

Migratory connectivity analysis

by EURING Migration Atlas

Carduelis flammea (EURING code 16630)

1.1 Connectivity between individuals

The analysis evaluated 202 individuals (404 encounters) filtered from a total of 104038 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from clustering, with a number of first-level clusters = 2 (Table 16630-1; Figure 16630-1).

Table 16630-1. 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	202	0.760	0.001	0.680	0.875	2	0.673
1	1	169	0.508	0.001	0.310	0.688	9	0.442
2	1	33	0.497	0.001	0.287	0.810	4	0.674
21	2	23	0.818	0.001	0.746	0.996	2	0.705
22	2	5	-	-	-	-	-	-
23	2	4	-	-	-	-	-	-
24	2	1	-	-	-	-	-	-
211	3	3	-	-	-	-	-	-
212	3	20	0.908	0.001	0.479	0.995	8	0.546

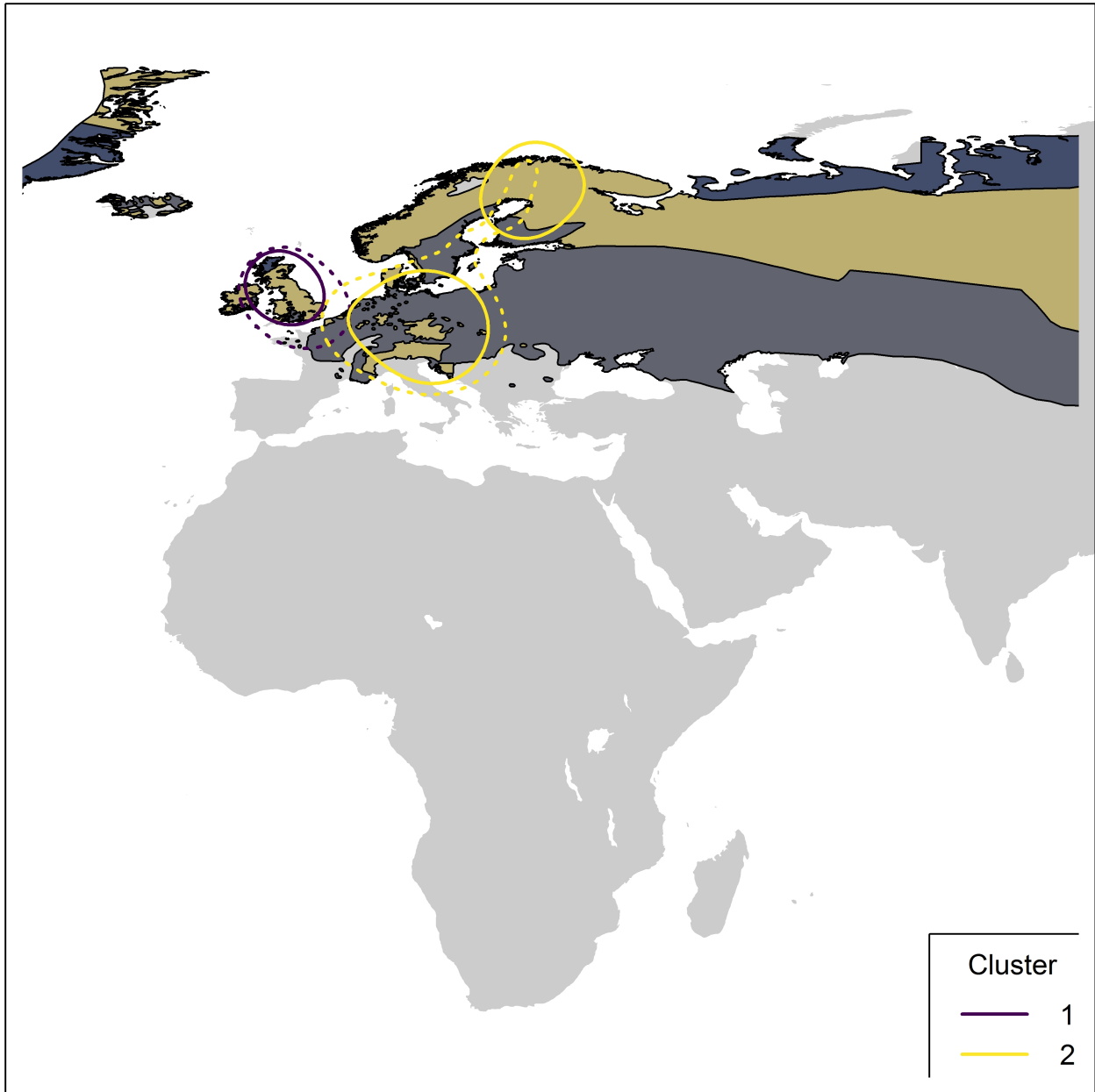


Figure 16630-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 16630-2) and stratified sampling of individuals within the breeding range (Figure 16630-3) and the non breeding range (Figure 16630-4). 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.

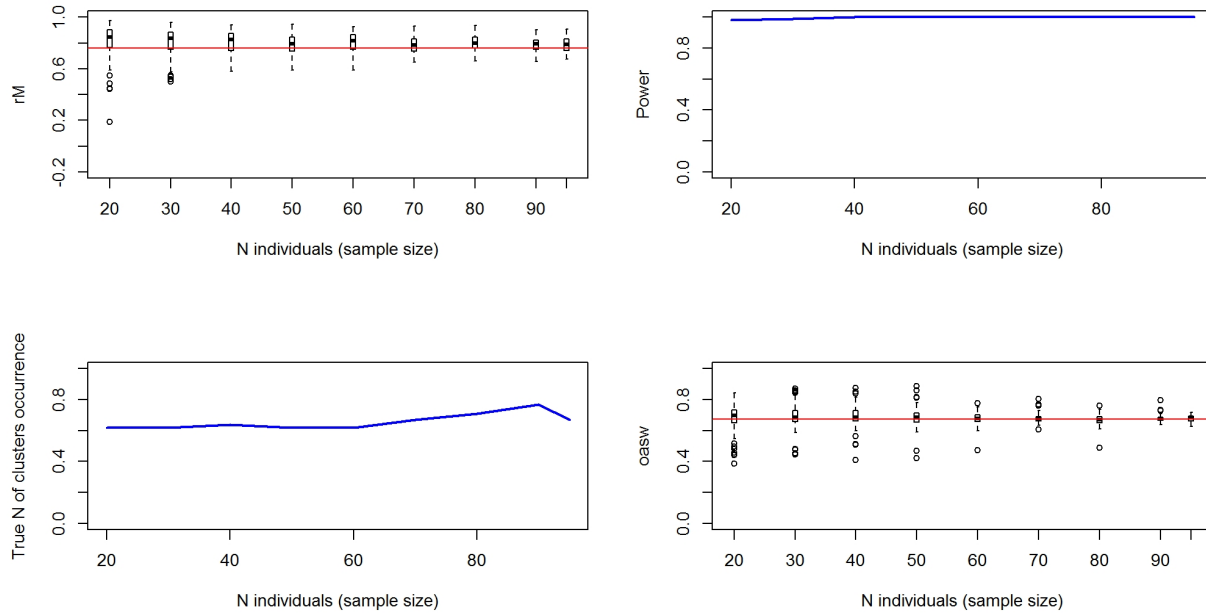


Figure 16630-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

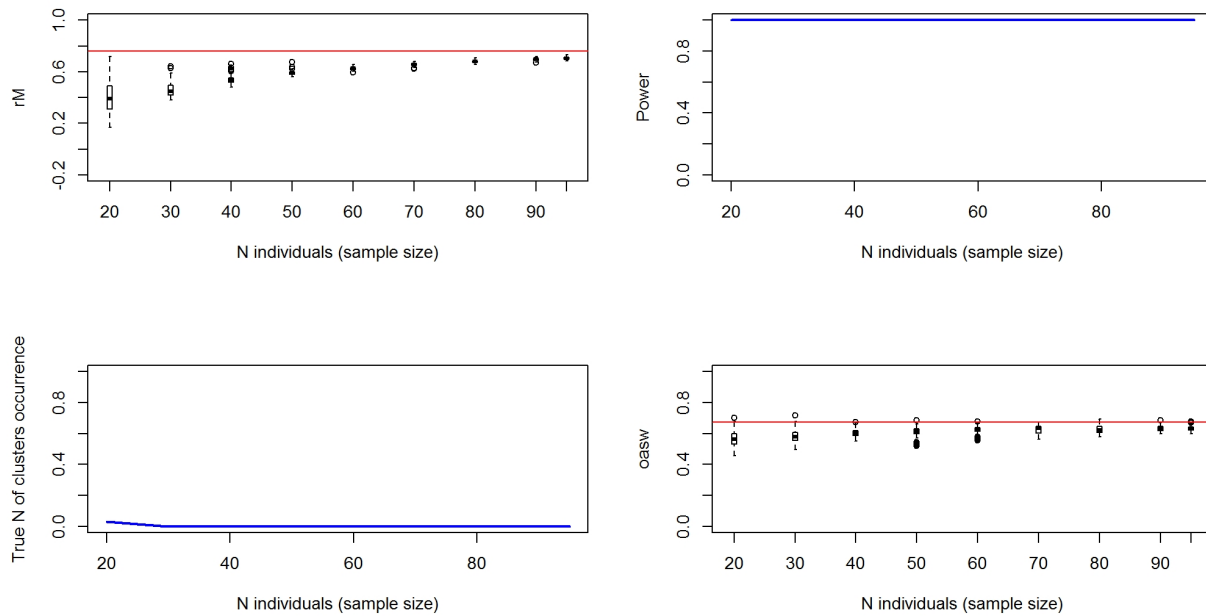


Figure 16630-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

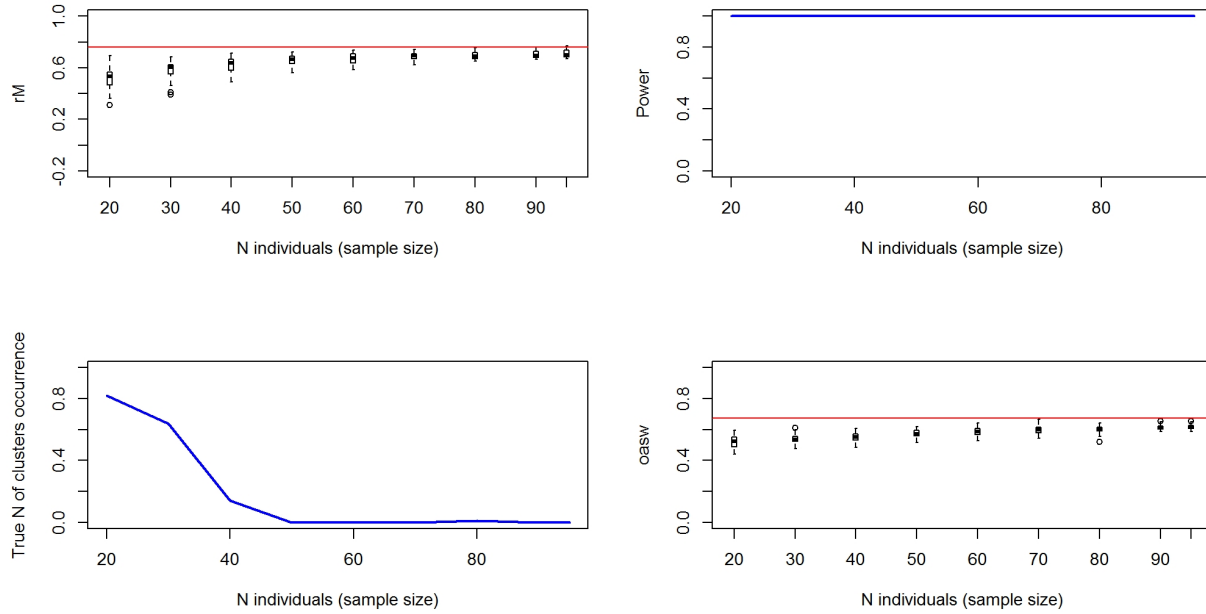


Figure 16630-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 ($p = 0.664$); Figure 16630-5).

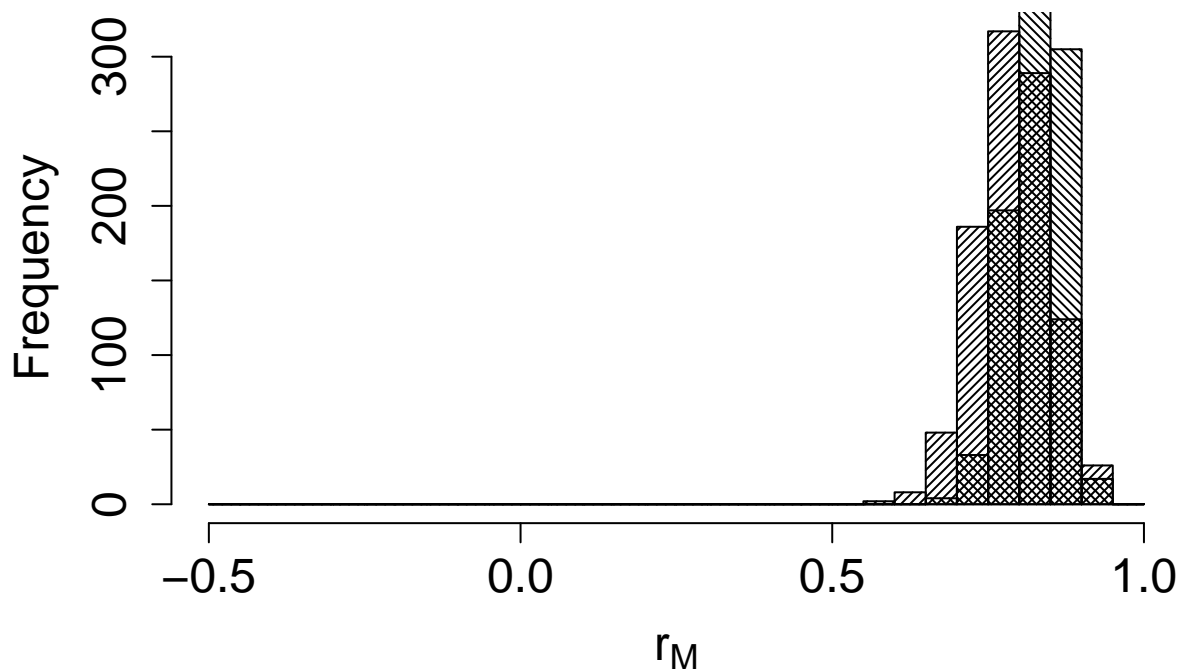


Figure 16630-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low connectivity ($MC = 0.093$; $MC = 0.089$ when adjusted for absolute abundance) between 5 breeding regions and 6 non breeding regions (Table 16630-2; Figure 16630-6).

Table 16630-2. 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	107040	Central Europe	1.000
North Europe	3119550	Central Europe	0.273
North Europe	3119550	East Europe	0.182
North Europe	3119550	North Europe	0.364
North Europe	3119550	West Europe	0.182
North-west Europe	974402	North-west Europe	0.952
North-west Europe	974402	South-central Europe	0.006
North-west Europe	974402	West Europe	0.042
South-central Europe	72800	Central Europe	1.000
West Europe	3892	West Europe	1.000

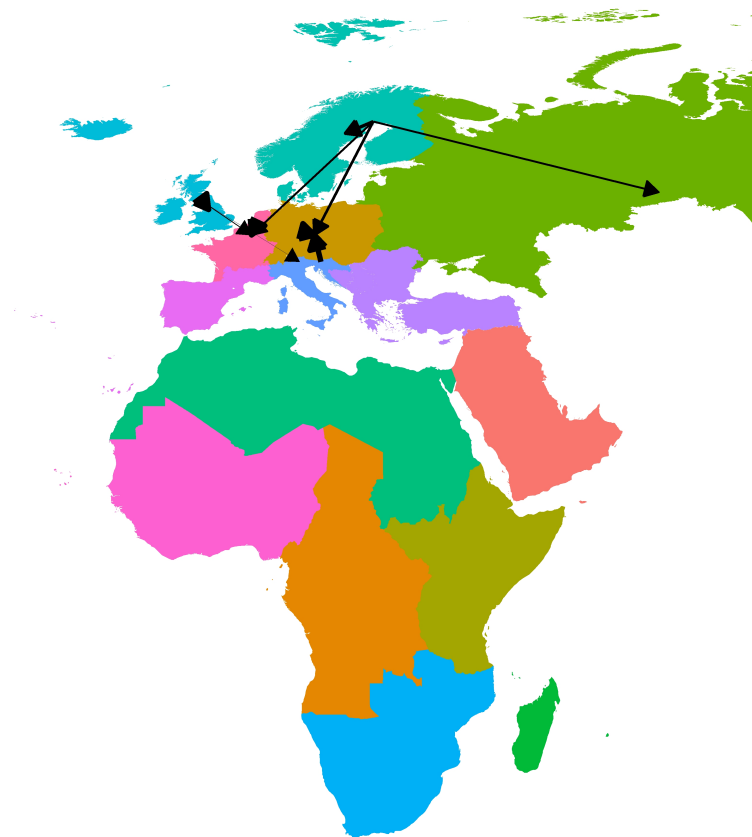


Figure 16630-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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>.