Migratory connectivity analysis

by EURING Migration Atlas

Carduelis spinus **(EURING code 16540)**

1.1 Connectivity between individuals

The analysis evaluated 1370 individuals (2740 encounters) filtered from a total of 340830 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 16540-1; Figure 16540-1).

Table 16540-1. 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	1370	0.692	0.001	0.657	0.727	2	0.628
1	1	183	0.109	0.007	0.027	0.217	2	0.381
2	1	1187	0.664	0.001	0.614	0.709	9	0.572
21	2	78	0.919	0.001	0.572	0.999	7	0.935
22	2	41	0.829	0.001	0.538	0.965	2	0.864
23	2	146	0.094	0.045	0.015	0.188	6	0.355
24	2	395	0.543	0.001	0.457	0.695	9	0.600
25	2	132	0.827	0.001	0.705	0.932	6	0.609
26	2	194	0.597	0.001	0.485	0.716	9	0.676
27	2	100	0.713	0.001	0.539	1.000	9	0.958
28	2	81	0.791	0.001	0.660	0.883	7	0.799
29	2	20	0.998	0.001	0.993	1.000	2	0.950
211	3	1	-	-	-	-	-	-
212	3	12	-	-	-	-	-	-
213	3	2	-	-	-	-	-	-
214	3	60	-0.047	1.000	-0.078	-0.023	-	-
215	3	1	-	-	-	-	-	-
216	3	1	-	-	-	-	-	-
217	3	1	-	-	-	-	-	-
221	3	3	-	-	-	-	-	-
222	3	38	0.518	0.008	0.329	0.926	2	0.801
241	3	162	0.767	0.001	0.533	0.928	9	0.910
242	3	24	0.822	0.001	0.613	0.963	3	0.839
243	3	45	0.742	0.001	0.549	0.906	8	0.876
244	3	14	-	-	-	-	-	-
245	3	24	0.077	0.141	-0.014	0.577	-	-
246	3	51	0.735	0.001	0.541	0.919	5	0.905

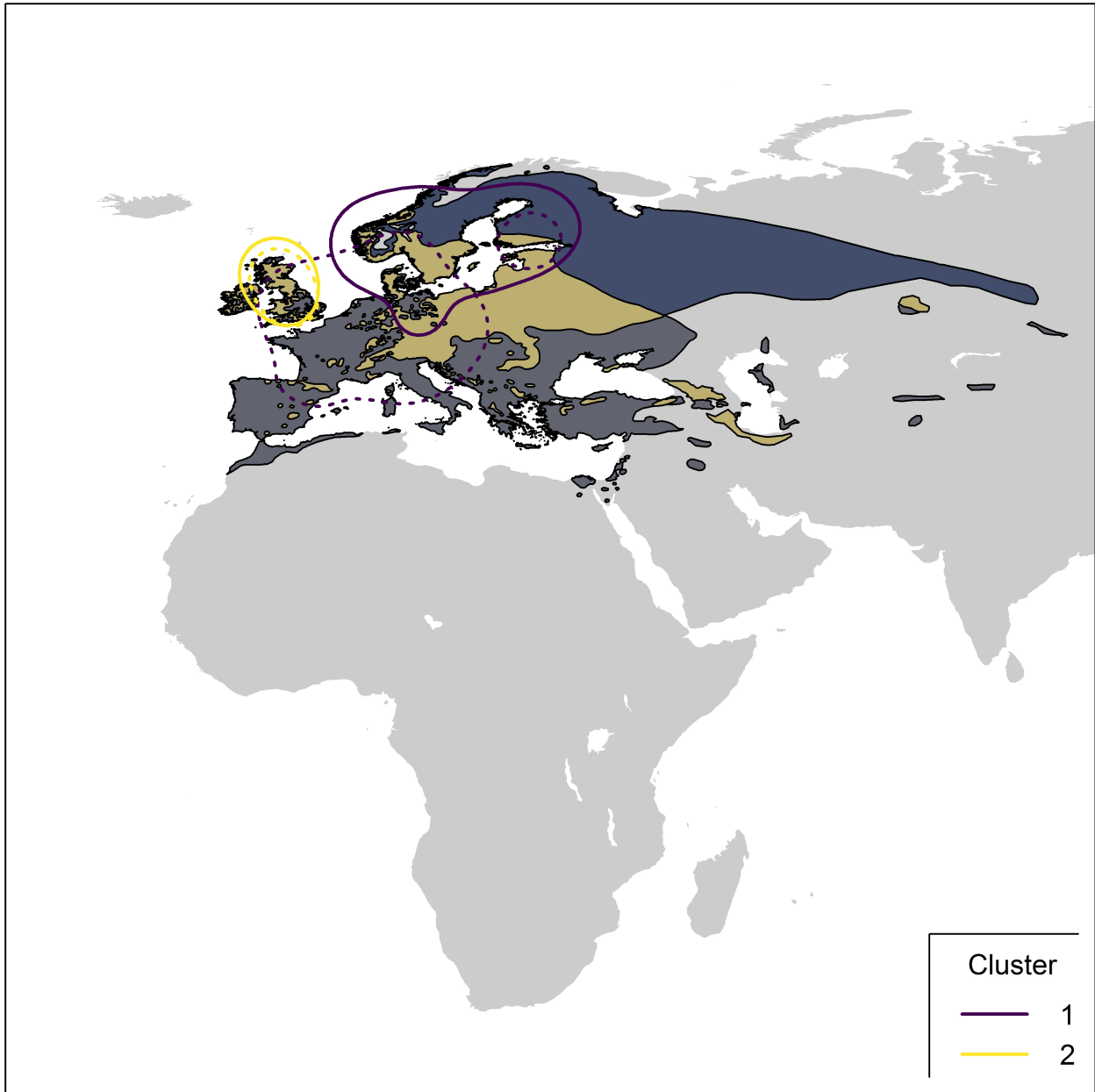| Cluster name	Level of clustering	N individuals	Migratory connectivity (r_M)	p-value	Lower 95% confidence limit	Upper 95% confidence limit	Best number of clusters	oasw
247	3	7	-	-	-	-	-	-
248	3	16	-	-	-	-	-	-
249	3	52	0.378	0.008	0.128	0.664	2	0.789
251	3	52	0.810	0.001	0.312	0.985	9	0.733
252	3	29	0.992	0.001	0.974	1.000	6	0.875
253	3	18	-	-	-	-	-	-
254	3	8	-	-	-	-	-	-
255	3	5	-	-	-	-	-	-
256	3	20	0.958	0.002	0.896	1.000	4	0.843
261	3	39	0.796	0.001	0.614	0.948	7	0.935
262	3	75	0.944	0.003	-0.031	0.994	2	0.968
263	3	7	-	-	-	-	-	-
264	3	7	-	-	-	-	-	-
265	3	6	-	-	-	-	-	-
266	3	29	0.616	0.008	0.180	1.000	5	0.897
267	3	7	-	-	-	-	-	-
268	3	10	-	-	-	-	-	-
269	3	14	-	-	-	-	-	-
271	3	24	0.926	0.020	-0.082	0.983	2	0.896
272	3	9	-	-	-	-	-	-
273	3	9	-	-	-	-	-	-
274	3	2	-	-	-	-	-	-
275	3	4	-	-	-	-	-	-
276	3	1	-	-	-	-	-	-
277	3	43	-	-	-	-	-	-
278	3	7	-	-	-	-	-	-
279	3	1	-	-	-	-	-	-
281	3	3	-	-	-	-	-	-
282	3	7	-	-	-	-	-	-
283	3	53	1.000	0.016	1.000	1.000	2	0.981
284	3	7	-	-	-	-	-	-
285	3	5	-	-	-	-	-	-
286	3	5	-	-	-	-	-	-
287	3	1	-	-	-	-	-	-
291	3	3	-	-	-	-	-	-
292	3	17	-	-	-	-	-	-

Figure 16540-1. 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 16540-2) and stratified sampling of individuals within the breeding range (Figure 16540-3) and the non breeding range (Figure 16540-4). 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.
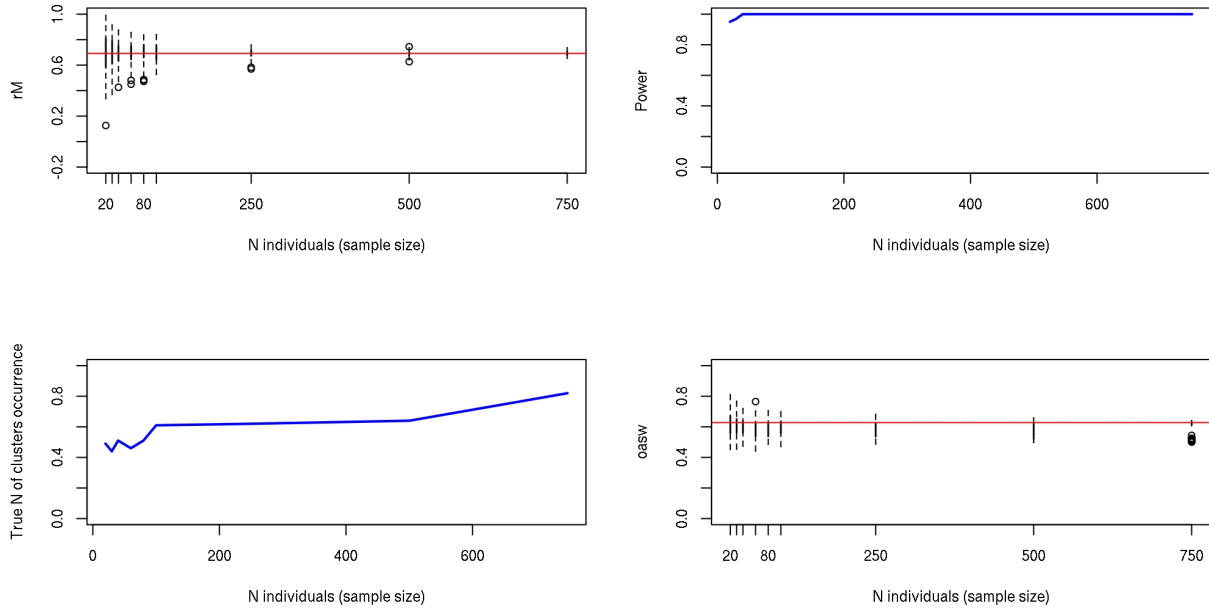

Figure 16540-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.
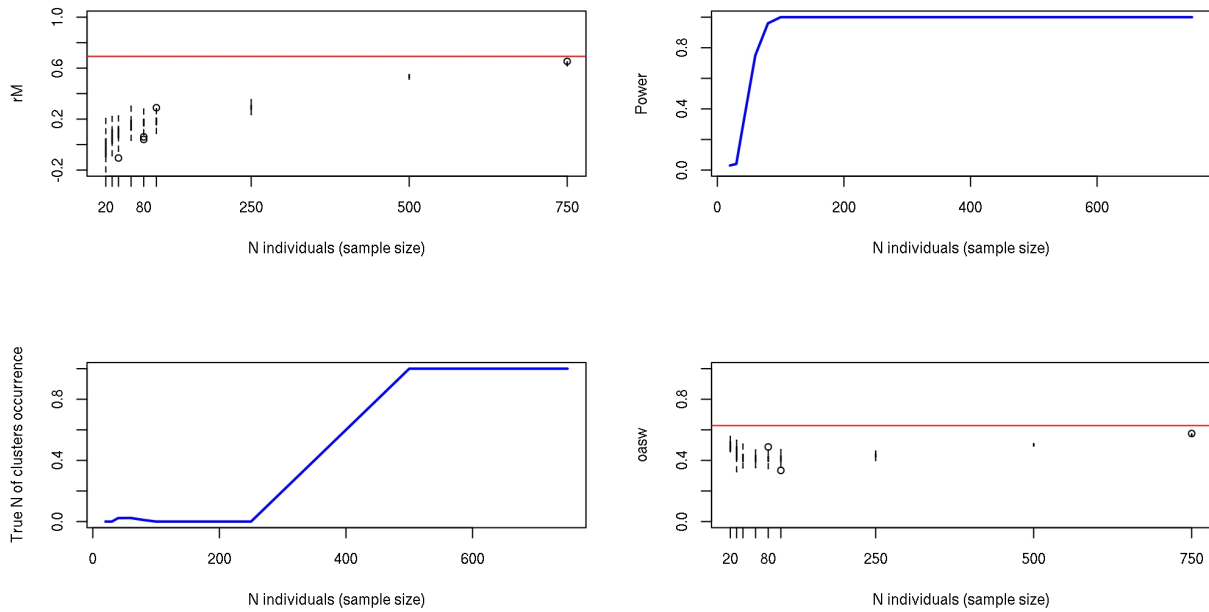

Figure 16540-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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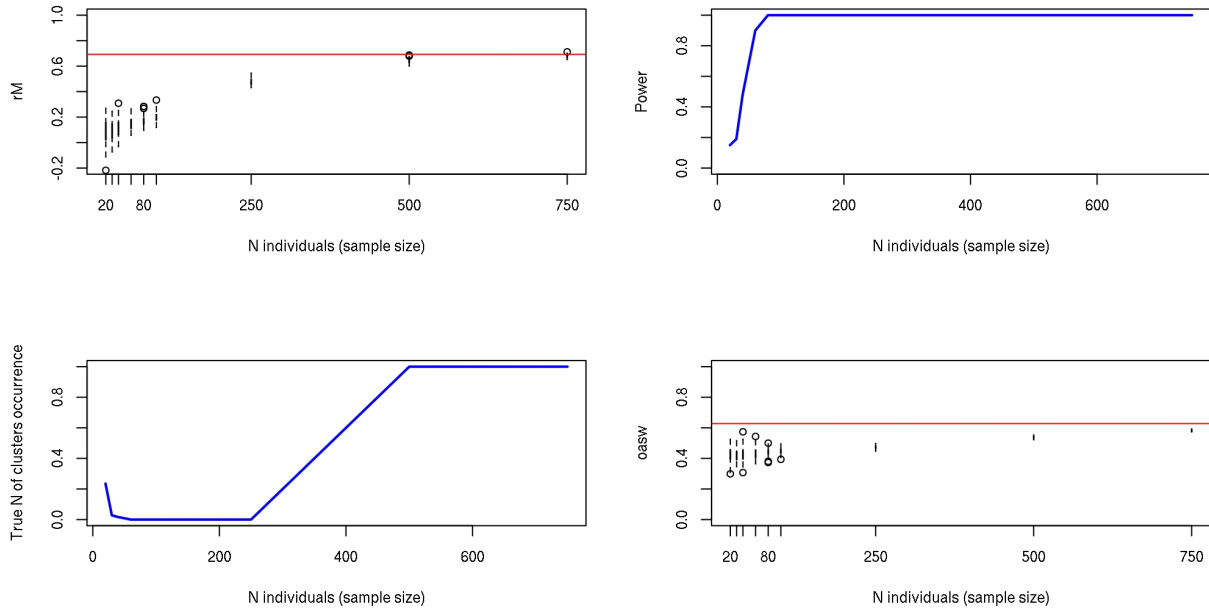

Figure 16540-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 16540-5).
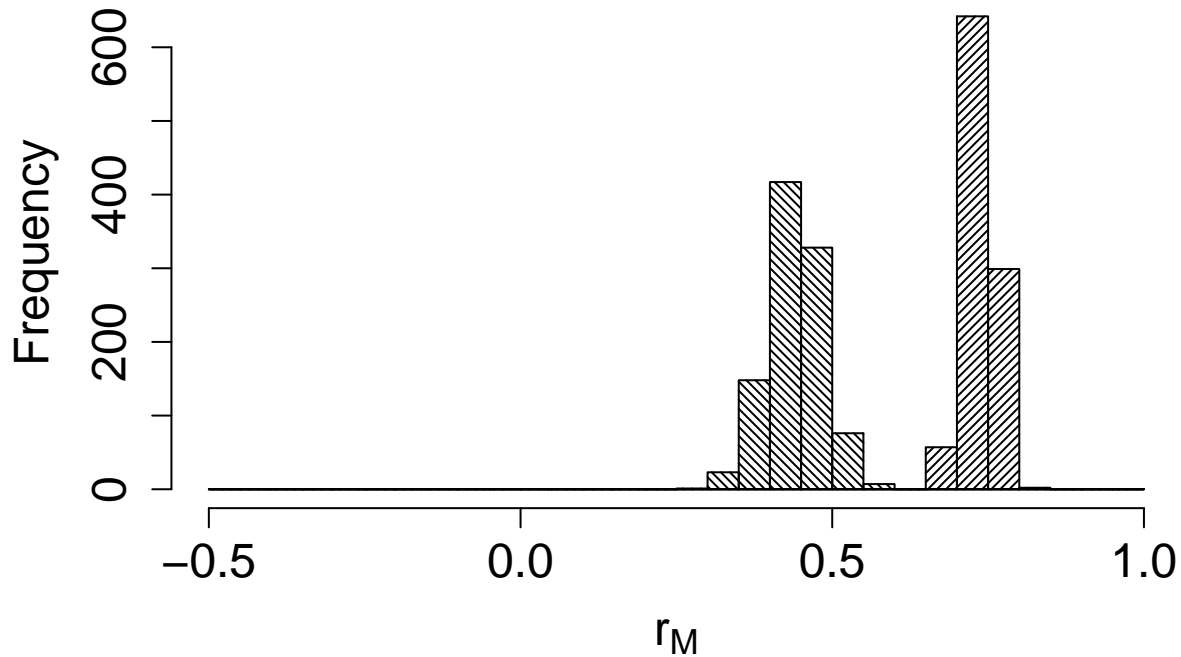
Figure 16540-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low connectivity (MC = 0.033; MC = 0.033 when adjusted for absolute abundance) between 5 breeding regions and 7 non breeding regions (Table 16540-2; Figure 16540-6).

Table 16540-2. 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	892320	Central Europe	0.550
Central Europe	892320	South-central Europe	0.100
Central Europe	892320	South-west Europe	0.150
Central Europe	892320	West Europe	0.200
East Europe	26429389	Central Europe	0.222
East Europe	26429389	North Europe	0.111
East Europe	26429389	North-west Europe	0.111
East Europe	26429389	South-central Europe	0.222
East Europe	26429389	South-west Europe	0.111
East Europe	26429389	West Europe	0.222
North Europe	6202404	Central Europe	0.175
North Europe	6202404	North Europe	0.237
North Europe	6202404	North-west Europe	0.113

| Breeding region	Abundance	Non breeding region	Transition probability
North Europe	6202404	South-central Europe	0.062
North Europe	6202404	South-east Europe	0.006
North Europe	6202404	South-west Europe	0.040
North Europe	6202404	West Europe	0.367
North-west Europe	1039998	North-west Europe	0.992
North-west Europe	1039998	West Europe	0.008
West Europe	2396	South-west Europe	0.250
West Europe	2396	West Europe	0.750
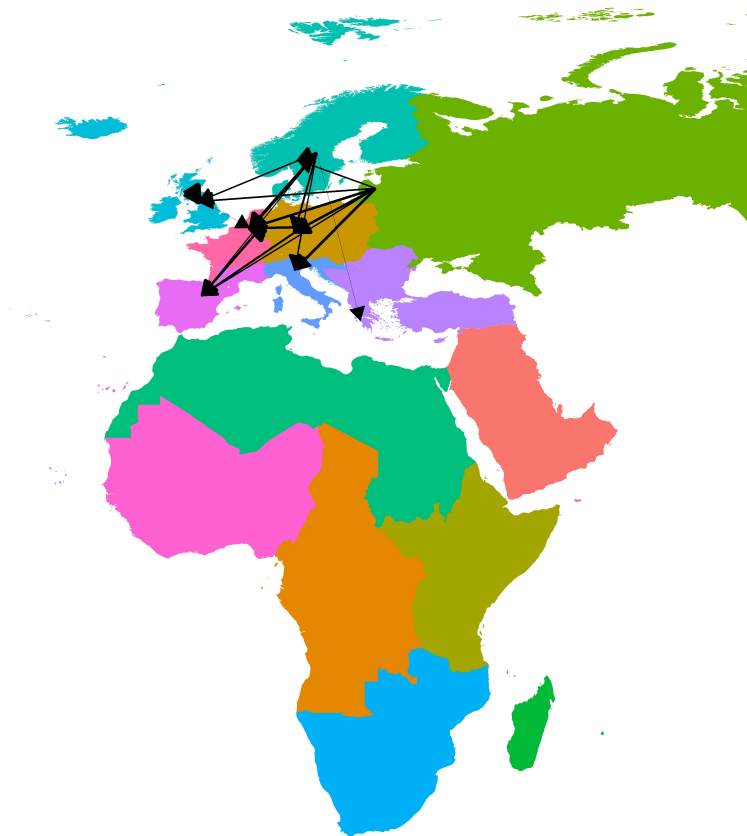
Figure 16540-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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.