

Migratory connectivity analysis

by EURING Migration Atlas

Turdus philomelos (EURING code 12000)

1.1 Connectivity between individuals

The analysis evaluated 5137 individuals (10274 encounters) filtered from a total of 149613 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 = 3 (Table 12000-1; Figure 12000-1).

Table 12000-1. 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	5137	0.573	0.001	0.552	0.593	3	0.520
1	1	1656	0.286	0.001	0.233	0.338	9	0.370
2	1	2869	0.706	0.001	0.662	0.749	4	0.443
3	1	612	0.201	0.001	0.124	0.273	2	0.319

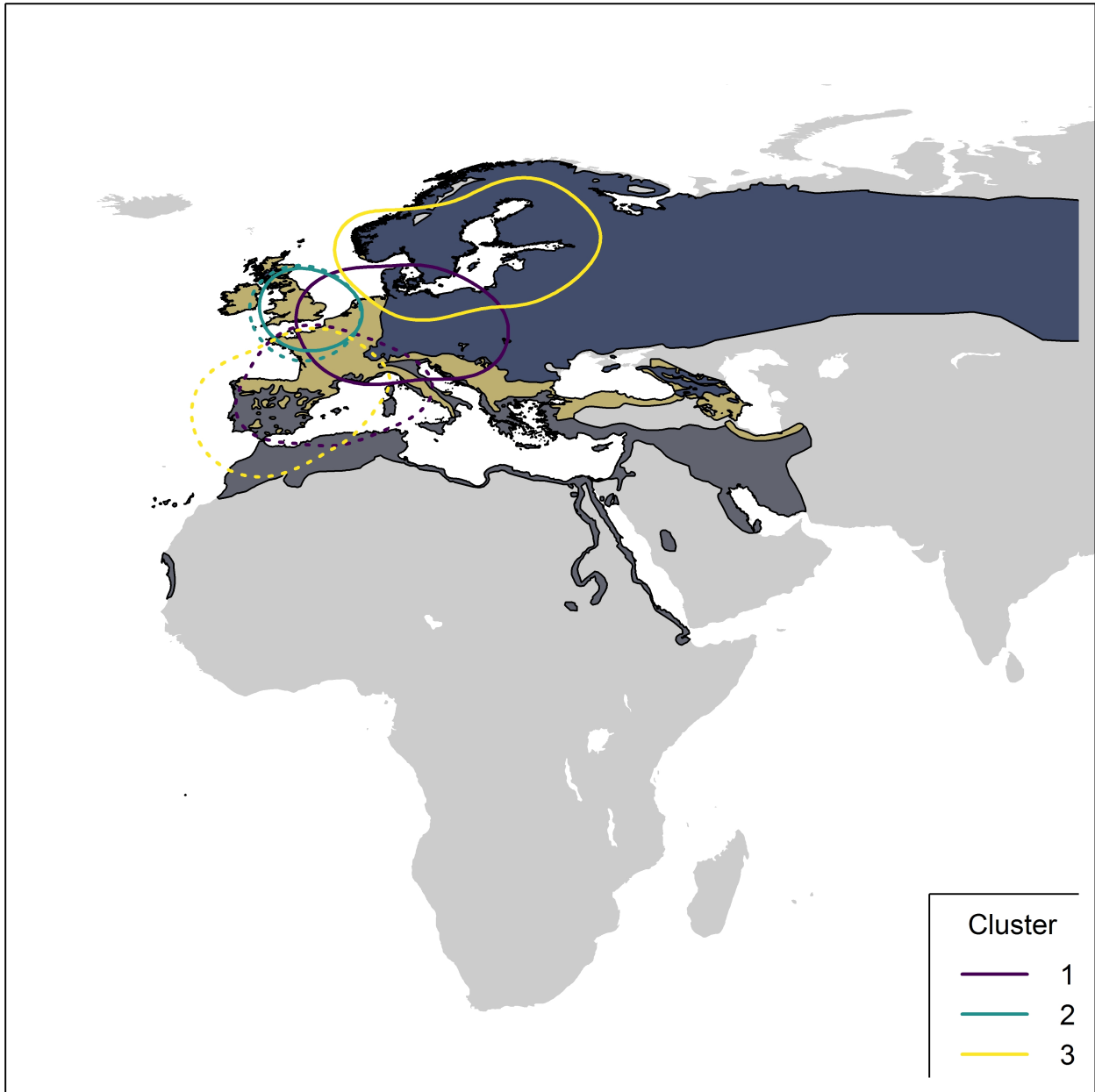


Figure 12000-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 12000-2) and stratified sampling of individuals within the breeding range (Figure 12000-3) and the non breeding range (Figure 12000-4). 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.

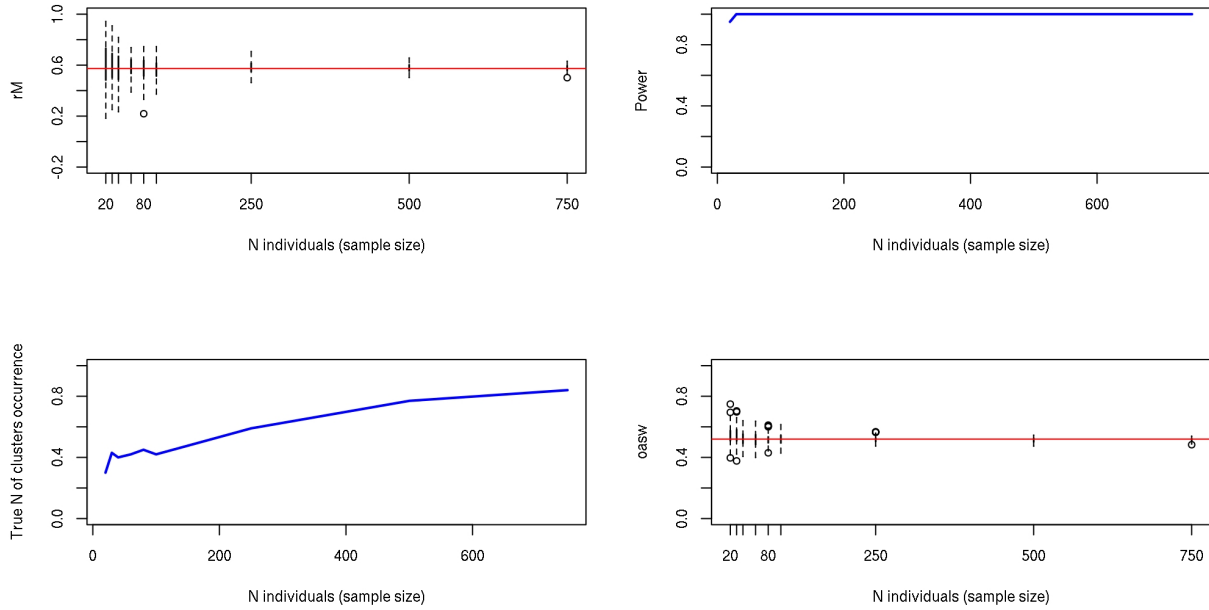


Figure 12000-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

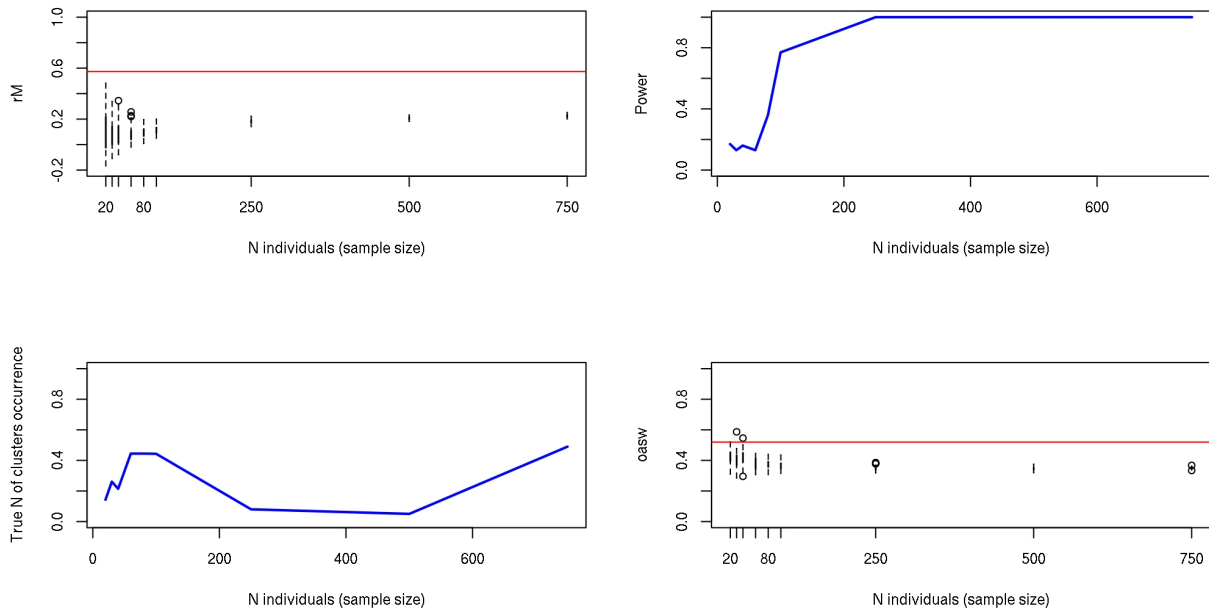


Figure 12000-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

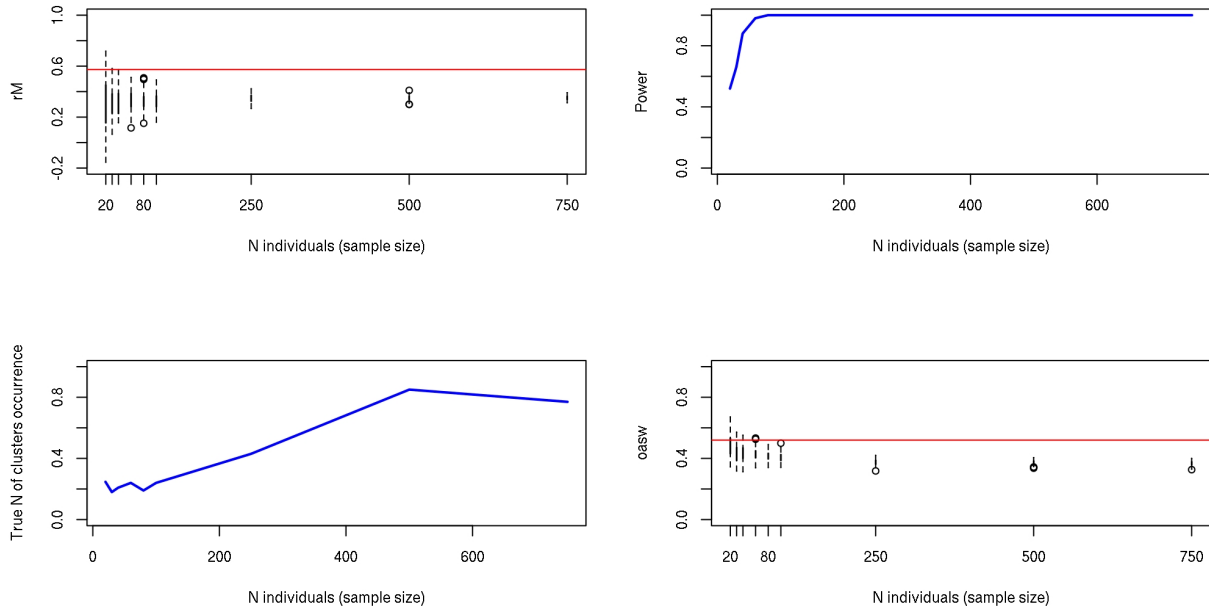


Figure 12000-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 12000-5).

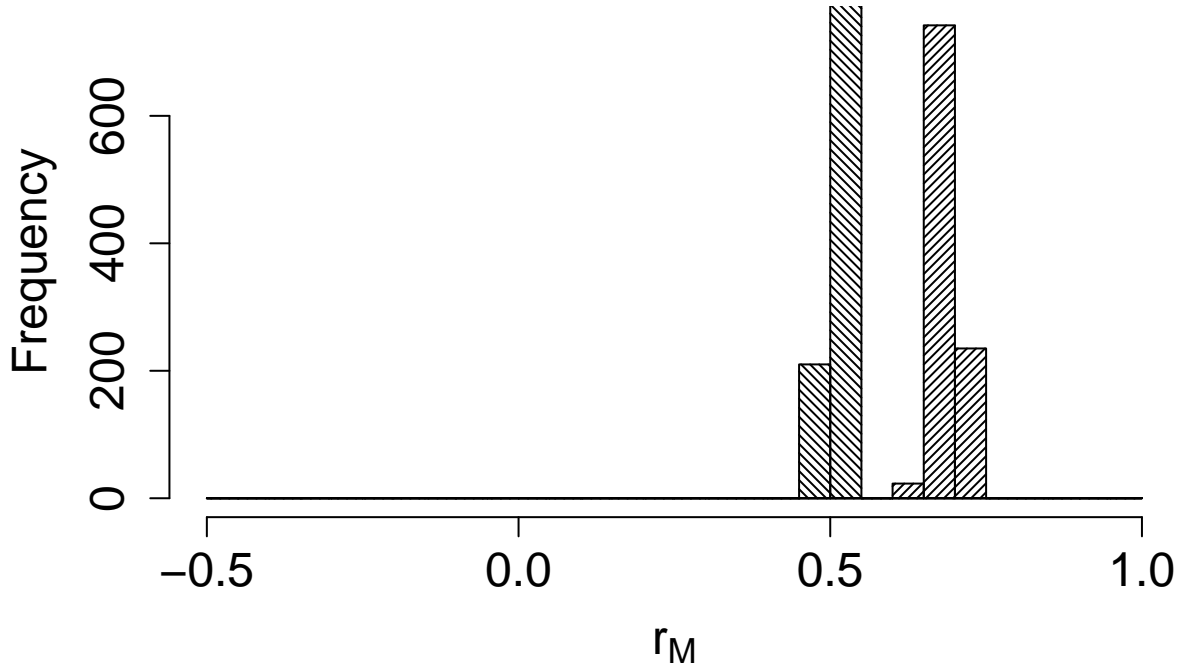


Figure 12000-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low/moderate connectivity ($MC = 0.236$; $MC = 0.236$ when adjusted for absolute abundance) between 8 breeding regions and 8 non breeding regions (Table 12000-2; Figure 12000-6).

Table 12000-2. 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	10443500	Central Europe	0.004
Central Europe	10443500	North Africa	0.060
Central Europe	10443500	North-west Europe	0.003
Central Europe	10443500	South-central Europe	0.242
Central Europe	10443500	South-west Europe	0.608
Central Europe	10443500	West Europe	0.083
East Europe	24728217	East Europe	0.011
East Europe	24728217	North Africa	0.011
East Europe	24728217	South-central Europe	0.187
East Europe	24728217	South-east Europe	0.055
East Europe	24728217	South-west Europe	0.615
East Europe	24728217	West Europe	0.121
North Europe	9480000	North Africa	0.027

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	9480000	North-west Europe	0.010
North Europe	9480000	South-central Europe	0.027
North Europe	9480000	South-west Europe	0.782
North Europe	9480000	West Europe	0.154
North-west Europe	5211410	North-west Europe	0.955
North-west Europe	5211410	South-west Europe	0.016
North-west Europe	5211410	West Europe	0.030
South-central Europe	2260000	South-central Europe	0.750
South-central Europe	2260000	South-west Europe	0.250
South-east Europe	4840000	South-central Europe	0.250
South-east Europe	4840000	South-east Europe	0.750
South-west Europe	2079864	South-west Europe	1.000
West Europe	3586078	North Africa	0.010
West Europe	3586078	North-west Europe	0.035
West Europe	3586078	South-central Europe	0.015
West Europe	3586078	South-west Europe	0.296
West Europe	3586078	West Europe	0.643



Figure 12000-6. 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>.