

Migratory connectivity analysis

by EURING Migration Atlas

Recurvirostra avosetta (EURING code 04560)

1.1 Connectivity between individuals

The analysis evaluated 372 individuals (744 encounters) filtered from a total of 19974 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 04560-1; Figure 04560-1).

Table 04560-1. 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	372	0.226	0.001	0.091	0.365	2	0.513
1	1	254	0.465	0.001	0.288	0.598	4	0.475
2	1	118	0.147	0.057	-0.068	0.465	2	0.783
21	2	113	0.116	0.051	-0.032	0.298	9	0.440
22	2	5	-	-	-	-	-	-

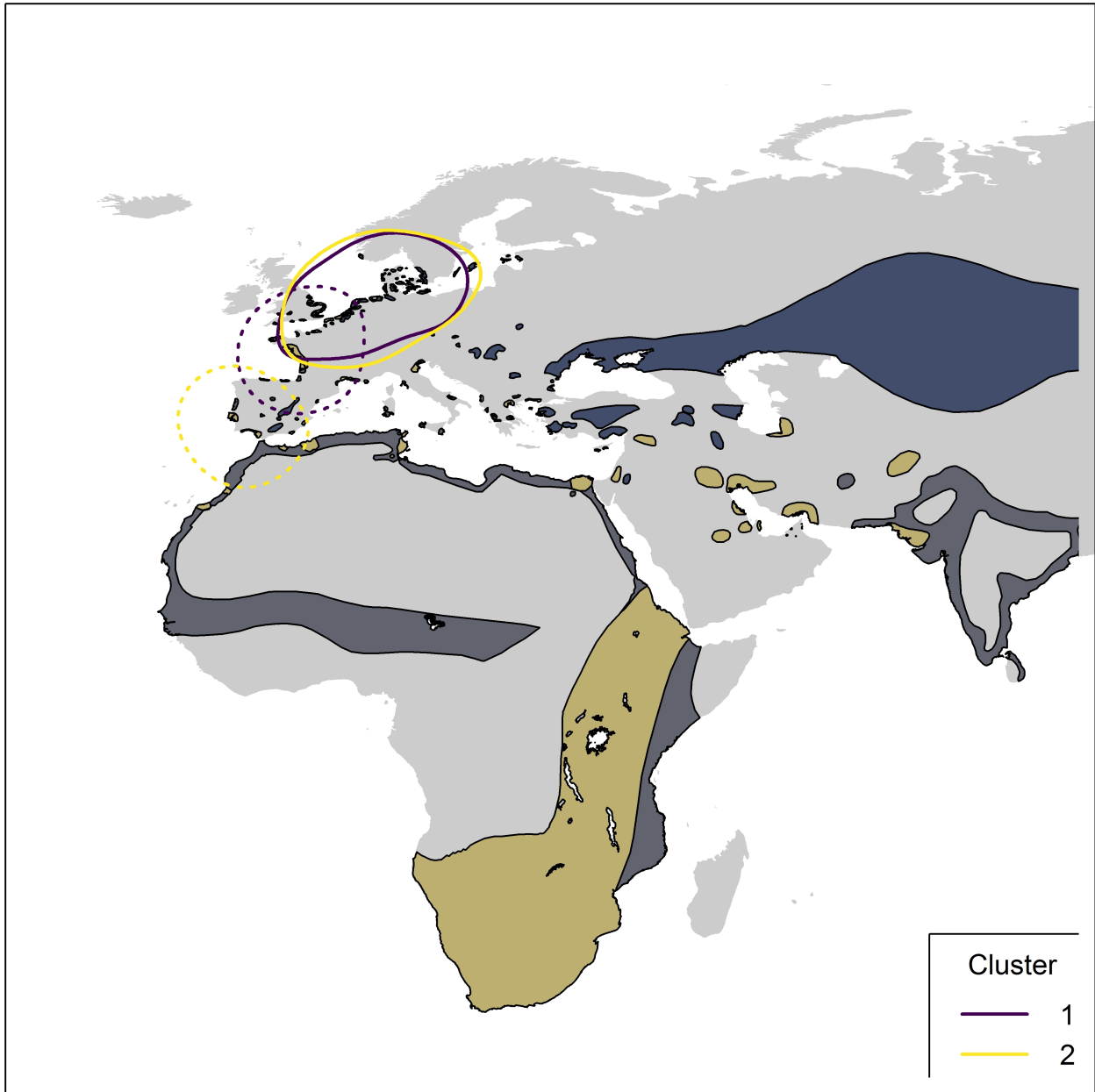


Figure 04560-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 04560-2) and stratified sampling of individuals within the breeding range (Figure 04560-3) and the non breeding range (Figure 04560-4). 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.

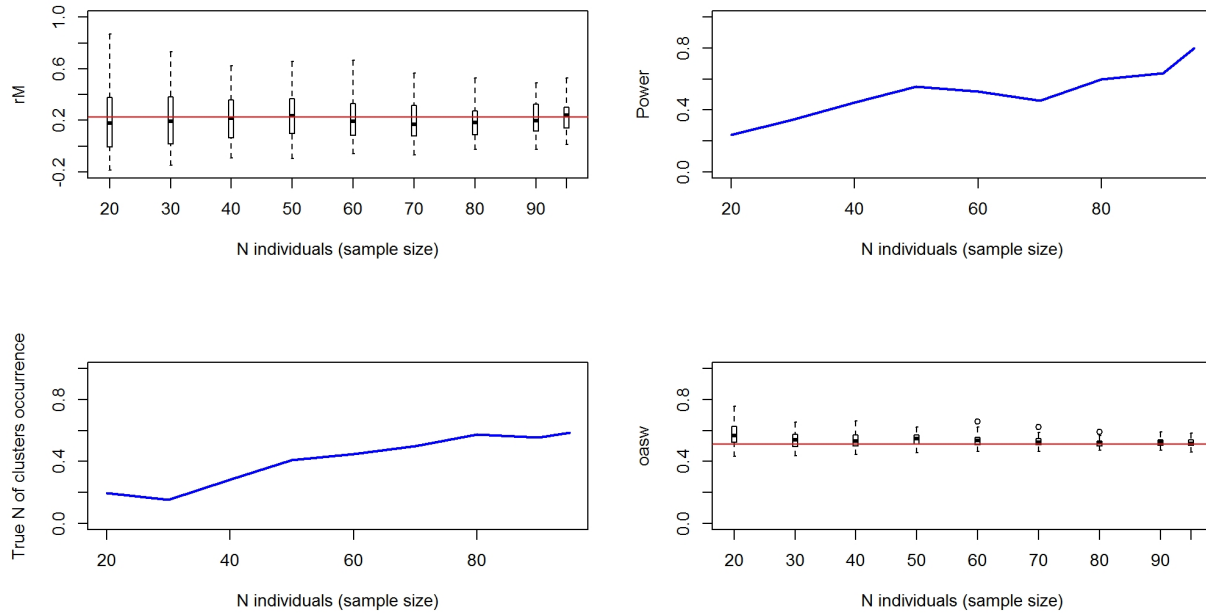


Figure 04560-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

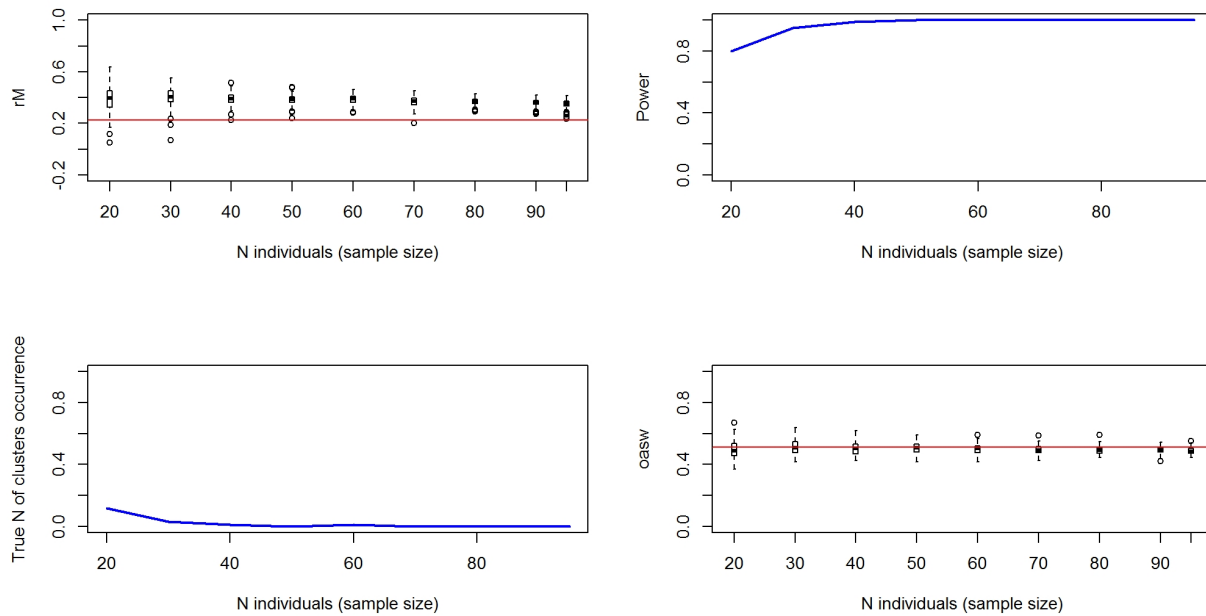


Figure 04560-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

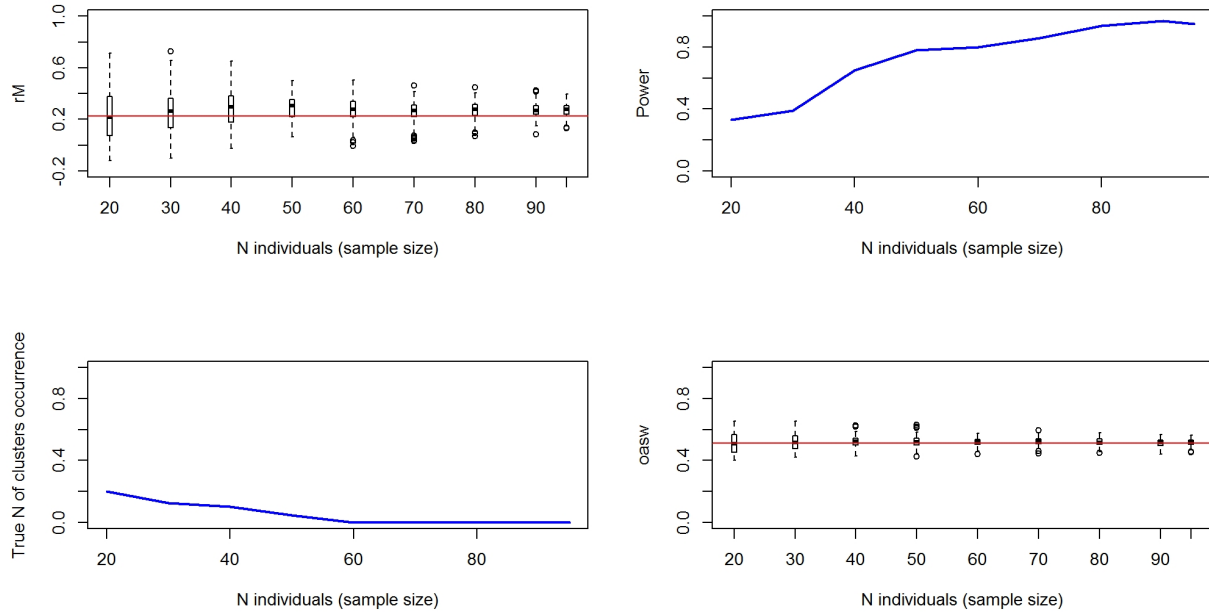


Figure 04560-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

The comparison between the bootstrapped distribution of r_M values from live recaptures and dead recoveries is significant ($p = 0.006$); Figure 04560-5).

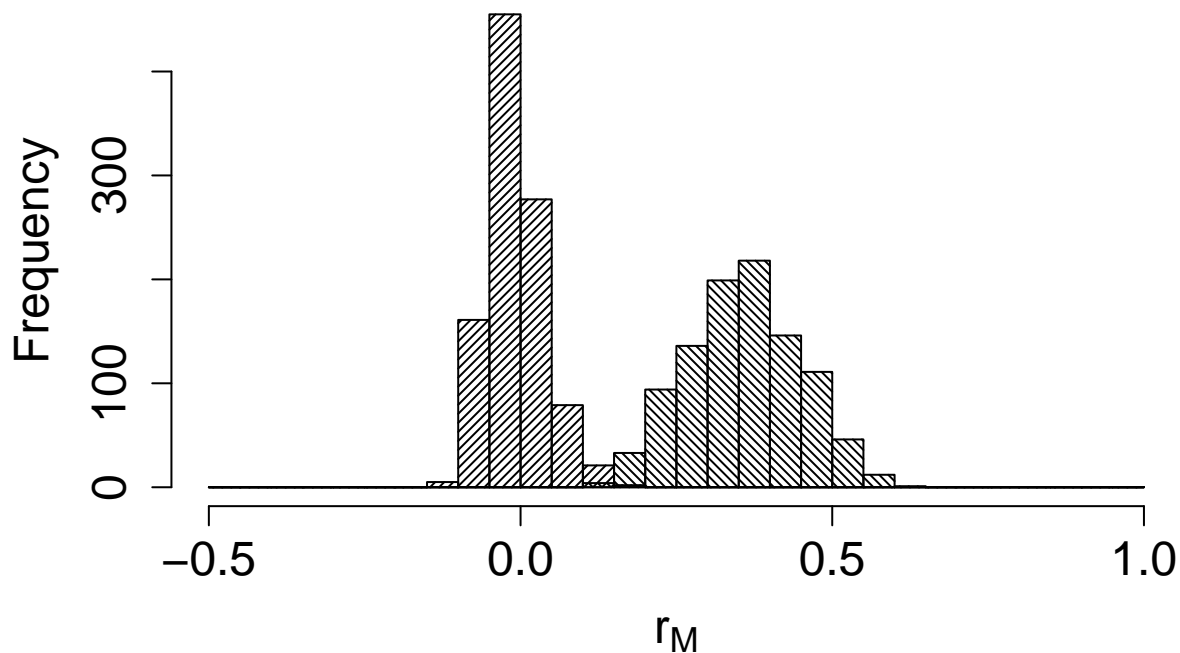


Figure 04560-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low/moderate connectivity ($MC = 0.298$; $MC = 0.295$ when adjusted for absolute abundance) between 7 breeding regions and 7 non breeding regions (Table 04560-2; Figure 04560-6).

Table 04560-2. 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	14434	North Africa	0.132
Central Europe	14434	South-east Europe	0.075
Central Europe	14434	South-west Europe	0.302
Central Europe	14434	West Europe	0.491
East Europe	15471	South-east Europe	0.667
East Europe	15471	South-west Europe	0.333
North Europe	8400	North Africa	0.007
North Europe	8400	South-central Europe	0.007
North Europe	8400	South-west Europe	0.281
North Europe	8400	West Europe	0.704
North-west Europe	3000	North-west Europe	0.571
North-west Europe	3000	South-west Europe	0.107
North-west Europe	3000	West Europe	0.321

Breeding region	Abundance	Non breeding region	Transition probability
South-central Europe	3873	South-central Europe	1.000
South-west Europe	59256	South-west Europe	0.750
South-west Europe	59256	West Africa	0.250
West Europe	16949	North Africa	0.061
West Europe	16949	North-west Europe	0.007
West Europe	16949	South-west Europe	0.351
West Europe	16949	West Africa	0.027
West Europe	16949	West Europe	0.554

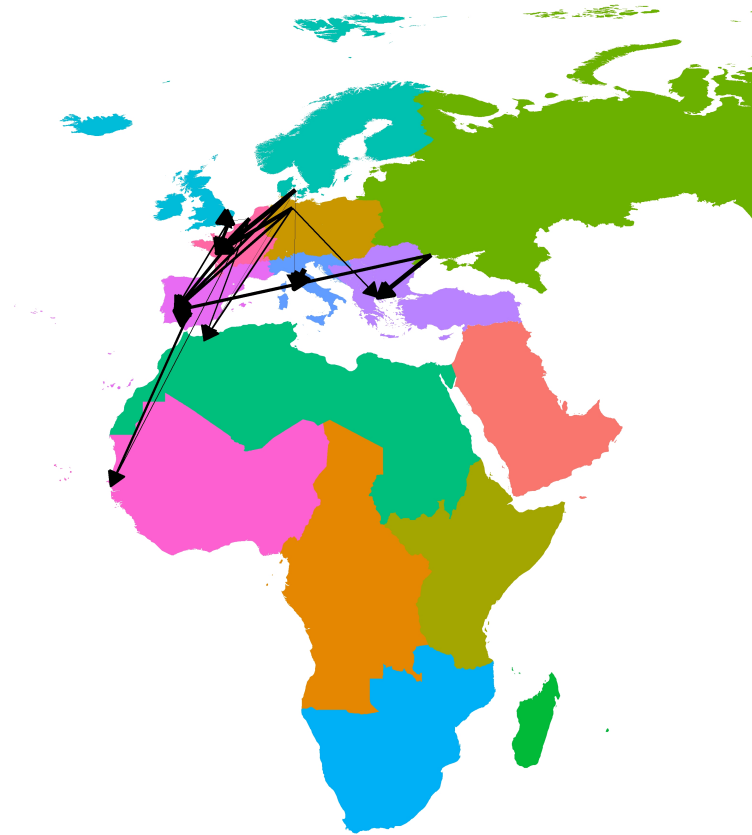


Figure 04560-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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>.