**Identifying a migratory divide: a method tested by simulation**

I developed this R code to run the simulations presented in Appendix 2 of the publication [Guillaumet et al. 2011. Behavioral Ecology]. The objective was to test the ability of the method I proposed in this paper to:

1) Correctly identify a migratory divide based on geographic locations in the breeding and winter seasons; and

2) Compare the relative explanatory power of a parallel migratory system versus a flyway migratory system, the latter relying on the previously identified migratory divide (for more information, see the document 'Appendix 2 of Guillaumet et al 2011_Behavioral Ecology', and particularly Fig. A2.1).

The comprehensive R function called *test_migratory_connectivity* only requires a data set (real or simulated) as input. Note that the library *gtools* is required to create one of the simulated data sets provided as example.

The function returns a Figure with 3 panels: 1) on top, the position of the putative migratory divide, corresponding to the partitioning yielding the lowest Akaike Information Criterion (AICc), is shown by a vertical dashed line; each individual is then given a color corresponding to its ascribed flyway; the two bottom panels give a visual representation of the explanatory power of the parallel (left) and flyway migratory systems (right), in agreement with aforementioned Fig. A2.1. The relative (quantitative) explanatory power of these two systems is obtained using an Information Theoretic Approach (Akaike Weight) returned by the function as a Table.

After loading the library (*gtools*) and the *test_migratory_connectivity* function, you can run some of the provided examples such as:

# 2 - Simulate and test a data set consistent with a flyway migration system:

# Central migratory divide' and balanced sample size on each flyway

n = 100; long_col = 1: n

long_w = rep(NA, n) ; for(i in 1 : n) ifelse(i <= 50, long_w[i] <- 25 + rnorm(1, sd = 5), long_w[i] <- 75 + rnorm(1, sd = 5))

data_f = as.data.frame(cbind(long_col = long_col, long_w = long_w, flyway_col = rep(0, n)))

test_migratory_connectivity(data = data_f); close.screen(all = TRUE)

As expected based on the simulated data set, you can see that: 1) the position of the putative migratory divide is central in this case (but see example # 3 for a different scenario); and 2) Akaike weight of the Flyway migration system is ~ 1 (versus ~ 0 for the parallel system), supporting a flyway migratory system; you should also get a figure similar to Fig. 1 below:

**Fig. 1**



Position of the putative migratory divide

AICc

Longitude Breeding

Parallel migration

Longitude Winter

Longitude Breeding

Flyway system

Longitude Winter

M          A

Migratory Flyway