

# Applications of landscape genetics in conservation biology: concepts and challenges

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**Abstract** Landscape genetics plays an increasingly important role in the management and conservation of species. Here, we highlight some of the opportunities and challenges in using landscape genetic approaches in conservation biology. We first discuss challenges related to sampling design and introduce several recent methodological developments in landscape genetics (analyses based on pairwise relatedness, the application of Bayesian methods, inference from landscape resistance and a shift from population-based to individual-based analyses). We then show how simulations can foster the field of landscape genetics and, finally, elaborate on technical developments in sequencing techniques that will dramatically improve

our ability to study genetic variation in wild species, opening up new and unprecedented avenues for genetic analysis in conservation biology.

**Keywords** Bayesian analysis · Conservation biology · Genotyping · Isolation by distance · Landscape resistance · Sampling design · Simulation modelling

## Introduction

Habitat fragmentation and climate change have negative impacts on populations, and they are considered to be main

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causes of biodiversity loss and therefore a major issue of conservation biology (Fischer and Lindenmayer 2007; Lindenmayer et al. 2008; Heller and Zavaleta 2009). Thus there is a growing need for natural resource managers to evaluate the impact of proposed management actions on the extent of habitats and the degree of fragmentation of these habitats (Fahrig and Merriam 1985). Habitat loss and fragmentation create discontinuities (i.e. patchiness) in the distribution of critical resources (e.g. food, cover, water) or environmental conditions (e.g. microclimate). From the perspective of an organism, such discontinuities in the distribution of suitable habitat lead to a reduction of connectivity among population fragments (Kindlmann and Burel 2008). As habitat is lost and populations fragmented, functional connectivity through individual exchange and gene flow becomes critically important (Fischer and Lindenmayer 2007). Specifically, subdivision and isolation of populations leads to reduced dispersal success and patch colonization rates, which may result in a decline in the persistence of populations and an enhanced probability of regional extinction across a landscape (Lande 1987; With and King 1999). In addition, metapopulation theory shows that population extinction and recolonization has substantial effects on the genetic differentiation of populations (Wade and McCauley 1988).

Gene flow among populations, either by exchange of individuals in animals, pollen and seed in plants or spores in cryptogams, is necessary to maintain the long-term viability of populations. Gene flow maintains local genetic variation by counteracting genetic drift and spreads potentially adaptive genes. From the perspective of conservation biology, it is thus essential to infer the functional connectivity of populations across landscapes (Van Dyck and Baguette 2005). While there are a number of approaches that have been used to estimate functional connectivity (O'Brien et al. 2006; Fall et al. 2007), its ultimate validation is based on gene flow estimation (Cushman 2006; Cushman et al. 2009a).

Molecular methods offer an increasingly powerful approach to quantifying gene flow across landscapes. A number of tools are currently available to investigate genetic variation in space *and* time, as well as its relationships to environmental conditions. This has led to the research field of *landscape genetics*, which integrates population genetics, landscape ecology and spatial statistics (Manel et al. 2003; Storfer et al. 2007; Holderegger and Wagner 2008). Landscape genetics seeks to elucidate how genetic variation (i.e. neutral and adaptive component) is affected by landscape and environmental variables. Taking advantage of recent statistical developments (e.g. in the field of spatial statistics or Bayesian analysis) it aims to detect the impact of fragmentation on gene flow and to determine how selection and environmental variation shapes adaptive genetic variation in natural populations.

Applications of landscape genetics to conservation typically employ spatial statistical analysis of genetic structure to infer gene flow in space and time (i.e. as a spatial-temporal process, Epperson 2003; Storfer et al. 2007; Anderson et al. 2010). Although landscape genetics is gaining increasing interest, there are still few examples where landscape genetic approaches have been successfully applied to the practical conservation management of species (but see e.g. Epps et al. 2005; Vignieri 2005; Riley et al. 2006; Segelbacher et al. 2008).

In general, landscape genetics often involves spatial and temporal processes that differ significantly from those modelled in population genetics (Epperson et al. 2010). Existing population genetic models assume large population sizes, have high degrees of spatial symmetry and are characterised by many simplifications regarding the life history of species. Appropriate landscape genetic models will need to deal with less symmetry and often greater detailed realism of life history and movement behaviour. However, even in symmetrical space-time processes such as two-dimensional isotropic isolation by distance, there is a high level of stochasticity in the spatial genetic structure created. Hence appropriate models need to maintain some spatial replication (i.e. multiple spatial comparisons) as well to average over multiple genetic markers for adequate statistical power (Epperson 2004, 2007; Cushman et al. 2009b). Effects of spatial scale (i.e. study area extent, spatial sampling design and scale of the processes studied) are critical (Anderson et al. 2010) as the spatial autocorrelation of allele frequencies generally decreases as distance increases (Vekemans and Hardy 2004). Temporal scale, in particular the length of time that a process or the effect of a landscape feature (the term is used here for any heterogeneity in landscape or environmental factors) has been acting is another important determinant of spatial genetic structure. In large populations, for example, it takes about 20–50 generations for most short distance spatial autocorrelation to build up under isolation by distance, and further back in time coalescent events become nearly independent of spatial location (Barton and Wilson 1995). Spatial dimensionality, i.e. the number of spatial dimensions that a studied process effectively acts in, is also critical. For example, populations of a riparian plant species located along a river effectively exist in only one spatial dimension. Generally, one-dimensional systems have greater stochasticity than two-dimensional systems, as well as different amounts of autocorrelation (Epperson 2003).

In the present article, we highlight some of the opportunities and challenges in using landscape genetic approaches in conservation biology. We first discuss challenges related to sampling design and recent methodological developments in landscape genetic analysis, i.e. analyses based on pairwise relatedness, the application of Bayesian

methods, inference from landscape resistance and the shift from population-based to individual-based analyses. We then show how simulations can foster the field of landscape genetics and, finally, we briefly elaborate on technical developments in sequencing techniques that will dramatically improve our ability to study genetic variation in wild species.

### Problems of sampling design

Most research projects start with a particular problem or a distinct question, which should be developed in the form of a statistically falsifiable hypothesis. Yet in the published landscape genetic literature, distinct questions, let alone proper hypotheses, have rarely been stated. In a recent review of 174 landscape genetics studies published from 1998 to 2008, only one-third had an explicit study design (Storfer et al. 2010). One explanation for this shortcoming is that there is usually only limited information available on how landscape features influence the movement and behaviour of animals or on how they affect dispersal in plants. For example, while it may be reasonable to assume that a six-lane, fenced motorway acts as a barrier to animal movement, we may know almost nothing about the effects of open fields, different forest types or varying river currents on animal movement or plant dispersal. Most landscape genetic studies simply ask general questions such as: “Which landscape elements influence the movement or dispersal of animals and plants?” In the absence of any prior knowledge, landscape geneticists therefore tend to sample data on many environmental factors or landscape features. As a null hypothesis, they assume that only geographic distance determines genetic affinity and that an isolation by distance pattern is present (Hutchison and Templeton 1999). However, many applications of landscape genetics in conservation biology will require the development of more sophisticated alternative hypotheses. Recently, Cushman and Landguth (*in press b*) showed that a naive correlational approach can lead to strong spurious correlations leading to false inferences. They emphasized the importance of explicit sampling designs and more sophisticated methods that reject incorrect causal models and provide increased support for the correct driving processes.

It appears that landscape geneticists often only intuitively think about appropriate scales of sampling and the pattern in which genetic samples should be taken (Muirhead et al. 2008). However, there is another, often neglected facet to landscape genetic sampling, namely the resolution in terms of scale and content of the landscape ecological data to be gathered. When investigating the influence of landscape features on gene flow, there is

general agreement that the scale at which genetic samples should be taken must be at least as large as the movement distance of the animal species studied or the dispersal distance of seed and pollen in plants. However, which type of animal movement should be considered? Is it the everyday movement within home-ranges or the episodic movement during dispersal (Baguette and Van Dyck 2007)? Is it the seasonal migration among habitat patches? Clearly, the answer depends on the particular research question to be answered. To define the appropriate spatial scale, researchers mostly rely on available ecological and demographic information on movement and dispersal distances (Sutherland et al. 2000; Bowman et al. 2002). However, caution is needed here. Recent genetic studies investigating contemporary gene flow and migration have often found that pollen and seed dispersal in plants as well as movement in animals far exceed estimates from ecological or demographic studies (both with respect to distance and frequency (Holderegger and Wagner 2008)). Landscape geneticists therefore need to take into account that they might infer gene flow over unexpectedly large distances and that they need to consider landscape features and their configuration over extended spatial scales. This problem of defining the appropriate scale are less critical when testing the genetic effects of a single explicit landscape structure such as a road or a mountain ridge, rather than searching for the general effects of a landscape (Marsh et al. 2008).

Another important consideration in landscape genetic studies is the replication of study areas. The effects of landscape patterns on population genetic processes are a classic example of a landscape-level process (McGarigal and Cushman 2002). To obtain rigorous inferences about pattern-process relationships it would be essential to a priori select a representative sample of study landscapes. Through sampling multiple representative landscapes and treating them as independent observations of the pattern-process relationship, it is possible to rigorously test for the generality of landscape genetic inference. However, nearly all past landscape genetic studies have been based on associations between gene flow estimates and landscape structure in a single species within a single landscape.

Historically, population genetics has sampled individuals that were grouped according to pre-defined, spatially delimited populations and used classical population genetics models such as Wright’s Island model to analyse the data (Wright 1943). However, during the past few years, landscape genetics has developed into a field progressively adopting individual-based statistical analysis (Manel et al. 2005). Landscape genetics studies now often apply Bayesian clustering techniques to group samples into populations in a more objective way (Storfer et al. 2010). Schwartz and McKelvey (2009) recently investigated the

effects of sampling design (e.g. random, stratified or transect sampling) on the performance of STRUCTURE (Pritchard et al. 2000), the most widely applied Bayesian clustering approach. They showed that in situations where near-neighbour mating creates patterns of long range isolation-by distance, STRUCTURE identifies different numbers of clusters depending on the sampling scheme applied. As genetic gradients are probably common in nature, STRUCTURE may thus provide misleading population circumscriptions. Unfortunately, the effects of sampling scheme on individual-based landscape genetic analyses are yet largely unknown and substantial simulation experiments are required to evaluate their potential impact. Further, in reality and especially so in conservation biology, many landscape genetic studies rely on opportunistic sampling, e.g. samples are obtained from hunters or harvesters in the case of larger vertebrates (Schwartz and McKelvey 2009). Alternatively, samples are often taken at locations where animals are most easily caught or trapped, e.g. ponds in the case of anurans (Angelone and Holderegger 2009). Hence, the corresponding sampling is largely non-random. In contrast, it should be possible to apply more regular sampling schemes for smaller animals such as ground-dwelling common insects or for many sessile plant species. A useful recommendation is that, prior to analyzing population structure, researchers should determine the patterns of local autocorrelation and then carefully consider how these patterns may influence the results (Fortin and Dale 2005; Schwartz and McKelvey 2009).

Other critical attributes of scale in landscape genetics that have been largely overlooked are the grain, extent and thematic resolution at which the landscape is represented (Anderson et al. 2010). These factors together define the spatial pattern of landscape features to which spatial patterns of genetic distance or differentiation among individuals or populations is correlated. A mismatch of the scale at which data are analyzed and the scale at which pattern-process relationships function can readily lead to incorrect inferences (Wiens 1989; Dungan et al. 2002; Thompson and McGarigal 2002). In landscape genetics spatial resolution is still an almost unexplored area. Often, landscape information is gathered from existing GIS data bases that have fixed resolution (grid-cell size or grain), a fixed number of landscape features or environmental factors considered and a given known level of uncertainty. A spatial resolution of  $25 \times 25$  m grid size, coarse information on topography and climatic conditions and a simple categorisation of the land cover into open land, forest, settlements, roads etc. can be sufficient to study landscape effects on movement and gene flow in larger vertebrates such as mountain lions or roe deer. On the other hand such a low resolution of landscape data is probably inappropriate for the analysis of small mammals such as mice and

voles, let alone insects, which might be affected by subtle changes in habitats at very small spatial scales. Simulation models can be used to evaluate the sensitivity of pattern-process inferences in landscape genetics to misspecification of the extent, grain and thematic resolution of the landscape. Cushman and Landguth (in press b) demonstrate very high sensitivity to incorrect specification of landscape resistance hypotheses (thematic resolution), but apparently much lower sensitivity to incorrect landscape grain. Thus, to obtain reliable inferences about relationships between landscape patterns and gene flow processes it is essential to carefully consider the thematic resolution of landscape data. It is surprising that the effects of the resolution of landscape data have received so little attention in the landscape genetic literature. Successful future application of landscape genetics to conservation biology requires that these problems of resolution be addressed in much more detail.

### Inferring isolation by distance and dispersal barriers using pairwise relatedness between individuals

Within a homogeneous habitat spatial genetic structure (SGS) arises whenever gene dispersal distances are limited due to local genetic drift. Wright (1943) called this phenomenon “isolation by distance” and showed that the neighbourhood size, defined as  $N_b = 4\pi D\sigma^2$  where  $D$  is the effective population density and  $\sigma^2$  is half of the mean square parent-offspring distance, largely determines the intensity of genetic differentiation. Malecot (1948) addressed the question of how relatedness between individuals decreases with spatial distance under isolation by distance. His approach was refined in subsequent works, leading to methods able to infer  $N_b$  from spatial genotypic data (e.g. Rousset 1997, 2000; Hardy and Vekemans 1999; Epperson 2007). Hence, SGS can provide information on gene dispersal distances through synthetic parameters,  $N_b$  and  $\sigma$ , leading to so called “indirect” estimates. Because SGS builds up over several generations before reaching a quasi-equilibrium state, SGS-based inferences of gene dispersal refer to past dispersal and assume drift-dispersal equilibrium, isotropic dispersal and constant density in space and time.

Several methods have been used to characterize SGS using genotypic data. For example, Rousset (2000) introduced a genetic distance metric between individuals ( $a_r$ ) analogue to pairwise  $F_{ST}/(1 - F_{ST})$  measures between populations. He quantified SGS by the rate of increase of  $a_r$  with the logarithm of distance, showing that, in a two-dimensional population, the rate is inversely proportional to  $N_b$ . As  $N_b = 4\pi D\sigma^2$ ,  $\sigma$  can then be extracted if the value of  $D$  is known (Epperson 2007). SGS has often been characterized by spatial autocorrelograms using Moran's  $I$

statistic applied on allele frequencies measured at the individual level (Sokal and Wartenberg 1983; Epperson 1995, 2003). Hardy and Vekemans (1999) showed that Moran's  $I$  statistic estimates the mean relatedness between individuals separated by a given distance class. They adapted the approach proposed by Rousset (2000) to estimate  $N_b$  using the distance decay of pairwise kinship coefficients, a metric that can be applied to selfing organisms, haploid genomes, or using dominant markers, unlike the  $a_r$  metric (Hardy and Vekemans 1999; Hardy et al. 2006). Two free software programs implement these approaches: GENEPOP (Rousset 2008) uses the  $a_r$  metric or an alternative estimator ( $e_r$ ) with better statistical properties (Watts et al. 2007), and SPAGeDi (Hardy and Vekemans 2002), which applies the  $a_r$  metric or other estimators of kinship coefficients.

SGS-based estimates are valuable for a first estimation of gene dispersal distances (through the synthetic parameter  $\sigma$ ) while other methods are required to obtain exact details on patterns of gene flow (shape of dispersal curves, anisotropy, asymmetrical contributions of fathers to offspring etc.). Most comparisons between SGS-based estimates and direct estimates of gene flow (e.g. using parentage analysis) find that they are congruent within a factor of two (Rousset 2000; Fenster et al. 2003; Oddou-Muratorio et al. 2004). However, they are only reliable if gene dispersal processes are sufficiently homogenous throughout the landscape (i.e. no major barriers). Therefore, Born et al. (2008) suggest to apply a Bayesian clustering technique first to identify potential discontinuities that might reflect major barriers or historical effects and to only then estimate gene dispersal distances within genetic clusters.

Most applications of landscape genetics to conservation biology involve heterogeneous landscapes, seeking to detect genetic discontinuities reflecting major barriers to gene flow diverging populations. Once pre-defined hypotheses are formulated regarding the location of physical barriers, pairwise relatedness measures between individuals can be used to test these hypotheses by contrasting kinship among pairs of individuals belonging to the same putative gene pool ("intra-group") versus individuals belonging to separated gene pools ("inter-group"), or for pairs of individuals located on the same side of a putative barrier versus individuals from different sides of the barrier (Hardy and Vekemans 2002). Such contrasts can be applied to situations relevant to conservation, such as roads, streams or mountain ranges.

It should be noted that formal testing for differences between intra-group and inter-group curves is challenging. While randomization of the spatial positions of individuals provides an adequate way to test the slope of the intra-group curve (test of isolation by distance), it is not

adequate to test the slope of the inter-group curve. The problem arises because an ideal randomization test should separate the spatial correlation of allele frequencies between putative gene pools from the spatial structure within each gene pool, whereas randomization of spatial positions only separates the latter. As a result, such tests can produce many false negatives, a problem similar to problems associated with partial Mantel tests (Raufaste and Rousset 2001). Alternative testing procedures, such as restricted randomization procedures (Fortin and Dale 2005) are clearly needed.

A limitation of inferences based on isolation by distance mathematical models is that the results strongly depend on the assumption of migration-drift equilibrium (Rousset 1997). However, applications of landscape genetics to conservation biology will often deal with non-equilibrium situations, because of the highly dynamic nature of modern human influenced landscapes (Lindenmayer et al. 2008). Both theory and simulations (the latter rely not on equilibrium, but "quasi-equilibrium" from recent generations) have shown that the patterns of isolation by distance expected under scenarios of range expansion or other non-equilibrium models can differ dramatically from those under equilibrium models (Slatkin 1993). As a consequence, a future field of investigation for landscape geneticists is the study of population genetic structure and isolation by distance under computer-simulated dynamical models of spatial expansion, contraction, fusion and fission of populations.

## Bayesian methods

The Bayesian approach shows promise for addressing conservation biology issues (Ellison 2004). Briefly, Bayesian statistics is a framework of statistical inference which aims at calculating posterior probability distributions for parameters of interest, using prior distributions for these parameters, updated based on the data. The characteristics of Bayesian analysis that are attractive to landscape genetics include their ability to be used to (1) tackle complex inference problems using computationally intensive techniques, (2) model individual genetic variability with hierarchical individual-based approaches, and (3) incorporate background information into the specification of population structure models via spatially explicit priors.

An example of a hierarchical individual-based Bayesian model that has been successfully applied in landscape genetics is the algorithm implemented in the program STRUCTURE (Pritchard et al. 2000). The program estimates admixture coefficients representing the proportions of each individual genome originating from a number of unknown source populations. Correctly assessing admixture

is a fundamental step in understanding the short-term evolution of species and the relative influence of landscape features on population structure. Since admixture may result from processes that are intrinsically spatial, for example following regional migration of populations, recent improvements of Bayesian assignment methods have incorporated geographically explicit prior distributions in their models (see Chen et al. 2007). Landscape ecologists have long understood that spatial autocorrelation and geographic trends in the data could bias parameter inference (Lichstein et al. 2002). To overcome this issue, Durand et al. (2009) have proposed an algorithm that includes spatial autocorrelation and geographic trends within an individual model of admixture. Implemented in the program TESS, their algorithm has been used to document the existence of a contact zone for the killifish *Fundulus heteroclitus* (Durand et al. 2009), study the population structure of caribou (*Rangifer tarandus*) in the Rocky Mountains and evaluate the permeability of rivers to racoon (*Procyon lotor*) gene flow in Ontario (Cullingham et al. 2009; McDevitt et al. 2009).

Bayesian methods have also been proposed for inferring contemporary or recent migration rates using individual multilocus genotypes (Wilson and Rannala 2003). An important aspect of these models is that they can incorporate the effects of environmental or landscape variables (Foll and Gaggiotti 2006; Faubet and Gaggiotti 2008). Bayesian population genetic methods can also be applied to describe potential adaptations in species, by identifying outlier loci physically linked to genes under selection through separating neutral effects from adaptive effects based on locus-specific population differentiation coefficients (Beaumont and Balding 2004). For instance, Foll and Gaggiotti (2008) applied this method to the periwinkle *Littorina saxatilis* and identified 21 molecular markers of adaptive relevance.

Another important class of Bayesian methods deals with the inference of demographic parameters using genealogy (Kuhner 2009). Coalescent genealogy samplers are Bayesian programs that aim to estimate parameters influencing the demographic history of species. Such parameters include effective population sizes, growth rates, migration rates or divergence times between populations. Coalescent genealogy sampler approaches are particularly useful in landscape genetics and conservation because they can consider non-equilibrium dynamics and recent divergence of populations. For example, the program BEAST has a nonparametric model of population growth based on a Bayesian skyline plot, which is a graph showing the curve of inferred population size over time (Drummond and Rambaut 2007). The software IM considers two populations that have recently diverged from a common ancestor. This program estimates the divergence time and migration

rates between the diverging populations (Hey and Nielsen 2004).

Although sophisticated models of population structure and demography can be implemented by coalescent genealogy samplers, they are currently restricted to a particular set of scenarios. Hence, there is a need to consider more flexible methods. One of these methods, Approximate Bayesian Computation (ABC) is well-suited to complex problems (e.g. a large number of markers), which would be intractable using likelihood methods (Beaumont et al. 2002). ABC is based on simulations of population genetic models using parameters drawn from prior distributions. A set of summary statistics is then calculated for each simulated sample and compared with the values for the observed sample. Parameters generating summary statistics close enough to the observed data are retained to form an approximate sample from the posterior distribution (Marjoram and Tavaré 2006; Blum and Francois 2010).

ABC approaches can estimate effective population sizes (Tallmon et al. 2004, 2008), migration rates after spatial expansion (Hamilton et al. 2005), levels of genetic introgression and admixture (Excoffier et al. 2005) or divergence time and gene flow in phylogeographic models (Hickerson et al. 2006). ABC has been successfully applied to inferring the demographic history of the cane toad *Bufo marinus* (Estoup et al. 2004), *Drosophila melanogaster* (Thornton and Andolfatto 2006), the model plant *Arabidopsis thaliana* in Europe (Francois et al. 2008) or the bullhead *Cottus gobio* in the Swiss Rhine basin (Neuenschwander et al. 2008b). The latter two studies used individual-based simulation programs designed for the study of the evolution of life history traits and population genetics in a spatially explicit framework (Currat et al. 2004; Guillaume and Rougemont 2006; Strand and Niehaus 2007). ABC analyses are greatly facilitated by the availability of powerful coalescent simulation programs such as MS (Hudson 2002) or SIMCOAL (Laval and Excoffier 2004).

An increasing use of Bayesian methods in landscape genetic applications to conservation biology is expected because of their flexibility in developing solutions for the complexity of processes in species of conservation concern such as small populations size and complex patterns of dispersion (Beaumont and Rannala 2004; Storfer et al. 2007). Individual-based simulation is also becoming increasingly useful in landscape ecology and genetics (e.g. Dunning et al. 1995; Wagner et al. 2006). However, the use of Bayesian approaches also generates problems. For instance, the interpretation of a high number of parameters fixed by the user to reach convergence is not always easy and may require caution and eventually the help of an experimented user.

### **Inference from landscape resistance: from populations to individuals**

In the past, most landscape analyses have represented landscapes as mosaics of categorically different patches. However, in conservation biology it is important to recognize that ecological systems are often more accurately described as multi-scale gradient systems than as categorical hierarchies (Evans and Cushman 2009). In some cases, such as pond and lake systems, oceanic islands or strongly isolated fragmented populations classic Wright-Fisher population genetic models are appropriate. In other cases where the population is continuously distributed in a uniform environment, an isolation by distance model is appropriate (Wright 1943). In many cases however, populations have marked internal structure, and it is often difficult to define discrete boundaries among populations. In such cases, it may be desirable to adopt a gradient perspective on population structure that allows flexible analysis of pattern-process relationships across multiple spatial scales (Anderson et al. 2010). Cushman and Landguth (in press a) used an individual-level, gradient framework for landscape genetics that allows the integration of Wright-Fisher discrete, panmictic populations and isolation by distance (Wright 1943) as special cases in a generalized model of population structure in complex landscapes. This integration allows the use of idealized simple models when they match the pattern-process relationship of a study system, while simultaneously allowing analysis of spatially more complex pattern-process relationships within the same analytical framework. By representing both the genetic dependent variables and the landscape resistance variables as continuous gradients, it is then possible to test competing hypotheses of the effects of landscape structure on gene flow in one synthetic analysis.

Hypothesis testing in landscape genetics entails large risks of incorrect attribution of causality behind observed genetic patterns (Cushman and Landguth in press a). A few authors have tested one or a few landscape resistance models against global panmixia, barriers or isolation by distance. These studies usually interpret the higher support for one of their models as definitive evidence that the model is correct and reflects the factors affecting population connectivity. On the other hand, using a multi-hypothesis, causal modeling approach Cushman et al. (2006) showed that gradients of landscape structure were the predominant drivers of gene flow in a study population of black bears and neither a classic Wright-Fisher discretely bounded, panmictic population structure nor a simple alternative of isolation by distance could be supported.

Moving from representing populations as discrete, non-overlapping patches to gradients of differentially related individuals in complex landscapes should improve our

ability to understand population structure and gene flow in complex and dynamical landscapes. There is a need to predict regional conservation corridors and quantify the degree of expected connectivity between specific areas (e.g. Fall et al. 2007; McRae and Beier 2007). Rigorous identification of the factors that drive gene flow in complex landscapes and the scales at which they are operative is a foundation of reliable mapping of conservation corridors. Specifically, reliable mapping of corridors must be based on a correct representation of the local resistance of the landscape relative to the organism of focus (Cushman et al. 2009a). With such understanding it becomes possible to predict optimal movement corridors for species of concern. This is essential for informed management and conservation planning, as corridors built from false assumptions regarding landscape resistance will likely fail to deliver the desired conservation benefits.

### **Simulation modelling**

In landscape genetic applications to conservation biology, a key approach is the combination of empirical analyses of genetic patterns with computer simulation to identify relevant processes (Cushman 2006; Epperson et al. 2010). This increases our criterion for validation, as a relevant process would have to be supported by both empirical analysis and theory. Specifically, simulations allow the formal exploration of how predictions of classical population genetics regarding drift, selection, genetic diversity and effective population size change as a function of increasingly complex landscapes.

Recently the development of new simulation programs opens new perspectives of investigation. For example, it is possible to simulate the evolution of populations and estimate gene flow in complex landscapes. Currat et al. (2004) introduced the software SPLATCHE (<http://cmpg.unibe.ch/software/splatche/>) that allows the incorporation of various effects of the environment in simulations of migration in the case of population expansion and generates the molecular genetic diversity of one or several samples drawn from the simulated species.

Landguth and Cushman (2010) have developed the software CDPOP as an individual-based spatially explicit population dynamics and population genetic program that simulates mating, dispersal and genetic exchange as probabilistic functions of cost distance among individuals within the context of complex resistant landscapes. This model has been utilized to explore a number of pattern-process issues central to the reliable application of landscape genetics to conservation biology as e.g. the evaluation of the power of statistical methods to infer relationships between landscape patterns and gene flow or the sensitivity of landscape

genetic inference to the scale of landscape data (Cushman and Landguth [in press a, b](#)).

Another approach is used by IBDSIM (Leblois et al. 2009), a package for the simulation of genotypic data under isolation by distance. It is based on a backward “generation by generation” coalescent algorithm allowing the consideration of various isolation-by-distance models with discrete populations as well as continuous populations.

Landscape genetics simulation would be of particular relevance if natural selection could be added to the simulation as evolutionary processes are driven by the combination of selection, gene flow, drift and mutation, with selection playing the dominant role in adaptation. Without a spatially explicit model of selection within complex landscapes it is difficult to explore the interactions between different evolutionary processes. One of the programs implementing such a model is QUNTINEMO (<http://www2.unil.ch/popgen/software/quantinemo/>) (Neuenschwander et al. 2008a), which is an individual-based, genetically explicit stochastic simulation program. It was developed to investigate the effects of selection, mutation, recombination and drift on quantitative traits with varying architectures in structured populations connected by gene flow and located in a heterogeneous habitat. The implementation of a generalized spatially landscape explicit evolution model is an exciting undertaking that is currently the focus of much research, and we hopefully anticipate that such models will be available for broader use by conservation planning within the next few years.

### Perspectives of upcoming sequencing technologies

New DNA sequence technologies will have a number of implications for studies of genetic variation, gene flow, mutation and selection in an explicit spatial manner over entire landscapes. Since 2005, several sequencing platforms have become available, reducing the cost of DNA sequencing by over two orders of magnitude (Shendure and Ji 2008). The 454 system (Roche) was the first of the second-generation sequencing platforms available as a commercial product (Margulies et al. 2005). More recently, two other second-generation DNA sequencers are increasingly attracting attention from the scientific community: the Genetic Analyzer/Solexa (Illumina) and the Solid DNA Sequencer (Applied Biosystems). In the next few years, other sequencing systems (i.e. “next next” generation sequencers) based on nanotechnologies will become available, even opening the door for low cost whole genome sequencing. The approaches developed by Visigen Biotechnologies ([visigenbio.com](http://visigenbio.com)) and Pacific Biosciences ([www.pacificbiosciences.com](http://www.pacificbiosciences.com); Eid et al. 2009)

appear to be particularly attractive and have the goal of sequencing whole mammalian genomes within minutes.

The new sequencing technologies have already made it possible to generate massive amounts of DNA sequence data for non-model species. For instance, the search for DNA regions of adaptive relevance, the identification of SNP markers for massive genotyping exercises is now possible even in rare species of conservation importance, with relatively low expenses in costs and time. These new sequence technologies also replace the tedious and expensive identification of microsatellite markers using traditional cloning methods (Abdelkrim et al. 2009). Even low coverage whole genome data can identify a large number of suitable microsatellite loci; the most commonly used molecular marker type in landscape genetics (Storfer et al. 2010).

A larger coverage of the genome will enable us to get a far better understanding of the genetic variation of individuals and populations. High resolution will also enhance our understanding of the effects of gene flow and the demographic history of populations, both critical parameters in small endangered populations. Additionally, large datasets will allow the identification of genomic regions under selection. Comparing neutral and adaptive genetic variation then would give us insight into the impact of drift and selection in natural populations, and we could improve our understanding of local adaptation in both individuals and populations.

If this becomes possible, then the sampling of study individuals, bioinformatics, computing time and data storage will replace genotyping as the limiting factors in genetic analysis (Manel and Segelbacher 2009). With respect to landscape genetics and conservation biology, sampling and field work might then become the restricting parts of an investigation, while genetic analysis no longer exerts relevant limits. In any case, we believe that, in the near future, genetic investigations will play an even more important role in conservation biology and practical management. The next technical revolution will complement our increasingly varied and powerful analytical approaches to analyze genetic variation, both neutral and adaptive, within landscapes.

### Conclusions

Landscape genetic methods provide a powerful framework for directly analyzing relationships between population processes and landscape structure at relevant spatial and temporal scales. For instance, it enables researchers to test multiple competing hypotheses about the role of specific landscape features and environmental conditions in affecting population connectivity. More generally, it increases

our ability to make detailed inferences about movement and gene flow and potentially adaptation at the landscape level. These advances will prove to be exceptionally valuable to efforts in applied conservation biology. For example, understanding the landscape features that drive gene flow, the spatial scales at which they act, and the temporal dynamics of their effects on population substructure is essential to effectively use genetic data as a tool for evaluating population status and fragmentation. In addition, using this understanding to predict, localize and implement empirically based conservation corridors should greatly improve the successfulness of efforts to promote landscape connectivity of species at risk due to fragmentation. The potential of landscape genetics to address large-scale connectivity questions is particularly important in the face of global climate change, which is coupled with accelerating habitat loss and degradation. Finally, it is the combination of various analytical approaches with simulation modeling, which will be of particular help to interpret landscape genetic results and to infer adequate strategies in conservation management.

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