Migratory connectivity analysis

by EURING Migration Atlas

Cettia cetti (EURING code 12200)

1.1 Connectivity between individuals

The analysis evaluated 4115 individuals (8230 encounters) filtered from a total of 151249 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 = 3 (Table 12200-1; Figure 12200-1).
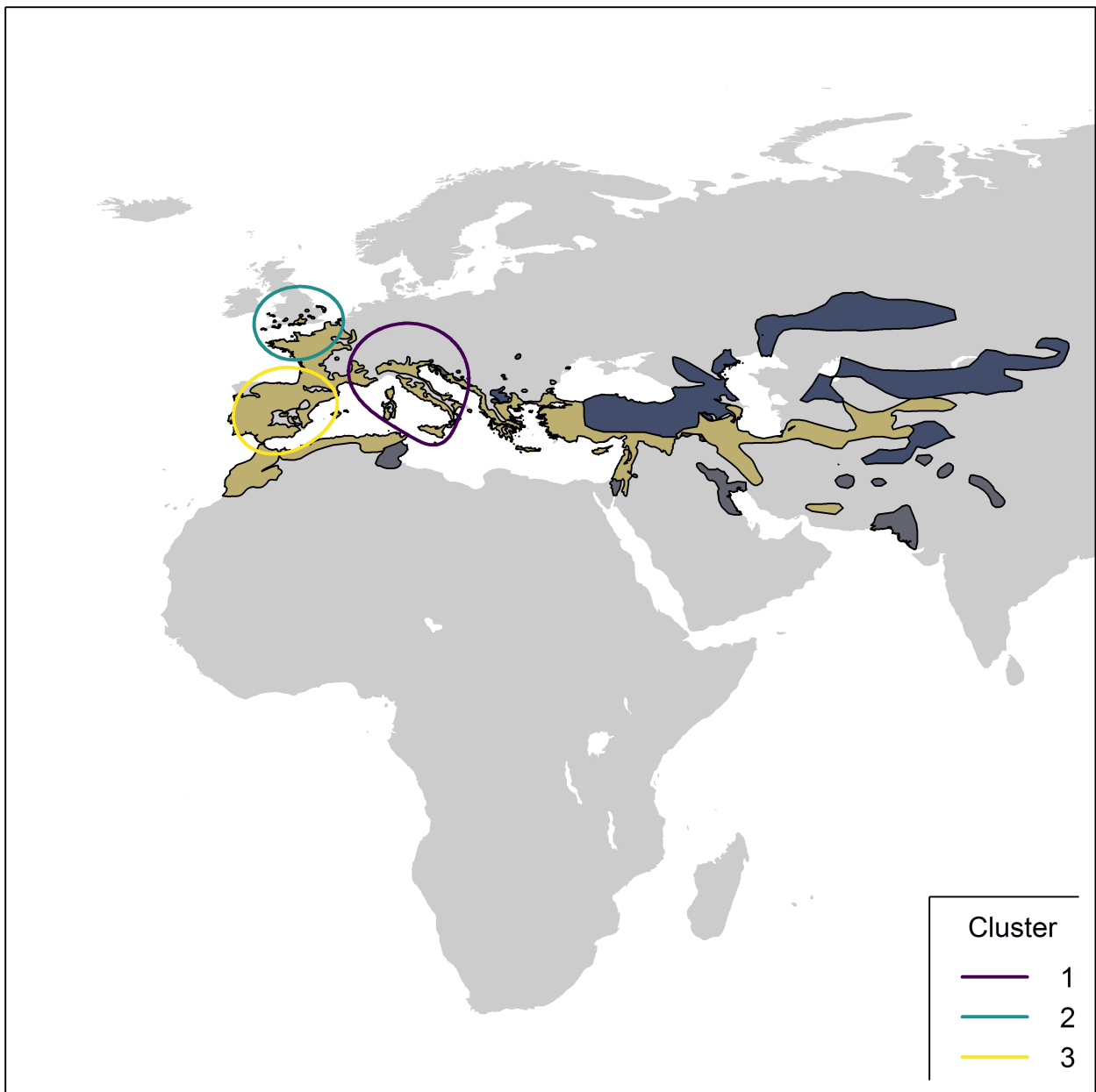
Table 12200-1. Results from the migratory connectivity analysis. For each cluster, the degree of connectivity (r_M), its statistical significance (p-value) and 95% confidence interval limits are shown. When the p-value is less than or equal to 0.1, the degree of clustering structure (oasw) and the best 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	4115	1.000	0.001	0.999	1.000	3	0.667
1	1	1233	0.999	0.001	0.999	1.000	3	0.746
2	1	329	0.998	0.001	0.997	0.999	8	0.723
3	1	2553	0.995	0.001	0.992	0.998	8	0.668
11	2	134	1.000	0.001	1.000	1.000	8	0.979
12	2	59	1.000	0.001	1.000	1.000	2	0.970
13	2	1040	0.992	0.001	0.985	0.998	9	0.548
21	2	22	0.975	0.001	0.947	1.000	3	0.902
22	2	56	0.988	0.001	0.624	1.000	2	0.936
23	2	86	0.971	0.001	0.884	1.000	9	0.808
24	2	57	1.000	0.001	1.000	1.000	4	0.984
25	2	27	0.872	0.001	0.643	1.000	6	0.803
26	2	14	-	-	-	-	-	-
27	2	38	0.999	0.001	0.998	1.000	7	0.955
28	2	29	0.998	0.001	0.993	1.000	5	0.966
31	2	225	0.990	0.001	0.977	1.000	9	0.876
32	2	131	0.990	0.001	0.973	1.000	9	0.901
33	2	284	0.996	0.001	0.991	1.000	9	0.713
34	2	196	0.912	0.001	0.831	0.997	5	0.653
35	2	444	0.986	0.001	0.974	0.996	6	0.644
36	2	873	0.885	0.001	0.789	0.969	2	0.816
37	2	271	0.818	0.001	0.668	0.988	6	0.733
38	2	129	1.000	0.001	1.000	1.000	9	0.958
111	3	2	-	-	-	-	-	-
112	3	6	-	-	-	-	-	-
113	3	19	-	-	-	-	-	-
114	3	20	-	-	-	-	-	-

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
115	3	5	-	-	-	-	-	-
116	3	7	-	-	-	-	-	-
117	3	2	-	-	-	-	-	-
118	3	73	1.000	0.001	1.000	1.000	2	1.000
121	3	4	-	-	-	-	-	-
122	3	55	1.000	0.001	1.000	1.000	4	0.943
131	3	30	0.978	0.001	0.948	0.988	2	0.883
132	3	106	1.000	0.001	1.000	1.000	2	0.969
133	3	78	1.000	0.001	0.999	1.000	9	0.913
134	3	219	1.000	0.001	1.000	1.000	7	0.800
135	3	142	1.000	0.001	0.999	1.000	6	0.960
136	3	87	1.000	0.001	1.000	1.000	9	0.952
137	3	69	0.996	0.001	0.985	1.000	2	0.963
138	3	152	0.857	0.001	0.770	0.960	9	0.869
139	3	157	1.000	0.001	1.000	1.000	9	0.972
211	3	18	-	-	-	-	-	-
212	3	1	-	-	-	-	-	-
213	3	3	-	-	-	-	-	-
221	3	54	0.959	0.001	0.416	1.000	7	0.944
222	3	2	-	-	-	-	-	-
231	3	1	-	-	-	-	-	-
232	3	4	-	-	-	-	-	-
233	3	19	-	-	-	-	-	-
234	3	11	-	-	-	-	-	-
235	3	12	-	-	-	-	-	-
236	3	4	-	-	-	-	-	-
237	3	8	-	-	-	-	-	-
238	3	7	-	-	-	-	-	-
239	3	20	-	-	-	-	-	-
241	3	44	0.343	0.141	-0.054	1.000	-	-
242	3	5	-	-	-	-	-	-
243	3	4	-	-	-	-	-	-
244	3	4	-	-	-	-	-	-
251	3	3	-	-	-	-	-	-
252	3	8	-	-	-	-	-	-
253	3	1	-	-	-	-	-	-
254	3	3	-	-	-	-	-	-
255	3	10	-	-	-	-	-	-
256	3	2	-	-	-	-	-	-
271	3	3	-	-	-	-	-	-
272	3	5	-	-	-	-	-	-
273	3	11	-	-	-	-	-	-
274	3	11	-	-	-	-	-	-
275	3	2	-	-	-	-	-	-
276	3	5	-	-	-	-	-	-
277	3	1	-	-	-	-	-	-
281	3	8	-	-	-	-	-	-
282	3	14	-	-	-	-	-	-
283	3	2	-	-	-	-	-	-
284	3	4	-	-	-	-	-	-

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
285	3	1	-	-	-	-	-	-
311	3	50	0.719	0.002	-0.044	1.000	3	0.934
312	3	33	0.987	0.001	0.971	1.000	5	1.000
313	3	30	0.972	0.001	0.800	1.000	7	0.933
314	3	50	0.998	0.001	0.172	0.999	2	0.950
315	3	9	-	-	-	-	-	-
316	3	2	-	-	-	-	-	-
317	3	24	0.802	0.005	0.659	1.000	2	0.933
318	3	26	0.135	0.106	0.027	1.000	-	-
319	3	1	-	-	-	-	-	-
321	3	11	-	-	-	-	-	-
322	3	13	-	-	-	-	-	-
323	3	2	-	-	-	-	-	-
324	3	9	-	-	-	-	-	-
325	3	34	1.000	0.001	1.000	1.000	4	0.971
326	3	3	-	-	-	-	-	-
327	3	23	-	-	-	-	-	-
328	3	31	-	-	-	-	-	-
329	3	5	-	-	-	-	-	-
331	3	19	-	-	-	-	-	-
332	3	40	1.000	0.001	1.000	1.000	7	0.946
333	3	47	0.947	0.001	0.736	0.991	8	0.801
334	3	31	0.997	0.001	0.994	0.999	6	0.892
335	3	34	0.933	0.001	0.878	0.999	4	0.892
336	3	46	1.000	0.001	1.000	1.000	4	0.951
337	3	26	0.836	0.001	0.542	1.000	6	0.962
338	3	14	-	-	-	-	-	-
339	3	27	1.000	0.001	1.000	1.000	3	1.000
341	3	36	0.297	0.004	0.103	1.000	5	0.891
342	3	27	0.920	0.001	0.899	1.000	6	0.889
343	3	104	0.982	0.001	0.976	0.999	9	0.851
344	3	16	-	-	-	-	-	-
345	3	13	-	-	-	-	-	-
351	3	120	0.947	0.001	0.877	0.986	9	0.818
352	3	120	0.968	0.001	0.938	0.992	9	0.903
353	3	40	0.808	0.001	0.496	1.000	5	0.933
354	3	50	0.976	0.001	0.930	1.000	5	0.966
355	3	43	1.000	0.001	1.000	1.000	4	0.979
356	3	71	0.965	0.001	0.871	1.000	8	0.904
361	3	47	0.912	0.001	0.860	1.000	5	0.918
362	3	826	0.765	0.001	0.609	0.987	9	0.641
371	3	82	0.979	0.001	0.949	1.000	9	0.899
372	3	12	-	-	-	-	-	-
373	3	56	0.863	0.001	0.673	1.000	6	0.982
374	3	38	0.900	0.001	0.737	1.000	5	0.929
375	3	59	0.970	0.001	0.920	0.998	8	0.927
376	3	24	0.839	0.001	0.824	1.000	3	0.893
381	3	8	-	-	-	-	-	-
382	3	1	-	-	-	-	-	-
383	3	36	1.000	0.027	1.000	1.000	2	0.972

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
384	3	17	-	-	-	-	-	-
385	3	2	-	-	-	-	-	-
386	3	24	1.000	0.001	1.000	1.000	2	1.000
387	3	10	-	-	-	-	-	-
388	3	29	-	-	-	-	-	-
389	3	2	-	-	-	-	-	-

Figure 12200-1. 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 12200-2) and stratified sampling of individuals within the breeding range (Figure 12200-3) and the non breeding range (Figure 12200-4). 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.
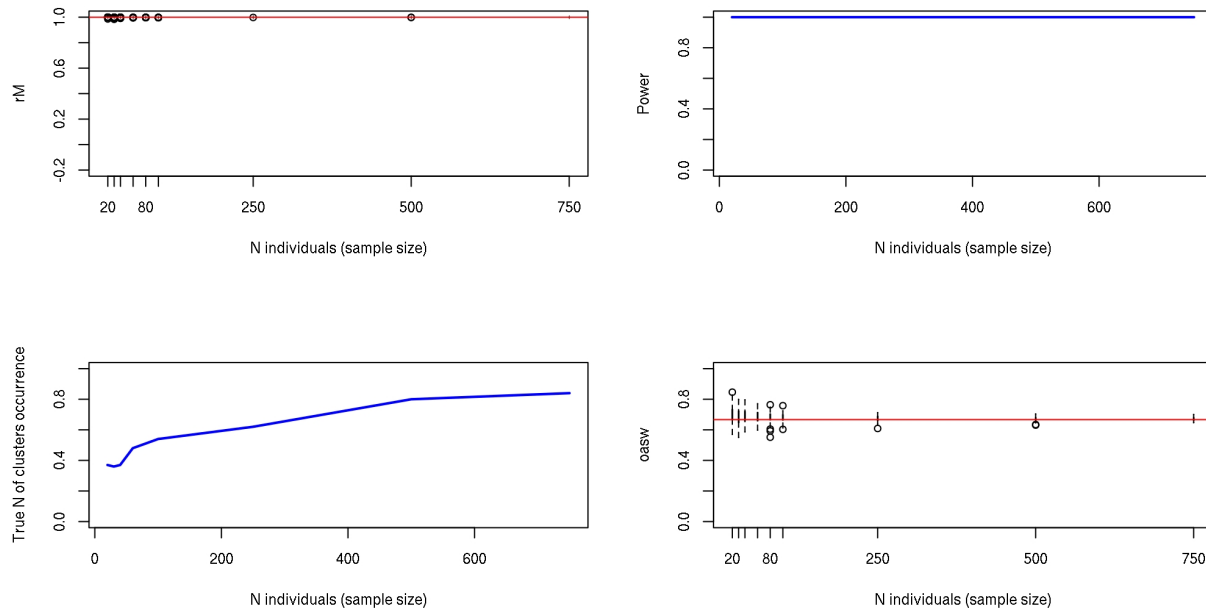
Figure 12200-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.
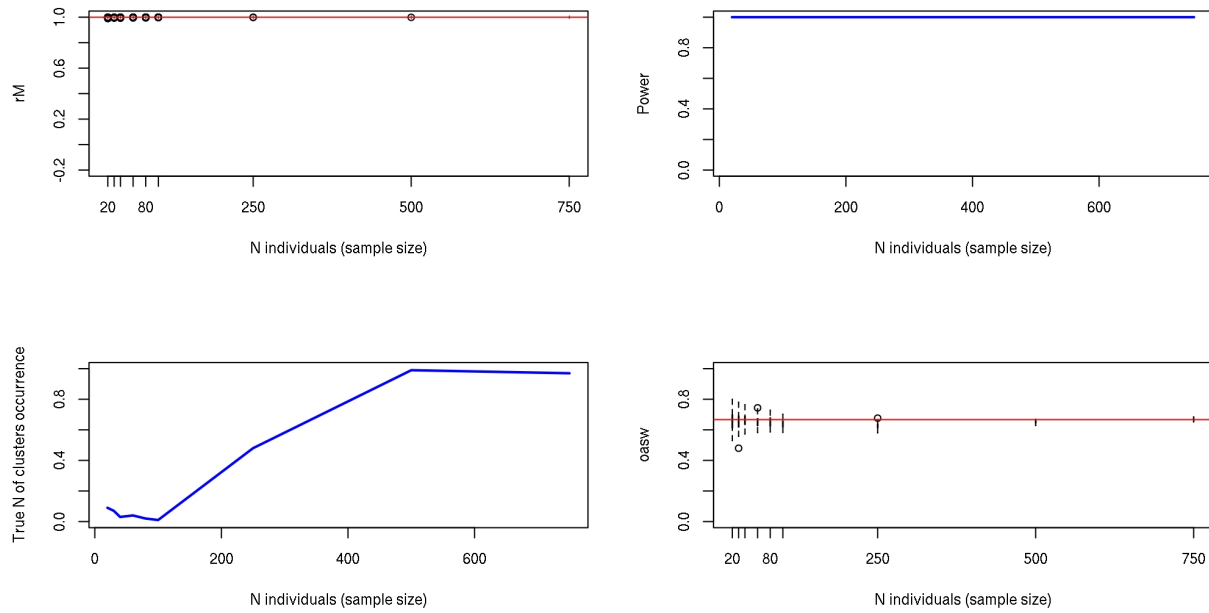
Figure 12200-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.
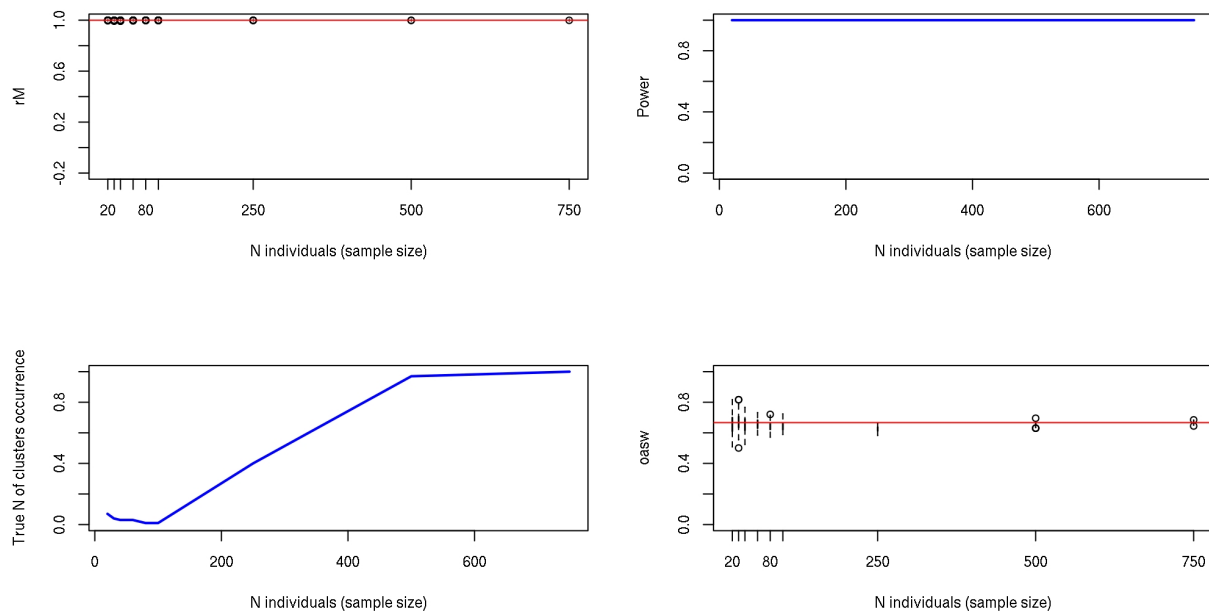
Figure 12200-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 12200-5.
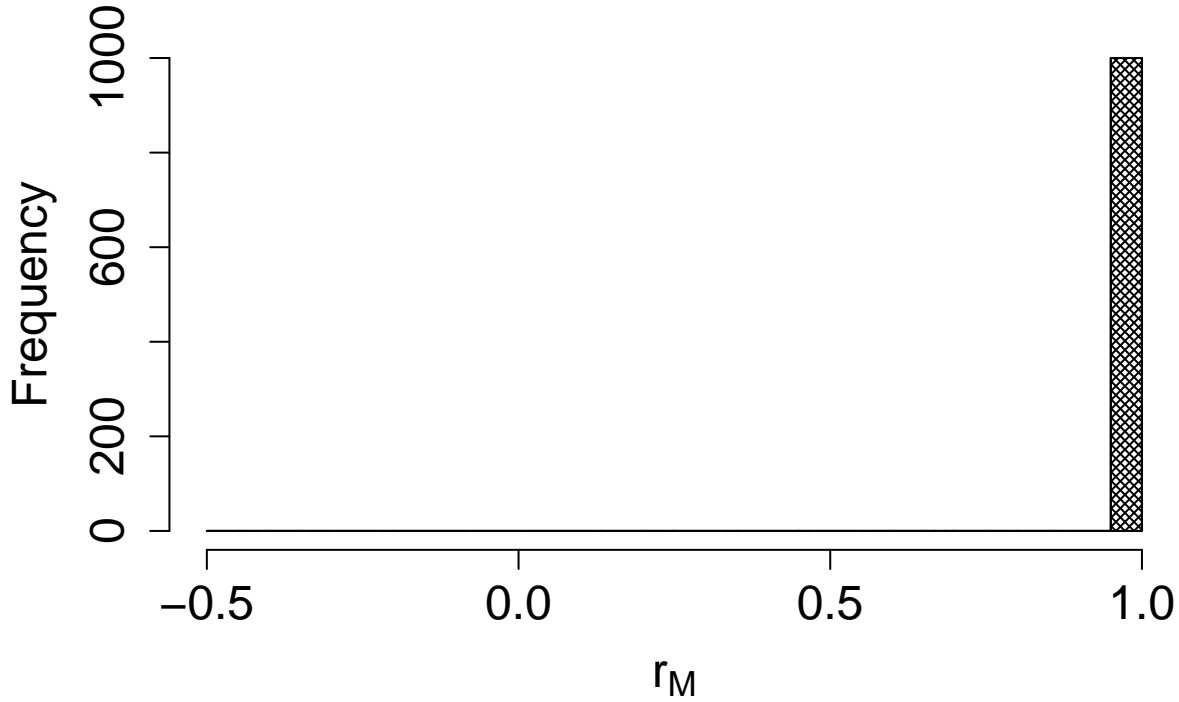
Figure 12200-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows high connectivity (MC = 1; MC = 1 when adjusted for absolute abundance) between 6 breeding regions and 6 non breeding regions (Table 12200-2; Figure 12200-6).

Table 12200-2. 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
Arabian peninsula	1000	Arabian peninsula	1
North-west Europe	4000	North-west Europe	1
South-central Europe	910760	South-central Europe	1
South-east Europe	910141	South-east Europe	1
South-west Europe	3171215	South-west Europe	1
West Europe	37334	West Europe	1

Figure 12200-6. 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.