

Migratory connectivity analysis

by EURING Migration Atlas

Vanellus vanellus (EURING code 04930)

1.1 Connectivity between individuals

The analysis evaluated 3646 individuals (7292 encounters) filtered from a total of 49037 records in the EURING databank which were considered for the Atlas. The species shows a significant connectivity from pattern transference (Table 04930-1; Figure 04930-1).

Table 04930-1. 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	3646	0.091	0.001	0.071	0.112	2	0.38

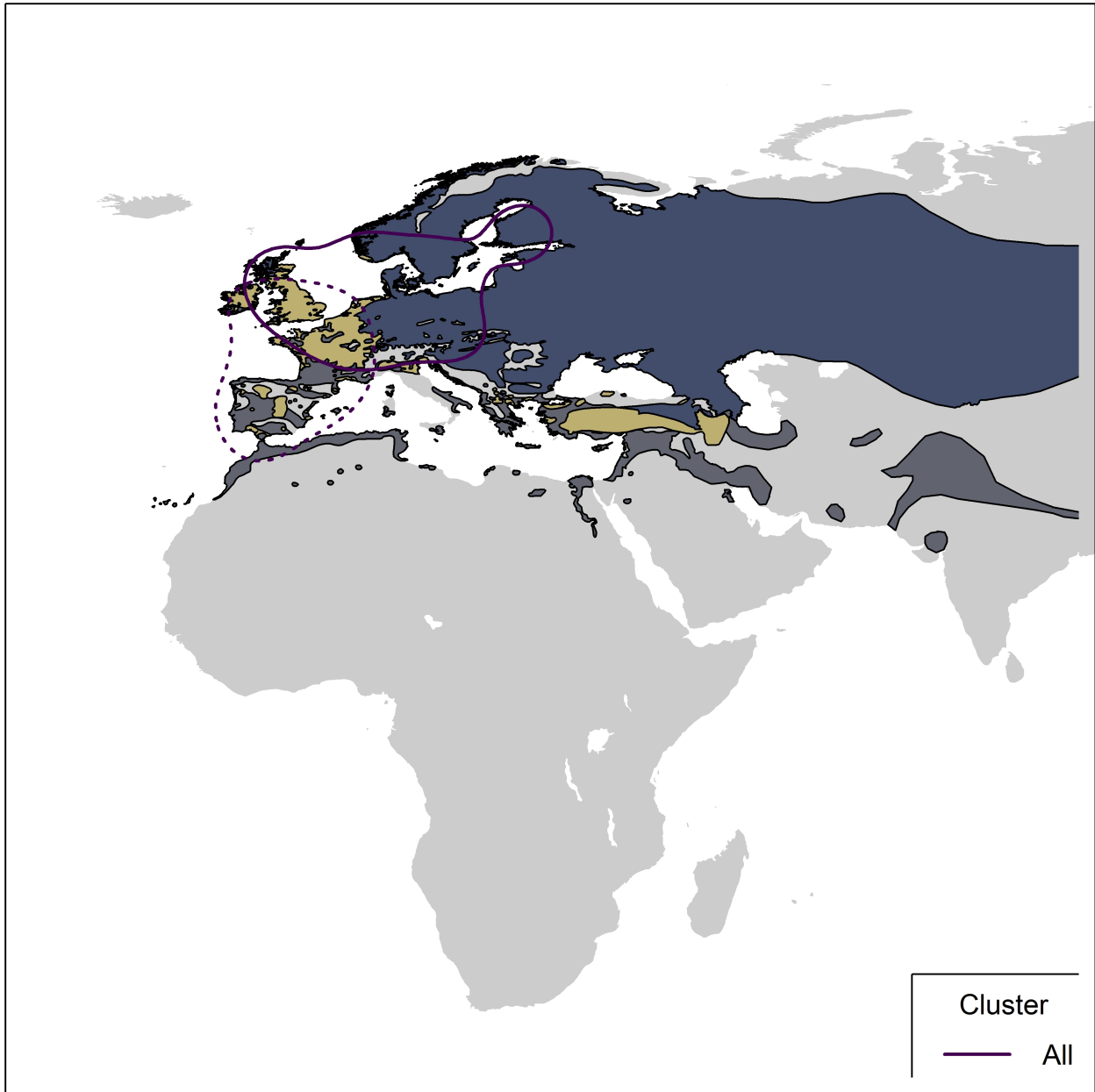


Figure 04930-1. Map showing 95% kernel contours of of first-level clusters identified by the migratory connectivity analysis, if any, or 95% kernel contours of all encounters, in case of no clustering structure. Solid lines indicate the clusters in the breeding range, dotted lines those in the non-breeding 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 04930-2) and stratified sampling of individuals within the breeding range (Figure 04930-3) and the non breeding range (Figure 04930-4). 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.

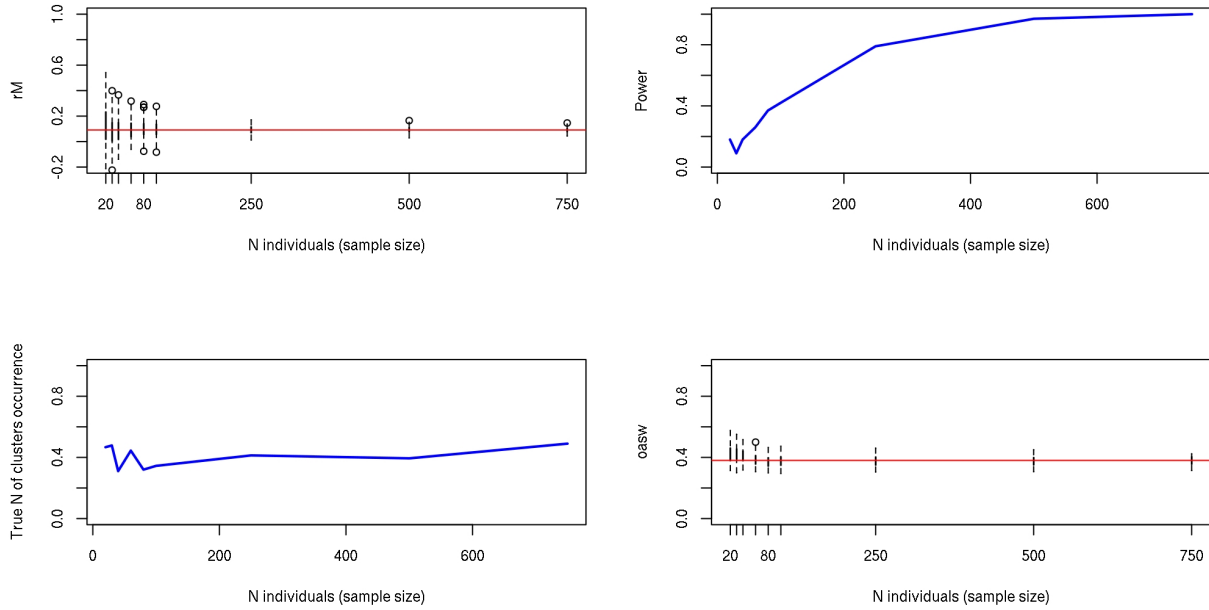


Figure 04930-2. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis (i.e. proportion of times the analyses on the subset of individuals was significant). Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed value (red line) of clustering intensity.

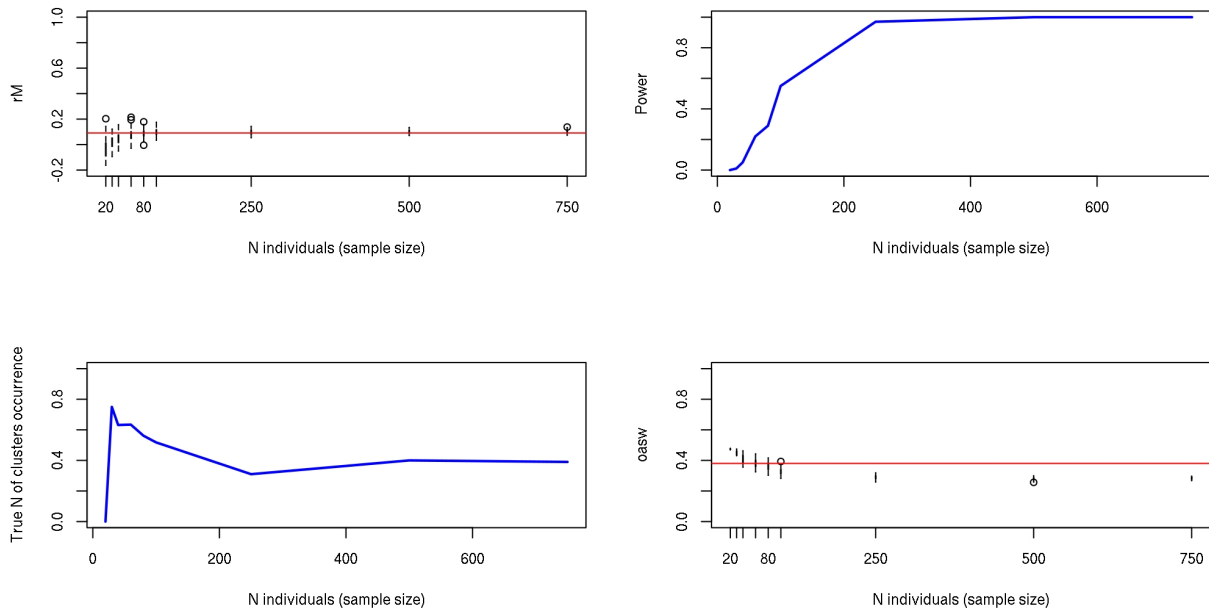


Figure 04930-3. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the

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

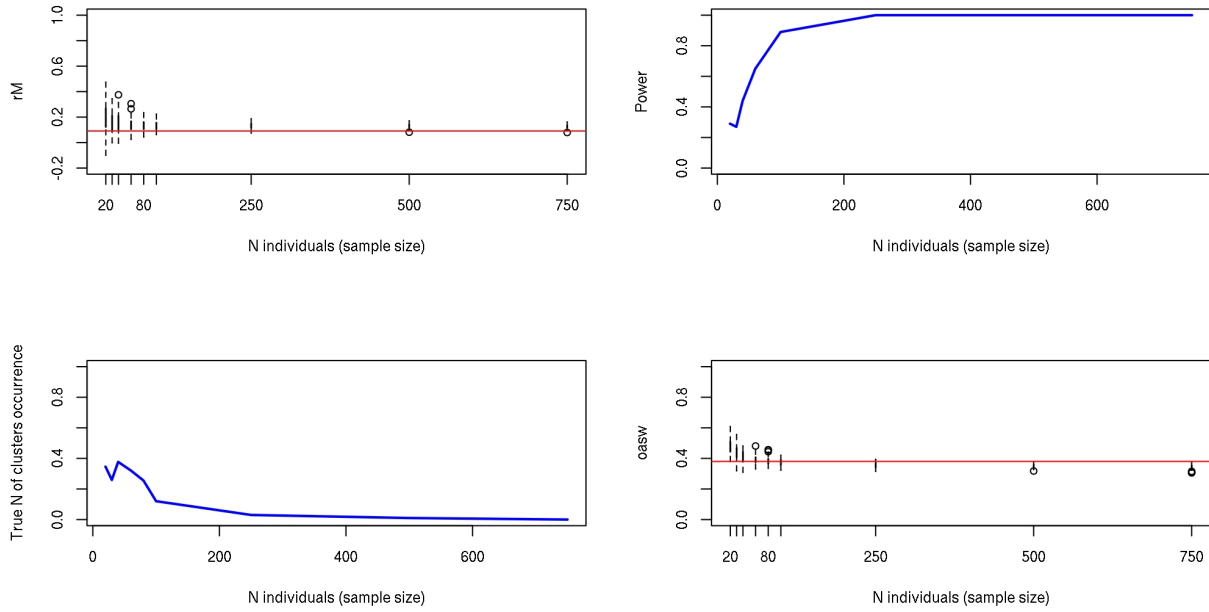


Figure 04930-4. Top left: simulated distribution (boxplots) and observed value (red line) of connectivity. Top right: Simulated power of the analysis. Bottom left: Proportion of times the analysis provides the observed best number of cluster. Bottom right: simulated distribution (boxplots) and observed 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 ($p = 0.213$); Figure 04930-5).

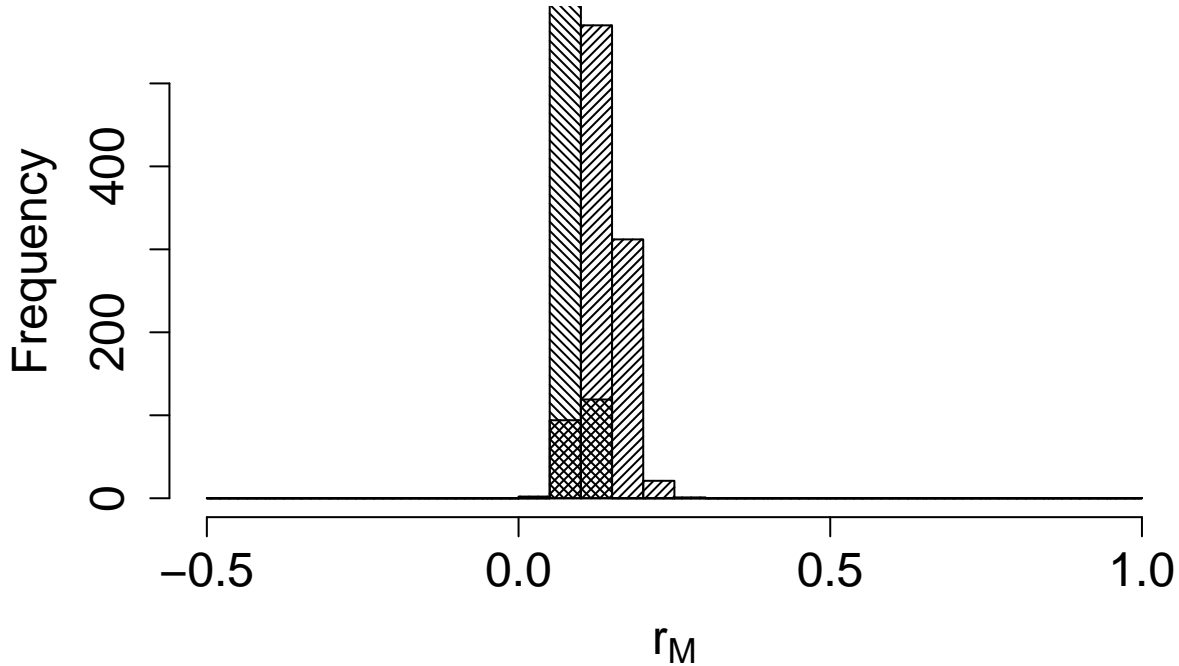


Figure 04930-5. Comparison between the bootstrapped distributions of connectivity value for alive recaptures (filling lines with angle=45°) and dead recoveries (filling lines with angle=375°).

2. Connectivity between pre-defined regions

The species shows low connectivity ($MC = 0.093$; $MC = 0.092$ when adjusted for absolute abundance) between 5 breeding regions and 8 non breeding regions (Table 04930-2; Figure 04930-6).

Table 04930-2. 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	471720	Central Europe	0.001
Central Europe	471720	North Africa	0.028
Central Europe	471720	North-west Europe	0.009
Central Europe	471720	South-central Europe	0.087
Central Europe	471720	South-east Europe	0.001
Central Europe	471720	South-west Europe	0.395
Central Europe	471720	West Europe	0.478
East Europe	2339141	North Africa	0.019
East Europe	2339141	North-west Europe	0.056
East Europe	2339141	South-central Europe	0.019
East Europe	2339141	South-west Europe	0.278
East Europe	2339141	West Europe	0.630
North Europe	394507	Central Europe	0.004

Breeding region	Abundance	Non breeding region	Transition probability
North Europe	394507	North Africa	0.027
North Europe	394507	North Europe	0.004
North Europe	394507	North-west Europe	0.096
North Europe	394507	South-central Europe	0.008
North Europe	394507	South-west Europe	0.379
North Europe	394507	West Europe	0.483
North-west Europe	284000	North Africa	0.010
North-west Europe	284000	North-west Europe	0.463
North-west Europe	284000	South-west Europe	0.265
North-west Europe	284000	West Europe	0.263
West Europe	423729	North Africa	0.028
West Europe	423729	North-west Europe	0.016
West Europe	423729	South-central Europe	0.003
West Europe	423729	South-west Europe	0.359
West Europe	423729	West Europe	0.595

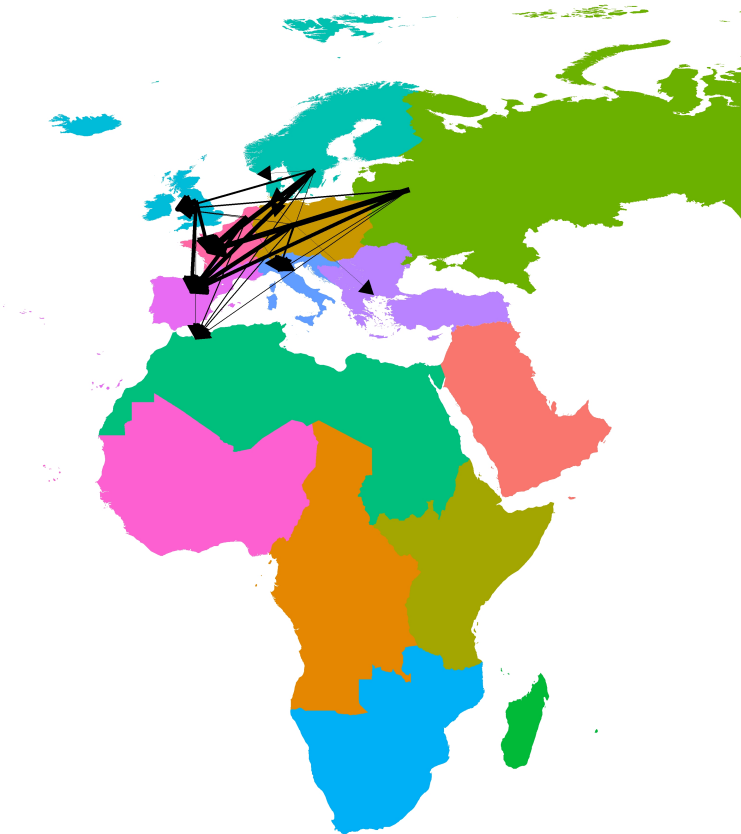


Figure 04930-6. Map showing pre-defined regions in different colours, with black arrows linking centroids of individual encounters in different regions. Arrow width is proportional to transition probability.

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>.