

# Migratory connectivity analysis

by EURING Migration Atlas

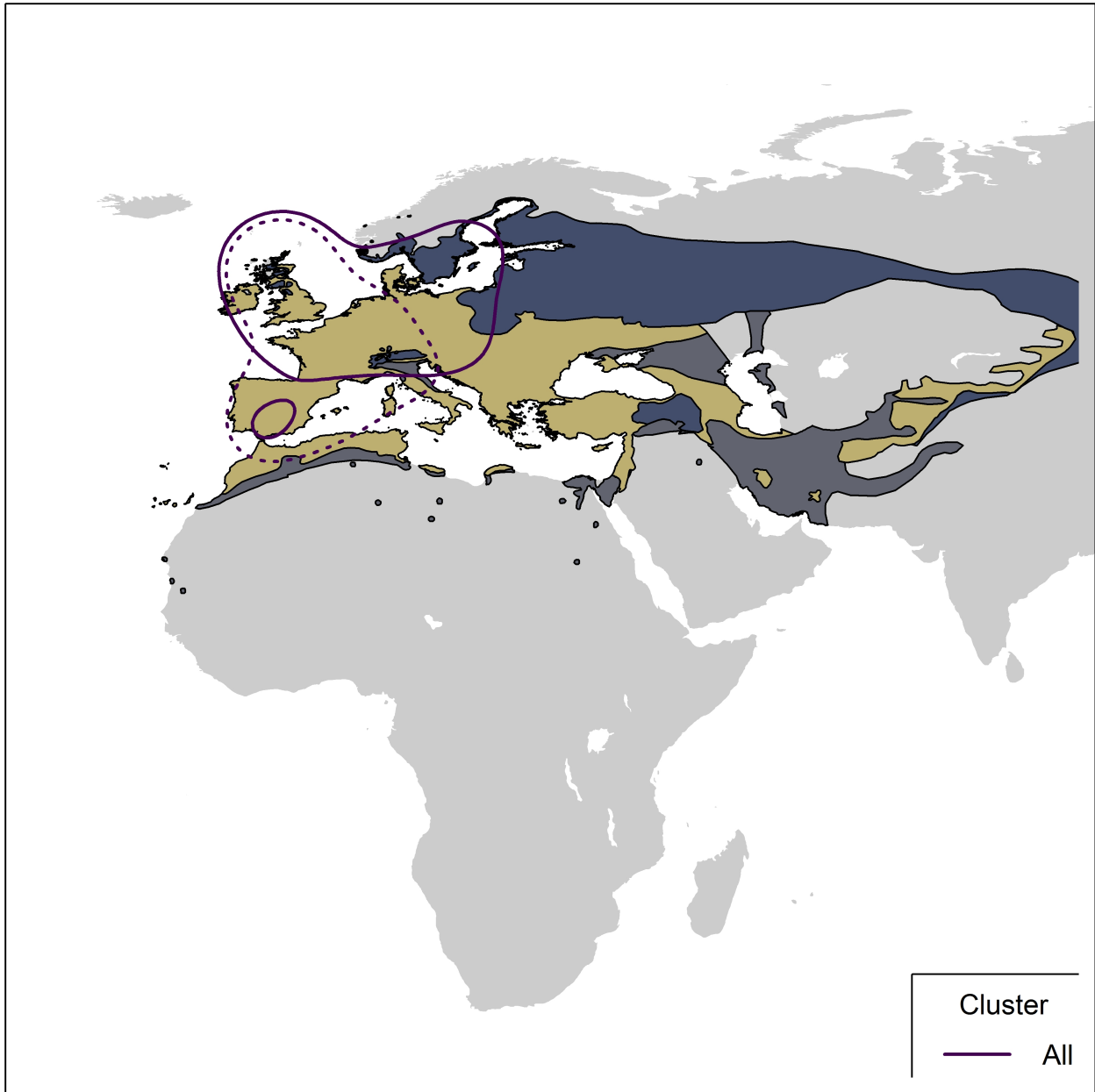
*Carduelis cannabina* (EURING code 16600)

## 1.1 Connectivity between individuals

The analysis evaluated 491 individuals (982 encounters) filtered from a total of 77439 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 16600-1; Figure 16600-1).

**Table 16600-1.** 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	491	0.528	0.001	0.459	0.601	9	0.479

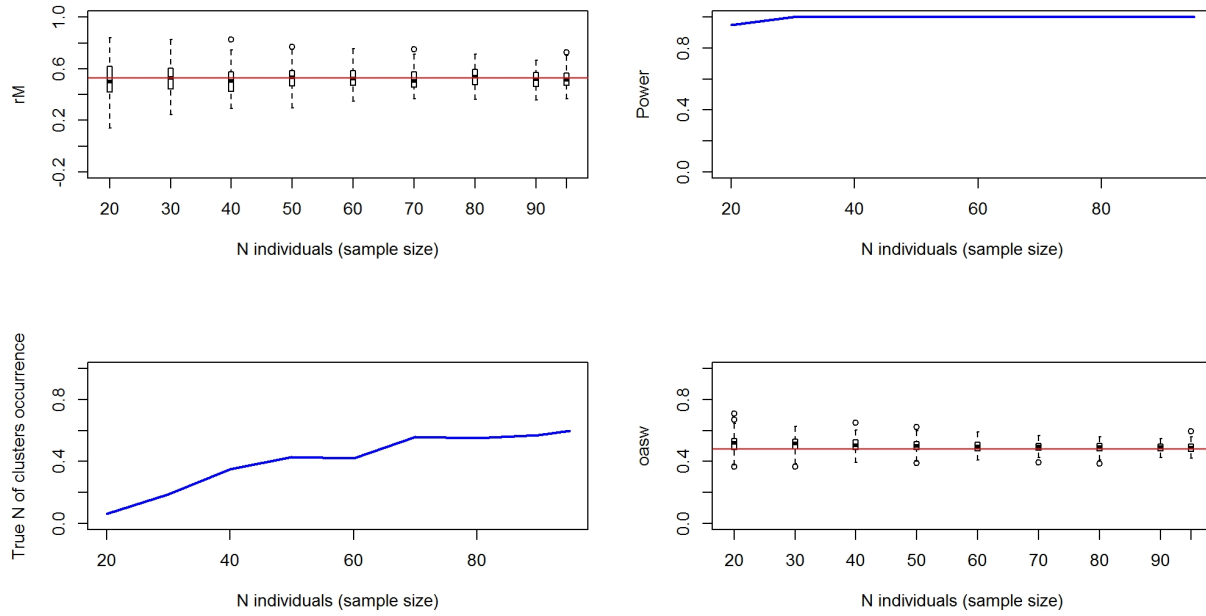


**Figure 16600-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

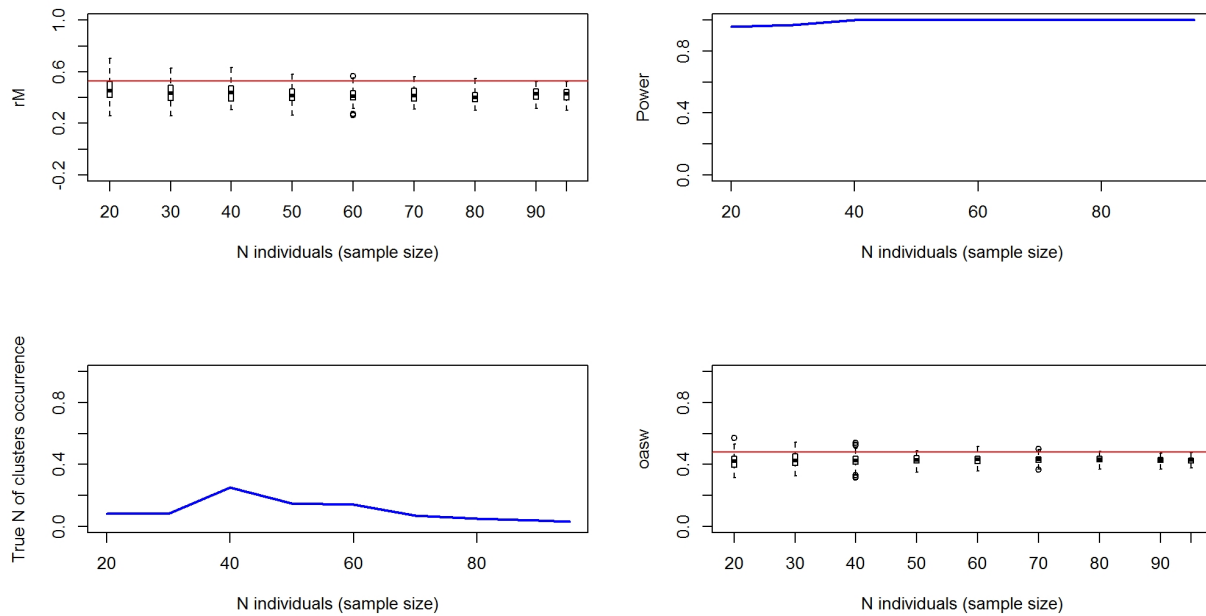
## 1.2 Sensitivity analysis

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 16600-2) and stratified sampling of individuals within the breeding range (Figure 16600-3) and the non breeding range (Figure 16600-4). 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.

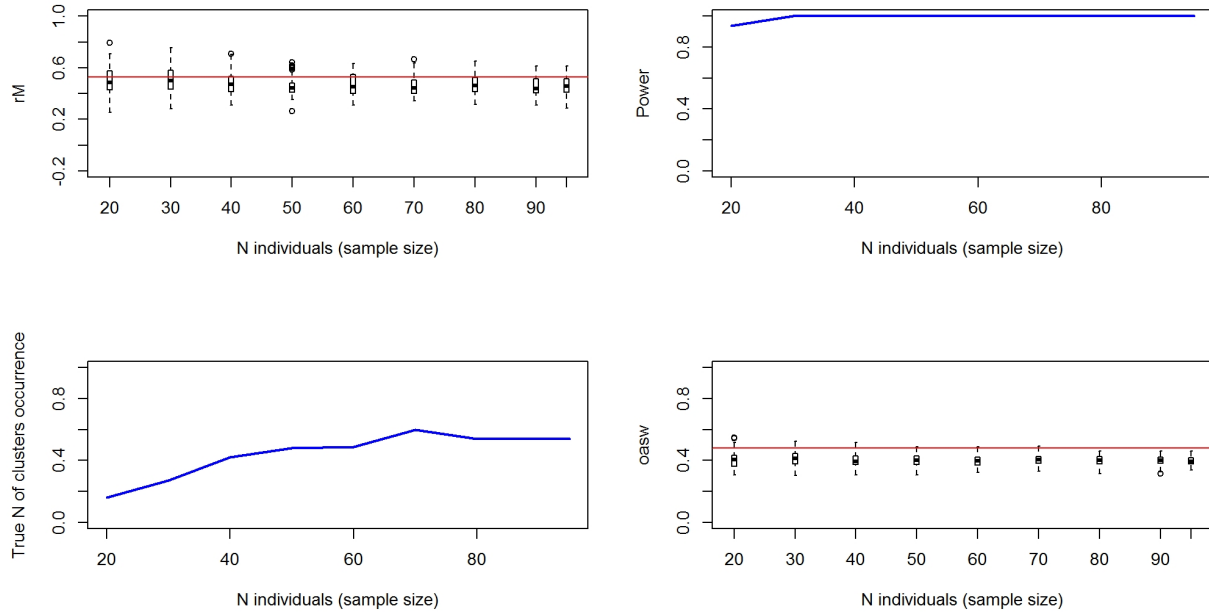


**Figure 16600-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



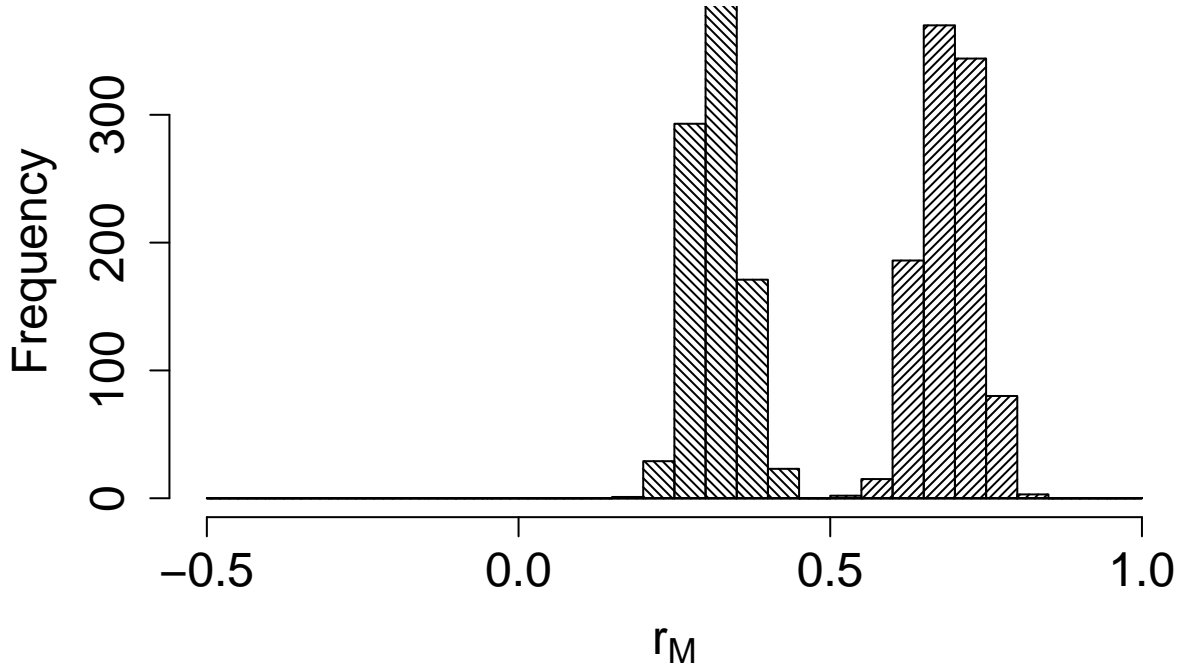
**Figure 16600-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 16600-4.** 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 16600-5).



**Figure 16600-5.** 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 high connectivity (MC = 0.914; MC = 0.914 when adjusted for absolute abundance) between 8 breeding regions and 8 non breeding regions (Table 16600-2; Figure 16600-6).

**Table 16600-2.** 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	2886130	Central Europe	0.119
Central Europe	2886130	South-central Europe	0.220
Central Europe	2886130	South-west Europe	0.534
Central Europe	2886130	West Europe	0.127
East Europe	3864227	Central Europe	0.400
East Europe	3864227	East Europe	0.200
East Europe	3864227	South-central Europe	0.400
North Europe	463600	Central Europe	0.048
North Europe	463600	South-central Europe	0.095
North Europe	463600	South-west Europe	0.548
North Europe	463600	West Europe	0.310
North-west Europe	1683513	North-west Europe	0.742
North-west Europe	1683513	South-west Europe	0.115

Breeding region	Abundance	Non breeding region	Transition probability
North-west Europe	1683513	West Europe	0.143
South-central Europe	1098569	South-central Europe	1.000
South-east Europe	14186000	South-east Europe	1.000
South-west Europe	23410897	South-west Europe	1.000
West Europe	1233718	North Africa	0.018
West Europe	1233718	North-west Europe	0.018
West Europe	1233718	South-west Europe	0.561
West Europe	1233718	West Europe	0.404



**Figure 16600-6.** 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>.