

# Migratory connectivity analysis

by EURING Migration Atlas

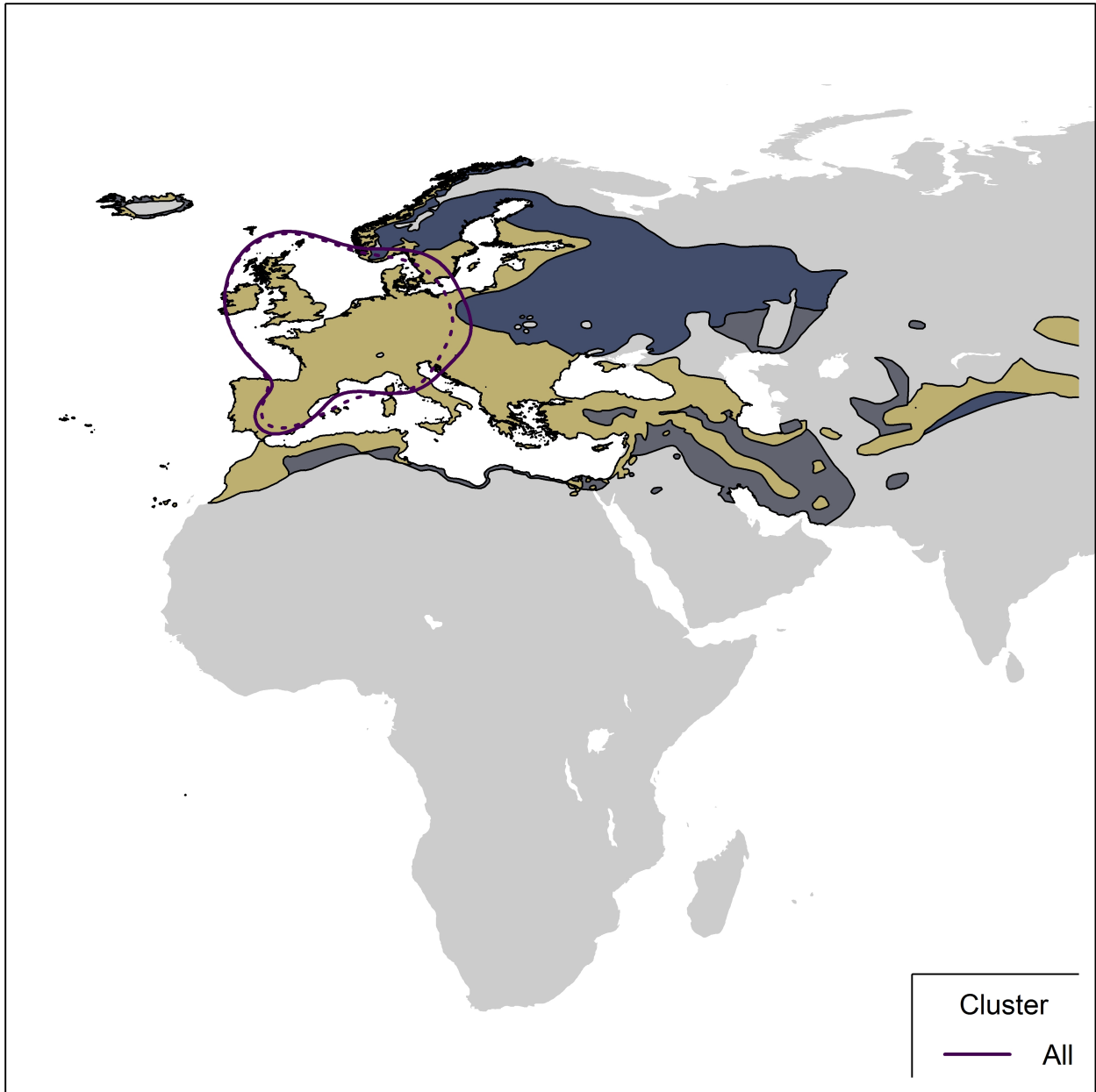
*Turdus merula* (EURING code 11870)

## 1.1 Connectivity between individuals

The analysis evaluated 19220 individuals (38440 encounters) filtered from a total of 850788 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 11870-1; Figure 11870-1).

**Table 11870-1.** 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	19220	0.909	0.001	0.901	0.917	3	0.491

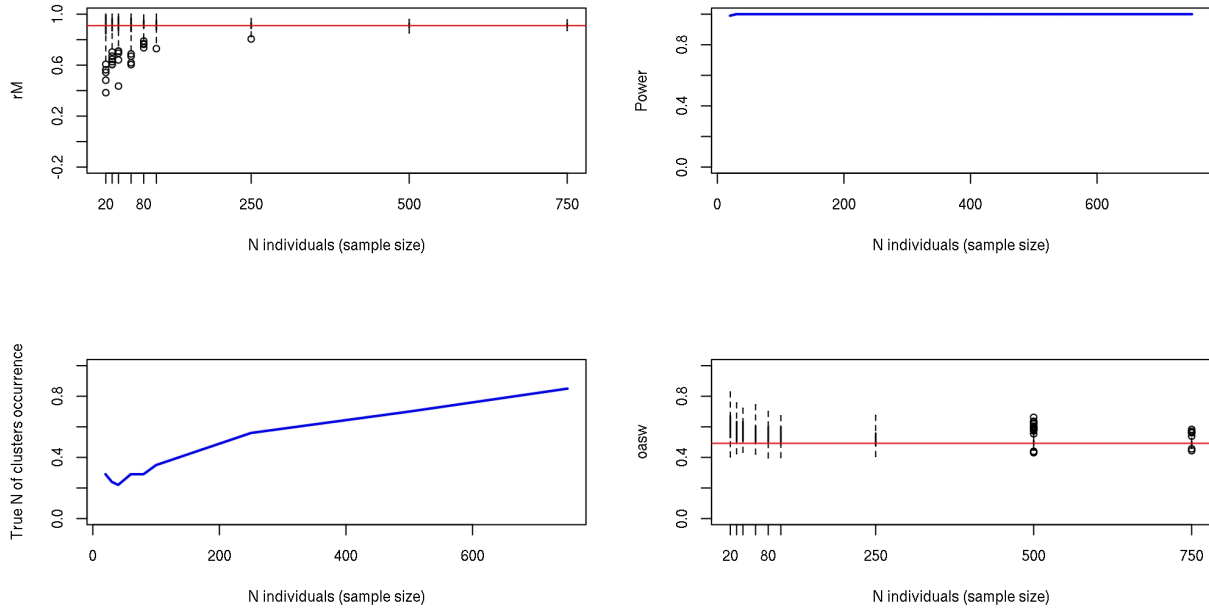


**Figure 11870-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

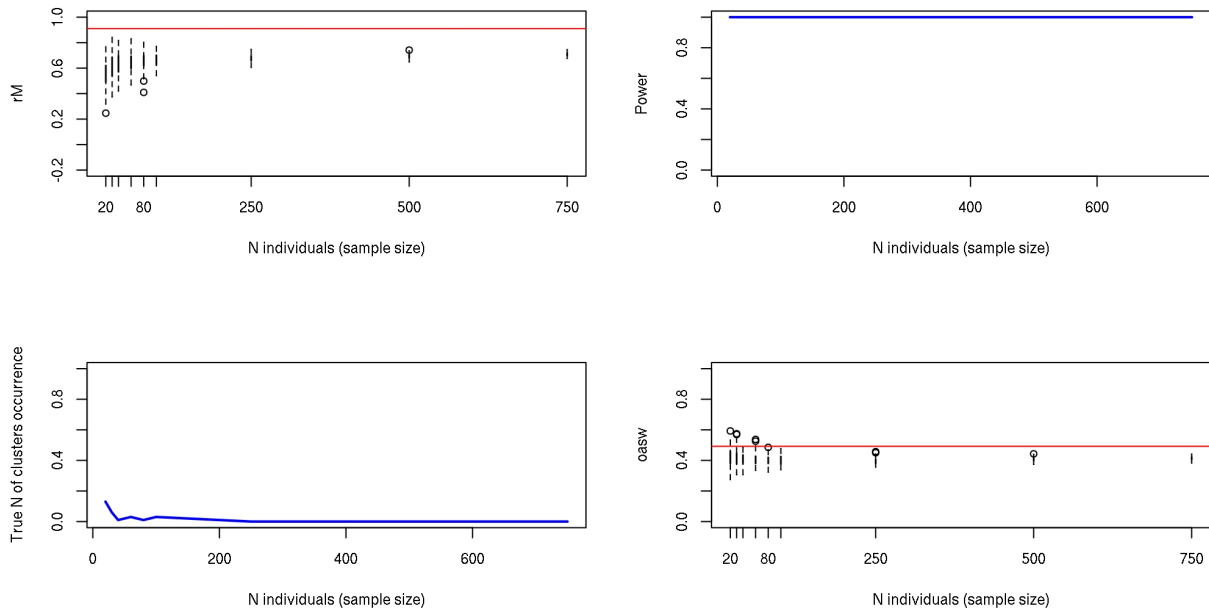
## 1.2 Sensitivity analysis

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 11870-2) and stratified sampling of individuals within the breeding range (Figure 11870-3) and the non breeding range (Figure 11870-4). 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.

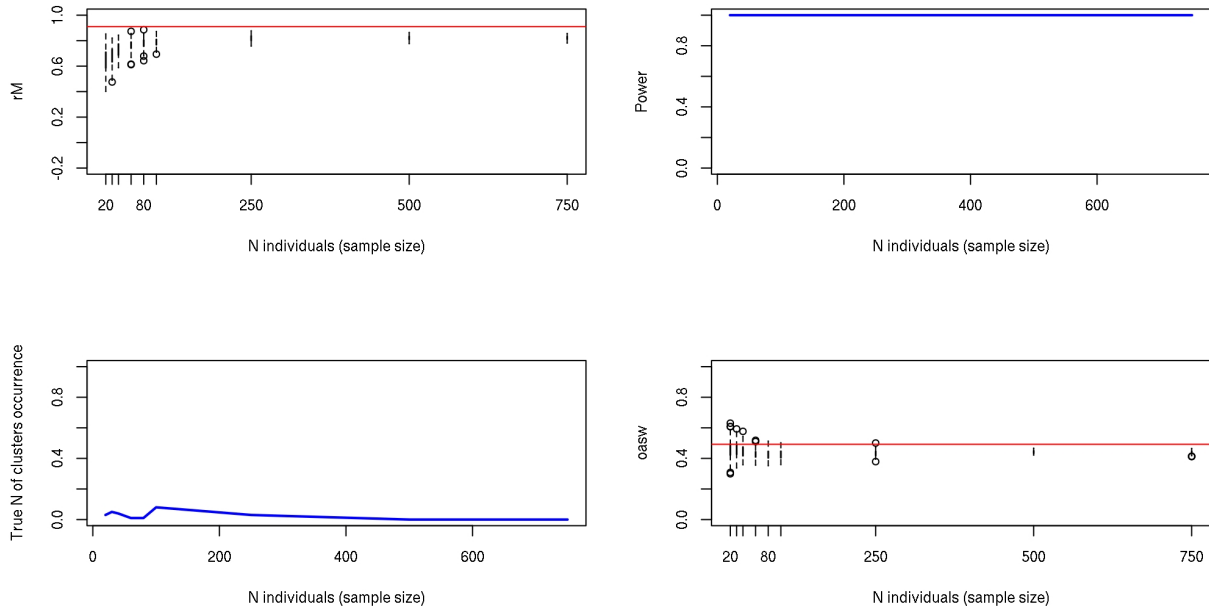


**Figure 11870-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



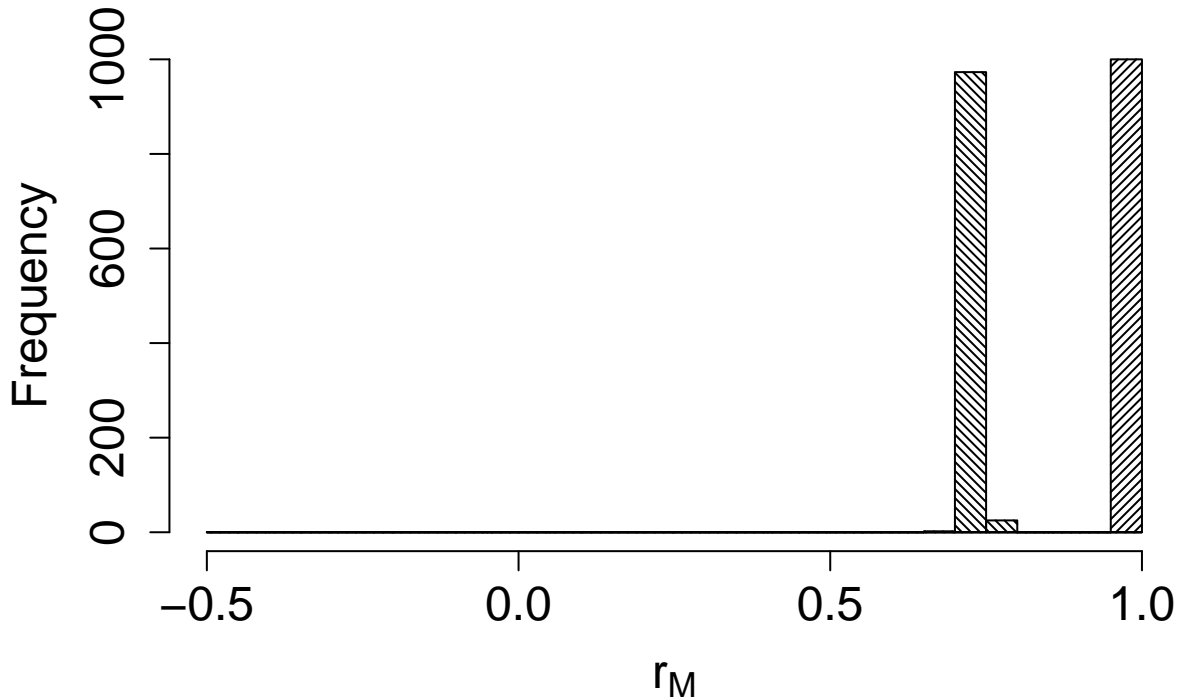
**Figure 11870-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 11870-4.** 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 11870-5).



**Figure 11870-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

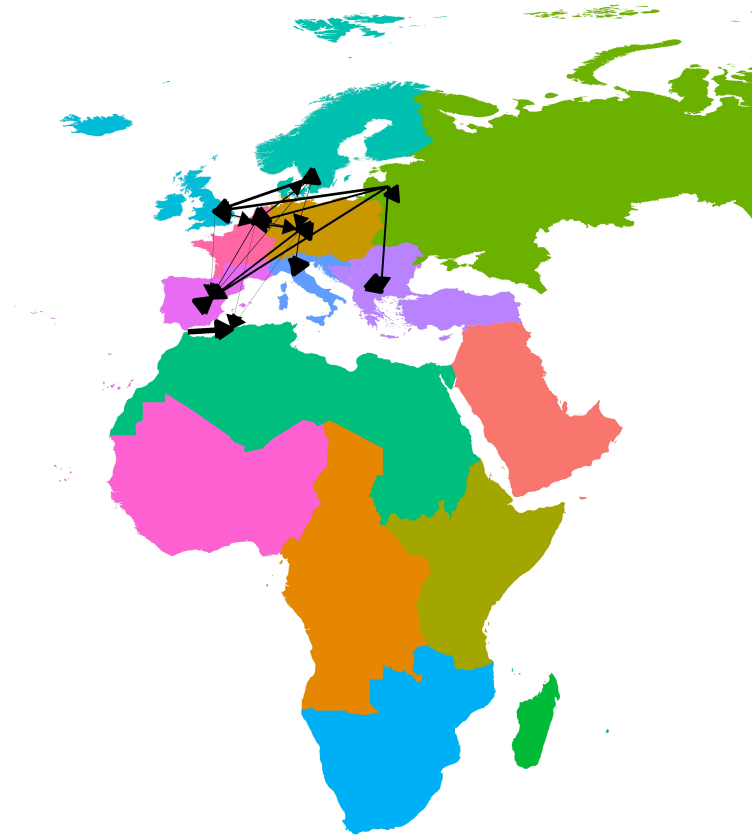
## 2. Connectivity between pre-defined regions

The species shows moderate/high connectivity ( $MC = 0.741$ ;  $MC = 0.741$  when adjusted for absolute abundance) between 9 breeding regions and 9 non breeding regions (Table 11870-2; Figure 11870-6).

**Table 11870-2.** 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	34873500	Central Europe	0.759
Central Europe	34873500	North Africa	0.002
Central Europe	34873500	North-west Europe	0.024
Central Europe	34873500	South-central Europe	0.029
Central Europe	34873500	South-west Europe	0.121
Central Europe	34873500	West Europe	0.066
East Europe	11426240	East Europe	0.294
East Europe	11426240	North-west Europe	0.235
East Europe	11426240	South-east Europe	0.118
East Europe	11426240	South-west Europe	0.176
East Europe	11426240	West Europe	0.176
North Africa	1000	North Africa	1.000
North Europe	9568000	Central Europe	0.015

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	9568000	North Europe	0.656
North Europe	9568000	North-west Europe	0.257
North Europe	9568000	South-west Europe	0.008
North Europe	9568000	West Europe	0.064
North-west Europe	17722867	North-west Europe	0.999
North-west Europe	17722867	South-west Europe	0.000
North-west Europe	17722867	West Europe	0.001
South-central Europe	14146236	South-central Europe	1.000
South-east Europe	16590600	South-east Europe	1.000
South-west Europe	26594956	South-west Europe	1.000
West Europe	10294637	Central Europe	0.004
West Europe	10294637	North Africa	0.000
West Europe	10294637	North Europe	0.000
West Europe	10294637	North-west Europe	0.014
West Europe	10294637	South-west Europe	0.026
West Europe	10294637	West Europe	0.955



**Figure 11870-6.** 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>.