Migratory connectivity analysis

by EURING Migration Atlas

Regulus regulus **(EURING code 13140)**

1.1 Connectivity between individuals

The analysis evaluated 220 individuals (440 encounters) filtered from a total of 203792 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 13140-1; Figure 13140-1).

Table 13140-1. 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	220	1.000	0.001	0.998	1	2	0.554
1	1	35	1.000	0.001	1.000	1	2	0.826
2	1	185	0.999	0.001	0.994	1	9	0.503
11	2	33	1.000	0.001	1.000	1	2	0.800
12	2	2	-	-	-	-	-	-
21	2	26	1.000	0.001	1.000	1	6	0.788
22	2	1	-	-	-	-	-	-
23	2	11	-	-	-	-	-	-
24	2	29	0.999	0.001	0.996	1	3	0.734
25	2	45	1.000	0.001	1.000	1	9	0.615
26	2	18	-	-	-	-	-	-
27	2	26	1.000	0.001	1.000	1	9	0.620
28	2	23	0.934	0.001	0.810	1	2	0.712
29	2	6	-	-	-	-	-	-
111	3	30	1.000	0.001	0.999	1	4	0.754
112	3	3	-	-	-	-	-	-
211	3	3	-	-	-	-	-	-
212	3	1	-	-	-	-	-	-
213	3	4	-	-	-	-	-	-
214	3	3	-	-	-	-	-	-
215	3	7	-	-	-	-	-	-
216	3	8	-	-	-	-	-	-
241	3	17	-	-	-	-	-	-
242	3	2	-	-	-	-	-	-
243	3	10	-	-	-	-	-	-
251	3	4	-	-	-	-	-	-
252	3	8	-	-	-	-	-	-

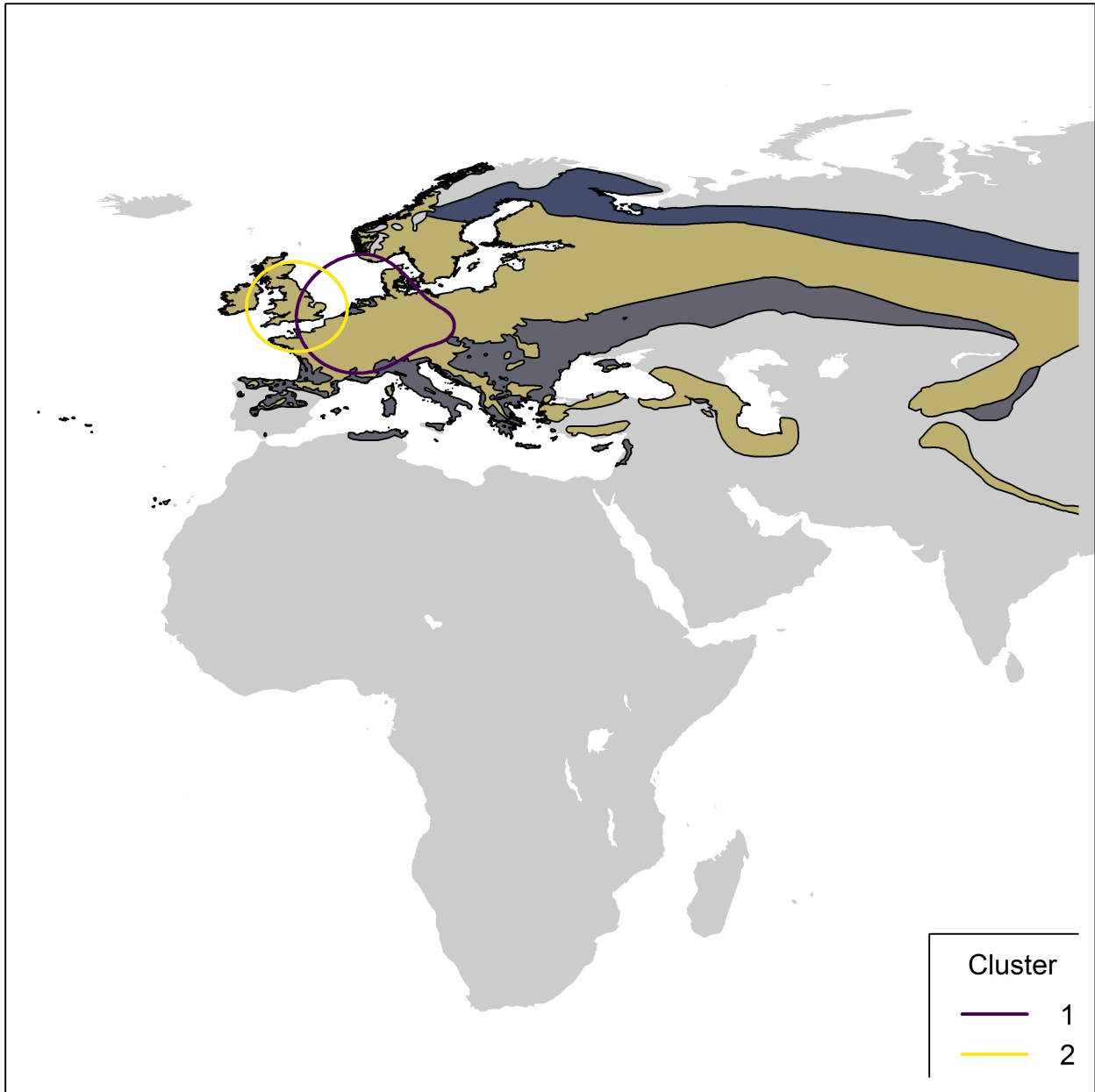| Cluster name	Level of clustering	N individuals	Migratory connectivity (r_M)	p-value	Lower 95% confidence limit	Upper 95% confidence limit	Best number of clusters	oasw
253	3	7	-	-	-	-	-	-
254	3	5	-	-	-	-	-	-
255	3	6	-	-	-	-	-	-
256	3	8	-	-	-	-	-	-
257	3	2	-	-	-	-	-	-
258	3	2	-	-	-	-	-	-
259	3	3	-	-	-	-	-	-
271	3	7	-	-	-	-	-	-
272	3	1	-	-	-	-	-	-
273	3	2	-	-	-	-	-	-
274	3	3	-	-	-	-	-	-
275	3	1	-	-	-	-	-	-
276	3	2	-	-	-	-	-	-
277	3	7	-	-	-	-	-	-
278	3	1	-	-	-	-	-	-
279	3	2	-	-	-	-	-	-
281	3	8	-	-	-	-	-	-
282	3	15	-	-	-	-	-	-

Figure 13140-1. 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 13140-2) and stratified sampling of individuals within the breeding range (Figure 13140-3) and the non breeding range (Figure 13140-4). 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.
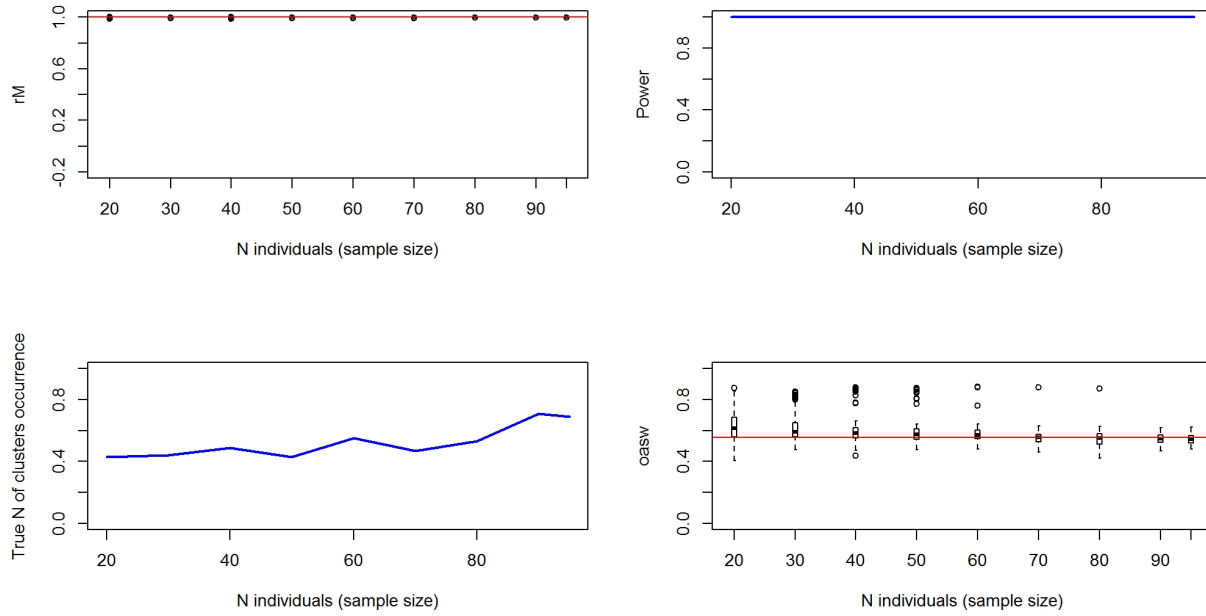

Figure 13140-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.
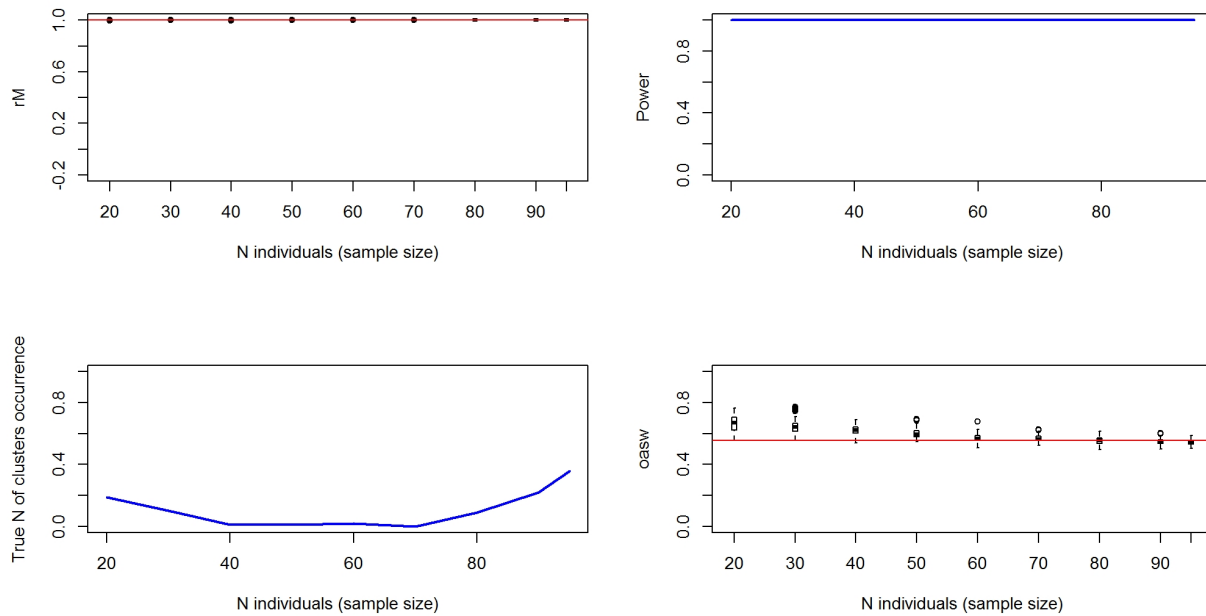

Figure 13140-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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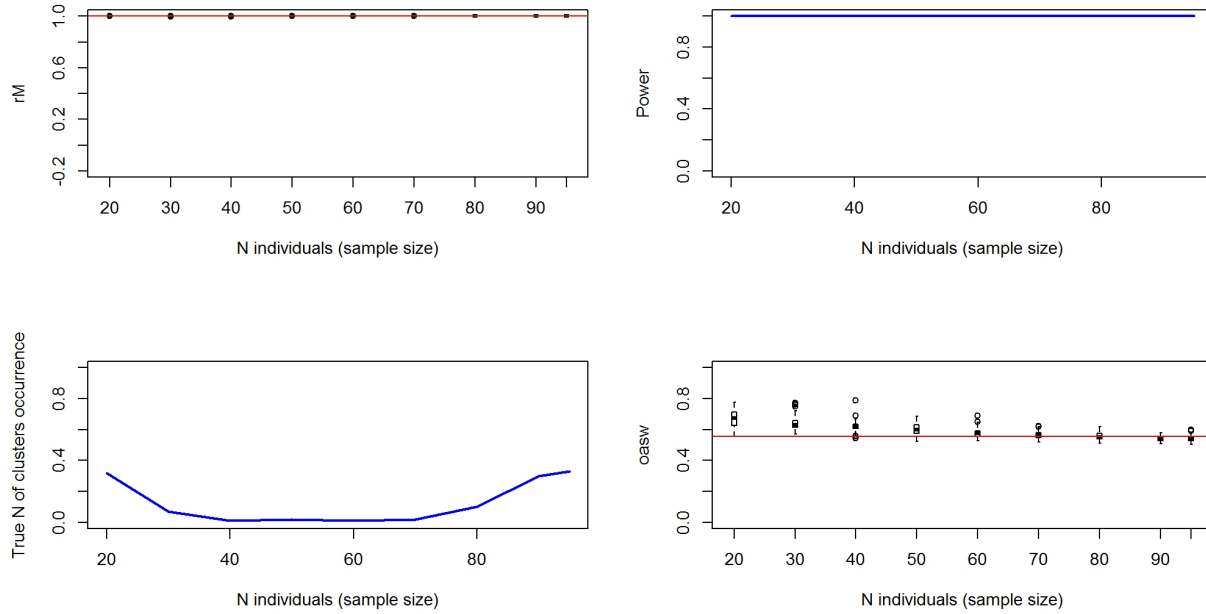

Figure 13140-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

2. Connectivity between pre-defined regions

The species shows high connectivity (MC = 1; MC = 1 when adjusted for absolute abundance) between 5 breeding regions and 5 non breeding regions (Table 13140-2; Figure 13140-6).

Table 13140-2. 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	5713100	Central Europe	1
North Europe	11188020	North Europe	1
North-west Europe	3303190	North-west Europe	1
South-west Europe	1165411	South-west Europe	1
West Europe	822014	West Europe	1

Figure 13140-6. 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.