

Migratory connectivity analysis

by EURING Migration Atlas

Erithacus rubecula (EURING code 10990)

1.1 Connectivity between individuals

The analysis evaluated 6621 individuals (13242 encounters) filtered from a total of 948232 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 10990-1; Figure 10990-1).

Table 10990-1. 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	6621	0.933	0.001	0.921	0.944	2	0.742
1	1	6101	0.922	0.001	0.902	0.942	9	0.420
2	1	520	0.706	0.001	0.644	0.775	9	0.674
21	2	56	0.143	0.014	0.051	0.337	7	0.306
22	2	35	0.887	0.001	0.812	0.980	3	0.717
23	2	63	0.801	0.001	0.728	0.904	9	0.579
24	2	46	0.885	0.001	0.818	1.000	3	0.754
25	2	100	0.901	0.001	0.858	0.997	2	0.819
26	2	98	1.000	0.001	0.999	1.000	9	0.918
27	2	39	1.000	0.001	1.000	1.000	4	0.885
28	2	77	0.972	0.001	0.955	1.000	8	0.866
29	2	6	-	-	-	-	-	-
221	3	3	-	-	-	-	-	-
222	3	29	0.897	0.001	0.741	1.000	9	0.727
223	3	3	-	-	-	-	-	-
231	3	5	-	-	-	-	-	-
232	3	6	-	-	-	-	-	-
233	3	7	-	-	-	-	-	-
234	3	8	-	-	-	-	-	-
235	3	2	-	-	-	-	-	-
236	3	4	-	-	-	-	-	-
237	3	18	-	-	-	-	-	-
238	3	8	-	-	-	-	-	-
239	3	5	-	-	-	-	-	-
241	3	8	-	-	-	-	-	-
242	3	30	1.000	0.001	1.000	1.000	6	0.732
243	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
251	3	96	0.855	0.001	0.838	0.990	8	0.682
252	3	4	-	-	-	-	-	-
261	3	1	-	-	-	-	-	-
262	3	1	-	-	-	-	-	-
263	3	24	0.796	0.009	0.365	1.000	3	0.893
264	3	53	1.000	0.019	1.000	1.000	2	0.981
265	3	8	-	-	-	-	-	-
266	3	2	-	-	-	-	-	-
267	3	2	-	-	-	-	-	-
268	3	4	-	-	-	-	-	-
269	3	3	-	-	-	-	-	-
271	3	34	1.000	0.001	1.000	1.000	3	0.914
272	3	3	-	-	-	-	-	-
273	3	1	-	-	-	-	-	-
274	3	1	-	-	-	-	-	-
281	3	1	-	-	-	-	-	-
282	3	1	-	-	-	-	-	-
283	3	32	1.000	0.001	1.000	1.000	4	0.998
284	3	21	1.000	0.001	1.000	1.000	4	0.905
285	3	4	-	-	-	-	-	-
286	3	5	-	-	-	-	-	-
287	3	7	-	-	-	-	-	-
288	3	6	-	-	-	-	-	-

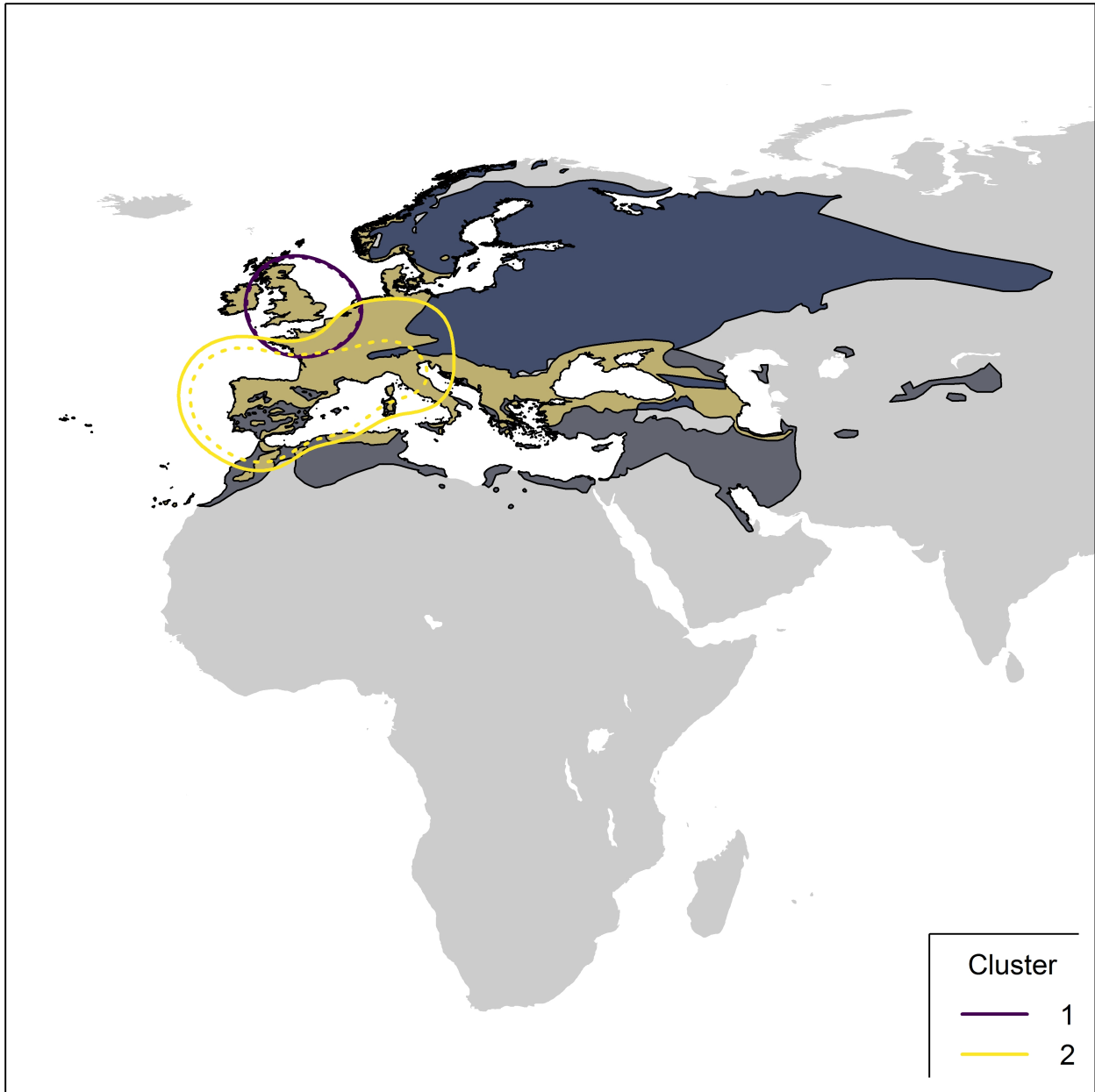


Figure 10990-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 10990-2) and stratified sampling of individuals within the breeding range (Figure 10990-3) and the non breeding range (Figure 10990-4). 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.

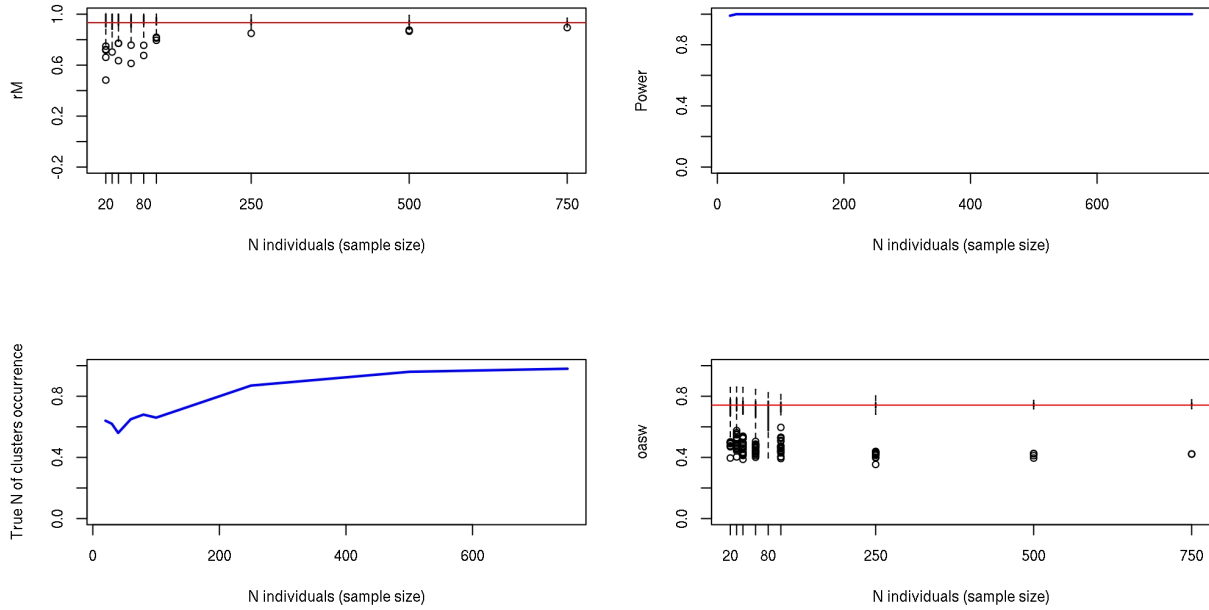


Figure 10990-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

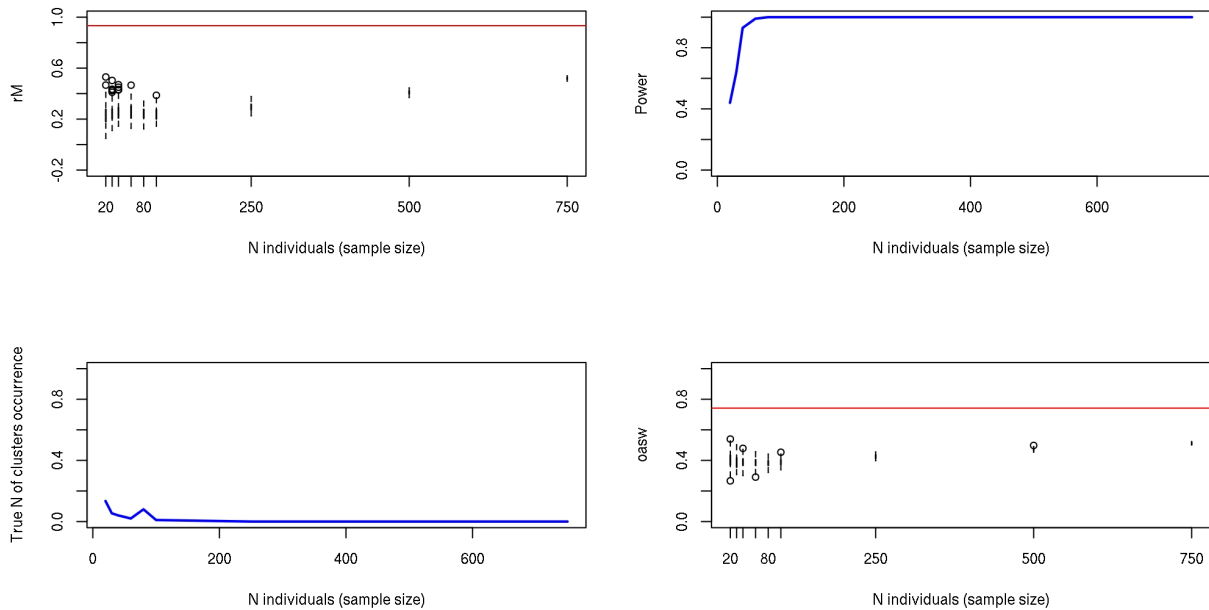


Figure 10990-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

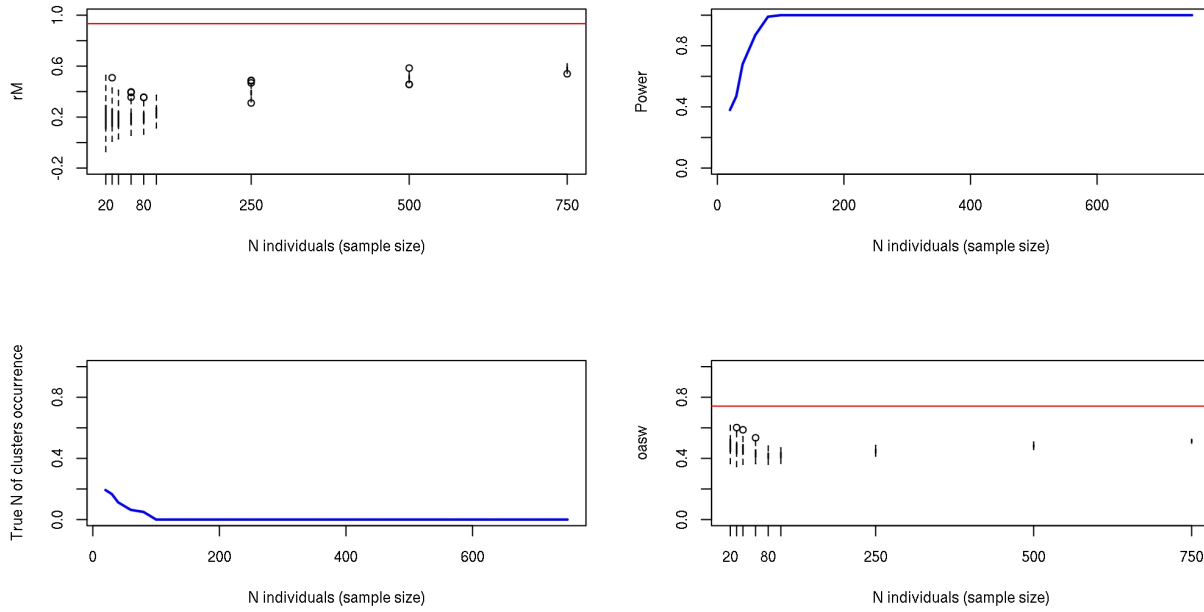


Figure 10990-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 10990-5).

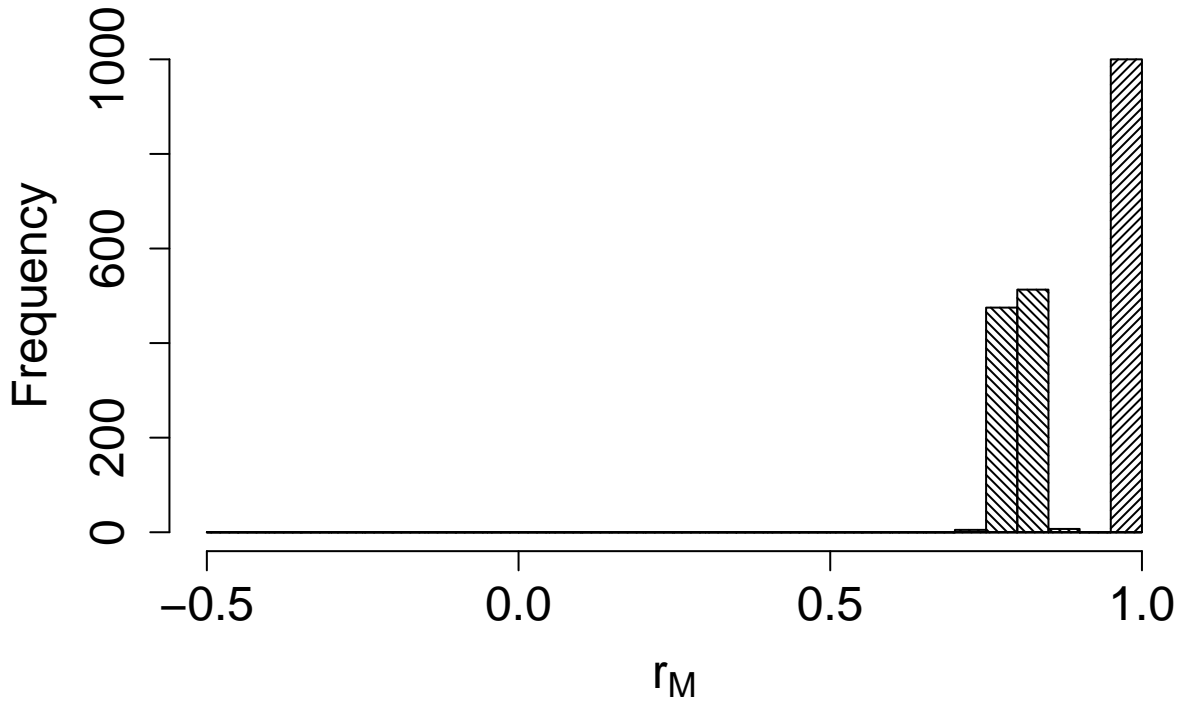


Figure 10990-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low connectivity ($MC = 0.123$; $MC = 0.123$ when adjusted for absolute abundance) between 8 breeding regions and 8 non breeding regions (Table 10990-2; Figure 10990-6).

Table 10990-2. 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	19239000	Central Europe	0.438
Central Europe	19239000	North Africa	0.054
Central Europe	19239000	South-central Europe	0.071
Central Europe	19239000	South-west Europe	0.321
Central Europe	19239000	West Europe	0.116
East Europe	46086387	Central Europe	0.100
East Europe	46086387	North Africa	0.200
East Europe	46086387	South-east Europe	0.200
East Europe	46086387	South-west Europe	0.300
East Europe	46086387	West Europe	0.200
North Africa	1000	North Africa	0.500
North Africa	1000	South-west Europe	0.500
North Europe	14011060	Central Europe	0.022

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	14011060	North Africa	0.244
North Europe	14011060	North Europe	0.089
North Europe	14011060	South-central Europe	0.111
North Europe	14011060	South-east Europe	0.011
North Europe	14011060	South-west Europe	0.367
North Europe	14011060	West Europe	0.156
North-west Europe	21636203	North-west Europe	0.999
North-west Europe	21636203	South-west Europe	0.000
North-west Europe	21636203	West Europe	0.001
South-central Europe	8425528	South-central Europe	1.000
South-west Europe	15332277	South-west Europe	1.000
West Europe	8888997	North Africa	0.003
West Europe	8888997	South-west Europe	0.038
West Europe	8888997	West Europe	0.959

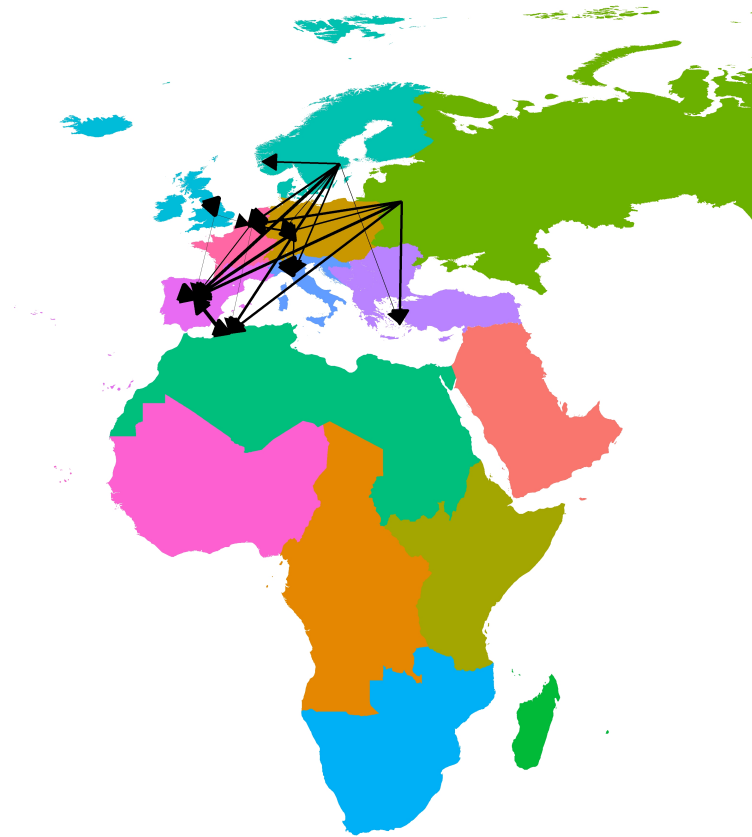


Figure 10990-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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>.