

Migratory connectivity analysis

by EURING Migration Atlas

Larus marinus (EURING code 06000)

1.1 Connectivity between individuals

The analysis evaluated 2380 individuals (4760 encounters) filtered from a total of 83825 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 = 6 (Table 06000-1; Figure 06000-1).

Table 06000-1. 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	2380	0.348	0.001	0.322	0.376	6	0.575
1	1	80	-0.021	0.592	-0.066	0.105	-	-
2	1	854	0.065	0.007	0.015	0.119	3	0.436
3	1	434	0.543	0.001	0.429	0.646	7	0.471
4	1	182	0.058	0.044	-0.005	0.148	4	0.451
5	1	675	0.355	0.001	0.283	0.428	8	0.404
6	1	155	0.336	0.001	0.182	0.482	4	0.483

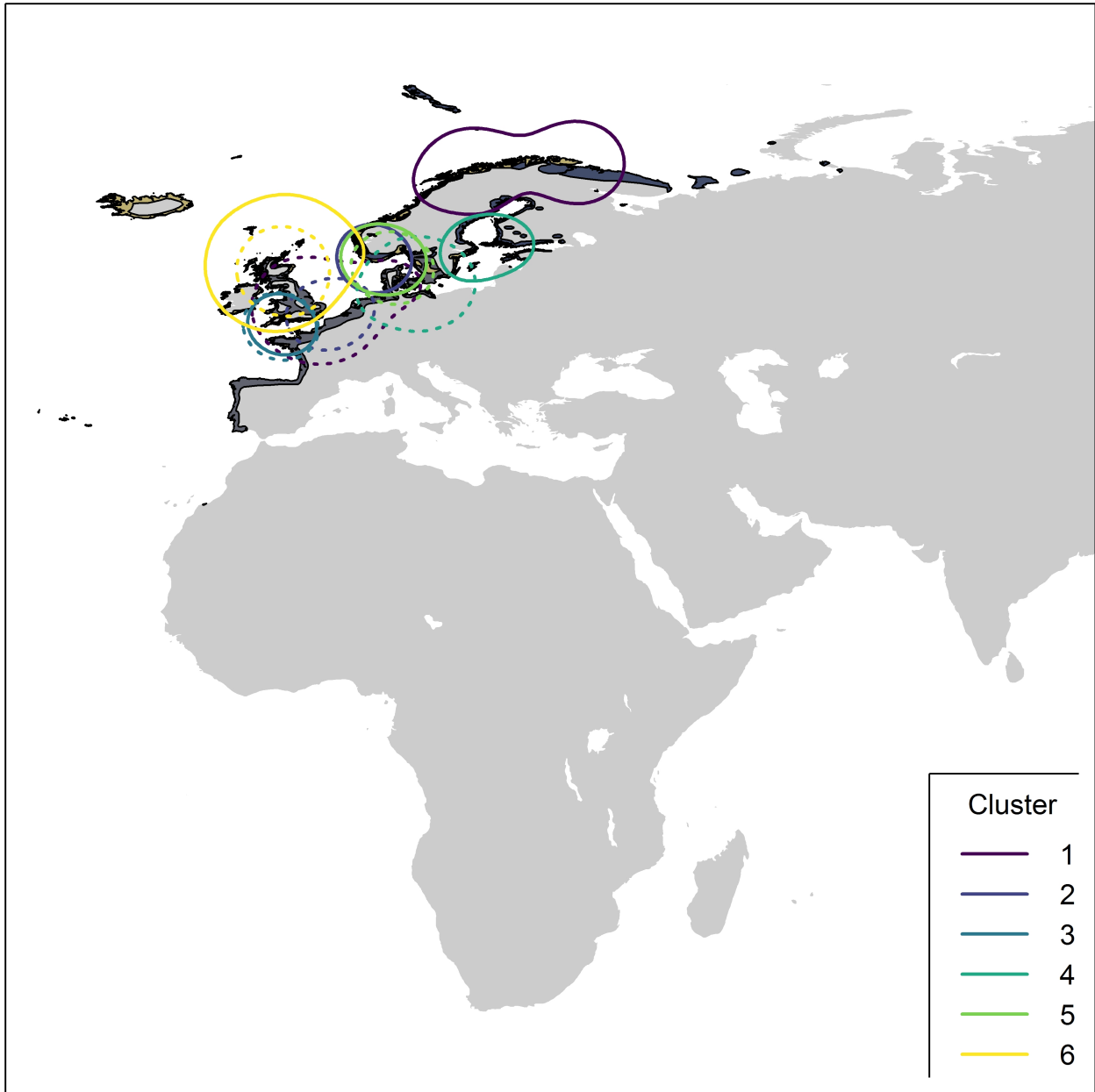


Figure 06000-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 06000-2) and stratified sampling of individuals within the breeding range (Figure 06000-3) and the non breeding range (Figure 06000-4). 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.

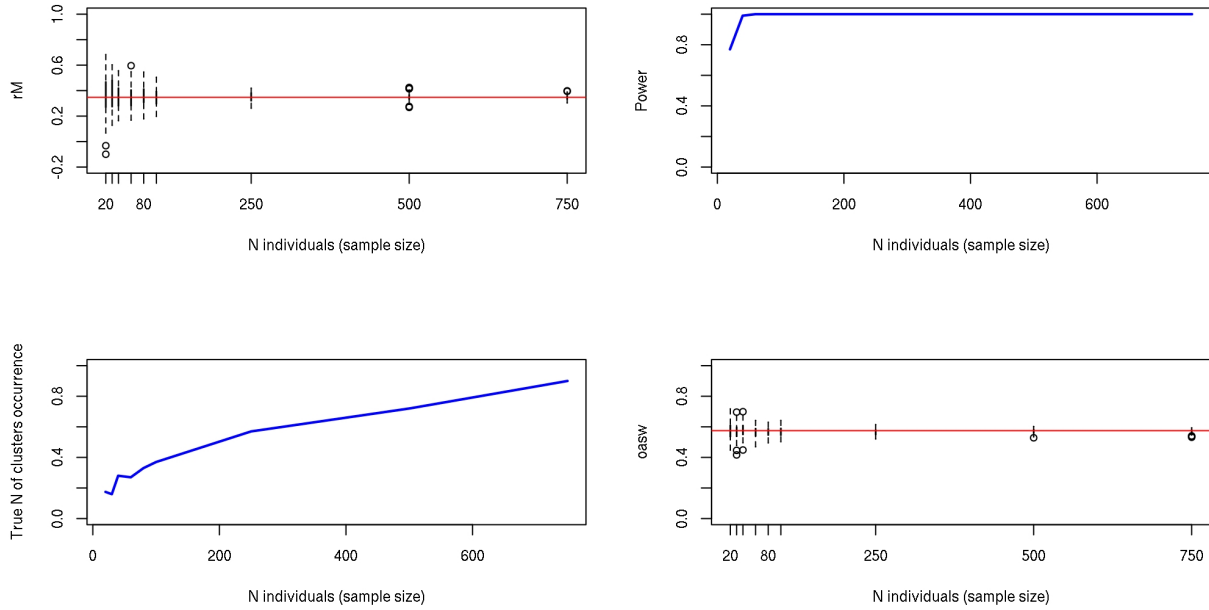


Figure 06000-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

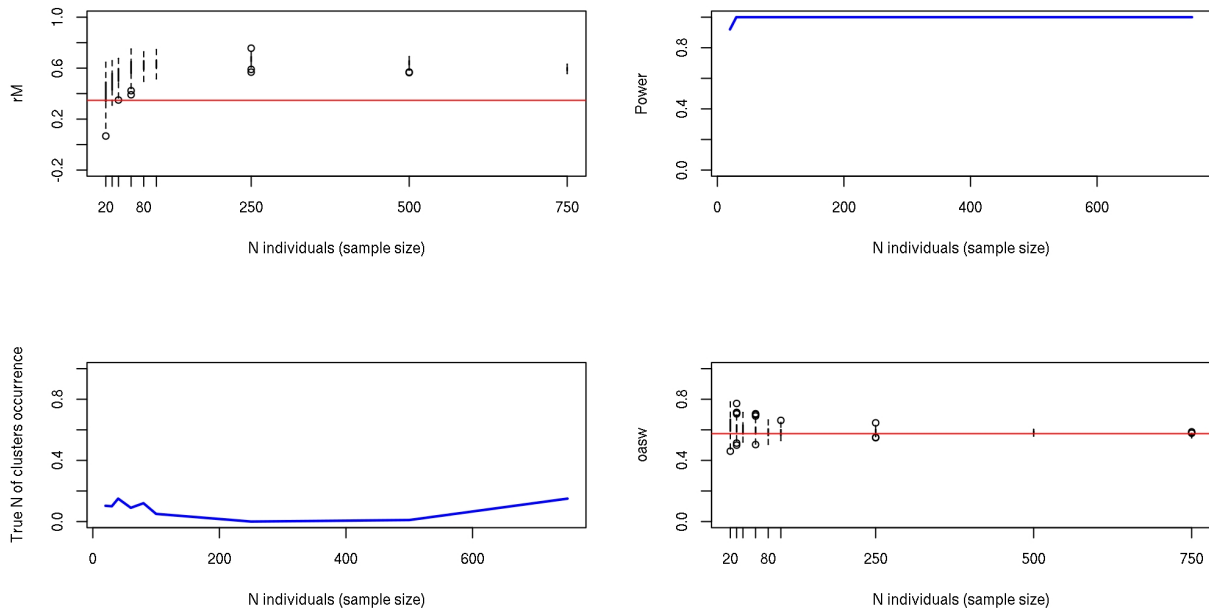


Figure 06000-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

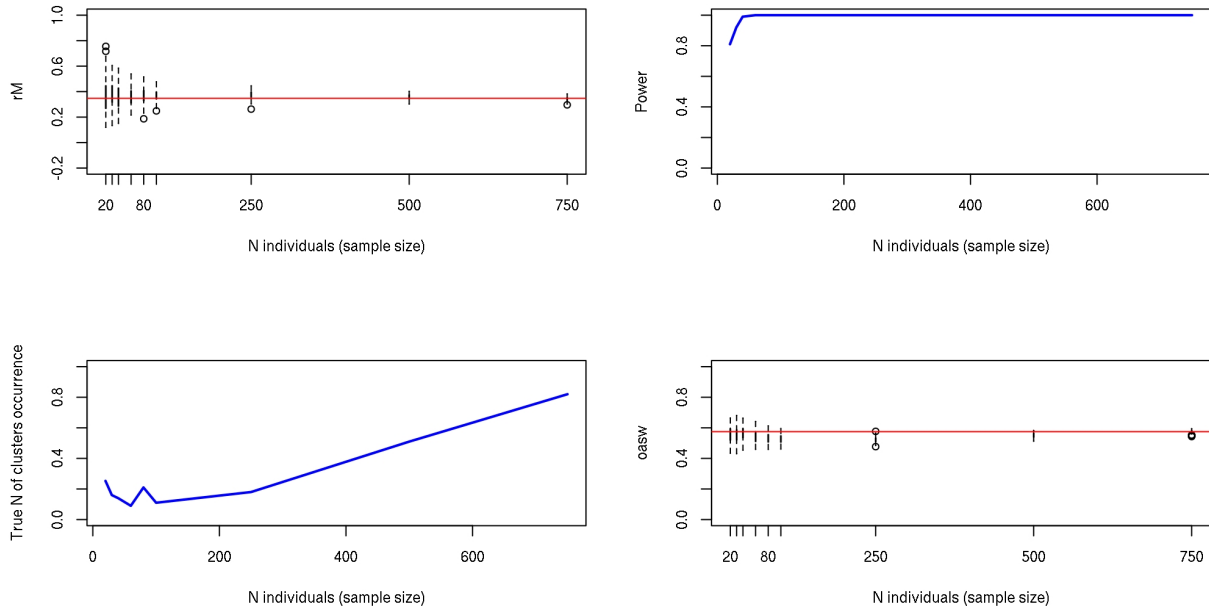


Figure 06000-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 ($p = 0.341$); Figure 06000-5).

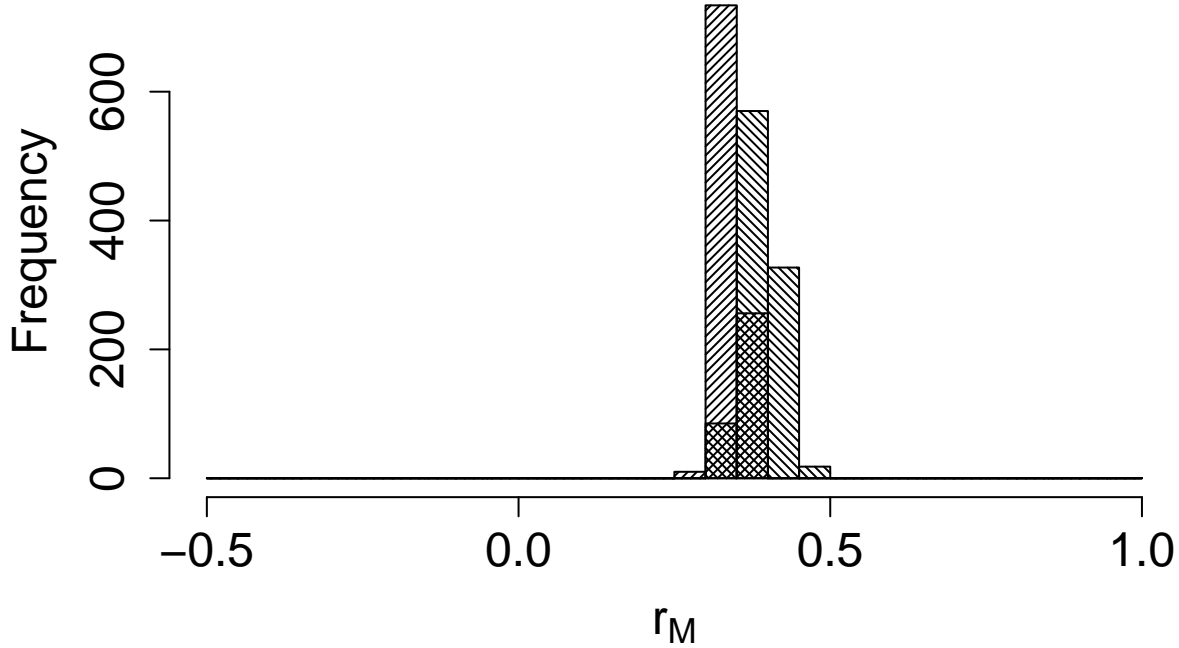


Figure 06000-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low connectivity ($MC = 0.181$; $MC = 0.18$ when adjusted for absolute abundance) between 4 breeding regions and 5 non breeding regions (Table 06000-2; Figure 06000-6).

Table 06000-2. 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
East Europe	11000	Central Europe	0.167
East Europe	11000	North Europe	0.500
East Europe	11000	North-west Europe	0.167
East Europe	11000	West Europe	0.167
North Europe	141550	Central Europe	0.056
North Europe	141550	North Europe	0.423
North Europe	141550	North-west Europe	0.185
North Europe	141550	South-west Europe	0.002
North Europe	141550	West Europe	0.334
North-west Europe	73890	North Europe	0.002
North-west Europe	73890	North-west Europe	0.919
North-west Europe	73890	South-west Europe	0.011
North-west Europe	73890	West Europe	0.068

Breeding region	Abundance	Non breeding region	Transition probability
West Europe	12830	North-west Europe	0.073
West Europe	12830	South-west Europe	0.007
West Europe	12830	West Europe	0.920



Figure 06000-6. 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>.