Migratory connectivity analysis

by EURING Migration Atlas

***Sterna hirundo* (EURING code 06150)**

1.1 Connectivity between individuals

The analysis evaluated 1089 individuals (2178 encounters) filtered from a total of 90316 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 = 2 (Table 06150-1; Figure 06150-1).

Table 06150-1. 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	1089	0.553	0.001	0.520	0.589	2	0.723
1	1	638	0.232	0.001	0.176	0.296	2	0.630
2	1	451	0.036	0.067	-0.001	0.084	9	0.479
11	2	420	0.015	0.301	-0.033	0.073	-	-
12	2	218	0.262	0.001	0.174	0.365	5	0.413

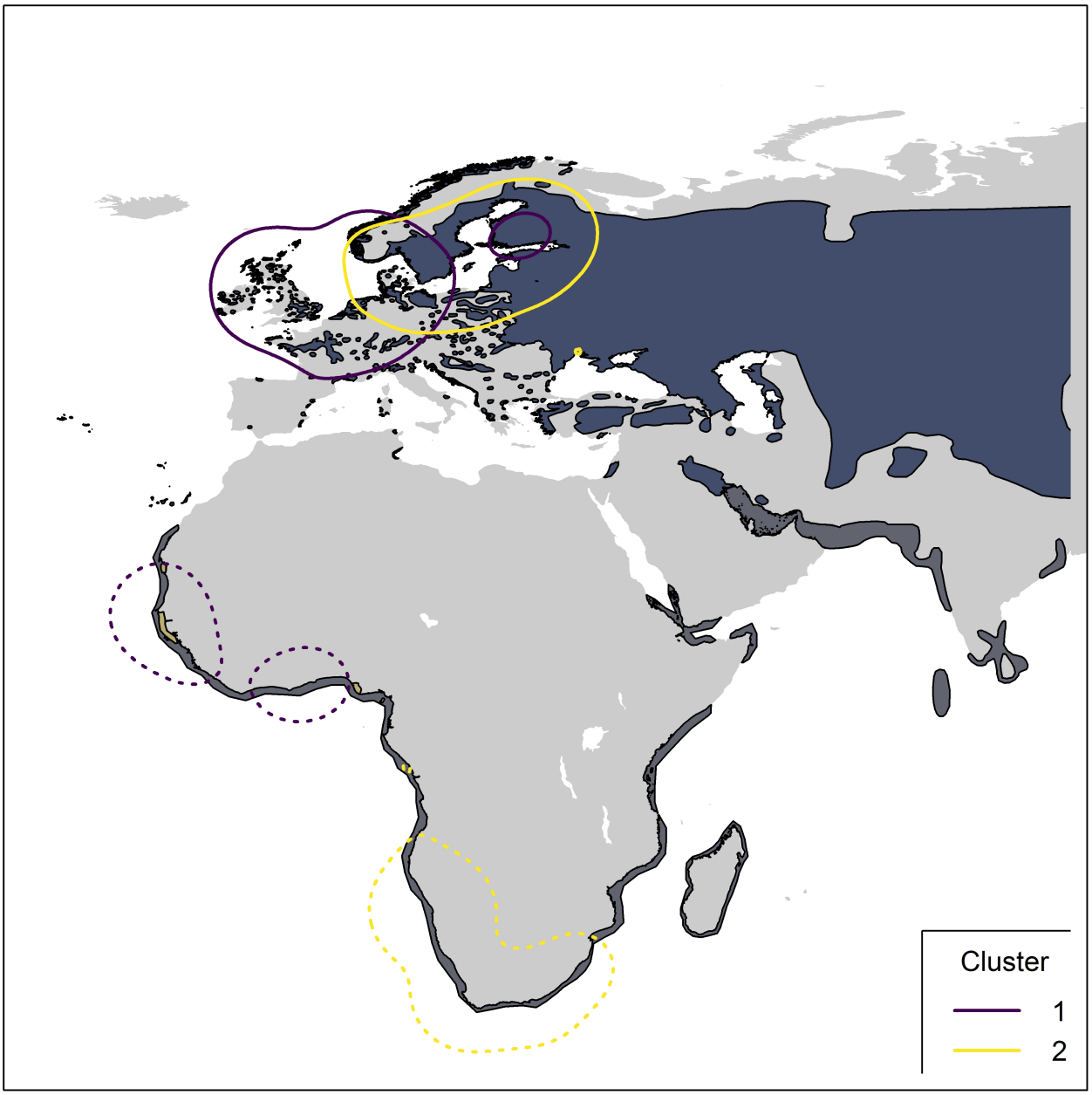

Figure 06150-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 06150-2) and stratified sampling of individuals within the breeding range (Figure 06150-3) and the non breeding range (Figure 06150-4). 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.

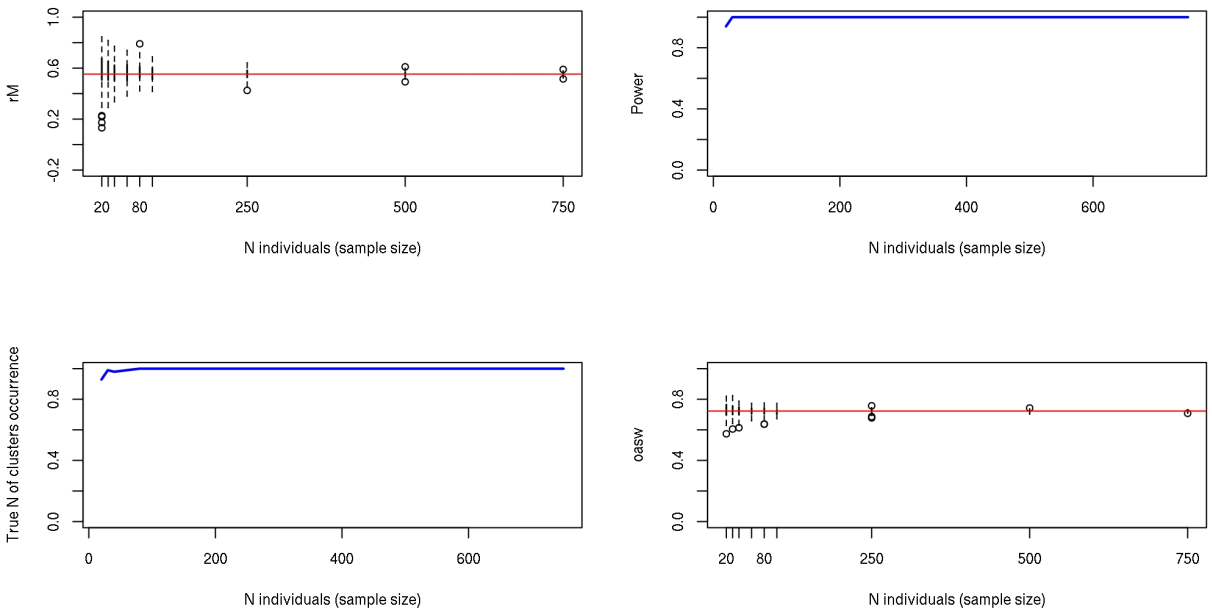

Figure 06150-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

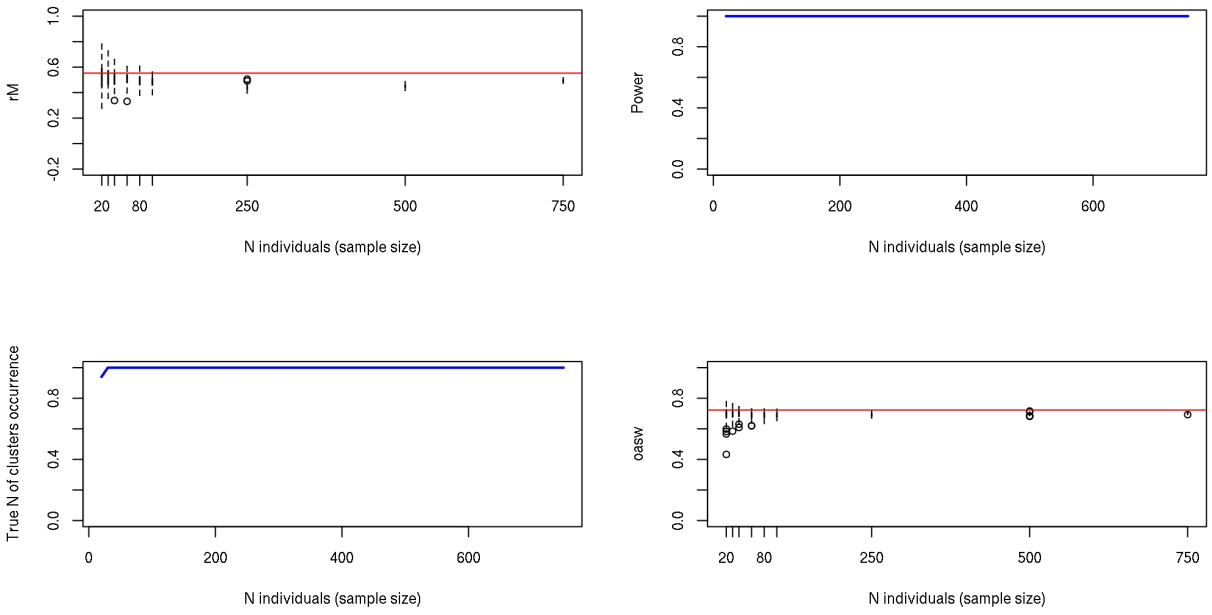

Figure 06150-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

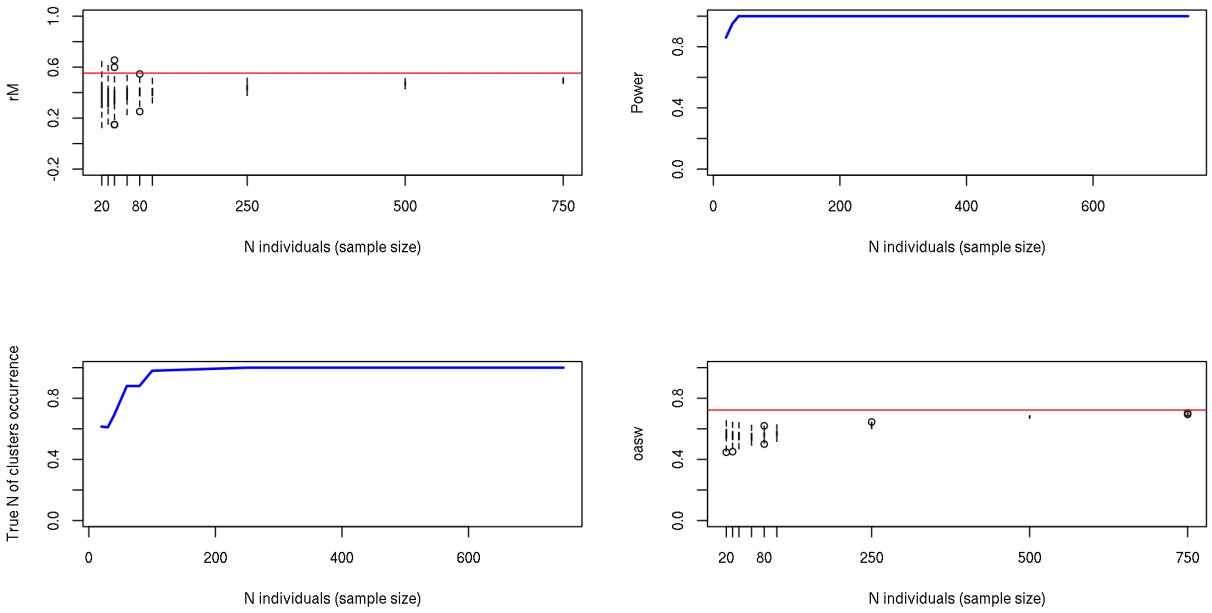

Figure 06150-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 ($p = 0.12$); Figure 06150-5).

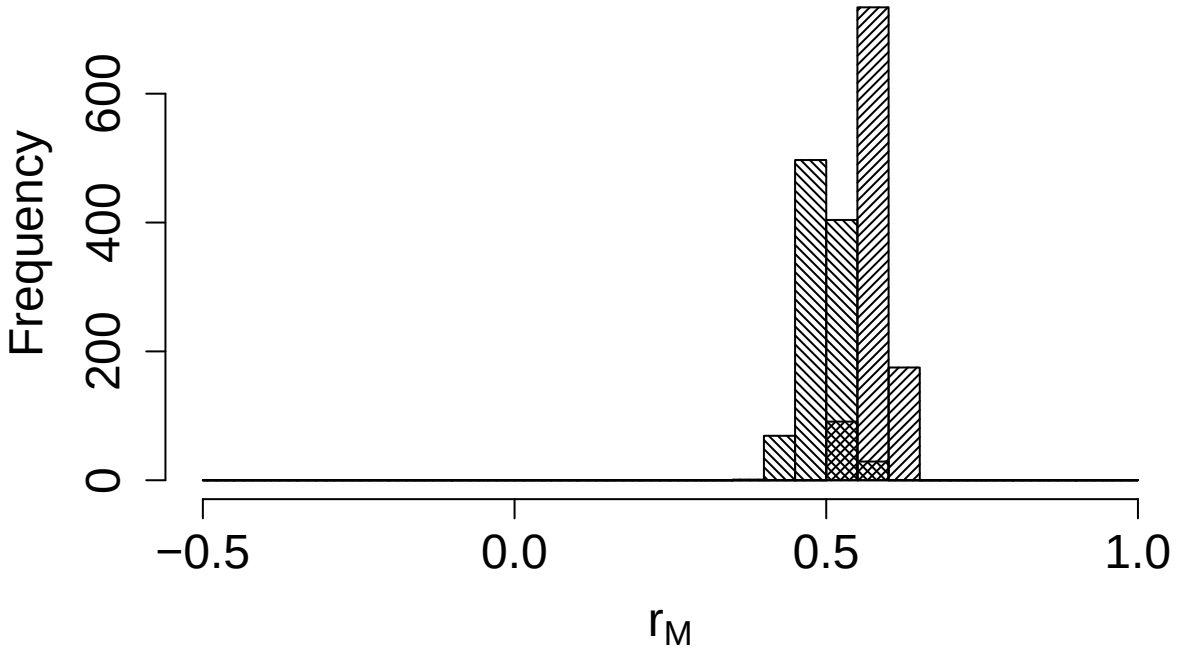

Figure 06150-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows moderate/high connectivity (MC = 0.664; MC = 0.664 when adjusted for absolute abundance) between 7 breeding regions and 4 non breeding regions (Table 06150-2; Figure 06150-6).

Table 06150-2. 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	39808	Central Africa	0.037
Central Europe	39808	South Africa	0.407
Central Europe	39808	West Africa	0.556
East Europe	526497	Central Africa	0.036
East Europe	526497	South Africa	0.964
North Europe	172011	Central Africa	0.091
North Europe	172011	South Africa	0.711
North Europe	172011	West Africa	0.198
North-west Europe	33480	North Africa	0.024
North-west Europe	33480	South Africa	0.015
North-west Europe	33480	West Africa	0.961
South-central Europe	10449	West Africa	1.000
South-west Europe	14730	West Africa	1.000

Breeding region	Abundance	Non breeding region	Transition probability
West Europe	51424	North Africa	0.012
West Europe	51424	South Africa	0.040
West Europe	51424	West Africa	0.947

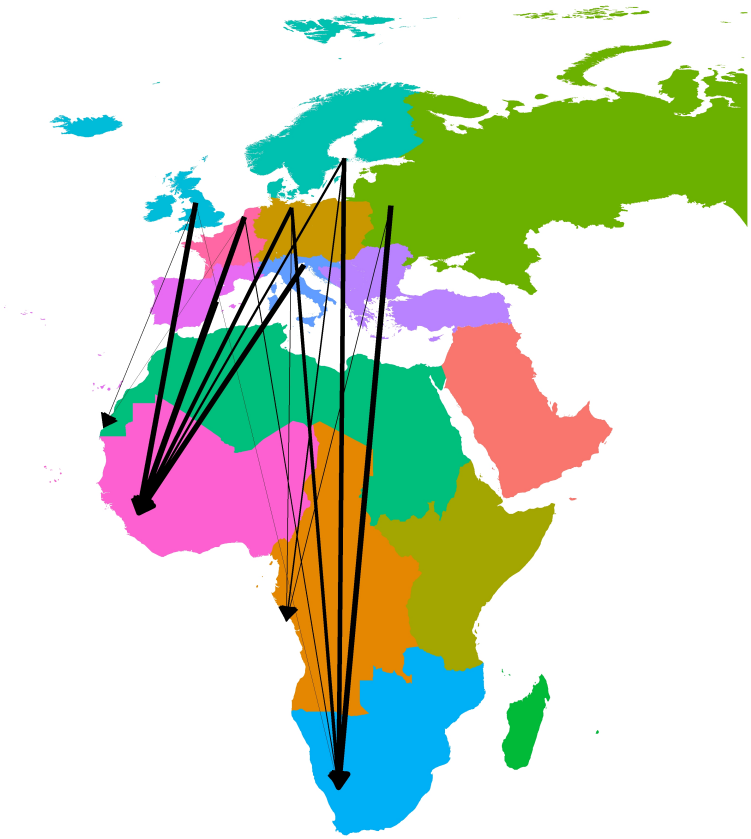

Figure 06150-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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.