Migratory connectivity analysis

by EURING Migration Atlas

Sula bassana **(EURING code 00710)**

1.1 Connectivity between individuals

The analysis evaluated 350 individuals (700 encounters) filtered from a total of 13769 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 00710-1; Figure 00710-1).

Table 00710-1. 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.

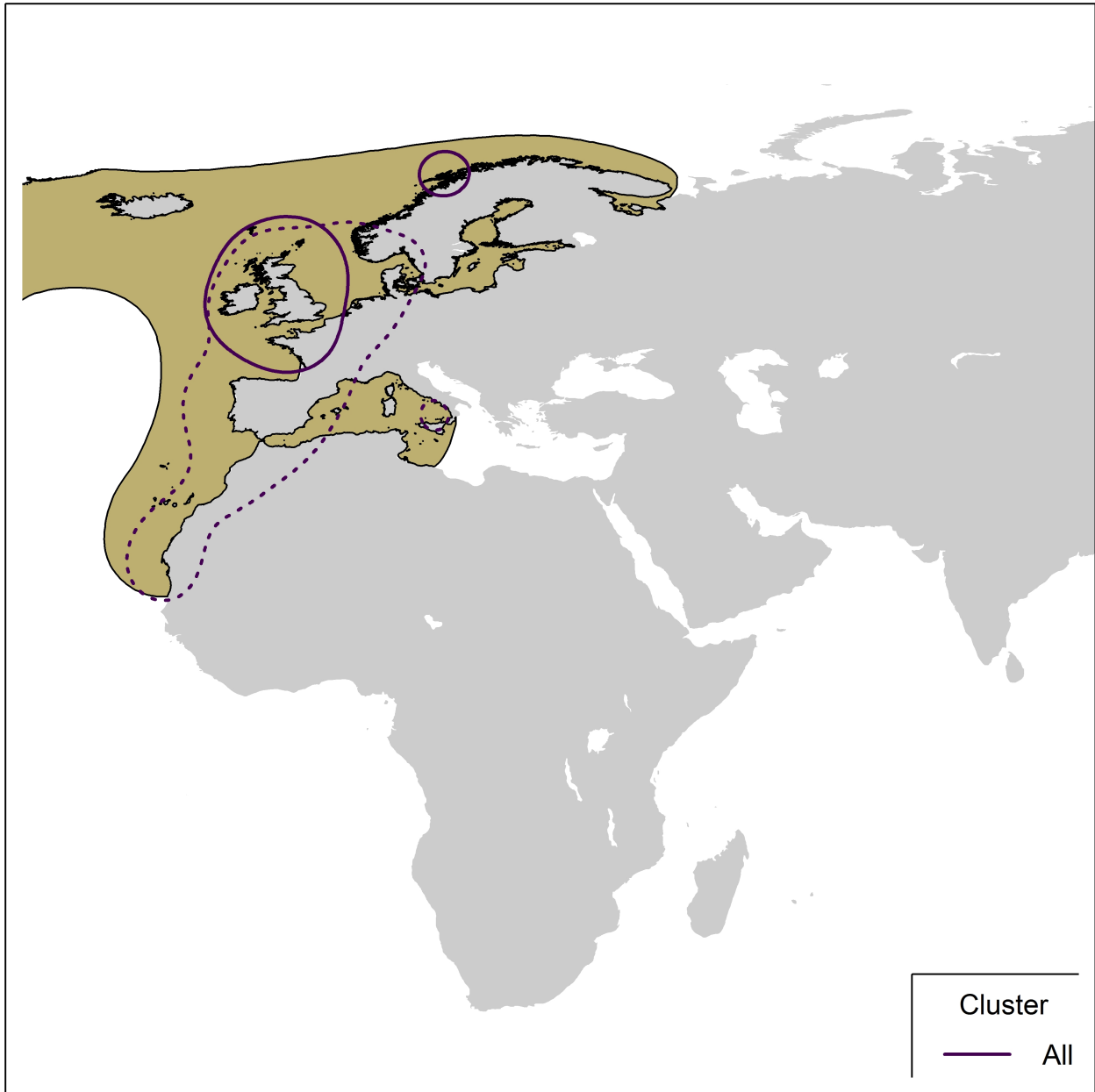| Cluster name	Level of clustering	N individuals	Migratory connectivity (r_M)	p-value	Lower 95% confidence limit	Upper 95% confidence limit	Best number of clusters	oasw
0	0	350	0.054	0.057	-0.016	0.136	2	0.413

Figure 00710-1. 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 00710-2) and stratified sampling of individuals within the breeding range (Figure 00710-3) and the non breeding range (Figure 00710-4). 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.
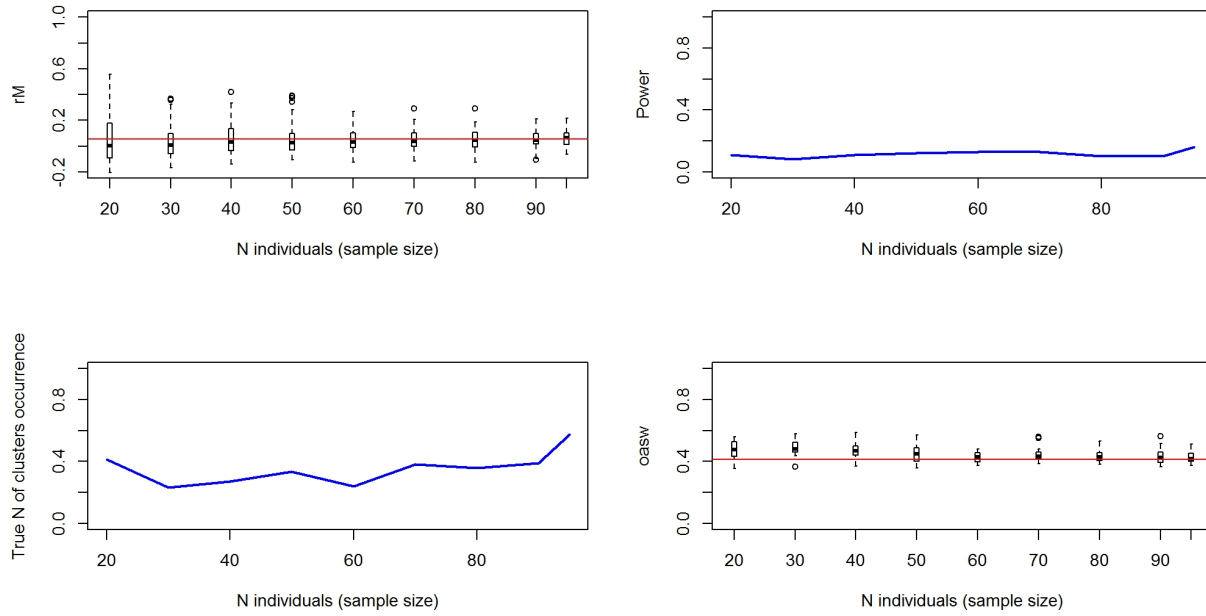

Figure 00710-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.
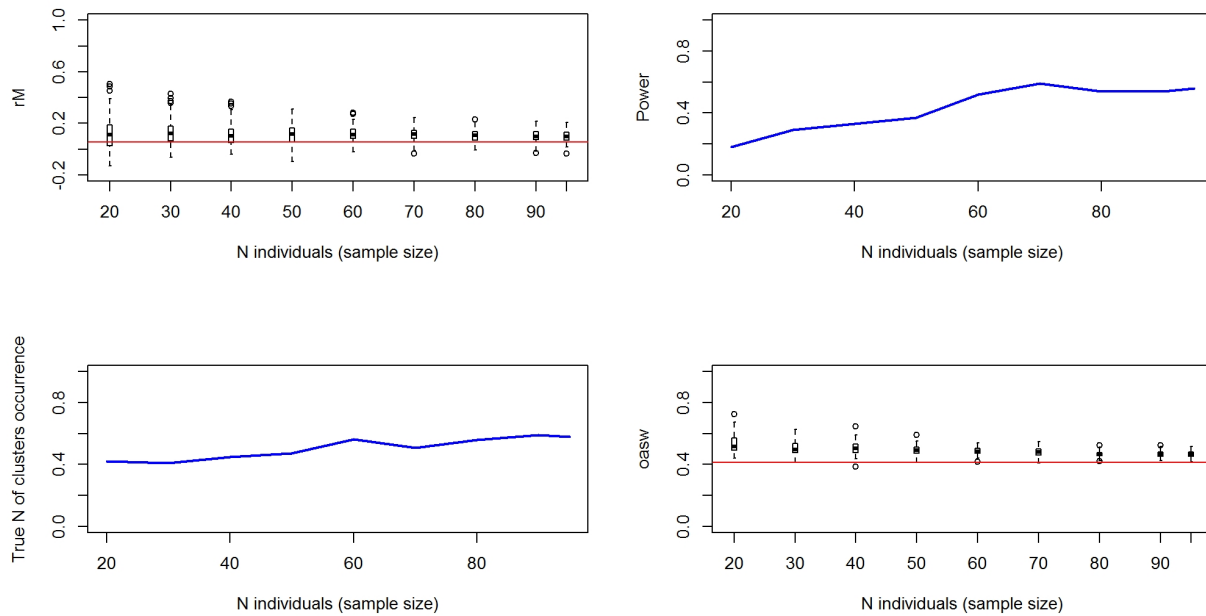

Figure 00710-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

Figure 00710-4. 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.
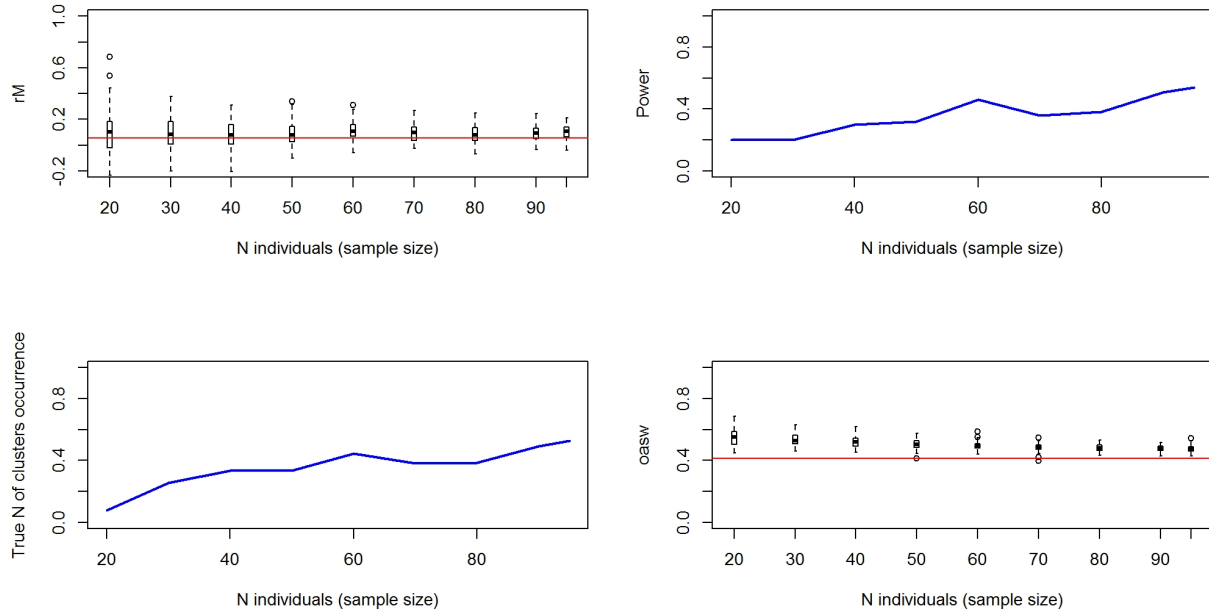
The comparison between the bootstrapped distribution of r_M values from live recaptures and dead recoveries is not significant (p = 0.322); Figure 00710-5).
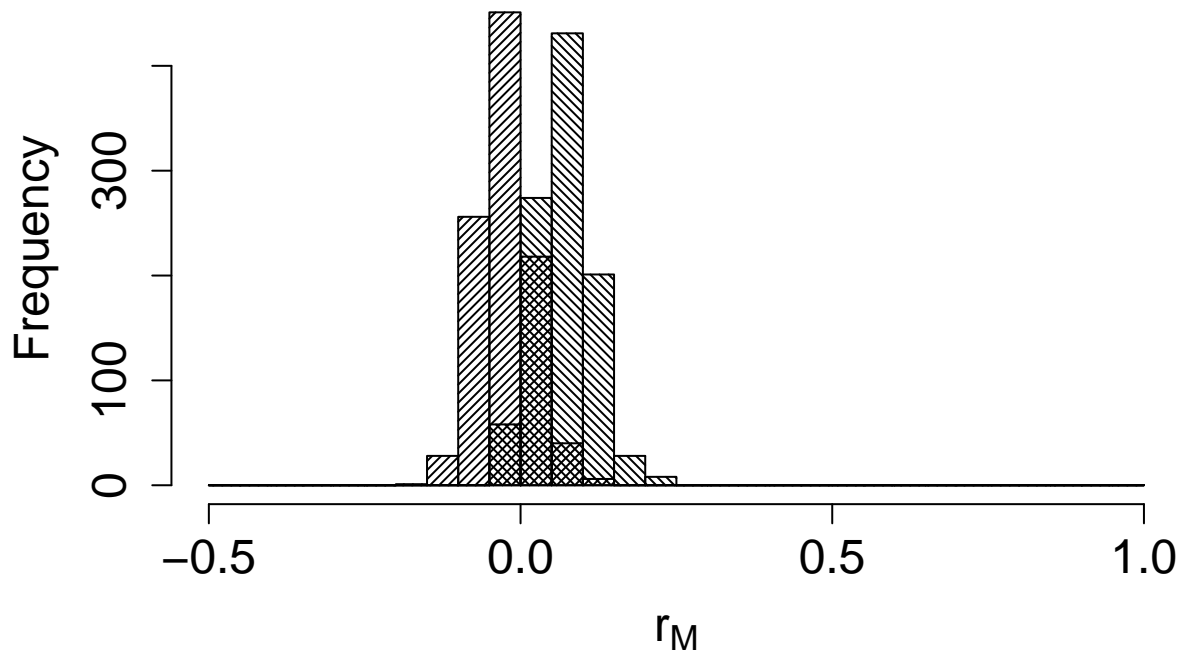
Figure 00710-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low connectivity (MC = 0.007; MC = 0.007 when adjusted for absolute abundance) between 3 breeding regions and 8 non breeding regions (Table 00710-2; Figure 00710-6).

Table 00710-2. 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
North Europe	19806	North Africa	0.033
North Europe	19806	North Europe	0.300
North Europe	19806	North-west Europe	0.300
North Europe	19806	South-west Europe	0.133
North Europe	19806	West Europe	0.233
North-west Europe	1303696	Central Europe	0.015
North-west Europe	1303696	North Africa	0.170
North-west Europe	1303696	North Europe	0.042
North-west Europe	1303696	North-west Europe	0.185
North-west Europe	1303696	South-central Europe	0.030
North-west Europe	1303696	South-west Europe	0.264
North-west Europe	1303696	West Africa	0.030
North-west Europe	1303696	West Europe	0.264

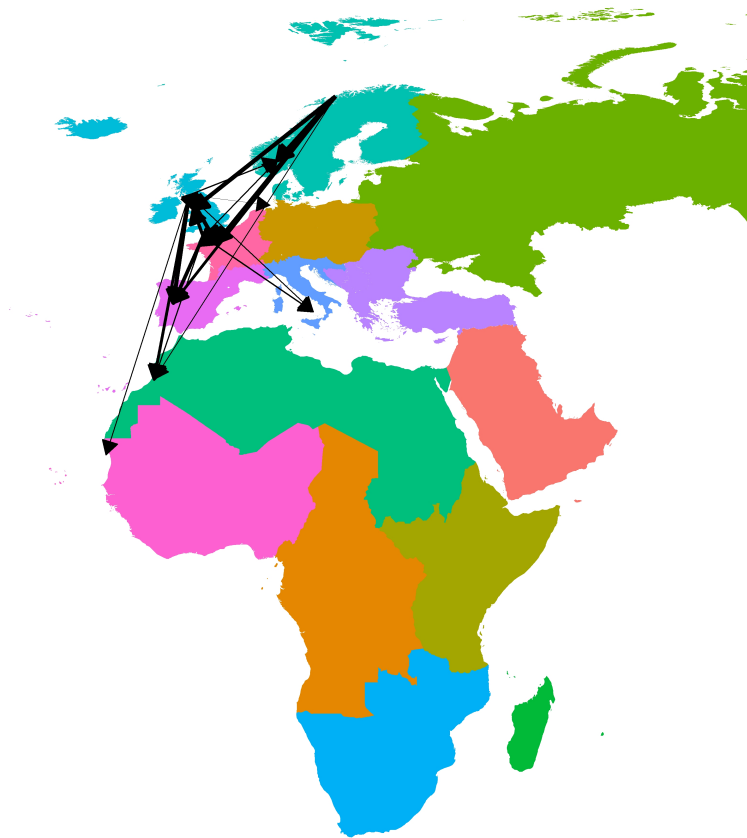| Breeding region	Abundance	Non breeding region	Transition probability
West Europe	21545	North Africa	0.036
West Europe	21545	North Europe	0.036
West Europe	21545	North-west Europe	0.182
West Europe	21545	South-central Europe	0.055
West Europe	21545	South-west Europe	0.218
West Europe	21545	West Europe	0.473

Figure 00710-6. 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.