**Detecting exceptional neutral genetic changes in resampled landscapes.**

INTRODUCTION

Global change, including climate change but also habitat destruction and fragmentation, have caused biodiversity to quickly decline in many parts of the world in the last century (Fischer & Lindenmayer, 2007; Butchart et al., 2010; Dirzo et al., 2014). The future of biodiversity is likely bleak (Bellard, Bertelsmeier, Leadley, Thuiller, & Courchamp, 2012), and thus there is an ever-increasing demand from ecosystem managers to evaluate and mitigate biodiversity loss, but also to assess current and proposed management plans (Brondizio, Settele, Díaz, & Ngo, 2019).

Global change ecology is still an emerging field and improvements are being made at a fast pace (Rands et al., 2010). Among the main axes of improvement followed by researchers, are increasing our understanding of synergies between drivers of ecosystem services and biodiversity loss, covering previously poorly described biodiversity (including genetic diversity), and increasing our predictive abilities, notably through model validation and development. Although global change trends, and associated uncertainty, have long been closely monitored and described (Sala et al., 2000; IPCC, 2014), more local information about within-landscape temporal changes is needed to further our ability to predict change (Randin et al., 2009; Potter, Arthur Woods, & Pincebourde, 2013; Yates et al., 2018).

Landscape genetics approaches are, and will continue to be, widely used for conservation biology purposes (Allendorf, Hohenlohe, & Luikart, 2010; Segelbacher et al., 2010; Harrisson, Pavlova, Telonis-Scott, & Sunnucks, 2014). Indeed, landscape genetics bridges an important gap in the field of molecular ecology: providing information about the interaction between micro-evolutionary processes and landscape features (Manel, Schwartz, Luikart, & Taberlet, 2003; Manel & Holderegger, 2013; Wagner & Fortin, 2013; Balkenhol, Cushman, Storfer, & Waits, 2015). Landscape genetics can therefore help us address a wide array of questions, such as how gene flow, and therefore movement (Bohonak, 1999; Clobert, Le Galliard, Cote, Meylan, & Massot, 2009), is affected by environmental heterogeneity (e.g. Wittische et al. 2019), how local landscape characteristics explain the spatial distribution of neutral and adaptive genetic information (e.g. Janes et al., 2014), or even how to locate genetic boundaries.

One of the main ongoing challenges for landscape geneticists, is to detect and predict where and when extraneous disturbance events influence the ecological dynamics and the evolution of species. Changes in genetic diversity can be the result of natural or anthropogenic disturbance at any temporal scale, from a local and abrupt change like a wildfire to a global and gradual change like climate warming (Manel & Holderegger, 2013). However, it is rarely possible to observe the effects of these events instantaneously and researchers are often left with their spatial legacies which may be cryptic. When a disturbance does not constitute a selective pressure, alleles are randomly transferred from a generation to the next and genetic drift happens leading to a loss of diversity. Common examples of situations where genetic drift occurs include geographic isolation, population bottleneck and massive migrations from previously isolated populations. The result of such events in a local population tend to alter the genetic distance of this population with surrounding populations (Segelbacher et al., 2010). Detecting changes in the genetic make-up of a population through time, including the nature of those changes, may describe what is happening at the demographic level, and therefore serve as an alarm for managers.

While the development of tools to identify aberrant loci (Frichot & François, 2015; Luu, Bazin, & Blum, 2017; Duruz et al., 2019) or classify population samples in genetically coherent clusters (Pritchard, Stephens, & Donnelly, 2000; Jombart, Devillard, & Balloux, 2010; Caye, Deist, Martins, Michel, & François, 2016; Verity & Nichols, 2016) is thriving, options offering to test whether a sample has truly changed relative to others, are less visible. Indeed, although one could use existing clustering methods, their relevance and performance on temporal datasets, where the objective is to find which population has indeed changed more significantly than others in the landscape, has not been evaluated.

A permutation-based statistical inference method for the analysis of spatial-temporal changes in community composition have recently been proposed (Legendre & Gauthier, 2014; Shimadzu, Dornelas, & Magurran, 2015). A number of applications of the method on composition data have been made on a range of systems (Legendre & Salvat, 2015; Winegardner, Legendre, Beisner, & Gregory-Eaves, 2017; Kuczynski, Legendre, & Grenouillet, 2018; Legendre & Condit, 2019) and its power and type 1 errors have recently been thoroughly tested through simulations (Legendre, 2018). Temporal Beta-diversity Indices (TBI; Legendre 2018) were designed to asses whether there are sites where the difference in community composition between survey times seems exceptionally large and it was suggested that one could use TBI on gene frequency data. The method involves estimating temporal change in each sampling site between two dates using a dissimilarity index/distance, testing the significance of each change through permutations, and partitioning the change into losses and gains. Comparing genetic data at two different dates separated by a known event may help us understand more about the ecological processes shaping the system, indicate the parts of the landscape where an event had the strongest effects, or highlight which sites should be investigated in the absence of an *a priori* known event.

Our paper seeks to describe how to find out find out which parts of a landscape have undergone atypical and substantial genetic change, for example after a disturbance event. We simulated scenarios where part of the landscape is affected by non-selective demographic changes mimicking the effects of common disturbance events. We then used TBI to measure changes in the gene pool of our populations, and evaluated the power and error rates associated with this approach. Finally, we illustrated the possibilities of this approach through applications on two real genetic datasets.