

# Migratory connectivity analysis

by EURING Migration Atlas

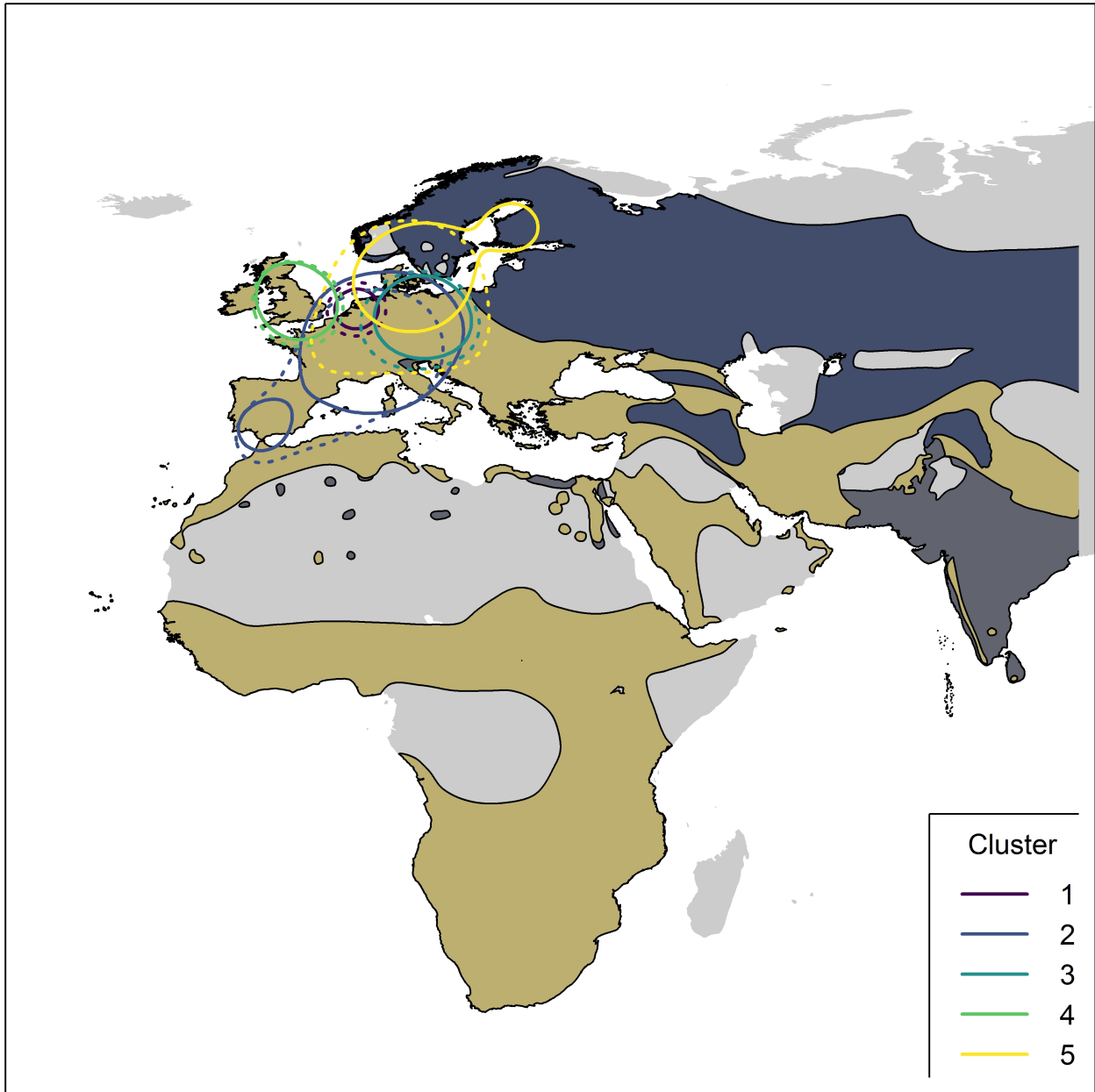
*Falco tinnunculus* (EURING code 03040)

## 1.1 Connectivity between individuals

The analysis evaluated 7662 individuals (15324 encounters) filtered from a total of 151060 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 = 5 (Table 03040-1; Figure 03040-1).

**Table 03040-1.** 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	7662	0.678	0.001	0.646	0.710	5	0.519
1	1	4079	0.736	0.001	0.648	0.801	2	0.441
2	1	946	0.640	0.001	0.585	0.692	3	0.692
3	1	1186	0.832	0.001	0.784	0.867	2	0.383
4	1	875	0.615	0.001	0.536	0.688	2	0.401
5	1	576	0.600	0.001	0.547	0.651	2	0.620
21	2	741	0.693	0.001	0.623	0.754	9	0.477
22	2	138	0.314	0.001	0.114	0.491	2	0.705
23	2	67	0.848	0.001	0.697	0.954	2	0.613
51	2	130	-0.014	0.575	-0.075	0.098	-	-
52	2	446	0.215	0.001	0.166	0.276	6	0.377
221	3	131	0.055	0.116	-0.006	0.167	-	-
222	3	7	-	-	-	-	-	-
231	3	16	-	-	-	-	-	-
232	3	51	0.764	0.001	0.176	0.931	5	0.549

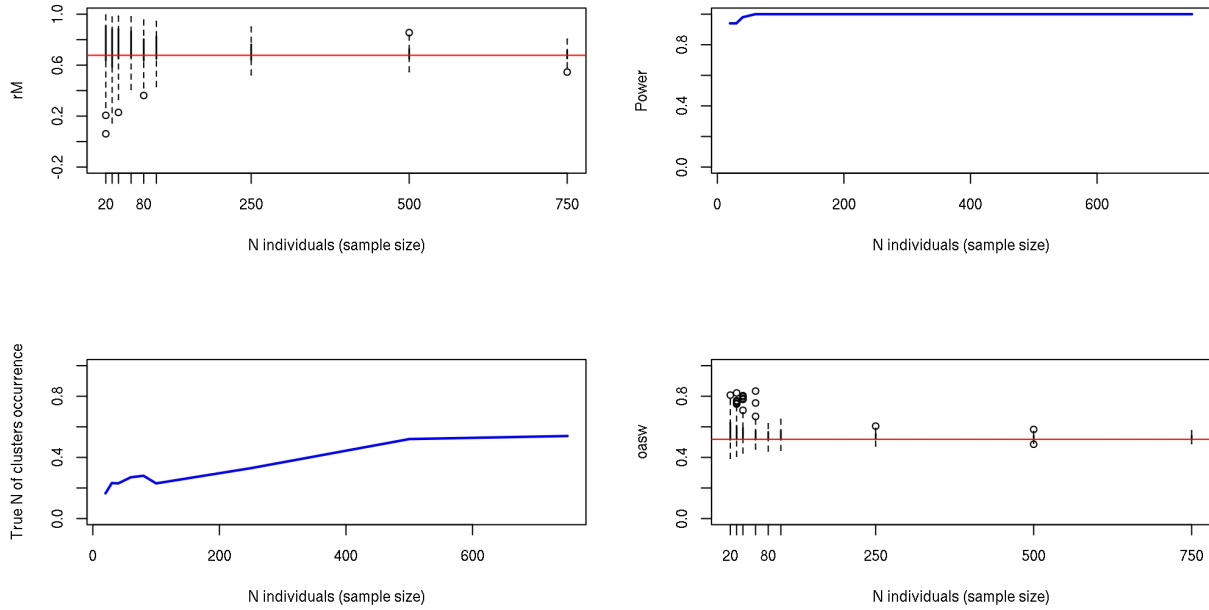


**Figure 03040-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

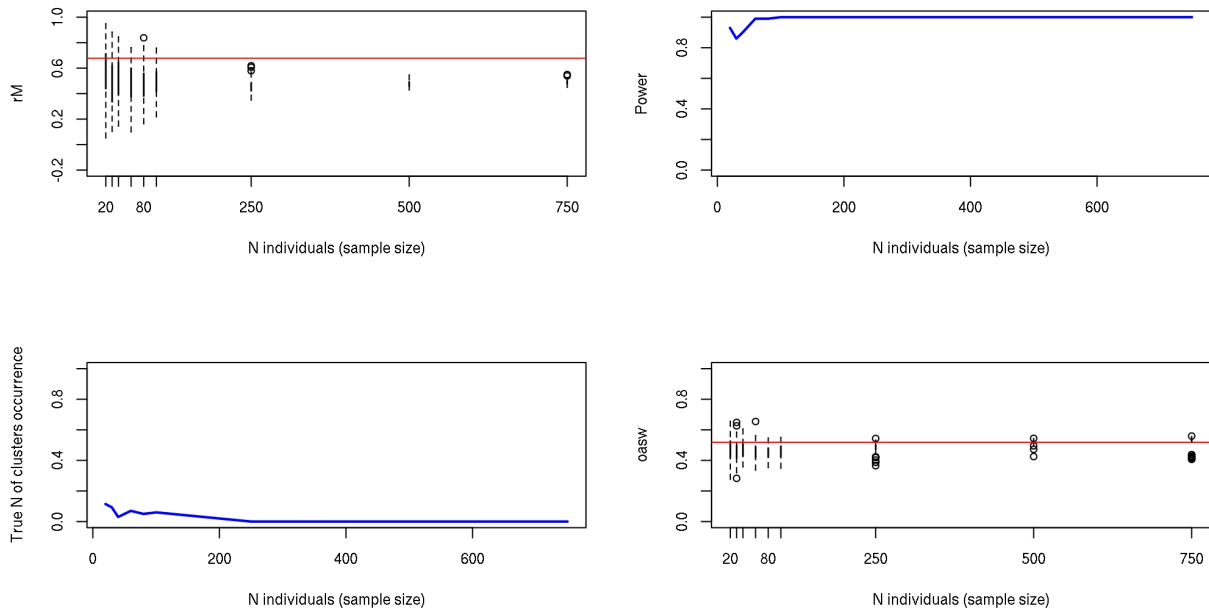
**1.2 Sensitivity analysis**

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 03040-2) and stratified sampling of individuals within the breeding range (Figure 03040-3) and the non breeding range (Figure 03040-4). 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.

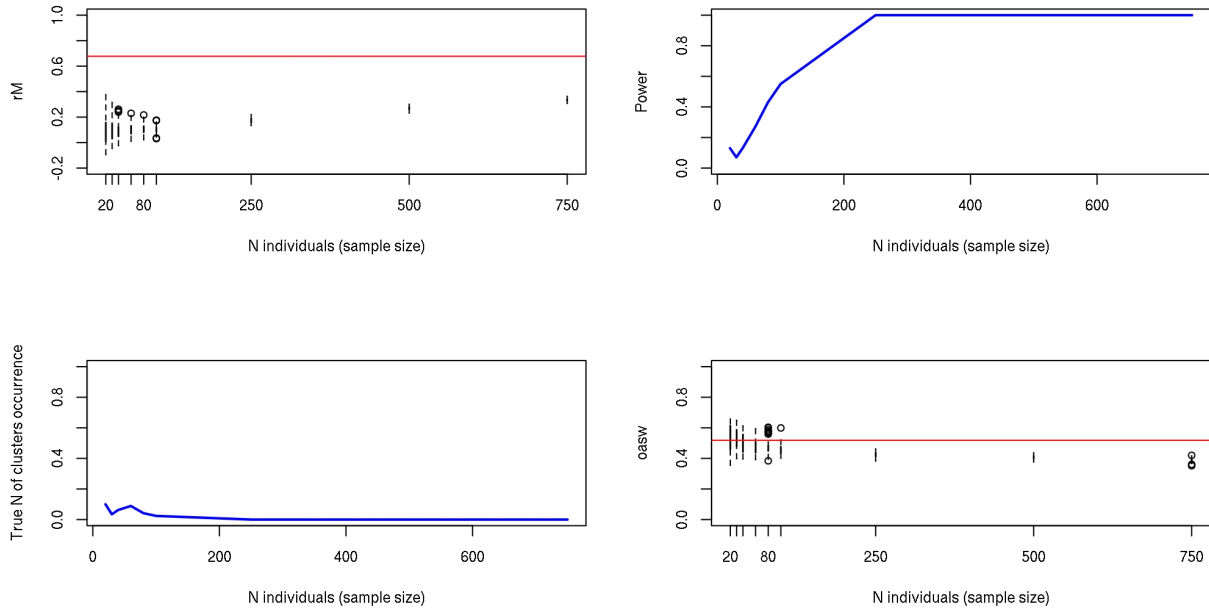


**Figure 03040-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



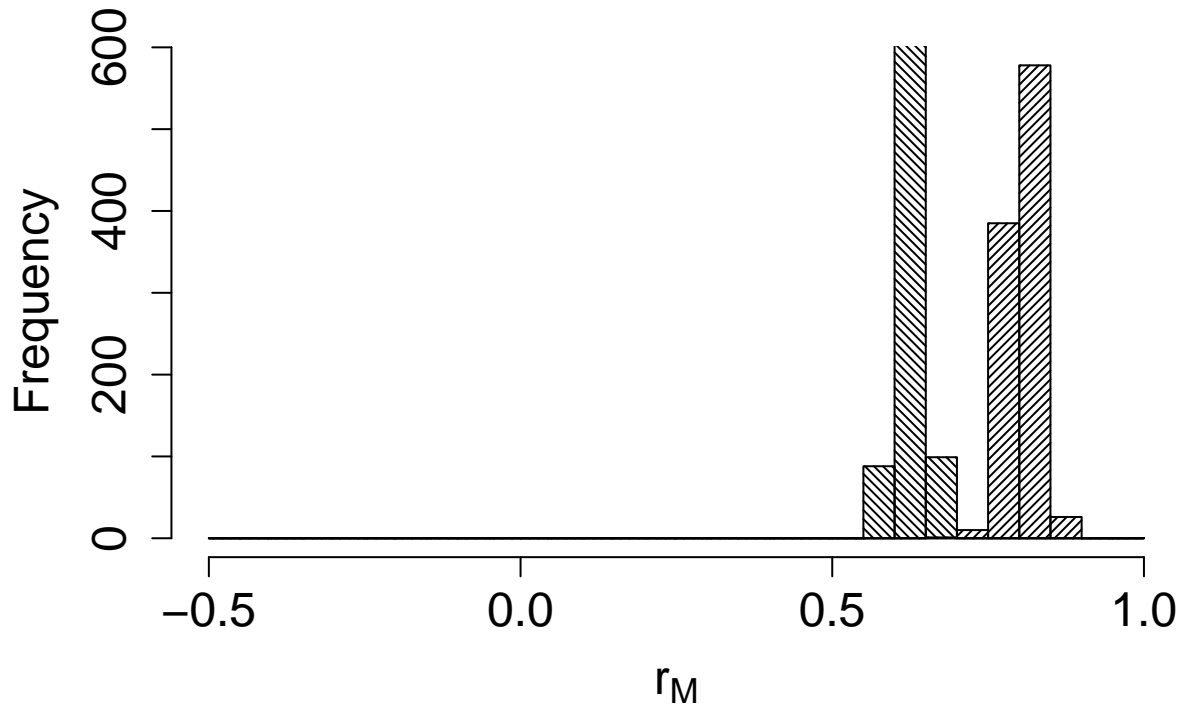
**Figure 03040-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 03040-4.** 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 03040-5).



**Figure 03040-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

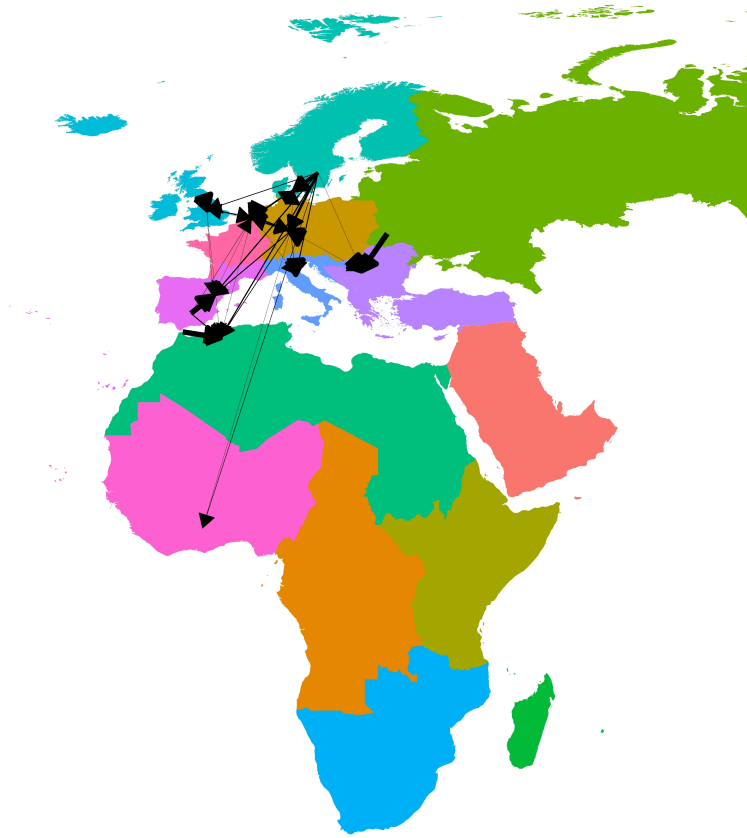
## 2. Connectivity between pre-defined regions

The species shows high connectivity (MC = 0.847; MC = 0.847 when adjusted for absolute abundance) between 9 breeding regions and 9 non breeding regions (Table 03040-2; Figure 03040-6).

**Table 03040-2.** 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	203200	Central Europe	0.870
Central Europe	203200	North Africa	0.018
Central Europe	203200	North Europe	0.006
Central Europe	203200	South-central Europe	0.014
Central Europe	203200	South-east Europe	0.001
Central Europe	203200	South-west Europe	0.034
Central Europe	203200	West Africa	0.001
Central Europe	203200	West Europe	0.056
East Europe	153881	South-east Europe	1.000
North Africa	7400	North Africa	1.000
North Europe	38300	Central Europe	0.229
North Europe	38300	North Africa	0.049
North Europe	38300	North Europe	0.503

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	38300	North-west Europe	0.017
North Europe	38300	South-central Europe	0.030
North Europe	38300	South-east Europe	0.007
North Europe	38300	South-west Europe	0.058
North Europe	38300	West Africa	0.009
North Europe	38300	West Europe	0.098
North-west Europe	146540	Central Europe	0.001
North-west Europe	146540	North Africa	0.001
North-west Europe	146540	North-west Europe	0.952
North-west Europe	146540	South-west Europe	0.005
North-west Europe	146540	West Europe	0.041
South-central Europe	46250	South-central Europe	1.000
South-east Europe	152900	South-east Europe	1.000
South-west Europe	119328	North Africa	0.042
South-west Europe	119328	South-west Europe	0.944
South-west Europe	119328	West Europe	0.014
West Europe	141116	Central Europe	0.045
West Europe	141116	North Africa	0.003
West Europe	141116	North Europe	0.001
West Europe	141116	North-west Europe	0.003
West Europe	141116	South-central Europe	0.000
West Europe	141116	South-west Europe	0.005
West Europe	141116	West Europe	0.943



**Figure 03040-6.** 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>.