# Migratory connectivity analysis

**by EURING Migration Atlas**
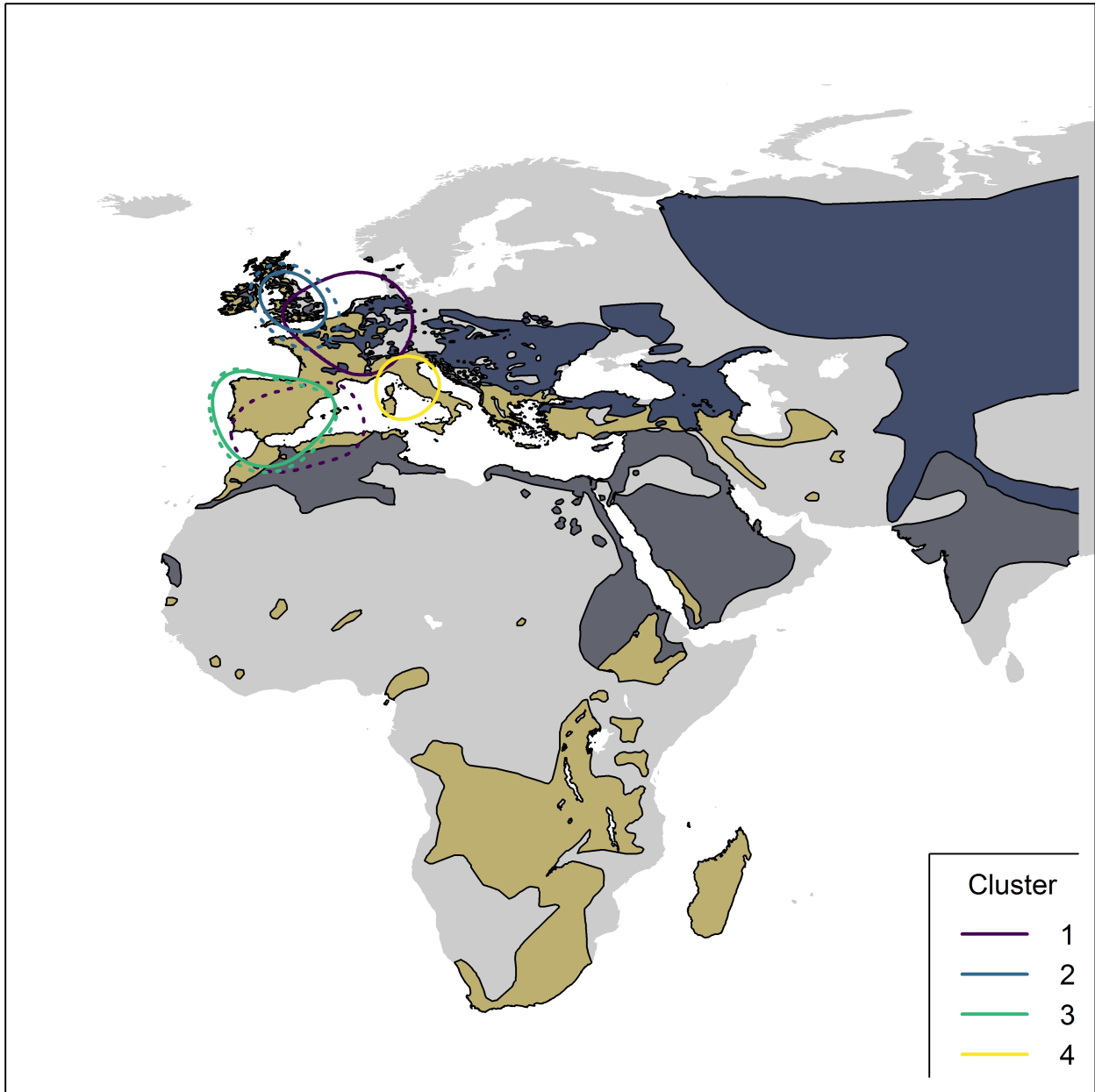
***Saxicola torquata*** **(EURING code 11390)**

## 1.1 Connectivity between individuals

The analysis evaluated 101 individuals (202 encounters) filtered from a total of 26569 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 11390-1; Figure 11390-1).

**Table 11390-1.** 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 | 101 | 0.262 | 0.001 | 0.169 | 0.413 | 4 | 0.579 |
| 1 | 1 | 35 | 0.099 | 0.148 | 0.019 | 0.368 | - | - |
| 2 | 1 | 28 | 0.633 | 0.001 | 0.371 | 0.993 | 5 | 0.695 |
| 3 | 1 | 30 | 0.869 | 0.001 | 0.713 | 1.000 | 9 | 0.682 |
| 4 | 1 | 8 | - | - | - | - | - | - |
| 21 | 2 | 2 | - | - | - | - | - | - |
| 22 | 2 | 9 | - | - | - | - | - | - |
| 23 | 2 | 14 | - | - | - | - | - | - |
| 24 | 2 | 2 | - | - | - | - | - | - |
| 25 | 2 | 1 | - | - | - | - | - | - |
| 31 | 2 | 3 | - | - | - | - | - | - |
| 32 | 2 | 10 | - | - | - | - | - | - |
| 33 | 2 | 1 | - | - | - | - | - | - |
| 34 | 2 | 4 | - | - | - | - | - | - |
| 35 | 2 | 2 | - | - | - | - | - | - |
| 36 | 2 | 3 | - | - | - | - | - | - |
| 37 | 2 | 2 | - | - | - | - | - | - |
| 38 | 2 | 2 | - | - | - | - | - | - |
| 39 | 2 | 3 | - | - | - | - | - | - |

**Figure 11390-1.** 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 11390-2) and stratified sampling of individuals within the breeding range (Figure 11390-3) and the non breeding range (Figure 11390-4). 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.
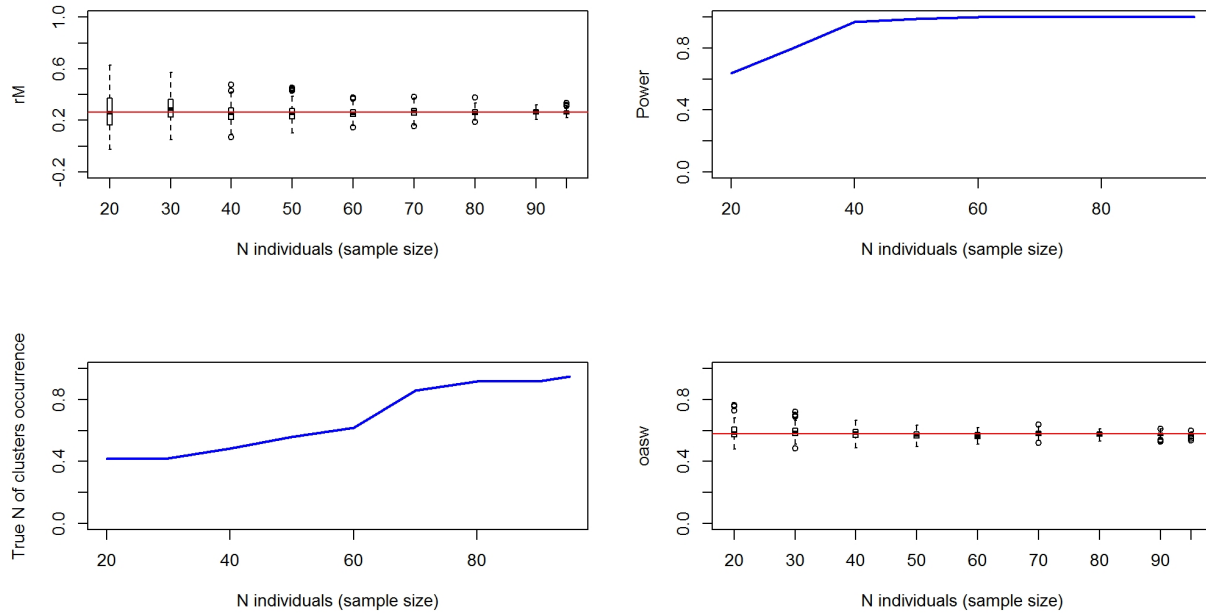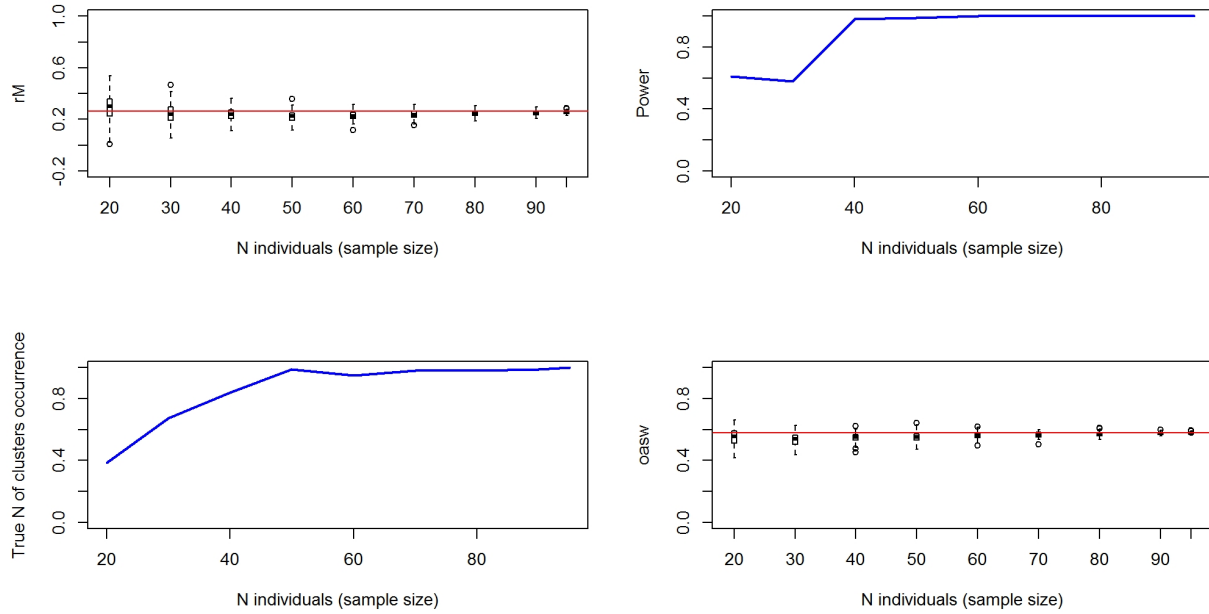


**Figure 11390-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.
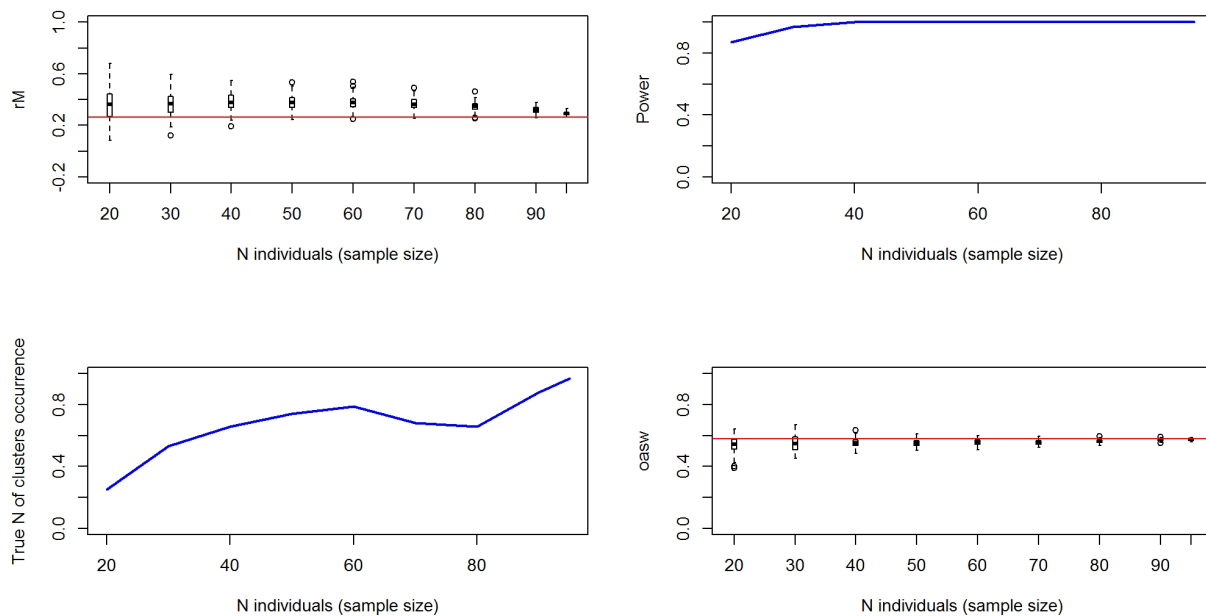


**Figure 11390-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 11390-4.** 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 = 0.558); Figure 11390-5).
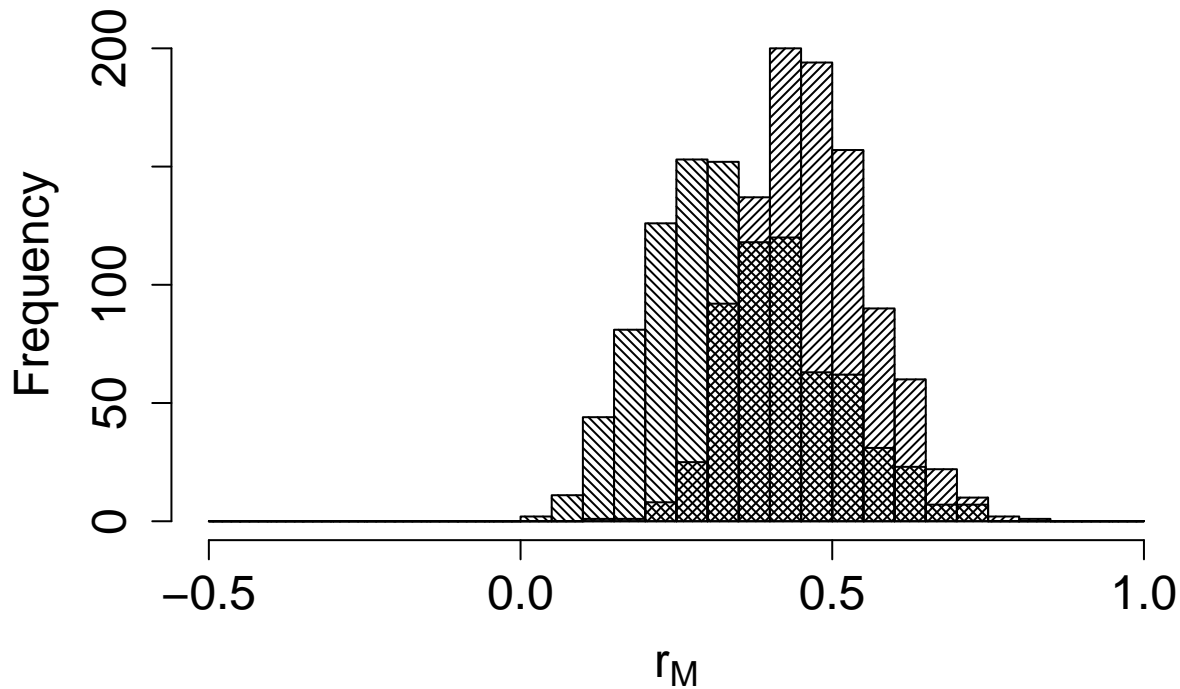
**Figure 11390-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

## 2. Connectivity between pre-defined regions

The species shows moderate/high connectivity (MC = 0.627; MC = 0.625 when adjusted for absolute abundance) between 5 breeding regions and 5 non breeding regions (Table 11390-2; Figure 11390-6).

**Table 11390-2.** 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 | 1177180 | North Africa | 0.545 |
| Central Europe | 1177180 | South-west Europe | 0.455 |
| North-west Europe | 261518 | North Africa | 0.032 |
| North-west Europe | 261518 | North-west Europe | 0.742 |
| North-west Europe | 261518 | South-west Europe | 0.129 |
| North-west Europe | 261518 | West Europe | 0.097 |
| South-central Europe | 1252891 | South-central Europe | 1.000 |
| South-west Europe | 9513233 | North Africa | 0.033 |
| South-west Europe | 9513233 | South-west Europe | 0.967 |
| West Europe | 564556 | North Africa | 0.333 |
| West Europe | 564556 | South-west Europe | 0.571 |
| West Europe | 564556 | West Europe | 0.095 |
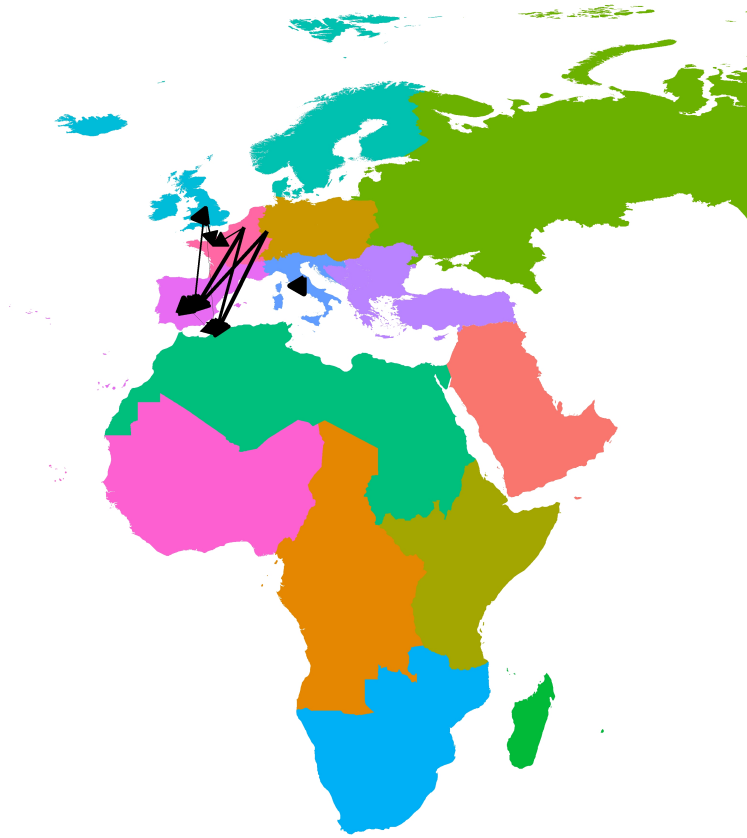
**Figure 11390-6.** Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

## 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.