

Landscape genetics, born of the association of genetics, ecology and spatial statistics, aims to "highlight the linkage between the spatial context of ecological dynamics and evolutionary processes, which is revealed in genetic signature that reflect the underlying forces shaping evolutionary and ecological trajectories". Gene flows and isolation by landscape resistance (IBR) are two important questions in landscape genetics and has been widely studied since the last 20 years. In most of these studies, least-cost path analysis is used as the standard approach to explain the genetic distance.

Several authors have discussed conceptual and methodological topics like the importance of the adequacy of spatial and temporal scales or the pertinence of the least-cost distance which assumes that gene flows are restricted to a single and optimal pathways. Nevertheless, the way to choose resistance values (also called friction or impedance values) stays the central problem. It must depend on the objectives of the study and on the conceptual meaning of these values. Moreover, sensitivity analysis showed that poor choices of resistance values can dramatically blur the results.

As far as we know, resistance values are mostly based on i) expert judgements, ii) massive try-and-error approaches or iii) resource selection functions (point and home range selection functions). However, these approaches present the defect of being arbitrary (i), CPU intensive (ii) and conceptually misleading (iii), respectively. In this communication, we propose to use a simple and iterative statistical approach to choose resistance values based on the optimization of a Matrix Selection Function (Zeller et al., 2012). Our approach is expected to be less subjective, more CPU efficient and to be more adapted to the spatial dynamic of gene flows.