

Migratory connectivity analysis

by EURING Migration Atlas

Carduelis chloris (EURING code 16490)

1.1 Connectivity between individuals

The analysis evaluated 8814 individuals (17628 encounters) filtered from a total of 581160 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 16490-1; Figure 16490-1).

Table 16490-1. 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	8814	0.967	0.001	0.961	0.973	2	0.581
1	1	1811	0.861	0.001	0.838	0.882	3	0.515
2	1	7003	0.972	0.001	0.963	0.980	4	0.544
11	2	548	0.804	0.001	0.745	0.859	2	0.583
12	2	741	0.553	0.001	0.500	0.611	9	0.441
13	2	522	0.813	0.001	0.753	0.872	3	0.651
21	2	1330	0.804	0.001	0.734	0.856	2	0.693
22	2	4764	0.889	0.001	0.851	0.921	3	0.462
23	2	239	0.751	0.001	0.624	0.895	4	0.744
24	2	670	0.943	0.001	0.896	0.982	9	0.651
111	3	76	0.923	0.001	0.855	0.997	9	0.890
112	3	472	0.716	0.001	0.629	0.797	6	0.467
131	3	78	0.790	0.001	0.647	0.887	3	0.631
132	3	421	0.818	0.001	0.712	0.910	7	0.645
133	3	23	0.608	0.002	0.355	0.928	2	0.769
211	3	1190	0.408	0.001	0.332	0.501	2	0.504
212	3	140	0.777	0.001	0.688	0.864	2	0.649
231	3	7	-	-	-	-	-	-
232	3	83	0.589	0.001	0.390	1.000	9	0.764
233	3	111	1.000	0.001	0.999	1.000	7	0.962
234	3	38	0.913	0.001	0.811	1.000	9	0.708
241	3	98	0.891	0.001	0.845	0.978	8	0.615
242	3	76	0.973	0.001	0.927	0.998	2	0.702
243	3	37	0.980	0.001	0.762	0.990	2	0.892
244	3	41	0.698	0.001	0.328	0.942	9	0.712
245	3	46	0.121	0.172	-0.011	0.930	-	-
246	3	150	0.780	0.001	0.645	0.911	9	0.708

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
247	3	140	0.699	0.001	0.556	0.903	6	0.913
248	3	63	0.422	0.001	0.259	0.597	9	0.625
249	3	19	-	-	-	-	-	-

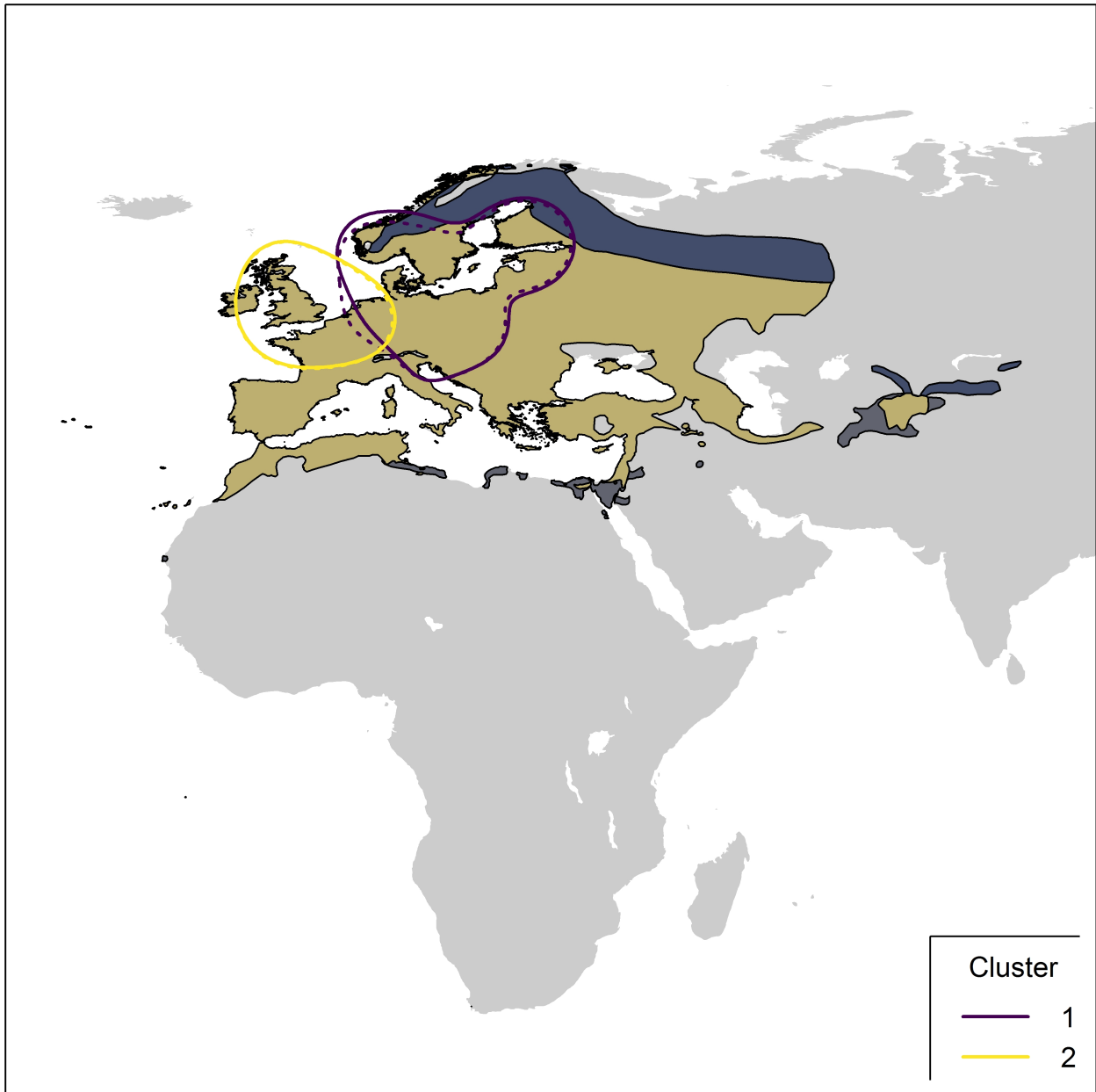


Figure 16490-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 16490-2) and stratified sampling of individuals within the breeding range (Figure 16490-3) and the non breeding range (Figure 16490-4). 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.

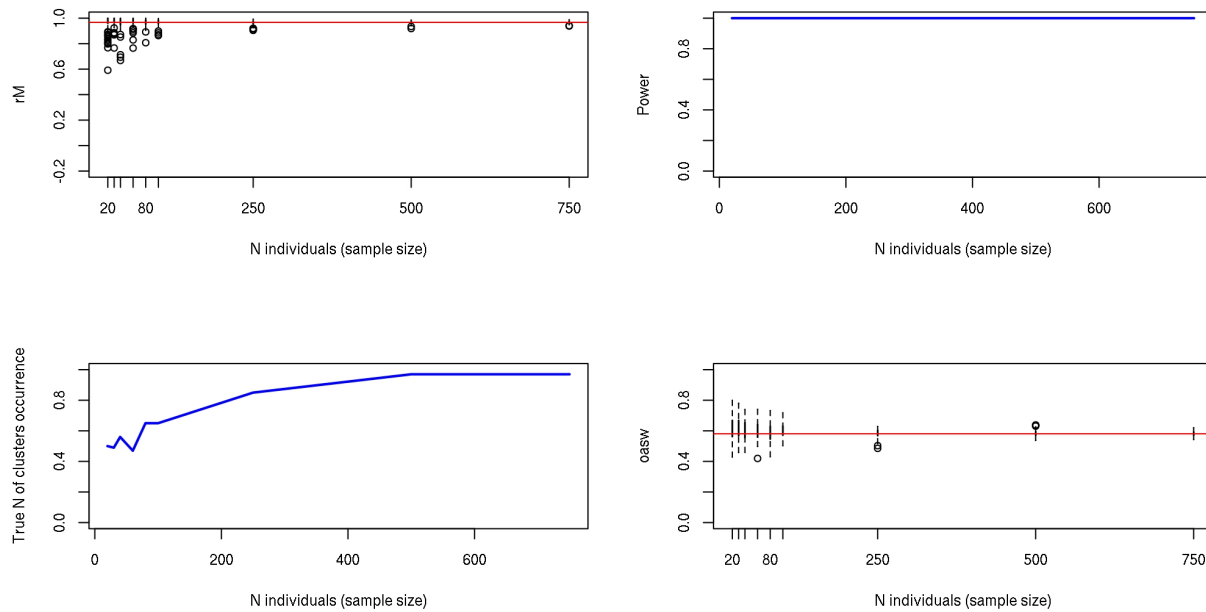


Figure 16490-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

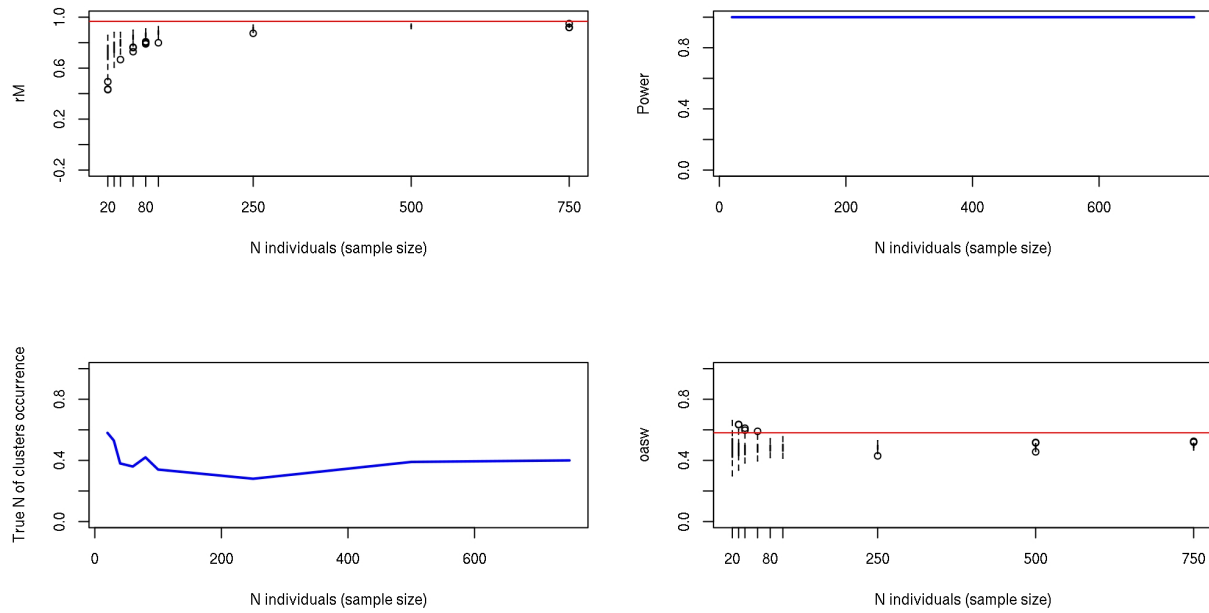


Figure 16490-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

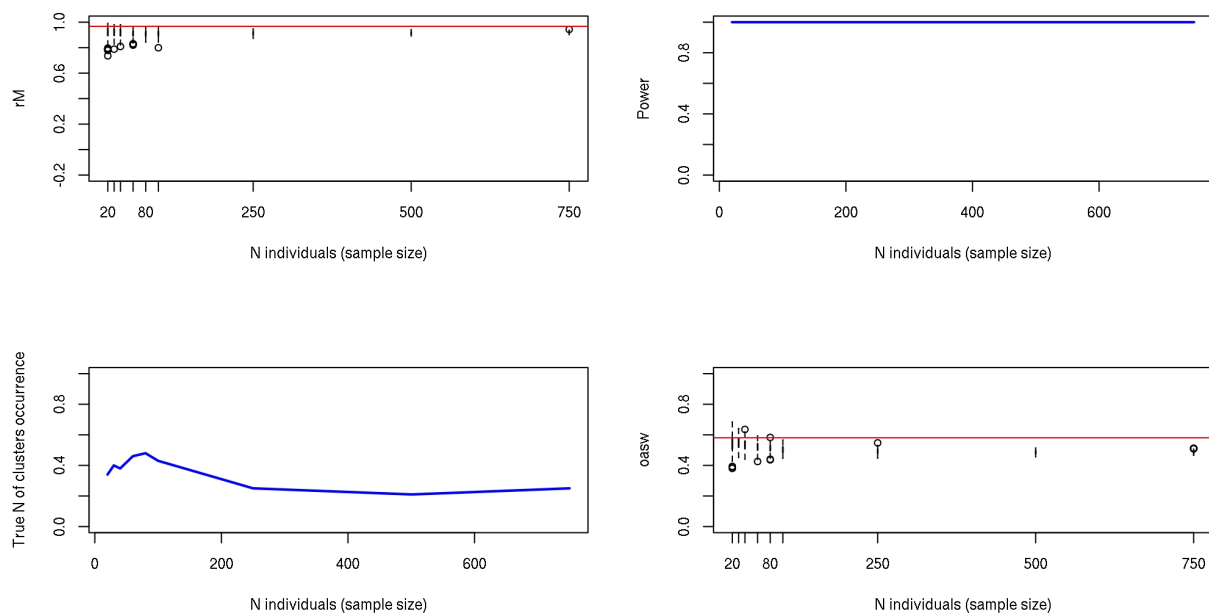


Figure 16490-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 ($p = 0.223$); Figure 16490-5).

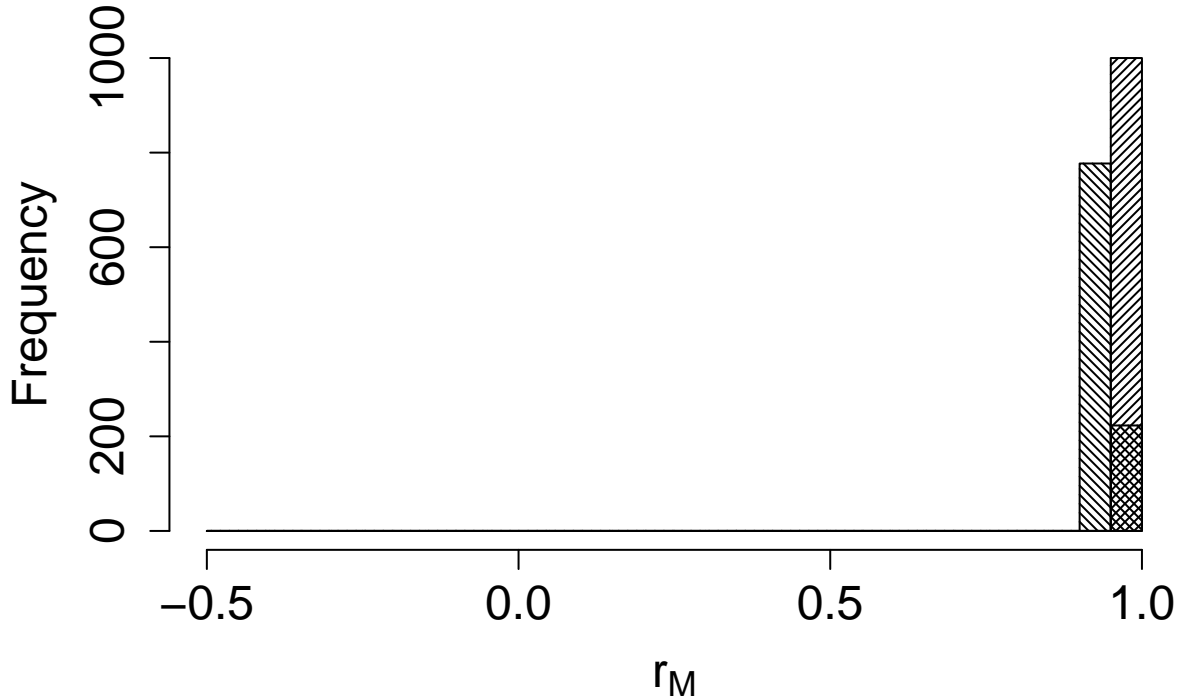


Figure 16490-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows high connectivity ($MC = 0.926$; $MC = 0.926$ when adjusted for absolute abundance) between 8 breeding regions and 9 non breeding regions (Table 16490-2; Figure 16490-6).

Table 16490-2. 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	10532100	Central Europe	0.888
Central Europe	10532100	North Europe	0.001
Central Europe	10532100	South-central Europe	0.018
Central Europe	10532100	South-east Europe	0.003
Central Europe	10532100	South-west Europe	0.020
Central Europe	10532100	West Europe	0.070
East Europe	6887867	Central Europe	0.250
East Europe	6887867	East Europe	0.719
East Europe	6887867	South-west Europe	0.016
East Europe	6887867	West Europe	0.016

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	2983000	Central Europe	0.024
North Europe	2983000	East Europe	0.006
North Europe	2983000	North Europe	0.910
North Europe	2983000	North-west Europe	0.006
North Europe	2983000	South-west Europe	0.001
North Europe	2983000	West Europe	0.052
North-west Europe	4626337	North-west Europe	0.998
North-west Europe	4626337	South-west Europe	0.000
North-west Europe	4626337	West Europe	0.002
South-central Europe	2089874	Central Europe	0.010
South-central Europe	2089874	South-central Europe	0.990
South-east Europe	5235000	South-east Europe	1.000
South-west Europe	19351724	North Africa	0.009
South-west Europe	19351724	South-west Europe	0.991
West Europe	2561911	North Europe	0.001
West Europe	2561911	North-west Europe	0.001
West Europe	2561911	South-west Europe	0.014
West Europe	2561911	West Europe	0.984

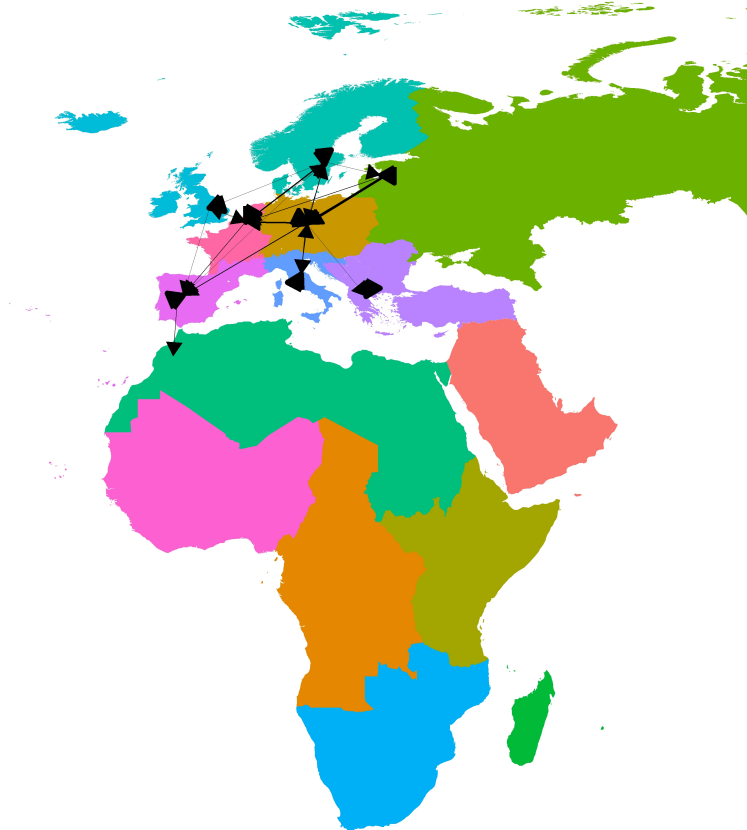


Figure 16490-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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>.