

# Migratory connectivity analysis

by EURING Migration Atlas

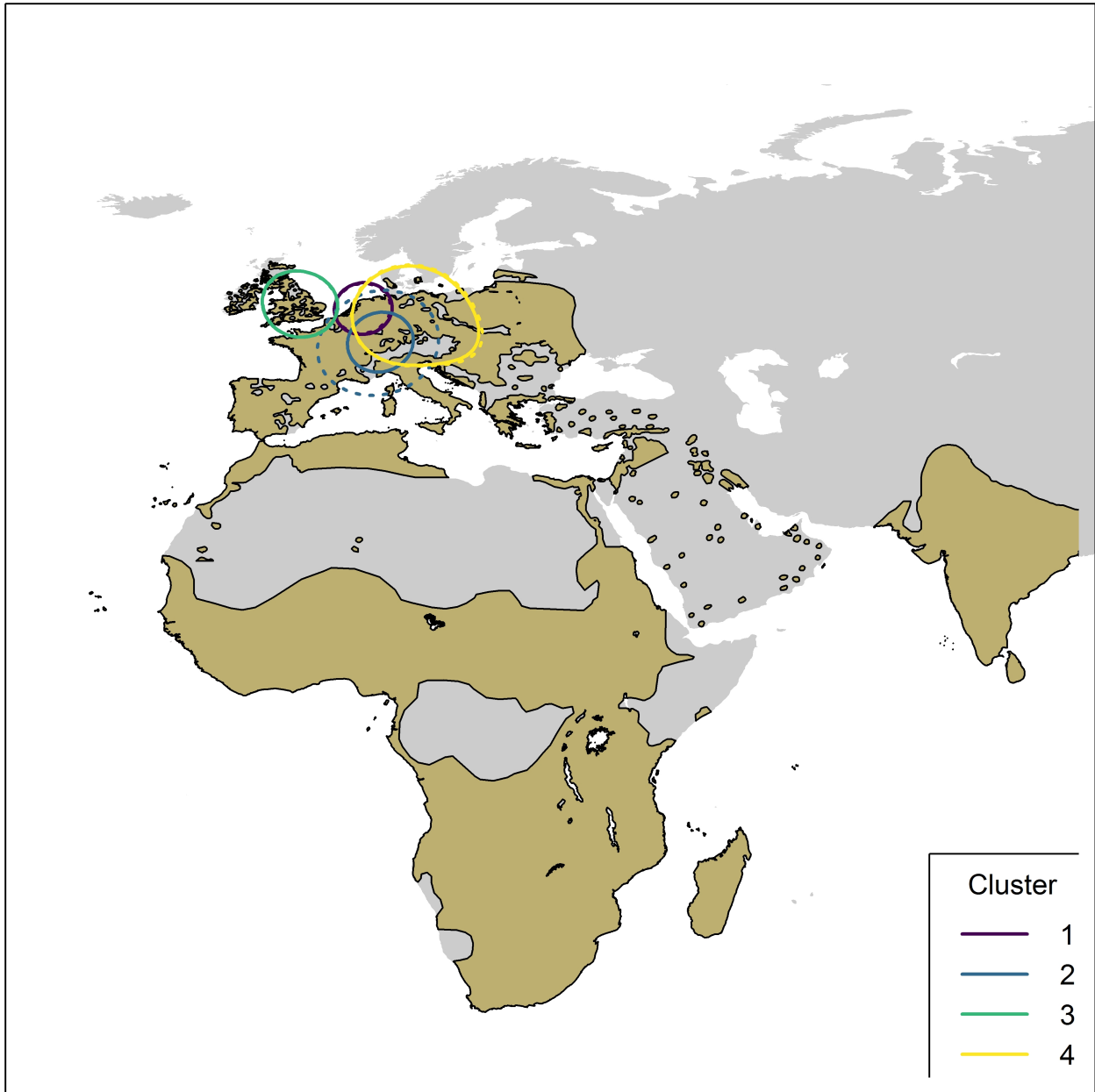
*Tyto alba* (EURING code 07350)

## 1.1 Connectivity between individuals

The analysis evaluated 15676 individuals (31352 encounters) filtered from a total of 212929 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from clustering, with a number of first-level clusters = 4 (Table 07350-1; Figure 07350-1).

**Table 07350-1.** 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	15676	0.932	0.001	0.921	0.941	4	0.510
1	1	6953	0.784	0.001	0.759	0.807	2	0.452
2	1	3023	0.815	0.001	0.730	0.875	2	0.393
3	1	3016	0.970	0.001	0.961	0.977	2	0.446
4	1	2684	0.902	0.001	0.858	0.930	2	0.616
41	2	2245	0.602	0.001	0.552	0.654	4	0.444
42	2	439	0.934	0.001	0.867	0.963	3	0.509
421	3	271	0.713	0.001	0.590	0.810	4	0.452
422	3	160	0.728	0.001	0.618	0.819	2	0.541
423	3	8	-	-	-	-	-	-

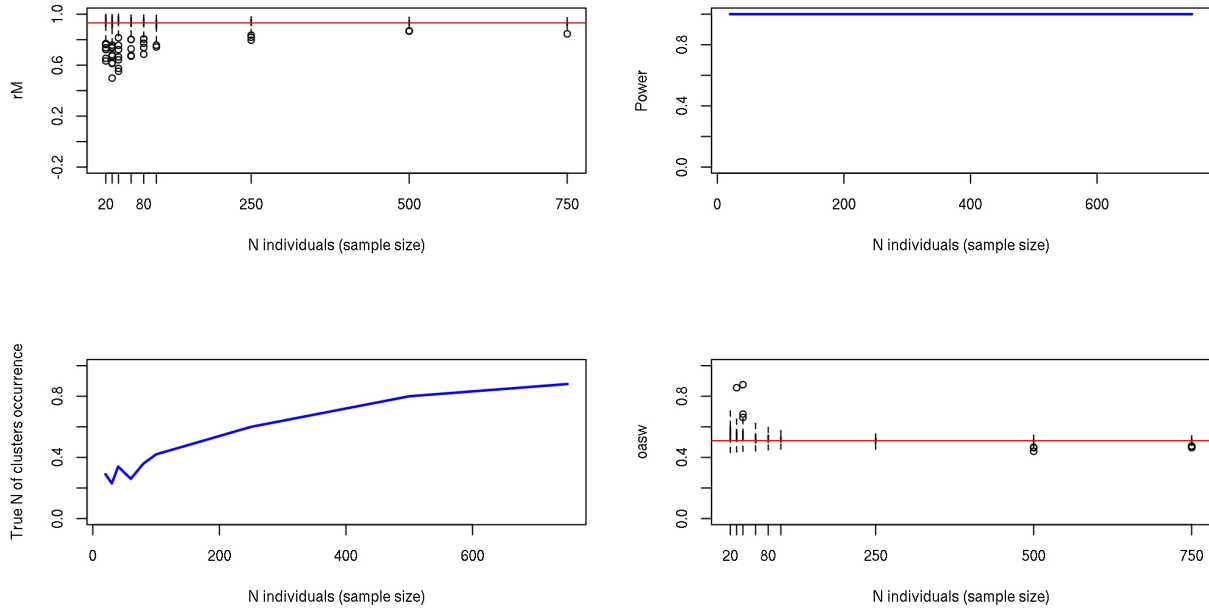


**Figure 07350-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

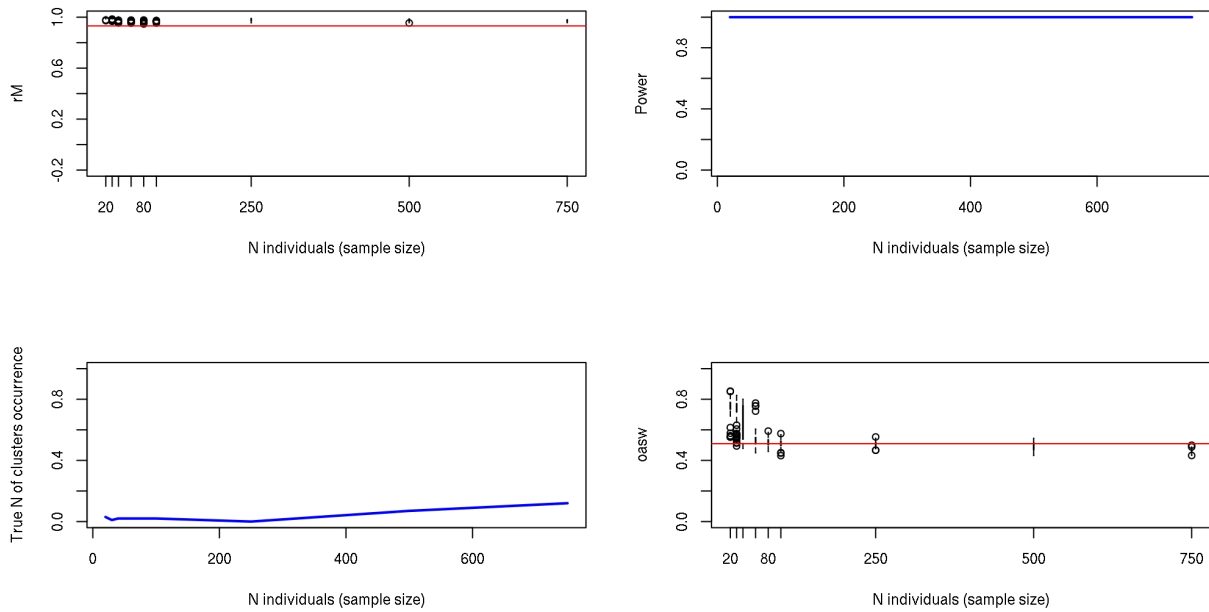
## 1.2 Sensitivity analysis

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 07350-2) and stratified sampling of individuals within the breeding range (Figure 07350-3) and the non breeding range (Figure 07350-4). 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.

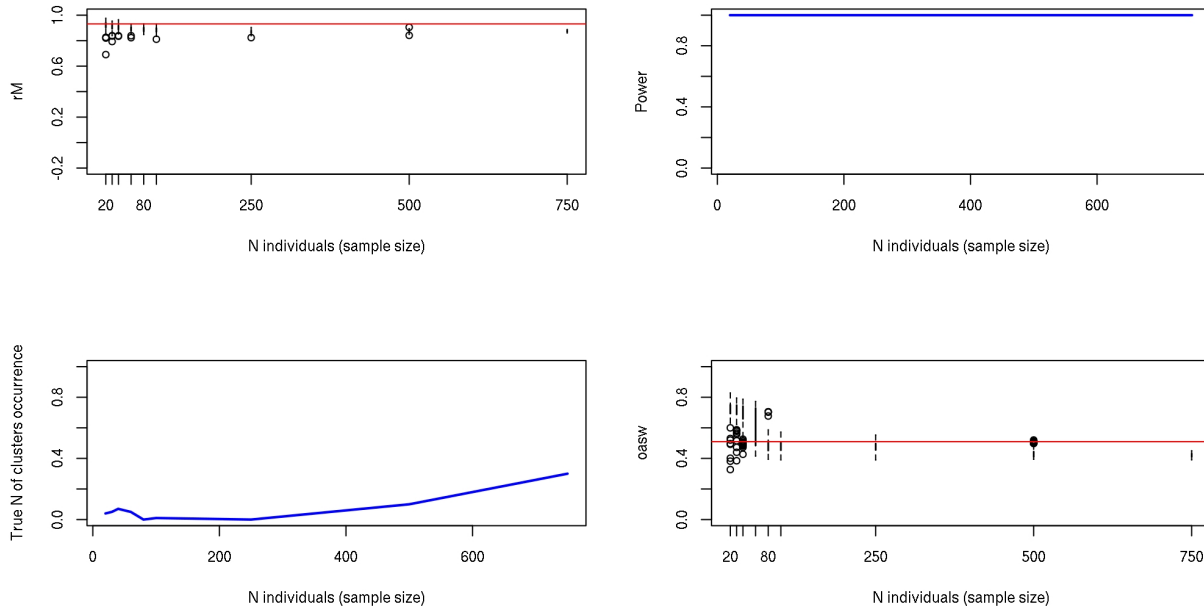


**Figure 07350-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



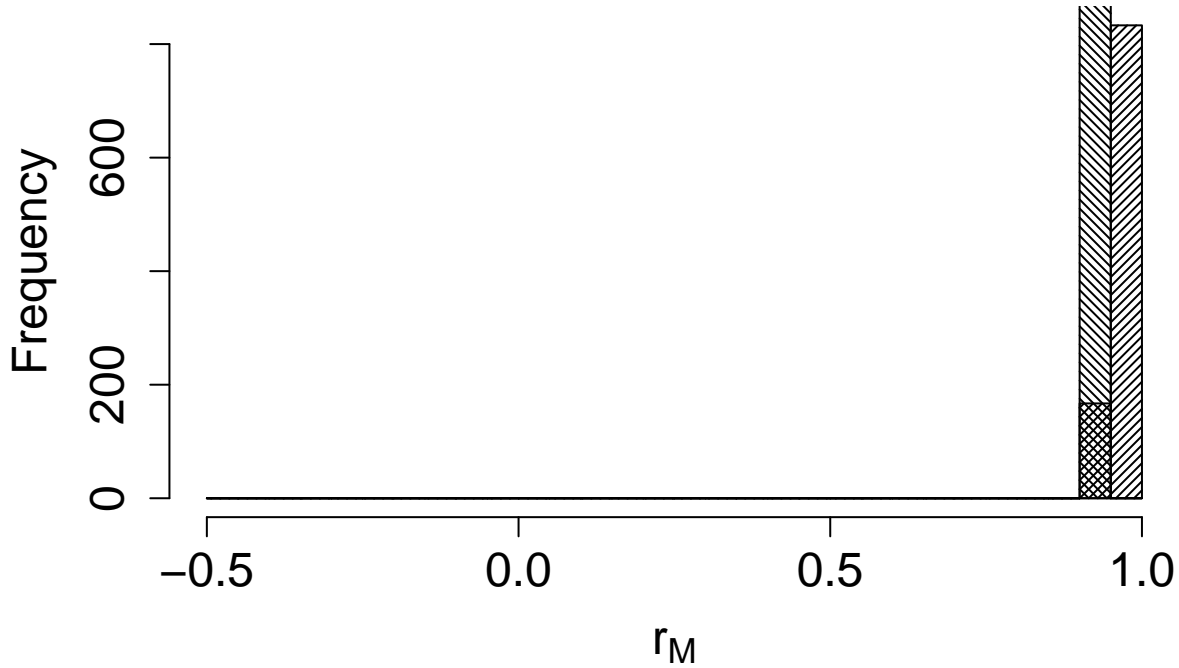
**Figure 07350-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 07350-4.** 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 ( $p = 0.167$ ); Figure 07350-5).



**Figure 07350-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

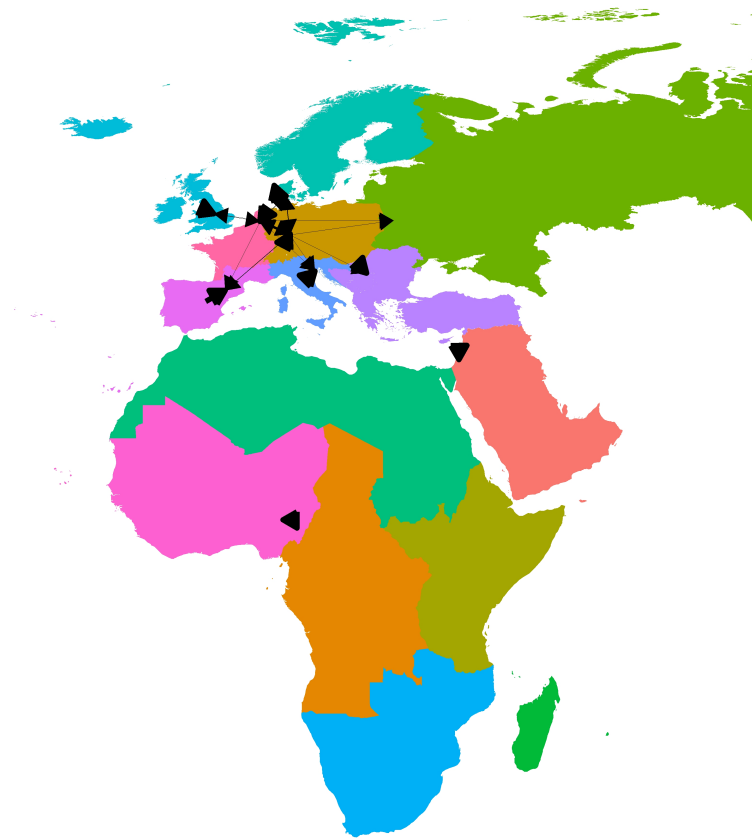
## 2. Connectivity between pre-defined regions

The species shows high connectivity (MC = 0.978; MC = 0.978 when adjusted for absolute abundance) between 9 breeding regions and 10 non breeding regions (Table 07350-2; Figure 07350-6).

**Table 07350-2.** 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
Arabian peninsula	1000	Arabian peninsula	1.000
Central Europe	55071	Central Europe	0.915
Central Europe	55071	East Europe	0.001
Central Europe	55071	North Europe	0.001
Central Europe	55071	South-central Europe	0.004
Central Europe	55071	South-east Europe	0.001
Central Europe	55071	South-west Europe	0.009
Central Europe	55071	West Europe	0.070
North Europe	130	Central Europe	0.026
North Europe	130	North Europe	0.966
North Europe	130	West Europe	0.009
North-west Europe	8900	North-west Europe	1.000
North-west Europe	8900	West Europe	0.000

Breeding region	Abundance	Non breeding region	Transition probability
South-central Europe	24121	South-central Europe	1.000
South-east Europe	27056	South-east Europe	1.000
South-west Europe	171845	South-west Europe	1.000
West Africa	1000	West Africa	1.000
West Europe	52695	Central Europe	0.040
West Europe	52695	East Europe	0.000
West Europe	52695	North Europe	0.000
West Europe	52695	North-west Europe	0.000
West Europe	52695	South-central Europe	0.000
West Europe	52695	South-west Europe	0.006
West Europe	52695	West Europe	0.953



**Figure 07350-6.** 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>.