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

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Running title: Spatio-temporal genetic change

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). This can constitute a clue for population geneticists that a disturbance event happened. 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.

*A lack of specific tools*

While the development of tools to identify aberrant loci (REFs LFMM, PCAdapt...) or classify population samples in genetically coherent clusters (REFs DAPC, STRUCTURE) is thriving, there are few options offering to test whether a sample is truly different from others. Ordination (e.g. PCA) offers clues as to which samples are different and is very valuable as an exploratory technique. Ordination has been used in classification tools such as DAPC (REF) which as it seeks to group samples may indicate which samples are different although the focus is not on finding singularly outlying samples. Furthermore, the relevance and performance of DAPC on temporal datasets, where the objective is to find which population has indeed changed more significantly than others in the landscape, has not evaluated.

*A glimmer of hope brought by community ecology*

Two statistical inference methods have recently been proposed and tested for the analysis of spatial-temporal changes in community composition. Namely they are Local Contributions to Beta Diversity (LCBD; Legendre, P., & De Cáceres 2013) for the spatial question of whether there are sites where the difference in community composition between samples seems exceptionally large and Temporal Beta diversity Indices (TBI; Legendre 2019) for the temporal question of whether there are sites where the difference in community composition between survey times seems exceptionally large. Legendre (2019) suggested that comparing genetic data at two different dates separated by a known event may indicate the locations where the event had strong effects, or that in the absence of an *a priori* event these sites should be investigated to learn about what caused the exceptional genetic change. Using genetic data to shed light on the causes and/or consequences of a local genetic change can also be done for LCBD.

A statistical method for the analysis of temporal beta diversity has recently been described by Legendre (2019). The objective is to compare observations made during two separate surveys through time, involving several sites. The method has two distinct parts: (1) estimate the change in each geographic sampling unit (site) between time 1 (abbreviated T1) and time 2 (T2), using an appro- priate dissimilarity index, called a temporal beta-diversity index (TBI), and test the significance of that change to identify the sites where the change has been exceptionally important; these sites may be worth examining to identify the causes of the differences. And (2) partition the dissimi- larity information into finer indices of losses and gains of species, or of abundances-per-species, which may tell us something about the processes at work in the system, which may have generated these changes. Applications of that method have already been published in palaeoecology (Winegardner et al. 2017) and in the study of freshwater (Kuczynski et al. 2018) and marine animal communities (Legendre & Salvat 2015). Three other ecological applica- tions of the method are presented in the Legendre (2019) paper.

*What this paper is about*

Our paper seeks to describe how to find out find out which parts of a landscape have undergone atypical and substantial genetic change after a disturbance event. We simulated two 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 subpopulations and used a permutation-based approach to distinguish exceptionally different sites.

METHODS

*Simulation experiments*

a) Simulation parameters

We modeled the effects of disturbance on the genetic diversity using the spatially-explicit gene flow simulation software CDMetaPOP (Landguth et al. 2017). CDMetaPOP simulates dispersal and mating of individuals across a landscape, and allows to define the initial genetic structure, spatial distribution of individuals, dispersal characteristics, and life history traits of the population. For each scenario we simulated 1000 replicates, with 25 interconnected populations, 100 bi-allelic loci and maximum carrying capacity of 100 individuals per population. X% (5 vs 50 atm) of individuals within a population may migrate at each generation. 220 generations. Dispersal kernel equation.

b) Simulation scenarios

The first scenario involves modelling a massive extraneous migration from a previously isolated 26th population. This population was simulated during the same number of generations and the cost distance between the 13th (central) and the 26th (isolated) populations is set to 0 between the 200th and 201st generations, mimicking a mass migration event between the two. The 26th population is then isolated again by resetting the cost distance to an unreachable number.

The second scenario involves modelling a demographic bottleneck through massive mortality. To do that, the carrying capacity of the 13th population (central), was set to 10% of its original value between the 200th and 201st generations.

Massive extraneous migration/Bottleneck

*Genetic dissimilarity*

Chord distance has been commonly used in both community ecology (Orlóci 1967; Legendre & Borcard 2018) and population genetics (Cavalli-Sforza & Edwards 1967; Balkenhol et al. 2016). We chose chord distance because it has already been tested for use with TBI with non-genetic data (Legendre 2019) and because it may be more appropriate than other indices of genetic dissimilarity when most of the variation among populations is due to recent changes (Takezaki & Nei 1996; Kalinowski 2002) as it does not assume populations are in drift-mutation equilibrium.

*Estimating type I and type II errors*

a) Permutation approach

b) Two-step criterion

RESULTS

DISCUSSION

A few systems are consistently monitored through time (e.g. REFs LTER...) and/or exhaustively sampled in space (e.g. REFs Fushan...).

REFERENCES