

Migratory connectivity analysis

by EURING Migration Atlas

Parus major (EURING code 14640)

1.1 Connectivity between individuals

The analysis evaluated 36506 individuals (73012 encounters) filtered from a total of 2194248 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 14640-1; Figure 14640-1).

Table 14640-1. 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	36506	0.994	0.001	0.993	0.995	2	0.614
1	1	31073	0.991	0.001	0.989	0.993	9	0.519
2	1	5433	0.982	0.001	0.976	0.988	3	0.685
11	2	2544	0.970	0.001	0.956	0.982	9	0.667
12	2	5280	0.756	0.001	0.688	0.822	9	0.498
13	2	5669	0.924	0.001	0.888	0.953	9	0.656
14	2	2373	0.888	0.001	0.861	0.913	9	0.639
15	2	8398	0.986	0.001	0.964	0.999	8	0.500
16	2	1117	0.906	0.001	0.875	0.933	8	0.490
17	2	697	0.995	0.001	0.992	0.998	2	0.734
18	2	707	0.979	0.001	0.945	1.000	7	0.692
19	2	4288	0.998	0.001	0.996	1.000	2	0.628
21	2	750	0.882	0.001	0.838	0.922	6	0.610
22	2	4022	0.981	0.001	0.974	0.988	9	0.648
23	2	661	0.963	0.001	0.931	0.986	5	0.623
111	3	80	0.989	0.001	0.968	0.998	2	0.777
112	3	262	0.938	0.001	0.872	0.985	5	0.583
113	3	343	0.936	0.001	0.893	0.998	6	0.943
114	3	202	0.939	0.001	0.902	0.976	8	0.760
115	3	136	0.901	0.001	0.832	0.999	7	0.720
116	3	256	0.987	0.001	0.986	0.999	9	0.920
117	3	142	0.991	0.001	0.986	0.995	2	0.934
118	3	610	0.977	0.001	0.914	0.997	3	0.939
119	3	513	0.969	0.001	0.944	0.986	4	0.766
131	3	685	0.915	0.001	0.852	0.953	4	0.681
132	3	683	0.916	0.001	0.761	0.973	6	0.766
133	3	103	0.916	0.001	0.849	0.970	2	0.848

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
134	3	187	0.860	0.001	0.787	0.939	9	0.758
135	3	1771	0.913	0.001	0.828	0.969	7	0.762
136	3	846	0.878	0.001	0.839	0.931	6	0.751
137	3	518	0.948	0.001	0.915	0.975	9	0.653
138	3	313	0.858	0.001	0.789	0.931	9	0.643
139	3	563	0.940	0.001	0.897	0.974	7	0.894
141	3	133	0.958	0.001	0.873	0.983	2	0.911
142	3	182	0.932	0.001	0.872	0.972	2	0.870
143	3	113	0.953	0.001	0.863	0.978	8	0.642
144	3	128	0.862	0.001	0.693	0.935	6	0.654
145	3	314	0.918	0.001	0.789	0.992	9	0.783
146	3	210	0.971	0.001	0.852	0.991	9	0.808
147	3	68	0.985	0.001	0.971	0.997	6	0.814
148	3	241	0.935	0.001	0.843	0.975	6	0.840
149	3	984	0.974	0.001	0.870	0.993	2	0.924
151	3	401	0.916	0.001	0.910	0.996	8	0.733
152	3	782	0.923	0.001	0.876	0.999	7	0.650
153	3	1166	0.969	0.001	0.934	0.995	8	0.657
154	3	1601	0.996	0.001	0.992	0.999	6	0.592
155	3	780	0.977	0.001	0.962	0.989	9	0.665
156	3	85	0.998	0.001	0.972	1.000	9	0.691
157	3	1339	0.987	0.001	0.965	0.998	4	0.574
158	3	2244	0.961	0.001	0.932	0.984	8	0.859
171	3	288	0.965	0.001	0.929	0.990	3	0.674
172	3	409	0.981	0.001	0.961	0.995	9	0.723
181	3	87	0.995	0.001	0.992	0.998	9	0.785
182	3	186	0.995	0.001	0.992	1.000	9	0.700
183	3	81	0.916	0.001	0.881	0.995	6	0.647
184	3	32	1.000	0.001	1.000	1.000	7	0.938
185	3	102	0.999	0.001	0.998	1.000	9	0.798
186	3	183	0.994	0.001	0.984	1.000	2	0.762
187	3	36	0.999	0.001	0.995	1.000	2	0.696
191	3	873	0.997	0.001	0.991	1.000	3	0.584
192	3	3415	0.997	0.001	0.993	0.999	9	0.616
211	3	41	0.988	0.001	0.969	0.999	2	0.909
212	3	48	0.912	0.001	0.743	1.000	7	0.780
213	3	237	0.941	0.001	0.911	1.000	7	0.861
214	3	129	0.957	0.001	0.931	0.978	2	0.825
215	3	80	0.872	0.001	0.790	0.960	8	0.818
216	3	215	0.788	0.001	0.507	0.950	9	0.619
221	3	146	0.896	0.001	0.758	0.942	9	0.716
222	3	1125	0.961	0.001	0.937	0.981	6	0.631
223	3	251	0.801	0.001	0.682	0.939	9	0.638
224	3	168	0.982	0.001	0.960	0.995	2	0.736
225	3	685	0.910	0.001	0.854	0.963	9	0.737
226	3	273	0.971	0.001	0.938	0.996	8	0.640
227	3	331	0.978	0.001	0.959	0.997	3	0.739
228	3	929	0.975	0.001	0.940	0.996	2	0.926
229	3	114	0.957	0.001	0.929	0.996	9	0.720
231	3	173	0.853	0.001	0.757	0.963	2	0.687

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	123	0.998	0.001	0.997	0.999	9	0.794
233	3	279	0.916	0.001	0.843	0.983	6	0.586
234	3	24	0.404	0.015	0.197	0.991	6	0.659
235	3	62	0.833	0.001	0.675	0.959	5	0.472

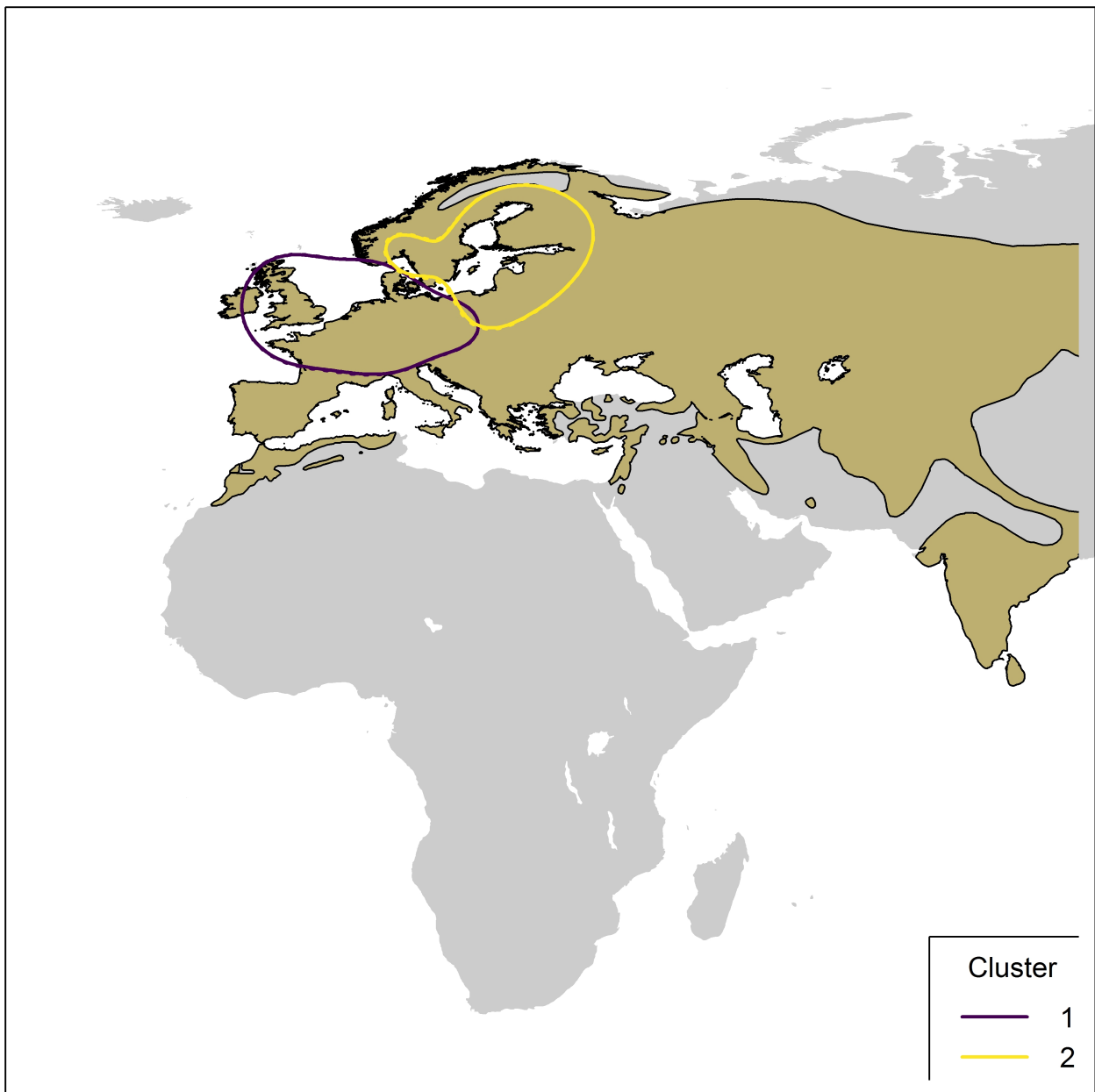


Figure 14640-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 14640-2) and stratified sampling of individuals within the breeding range (Figure 14640-3) and the non breeding range (Figure 14640-4). 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.

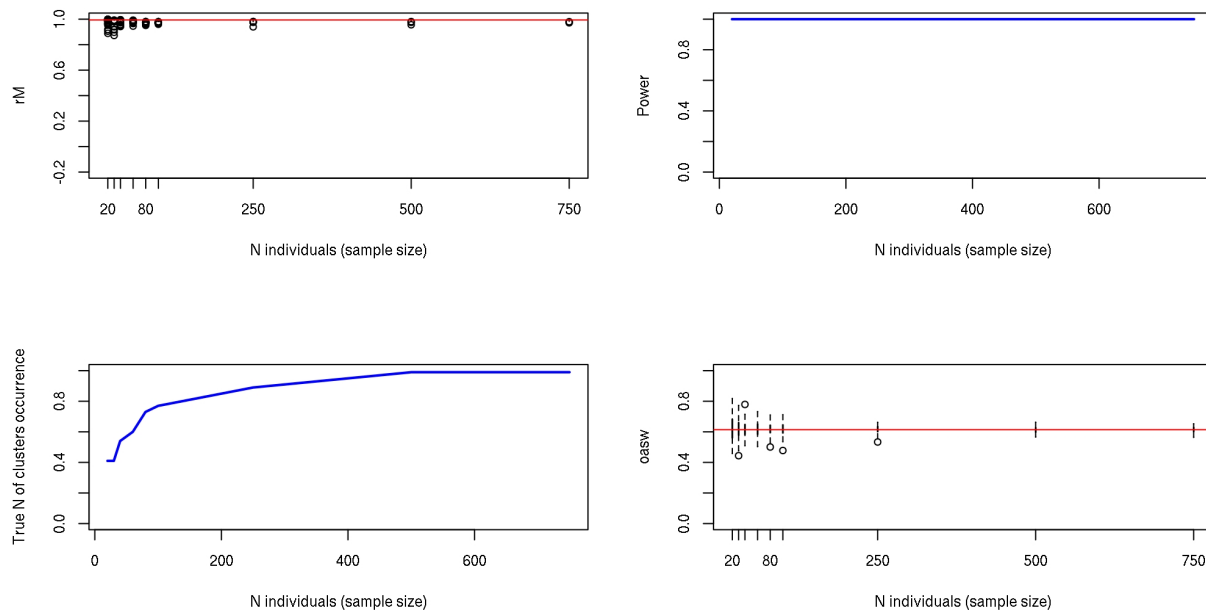


Figure 14640-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

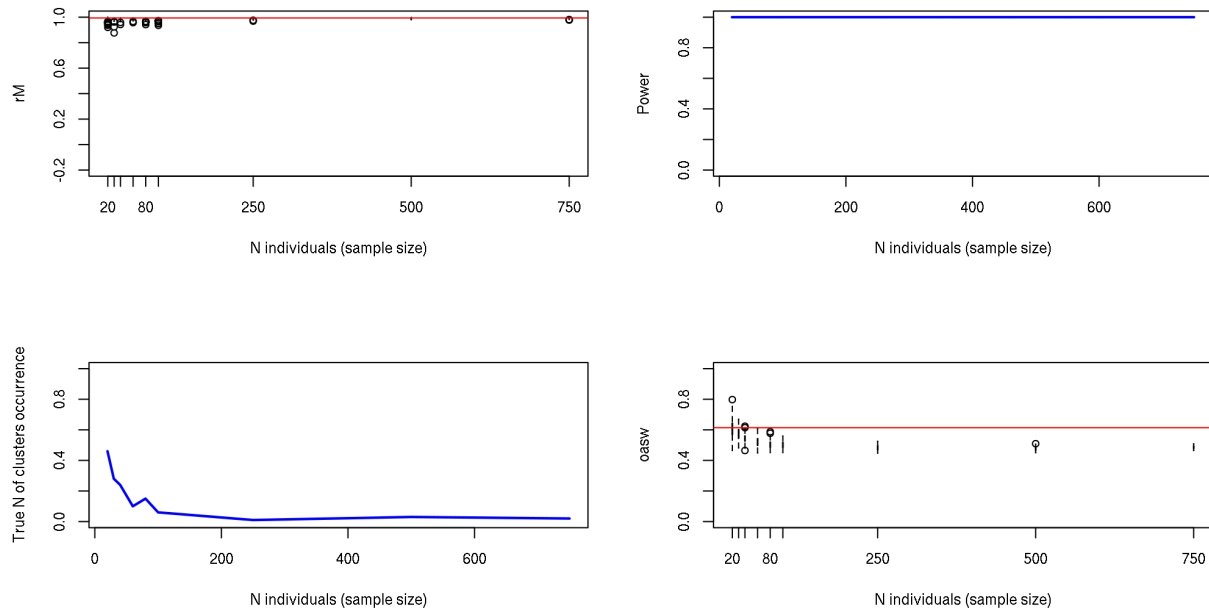


Figure 14640-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

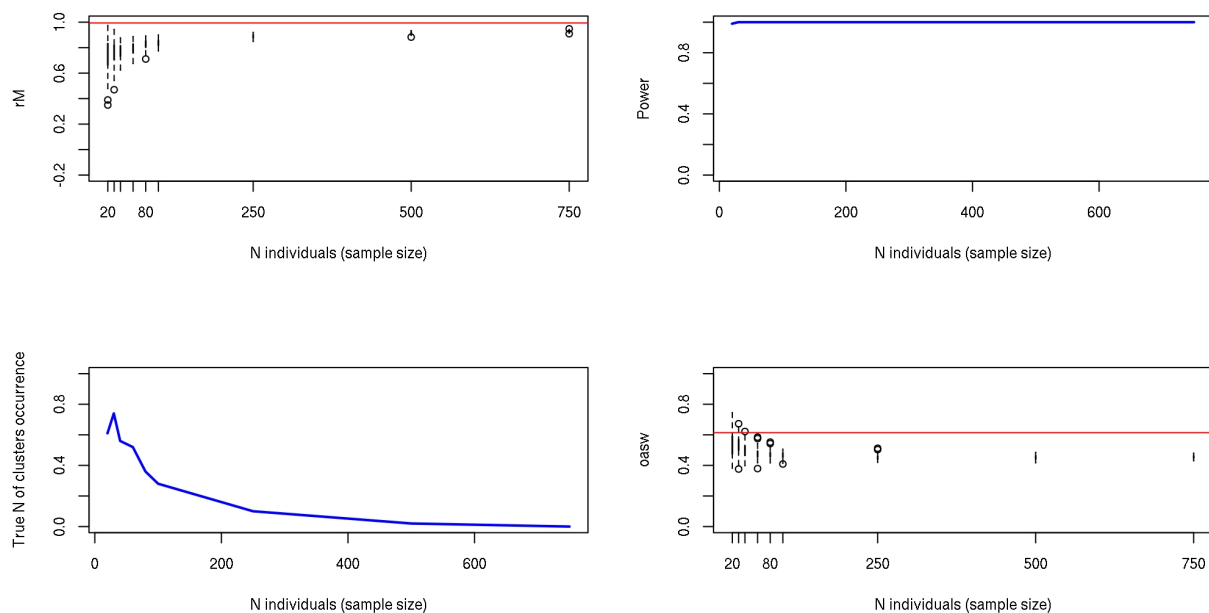


Figure 14640-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 ($p = 0.822$); Figure 14640-5).

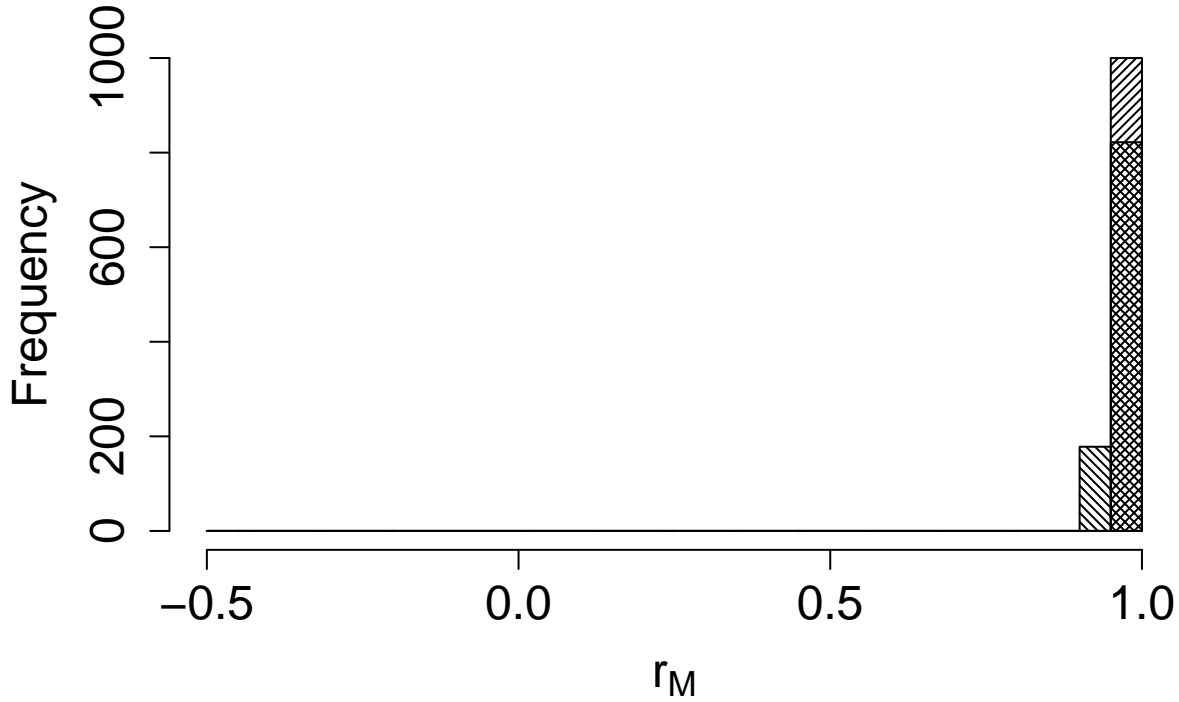


Figure 14640-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows high connectivity ($MC = 0.964$; $MC = 0.964$ when adjusted for absolute abundance) between 9 breeding regions and 9 non breeding regions (Table 14640-2; Figure 14640-6).

Table 14640-2. 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	39881700	Central Europe	0.975
Central Europe	39881700	East Europe	0.001
Central Europe	39881700	North Europe	0.000
Central Europe	39881700	South-central Europe	0.000
Central Europe	39881700	South-west Europe	0.008
Central Europe	39881700	West Europe	0.015
East Europe	41181401	Central Europe	0.054
East Europe	41181401	East Europe	0.917
East Europe	41181401	North Europe	0.006
East Europe	41181401	South-central Europe	0.002

Breeding region	Abundance	Non breeding region	Transition probability
East Europe	41181401	South-west Europe	0.002
East Europe	41181401	West Europe	0.019
North Africa	1000	North Africa	1.000
North Europe	12405000	East Europe	0.001
North Europe	12405000	North Europe	0.999
North Europe	12405000	West Europe	0.000
North-west Europe	7115807	North-west Europe	1.000
South-central Europe	8396870	South-central Europe	1.000
South-east Europe	27380000	South-east Europe	1.000
South-west Europe	23123212	South-west Europe	1.000
West Europe	10605892	Central Europe	0.001
West Europe	10605892	South-west Europe	0.000
West Europe	10605892	West Europe	0.998



Figure 14640-6. 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>.