Migratory connectivity analysis

by EURING Migration Atlas

Fringilla coelebs **(EURING code 16360)**

1.1 Connectivity between individuals

The analysis evaluated 2682 individuals (5364 encounters) filtered from a total of 367061 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 16360-1; Figure 16360-1).

Table 16360-1. 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	2682	0.857	0.001	0.831	0.883	4	0.491

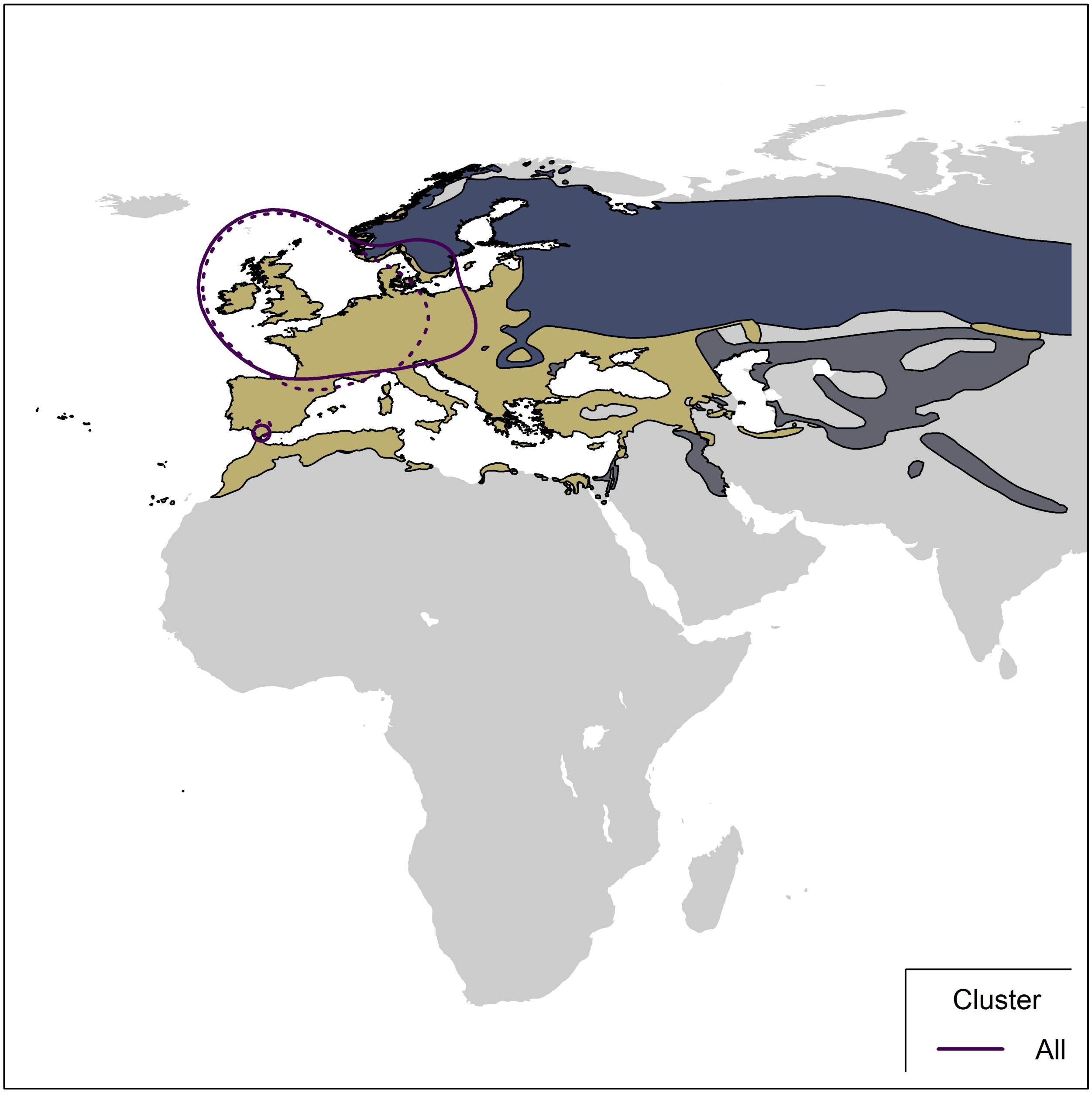

Figure 16360-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 16360-2) and stratified sampling of individuals within the breeding range (Figure 16360-3) and the non breeding range (Figure 16360-4). 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.

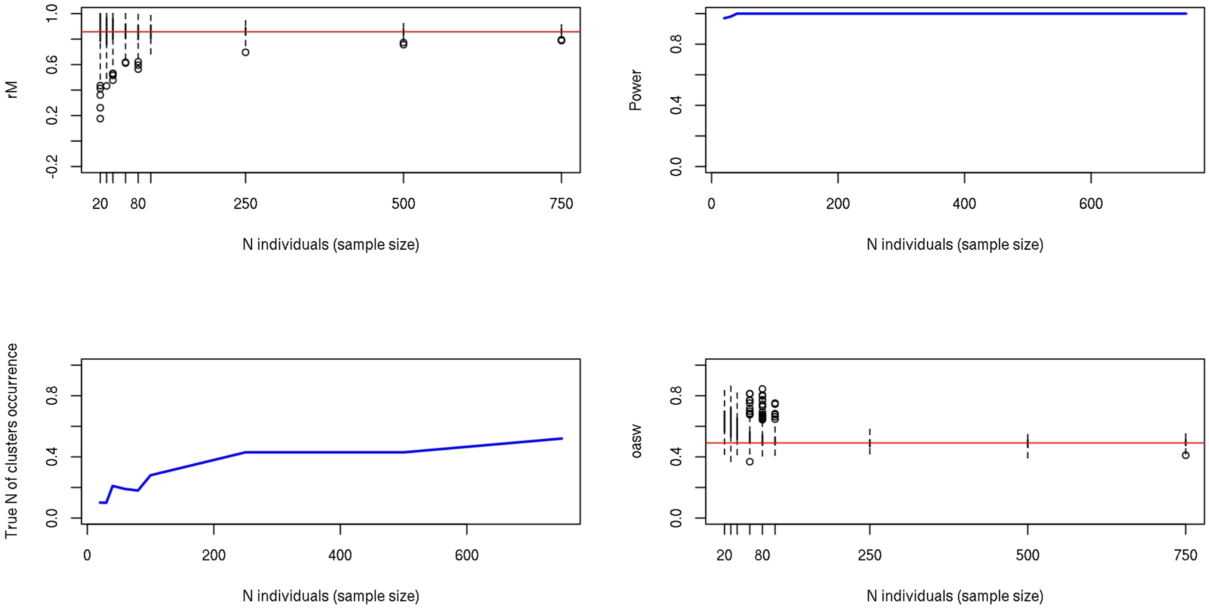

Figure 16360-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

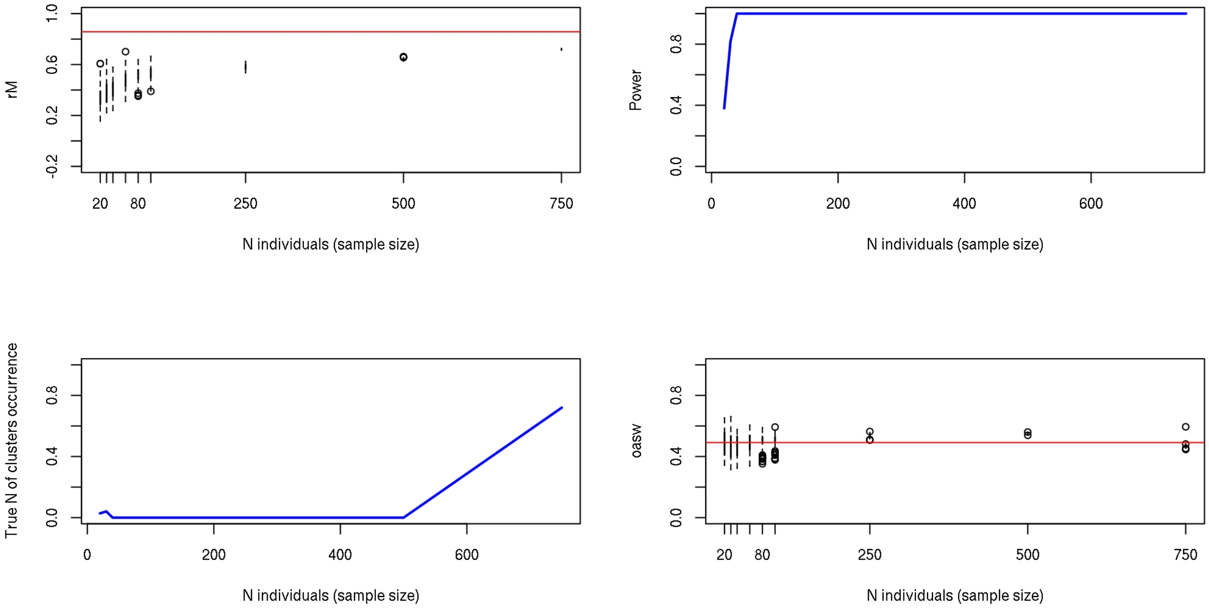

Figure 16360-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

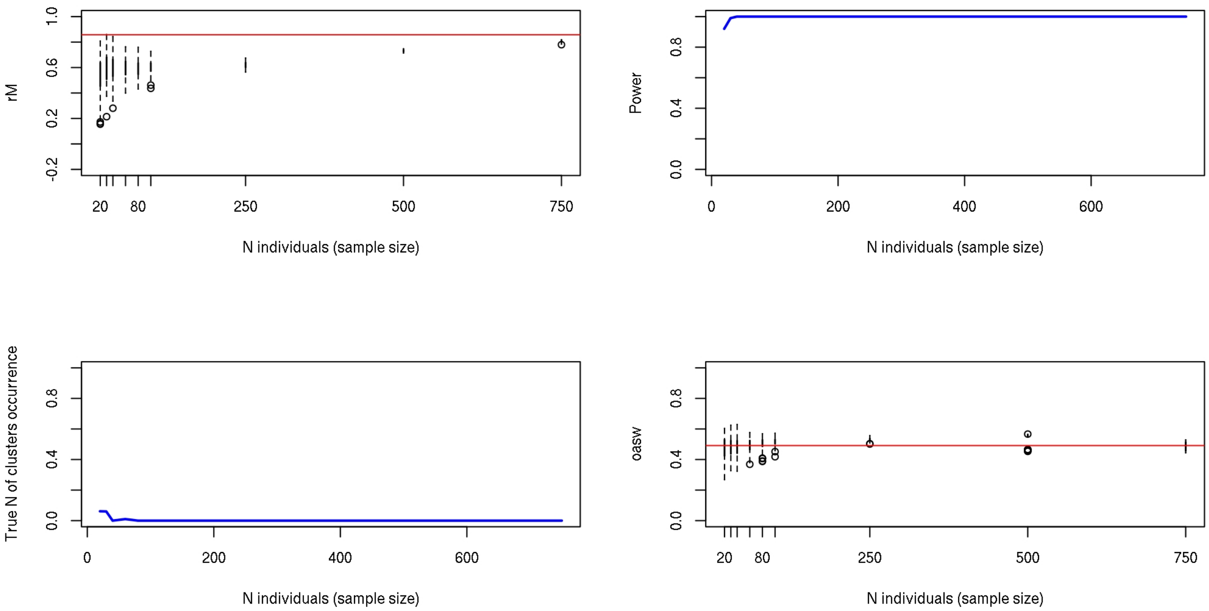

Figure 16360-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

The comparison between the bootstrapped distribution of r_M values from live recaptures and dead recoveries is significant ($p < 0.001$); Figure 16360-5).

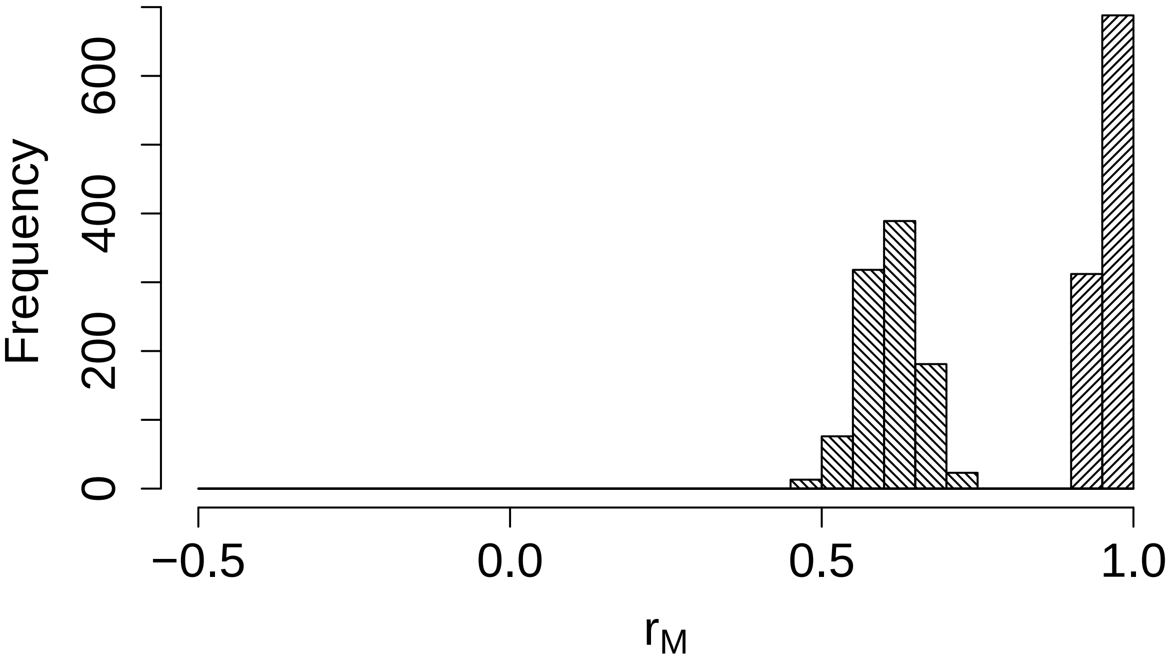

Figure 16360-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows no connectivity (MC = -0.03; MC = -0.03 when adjusted for absolute abundance) between 8 breeding regions and 9 non breeding regions (Table 16360-2; Figure 16360-6).

Table 16360-2. 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	62006000	Central Europe	0.496
Central Europe	62006000	North Africa	0.007
Central Europe	62006000	North-west Europe	0.014
Central Europe	62006000	South-central Europe	0.142
Central Europe	62006000	South-west Europe	0.220
Central Europe	62006000	West Europe	0.121
East Europe	221743221	Arabian peninsula	0.062
East Europe	221743221	Central Europe	0.125
East Europe	221743221	East Europe	0.125
East Europe	221743221	South-central Europe	0.062
East Europe	221743221	South-west Europe	0.500
East Europe	221743221	West Europe	0.125
North Africa	1000	North Africa	1.000

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	41380000	North Europe	0.188
North Europe	41380000	North-west Europe	0.312
North Europe	41380000	South-west Europe	0.152
North Europe	41380000	West Europe	0.348
North-west Europe	18116863	North-west Europe	1.000
South-central Europe	12359453	South-central Europe	1.000
South-west Europe	36917479	South-west Europe	1.000
West Europe	18424224	Central Europe	0.006
West Europe	18424224	West Europe	0.994

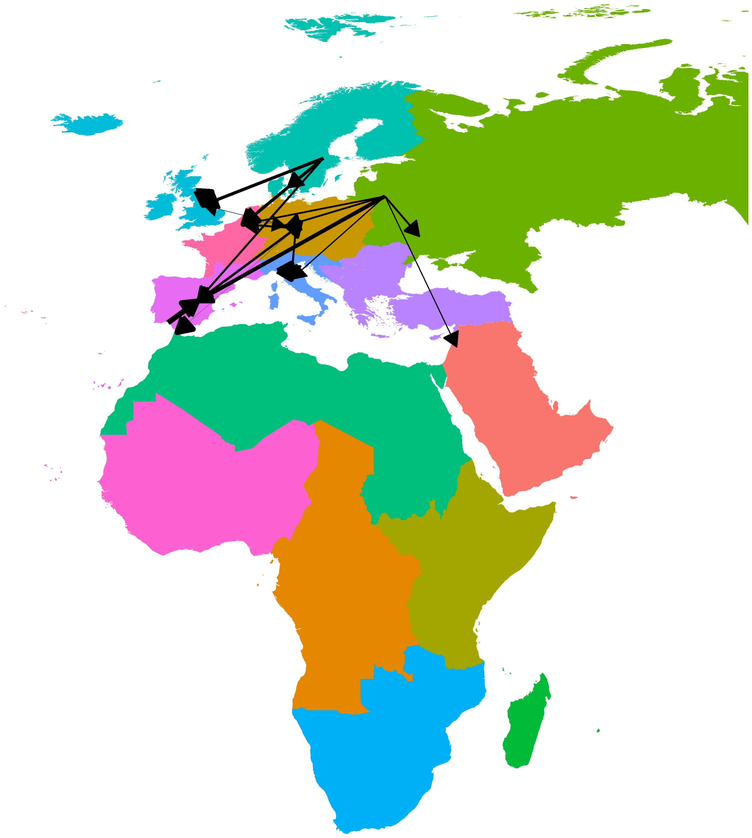

Figure 16360-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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.