

Migratory connectivity analysis

by EURING Migration Atlas

Ciconia ciconia (EURING code 01340)

1.1 Connectivity between individuals

The analysis evaluated 3783 individuals (7566 encounters) filtered from a total of 321995 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 01340-1; Figure 01340-1).

Table 01340-1. 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	3783	0.159	0.001	0.139	0.178	2	0.845
1	1	3487	0.216	0.001	0.185	0.250	2	0.605
2	1	296	-0.004	0.515	-0.049	0.065	-	-
11	2	3014	0.142	0.001	0.082	0.206	2	0.608
12	2	473	0.194	0.001	0.083	0.297	2	0.777
111	3	461	0.561	0.001	0.445	0.664	2	0.902
112	3	2553	0.135	0.001	0.059	0.209	9	0.465
121	3	414	0.122	0.001	0.065	0.192	3	0.550
122	3	59	0.189	0.006	0.040	0.383	4	0.613

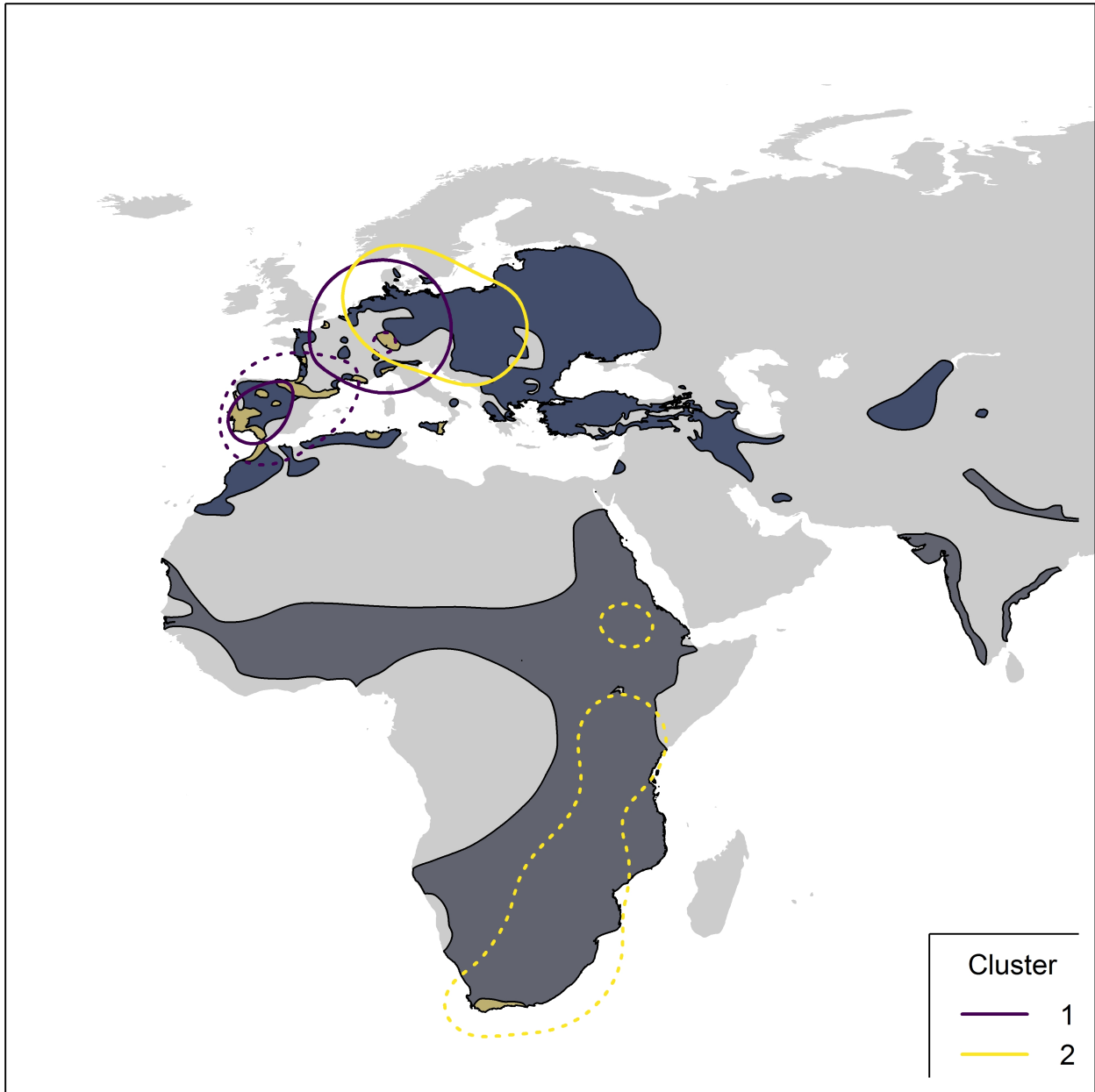


Figure 01340-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 01340-2) and stratified sampling of individuals within the breeding range (Figure 01340-3) and the non breeding range (Figure 01340-4). 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.

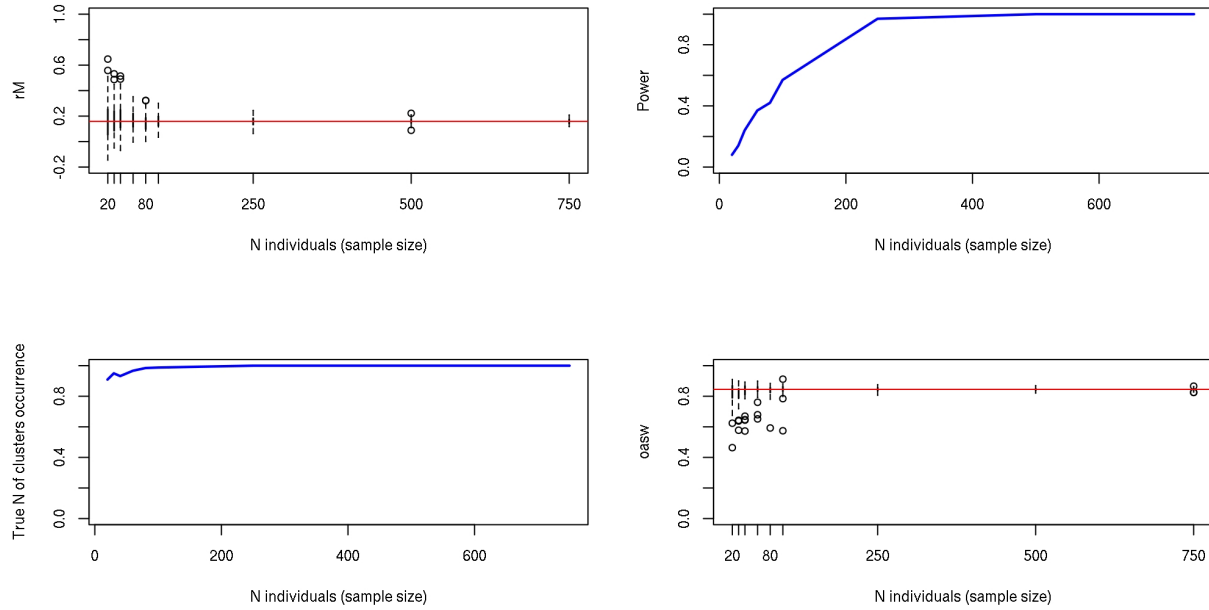


Figure 01340-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

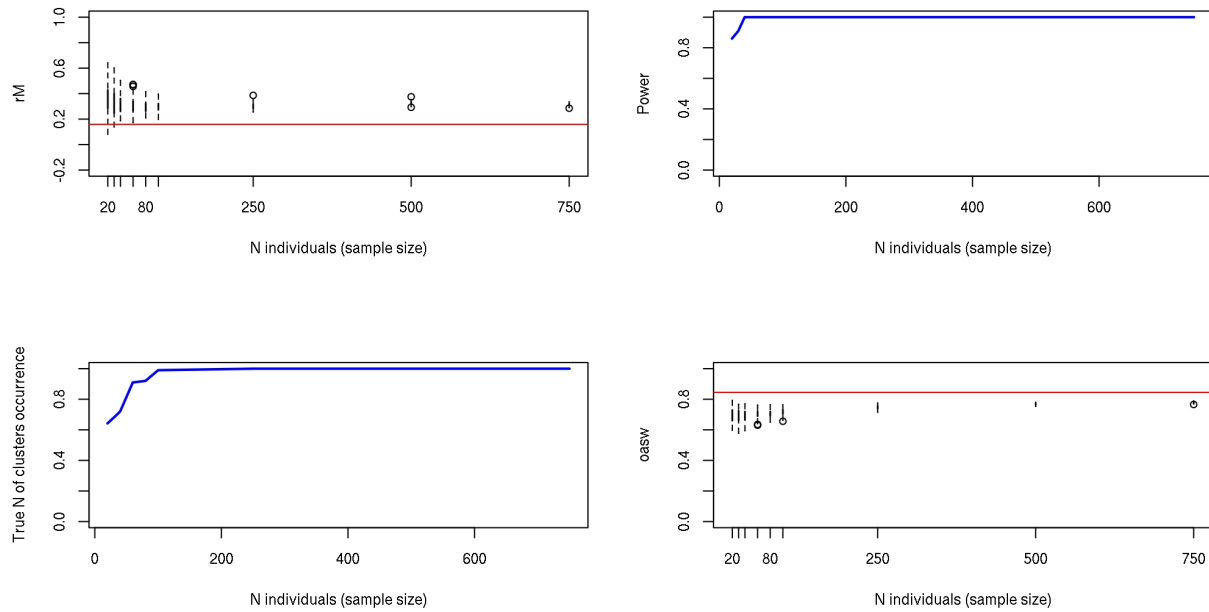


Figure 01340-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

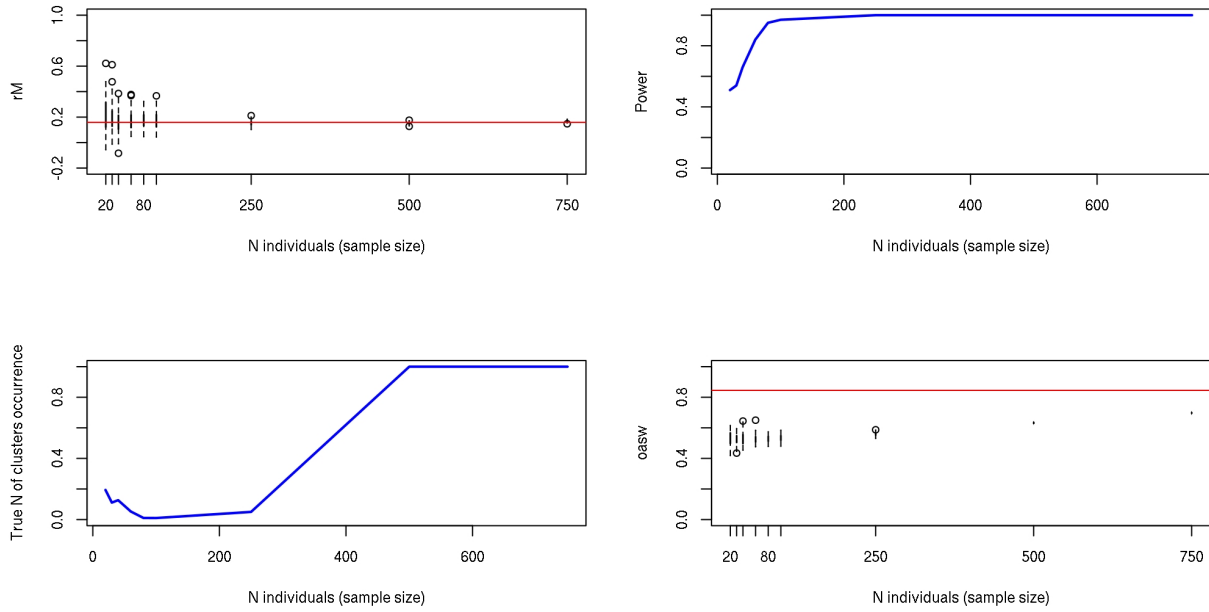


Figure 01340-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 01340-5).

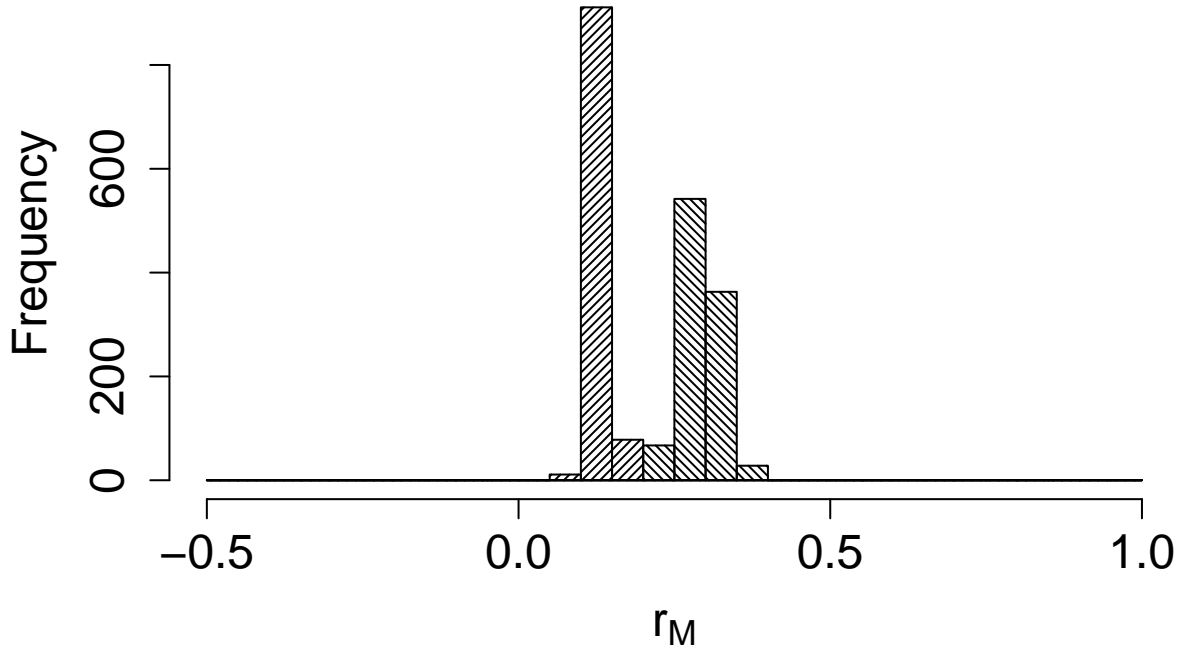


Figure 01340-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low/moderate connectivity ($MC = 0.335$; $MC = 0.335$ when adjusted for absolute abundance) between 7 breeding regions and 8 non breeding regions (Table 01340-2; Figure 01340-6).

Table 01340-2. 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	130523	Central Africa	0.002
Central Europe	130523	Central Europe	0.105
Central Europe	130523	East Africa	0.020
Central Europe	130523	North Africa	0.009
Central Europe	130523	South Africa	0.069
Central Europe	130523	South-west Europe	0.754
Central Europe	130523	West Africa	0.006
Central Europe	130523	West Europe	0.036
East Europe	190800	Central Africa	0.067
East Europe	190800	East Africa	0.200
East Europe	190800	North Africa	0.133
East Europe	190800	South Africa	0.467
East Europe	190800	West Africa	0.133

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	2	Central Europe	0.023
North Europe	2	East Africa	0.068
North Europe	2	North Africa	0.068
North Europe	2	South Africa	0.295
North Europe	2	South-west Europe	0.545
South-central Europe	3193	North Africa	0.111
South-central Europe	3193	South Africa	0.889
South-east Europe	45856	East Africa	0.167
South-east Europe	45856	North Africa	0.167
South-east Europe	45856	South Africa	0.583
South-east Europe	45856	South-west Europe	0.083
South-west Europe	89174	East Africa	0.002
South-west Europe	89174	North Africa	0.038
South-west Europe	89174	South-west Europe	0.852
South-west Europe	89174	West Africa	0.103
South-west Europe	89174	West Europe	0.004
West Europe	4008	Central Europe	0.005
West Europe	4008	North Africa	0.003
West Europe	4008	South-west Europe	0.893
West Europe	4008	West Africa	0.010
West Europe	4008	West Europe	0.089

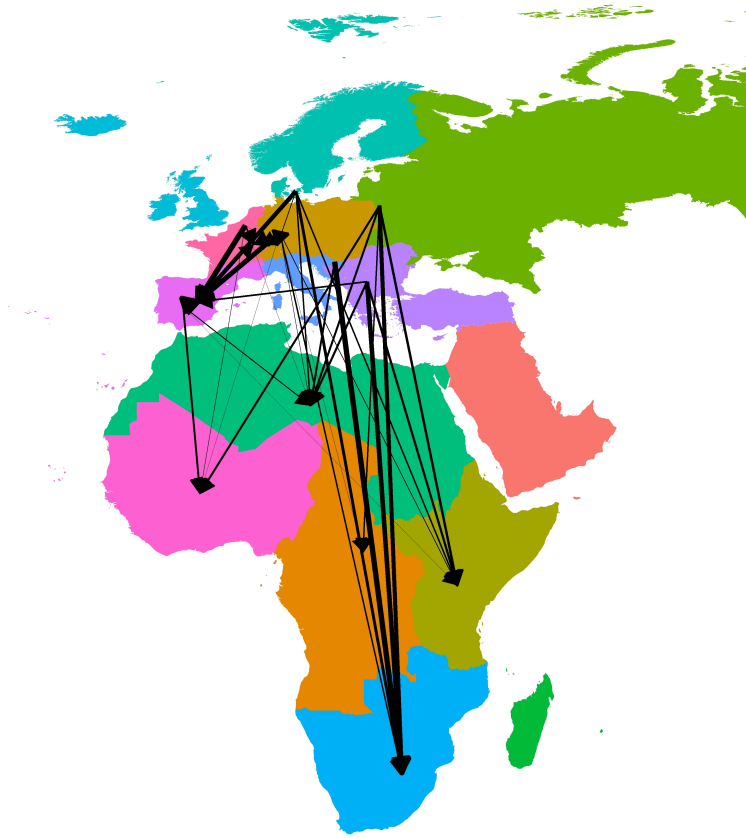


Figure 01340-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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>.