

Migratory connectivity analysis

by EURING Migration Atlas

Larus canus (EURING code 05900)

1.1 Connectivity between individuals

The analysis evaluated 3878 individuals (7756 encounters) filtered from a total of 152015 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 05900-1; Figure 05900-1).

Table 05900-1. 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	3878	0.213	0.001	0.191	0.238	2	0.406

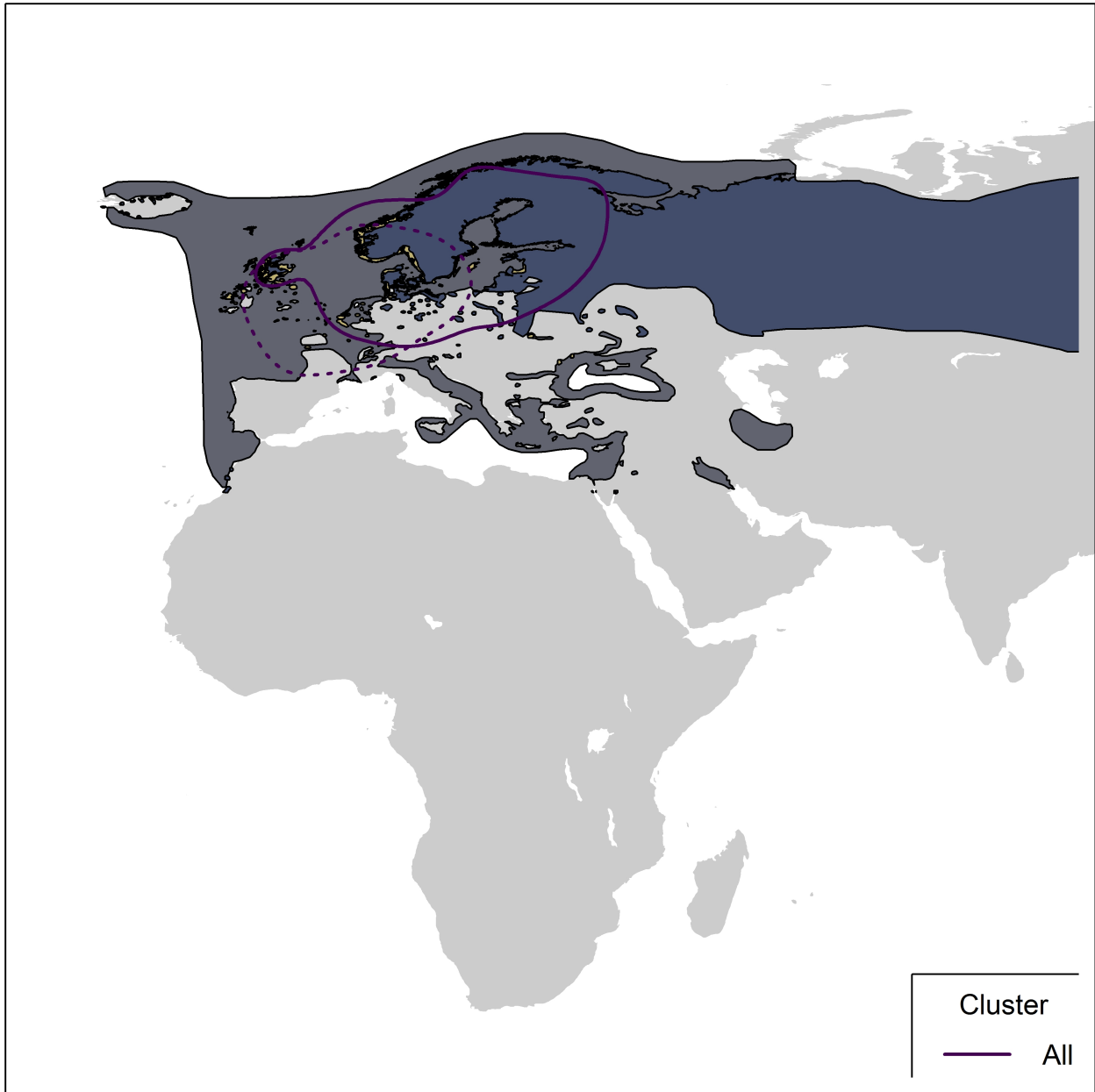


Figure 05900-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 05900-2) and stratified sampling of individuals within the breeding range (Figure 05900-3) and the non breeding range (Figure 05900-4). 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.

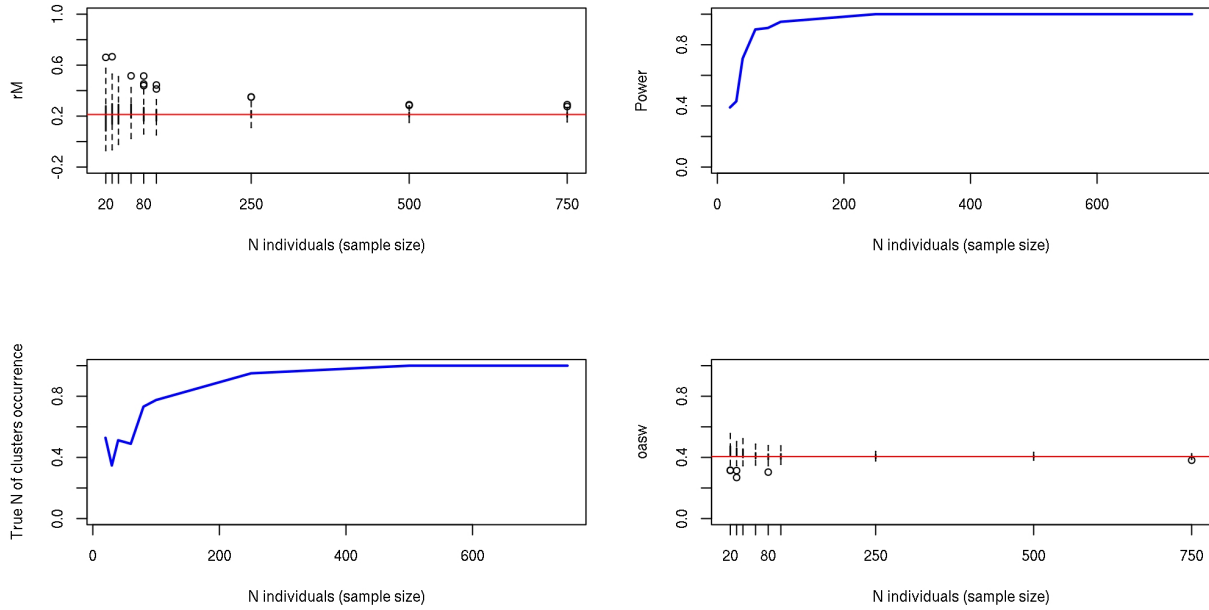


Figure 05900-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

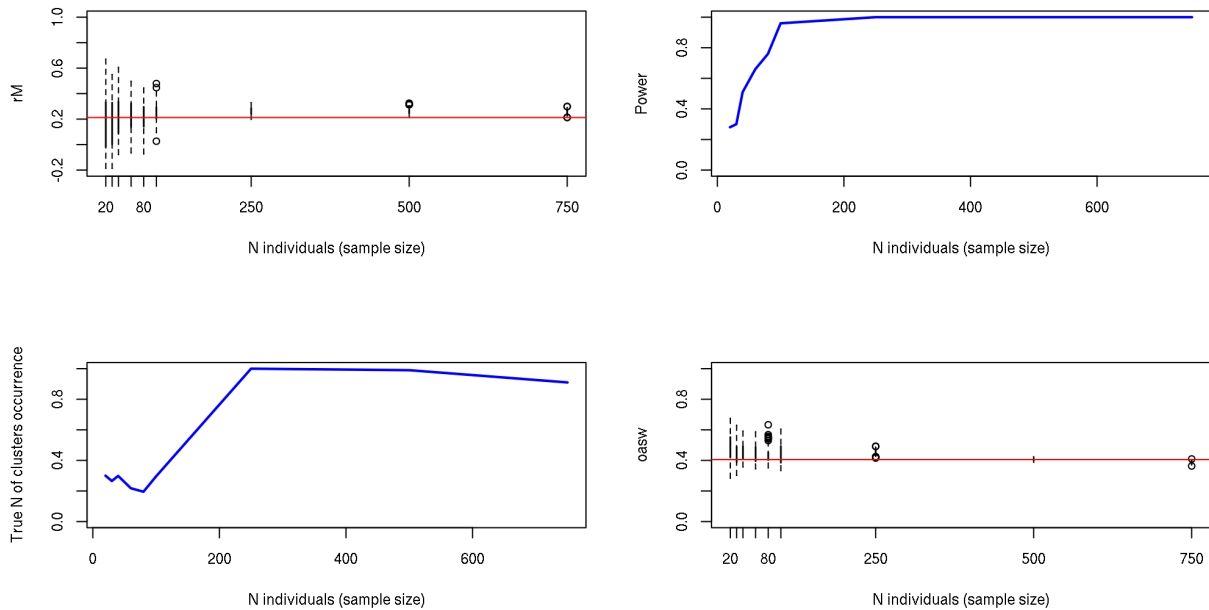


Figure 05900-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

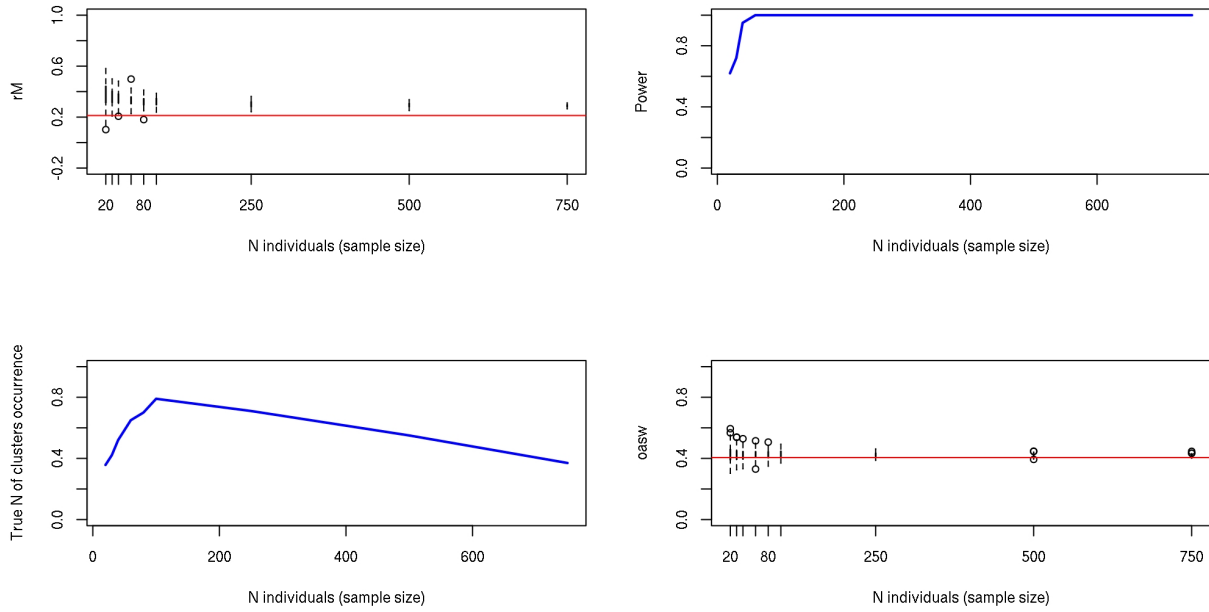


Figure 05900-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 ($p = 0.199$); Figure 05900-5).

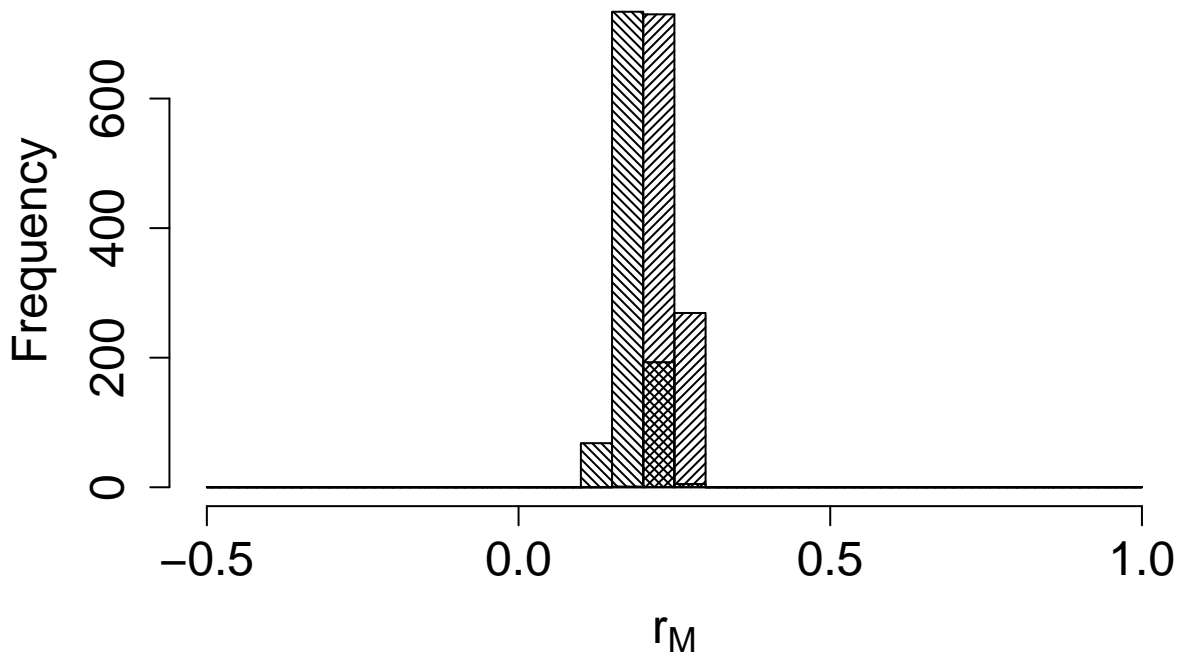


Figure 05900-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low connectivity ($MC = 0.111$; $MC = 0.111$ when adjusted for absolute abundance) between 5 breeding regions and 9 non breeding regions (Table 05900-2; Figure 05900-6).

Table 05900-2. 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	48026	Central Europe	0.154
Central Europe	48026	North Europe	0.025
Central Europe	48026	North-west Europe	0.145
Central Europe	48026	South-central Europe	0.005
Central Europe	48026	South-west Europe	0.011
Central Europe	48026	West Europe	0.660
East Europe	879927	Central Europe	0.100
East Europe	879927	East Europe	0.015
East Europe	879927	North Europe	0.267
East Europe	879927	North-west Europe	0.042
East Europe	879927	South-central Europe	0.006
East Europe	879927	West Europe	0.570
North Europe	681003	Central Europe	0.066

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	681003	East Europe	0.004
North Europe	681003	North Africa	0.000
North Europe	681003	North Europe	0.361
North Europe	681003	North-west Europe	0.171
North Europe	681003	South-central Europe	0.000
North Europe	681003	South-east Europe	0.000
North Europe	681003	South-west Europe	0.010
North Europe	681003	West Europe	0.387
North-west Europe	103254	North Europe	0.013
North-west Europe	103254	North-west Europe	0.960
North-west Europe	103254	West Europe	0.027
West Europe	8670	North-west Europe	0.198
West Europe	8670	South-west Europe	0.018
West Europe	8670	West Europe	0.784



Figure 05900-6. 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>.