# Migratory connectivity analysis

## by EURING Migration Atlas

***Parus montanus* (EURING code 14420)**

## 1.1 Connectivity between individuals

The analysis evaluated 448 individuals (896 encounters) filtered from a total of 115767 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 = 2 (Table 14420-1; Figure 14420-1).

**Table 14420-1.** 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 | 448 | 1.000 | 0.001 | 0.999 | 1.000 | 2 | 0.732 |
| 1 | 1 | 272 | 1.000 | 0.001 | 1.000 | 1.000 | 3 | 0.704 |
| 2 | 1 | 176 | 0.994 | 0.001 | 0.980 | 1.000 | 9 | 0.633 |
| 11 | 2 | 62 | 0.996 | 0.001 | 0.993 | 0.999 | 2 | 0.550 |
| 12 | 2 | 66 | 1.000 | 0.001 | 1.000 | 1.000 | 9 | 0.701 |
| 13 | 2 | 144 | 1.000 | 0.001 | 0.999 | 1.000 | 9 | 0.690 |
| 21 | 2 | 14 | - | - | - | - | - | - |
| 22 | 2 | 9 | - | - | - | - | - | - |
| 23 | 2 | 2 | - | - | - | - | - | - |
| 24 | 2 | 40 | 1.000 | 0.001 | 0.999 | 1.000 | 3 | 0.832 |
| 25 | 2 | 24 | 0.969 | 0.001 | 0.956 | 1.000 | 4 | 0.856 |
| 26 | 2 | 20 | 0.993 | 0.001 | 0.987 | 0.999 | 4 | 0.712 |
| 27 | 2 | 38 | 0.999 | 0.001 | 0.997 | 1.000 | 6 | 0.895 |
| 28 | 2 | 11 | - | - | - | - | - | - |
| 29 | 2 | 18 | - | - | - | - | - | - |
| 111 | 3 | 37 | 0.990 | 0.001 | 0.975 | 0.997 | 2 | 0.558 |
| 112 | 3 | 25 | 0.999 | 0.001 | 0.997 | 1.000 | 7 | 0.689 |
| 121 | 3 | 3 | - | - | - | - | - | - |
| 122 | 3 | 8 | - | - | - | - | - | - |
| 123 | 3 | 23 | 0.988 | 0.001 | 0.885 | 1.000 | 6 | 0.943 |
| 124 | 3 | 8 | - | - | - | - | - | - |
| 125 | 3 | 10 | - | - | - | - | - | - |
| 126 | 3 | 2 | - | - | - | - | - | - |
| 127 | 3 | 7 | - | - | - | - | - | - |
| 128 | 3 | 3 | - | - | - | - | - | - |
| 129 | 3 | 2 | - | - | - | - | - | - |
| 131 | 3 | 45 | 1.000 | 0.001 | 1.000 | 1.000 | 8 | 0.978 |

| 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 |
|---|---|---|---|---|---|---|---|---|
| 132 | 3 | 25 | 1.000 | 0.001 | 0.986 | 1.000 | 2 | 0.914 |
| 133 | 3 | 10 | - | - | - | - | - | - |
| 134 | 3 | 18 | - | - | - | - | - | - |
| 135 | 3 | 12 | - | - | - | - | - | - |
| 136 | 3 | 9 | - | - | - | - | - | - |
| 137 | 3 | 20 | 0.996 | 0.001 | 0.989 | 1.000 | 2 | 0.973 |
| 138 | 3 | 4 | - | - | - | - | - | - |
| 139 | 3 | 1 | - | - | - | - | - | - |
| 241 | 3 | 30 | 0.996 | 0.001 | 0.980 | 1.000 | 4 | 0.840 |
| 242 | 3 | 8 | - | - | - | - | - | - |
| 243 | 3 | 2 | - | - | - | - | - | - |
| 251 | 3 | 11 | - | - | - | - | - | - |
| 252 | 3 | 1 | - | - | - | - | - | - |
| 253 | 3 | 1 | - | - | - | - | - | - |
| 254 | 3 | 11 | - | - | - | - | - | - |
| 261 | 3 | 5 | - | - | - | - | - | - |
| 262 | 3 | 6 | - | - | - | - | - | - |
| 263 | 3 | 5 | - | - | - | - | - | - |
| 264 | 3 | 4 | - | - | - | - | - | - |
| 271 | 3 | 7 | - | - | - | - | - | - |
| 272 | 3 | 2 | - | - | - | - | - | - |
| 273 | 3 | 25 | 0.546 | 0.002 | 0.007 | 0.784 | 3 | 0.648 |
| 274 | 3 | 1 | - | - | - | - | - | - |
| 275 | 3 | 2 | - | - | - | - | - | - |
| 276 | 3 | 1 | - | - | - | - | - | - |

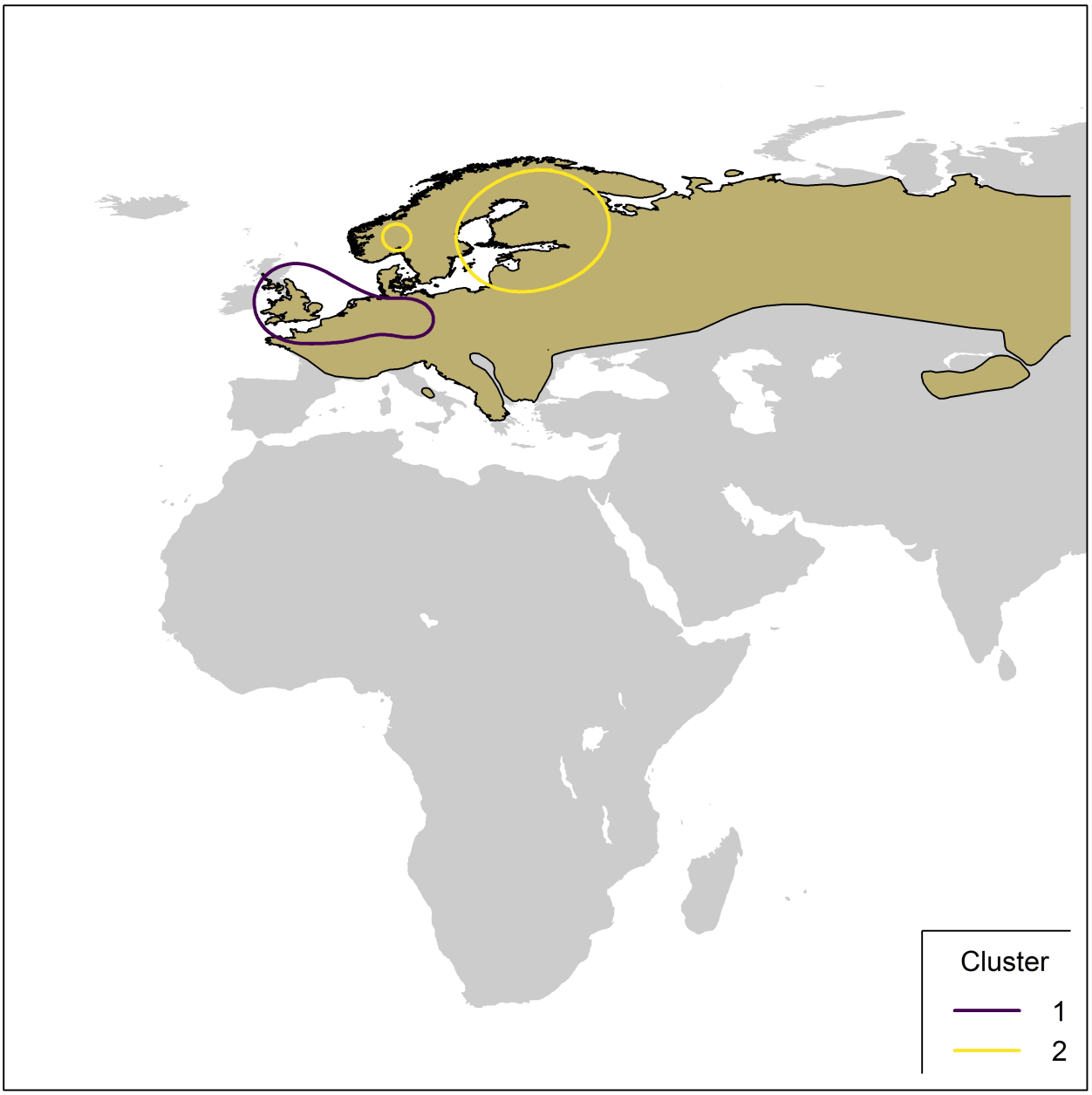


**Figure 14420-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 14420-2) and stratified sampling of individuals within the breeding range (Figure 14420-3) and the non breeding range (Figure 14420-4). 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.

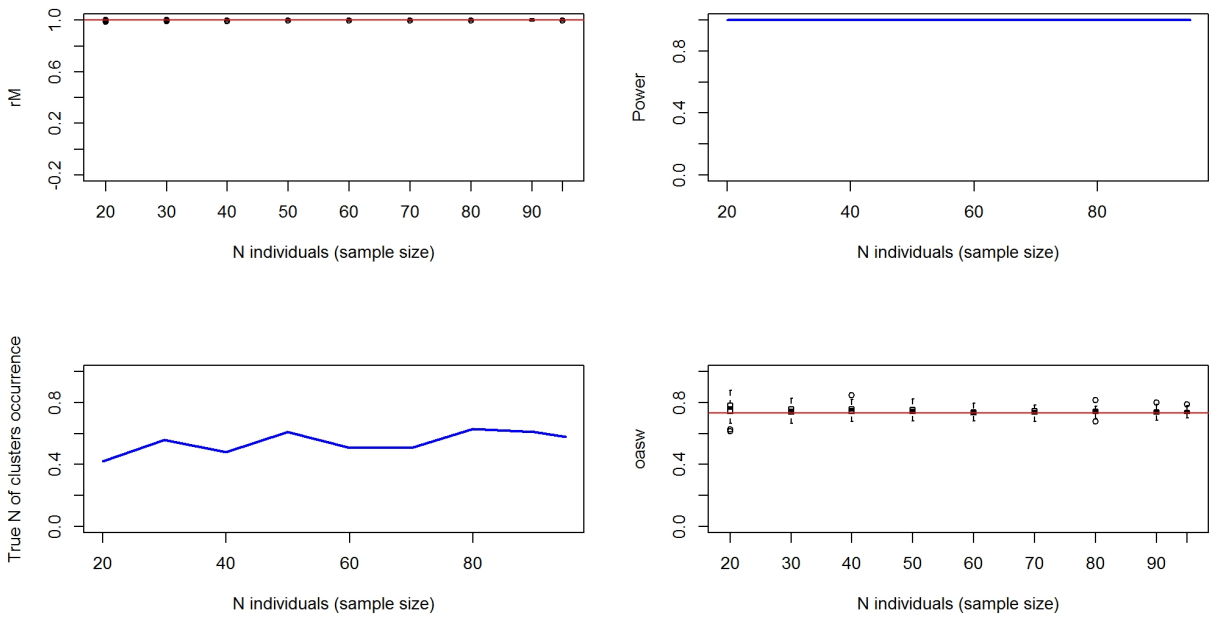


**Figure 14420-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

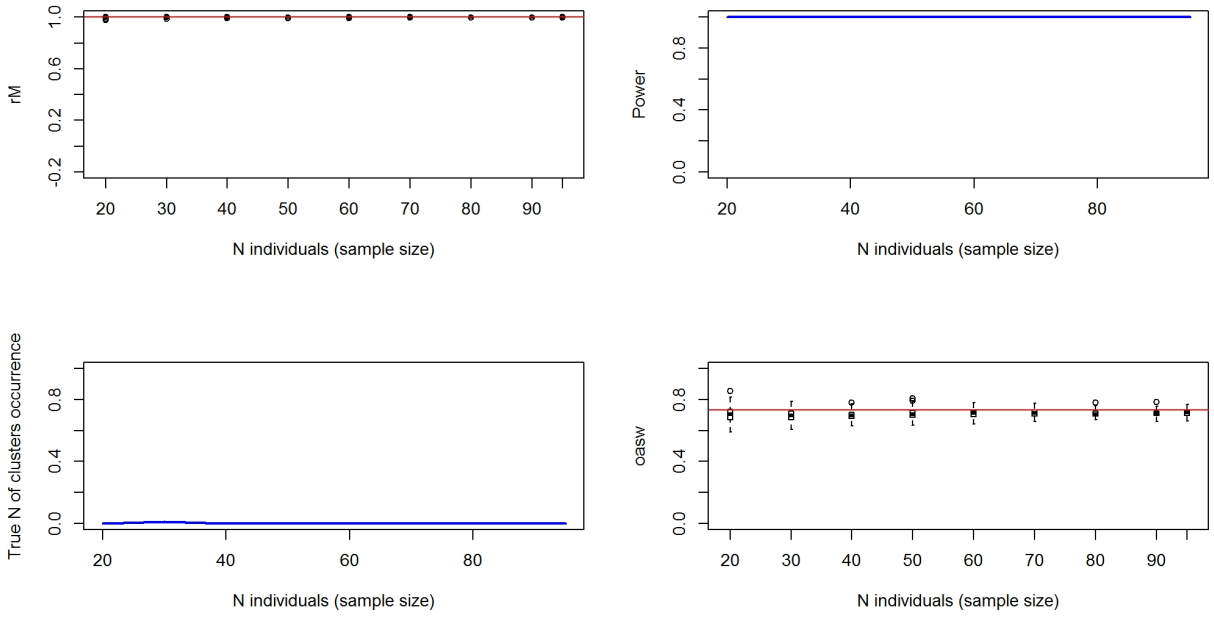


**Figure 14420-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

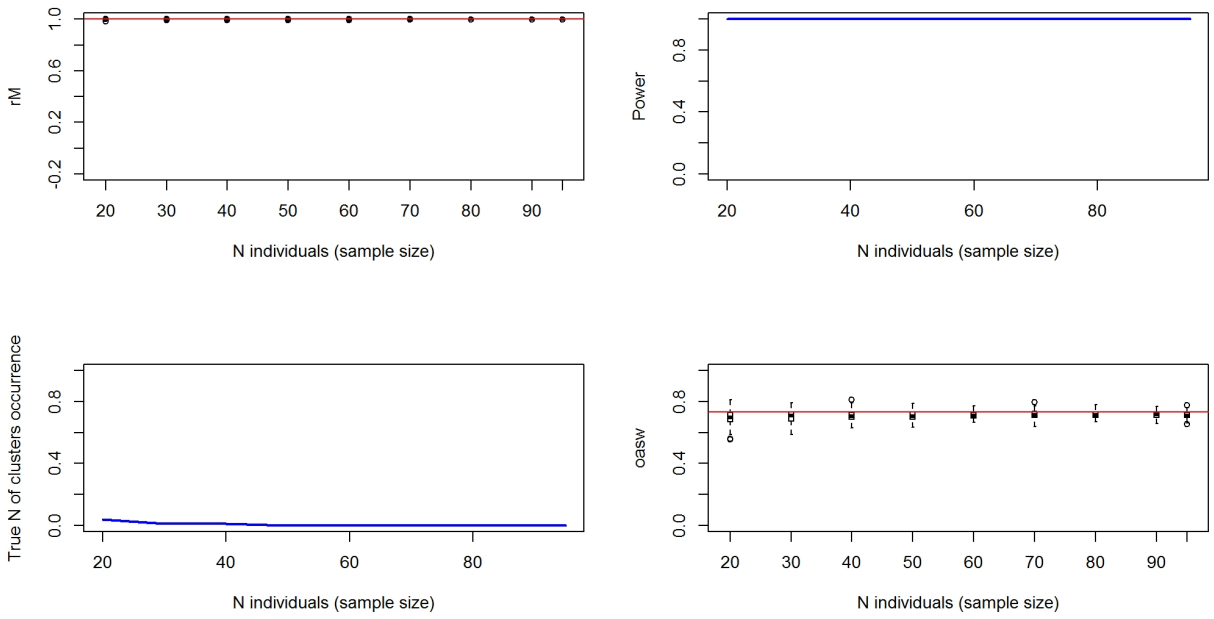


**Figure 14420-4.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 ($p = 1$); Figure 14420-5).

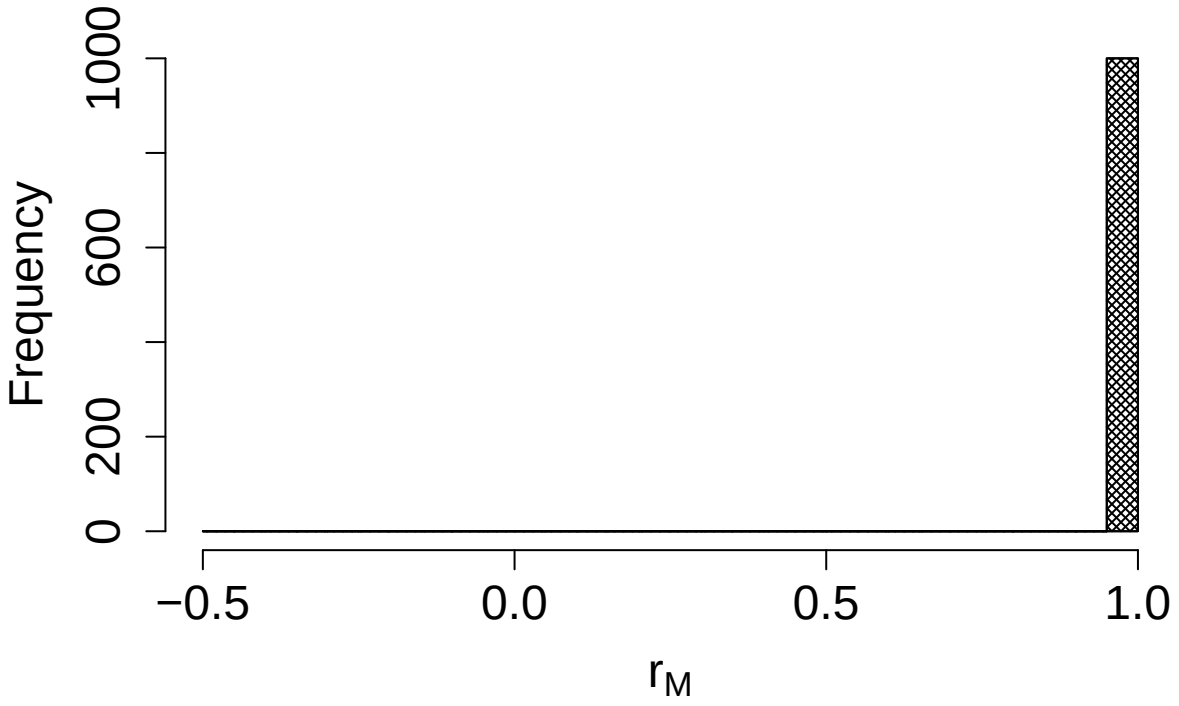


**Figure 14420-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

## 2. Connectivity between pre-defined regions

The species shows high connectivity (MC = 1; MC = 1 when adjusted for absolute abundance) between 4 breeding regions and 4 non breeding regions (Table 14420-2; Figure 14420-6).

**Table 14420-2.** 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 | 1410800 | Central Europe | 1 |
| North Europe | 4554000 | North Europe | 1 |
| North-west Europe | 6800 | North-west Europe | 1 |
| West Europe | 468618 | West Europe | 1 |

**Figure 14420-6.** 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.