

Migratory connectivity analysis

by EURING Migration Atlas

Fulica atra (EURING code 04290)

1.1 Connectivity between individuals

The analysis evaluated 3806 individuals (7612 encounters) filtered from a total of 132738 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 = 9 (Table 04290-1; Figure 04290-1).

Table 04290-1. 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	3806	0.838	0.001	0.818	0.857	9	0.614
1	1	1729	0.756	0.001	0.711	0.803	8	0.861
2	1	497	0.776	0.001	0.713	0.836	4	0.706
3	1	253	0.114	0.001	0.040	0.204	8	0.420
4	1	391	0.771	0.001	0.697	0.838	3	0.817
5	1	224	0.546	0.001	0.326	0.685	8	0.286
6	1	250	0.483	0.001	0.378	0.594	9	0.545
7	1	209	0.676	0.001	0.505	0.799	2	0.790
8	1	155	0.195	0.023	0.064	0.373	9	0.632
9	1	98	0.879	0.001	0.769	0.954	9	0.904
11	2	1436	0.371	0.001	0.232	0.554	3	0.887
12	2	20	-0.195	0.958	-0.175	0.157	-	-
13	2	93	0.812	0.001	0.691	0.911	6	0.796
14	2	43	0.225	0.011	0.039	0.473	9	0.482
15	2	25	0.692	0.001	0.474	0.973	3	0.773
16	2	27	0.086	0.081	-0.004	0.401	9	0.476
17	2	65	0.814	0.001	0.606	0.955	5	0.859
18	2	20	0.865	0.001	0.726	0.977	2	0.760
21	2	199	0.717	0.001	0.567	0.846	3	0.668
22	2	35	0.279	0.039	-0.130	0.620	2	0.417
23	2	123	0.979	0.001	0.807	0.998	2	0.968
24	2	140	0.800	0.001	0.632	0.927	9	0.547
41	2	26	0.136	0.034	0.061	0.431	4	0.501
42	2	350	0.755	0.001	0.635	0.851	8	0.853
43	2	15	-	-	-	-	-	-
61	2	41	0.563	0.001	0.450	0.986	4	0.866
62	2	22	0.140	0.131	0.003	0.453	-	-

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
63	2	11	-	-	-	-	-	-
64	2	29	0.520	0.001	0.317	0.811	3	0.569
65	2	87	0.633	0.001	0.337	0.837	9	0.608
66	2	10	-	-	-	-	-	-
67	2	14	-	-	-	-	-	-
68	2	14	-	-	-	-	-	-
69	2	22	0.669	0.001	0.458	0.881	6	0.640
71	2	192	0.645	0.001	0.505	0.779	2	0.716
72	2	17	-	-	-	-	-	-
81	2	17	-	-	-	-	-	-
82	2	8	-	-	-	-	-	-
83	2	82	0.014	0.382	-0.064	0.182	-	-
84	2	3	-	-	-	-	-	-
85	2	18	-	-	-	-	-	-
86	2	6	-	-	-	-	-	-
87	2	3	-	-	-	-	-	-
88	2	11	-	-	-	-	-	-
89	2	7	-	-	-	-	-	-
91	2	1	-	-	-	-	-	-
92	2	18	-	-	-	-	-	-
93	2	22	0.038	0.346	-0.094	0.374	-	-
94	2	28	0.321	0.001	0.139	0.646	8	0.791
95	2	3	-	-	-	-	-	-
96	2	21	1.000	0.005	-0.129	1.000	2	0.916
97	2	3	-	-	-	-	-	-
98	2	1	-	-	-	-	-	-
99	2	1	-	-	-	-	-	-
111	3	31	0.293	0.061	-0.071	0.748	2	0.757
112	3	1372	0.400	0.001	0.284	0.531	3	0.820
113	3	33	0.347	0.008	0.200	0.597	2	0.580
131	3	5	-	-	-	-	-	-
132	3	17	-	-	-	-	-	-
133	3	4	-	-	-	-	-	-
134	3	63	0.545	0.002	0.377	1.000	9	0.880
135	3	1	-	-	-	-	-	-
136	3	3	-	-	-	-	-	-
151	3	3	-	-	-	-	-	-
152	3	2	-	-	-	-	-	-
153	3	20	0.931	0.001	0.771	1.000	2	0.766
171	3	2	-	-	-	-	-	-
172	3	3	-	-	-	-	-	-
173	3	55	0.667	0.004	0.117	0.975	2	0.890
174	3	3	-	-	-	-	-	-
175	3	2	-	-	-	-	-	-
181	3	3	-	-	-	-	-	-
182	3	17	-	-	-	-	-	-
211	3	24	0.692	0.001	0.292	0.890	5	0.488
212	3	18	-	-	-	-	-	-
213	3	157	0.819	0.001	0.758	0.938	3	0.752
231	3	122	0.929	0.001	0.687	0.991	2	0.953

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
232	3	1	-	-	-	-	-	-
241	3	12	-	-	-	-	-	-
242	3	36	0.580	0.001	0.383	0.915	3	0.708
243	3	26	0.155	0.117	-0.108	0.596	-	-
244	3	46	0.632	0.001	0.463	0.869	8	0.732
245	3	4	-	-	-	-	-	-
246	3	4	-	-	-	-	-	-
247	3	1	-	-	-	-	-	-
248	3	7	-	-	-	-	-	-
249	3	4	-	-	-	-	-	-
411	3	8	-	-	-	-	-	-
412	3	3	-	-	-	-	-	-
413	3	13	-	-	-	-	-	-
414	3	2	-	-	-	-	-	-
421	3	2	-	-	-	-	-	-
422	3	4	-	-	-	-	-	-
423	3	3	-	-	-	-	-	-
424	3	32	0.387	0.002	0.197	0.662	3	0.413
425	3	5	-	-	-	-	-	-
426	3	298	0.272	0.013	0.146	0.674	2	0.925
427	3	5	-	-	-	-	-	-
428	3	1	-	-	-	-	-	-
611	3	1	-	-	-	-	-	-
612	3	8	-	-	-	-	-	-
613	3	30	0.925	0.002	0.027	0.983	2	0.889
614	3	2	-	-	-	-	-	-
641	3	17	-	-	-	-	-	-
642	3	10	-	-	-	-	-	-
643	3	2	-	-	-	-	-	-
651	3	4	-	-	-	-	-	-
652	3	2	-	-	-	-	-	-
653	3	3	-	-	-	-	-	-
654	3	60	0.243	0.043	0.078	0.842	9	0.770
655	3	3	-	-	-	-	-	-
656	3	1	-	-	-	-	-	-
657	3	12	-	-	-	-	-	-
658	3	1	-	-	-	-	-	-
659	3	1	-	-	-	-	-	-
691	3	4	-	-	-	-	-	-
692	3	5	-	-	-	-	-	-
693	3	6	-	-	-	-	-	-
694	3	3	-	-	-	-	-	-
695	3	3	-	-	-	-	-	-
696	3	1	-	-	-	-	-	-
711	3	167	0.415	0.001	0.251	0.600	3	0.730
712	3	25	0.613	0.004	0.071	0.913	4	0.591
941	3	6	-	-	-	-	-	-
942	3	3	-	-	-	-	-	-
943	3	2	-	-	-	-	-	-
944	3	3	-	-	-	-	-	-

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
945	3	4	-	-	-	-	-	-
946	3	7	-	-	-	-	-	-
947	3	1	-	-	-	-	-	-
948	3	2	-	-	-	-	-	-
961	3	20	0.998	0.050	-0.177	1.000	2	0.938
962	3	1	-	-	-	-	-	-

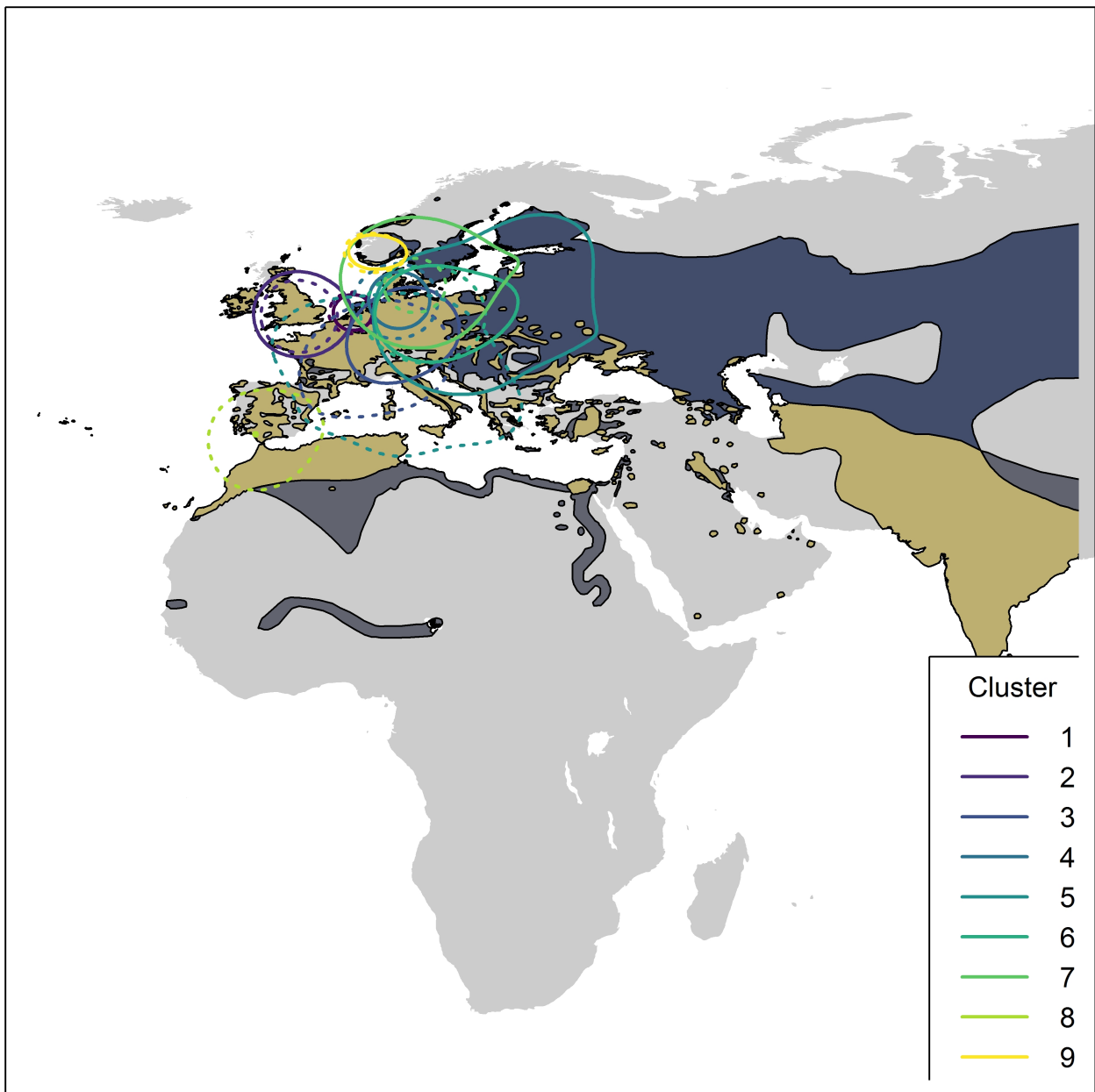


Figure 04290-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure.

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 04290-2) and stratified sampling of individuals within the breeding range (Figure 04290-3) and the non breeding range (Figure 04290-4). 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.

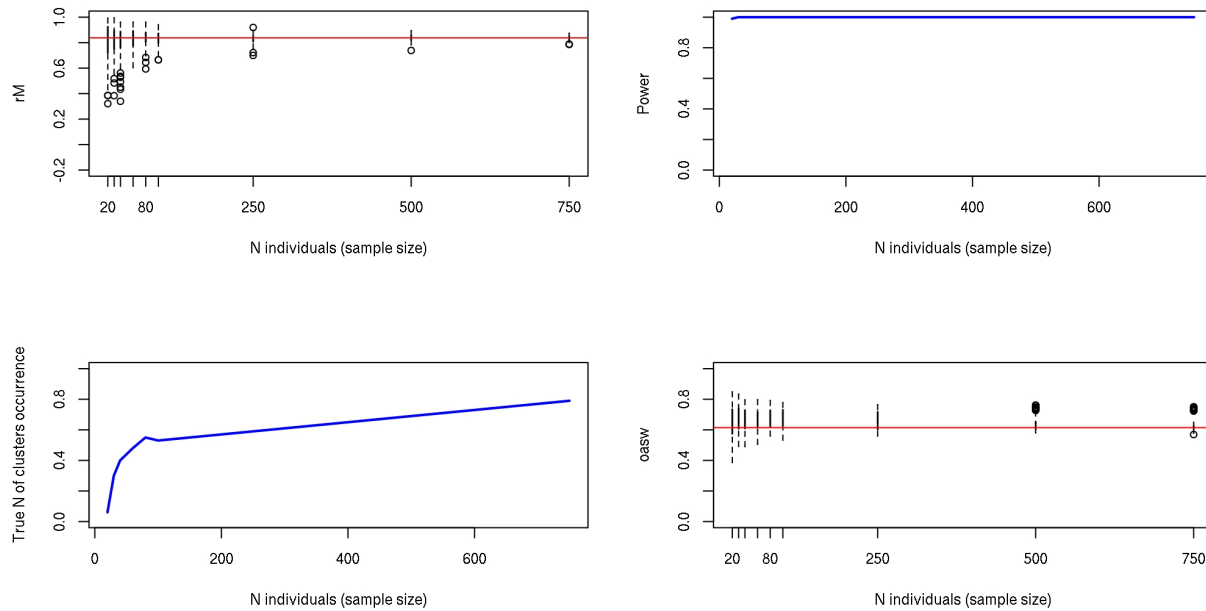


Figure 04290-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

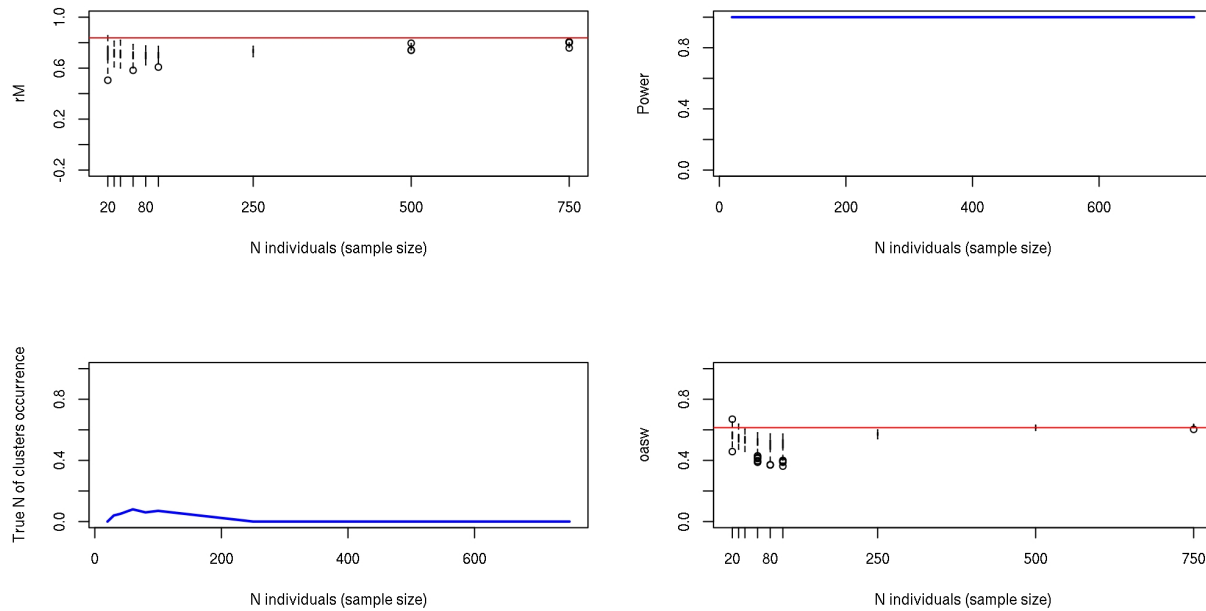


Figure 04290-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

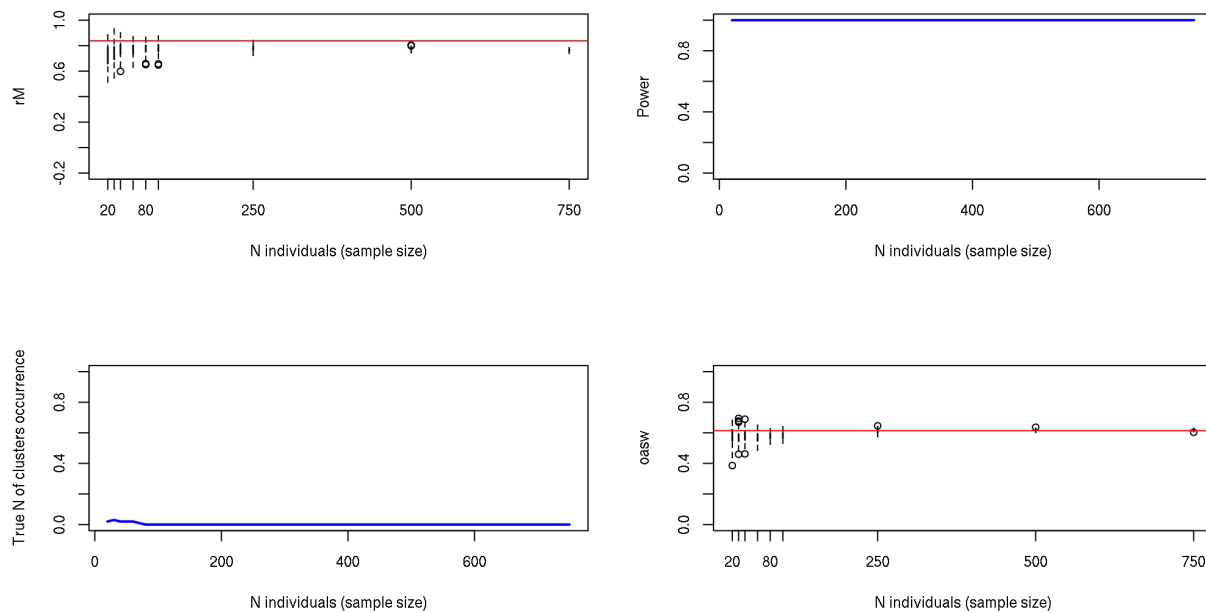


Figure 04290-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 04290-5).

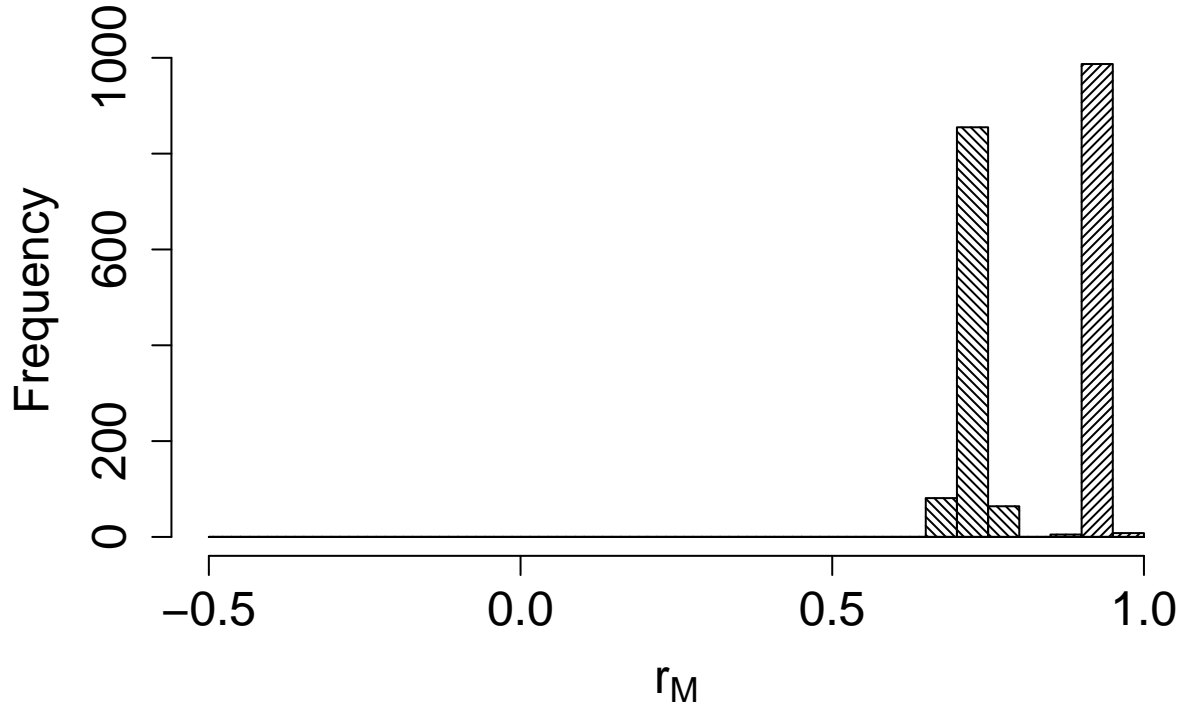


Figure 04290-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low/moderate connectivity ($MC = 0.342$; $MC = 0.342$ when adjusted for absolute abundance) between 8 breeding regions and 10 non breeding regions (Table 04290-2; Figure 04290-6).

Table 04290-2. 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	418518	Central Europe	0.758
Central Europe	418518	North Africa	0.004
Central Europe	418518	North Europe	0.001
Central Europe	418518	North-west Europe	0.002
Central Europe	418518	South-central Europe	0.092
Central Europe	418518	South-east Europe	0.008
Central Europe	418518	South-west Europe	0.038
Central Europe	418518	West Europe	0.098
East Europe	971000	Arabian peninsula	0.010
East Europe	971000	Central Europe	0.286

Breeding region	Abundance	Non breeding region	Transition probability
East Europe	971000	East Europe	0.031
East Europe	971000	North Africa	0.010
East Europe	971000	North Europe	0.031
East Europe	971000	North-west Europe	0.010
East Europe	971000	South-central Europe	0.255
East Europe	971000	South-east Europe	0.061
East Europe	971000	South-west Europe	0.092
East Europe	971000	West Europe	0.214
North Europe	69000	Central Europe	0.058
North Europe	69000	North Europe	0.765
North Europe	69000	North-west Europe	0.011
North Europe	69000	South-central Europe	0.017
North Europe	69000	South-west Europe	0.006
North Europe	69000	West Europe	0.144
North-west Europe	68924	North-west Europe	0.985
North-west Europe	68924	South-west Europe	0.002
North-west Europe	68924	West Europe	0.013
South-central Europe	42718	South-central Europe	1.000
South-east Europe	268408	South-central Europe	0.500
South-east Europe	268408	South-east Europe	0.500
South-west Europe	146592	North Africa	0.248
South-west Europe	146592	North Europe	0.006
South-west Europe	146592	South-central Europe	0.006
South-west Europe	146592	South-west Europe	0.732
South-west Europe	146592	West Europe	0.006
West Europe	466491	Central Europe	0.004
West Europe	466491	North Europe	0.001
West Europe	466491	North-west Europe	0.005
West Europe	466491	South-west Europe	0.006
West Europe	466491	West Europe	0.985

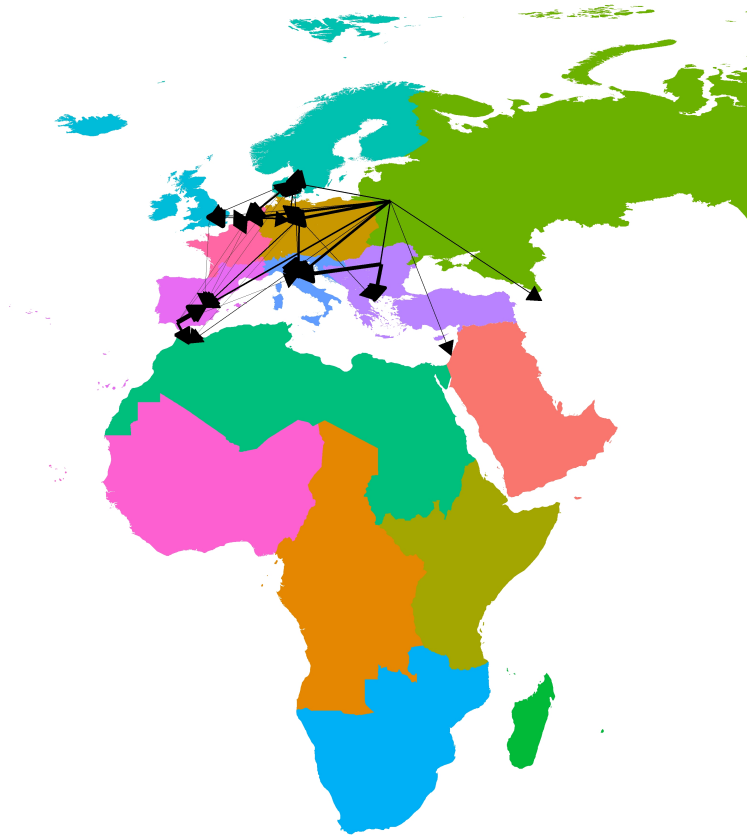


Figure 04290-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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>.