

Migratory connectivity analysis

by EURING Migration Atlas

Columba palumbus (EURING code 06700)

1.1 Connectivity between individuals

The analysis evaluated 1522 individuals (3044 encounters) filtered from a total of 27670 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 06700-1; Figure 06700-1).

Table 06700-1. 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	1522	0.674	0.001	0.639	0.71	6	0.419

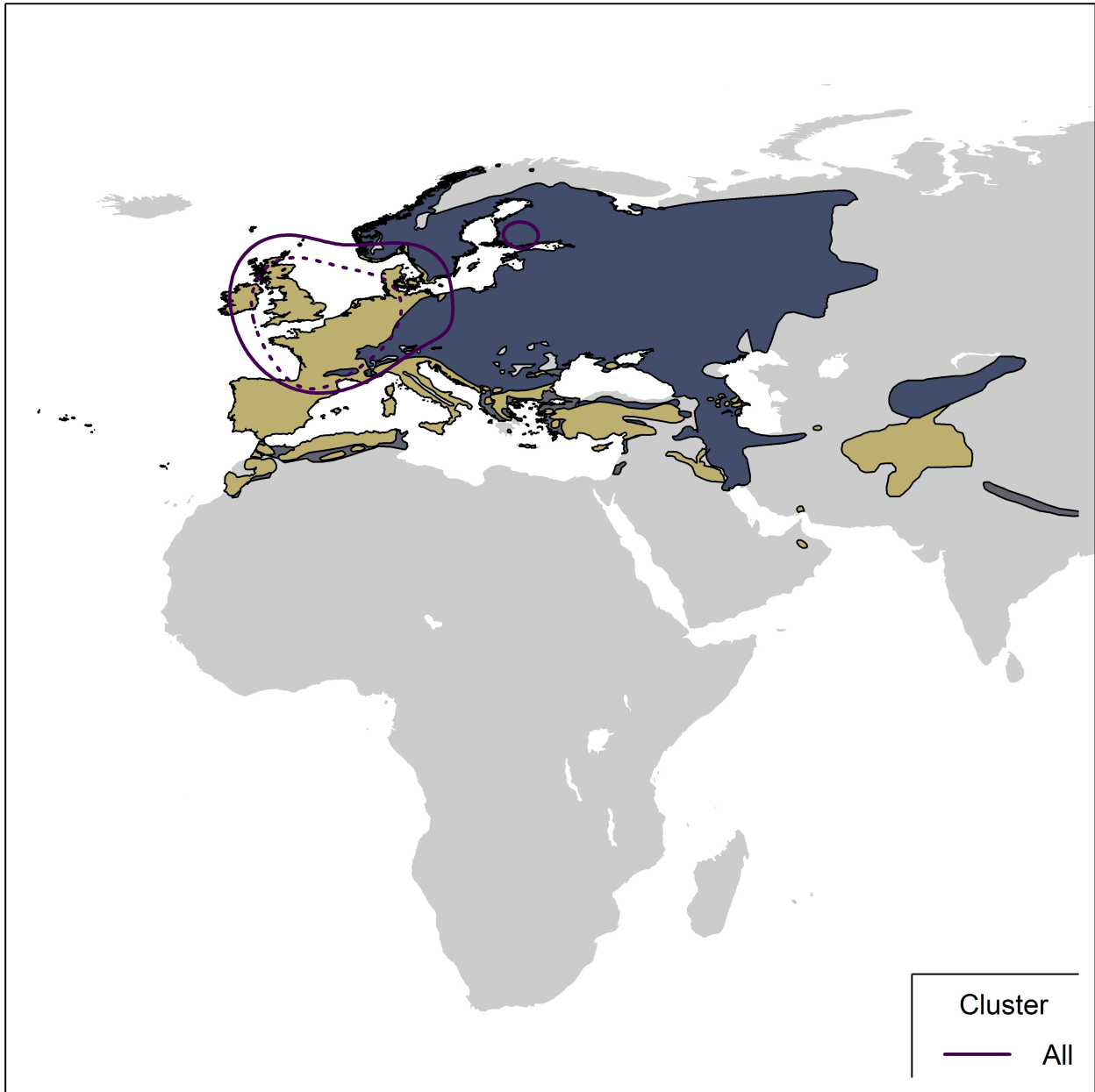


Figure 06700-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 06700-2) and stratified sampling of individuals within the breeding range (Figure 06700-3) and the non breeding range (Figure 06700-4). 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.

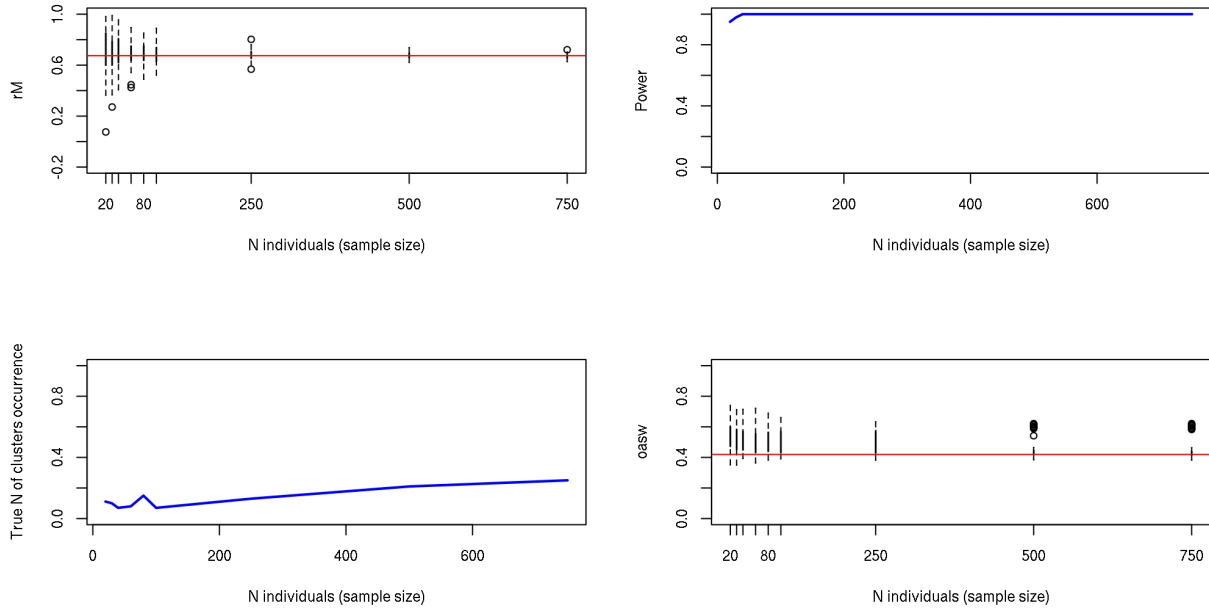


Figure 06700-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

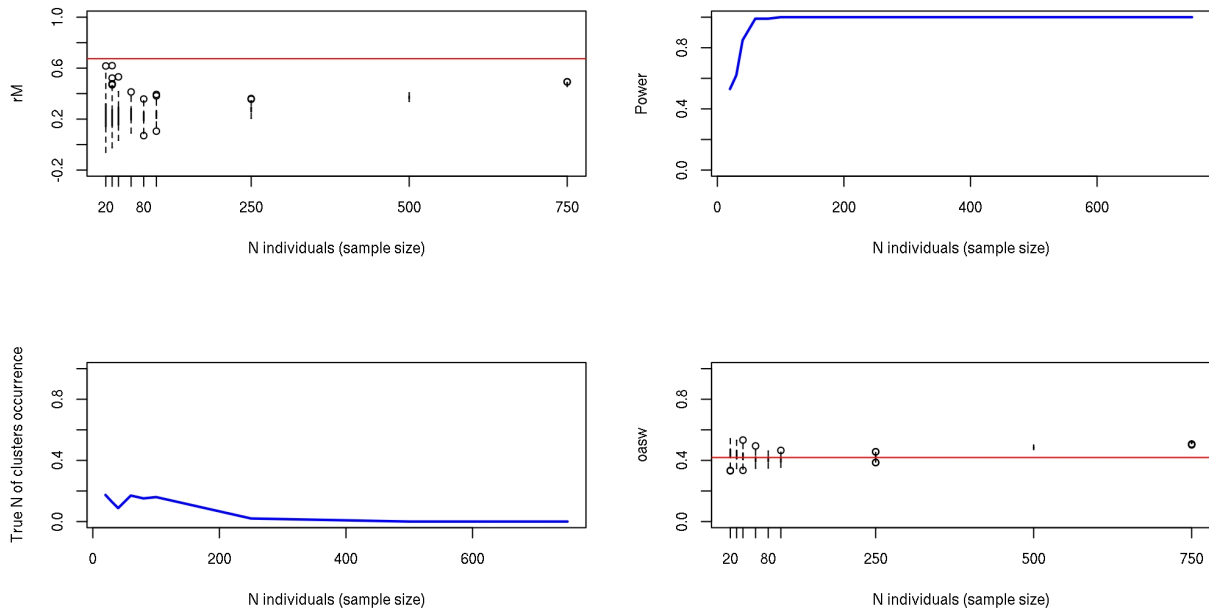


Figure 06700-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

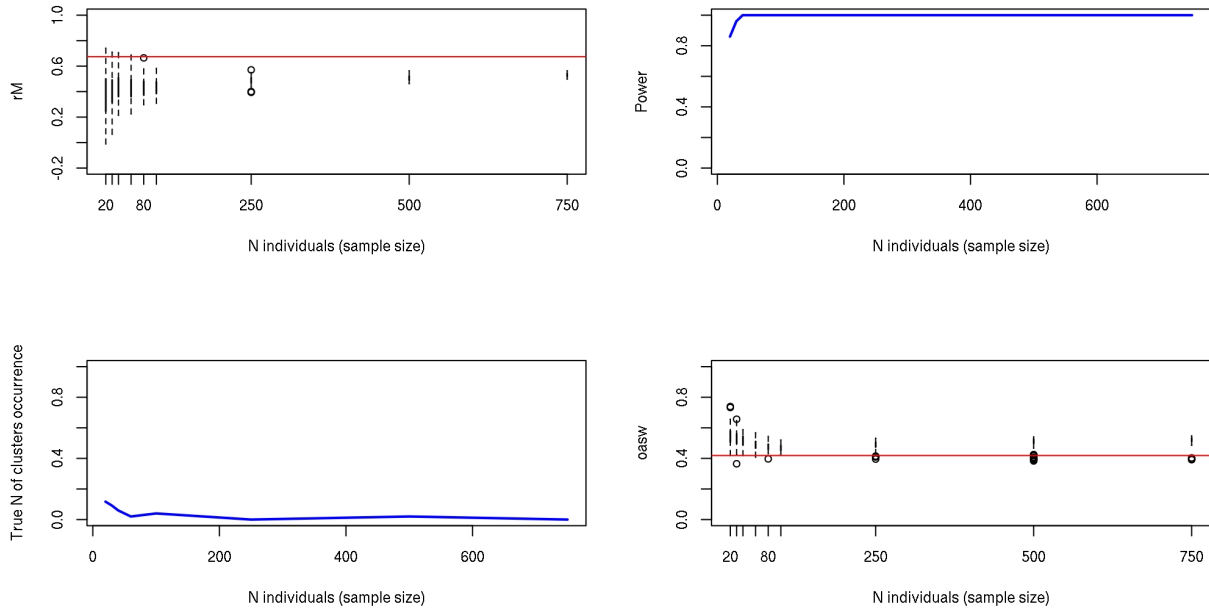


Figure 06700-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 06700-5).

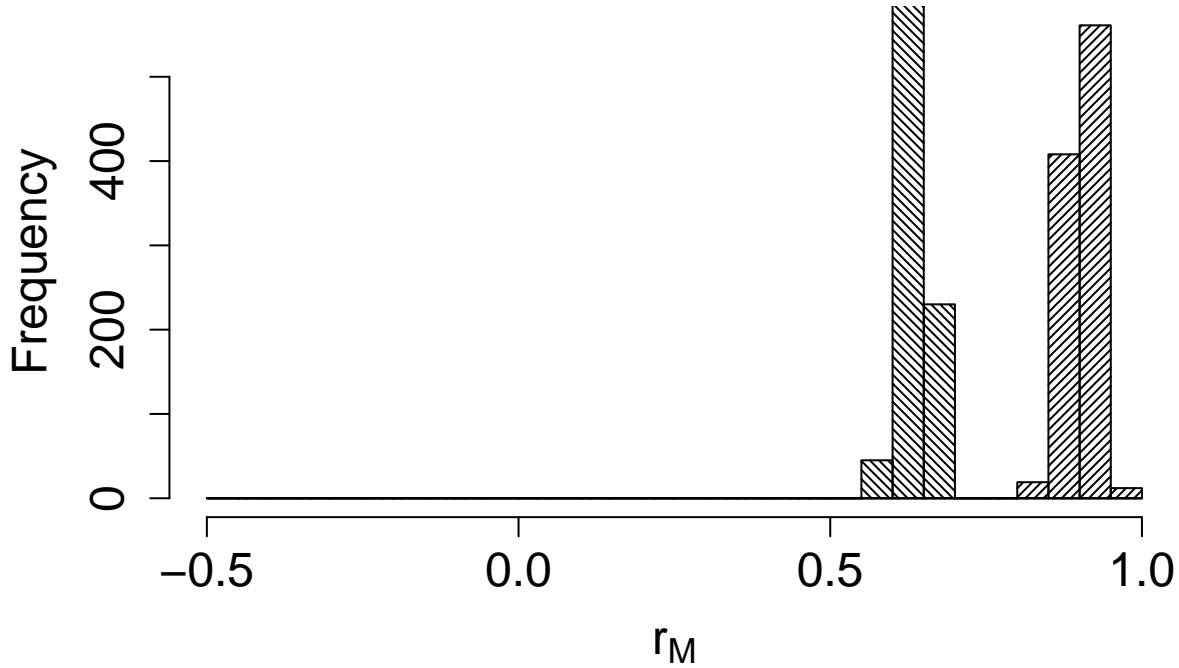


Figure 06700-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low/moderate connectivity ($MC = 0.382$; $MC = 0.382$ when adjusted for absolute abundance) between 7 breeding regions and 6 non breeding regions (Table 06700-2; Figure 06700-6).

Table 06700-2. 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	8969850	Central Europe	0.450
Central Europe	8969850	North Europe	0.007
Central Europe	8969850	South-central Europe	0.054
Central Europe	8969850	South-west Europe	0.181
Central Europe	8969850	West Europe	0.309
East Europe	2717907	South-west Europe	0.500
East Europe	2717907	West Europe	0.500
North Europe	4729002	Central Europe	0.080
North Europe	4729002	North Europe	0.219
North Europe	4729002	North-west Europe	0.007
North Europe	4729002	South-central Europe	0.007
North Europe	4729002	South-west Europe	0.263
North Europe	4729002	West Europe	0.423

Breeding region	Abundance	Non breeding region	Transition probability
North-west Europe	13601545	North-west Europe	0.977
North-west Europe	13601545	South-west Europe	0.002
North-west Europe	13601545	West Europe	0.022
South-central Europe	348853	South-central Europe	0.750
South-central Europe	348853	South-west Europe	0.250
South-west Europe	11737702	South-west Europe	0.800
South-west Europe	11737702	West Europe	0.200
West Europe	5720171	Central Europe	0.004
West Europe	5720171	North-west Europe	0.002
West Europe	5720171	South-west Europe	0.023
West Europe	5720171	West Europe	0.972

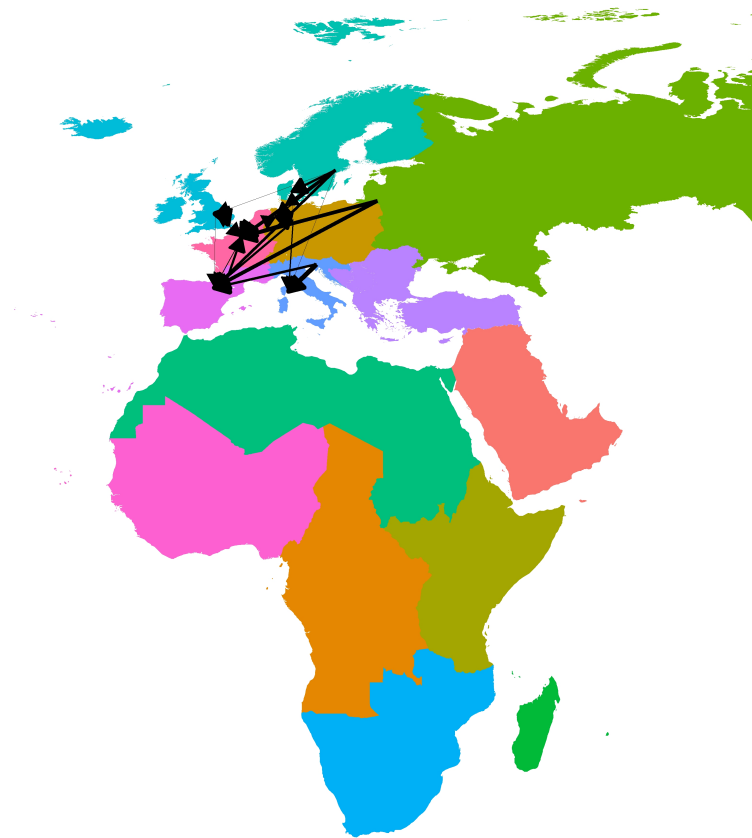


Figure 06700-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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>.