

# Migratory connectivity analysis

by EURING Migration Atlas

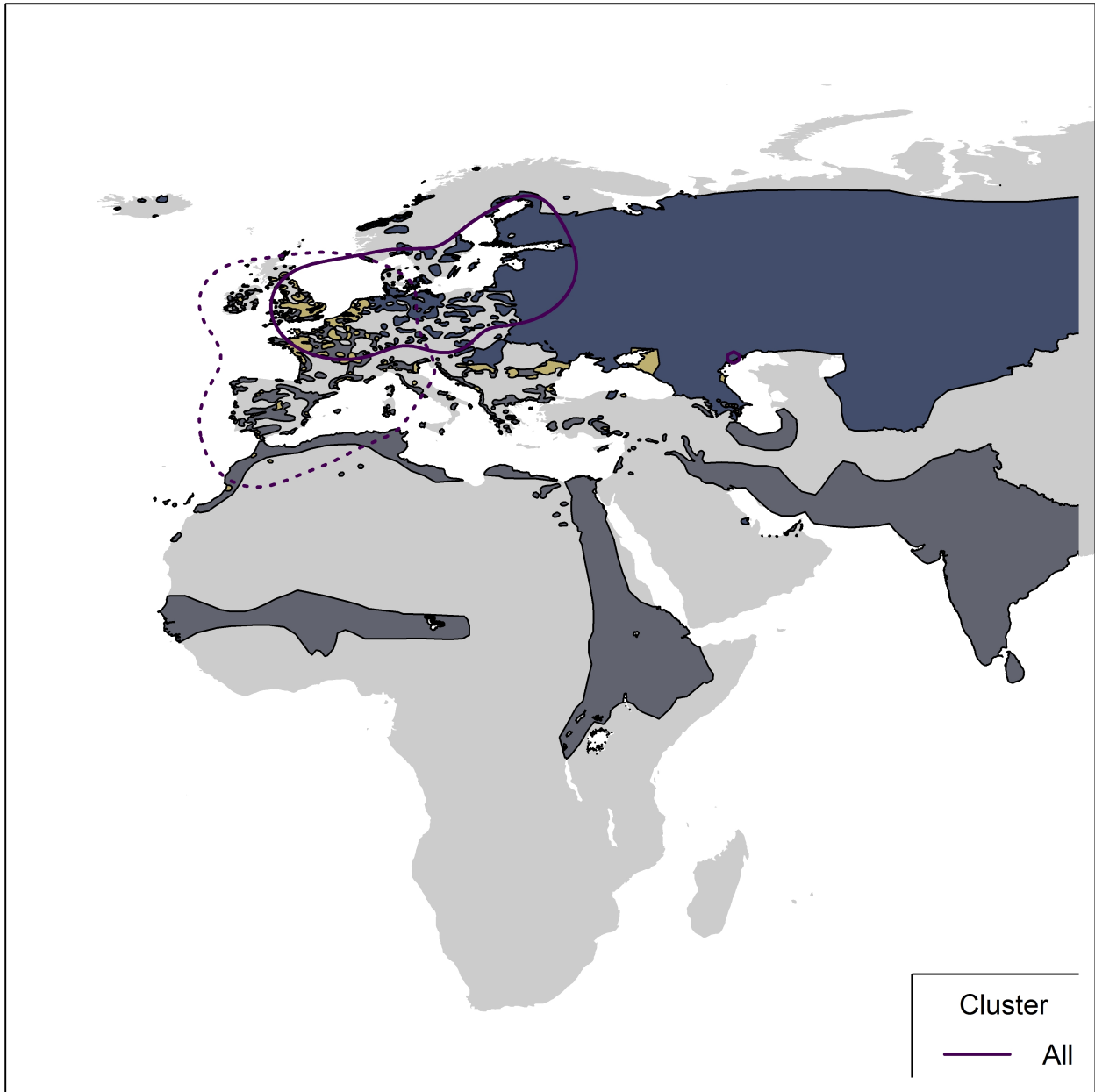
*Anas clypeata* (EURING code 01940)

## 1.1 Connectivity between individuals

The analysis evaluated 278 individuals (556 encounters) filtered from a total of 8612 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 01940-1; Figure 01940-1).

**Table 01940-1.** 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	278	0.342	0.001	0.207	0.471	4	0.392

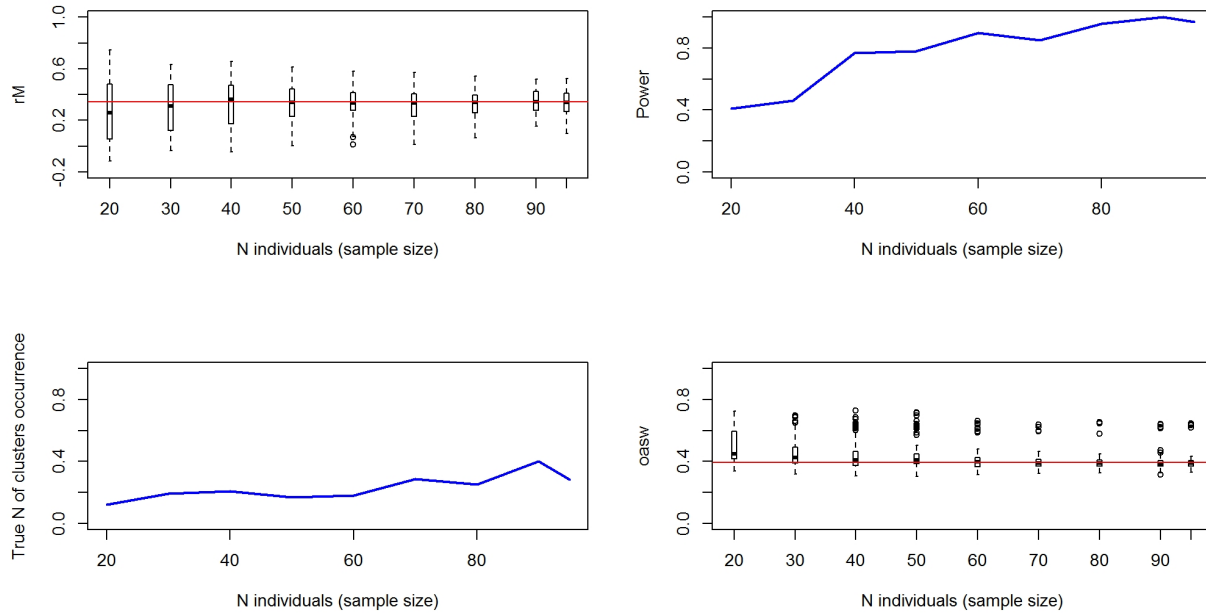


**Figure 01940-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

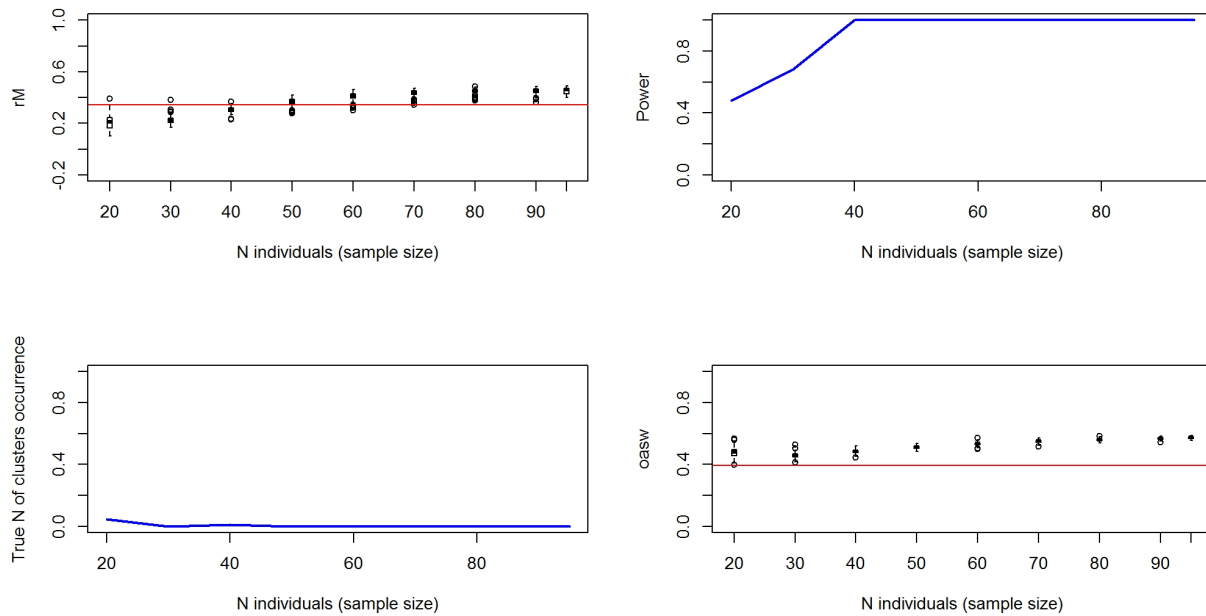
## 1.2 Sensitivity analysis

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 01940-2) and stratified sampling of individuals within the breeding range (Figure 01940-3) and the non breeding range (Figure 01940-4). 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.

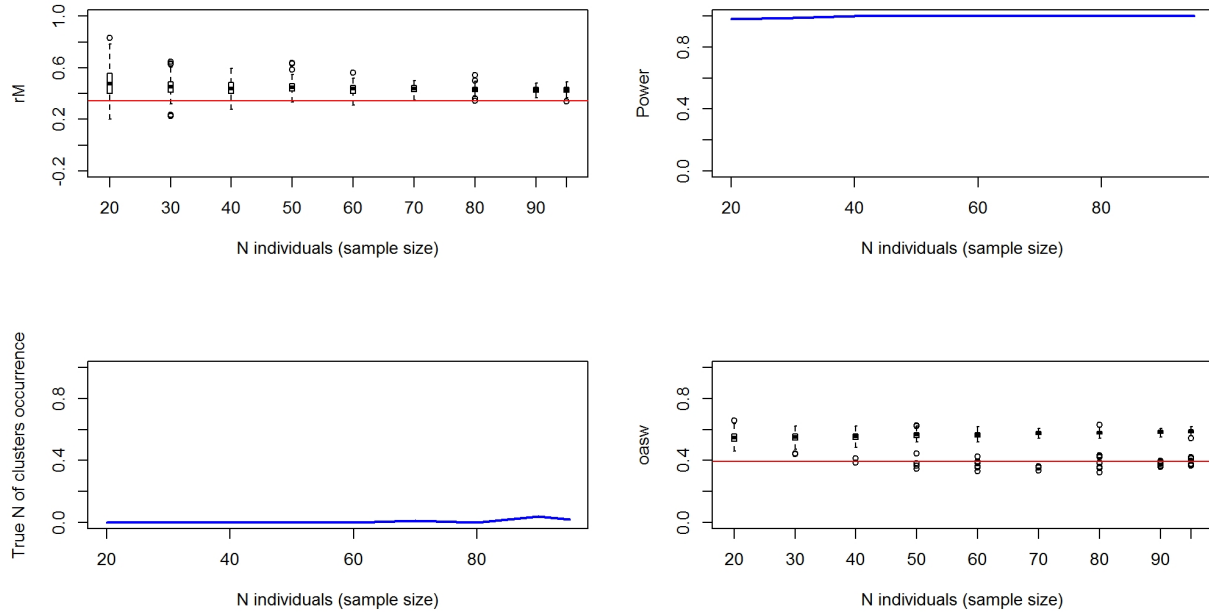


**Figure 01940-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



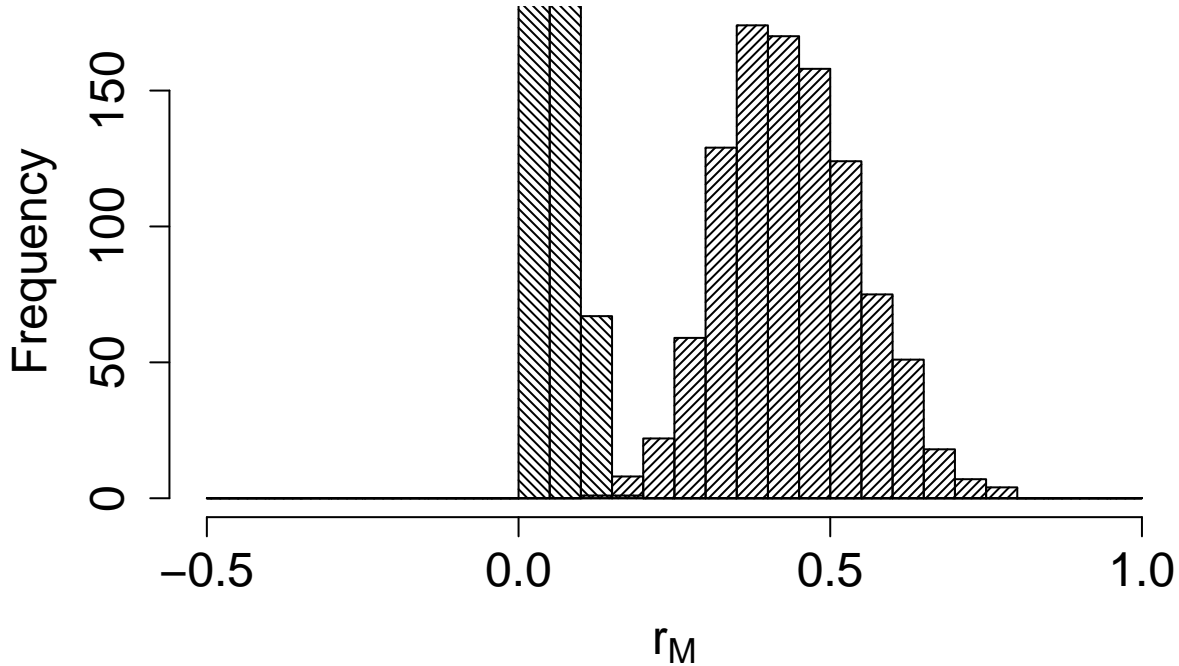
**Figure 01940-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 01940-4.** 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 ( $p = 0.002$ ); Figure 01940-5).



**Figure 01940-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

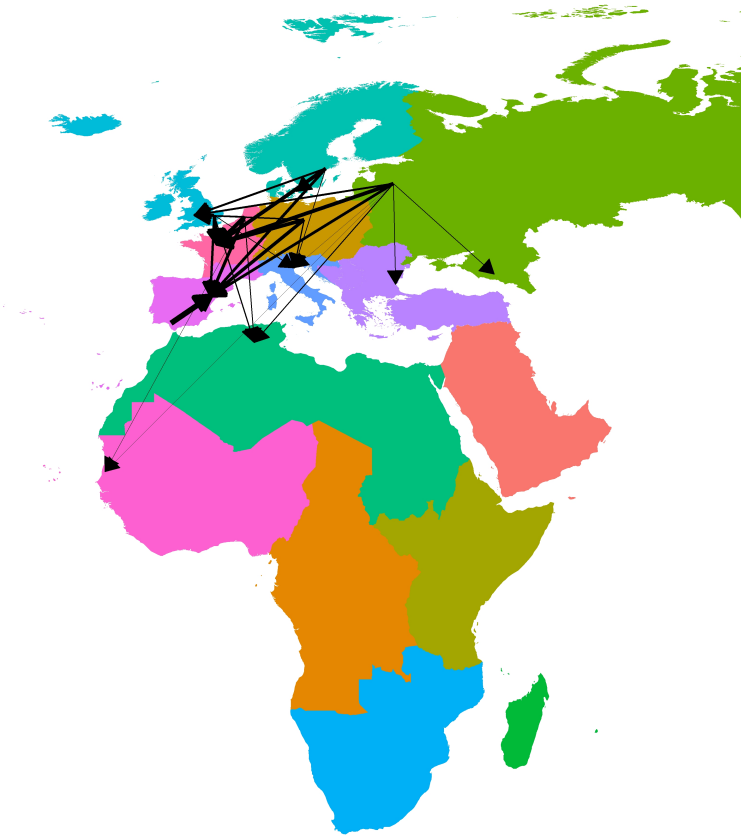
## 2. Connectivity between pre-defined regions

The species shows no connectivity ( $MC = -0.033$ ;  $MC = -0.034$  when adjusted for absolute abundance) between 6 breeding regions and 9 non breeding regions (Table 01940-2; Figure 01940-6).

**Table 01940-2.** 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	8190	North-west Europe	0.083
Central Europe	8190	South-central Europe	0.056
Central Europe	8190	South-west Europe	0.389
Central Europe	8190	West Europe	0.472
East Europe	336000	East Europe	0.024
East Europe	336000	North Africa	0.041
East Europe	336000	North-west Europe	0.122
East Europe	336000	South-central Europe	0.008
East Europe	336000	South-east Europe	0.024
East Europe	336000	South-west Europe	0.268
East Europe	336000	West Africa	0.008
East Europe	336000	West Europe	0.504
North Europe	35520	North Europe	0.056

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	35520	North-west Europe	0.167
North Europe	35520	South-central Europe	0.028
North Europe	35520	South-west Europe	0.278
North Europe	35520	West Europe	0.472
North-west Europe	1550	North Africa	0.062
North-west Europe	1550	North-west Europe	0.312
North-west Europe	1550	South-central Europe	0.031
North-west Europe	1550	South-west Europe	0.188
North-west Europe	1550	West Europe	0.406
South-west Europe	2386	South-west Europe	1.000
West Europe	16256	North Africa	0.040
West Europe	16256	North-west Europe	0.080
West Europe	16256	South-west Europe	0.340
West Europe	16256	West Africa	0.020
West Europe	16256	West Europe	0.520



**Figure 01940-6.** 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>.