Migratory connectivity analysis

by EURING Migration Atlas

***Strix aluco* (EURING code 07610)**

1.1 Connectivity between individuals

The analysis evaluated 9296 individuals (18592 encounters) filtered from a total of 80406 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 = 6 (Table 07610-1; Figure 07610-1).

Table 07610-1. 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	9296	0.998	0.001	0.997	0.998	6	0.613
1	1	947	0.992	0.001	0.987	0.996	2	0.512
2	1	1644	0.979	0.001	0.967	0.988	7	0.537
3	1	2235	0.987	0.001	0.984	0.991	7	0.531
4	1	789	0.995	0.001	0.990	0.998	2	0.860
5	1	1186	0.993	0.001	0.984	0.998	2	0.493
6	1	2495	0.931	0.001	0.918	0.943	4	0.379
11	2	391	0.974	0.001	0.946	0.993	6	0.496
12	2	556	0.991	0.001	0.985	0.995	3	0.553
21	2	406	0.938	0.001	0.886	0.969	8	0.407
22	2	136	0.938	0.001	0.908	0.977	6	0.582
23	2	372	0.906	0.001	0.868	0.937	8	0.454
24	2	75	0.856	0.001	0.733	0.958	2	0.571
25	2	40	0.921	0.001	0.803	0.993	5	0.740
26	2	355	0.858	0.001	0.765	0.943	6	0.483
27	2	260	0.896	0.001	0.859	0.935	6	0.528
31	2	421	0.937	0.001	0.896	0.967	3	0.642
32	2	529	0.823	0.001	0.725	0.915	4	0.571
33	2	352	0.879	0.001	0.834	0.916	4	0.453
34	2	201	0.957	0.001	0.930	0.976	4	0.647
35	2	136	0.949	0.001	0.919	0.971	2	0.709
36	2	227	0.838	0.001	0.747	0.927	2	0.520
37	2	369	0.877	0.001	0.797	0.941	3	0.561
41	2	754	0.971	0.001	0.940	0.990	5	0.489
42	2	35	0.975	0.001	0.941	0.999	7	0.674
121	3	355	0.979	0.001	0.962	0.990	9	0.528
122	3	112	0.975	0.001	0.922	0.998	6	0.760

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
123	3	89	0.944	0.001	0.889	0.984	3	0.639
221	3	25	0.774	0.001	0.620	0.962	2	0.515
222	3	5	-	-	-	-	-	-
223	3	78	0.865	0.001	0.715	0.949	2	0.471
224	3	17	-	-	-	-	-	-
225	3	10	-	-	-	-	-	-
226	3	1	-	-	-	-	-	-
241	3	15	-	-	-	-	-	-
242	3	60	0.803	0.001	0.591	0.928	9	0.536
251	3	14	-	-	-	-	-	-
252	3	11	-	-	-	-	-	-
253	3	6	-	-	-	-	-	-
254	3	8	-	-	-	-	-	-
255	3	1	-	-	-	-	-	-
271	3	32	0.909	0.001	0.806	0.947	5	0.486
272	3	66	0.761	0.005	0.024	0.941	2	0.894
273	3	32	0.501	0.001	0.319	0.766	6	0.387
274	3	18	-	-	-	-	-	-
275	3	94	0.357	0.001	0.148	0.571	2	0.478
276	3	18	-	-	-	-	-	-
311	3	217	0.897	0.001	0.849	0.940	3	0.606
312	3	162	0.794	0.001	0.677	0.915	3	0.549
313	3	42	0.705	0.001	0.593	0.918	9	0.530
321	3	283	0.760	0.001	0.658	0.835	2	0.489
322	3	105	0.874	0.001	0.727	0.949	2	0.772
323	3	89	0.744	0.001	0.635	0.863	2	0.537
324	3	52	0.633	0.001	0.367	0.815	4	0.498
341	3	40	0.595	0.001	0.294	0.795	2	0.456
342	3	25	0.361	0.005	0.169	0.747	3	0.446
343	3	96	0.693	0.001	0.605	0.804	2	0.536
344	3	40	0.446	0.007	0.060	0.897	2	0.353
351	3	104	0.701	0.001	0.596	0.826	4	0.494
352	3	32	0.855	0.001	0.691	0.965	2	0.693
361	3	170	0.769	0.001	0.545	0.912	4	0.517
362	3	57	0.775	0.001	0.595	0.935	7	0.506
371	3	131	0.786	0.001	0.709	0.906	7	0.492
372	3	110	0.547	0.001	0.378	0.731	2	0.550
373	3	128	0.886	0.001	0.825	0.938	2	0.585
421	3	9	-	-	-	-	-	-
422	3	6	-	-	-	-	-	-
423	3	8	-	-	-	-	-	-
424	3	5	-	-	-	-	-	-
425	3	4	-	-	-	-	-	-
426	3	2	-	-	-	-	-	-
427	3	1	-	-	-	-	-	-

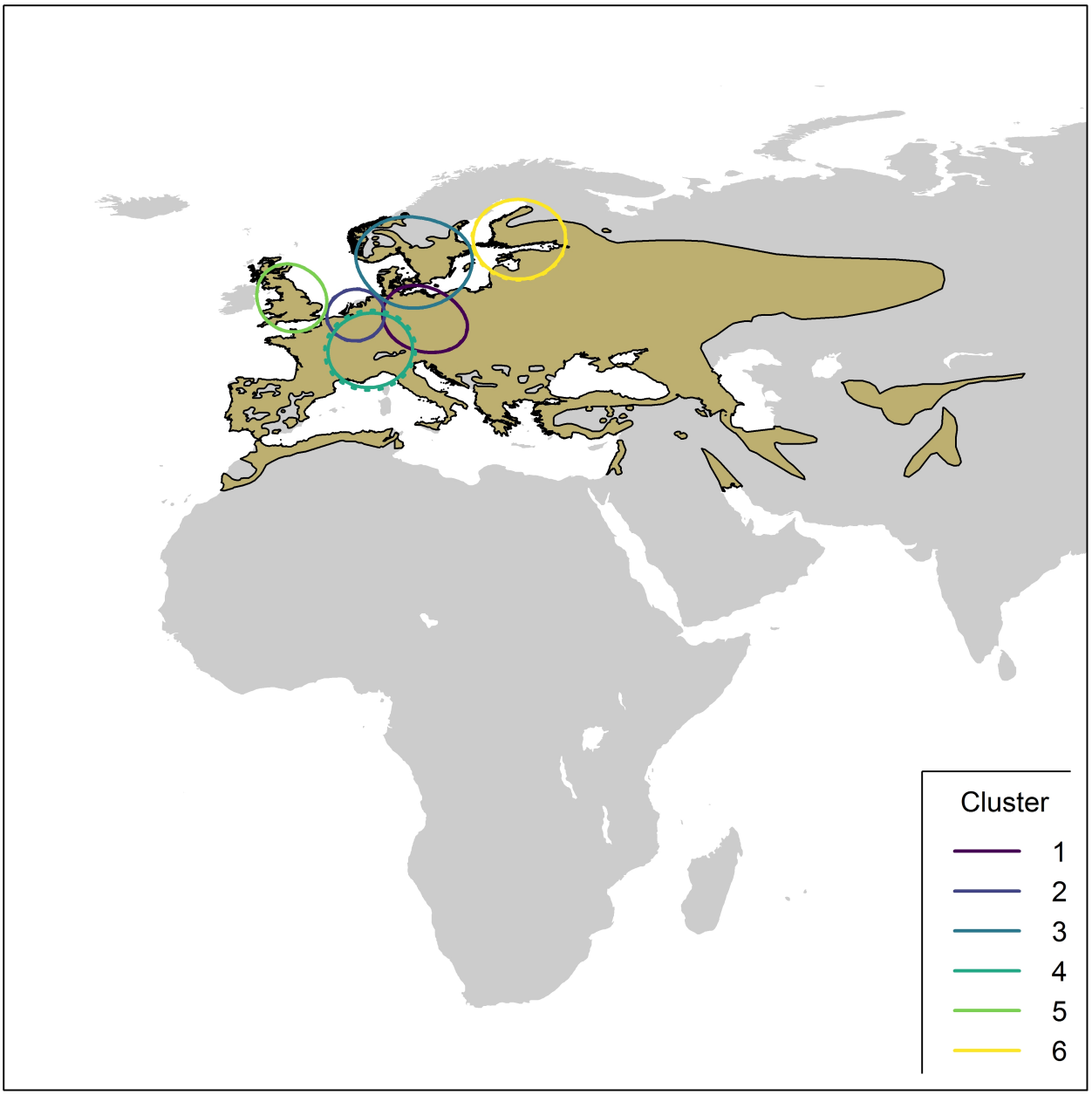

Figure 07610-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 07610-2) and stratified sampling of individuals within the breeding range (Figure 07610-3) and the non breeding range (Figure 07610-4). 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.

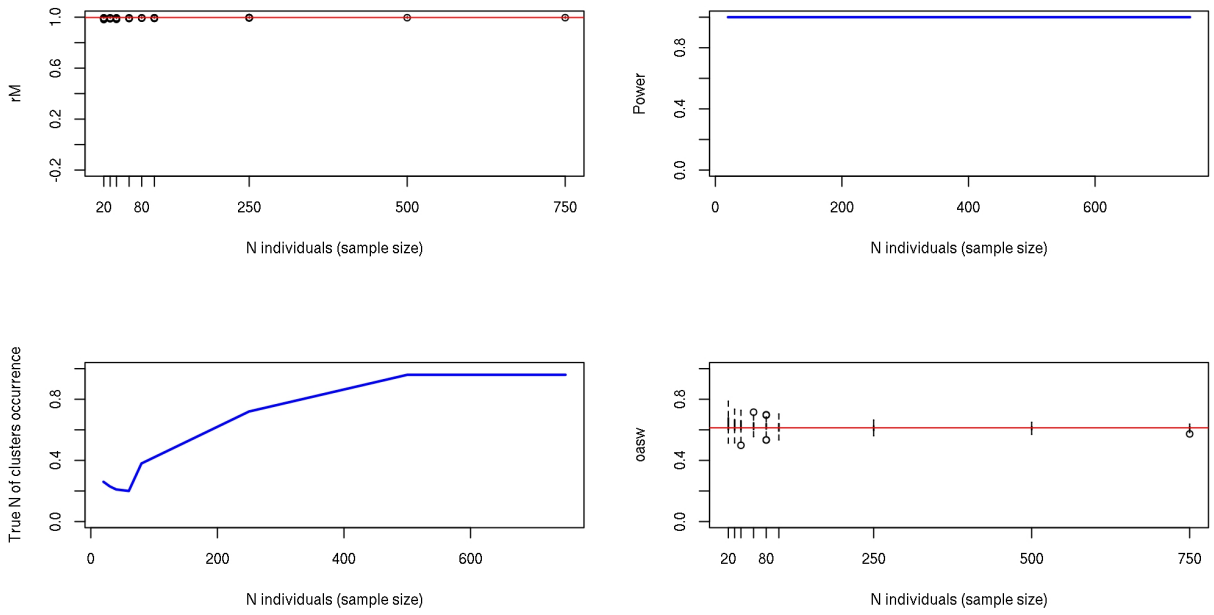

Figure 07610-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

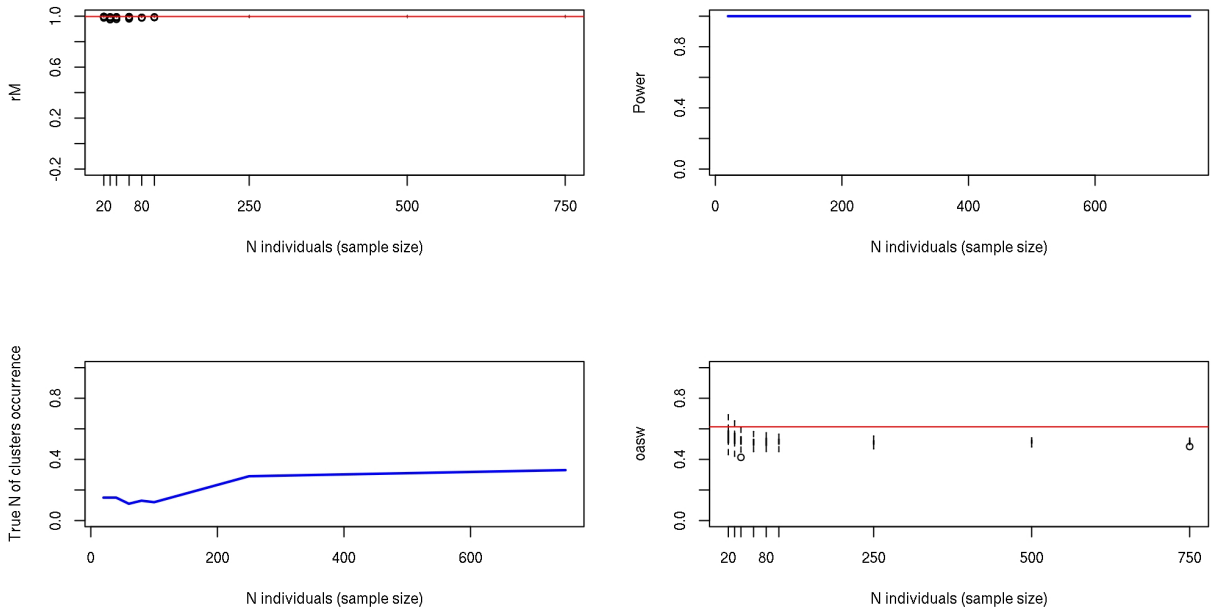

Figure 07610-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

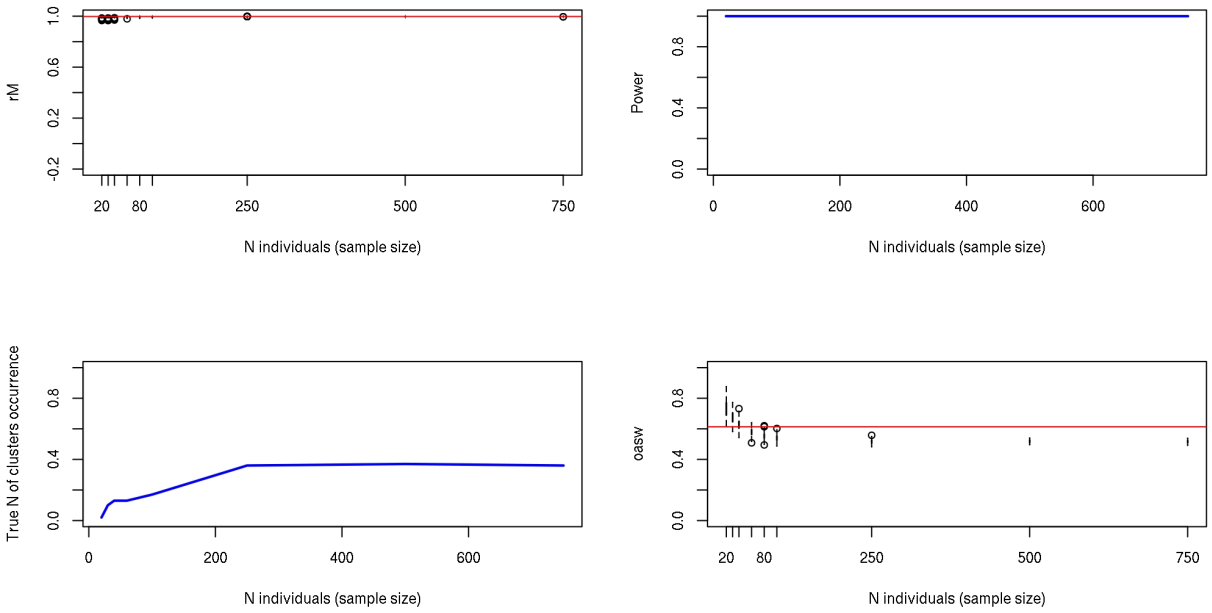

Figure 07610-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 ($p = 1$); Figure 07610-5).

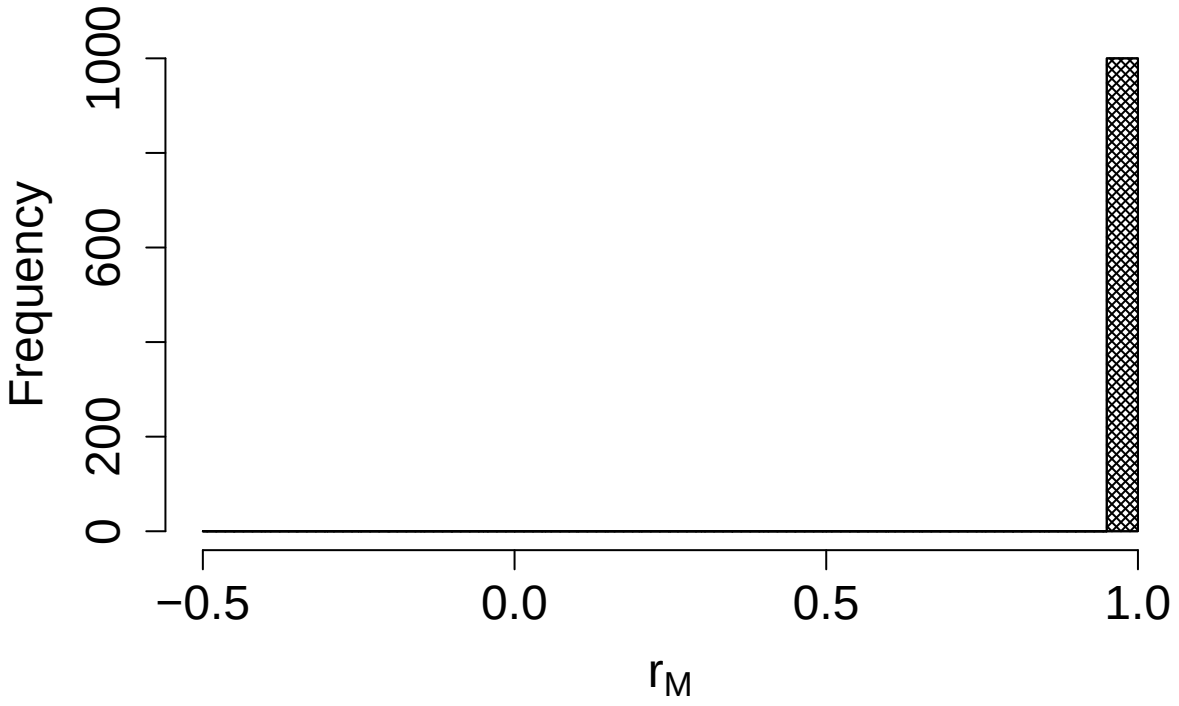

Figure 07610-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows high connectivity (MC = 0.993; MC = 0.993 when adjusted for absolute abundance) between 9 breeding regions and 9 non breeding regions (Table 07610-2; Figure 07610-6).

Table 07610-2. 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	350090	Central Europe	0.988
Central Europe	350090	East Europe	0.001
Central Europe	350090	North Europe	0.001
Central Europe	350090	South-central Europe	0.001
Central Europe	350090	West Europe	0.011
East Europe	290000	East Europe	1.000
North Africa	1000	North Africa	1.000
North Europe	53200	East Europe	0.003
North Europe	53200	North Europe	0.997
North-west Europe	100000	North-west Europe	1.000
South-central Europe	124100	South-central Europe	1.000
South-east Europe	286250	South-east Europe	1.000
South-west Europe	111201	South-west Europe	0.977

Breeding region	Abundance	Non breeding region	Transition probability
South-west Europe	111201	West Europe	0.023
West Europe	146913	Central Europe	0.014
West Europe	146913	West Europe	0.986

Figure 07610-6. 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.