**INTRODUCTION**

The rapid pace of global loss of genetic diversity (Leigh, Hendry, Vázquez‐Domínguez, & Friesen, 2019), is making it increasingly important to move beyond, single sampling/time, snapshot research (Draheim, Moore, Fortin, & Scribner, 2018). Spatial and temporal genetic variation can tell us a great deal about demography and population connectivity (Bradburd & Ralph, 2019; Lowe & Allendorf, 2010). Indeed, population genetics have proven to be essential to translating observed genetic variation into meaningful inferences regarding connectivity and demography that are necessary for conservation efforts. (Allendorf, Hohenlohe, & Luikart, 2010; Harrisson, Pavlova, Telonis-Scott, & Sunnucks, 2014; Segelbacher et al., 2010). In particular, landscape genetics provides information about the interaction between micro-evolutionary processes and landscape features (Balkenhol, Cushman, Storfer, & Waits, 2015; Manel & Holderegger, 2013; Manel, Schwartz, Luikart, & Taberlet, 2003; Wagner & Fortin, 2013). The field of landscape genetics has thus made enormous contributions to our understanding of how spatial heterogeneity influences population genetic processes. However, many situations such as outbreaks, invasions and species declines require researchers and managers to also look through a temporal lens.

Temporal variation in genetic diversity, and its drivers, are indeed at the crux of many conservation issues because they influence the evolution and persistence of a species through processes such as local adaptation, maladaptation, or divergent natural selection (Aeschbacher, Selby, Willis, & Coop, 2016; Bolnick & Nosil, 2007; Kremer et al., 2012). Comparing genetic data at two different dates, whether or not they were separated by an a priori known event, is a challenge because the genetic diversity of a population is dynamic, as beyond recombination and mutation constantly introducing new diversity, every demographic change creates genetic drift. Although it is rarely possible to directly observe the effects of landscape and climate change on spatial and temporal genetic variation, we may observe these effects through their population genetic legacies. Genetic legacies may not be detectable as rapidly as the demographic consequences of a landscape change for example but they may carry a signal of its effects for several generations (Bolliger, Lander, & Balkenhol, 2014; Epps & Keyghobadi, 2015). Researchers commonly use spatio-temporal population genetic legacies to study isolation-by-distance (Rousset, 1997; Wright, 1943), population bottlenecks (Gattepaille, Jakobsson, & Blum, 2013; Maruyama & Fuerstt, 1985), migration between isolated populations (Bezemer, Krauss, Roberts, & Hopper, 2019; Buschbom, Yanbaev, & Degen, 2011), and outbreak expansions (Larroque et al., 2019; Wittische, Janes, & James, 2019). Identifying meaningful and statistically significant relationships between temporal landscape-change and the spatial apportionment of genetic variation can give us important insights about the eco-evolutionary dynamics of a species, and be used to inform conservation strategies (e.g. Landguth, Holden, Mahalovich, & Cushman, 2017).

Spatio-temporal population genetics methods to detect significant past demographic events exist (Excoffier, Dupanloup, Huerta-Sánchez, Sousa, & Foll, 2013; Günther & Coop, 2013; Gutenkunst, Hernandez, Williamson, & Bustamante, 2009), but they are generally purpose-built for large genetic datasets, which span great sections or the whole genome, collected at a single point in time. Those methods often need additional input such as information about recombination processes (Gattepaille et al., 2013) and ascertainment bias (Marth, Czabarka, Murvai, & Sherry, 2004). The lack of phase information also limits the use of some methods because it is needed to account for parent of origin or identity by descent for each allele (Howie, Donnelly, & Marchini, 2009; Kong et al., 2013). Some other studies have directly used genetic differentiation metrics such as Fst, to evaluate temporal change between genetic datasets (e.g. Larroque et al 2019b; Segura-García et al., 2019). However, translating our spatial understanding of Fst-based results to the temporal dimension is not always straightforward. Indeed, appropriate use and interpretation of pairwise Fst requires that certain assumptions such as equal amounts of drift in both populations be respected (Bhatia, Patterson, Sankararaman, & Price, 2013) and translated in a temporal context. Additionally, disentangling spatial from temporal effects is a challenge because the additivity of genetic drift, means than genetic differentiation can be associated with both temporal structure or population divergence (Murray et al., 2016; Skoglund, Sjödin, Skoglund, Lascoux, & Jakobsson, 2014). Testing whether significant change, relative to the expected variation mostly associated with genetic drift, has occurred in a population based on limited time series genetic data remains a challenge.

One of the most crucial steps in this comparison is to evaluate the significance of the change. Indeed, without a mean to determine adequate significance thresholds for their analyses, decision makers and researchers would be left to arbitrarily set thresholds for what constitute change for their specific genetic dataset. Permutation-based approaches can be used to generate a distribution of values against which an observed value (here temporal change in genetic diversity) can be compared . Such 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).

Temporal Beta-diversity Indices (TBI; Legendre 2019) assess the significance of changes in community composition through time. Given the conceptual similarity between the question of how multi-species communities might change through time and our question of monitoring genetic change through time, we expect that TBI can be applied/modified for the analysis of multi-locus genotypic data. The method involves estimating temporal change in each sampling site between two dates using a dissimilarity index/distance, and testing the significance of each change through permutations. Although other permutation-based methods have been successful in answering other genetics questions (e.g. Churchill & Doerge, 1994; Fourtune et al., 2018; Prunier et al., 2013), and TBI has been extensively tested on community composition data (Legendre, 2019b), there is uncertainty about the performance of TBI, when applied to genetic data.

In this study, we build upon the temporal beta diversity indices framework to develop and apply a method, Temporal Genetic diversity Indices (TGI), to quantify and statistically assess temporal variation in spatial genetic diversity. Quantifying relative temporal genetic change among locations will allow us to infer past demographic events. Persisting spatial legacies in genetic diversity can also be used to identify sites that were most strongly impacted by previous demographic events. Such spatial legacies could also highlight which sites should be investigated if managers are not aware of an a priori known demographic event. To demonstrate the effectiveness and applicability of the approach we used a spatially-explicit gene flow simulator (Landguth, Bearlin, Day, & Dunham, 2017). We simulated multiple scenarios in which portions of a landscape are affected by different non-selective demographic changes. We then used TGI to measure changes in genetic make-up of our populations, and evaluated the power and error rates associated with this approach. The goal of our approach is to help researchers with limited time series of genetic data, to identify whether substantial change has occurred in one of the population they studied.

In testing the performance of our TGI approach, we explored how dispersal ability, the number of populations affected a demographic event, and time between two sampling efforts, affected temporal variation in genetic diversity. We also explored how different permutation algorithms in our framework affected our ability to identify statistically significant deviation from neutral expectations, based on simulated processes such as genetic drift. Performance was quantified using standard false positive/negative rates binary classification. We predicted that performance would be lower with increasing dispersal ability because of the homogenizing effect of a higher gene flow. We predict that the longer the time between samplings, regardless of when an event occurred between them, the harder it will be to identify where and when a demographic event occurred. Finally, we briefly showed that TGI testing works on microsatellite data.