

# Migratory connectivity analysis

by EURING Migration Atlas

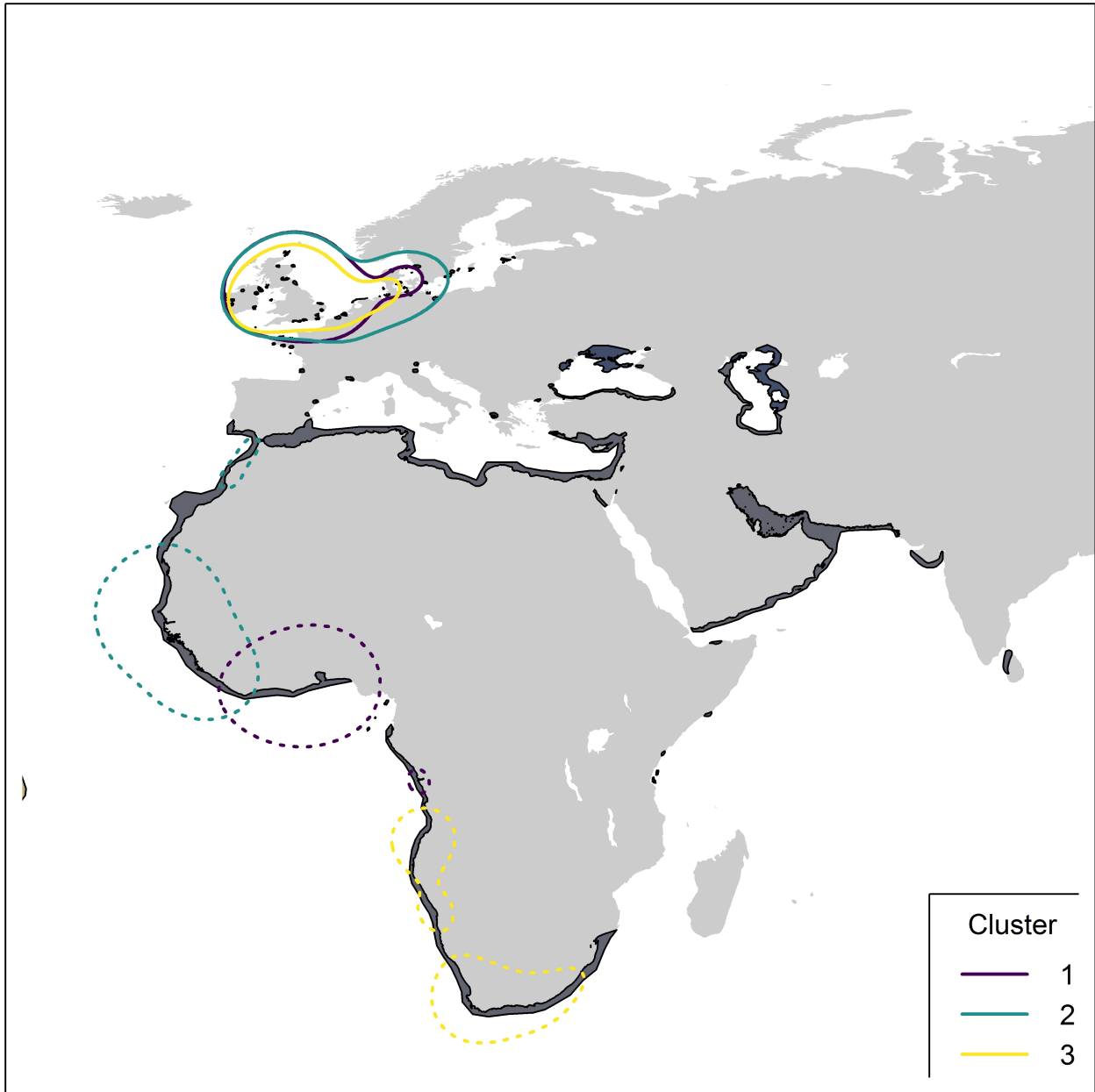
*Sterna sandvicensis* (EURING code 06110)

## 1.1 Connectivity between individuals

The analysis evaluated 423 individuals (846 encounters) filtered from a total of 56104 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 06110-1; Figure 06110-1).

**Table 06110-1.** 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	423	0.082	0.016	0.012	0.160	3	0.563
1	1	163	0.357	0.005	-0.058	0.658	2	0.714
2	1	210	0.123	0.026	-0.044	0.302	5	0.519
3	1	50	-0.041	0.805	-0.080	0.112	-	-
11	2	11	-	-	-	-	-	-
12	2	152	0.513	0.005	-0.050	0.763	2	0.587
21	2	21	-0.123	0.773	-0.179	0.334	-	-
22	2	56	-0.090	0.881	-0.159	0.061	-	-
23	2	36	-0.100	0.845	-0.135	0.045	-	-
24	2	17	-	-	-	-	-	-
25	2	80	0.008	0.432	-0.077	0.172	-	-
121	3	20	0.951	0.032	-0.037	0.983	2	0.877
122	3	132	0.032	0.257	-0.070	0.174	-	-

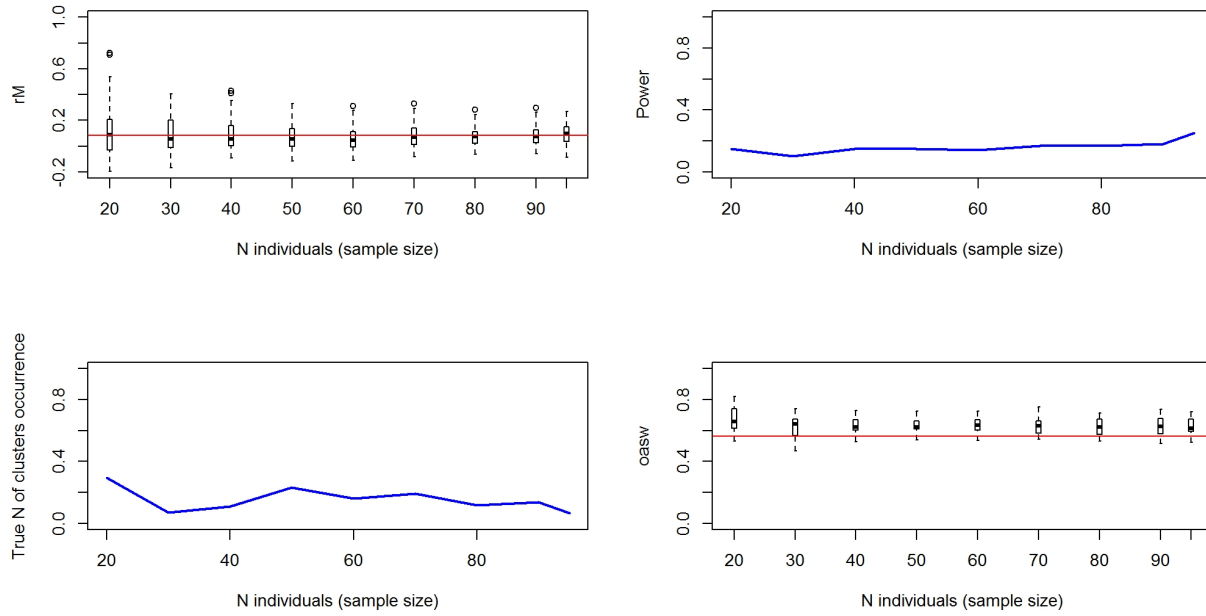


**Figure 06110-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

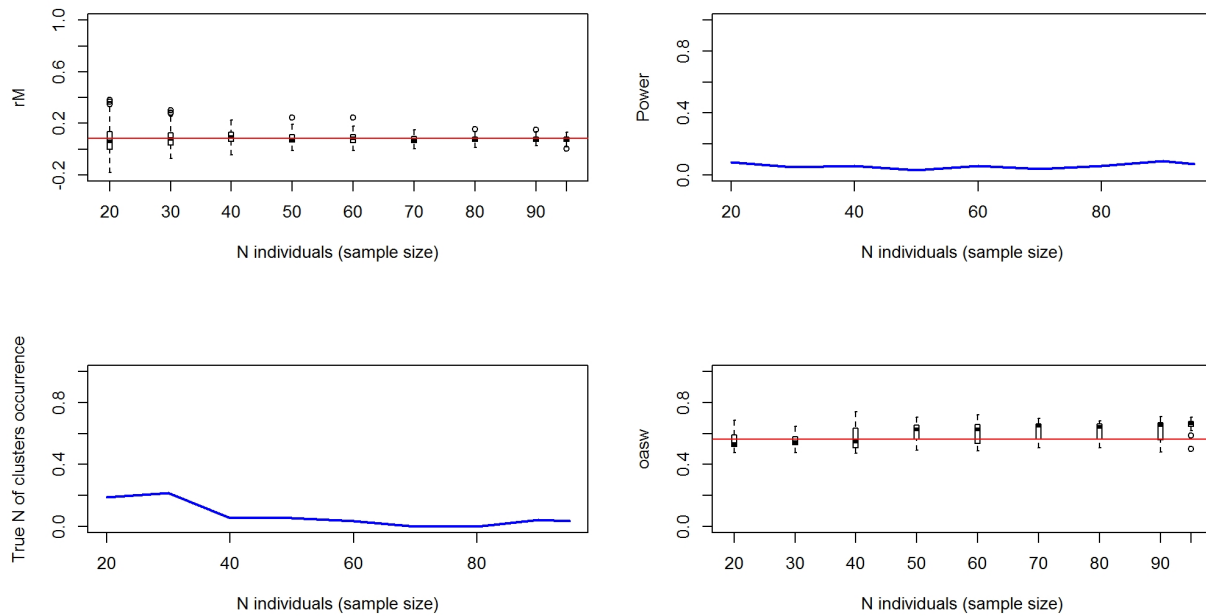
## 1.2 Sensitivity analysis

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 06110-2) and stratified sampling of individuals within the breeding range (Figure 06110-3) and the non breeding range (Figure 06110-4). 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.

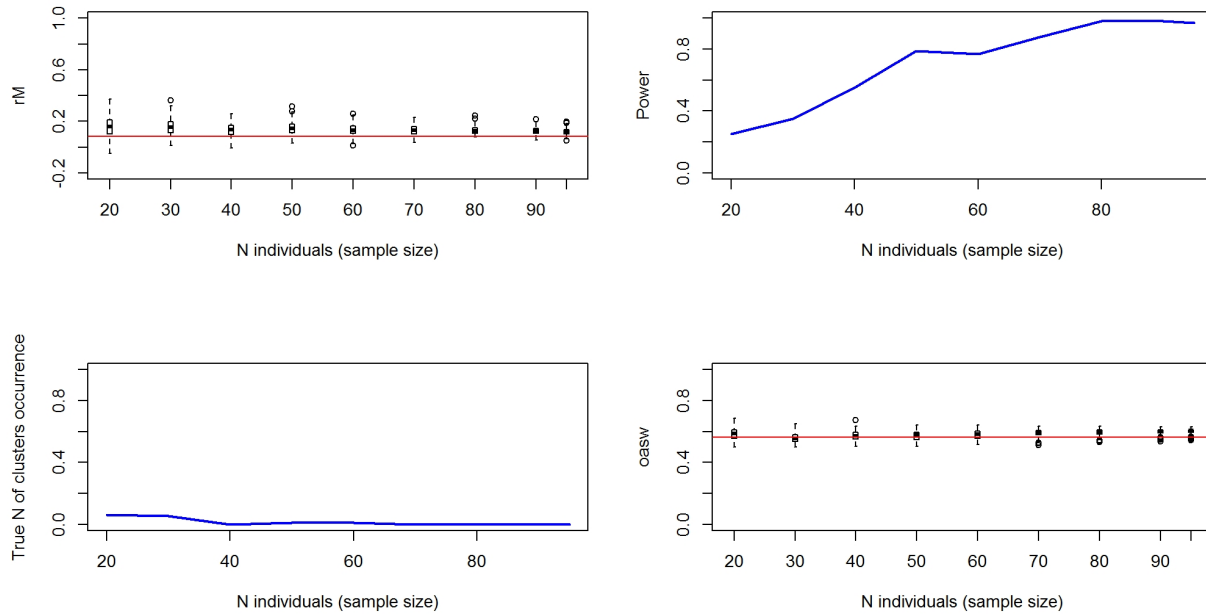


**Figure 06110-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



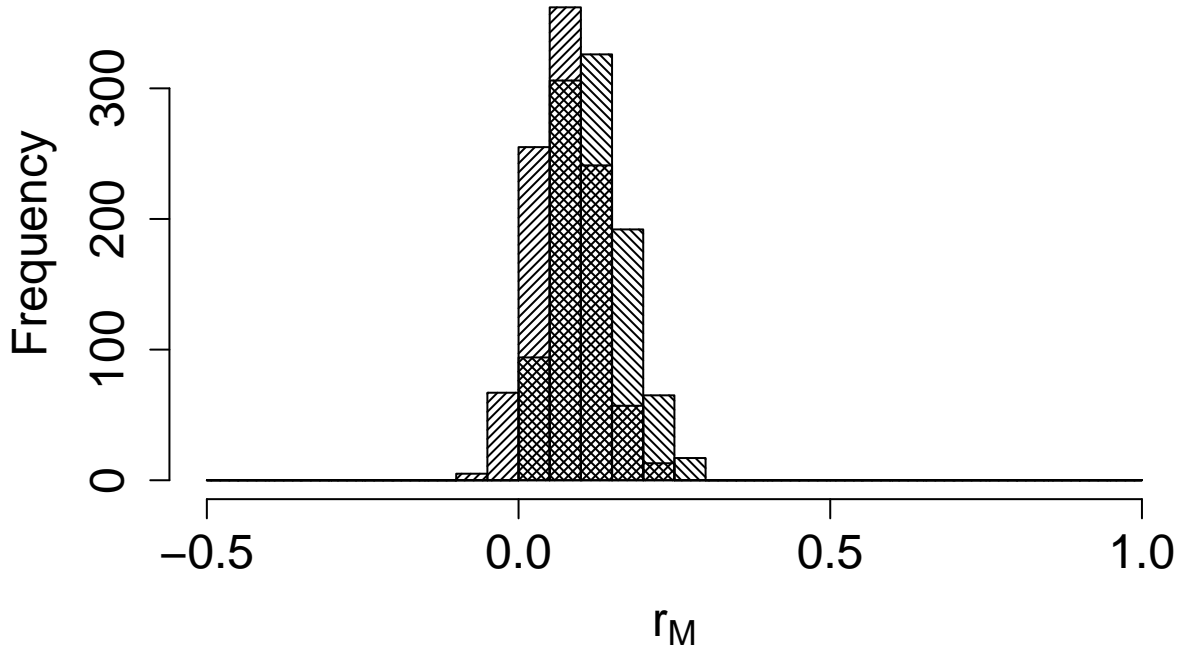
**Figure 06110-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 06110-4.** 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 ( $p = 0.711$ ); Figure 06110-5).



**Figure 06110-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

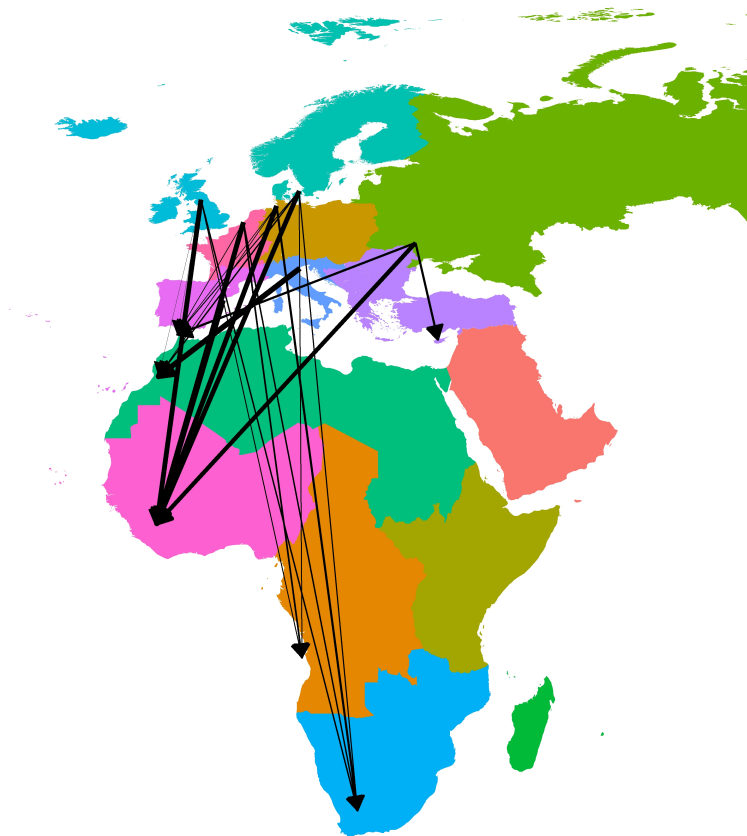
## 2. Connectivity between pre-defined regions

The species shows low connectivity ( $MC = 0.041$ ;  $MC = 0.038$  when adjusted for absolute abundance) between 7 breeding regions and 6 non breeding regions (Table 06110-2; Figure 06110-6).

**Table 06110-2.** 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	9882	North Africa	0.037
Central Europe	9882	South Africa	0.185
Central Europe	9882	South-west Europe	0.037
Central Europe	9882	West Africa	0.741
East Europe	93700	South-east Europe	0.200
East Europe	93700	South-west Europe	0.200
East Europe	93700	West Africa	0.600
North Europe	12520	Central Africa	0.043
North Europe	12520	North Africa	0.085
North Europe	12520	South Africa	0.064
North Europe	12520	South-west Europe	0.043
North Europe	12520	West Africa	0.766
North-west Europe	29454	Central Africa	0.053

Breeding region	Abundance	Non breeding region	Transition probability
North-west Europe	29454	North Africa	0.016
North-west Europe	29454	South Africa	0.092
North-west Europe	29454	South-west Europe	0.010
North-west Europe	29454	West Africa	0.829
South-central Europe	1619	North Africa	1.000
South-west Europe	12320	West Africa	1.000
West Europe	47797	Central Africa	0.105
West Europe	47797	South Africa	0.079
West Europe	47797	South-west Europe	0.026
West Europe	47797	West Africa	0.789



**Figure 06110-6.** 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>.