

# Migratory connectivity analysis

by EURING Migration Atlas

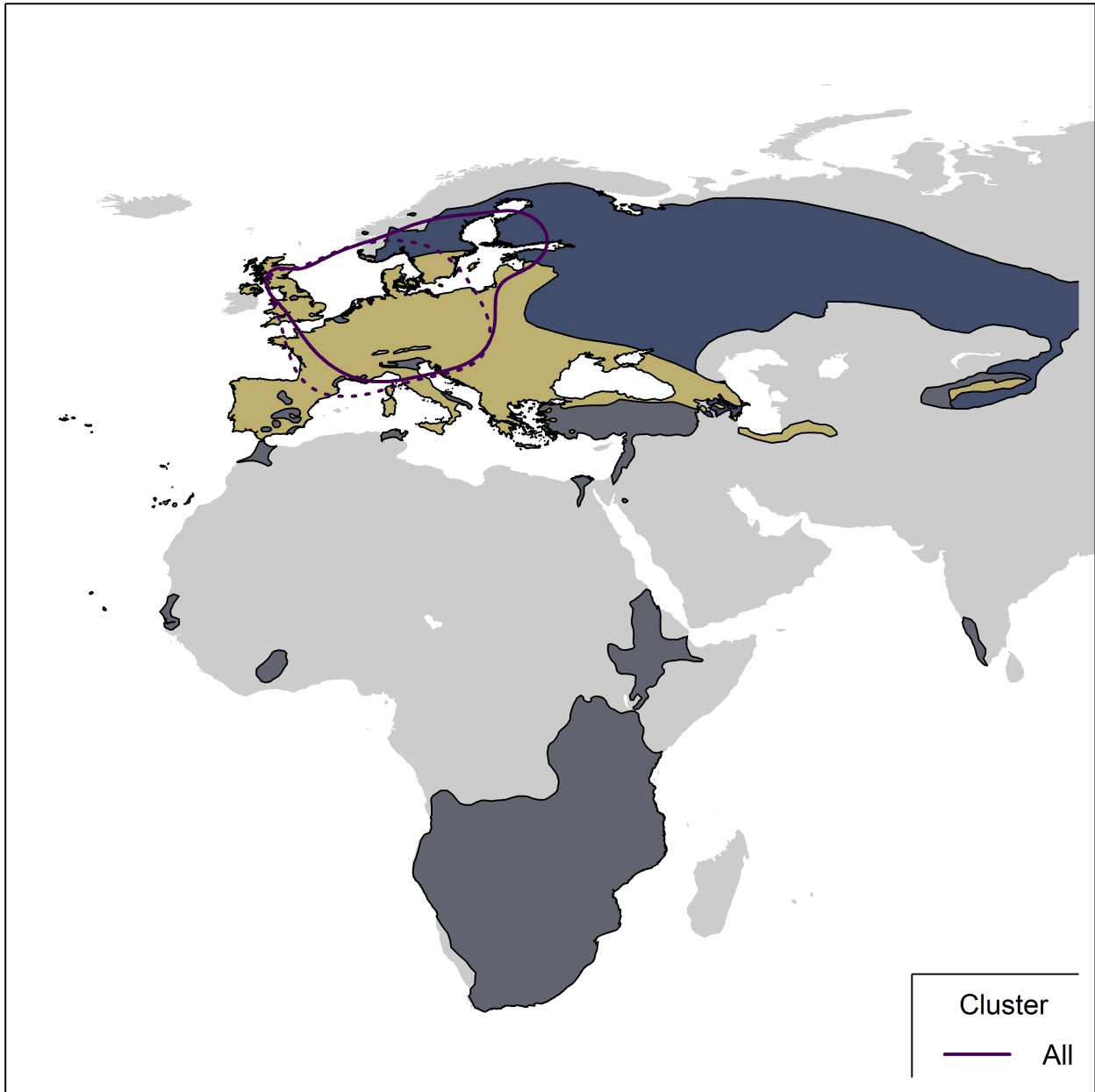
*Buteo buteo* (EURING code 02870)

## 1.1 Connectivity between individuals

The analysis evaluated 3509 individuals (7018 encounters) filtered from a total of 63054 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 02870-1; Figure 02870-1).

**Table 02870-1.** 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	3509	0.532	0.001	0.481	0.603	7	0.474

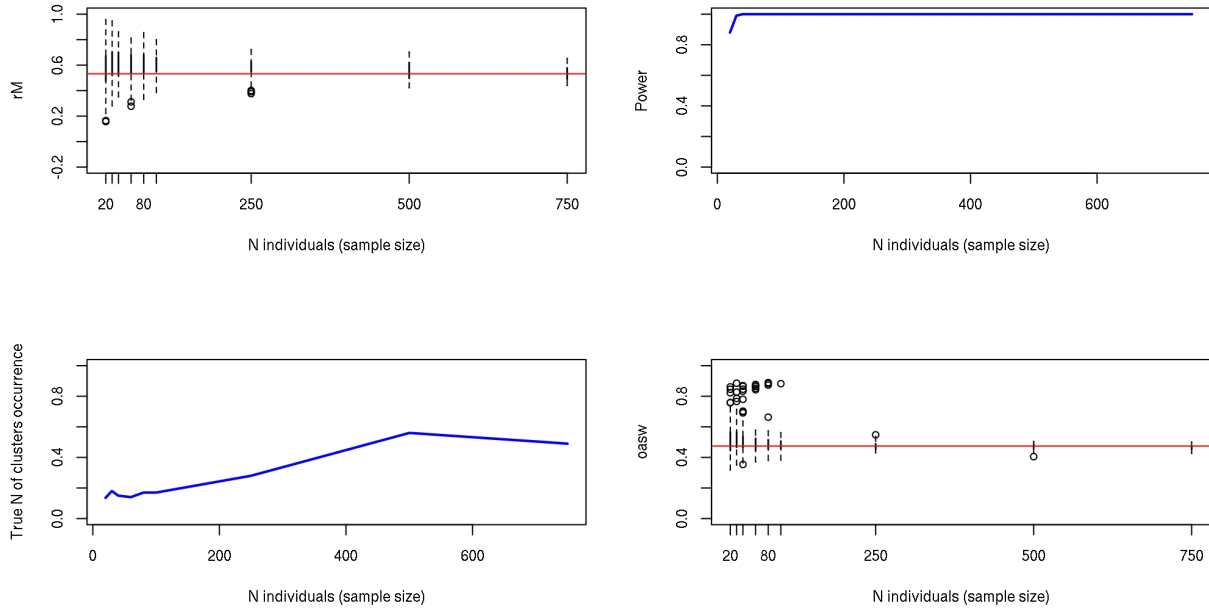


**Figure 02870-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

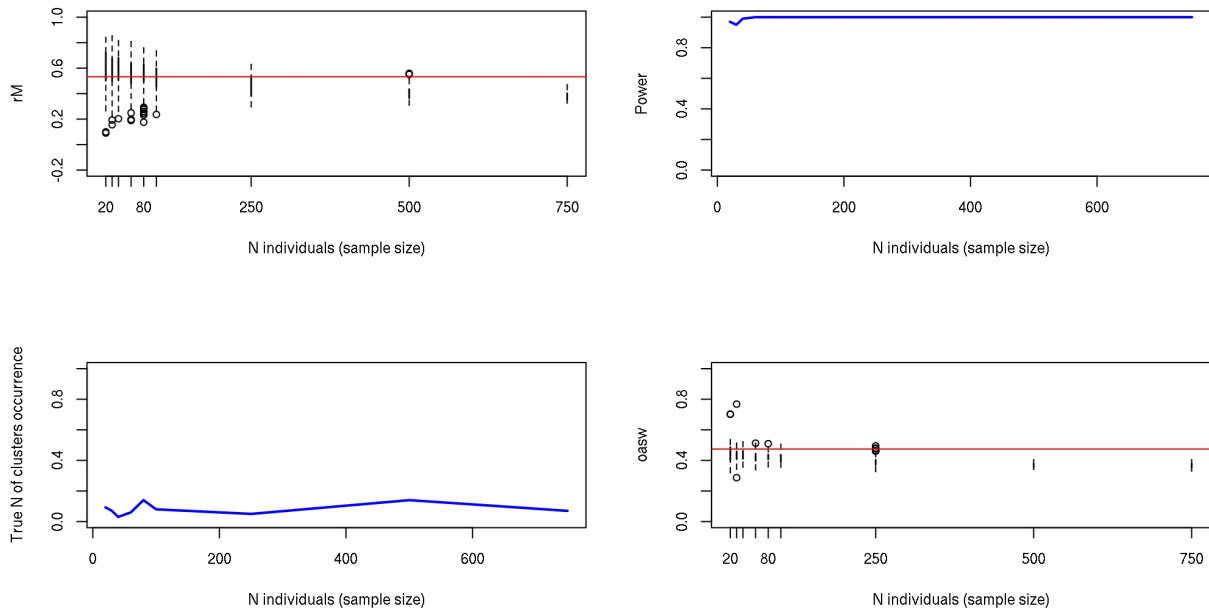
## 1.2 Sensitivity analysis

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 02870-2) and stratified sampling of individuals within the breeding range (Figure 02870-3) and the non breeding range (Figure 02870-4). 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.

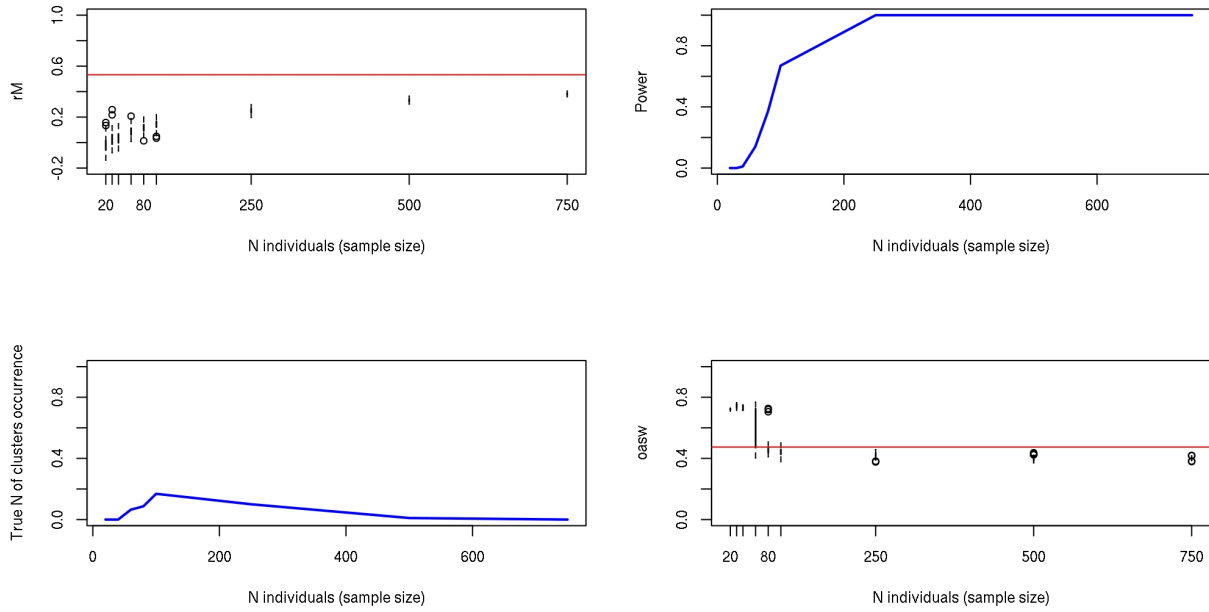


**Figure 02870-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



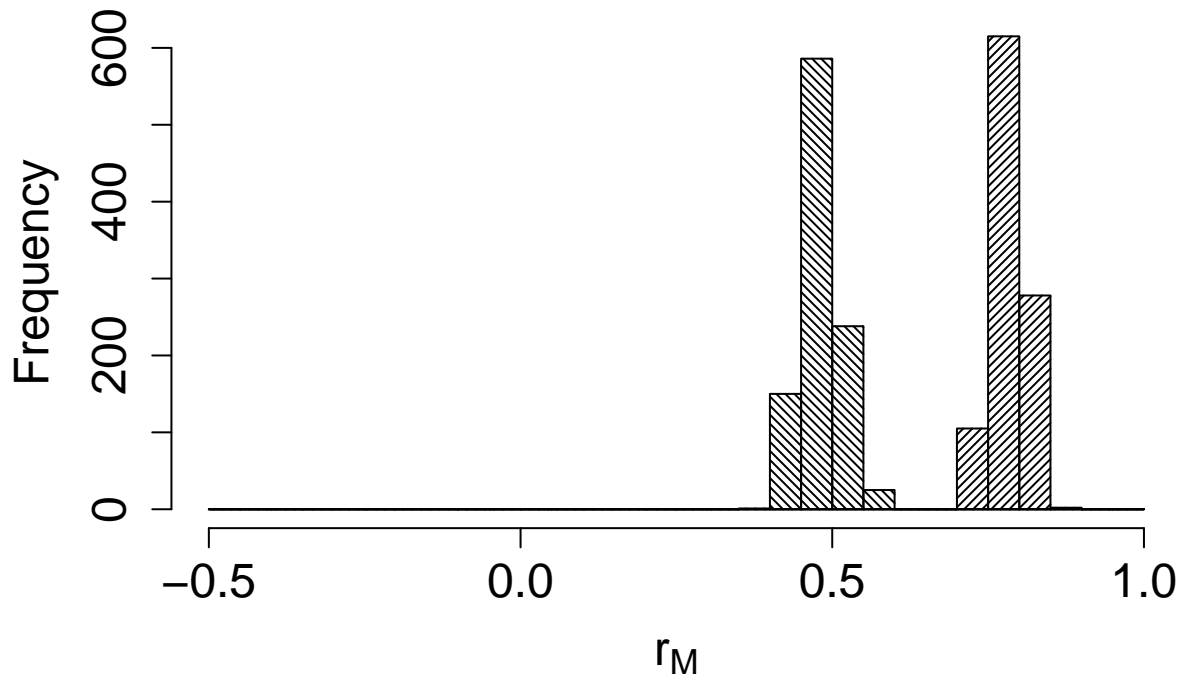
**Figure 02870-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 02870-4.** 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 02870-5).



**Figure 02870-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

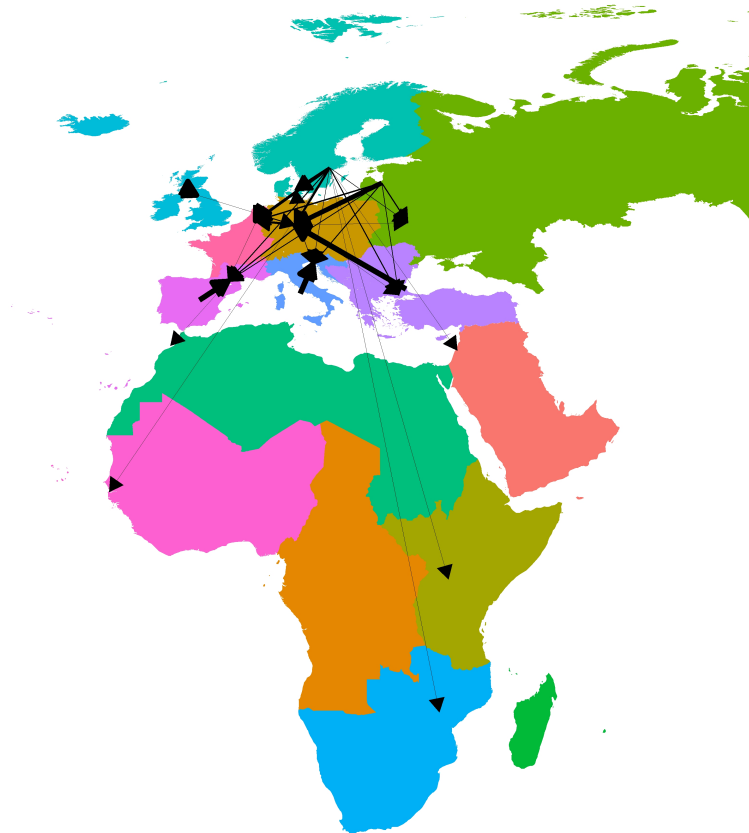
## 2. Connectivity between pre-defined regions

The species shows low/moderate connectivity ( $MC = 0.396$ ;  $MC = 0.396$  when adjusted for absolute abundance) between 8 breeding regions and 13 non breeding regions (Table 02870-2; Figure 02870-6).

**Table 02870-2.** 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	490050	Central Europe	0.762
Central Europe	490050	East Europe	0.001
Central Europe	490050	North Europe	0.003
Central Europe	490050	South-central Europe	0.012
Central Europe	490050	South-east Europe	0.003
Central Europe	490050	South-west Europe	0.051
Central Europe	490050	West Europe	0.169
East Europe	933520	Central Europe	0.765
East Europe	933520	East Europe	0.059
East Europe	933520	South-central Europe	0.039
East Europe	933520	South-east Europe	0.020
East Europe	933520	South-west Europe	0.039
East Europe	933520	West Europe	0.078

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	83200	Arabian peninsula	0.004
North Europe	83200	Central Europe	0.213
North Europe	83200	East Africa	0.001
North Europe	83200	East Europe	0.012
North Europe	83200	North Africa	0.003
North Europe	83200	North Europe	0.344
North Europe	83200	South Africa	0.004
North Europe	83200	South-central Europe	0.016
North Europe	83200	South-east Europe	0.051
North Europe	83200	South-west Europe	0.030
North Europe	83200	West Africa	0.001
North Europe	83200	West Europe	0.319
North-west Europe	139000	Central Europe	0.006
North-west Europe	139000	North-west Europe	0.994
South-central Europe	46192	South-central Europe	1.000
South-east Europe	124900	Central Europe	1.000
South-west Europe	153371	South-west Europe	1.000
West Europe	224353	Central Europe	0.031
West Europe	224353	South-west Europe	0.001
West Europe	224353	West Europe	0.969



**Figure 02870-6.** 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>.