Migratory connectivity analysis

by EURING Migration Atlas

Cygnus olor **(EURING code 01520)**

1.1 Connectivity between individuals

The analysis evaluated 24302 individuals (48604 encounters) filtered from a total of 627149 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 01520-1; Figure 01520-1).

Table 01520-1. 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	24302	0.965	0.001	0.963	0.967	2	0.548
1	1	11344	0.982	0.001	0.979	0.985	4	0.593
2	1	12958	0.896	0.001	0.889	0.902	5	0.416
11	2	2967	0.877	0.001	0.846	0.903	2	0.588
12	2	5450	0.915	0.001	0.900	0.929	3	0.510
13	2	2449	0.915	0.001	0.901	0.930	8	0.499
14	2	478	0.799	0.001	0.669	0.919	2	0.766
111	3	1010	0.855	0.001	0.806	0.894	9	0.632
112	3	1957	0.675	0.001	0.457	0.828	2	0.498
121	3	2463	0.876	0.001	0.832	0.914	4	0.506
122	3	1032	0.907	0.001	0.861	0.937	5	0.539
123	3	1955	0.714	0.001	0.670	0.756	3	0.430
141	3	353	0.457	0.001	0.373	0.575	8	0.626
142	3	125	0.420	0.002	0.118	0.741	3	0.404
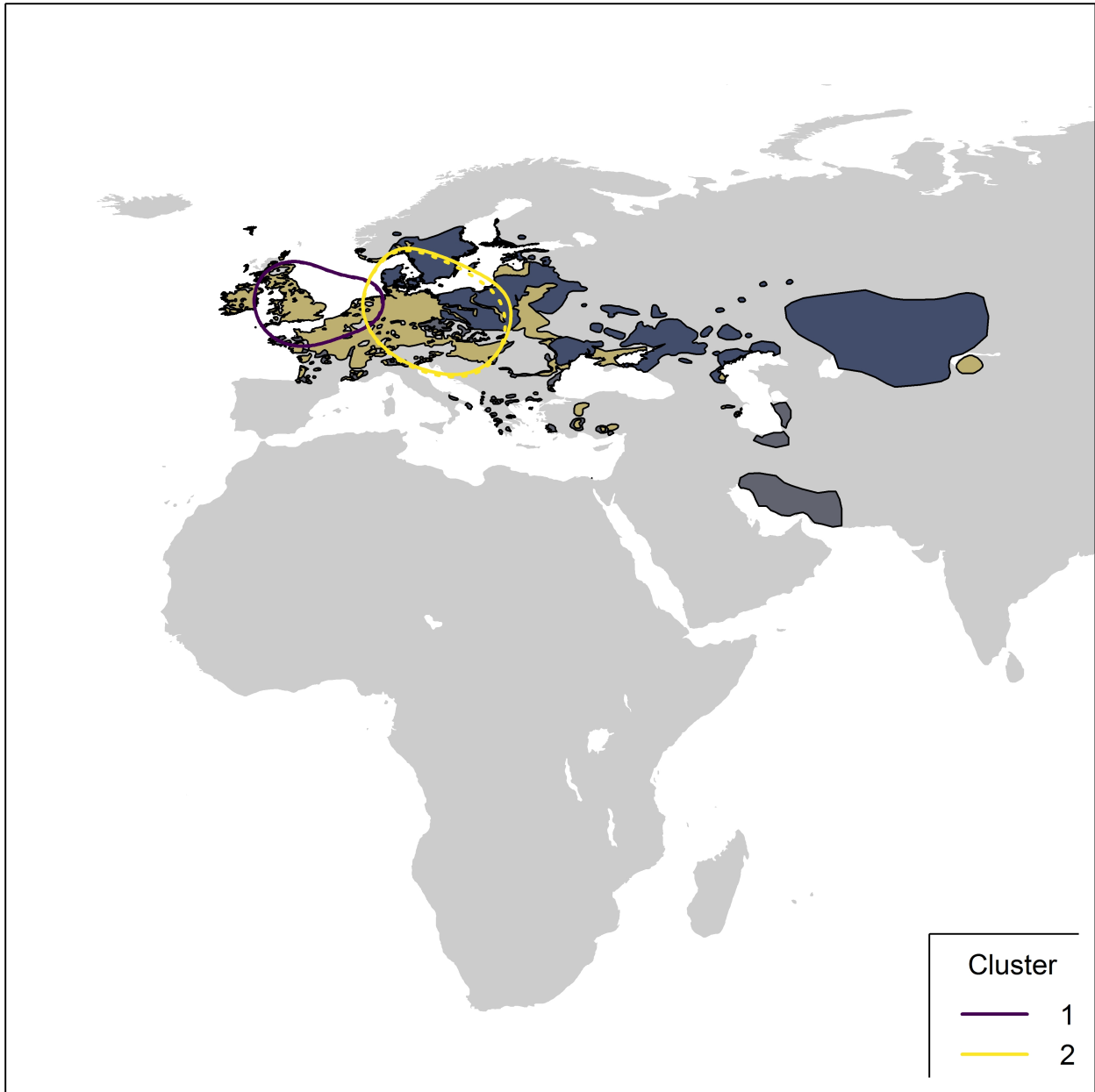
Figure 01520-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 01520-2) and stratified sampling of individuals within the breeding range (Figure 01520-3) and the non breeding range (Figure 01520-4). 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.
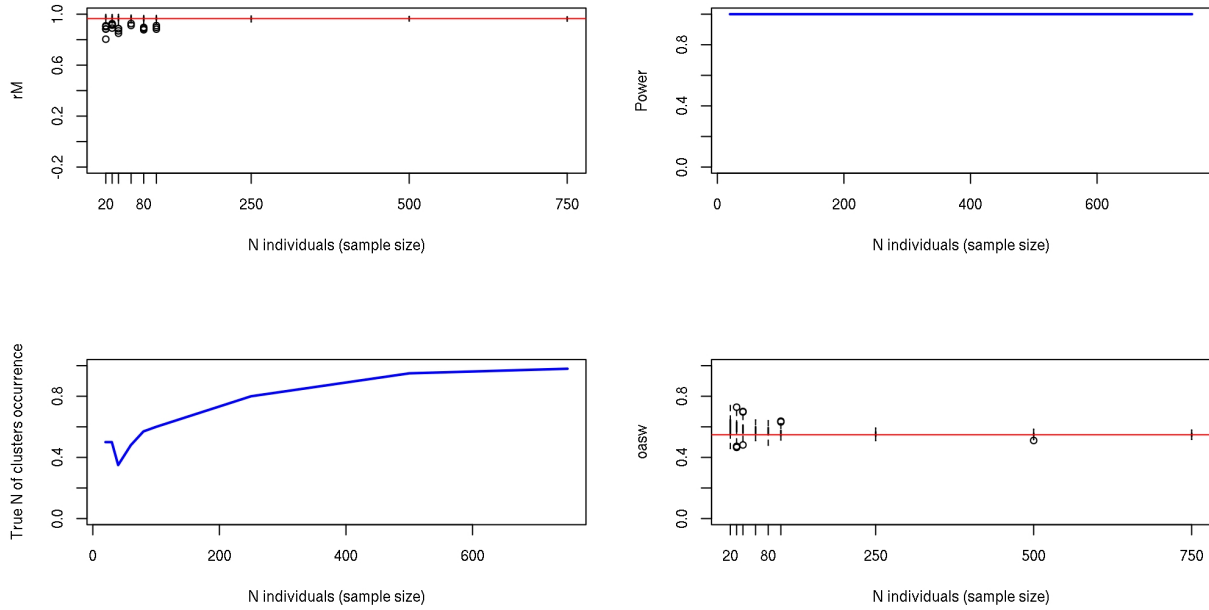

Figure 01520-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.
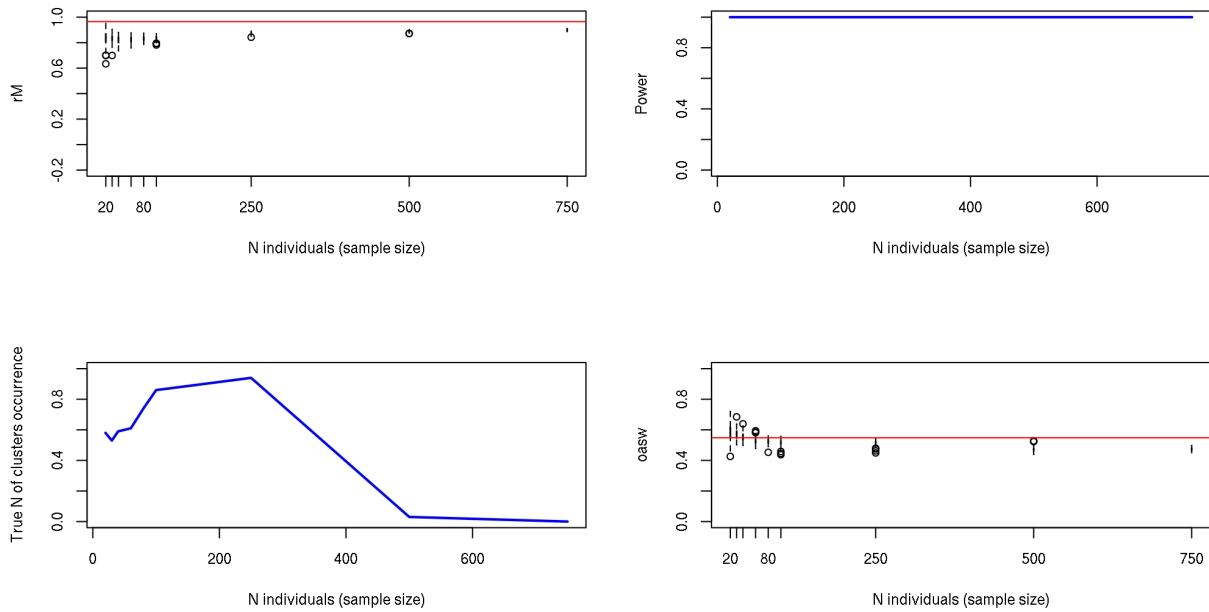

Figure 01520-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

Figure 01520-4. 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.
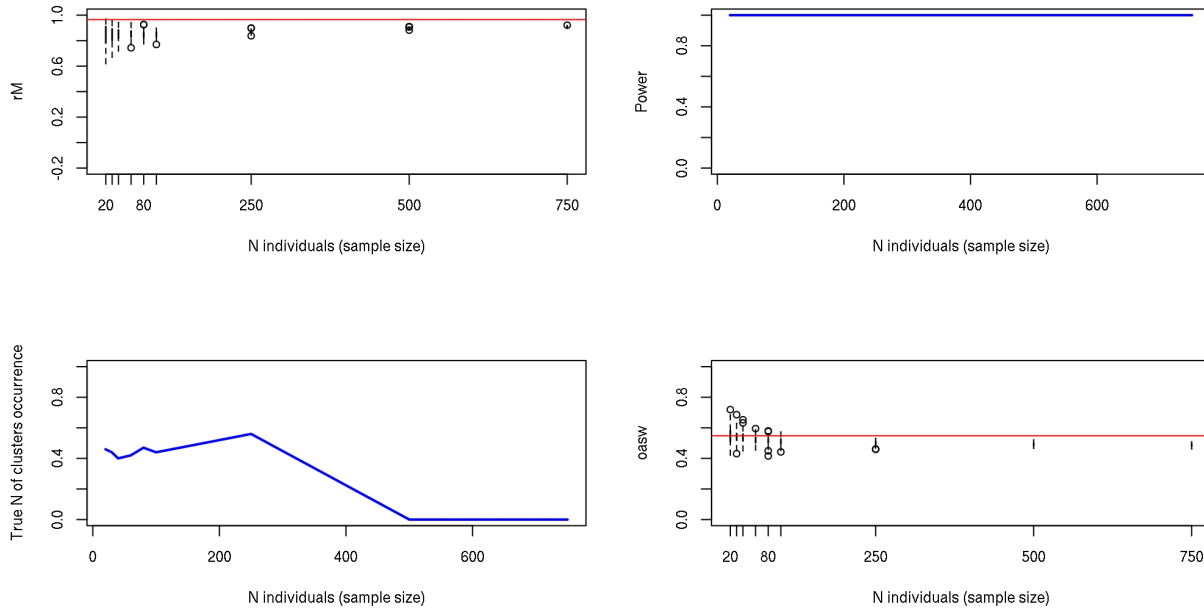
The comparison between the bootstrapped distribution of r_M values from live recaptures and dead recoveries is not significant (p = 1); Figure 01520-5).
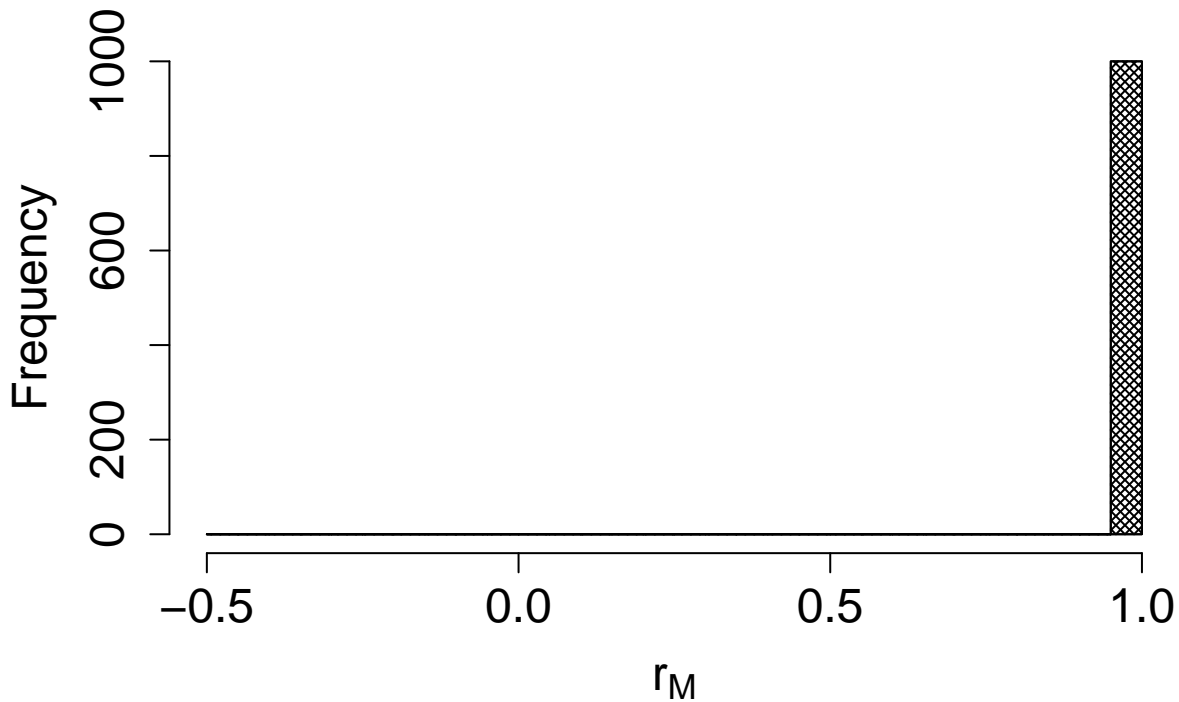
Figure 01520-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows moderate/high connectivity (MC = 0.709; MC = 0.709 when adjusted for absolute abundance) between 7 breeding regions and 7 non breeding regions (Table 01520-2; Figure 01520-6).

Table 01520-2. 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	46677	Central Europe	0.968
Central Europe	46677	East Europe	0.003
Central Europe	46677	North Europe	0.000
Central Europe	46677	North-west Europe	0.000
Central Europe	46677	South-central Europe	0.016
Central Europe	46677	South-east Europe	0.005
Central Europe	46677	West Europe	0.007
East Europe	43950	Central Europe	0.345
East Europe	43950	East Europe	0.491
East Europe	43950	North Europe	0.004
East Europe	43950	North-west Europe	0.004
East Europe	43950	South-central Europe	0.004
East Europe	43950	South-east Europe	0.124

Breeding region	Abundance	Non breeding region	Transition probability
East Europe	43950	West Europe	0.027
North Europe	51705	Central Europe	0.080
North Europe	51705	North Europe	0.915
North Europe	51705	North-west Europe	0.001
North Europe	51705	West Europe	0.004
North-west Europe	19920	North Europe	0.000
North-west Europe	19920	North-west Europe	0.999
North-west Europe	19920	West Europe	0.001
South-central Europe	3280	Central Europe	0.137
South-central Europe	3280	South-central Europe	0.863
South-east Europe	8829	Central Europe	0.500
South-east Europe	8829	South-east Europe	0.500
West Europe	23838	Central Europe	0.064
West Europe	23838	North Europe	0.003
West Europe	23838	North-west Europe	0.001
West Europe	23838	West Europe	0.932

Figure 01520-6. 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.