Migratory connectivity analysis

by EURING Migration Atlas

Aythya ferina (EURING code 01980)

1.1 Connectivity between individuals

The analysis evaluated 552 individuals (1104 encounters) filtered from a total of 24377 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 01980-1; Figure 01980-1).

Table 01980-1. Results from the migratory connectivity analysis. For each cluster, the degree of connectivity (r_M), its statistical significance (p-value) and 95% confidence interval limits are shown. When the p-value is less than or equal to 0.1, the degree of clustering structure (oasw) and the best number of clusters identified are reported.

Cluster name	Level of clustering	N individuals	Migratory connectivity (r_M)	p-value	Lower 95% confidence limit	Upper 95% confidence limit	Best number of clusters	oasw
0	0	552	0.193	0.001	0.121	0.268	5	0.415

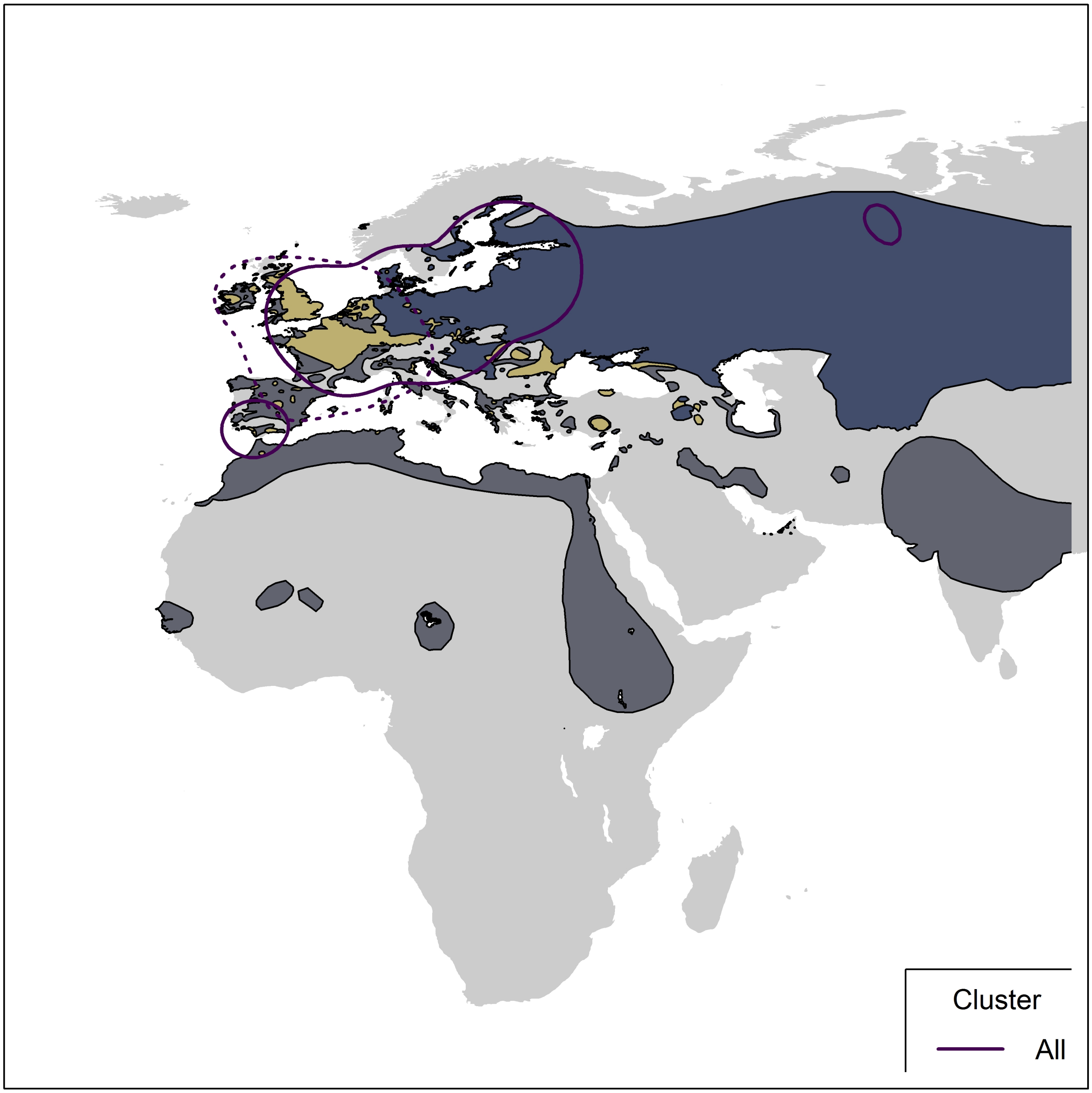

Figure 01980-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding range. Different contour colours correspond to different clusters, as reported in legend. The species distribution range is also shown (breeding range: blue; non-breeding range: dark grey; resident range: beige; from BirdLife International, 2019).

1.2 Sensitivity analysis

Results of power analysis and validation. Analyses at the species level were re-run on subsamples of individuals of decreasing size (100 repetitions per subsample size), according to simple random sampling of individuals (Figure 01980-2) and stratified sampling of individuals within the breeding range (Figure 01980-3) and the non breeding range (Figure 01980-4). For stratified sampling, we selected individuals with a probability inversely proportional to the number of observation in each country. Figures below report the results of the procedure.

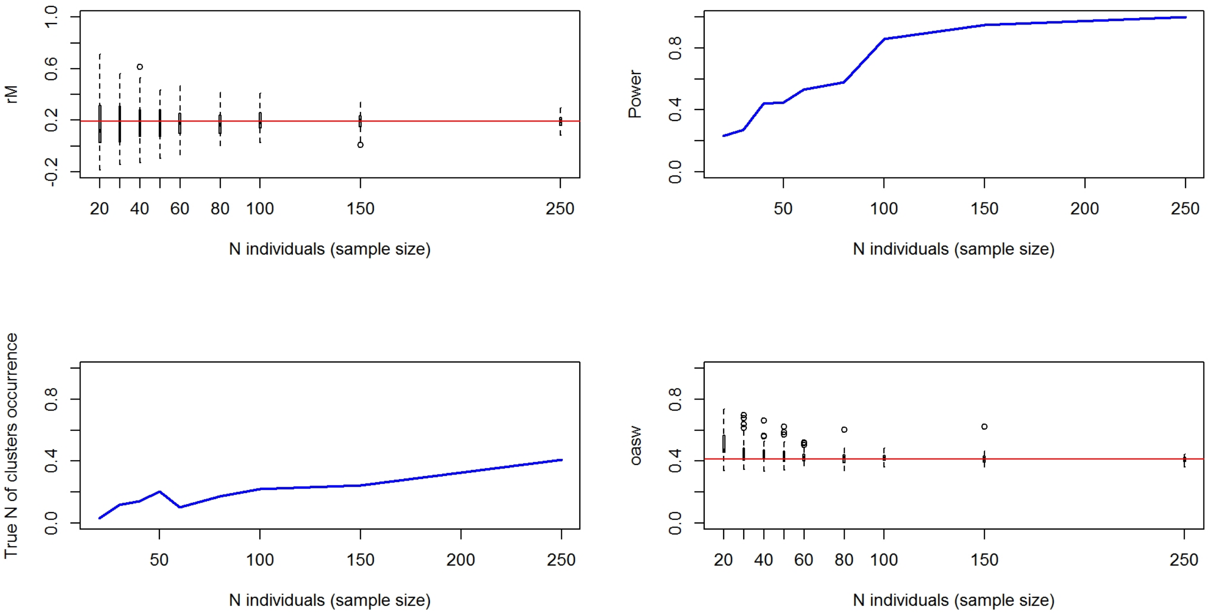

Figure 01980-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

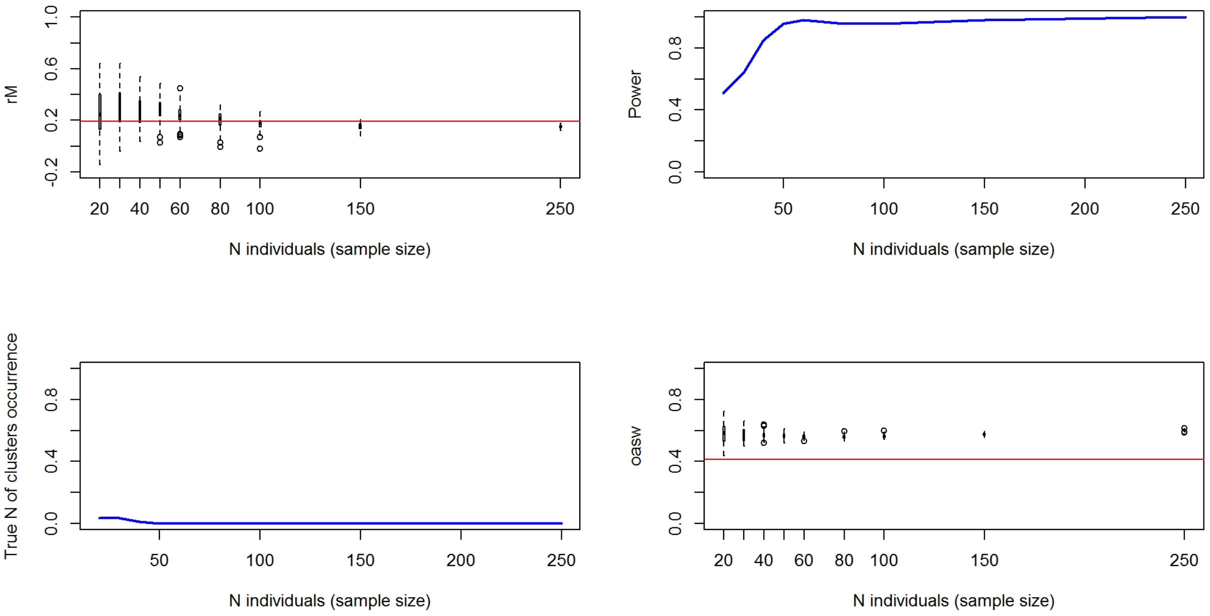

Figure 01980-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

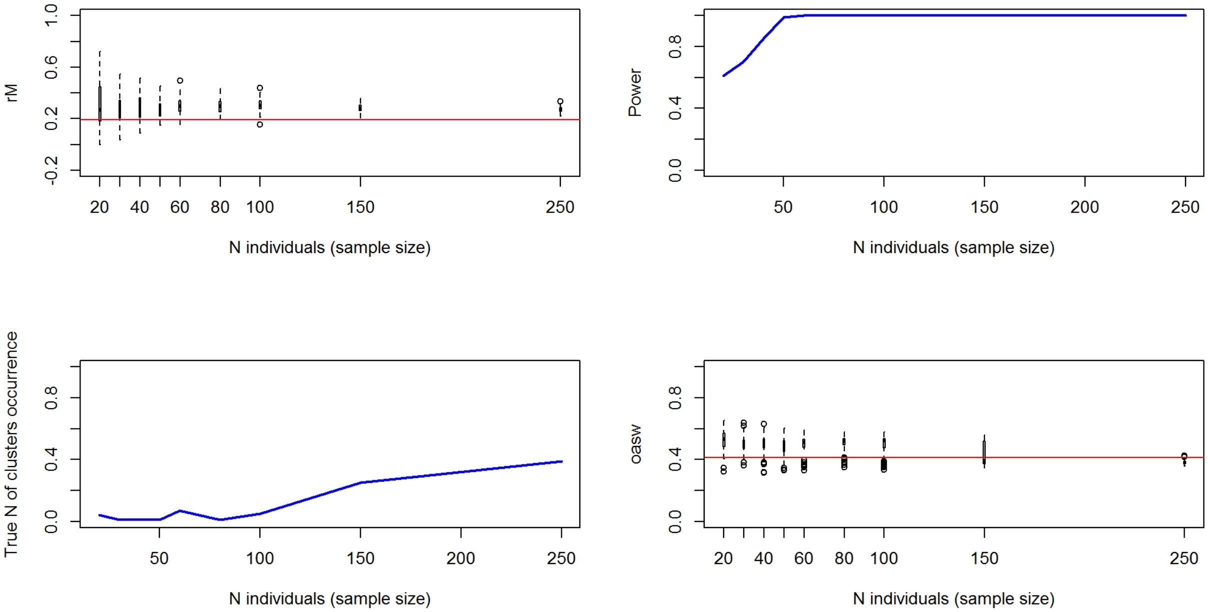

Figure 01980-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

The comparison between the bootstrapped distribution of r_M values from live recaptures and dead recoveries is not significant ($p = 0.655$); Figure 01980-5).

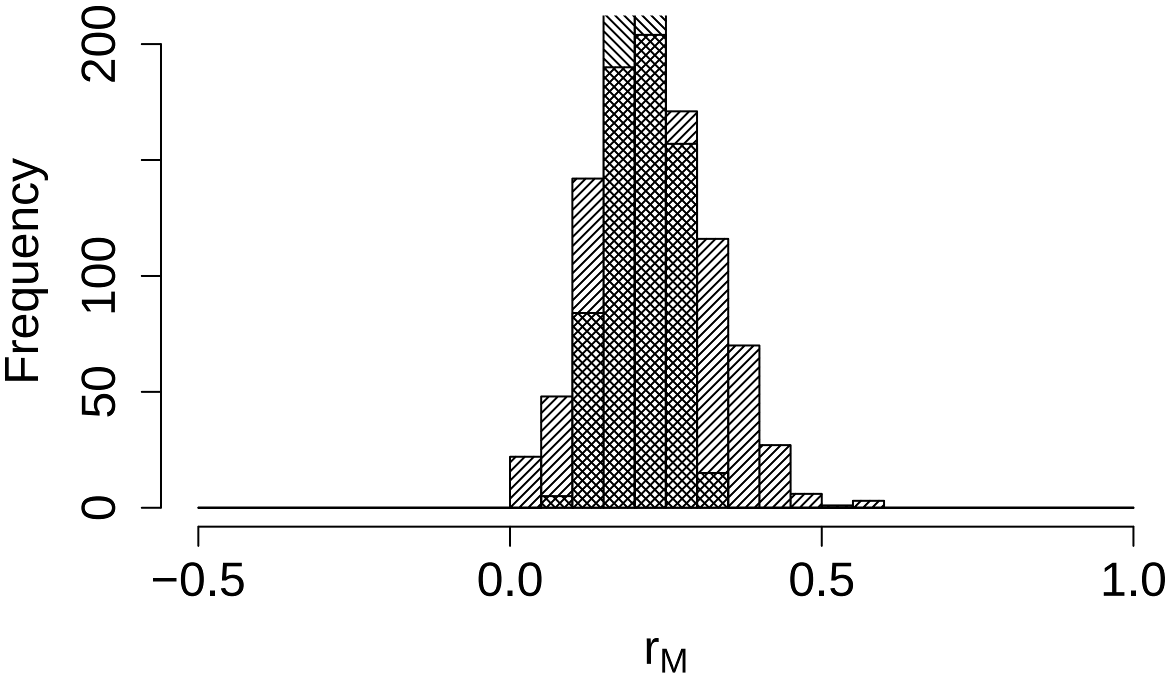

Figure 01980-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low/moderate connectivity (MC = 0.226; MC = 0.225 when adjusted for absolute abundance) between 8 breeding regions and 8 non breeding regions (Table 01980-2; Figure 01980-6).

Table 01980-2. Transition probabilities between pre-defined regions. Estimated abundance (number of individuals) in each breeding region is also reported.

Breeding region	Abundance	Non breeding region	Transition probability
Central Europe	91646	Central Europe	0.280
Central Europe	91646	North Africa	0.017
Central Europe	91646	North-west Europe	0.136
Central Europe	91646	South-central Europe	0.085
Central Europe	91646	South-east Europe	0.008
Central Europe	91646	South-west Europe	0.119
Central Europe	91646	West Europe	0.356
East Europe	270700	Central Europe	0.119
East Europe	270700	North Europe	0.007
East Europe	270700	North-west Europe	0.318
East Europe	270700	South-central Europe	0.014
East Europe	270700	South-east Europe	0.007
East Europe	270700	South-west Europe	0.091

Breeding region	Abundance	Non breeding region	Transition probability
East Europe	270700	West Europe	0.444
North Europe	28775	North-west Europe	0.375
North Europe	28775	South-west Europe	0.062
North Europe	28775	West Europe	0.562
North-west Europe	980	North Africa	0.025
North-west Europe	980	North-west Europe	0.675
North-west Europe	980	South-west Europe	0.025
North-west Europe	980	West Europe	0.275
South-central Europe	6500	South-central Europe	0.333
South-central Europe	6500	South-west Europe	0.667
South-east Europe	54093	Central Europe	1.000
South-west Europe	17015	North Africa	0.136
South-west Europe	17015	North-west Europe	0.045
South-west Europe	17015	South-central Europe	0.045
South-west Europe	17015	South-west Europe	0.636
South-west Europe	17015	West Europe	0.136
West Europe	13072	Central Europe	0.180
West Europe	13072	North-west Europe	0.080
West Europe	13072	South-east Europe	0.020
West Europe	13072	South-west Europe	0.220
West Europe	13072	West Europe	0.500

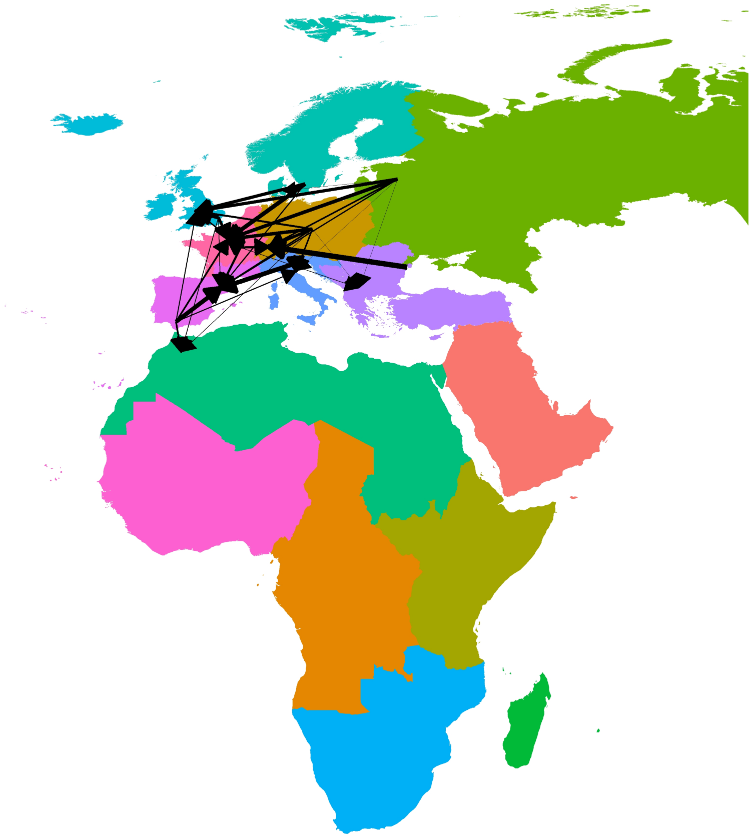

Figure 01980-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

Reference

BirdLife International and Handbook of the Birds of the World (2019). Bird species distribution maps of the world. Version 2019.1. Available at http://datazone.birdlife.org/species/requestdis.