

# Migratory connectivity analysis

by EURING Migration Atlas

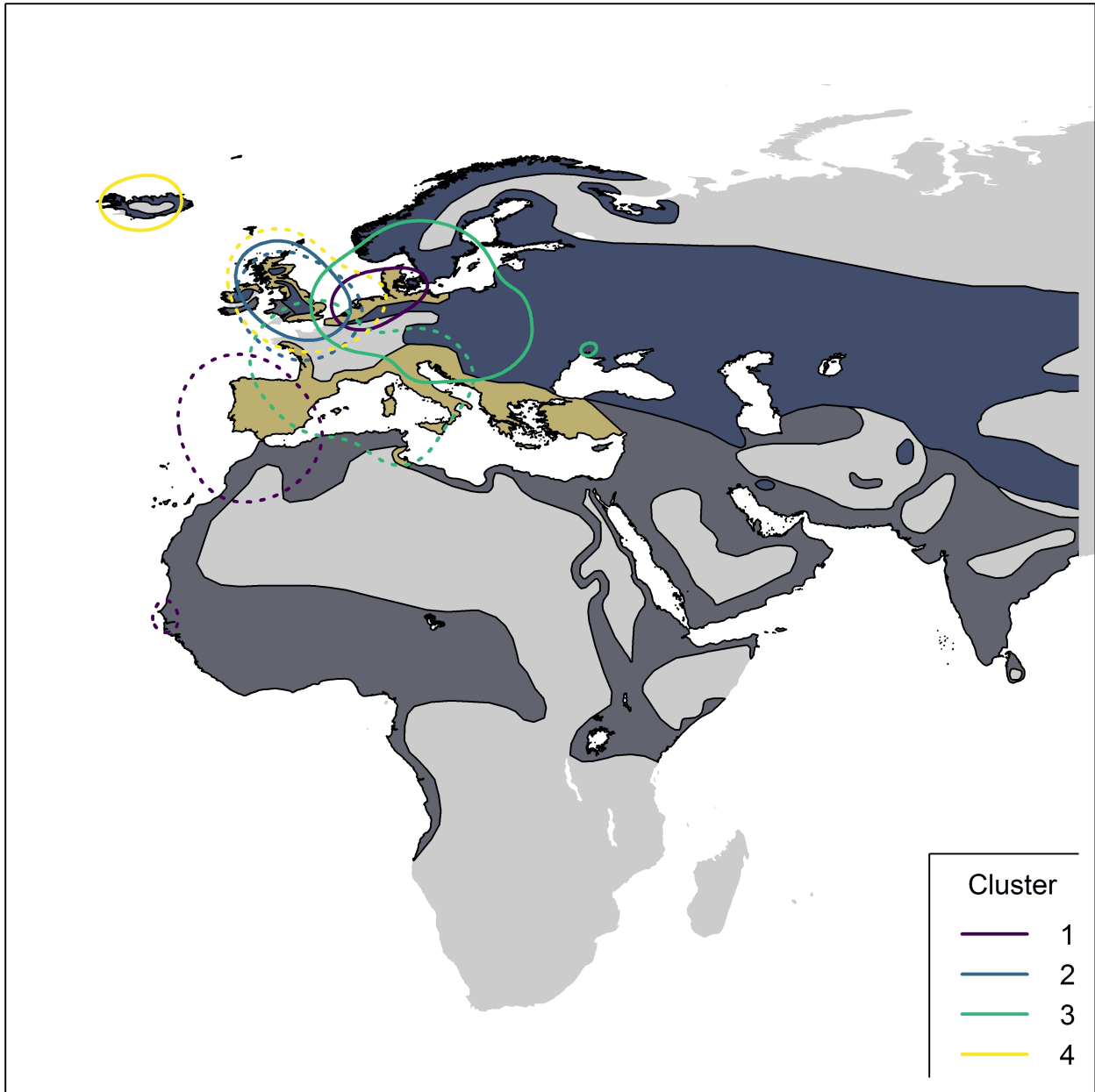
*Tringa totanus* (EURING code 05460)

## 1.1 Connectivity between individuals

The analysis evaluated 363 individuals (726 encounters) filtered from a total of 56578 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 05460-1; Figure 05460-1).

**Table 05460-1.** 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	363	0.283	0.001	0.212	0.369	4	0.530
1	1	73	0.351	0.003	-0.089	0.670	2	0.784
2	1	167	0.335	0.001	0.227	0.471	2	0.411
3	1	65	0.532	0.001	0.296	0.717	9	0.513
4	1	58	-0.036	0.819	-0.044	0.102	-	-
11	2	66	-0.012	0.635	-0.047	0.100	-	-
12	2	7	-	-	-	-	-	-
31	2	3	-	-	-	-	-	-
32	2	7	-	-	-	-	-	-
33	2	15	-	-	-	-	-	-
34	2	11	-	-	-	-	-	-
35	2	10	-	-	-	-	-	-
36	2	7	-	-	-	-	-	-
37	2	7	-	-	-	-	-	-
38	2	1	-	-	-	-	-	-
39	2	4	-	-	-	-	-	-

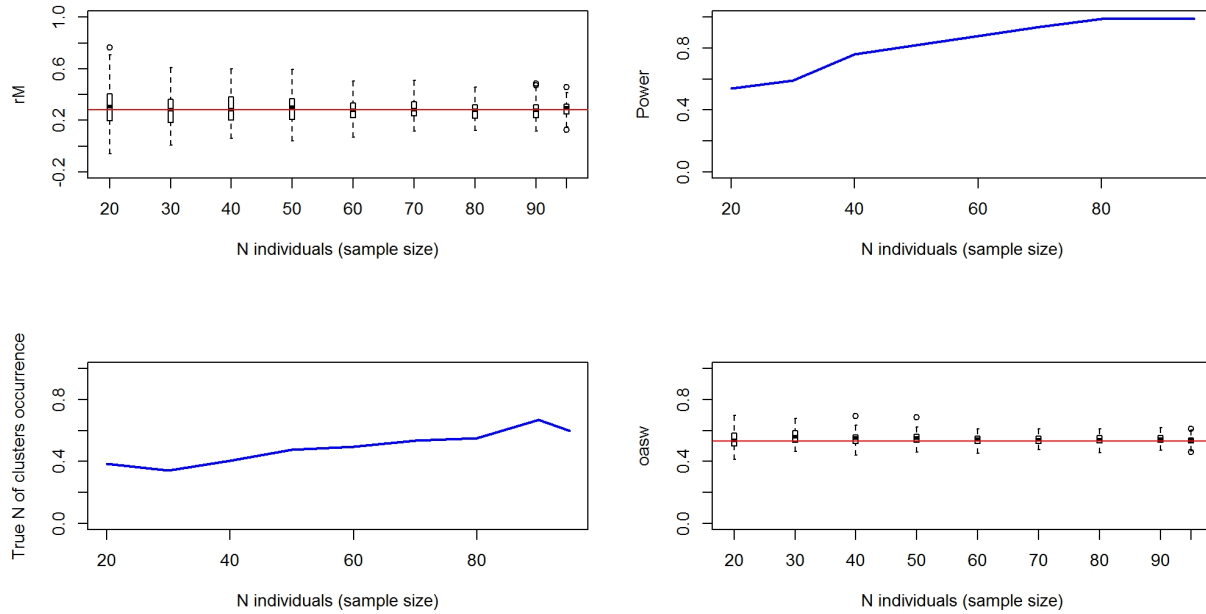


**Figure 05460-1.** Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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).

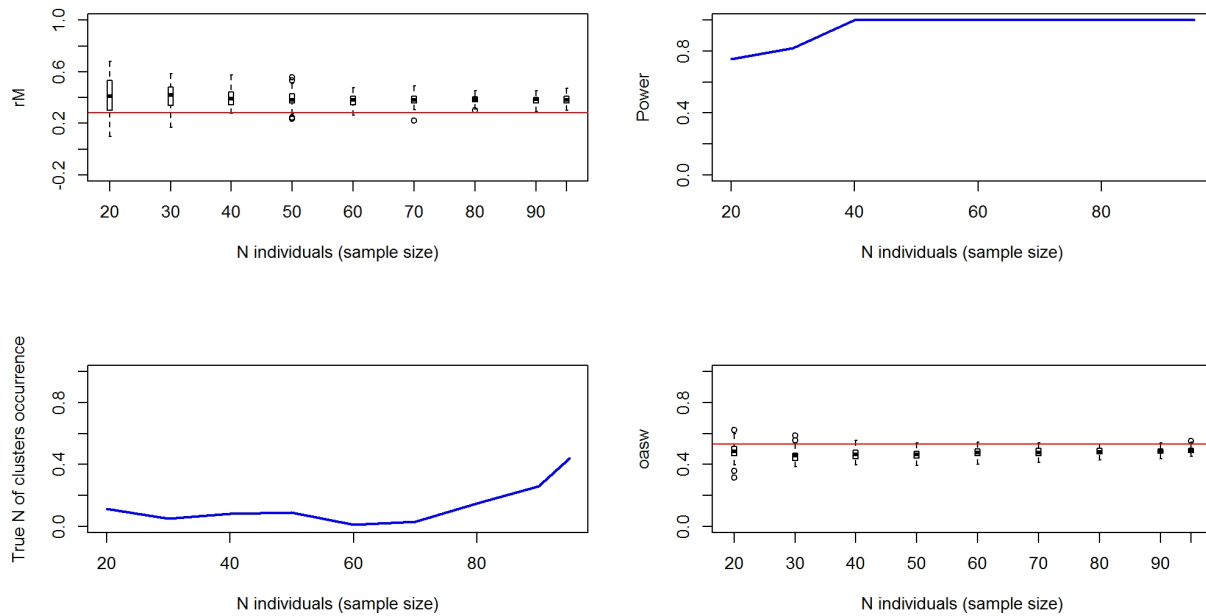
## 1.2 Sensitivity analysis

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 05460-2) and stratified sampling of individuals within the breeding range (Figure 05460-3) and the non breeding range (Figure 05460-4). 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.

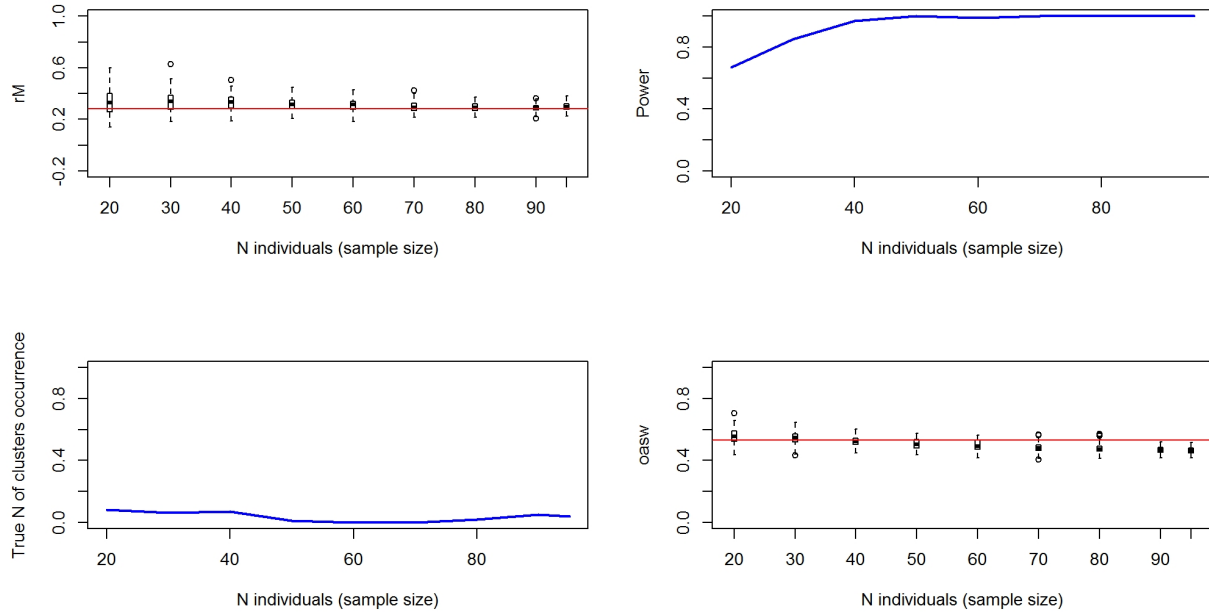


**Figure 05460-2.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.



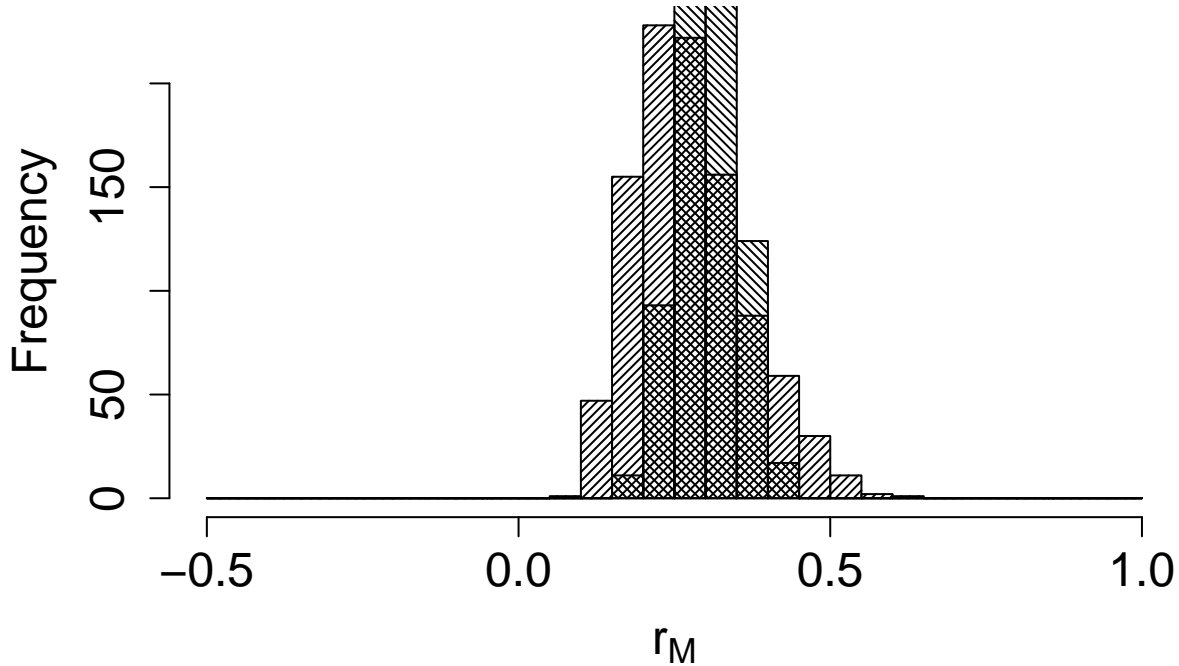
**Figure 05460-3.** Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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



**Figure 05460-4.** 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 ( $p = 0.587$ ); Figure 05460-5).



**Figure 05460-5.** Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

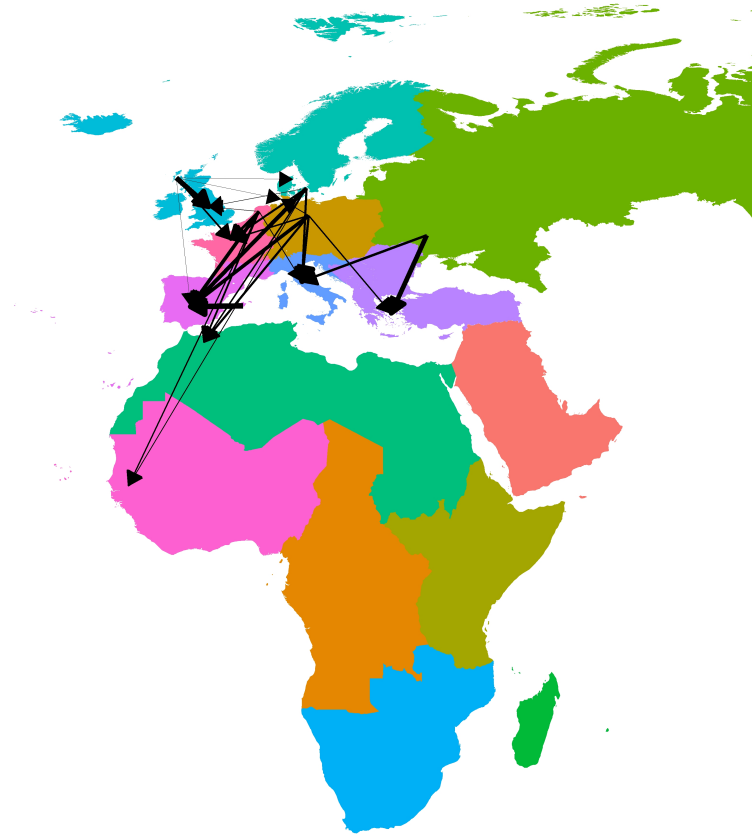
## 2. Connectivity between pre-defined regions

The species shows moderate/high connectivity ( $MC = 0.73$ ;  $MC = 0.729$  when adjusted for absolute abundance) between 7 breeding regions and 9 non breeding regions (Table 05460-2; Figure 05460-6).

**Table 05460-2.** 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	32985	Central Europe	0.038
Central Europe	32985	North Africa	0.154
Central Europe	32985	South-central Europe	0.192
Central Europe	32985	South-east Europe	0.077
Central Europe	32985	South-west Europe	0.423
Central Europe	32985	West Europe	0.115
East Europe	252724	South-central Europe	0.250
East Europe	252724	South-east Europe	0.750
North Europe	132530	North Africa	0.102
North Europe	132530	North-west Europe	0.017
North Europe	132530	South-central Europe	0.153
North Europe	132530	South-west Europe	0.542
North Europe	132530	West Africa	0.034

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	132530	West Europe	0.153
North-west Europe	331000	Central Europe	0.009
North-west Europe	331000	North Europe	0.005
North-west Europe	331000	North-west Europe	0.875
North-west Europe	331000	South-west Europe	0.005
North-west Europe	331000	West Europe	0.106
South-central Europe	2513	South-central Europe	1.000
South-west Europe	10271	South-west Europe	1.000
West Europe	39334	North Africa	0.145
West Europe	39334	North-west Europe	0.018
West Europe	39334	South-central Europe	0.036
West Europe	39334	South-west Europe	0.418
West Europe	39334	West Africa	0.091
West Europe	39334	West Europe	0.291



**Figure 05460-6.** 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>.