

Migratory connectivity analysis

by EURING Migration Atlas

Sturnus vulgaris (EURING code 15820)

1.1 Connectivity between individuals

The analysis evaluated 7038 individuals (14076 encounters) filtered from a total of 305052 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 15820-1; Figure 15820-1).

Table 15820-1. 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	7038	0.424	0.001	0.400	0.449	3	0.575
1	1	764	0.506	0.001	0.398	0.589	5	0.344
2	1	5048	0.883	0.001	0.864	0.899	3	0.545
3	1	1226	0.328	0.001	0.263	0.394	2	0.325
21	2	995	0.369	0.001	0.308	0.439	5	0.393
22	2	3340	0.804	0.001	0.774	0.837	2	0.473
23	2	713	0.894	0.001	0.838	0.935	9	0.676
231	3	9	-	-	-	-	-	-
232	3	33	0.609	0.001	0.288	0.871	6	0.694
233	3	59	0.656	0.001	0.468	0.841	5	0.590
234	3	130	0.662	0.001	0.542	0.796	2	0.512
235	3	48	0.900	0.001	0.310	0.983	2	0.877
236	3	36	0.479	0.005	0.149	0.753	2	0.459
237	3	69	0.634	0.001	0.429	0.852	9	0.723
238	3	313	0.797	0.001	0.584	0.974	8	0.950
239	3	16	-	-	-	-	-	-

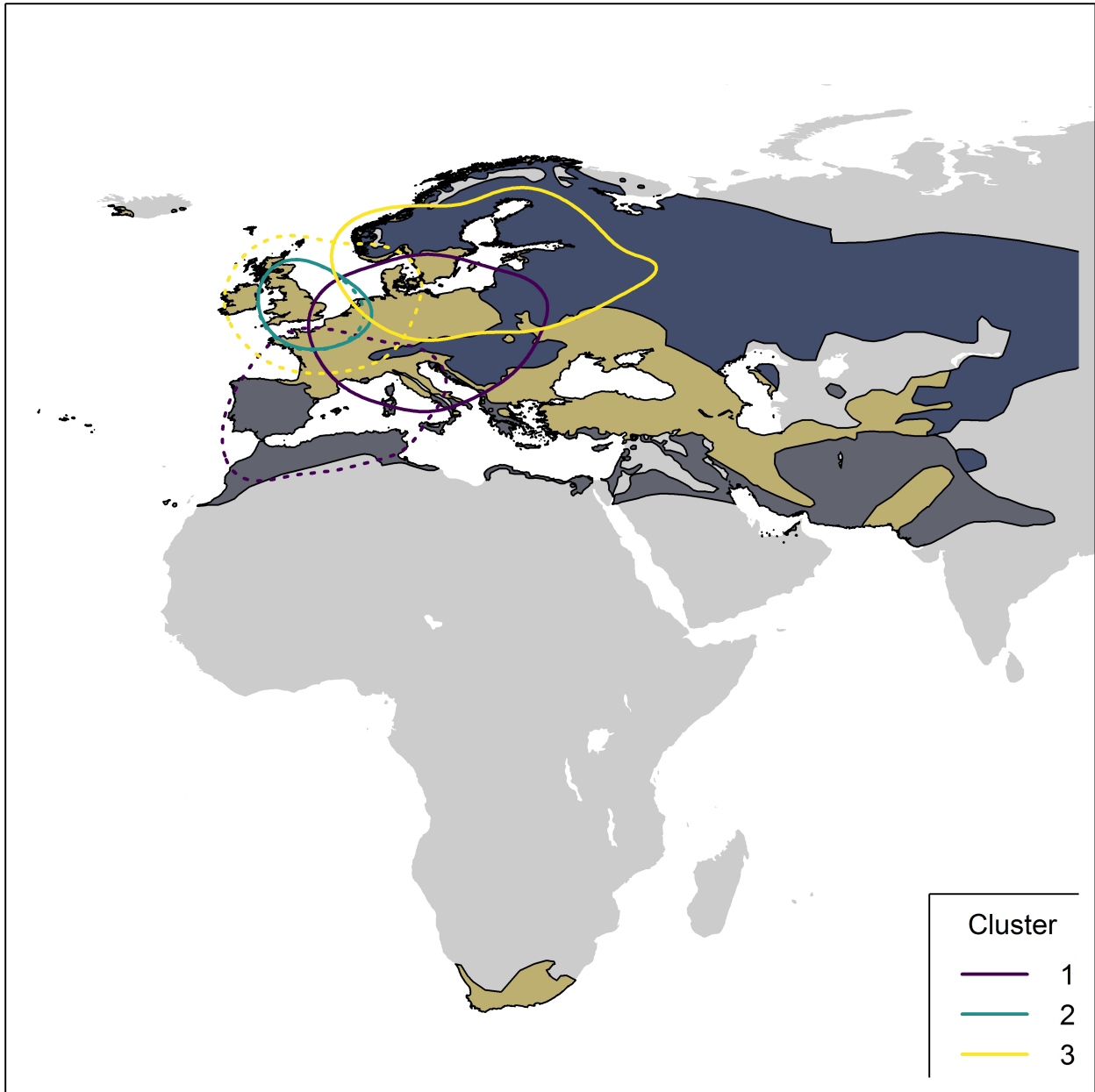


Figure 15820-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 15820-2) and stratified sampling of individuals within the breeding range (Figure 15820-3) and the non breeding range (Figure 15820-4). 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.

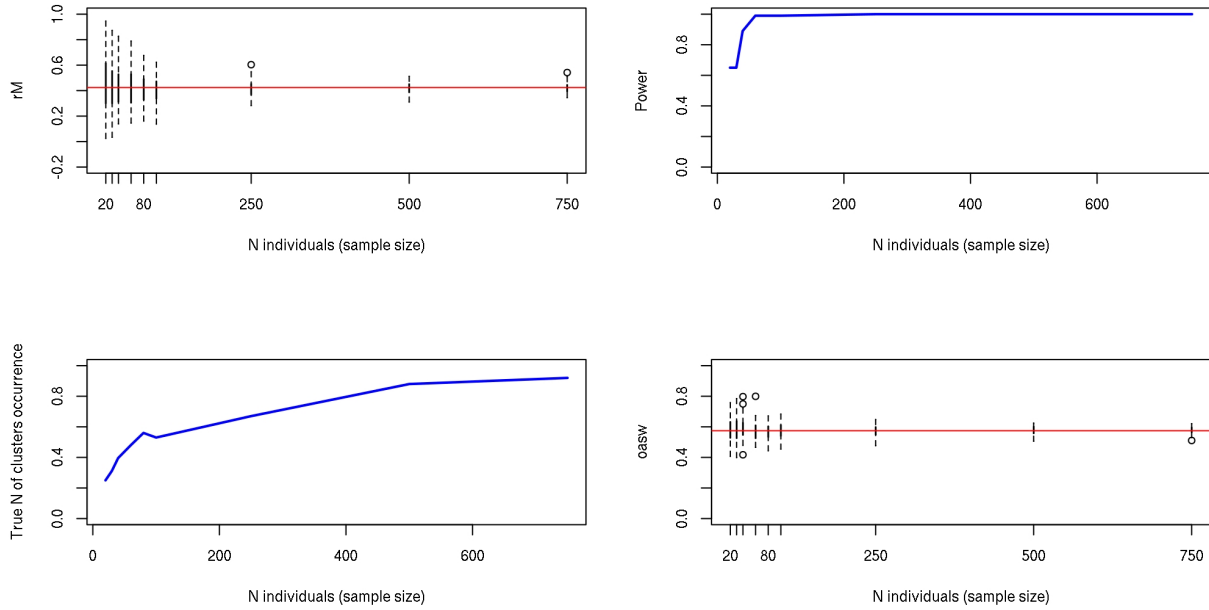


Figure 15820-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

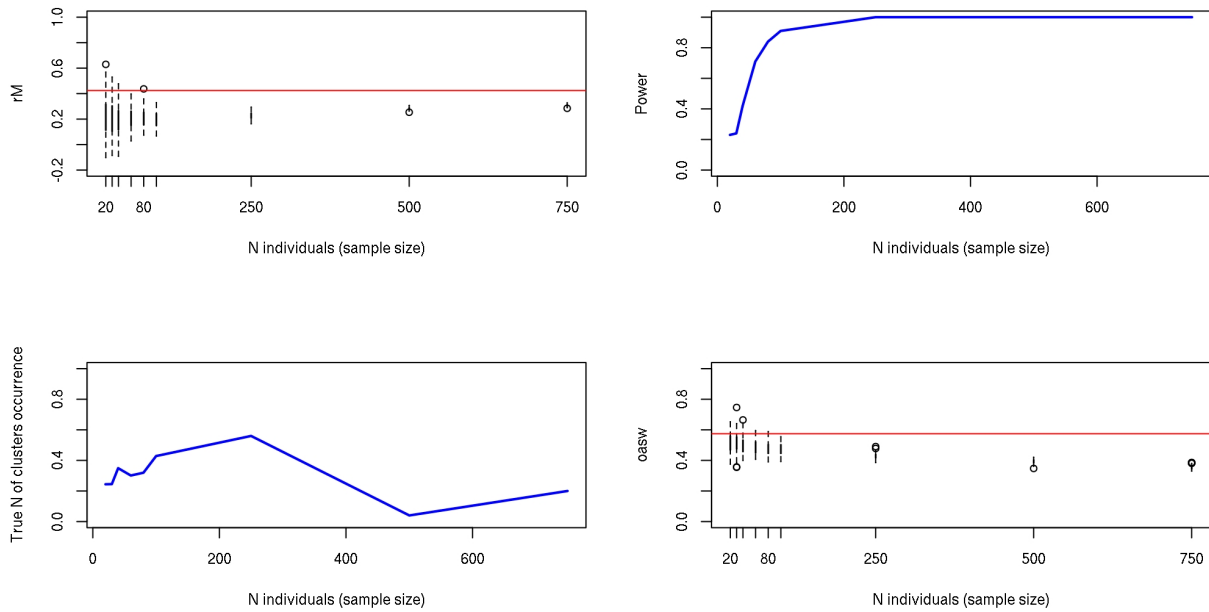


Figure 15820-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

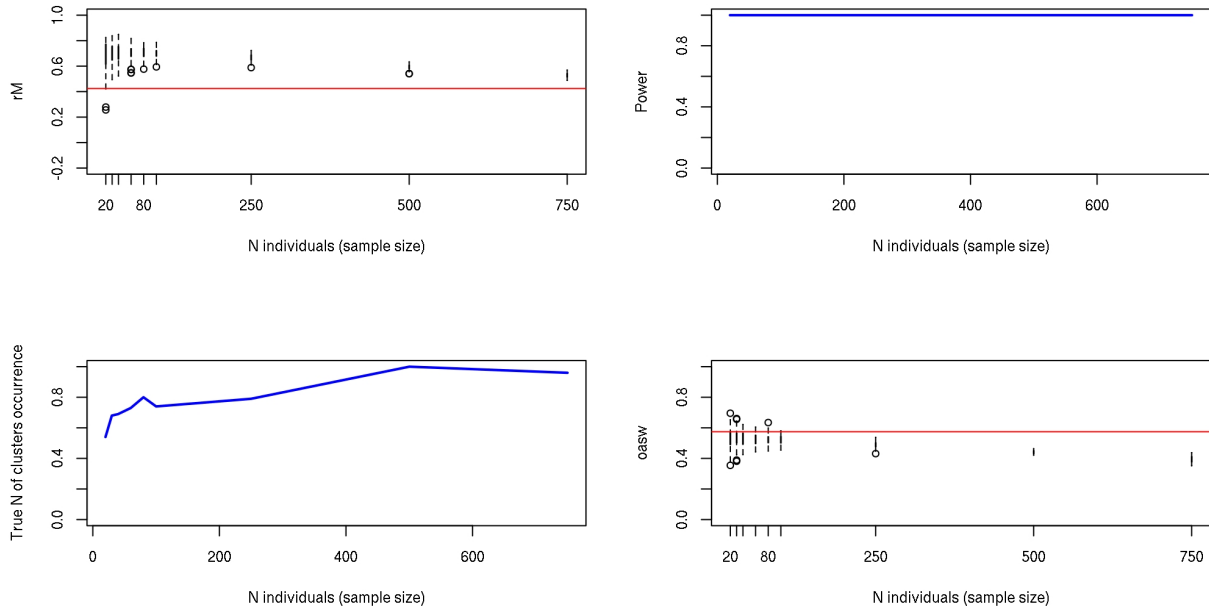


Figure 15820-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

The comparison between the bootstrapped distribution of r_M values from live recaptures and dead recoveries is significant ($p < 0.001$); Figure 15820-5).

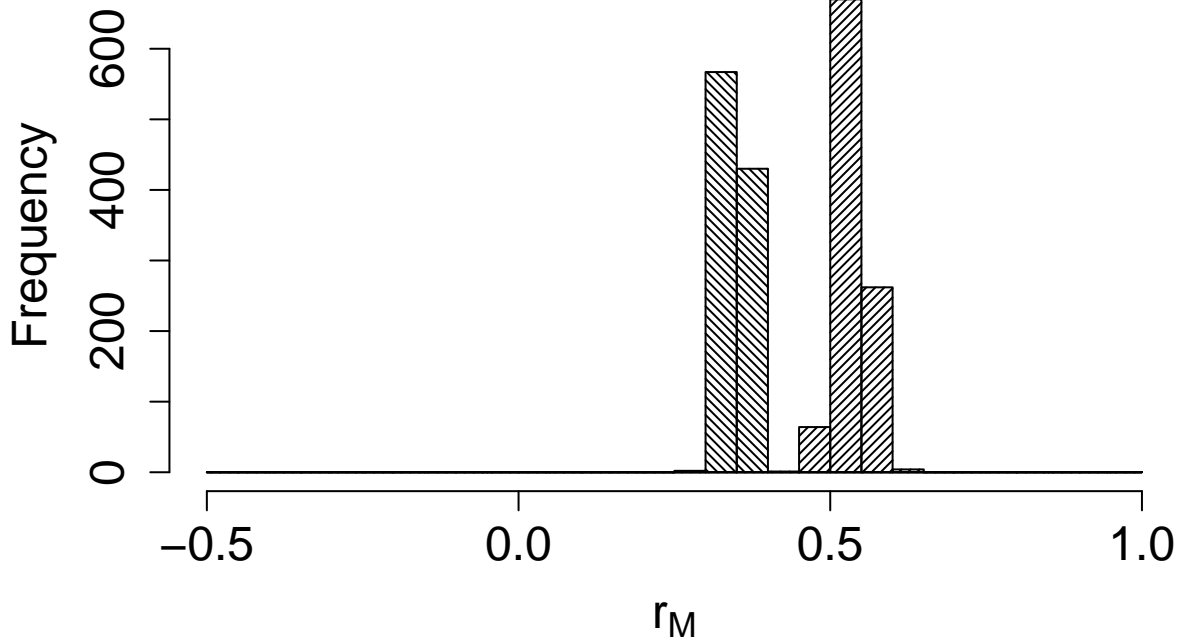


Figure 15820-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low/moderate connectivity ($MC = 0.275$; $MC = 0.274$ when adjusted for absolute abundance) between 8 breeding regions and 10 non breeding regions (Table 15820-2; Figure 15820-6).

Table 15820-2. 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	18690800	Central Europe	0.068
Central Europe	18690800	North Africa	0.213
Central Europe	18690800	North-west Europe	0.099
Central Europe	18690800	South-central Europe	0.068
Central Europe	18690800	South-west Europe	0.341
Central Europe	18690800	West Europe	0.212
East Europe	20273150	Arabian peninsula	0.018
East Europe	20273150	Central Europe	0.007
East Europe	20273150	East Europe	0.037
East Europe	20273150	North Europe	0.015
East Europe	20273150	North-west Europe	0.363
East Europe	20273150	South-central Europe	0.077
East Europe	20273150	South-east Europe	0.031

Breeding region	Abundance	Non breeding region	Transition probability
East Europe	20273150	South-west Europe	0.031
East Europe	20273150	West Europe	0.421
North Europe	2004000	Central Europe	0.009
North Europe	2004000	North Europe	0.109
North Europe	2004000	North-west Europe	0.647
North Europe	2004000	South-central Europe	0.003
North Europe	2004000	South-west Europe	0.006
North Europe	2004000	West Europe	0.226
North-west Europe	6559168	East Europe	0.000
North-west Europe	6559168	North-west Europe	0.999
North-west Europe	6559168	West Europe	0.001
South-central Europe	5830000	North Africa	0.333
South-central Europe	5830000	South-central Europe	0.667
South-east Europe	15223000	South-central Europe	1.000
South-west Europe	4753265	South-west Europe	1.000
West Europe	7005339	Central Europe	0.001
West Europe	7005339	North Africa	0.001
West Europe	7005339	North Europe	0.001
West Europe	7005339	North-west Europe	0.142
West Europe	7005339	South-west Europe	0.029
West Europe	7005339	West Europe	0.826

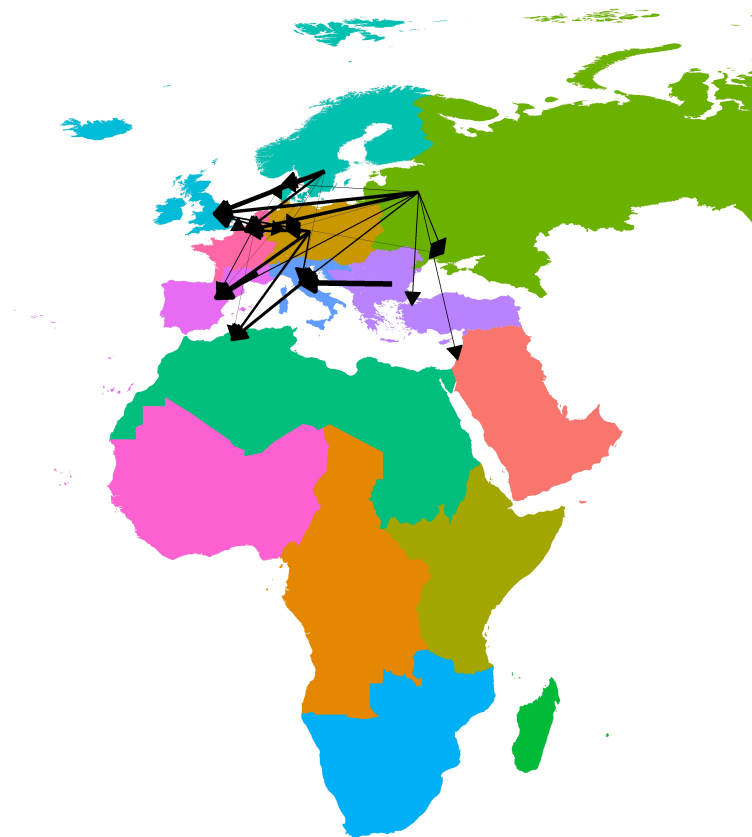


Figure 15820-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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>.