Migratory connectivity analysis
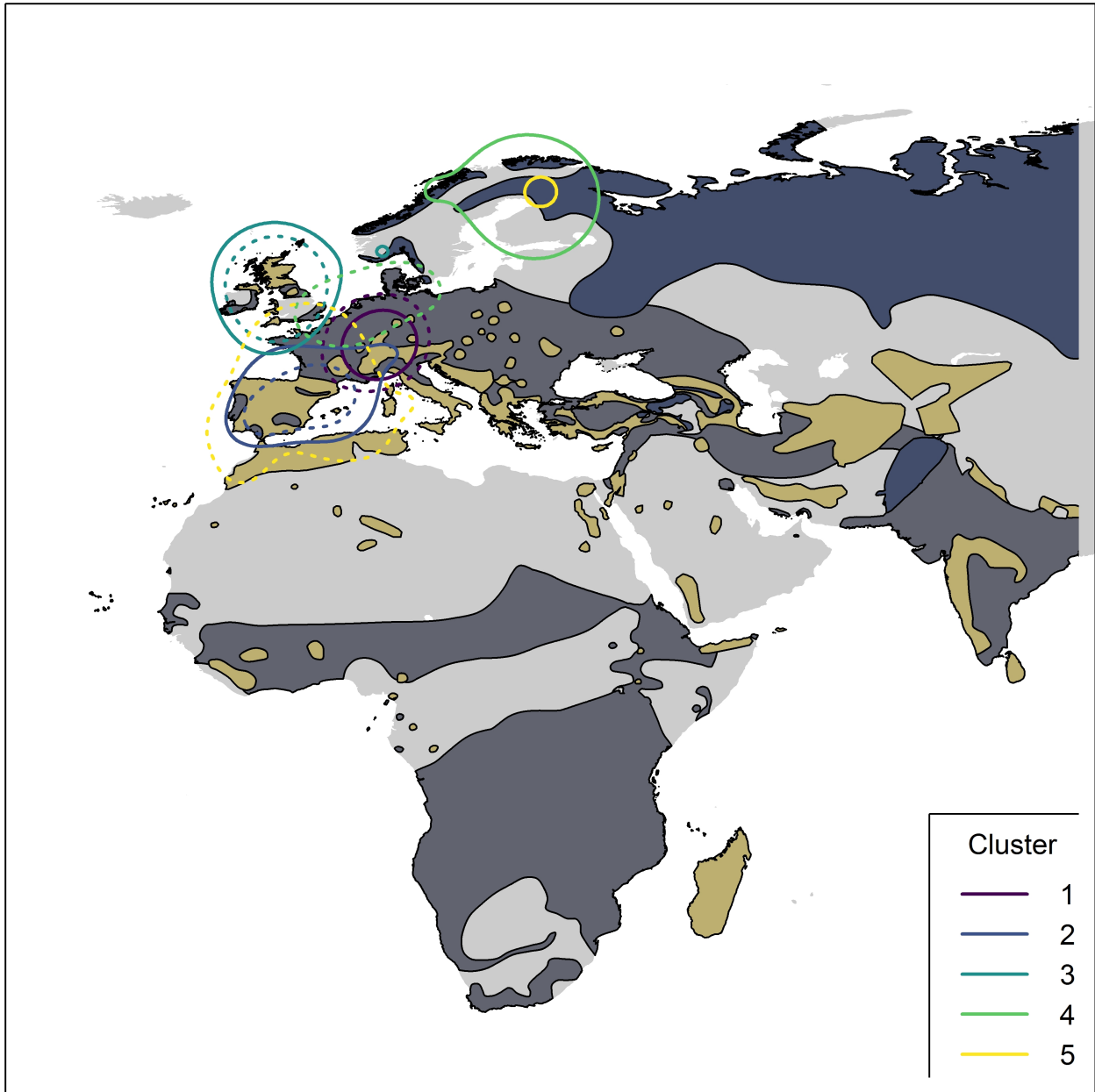
by EURING Migration Atlas

Falco peregrinus **(EURING code 03200)**

1.1 Connectivity between individuals

The analysis evaluated 238 individuals (476 encounters) filtered from a total of 17112 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 03200-1; Figure 03200-1).

Table 03200-1. 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	238	0.321	0.001	0.240	0.440	5	0.609
1	1	58	0.678	0.001	0.370	0.859	9	0.391
2	1	15	-	-	-	-	-	-
3	1	92	0.688	0.001	0.570	0.843	3	0.623
4	1	51	-0.072	0.851	-0.114	0.124	-	-
5	1	22	0.229	0.111	-0.130	0.605	-	-
31	2	71	0.641	0.001	0.528	0.807	2	0.338
32	2	13	-	-	-	-	-	-
33	2	8	-	-	-	-	-	-

Figure 03200-1. 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 03200-2) and stratified sampling of individuals within the breeding range (Figure 03200-3) and the non breeding range (Figure 03200-4). 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.
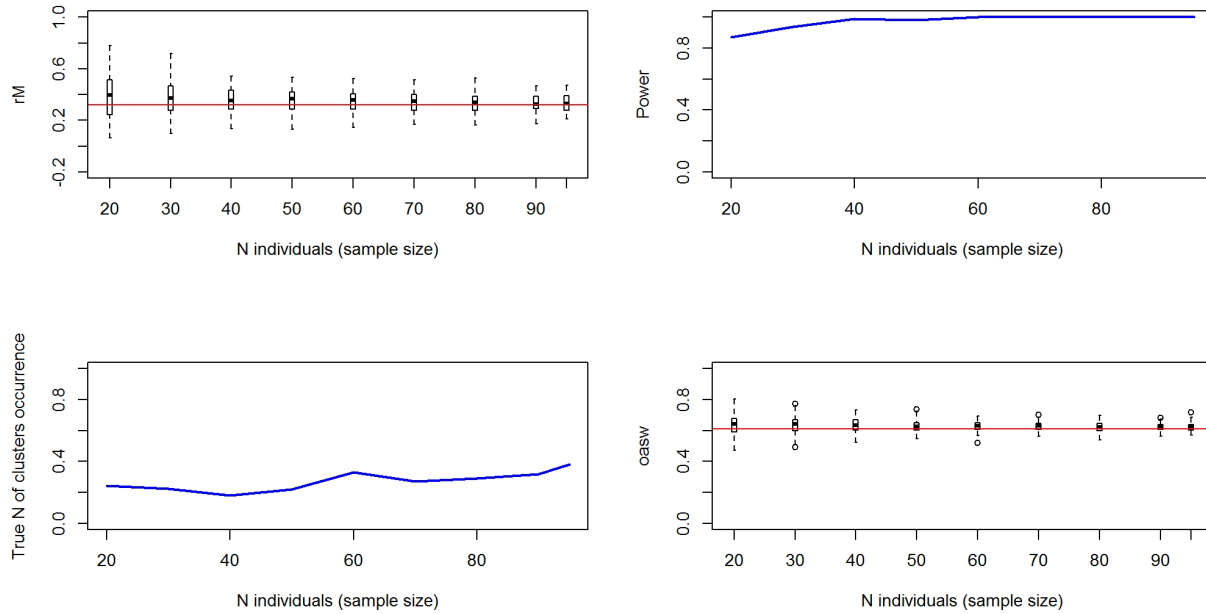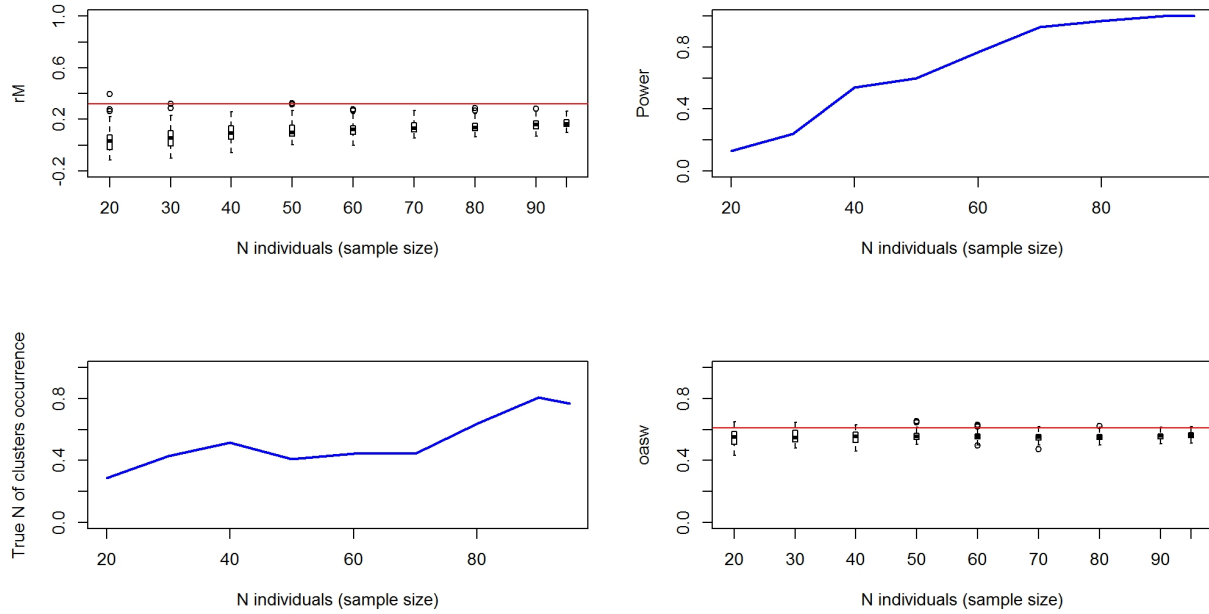

Figure 03200-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.
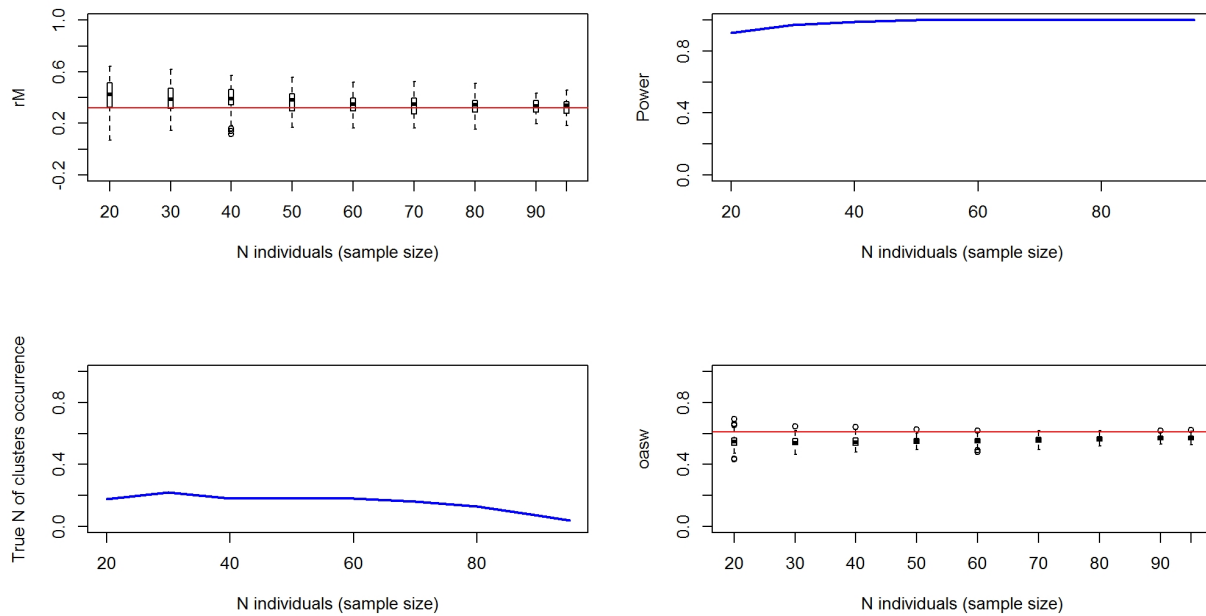
Figure 03200-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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


Figure 03200-4. 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 = 0.748); Figure 03200-5).
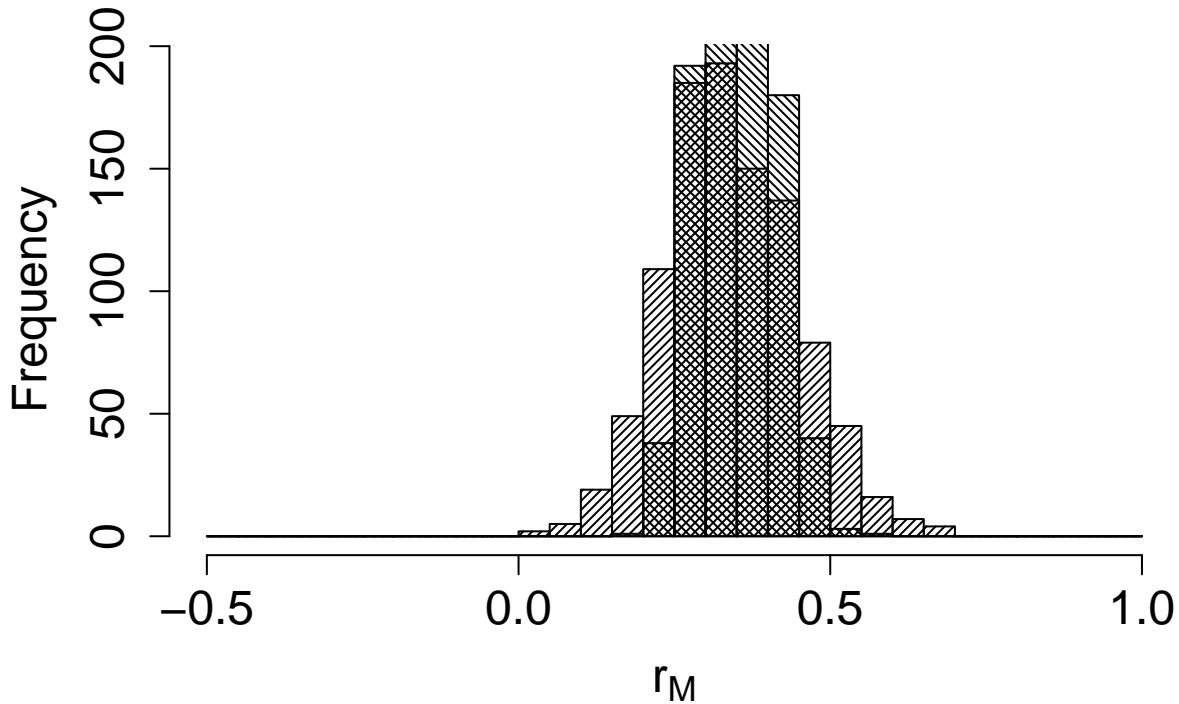
Figure 03200-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows moderate connectivity (MC = 0.434; MC = 0.429 when adjusted for absolute abundance) between 6 breeding regions and 8 non breeding regions (Table 03200-2; Figure 03200-6).

Table 03200-2. 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	3864	Central Europe	0.649
Central Europe	3864	South-west Europe	0.088
Central Europe	3864	West Europe	0.263
North Europe	2976	Central Europe	0.111
North Europe	2976	North Africa	0.037
North Europe	2976	North Europe	0.160
North Europe	2976	North-west Europe	0.160
North Europe	2976	South-central Europe	0.012
North Europe	2976	South-west Europe	0.123
North Europe	2976	West Africa	0.012
North Europe	2976	West Europe	0.383
North-west Europe	4030	North-west Europe	0.988
North-west Europe	4030	West Europe	0.012

Breeding region	Abundance	Non breeding region	Transition probability
South-central Europe	3060	South-central Europe	0.500
South-central Europe	3060	South-west Europe	0.500
South-west Europe	7201	South-west Europe	0.923
South-west Europe	7201	West Europe	0.077
West Europe	1268	West Europe	1.000
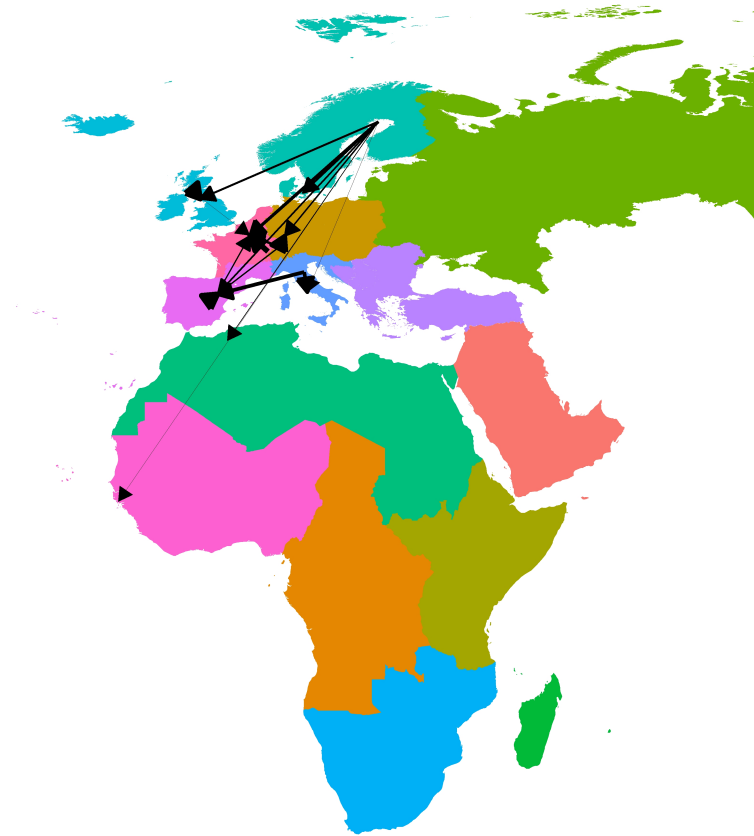
Figure 03200-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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.