# Migratory connectivity analysis

## by EURING Migration Atlas

### ***Pandion haliaetus*** **(EURING code 03010)**

## 1.1 Connectivity between individuals

The analysis evaluated 369 individuals (738 encounters) filtered from a total of 24680 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 03010-1; Figure 03010-1).

**Table 03010-1.** 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 | 369 | 0.285 | 0.001 | 0.221 | 0.35 | 4 | 0.476 |

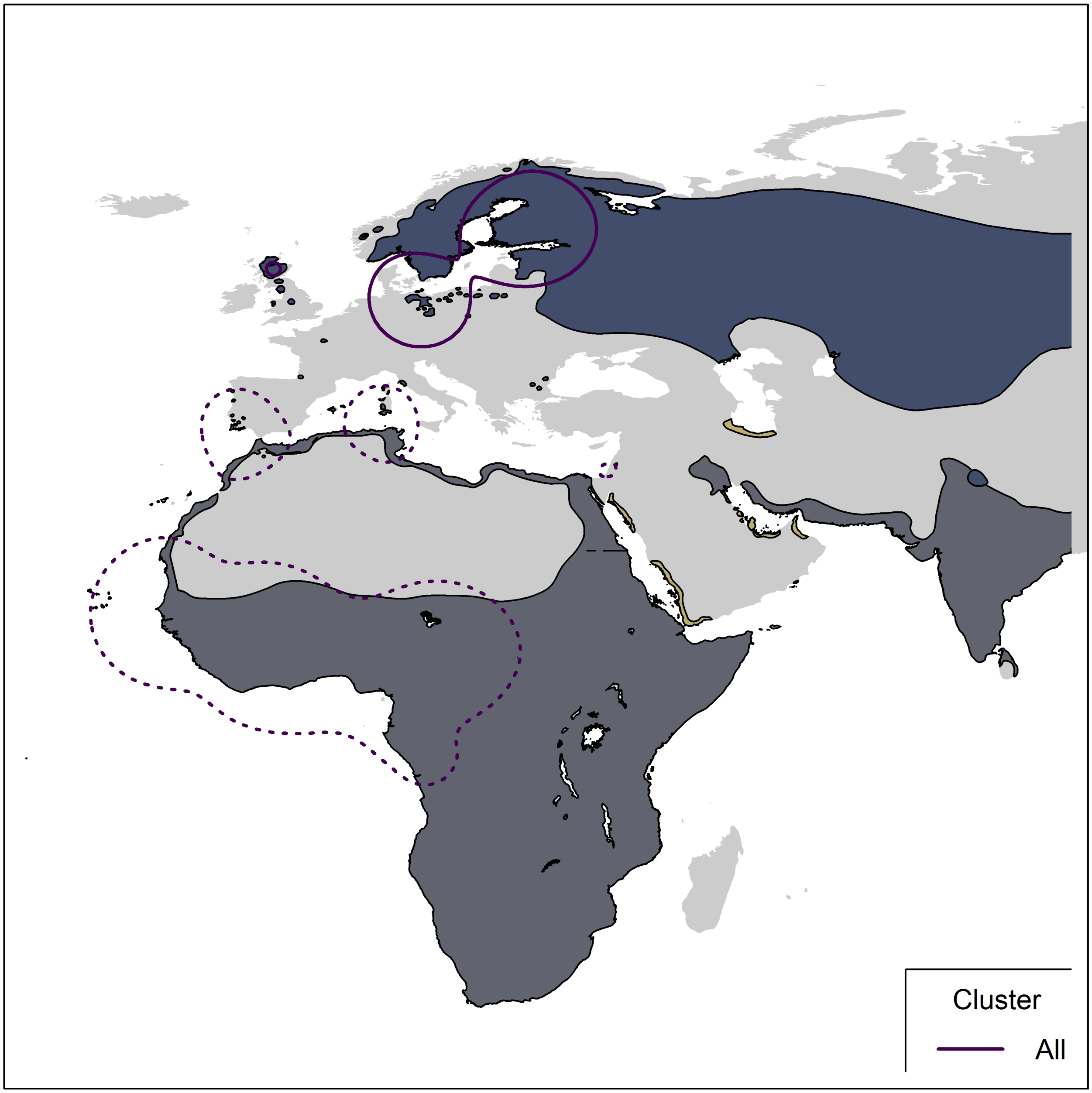

**Figure 03010-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 03010-2) and stratified sampling of individuals within the breeding range (Figure 03010-3) and the non breeding range (Figure 03010-4). 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.

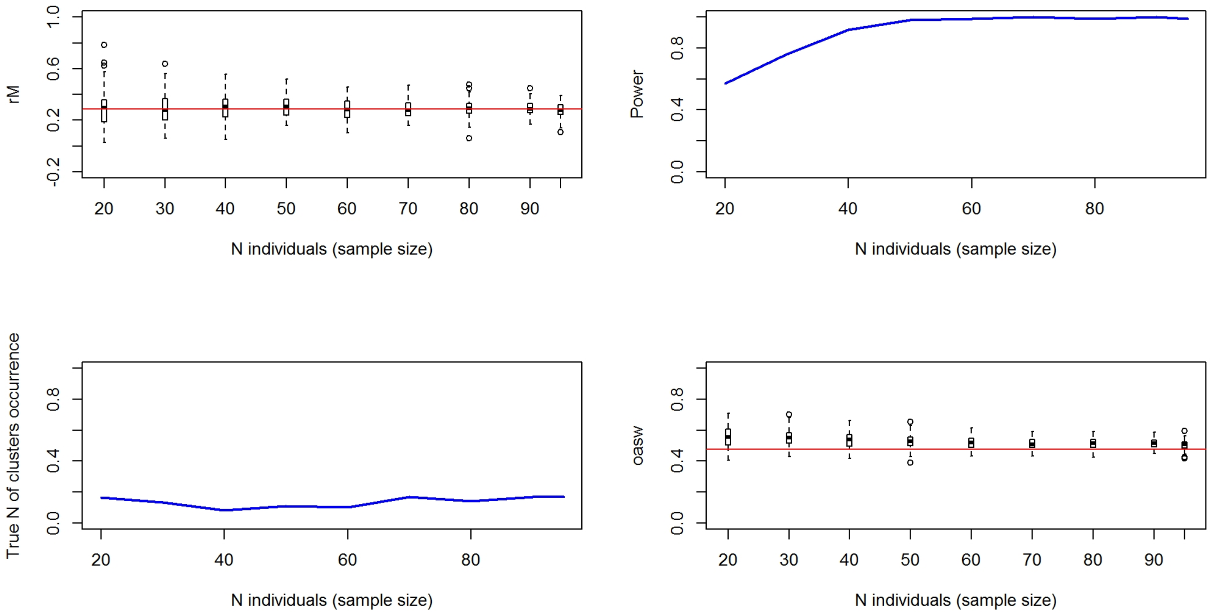

**Figure 03010-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

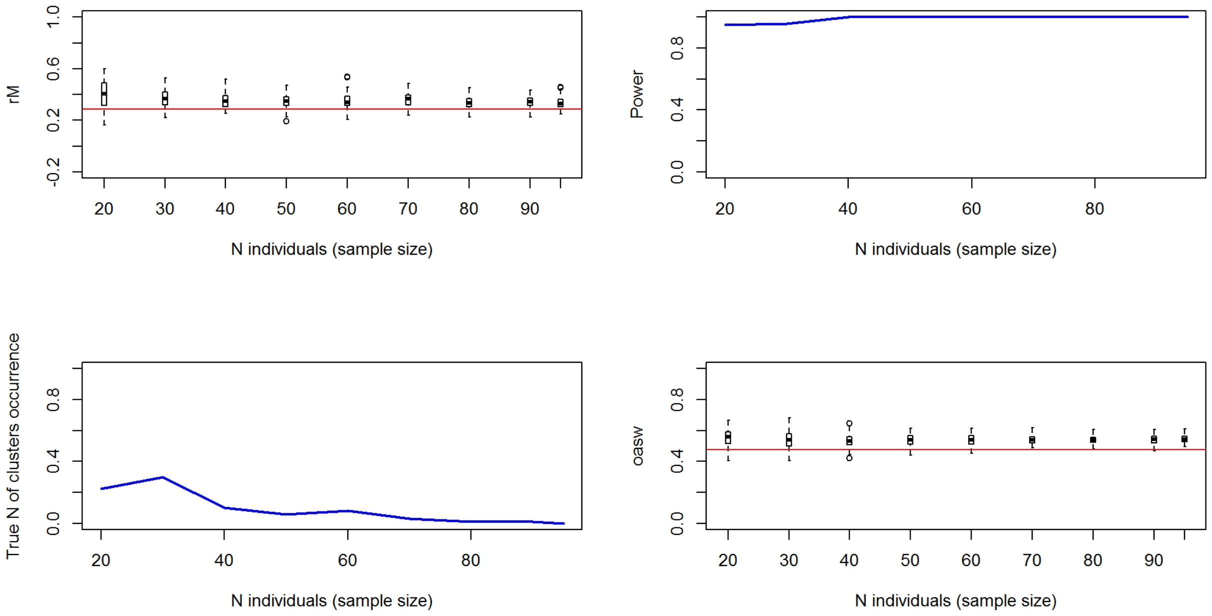

**Figure 03010-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

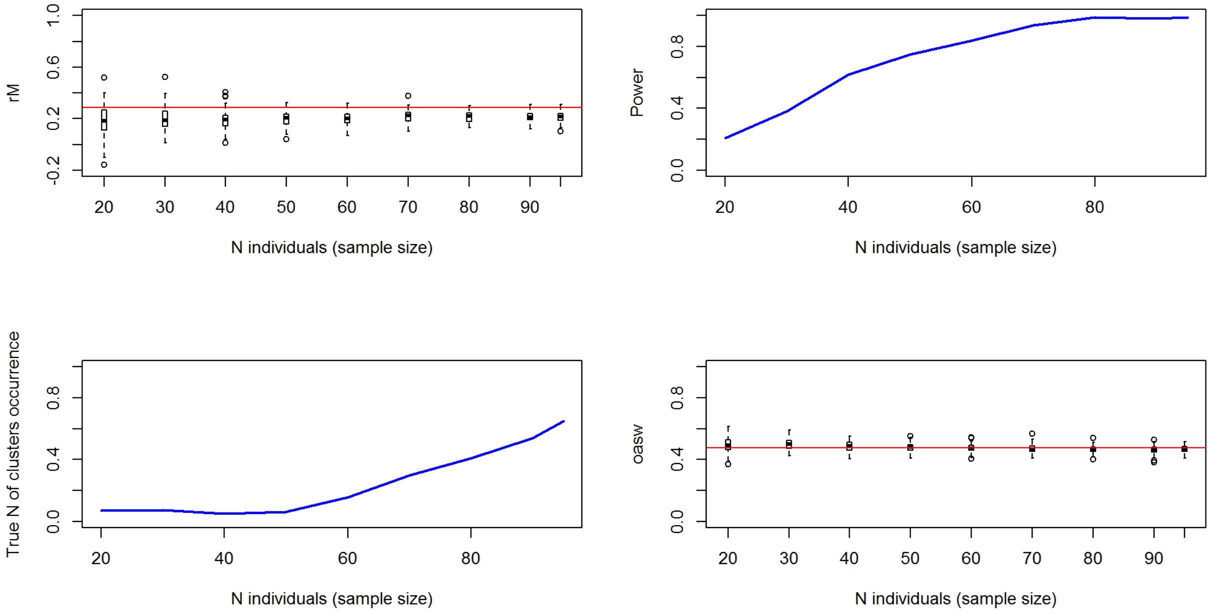

**Figure 03010-4.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

The comparison between the bootstrapped distribution of $r_M$ values from live recaptures and dead recoveries is significant ($p = 0.008$); Figure 03010-5).

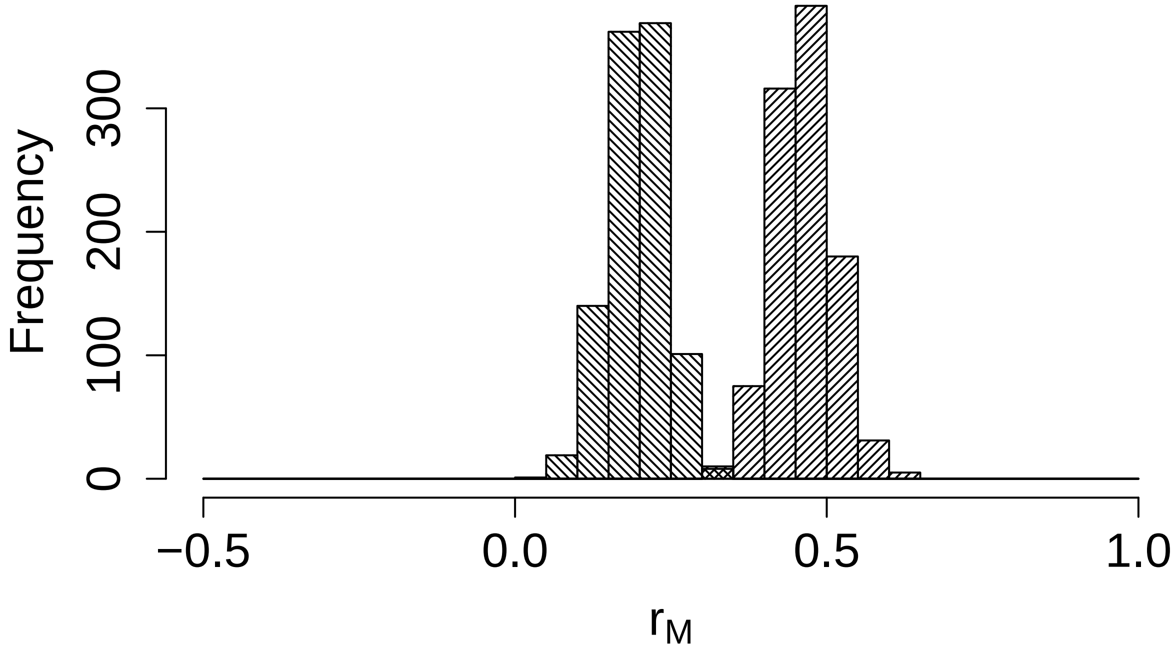

**Figure 03010-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

## 2. Connectivity between pre-defined regions

The species shows low connectivity (MC = 0.134; MC = 0.132 when adjusted for absolute abundance) between 6 breeding regions and 8 non breeding regions (Table 03010-2; Figure 03010-6).

**Table 03010-2.** 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 | 1488 | North Africa | 0.018 |
| Central Europe | 1488 | South-central Europe | 0.009 |
| Central Europe | 1488 | South-west Europe | 0.045 |
| Central Europe | 1488 | West Africa | 0.927 |
| East Europe | 6932 | Central Africa | 0.500 |
| East Europe | 6932 | South Africa | 0.500 |
| North Europe | 11571 | Arabian peninsula | 0.013 |
| North Europe | 11571 | Central Africa | 0.287 |
| North Europe | 11571 | East Africa | 0.017 |
| North Europe | 11571 | North Africa | 0.035 |
| North Europe | 11571 | South Africa | 0.022 |
| North Europe | 11571 | South-central Europe | 0.013 |
| North Europe | 11571 | South-west Europe | 0.004 |

| Breeding region | Abundance | Non breeding region | Transition probability |
|---|---:|---|---:|
| North Europe | 11571 | West Africa | 0.609 |
| North-west Europe | 450 | Central Africa | 0.083 |
| North-west Europe | 450 | North Africa | 0.083 |
| North-west Europe | 450 | South-west Europe | 0.042 |
| North-west Europe | 450 | West Africa | 0.792 |
| South-central Europe | 58 | South-central Europe | 1.000 |
| West Europe | 75 | South-west Europe | 1.000 |

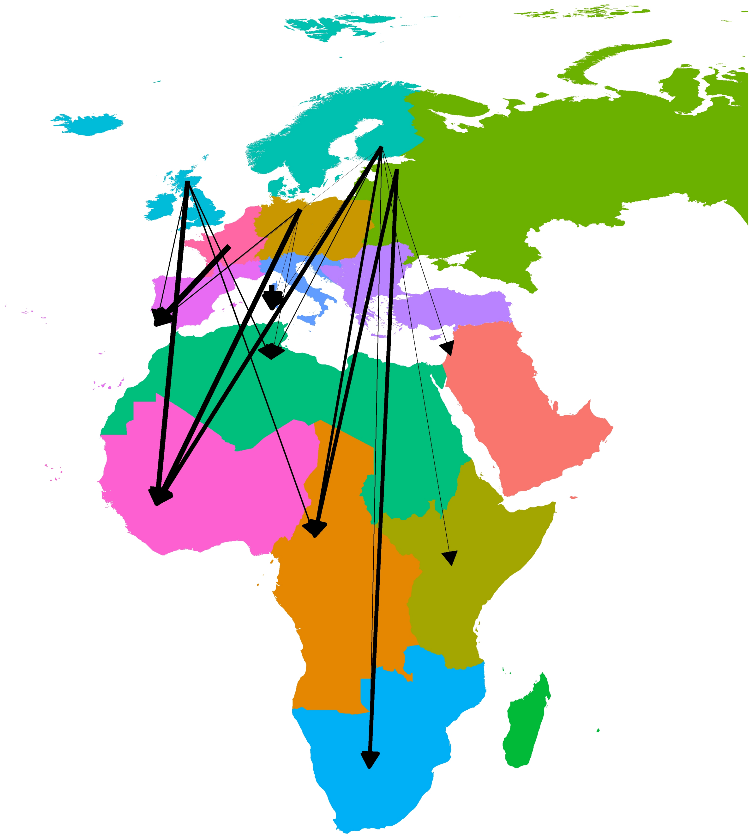

**Figure 03010-6.** Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

## 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.