

Migratory connectivity analysis

by EURING Migration Atlas

Rissa tridactyla (EURING code 06020)

1.1 Connectivity between individuals

The analysis evaluated 134 individuals (268 encounters) filtered from a total of 34833 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 06020-1; Figure 06020-1).

Table 06020-1. 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	134	0.159	0.002	0.052	0.296	2	0.495

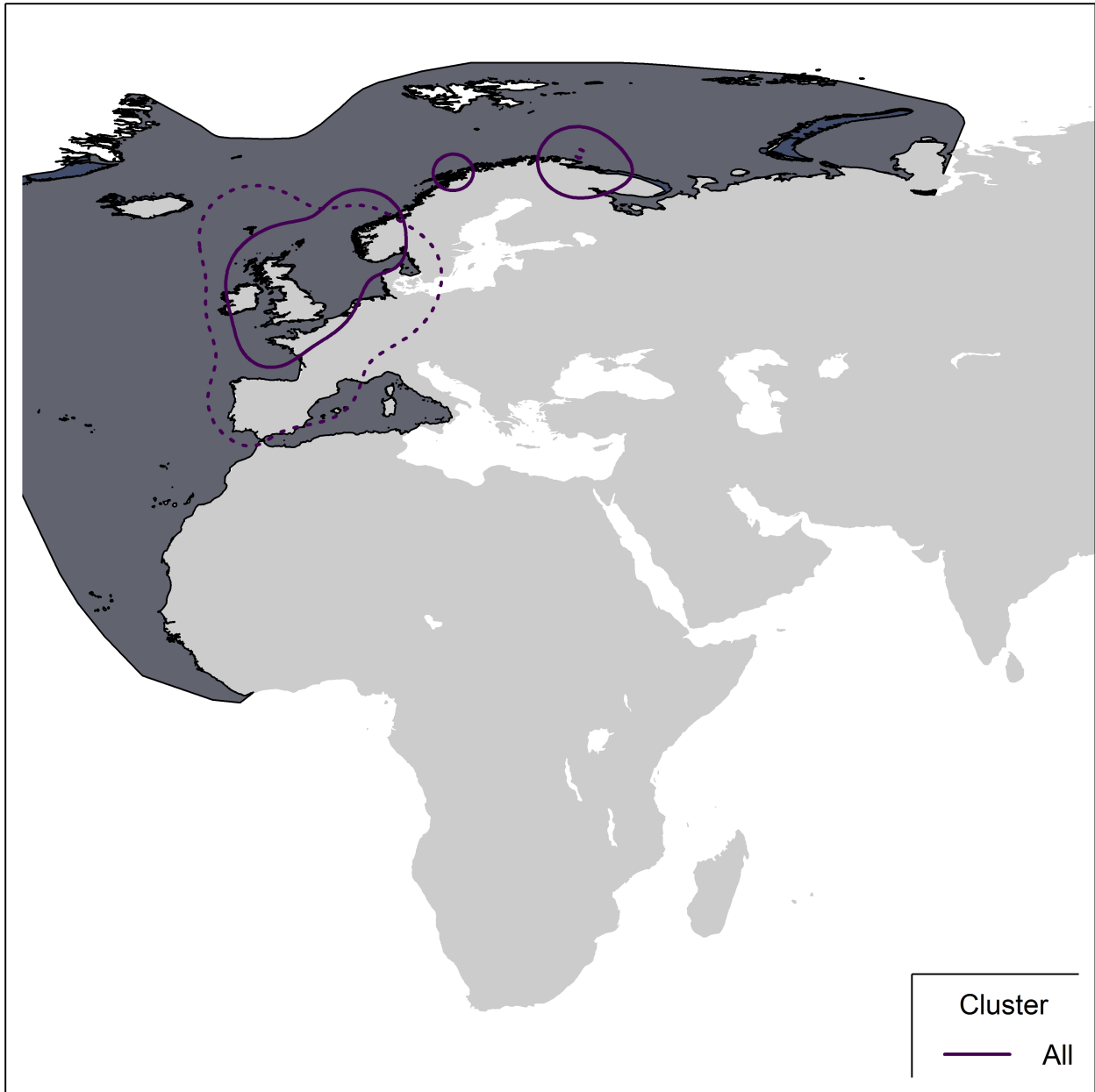


Figure 06020-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 06020-2) and stratified sampling of individuals within the breeding range (Figure 06020-3) and the non breeding range (Figure 06020-4). 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.

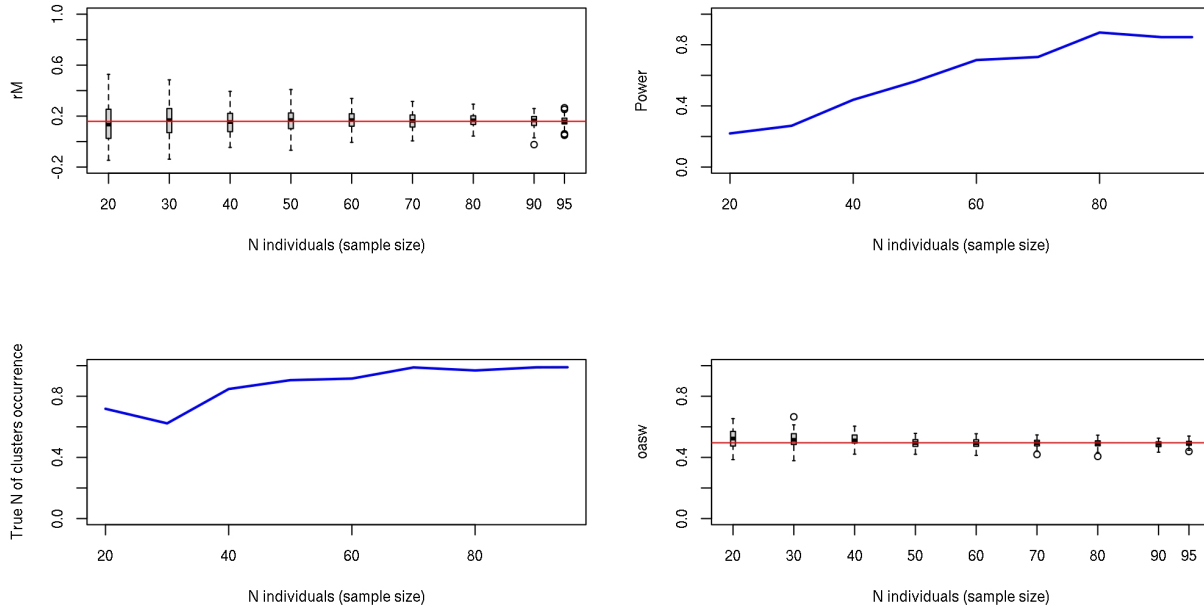


Figure 06020-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

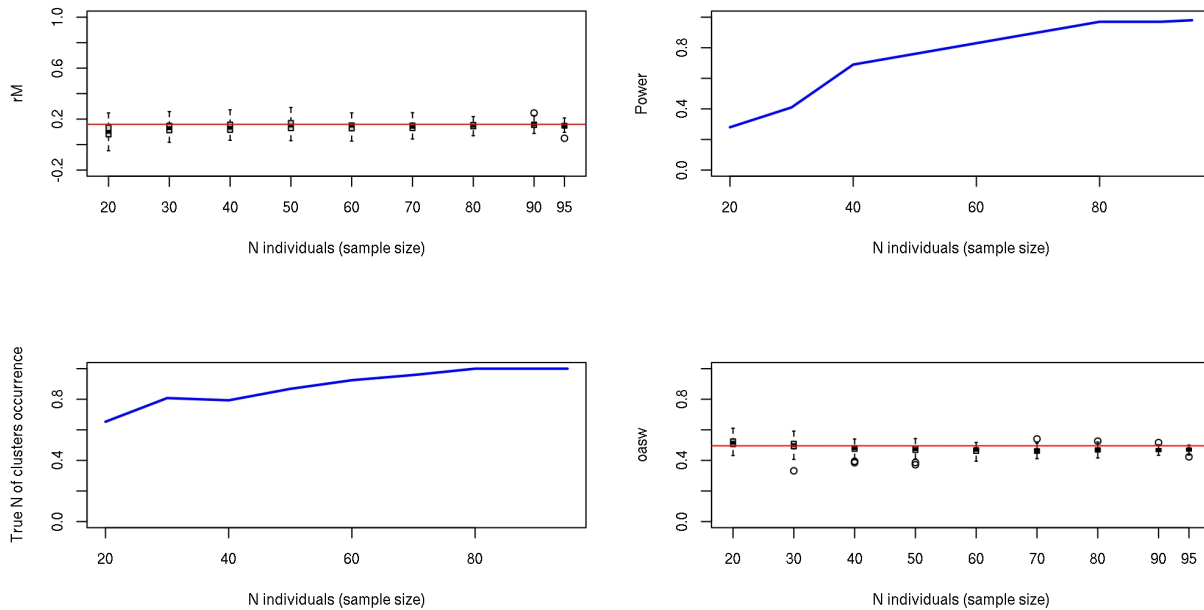


Figure 06020-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

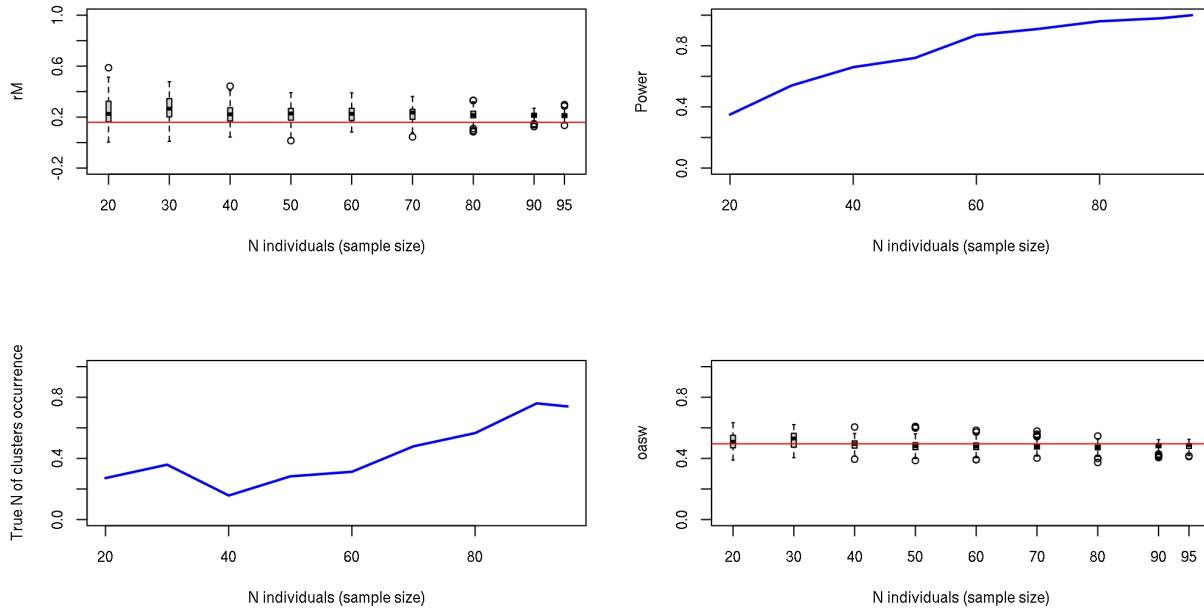


Figure 06020-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 ($p = 0.471$); Figure 06020-5).

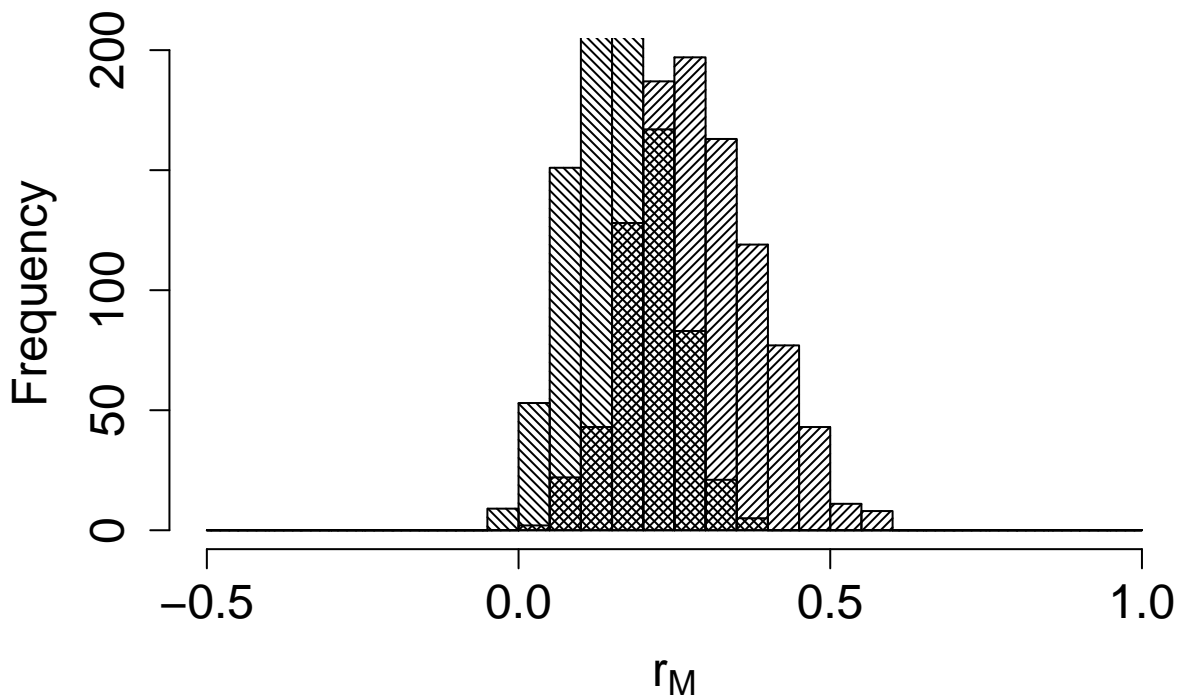


Figure 06020-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low connectivity ($MC = 0.091$; $MC = 0.081$ when adjusted for absolute abundance) between 4 breeding regions and 8 non breeding regions (Table 06020-2; Figure 06020-6).

Table 06020-2. 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
East Europe	600000	North Europe	0.400
East Europe	600000	North-west Europe	0.200
East Europe	600000	South-central Europe	0.200
East Europe	600000	West Europe	0.200
North Europe	1112752	Central Europe	0.136
North Europe	1112752	East Europe	0.023
North Europe	1112752	North Europe	0.182
North Europe	1112752	North-west Europe	0.409
North Europe	1112752	South-west Europe	0.045
North Europe	1112752	West Europe	0.205
North-west Europe	1977254	Central Europe	0.132
North-west Europe	1977254	North Africa	0.026
North-west Europe	1977254	North Europe	0.066

Breeding region	Abundance	Non breeding region	Transition probability
North-west Europe	1977254	North-west Europe	0.434
North-west Europe	1977254	South-west Europe	0.197
North-west Europe	1977254	West Europe	0.145
West Europe	10625	Central Europe	0.111
West Europe	10625	North Europe	0.222
West Europe	10625	North-west Europe	0.333
West Europe	10625	South-west Europe	0.111
West Europe	10625	West Europe	0.222

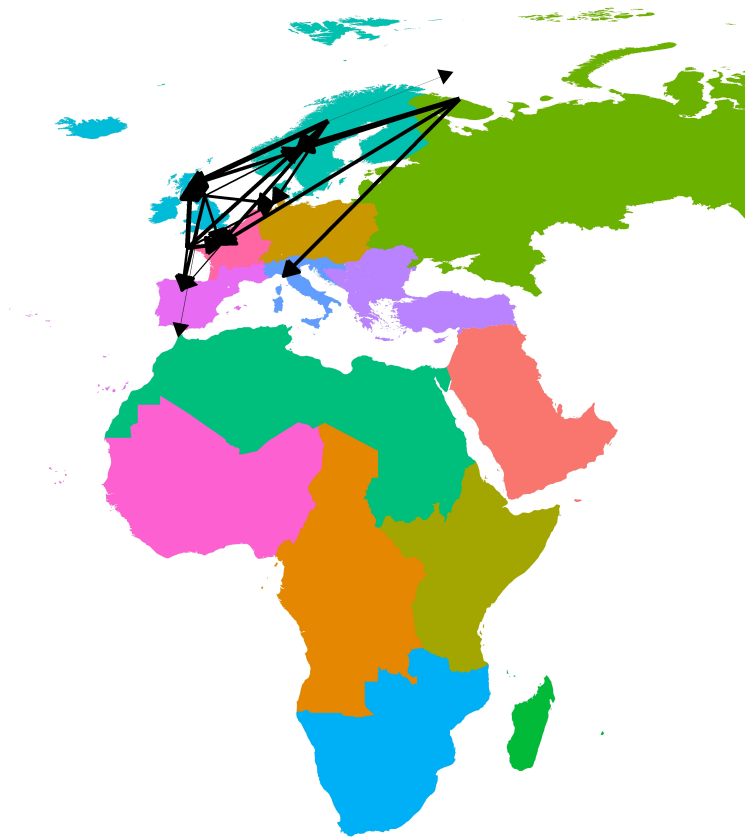


Figure 06020-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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>.