland	0.906
Green-winged orchid	–	–	–
Pyramidal orchid	distance to dune marram	distance to dune grassland	0.906
Southern marsh-orchid	distance to wetlands	distance to ponds and reservoirs	0.727
Lizard orchid	distance to dune heathland	distance to dune grassland	0.894
	distance to dune marram	distance to dune grassland	0.906
	distance to dune marram	distance to dune heathland	0.980

Table C2 continued

Species	Variable 1	Variable 2	Correlation (R ²)
Early-purple orchid	distance to (all) boundary features	distance to banks	0.892
	distance to hedges	distance to banks	0.815
	distance to hedges	distance to (all) boundary features	0.921
	distance to (all) scrub	distance to scrub	0.893
Jersey buttercup	distance to (all) scrub	distance to scrub	0.893
Ragged robin	distance to hedges	distance to banks	0.815
	distance to wetlands	distance to ponds and reservoirs	0.727
Autumn lady's-tresses	distance to dune heathland	distance to dune grassland	0.894

Step 3: Identification and reduction of Habitat Concentration Areas (HCAs)

The outputs from species distribution modelling consist of each cell in a landscape being assigned a value related to its suitability or the likelihood that the species of interest may occur there (depending on interpretation). In MaxEnt, the ClogLog outputs are bounded between 0 and 1, with higher values indicating greater suitability. For the purposes of selecting the most important areas in a landscape for protection, management, monitoring and connecting it can be necessary to use a threshold above which patches of land are considered to be most suitable. We refer to these areas as Habitat Concentration Areas (HCAs) (*sensu* WHCWG 2010).

Setting a binary threshold

To identify HCAs, we used an objective binary threshold known as maxSSS which maximises the sum of sensitivity (the percentage of correctly classified presences) and specificity (the percentage of correctly classified absences) (Liu et al. 2005; Peterson et al. 2011). Taking such an approach is not always appropriate but is supported for identifying conservation priorities (Guillera-Aroita et al. 2015) and has been widely used. These outputs were reduced further by a series of steps to (i) remove small, disaggregated patches expected to have little conservation value and (ii) parts of the landscape that were unsuitable but that may have been overlooked due to the assignment of landcover to one of 23 habitat classes and subsequent conversion to a 25 metre resolution raster for use in MaxEnt.

Removing small, isolated patches

Small, isolated HCAs were identified by using FRAGSTATS v4.2 software (McGarigal et al. 2012) to calculate the Proximity Index (Gustafson and Parker 1994) at a radius of 20 km to cover the full extent of Jersey, and Patch Area values. These were calculated with the 8-cell neighbourhood rule and we generated a Patch ID file to allow the results to be easily transferred to the HCA shapefiles (joining the PID field to the gridcode field of the polygon HCAs). The Proximity Index measures how isolated a patch may be but can be heavily influenced by patch size and subsequently attributes larger patches with smaller values than a comparable small patch (Hargis et al. 1998). This issue was circumvented by calculating a Modified Proximity Index (Bani et al. 2006) as

$$MPI = Proximity\ Index \times Patch\ Area \quad \text{Equation 1}$$

Patches with MPI < 0.6 were removed from each species' HCA layer, and were on average 0.116 ha in area (range: 0.063–1.688, SD: 0.105), resulting in average HCA decreases of 38.11 ha per species (range: 2.13–100.00, SD: 32.53).

Removing unsuitable habitat

Further areas of the HCAs were removed where they were considered to comprise unsuitable habitat using the **ERASE** tool (Analysis Tools) in ModelBuilder (Figure C4). These removals included water bodies, unnatural bare ground (e.g. roads), buildings and recreation fields, and are summarised in Table C3.

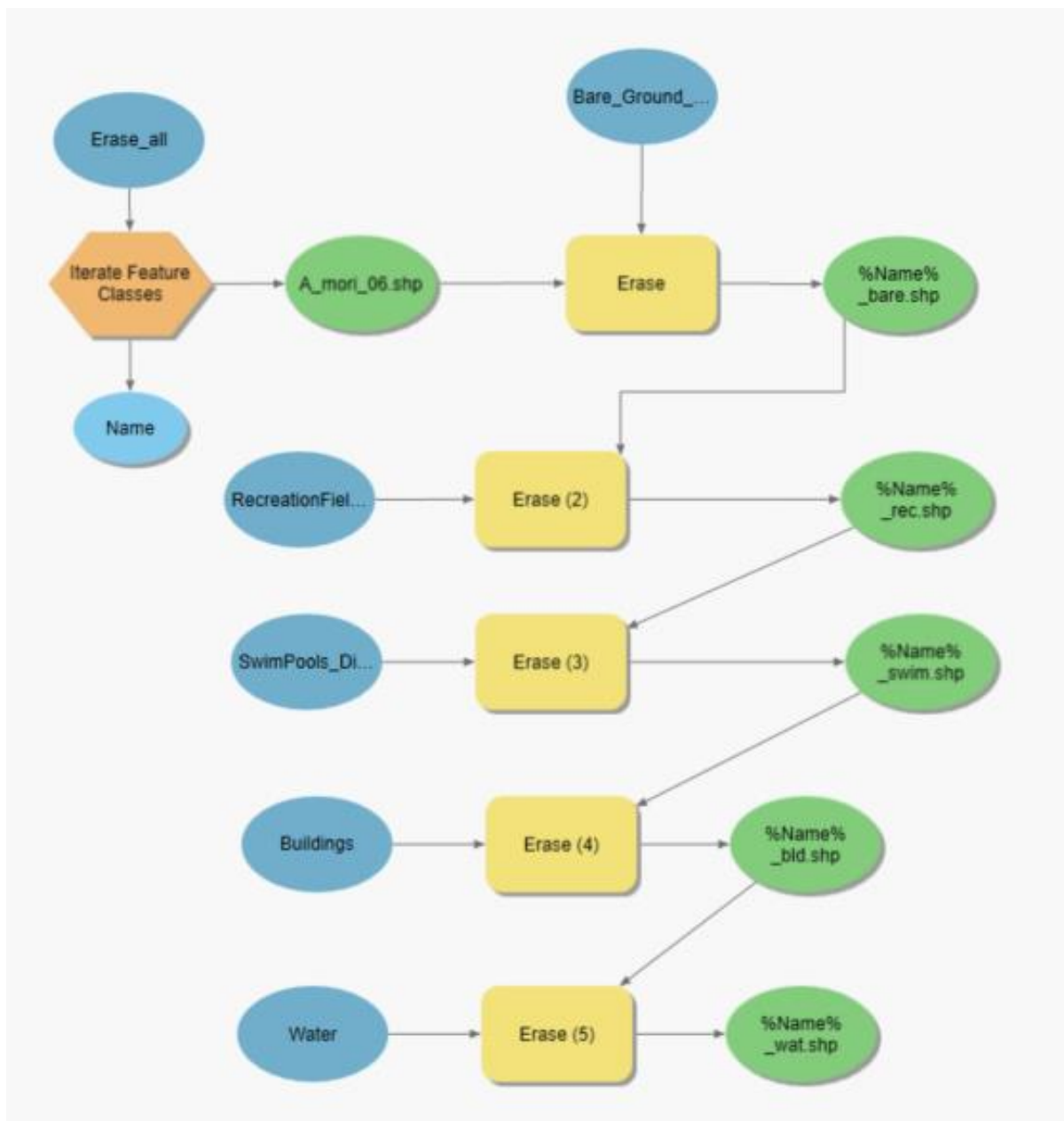


Figure C4 ModelBuilder scenario example for removal of unsuitable feature types from HCAs.

Table C3 Table showing the features removed from each species to produce a final Habitat Concentration Area (HCA), as indicated by '+’.

Species	Bare ground (unnatural)	Recreation fields	Swimming pools	Buildings	Water
Western toad	+	+	+	+	-
Grass snake	+	+	+	+	-
Bank vole	+	+	+	+	+
Common pipistrelle bats	+	+	+	-	+
Long-eared bats	+	+	+	-	+
Red squirrel	+	+	+	+	+
Field cricket	+	+	+	+	+
Waxcap fungi	+	+	+	+	+
Scaly stalkball	+	+	+	+	+
Green-winged orchid	+	+	+	+	+
Pyramidal orchid	+	+	+	+	+
Southern marsh-orchid	+	+	+	+	+
Lizard orchid	+	+	+	+	+
Early-purple orchid	+	+	+	+	+
Jersey buttercup	+	+	+	+	+
Ragged robin	+	+	+	+	+
Autumn lady's-tresses	+	+	+	+	+

HCA similarity and distribution

The overlaps between the final HCAs for each species were assessed in ArcGIS Pro using the **INTERSECT** tool (Analysis Tools) in ModelBuilder (Figure C5) to create new files for each pairwise combination of species. We subsequently summarised each file in ModelBuilder (Figure C6) to produce a text file for each species that was then imported and queried in Microsoft Excel. A combined HCA map was also generated by merging (**MERGE**; Data Management Tools) and dissolving (**DISSOLVE**; Data Management Tools) the individual species' HCAs in to a single shapefile. The HCAs for each focal species and the combined HCAs were then contrasted against the landscape designations given in Table 4 of the main document via the same intersection process, to identify the proportion of HCAs falling within each designation, and the proportion of each designation containing HCAs. The HCAs from each species were then overlaid to create a 'hotspot' map by converting the HCA shapefiles to rasters (**POLYGON TO RASTER**; Conversion Tools), reclassifying values ≥ 1 to 1, and 0 values and NODATA to 0 (**RECLASSIFY**; Spatial Analyst Tools). We then used the **WEIGHTED SUM** tool (Spatial Analyst Tools) to generate hotspot maps for the following scenarios; (i) all (17) focal species including built-up areas, (ii) all (17) focal species excluding built-up areas, (iii) all focal species that do not have a large ($\geq 10\%$) HCA component within built-up areas and (iv) only those species that do have a large ($\geq 10\%$) HCA component within built-up areas.

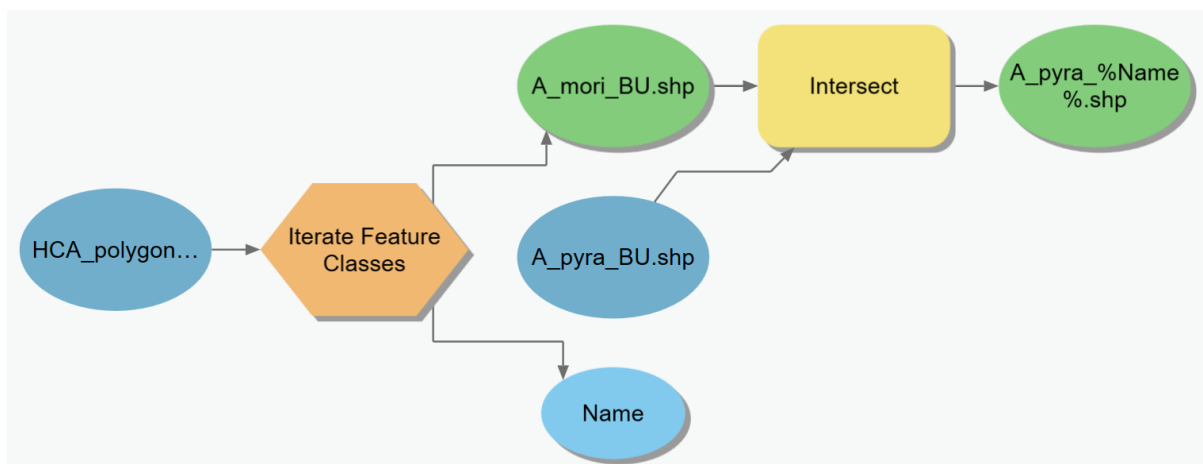


Figure C5 ModelBuilder scenario example used to calculate the intersect between HCAs for different species.

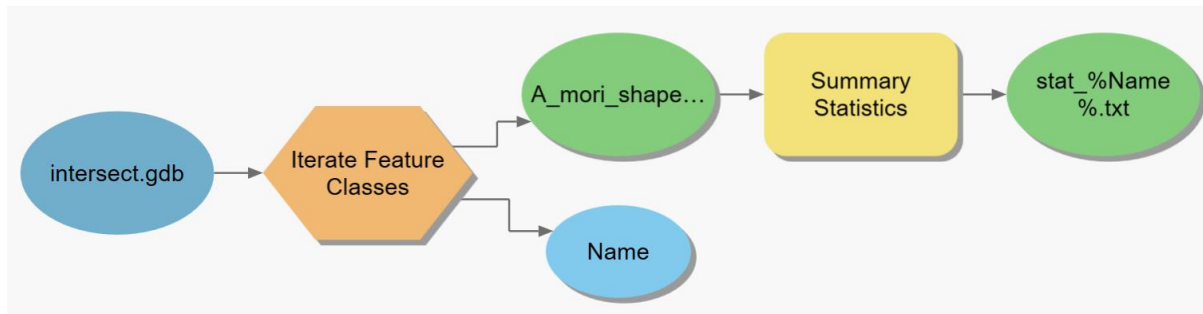


Figure C6 ModelBuilder scenario example used to summarise the area of intersections HCAs for different species combinations.

HCA validation

The coverage provided by the final HCAs as a representation of areas of conservation importance in Jersey were validated using occurrence data consisting of 10,113 records across 98 species (see Table 8 in the main document) restricted to records between 2007 and 2017 but of all geographic accuracies. This species set comprised a large number of species currently protected or proposed for protection, and a further 26 fungi species to provide good representation of this taxonomic group. From the merged and dissolved multi-species HCA map described in the previous step we generated a maximum of 1,000,000,000 random points (**CREATE RANDOM POINTS**; Tools) within the polygons. This step ensures that no small polygons are missed when calculating the next distance step. A Euclidean distance surface was then generated representing the distance to these HCA points with the **EUCLIDEAN DISTANCE** tool (Spatial Analyst Tools) with a 5 metre cell size. We then assessed the percentage of records that occurred within HCAs (i.e. distance = 0) and the average distances at which they occurred from HCAs by extracting the Euclidean distance values to the species occurrence points (**EXTRACT VALUES TO POINTS**; Spatial Analyst Tools) to create a point features file containing the Euclidean distance attributes at those locations, ensuring the output points features were masked to the Jersey base shapefile (*JsyDissolve.shp*). The variable geographic accuracy of data used in this step meant that records falling outside of HCAs may have actually occurred within them but that coordinate data was inaccurate. The inverse may also be true. A visual representation of the distribution of these records was also generated in the form of a hotspot map at a 100 metre resolution by first converting occurrence points to a raster for each species using the **POINT TO RASTER** tool (Conversion Tools) in ModelBuilder (Figure C7) (specifying the given resolutions of 100 metre cell size) and then using the **WEIGHTED SUM** tool (Spatial Analyst Tools) to generate hotspot maps for (i) all 98 species protected or proposed for protection,

(ii) 83 species excluding those analysed as focal species and (iii) the 26 fungi species. A final validation step was undertaken by qualitatively comparing areas identified by the Société Jersiaise Ornithology Section as being of high importance to local bird populations (see Appendix E) against our HCA predictions.

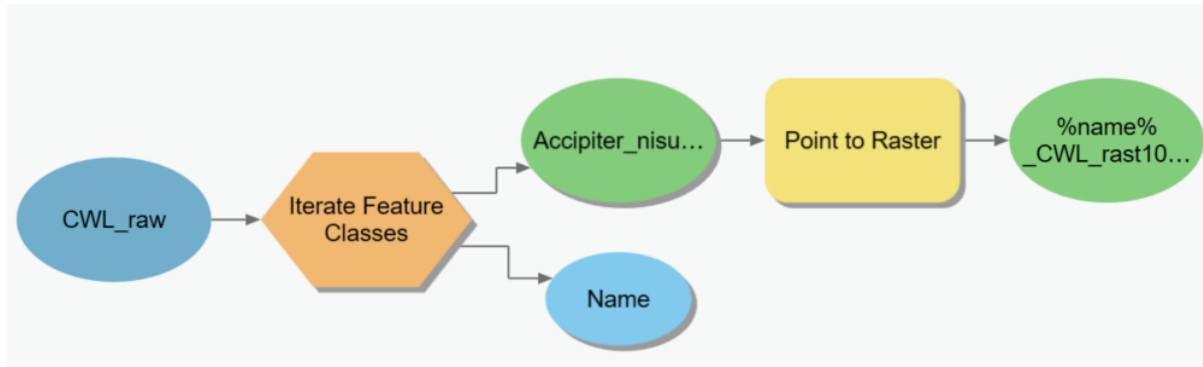


Figure C7 ModelBuilder scenario for converting occurrence points to rasters for multiple species with the POINT TO RASTER tool.

Step 4: Connectivity modelling

Several approaches can be taken to assess connectivity between predefined areas using methods such as graph and circuit theory or least-cost paths. Graphs can be envisaged as a network of nodes or habitat patches requiring connecting, joined by edges along which species may be able to disperse between two nodes. The ability of a species to move along an edge is dependent on the weight of the edge (McRae et al. 2008). Alternatively, least-cost paths follow the path of least resistance between two nodes. The results of connectivity modelling can be heavily influenced by how the model is parameterised, including the way in which nodes and resistance surfaces are defined.

Previous studies have applied different methods and considerations to identify the best corridors for wildlife, including using resource selection approaches (Abrahms et al. 2017), accounting for species movement and dispersal capabilities, the generation time of an organism, genetic connectivity, circuit theory, least-cost paths, and considering the fact that species may behave and move differently within their home-ranges compared to during dispersal (i.e. studies basing habitat selection on home-range studies may be incorrect if species select habitat differently during dispersal; they may be willing to use poorer habitats in order to achieve their dispersal aims and access resources). The results may also be influenced by the scale of the study and temporal changes in resistance.

Creating corridors for multiple species is regarded as best practice to identify robust connectivity networks, and reduces the risk of errors associated with single-species

approaches. Approaches to generating them include overlaying multiple single-species maps of linkages, or creating a single, multi-species network from the start (Marrotte et al. 2017).

Where to connect?

We used our HCAs as nodes for connectivity in the landscape. As built-up areas are generally unsuitable for protection, and the diversity of land-owners makes it difficult to inform management, we opted to remove built-up areas from HCAs prior to calculating least-cost paths and corridors. However, separate runs including HCAs within built-up areas were carried out for urban-dwelling species (defined as species with $\geq 10\%$ of their HCAs within built-up areas).

Creating resistance surfaces

Resistance surfaces can be created through many avenues, but should preferentially be parameterised based on quantitative genetic or movement data (Khosravi et al. 2018); however, these data are often lacking for single species, and more so for multi-species approaches. Alternatively, they can be generated by transforming measures of habitat suitability (Schoville et al. 2018) or be based on expert opinion (Sawyer et al. 2011). Resistance surfaces based on habitat suitability can also be calculated using additive or multiplicative approaches, and with different transformations of habitat suitability scores (e.g. Keeley et al. 2016).

Here we parameterise our resistance surfaces using a transformation of habitat suitability estimates. The habitat suitability estimates were the ClogLog outputs from the respective species' final MaxEnt output. These were transformed into a resistance surface using a linear negative transformation (Wilkinson and Starnes 2016) calculated as

$$R_{in} = ((1 - [\text{MaxEnt_output}]) * 100) + 1 \quad \text{Equation 2}$$

with values rescaled between 1 and 100 using the **RESCALE BY FUNCTION** tool (Spatial Analyst Tools). To this, we added further resistance for roads and other transport infrastructure (*Roadcentrelines.shp*) with resistance values dependent on their width (e.g. single, dual or triple lane), with wider roads given greater resistance. These values were based on their expected risk of mortality, either from traffic or exposure to predators. Built-up areas were also assigned higher resistance, using building density as a proxy (see Table 7 in the main document). Building densities ranged between 0 and 0.0053, and were rescaled between 0 (no built-up resistance) and 20 (high built-up resistance) with the **RESCALE BY FUNCTION** tool (Spatial Analyst Tools).

A final resistance layer was added consisting of boundary features. These can have both positive and negative influences on movement, providing shelter and other resources, or by serving as a physical barrier. The *Boundary.shp* shapefile was used, which contained 37 categories of which 36 were related to physical boundary features. Those listed as bank, hedge, ditch or wall were considered to aid dispersal of species and were assigned a small negative resistance value. Fences were assigned small positive values (1), and streams were not given a resistance value.

Conversion of linear shapefile features (e.g. boundaries and roads) to rasters can result in gaps or 'cracks', through which models may mistakenly predict least-cost routes to occur (Adriaensen et al. 2003; Rothley 2005; Theobald 2005). This can be resolved through the use of buffering the linear feature by half the diagonal cell distance, or through the use of a neighbourhood operation (e.g. Rothley 2005). Theobald (2005) provided an algorithm to check for cracks in linear features. We followed this, and visually inspected each 'crack' identified by the algorithm. None of the cracks identified in the boundary or road layers were true. Therefore, we made no further adjustments to these rasters before summing them with the transformed MaxEnt output. All resistance surface values are summarised in Table 9 of the main document. For each species, the four resistance surfaces (negative transformation of MaxEnt habitat suitability, roads, building density and boundary features) were summed using the **WEIGHTED SUM** tool (Spatial Analyst Tools) to produce a final resistance surface.

Though the transformed MaxEnt surfaces were for specific species, we treated them as representatives for a given ecosystem or niche, and carried out all further steps based on the aim of generating wildlife corridors that would encourage dispersal of the majority of Jersey's terrestrial animal species. Given the difficulties in modelling the dispersal of plant and fungi, we did not model these specifically but assumed a well-functioning landscape for animals would also benefit plants and fungi.

Modelling least-cost paths and corridors

We first used the Linkage Mapper toolbox (McRae and Kavanagh 2011) in ArcCatalog to build network and map linkages (connections) between HCAs across the resistance surface. We used the cost-weighted and Euclidean adjacency method and dropped corridors that intersected core areas (HCAs). Linkages were calculated without restriction across the whole island and then restricted to three separate scenarios equivalent to Maximum Euclidean corridor distances of (i) 250 m, (ii) 1000 m and (iii) 4000 m. These distance values were based on our review of known species movement capabilities (Appendix B) and are expected to represent a wide range of species. Linkage Mapper allows distances to be

assessed based on either Euclidean (straight-line) distance, or cost-weighted distance. The latter can be described as the cumulative cost of moving through each cell where the cost of a given cell is its resistance value multiplied by its size (i.e. 25 metres) (WHCWG 2010).

Corridors were designed excluding HCAs that occurred within built-up areas unless a focal species was considered to be an urban-dweller, in which case corridors were designed including HCAs occurring within built-up areas. This was based on the premise that HCAs occurring within built-up areas would be unsuitable for protection as they mainly consisted of gardens, buildings and other privately-owned features.

To identify linkage zones (sensu WHCWG 2010), normalised least-cost corridors were limited to cut-off values equivalent to a Euclidean corridor width of 100 metres across all scenarios, calculating the associated cost-weighted distance value based on the mean resistance values per metre in HCAs shown in Table C4 multiplied by 100. This relatively small value was used due to the fine-scale nature of the project. Similarities between corridor predictions were assessed between species to identify commonalities between them by overlaying them using the **WEIGHTED SUM** tool (Spatial Analyst Tools). Areas with greater overlap are therefore considered to have greater importance for overall connectivity, and can be used as targets for conservation management.

Table C4 Summary table of mean resistance values within HCAs either excluding or including HCAs within built-up areas, and the associated cost-weighted distance for Euclidean distances of 100 and 1000 metres. Cost-weighted distances are calculated as the mean resistance value per metre multiplied by 100 or 1000 respectively.

Species	Mean resistance per metre	Cost-weighted distance equivalent to 100 m	Cost-weighted distance equivalent to 1000 m
Excluding built-up HCAs			
Western toad	53.76	5376.00	53760.85
Grass snake	63.43	6343.00	63430.79
Bank vole	30.77	3077.00	30772.28
Common pipistrelle bat	70.53	7053.00	70528.37
Long-eared bats	46.99	4699.00	46985.96
Red squirrel	39.41	3941.00	39405.47
Field cricket	40.94	4094.00	40943.54
Waxcap fungi	62.38	6238.00	62384.44
Scaly stalkball	34.78	3478.00	34776.02
Green-winged orchid	45.27	4527.00	45266.33
Pyramidal orchid	34.26	3426.00	34260.81
Southern-marsh orchid	36.21	3621.00	36210.78
Lizard orchid	17.68	1768.00	17683.51
Early-purple orchid	3.19	319.00	3194.23
Jersey buttercup	38.16	3816.00	38163.91
Ragged robin	65.88	6588.00	65878.63
Autumn lady's-tresses	65.67	6567.00	65668.82
Including built-up HCAs			
Western toad	48.97	4897.00	48966.33
Common pipistrelle bat	71.41	7141.00	71414.23
Long-eared bats	47.20	4720.00	47204.90
Red squirrel	39.57	3957.00	39567.28
Autumn lady's-tresses	65.55	6555.00	65547.83

Step 5: Priorities for protection and restoration

Connectivity indices

We used the command interface of the graph software Conefor v2.6 (Saura and Torné 2009) (www.conefor.org) to assess the importance of HCAs based on five indices related to their contribution to landscape connectivity. The metrics were (i) the integral index of connectivity (*dIIC*) (Pascual-Hortal and Saura 2006), (ii) the probability of connectivity (*dPC*) (Saura and Pascual-Hortal 2007) and the (iii) *intra*, (iv) *flux* and (v) *connector* fractions of the *dPC* metric (Saura and Rubio 2010; Baranyi et al. 2011). The *intra* fraction is a measure of intra-patch connectivity, whereas the *flux* and *connector* fractions are measures of inter-patch connectivity. Higher values of these indices indicate a greater contribution to landscape connectivity. *dIIC* is a binary metric, whereas *dPC* is probabilistic.

Selecting and scoring nodes

To calculate the connectivity metrics, we used the HCAs as nodes, with their mean habitat suitability used to represent their value (calculated as the summed value of the inverse resistance surface within that polygon). We also input the cost-weighted distances calculated previously in Linkage Mapper as distance measures of connectivity within the connection file.

In order to obtain the inverse of resistance values for the HCAs, we used **RASTER CALCULATOR** (Spatial Analyst Tools) in ArcGIS Pro with the formula shown in Equation 3, where R is a species' resistance surface, r_{Max} is the maximum resistance value in that surface and r_{Min} is the minimum.

$$((R - r_{Max}) * -1) + r_{Min} \text{ Equation 3}$$

Following this, the values of the cells falling within each HCA were summed to assign each HCA with a value representing both its area and habitat suitability. This was done by first multiplying the inverted resistance values by 100,000, converting them to integers, converting the integer rasters to polygons, adding a new field to contain the original raster values, and dividing the integer values by 100,000 to populate the 'original' field with the inverse of the original raster resistance values. We then used the **INTERSECT** tool (Analysis Tools) to create a shapefile containing the new suitability values for each of the cells in each HCA, and calculated the node value of a HCA as the suitability value in a cell multiplied by the size of the HCA polygon (in hectares) occurring within that cell. These values were then

summed across all cells comprising a single HCA to assign a single habitat suitability value to each HCA.

Connection file

The connection file was in partial format, and consisted of the cost-weighted distance values calculated previously in Linkage Mapper between each pair of HCAs. We used a partial file as we had specified Linkage Mapper to drop corridors that intersected HCAs. Conefor requires a distance threshold to be set for each of the connectivity metrics used here. Therefore, we carried out runs at a single level equivalent to an intermediate Euclidean distance of 1000 metres with a probability of 0.01 for *dPC* indices. These cost-distance values were calculated separately for each species as the mean cell value falling within each HCA from the resistance rasters described above, and are shown in Table C4. They were calculated in a similar manner as that described above for calculating HCA suitability values, without the final summing step or inverting of the raster. We interpret these values as the resistance expected to occur within a cell in good quality habitat, given that they fall within predicted HCAs. Other distances (250 and 4000 m) were not assessed due to processing time constraints. We requested delta outputs, and kept all other settings as defaults.

Pearson's correlation tests were used to assess similarities between the five different indices with the **COR()** function in R. Only those deemed to hold unique value were retained for further assessment, and the Conefor node importance tables were then joined to the HCA polygons using the **ADD JOIN** tool (Data Management Tools), using Node ID / PID as the respective join fields. We then visualised the importance of each HCA based on the remaining indices. Following this, we converted the polygons to separate rasters for each of the three indices, and rescaled each raster to between 0 and 1 with a linear function with the **RESCALE BY FUNCTION** tool (Spatial Analyst Tools) to provide comparable outputs across species. We then reclassified nodata values to 0 to avoid gaps in the maps and used the **WEIGHTED SUM** tool (Spatial Analyst Tools) to sum the rasters and identify areas of high importance for connectivity based on each of the indices. Higher values reflected greater priorities for connectivity. From these, we overlaid the varying landcover designations to identify areas of high importance but low protection to provide priorities for protection. Overall prioritisation was then assessed based on landscape designations (see Table 4 in the main document) and contribution to connectivity. Following the premise that areas that are currently unprotected are at greater risk of loss, these were prioritised above areas already within statutory designations. Therefore, we evaluated areas separately based on their existing designation.

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