

Migratory connectivity analysis

by EURING Migration Atlas

Anas platyrhynchos (EURING code 01860)

1.1 Connectivity between individuals

The analysis evaluated 6333 individuals (12666 encounters) filtered from a total of 307587 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 01860-1; Figure 01860-1).

Table 01860-1. 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	6333	0.662	0.001	0.639	0.683	6	0.468

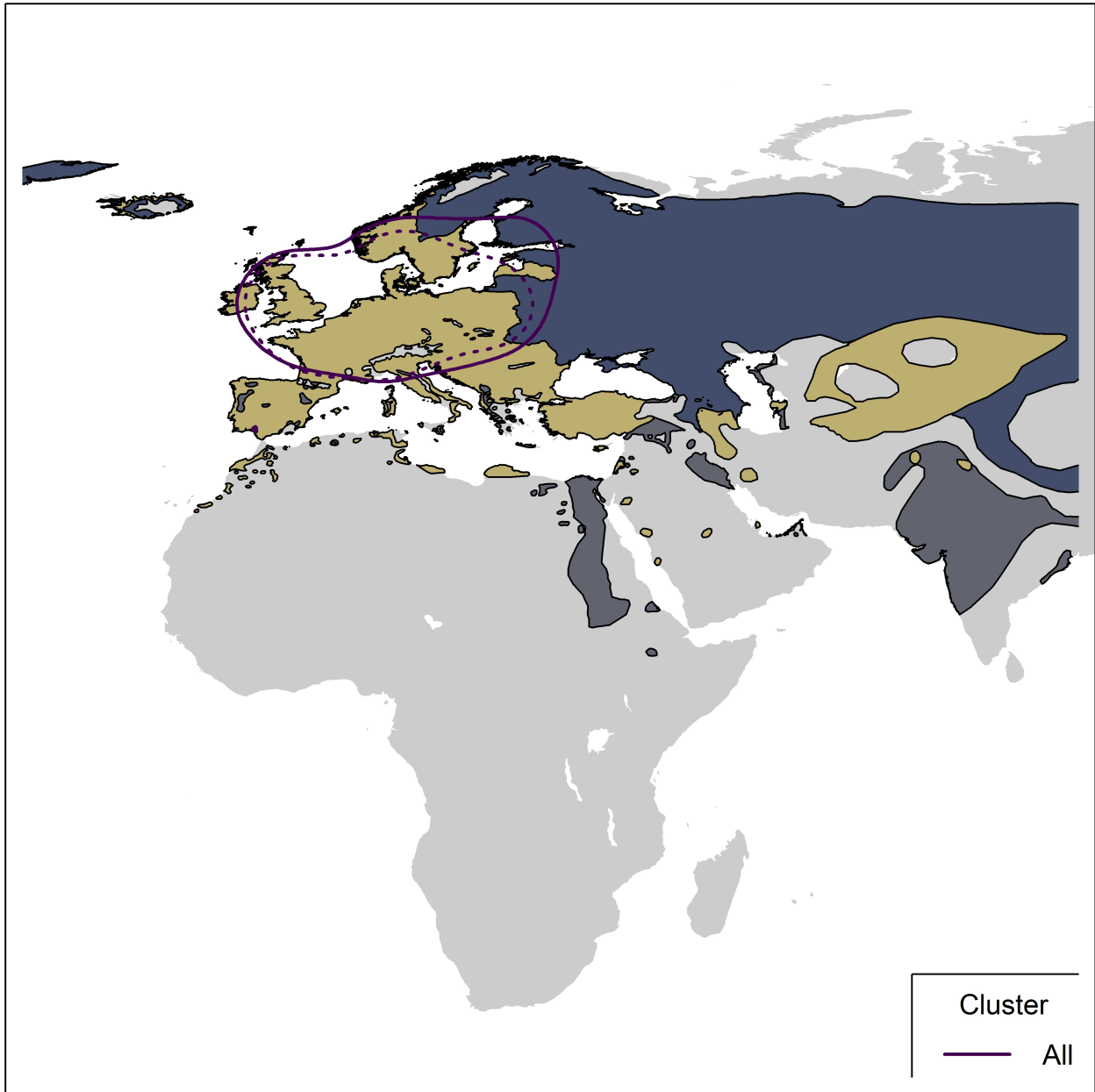


Figure 01860-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 01860-2) and stratified sampling of individuals within the breeding range (Figure 01860-3) and the non breeding range (Figure 01860-4). 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.

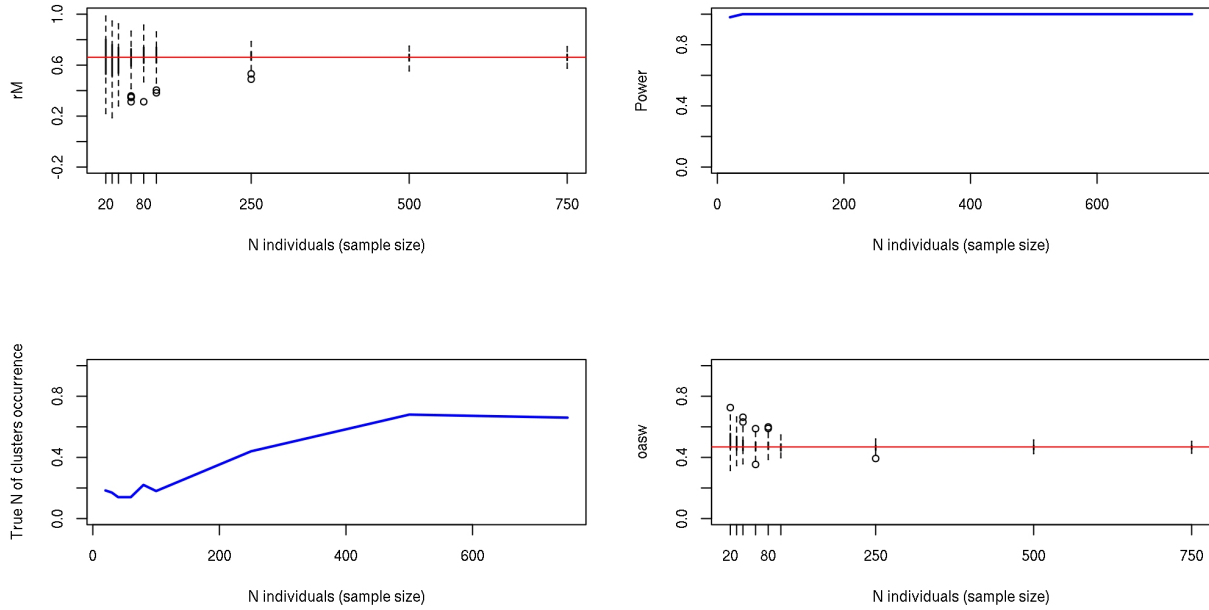


Figure 01860-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

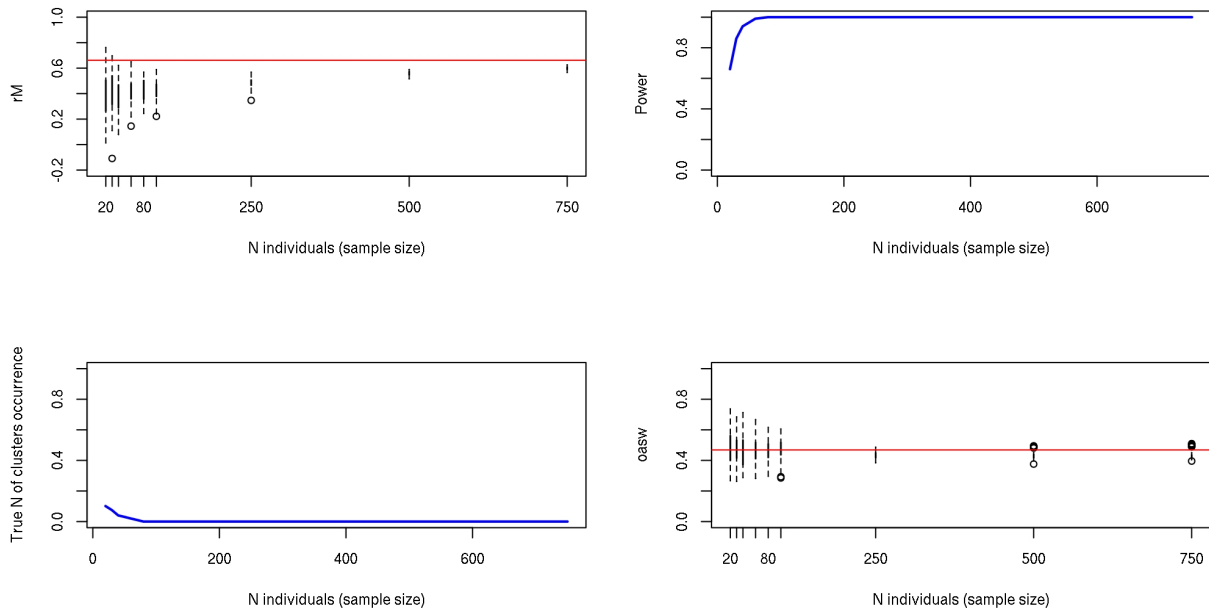


Figure 01860-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

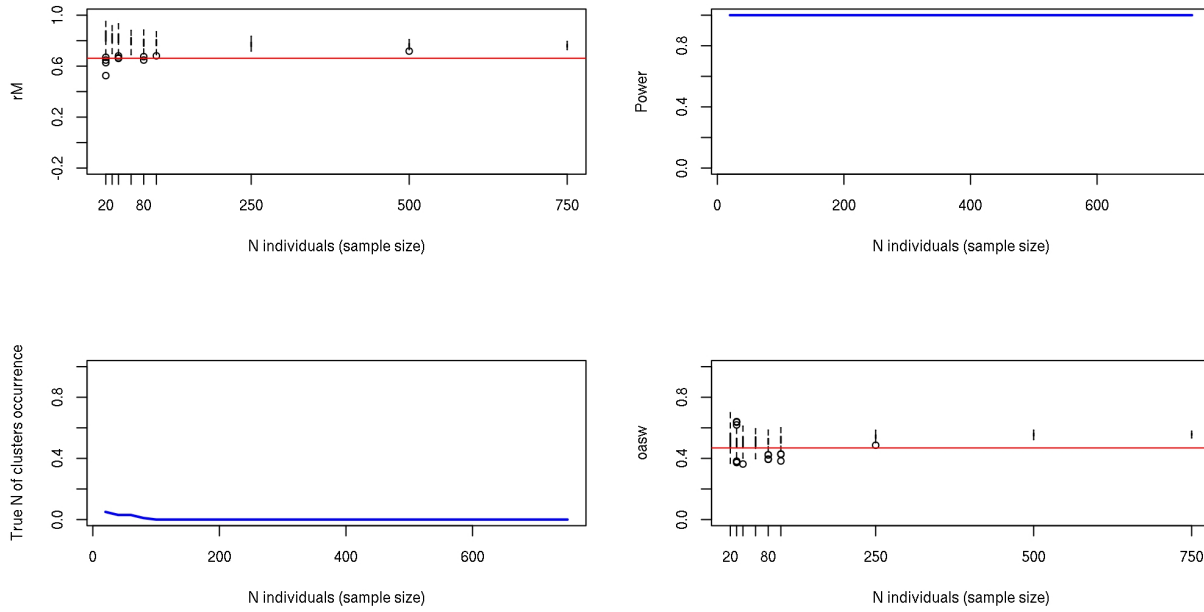


Figure 01860-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 01860-5).

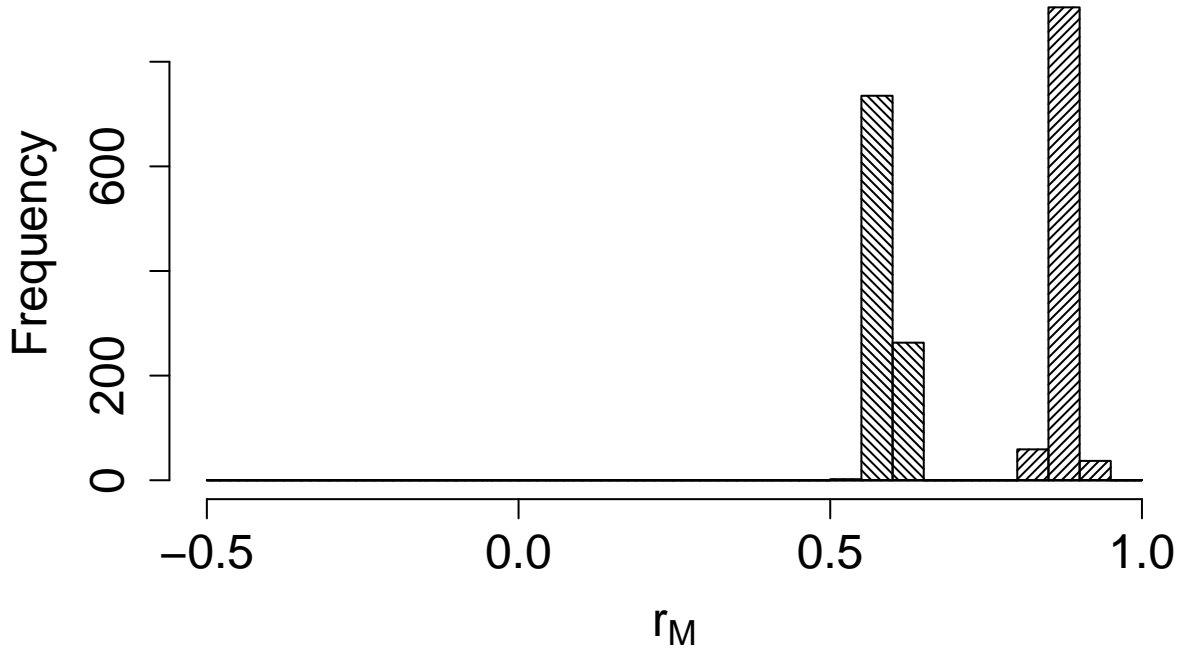


Figure 01860-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows moderate connectivity ($MC = 0.447$; $MC = 0.447$ when adjusted for absolute abundance) between 8 breeding regions and 9 non breeding regions (Table 01860-2; Figure 01860-6).

Table 01860-2. 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	1353030	Central Europe	0.875
Central Europe	1353030	North Europe	0.002
Central Europe	1353030	North-west Europe	0.007
Central Europe	1353030	South-central Europe	0.013
Central Europe	1353030	South-east Europe	0.001
Central Europe	1353030	South-west Europe	0.006
Central Europe	1353030	West Europe	0.096
East Europe	2981835	Central Europe	0.376
East Europe	2981835	East Europe	0.044
East Europe	2981835	North Africa	0.003
East Europe	2981835	North Europe	0.107
East Europe	2981835	North-west Europe	0.060
East Europe	2981835	South-central Europe	0.019

Breeding region	Abundance	Non breeding region	Transition probability
East Europe	2981835	South-east Europe	0.041
East Europe	2981835	South-west Europe	0.025
East Europe	2981835	West Europe	0.326
North Europe	977950	Central Europe	0.094
North Europe	977950	East Europe	0.001
North Europe	977950	North Europe	0.689
North Europe	977950	North-west Europe	0.101
North Europe	977950	South-central Europe	0.001
North Europe	977950	South-west Europe	0.001
North Europe	977950	West Europe	0.113
North-west Europe	262800	Central Europe	0.001
North-west Europe	262800	North Europe	0.001
North-west Europe	262800	North-west Europe	0.971
North-west Europe	262800	South-west Europe	0.003
North-west Europe	262800	West Europe	0.023
South-central Europe	124050	Central Europe	0.017
South-central Europe	124050	South-central Europe	0.879
South-central Europe	124050	South-east Europe	0.086
South-central Europe	124050	West Europe	0.017
South-east Europe	247051	Central Europe	1.000
South-west Europe	439862	Central Europe	0.006
South-west Europe	439862	North-west Europe	0.006
South-west Europe	439862	South-west Europe	0.911
South-west Europe	439862	West Europe	0.077
West Europe	1051112	Central Europe	0.013
West Europe	1051112	North Europe	0.007
West Europe	1051112	North-west Europe	0.062
West Europe	1051112	South-west Europe	0.005
West Europe	1051112	West Europe	0.913

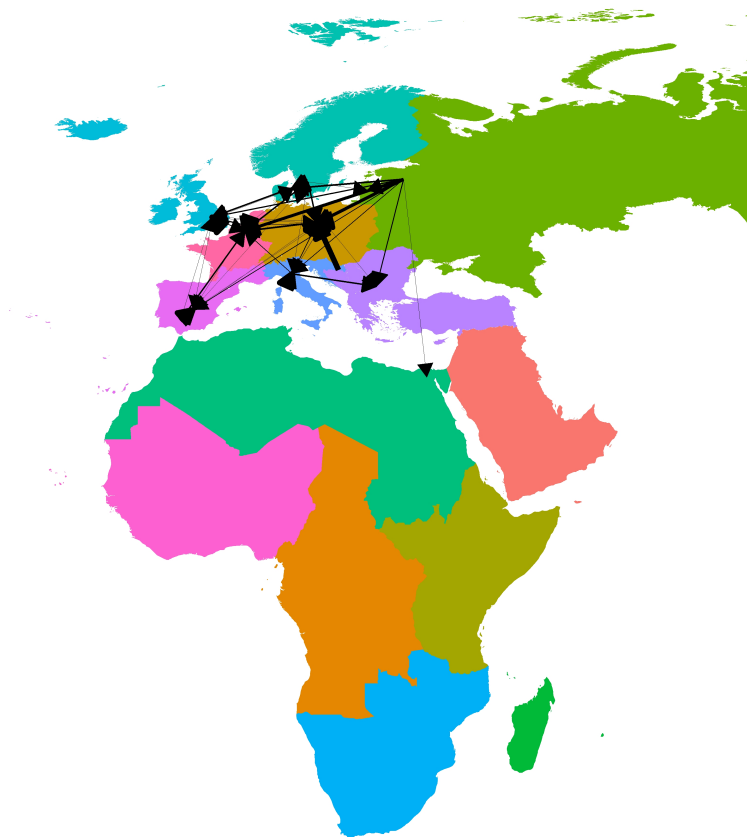


Figure 01860-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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>.