



**HAL**  
open science

## Functional connectivity in replicated urban landscapes in the land snail (*Cornu aspersum*)

Manon Balbi, Aude Ernoult, Pedro Poli, Luc Madec, Annie Guiller,  
Marie-Claire Martin, Jean Nabucet, Véronique Beaujouan, Eric Petit

### ► To cite this version:

Manon Balbi, Aude Ernoult, Pedro Poli, Luc Madec, Annie Guiller, et al.. Functional connectivity in replicated urban landscapes in the land snail (*Cornu aspersum*). *Molecular Ecology*, 2018, 27 (6), pp.1357-1370. 10.1111/mec.14521 . hal-01771481

**HAL Id: hal-01771481**

**<https://hal-univ-rennes1.archives-ouvertes.fr/hal-01771481>**

Submitted on 5 Jul 2018

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

MISS MANON BALBI (Orcid ID : 0000-0002-1915-8639)

Article type : Original Article

Title: Functional connectivity in replicated urban landscapes in the land snail (*Cornu aspersum*)

Running title: Connectivity in replicated urban landscapes

Authors :

Manon BALBI; UMR 6553 Ecosystems, Biodiversity, Evolution (Ecobio), CNRS, Université Rennes 1, 35042 Rennes, France; manon.balbi@gmail.com

Aude ERNOULT ; UMR 6553 Ecosystems, Biodiversity, Evolution (Ecobio), CNRS, Université Rennes 1, 35042 Rennes, France; aude.ernoult@univ-rennes1.fr

Pedro POLI ; UMR 6553 Ecosystems, Biodiversity, Evolution (Ecobio), CNRS, Université Rennes 1, 35042 Rennes, France; pvpoli@gmail.com

Luc MADEC; UMR 6553 Ecosystems, Biodiversity, Evolution (Ecobio), CNRS, Université Rennes 1, 35042 Rennes, France ; luc.madec@univ-rennes1.fr

Annie GUILLER ; Edysan FRE 3498, CNRS, Université de Picardie Jules Vernes, 80000 Amiens ; France ; annie.guiller@u-picardie.fr

Marie-Claire MARTIN ; UMR 6553 Ecosystems, Biodiversity, Evolution (Ecobio), CNRS, Université Rennes 1, 35042 Rennes, France; marie-claire.martin@univ-rennes1.fr

Accepted Article

Jean Nabucet ; UMR LETG, CNRS, Université de Rennes 2, EPHE-PSL, Université d'Angers, Université de Bretagne Occidentale, Université de Caen Normandie, Université de Nantes, Place du Recteur Henri Le Moal, 35043 Rennes Cedex, France ; jean.nabucet@uhb.fr

Véronique Beaujouan, Unité de Recherche Paysage et Ecologie ESA ; Agrocampus Ouest ; 49045 Angers ; France ; veronique.beaujouan@agrocampus-ouest.fr

Eric J. PETIT; ESE, Ecology and Ecosystem Health, Agrocampus Ouest, INRA, 35042 Rennes, France; eric.petit@inra.fr

Corresponding author: Manon Balbi, UMR 6553 Ecosystems, Biodiversity, Evolution (Ecobio), CNRS, Université Rennes 1, 263 Avenue Général Leclerc, 35042 Rennes Cedex, France; manon.balbi@gmail.com

## Abstract

Urban areas are highly fragmented and thereby exert strong constraints on individual dispersal. Despite this, some species manage to persist in urban areas, such as the garden snail, *Cornu aspersum*, which is common in cityscapes despite its low mobility. Using landscape genetic approaches, we combined study area replication and multi-scale analysis to determine how landscape composition, configuration, and connectivity influence snail dispersal across urban areas. At the overall landscape scale, areas with a high percentage of roads decreased genetic differentiation between populations. At the population scale, genetic differentiation was positively linked with building surface, the proportion of borders where wooded patches and roads appeared side-by-side and the proportion of borders combining wooded patches and other impervious areas. Analyses based on pairwise genetic distances validated the isolation-by-distance and isolation-by-resistance models for this land snail, with an equal fit to least-cost paths and circuit-theory-based models. Each of the 12 landscapes analyzed separately yielded specific relations to environmental features,

whereas analyses integrating all replicates highlighted general common effects. Our results suggest that urban transport infrastructures facilitate passive snail dispersal. At a local scale, corresponding to active dispersal, unfavorable habitats (wooded and impervious areas) isolate populations. This work upholds the use of replicated landscapes to increase the generalizability of landscape genetics results, and shows how multi-scale analyses provide insight to scale-dependent processes.

#### Keywords

gene flow, resistance-based models, urban, landscape genetics, Gastropoda, isolation by distance

#### Introduction

Cities are growing around the world, and they contain an increasing proportion of the human population (United Nations, 2015). Urbanization is regarded as a major threat to global biodiversity (Grimm et al., 2008; McKinney, 2006). Urban areas are characterized by their high degree of fragmentation, where habitat patches are generally restricted to small vegetated areas isolated from each other by an inhospitable matrix (Cadenasso, Pickett, & Schwarz, 2007; Forman, 2014). Habitat patches are also altered by multiple anthropic disturbances and frequent habitat transformation (Ramalho & Hobbs, 2012). Habitat fragmentation affects population genetic structure and dynamics, with potential deleterious effects on population persistence (Keyghobadi, 2007). To limit fragmentation effects, maintaining landscape connectivity (i.e. the degree to which the landscape facilitates or impedes movement, Taylor, Fahrig, Henein, & Merriam, 1993) is an important tool in

conservation biology. Landscape connectivity is influenced by structural (referring to the physical relationships of landscape elements) and functional (based on the movement of organisms through the landscape, Taylor, Fahrig, & With, 2006) components. Functional landscape connectivity can be assessed by associating genetic population structure with landscape features (Baguette, Blanchet, Legrand, Stevens, & Turlure, 2013; Manel, Schwartz, Luikart, & Taberlet, 2003). When applied to urban areas, landscape genetics approaches have shown that urbanization limits gene flow among populations and thus increases genetic differentiation (M. T. J. Johnson & Munshi-South, 2017). Urban areas act as barriers between non-urban populations located around cities (e.g. bobcats, *Lynx rufus*, Lee et al., 2012; pine marten, *Martes martes*, Ruiz-González et al., 2014; solitary bee, *Colletes floralis*, Davis, Murray, Fitzpatrick, Brown, & Paxton, 2010) and between intra-urban populations (e.g. white-footed mouse, *Peromyscus leucopus*, Munshi-South, 2012; Munshi-South & Kharchenko, 2010; Munshi-South, Zolnik, & Harris, 2016). Such barrier effects were linked to particular urban features such as major transport infrastructures (Holderegger & Di Giulio, 2010; Lee et al., 2012), buildings, bodies of water (common wall lizard, *Podarcis muralis*, Beninde et al., 2016, European hedgehog, *Erinaceus europaeus*, Braaker, Kormann, Bontadina, & Obrist, 2017). Moreover, features favoring gene flow, such as urban green spaces or canopy cover (M. T. J. Johnson & Munshi-South, 2017; Munshi-South, 2012), have also been identified. However, studies that focus on intra-urban populations are under-represented and knowledge is lacking on the way particular urban landscape features and connectivity influence genetic exchange, especially for organisms with restricted mobility (La Point, Balkenhol, Hale, Sadler, & van der Ree, 2015; Storfer, Murphy, Spear, Holderegger, & Waits, 2010).

Accepted Article

Major challenges remain in understanding dispersal processes across landscapes using landscape genetics approaches. These approaches are not always generalizable because they neglect two main issues, (1) landscapes replication and (2) multi-scale landscape analyses (Holderegger & Wagner, 2008; Pflüger & Balkenhol, 2014; Richardson, Brady, Wang, & Spear, 2016; Segelbacher et al., 2010). Landscape replication is necessary to expand the scope of inference of landscape genetics. Multiple and independent landscapes need to be evaluated (Segelbacher et al., 2010), with the landscape itself as a study unit. Replication offers the opportunity to extract general landscape effects across all replicates but also to focus on the specific contribution of each landscape. The few studies using replicated landscapes show that generalization was not straightforward and that extrapolating from one landscape to another could be misleading (Castillo et al., 2016; Hand et al., 2016; Richardson et al., 2016; Villemey et al., 2016). For example, by comparing twelve landscapes, Short Bull et al. (2011) found that the features influencing American black bear gene flow were different between landscapes and were those with the highest variation within each landscape. Landscape replicates should be homogeneous in terms of landscape characteristics when seeking generalization. At least, post-hoc statistical controls can justify that landscape metrics vary in the same way across landscapes. Urban landscapes are good candidates for keeping a certain level of homogeneity among replicates because cities broadly share similar compositions and fragmentation levels due to similarly altered environmental conditions (Groffman et al., 2017; Parris, 2016). However, to date no studies of urban gene flow have used replicated landscapes across multiple cities (M. T. J. Johnson & Munshi-South, 2017).

Accepted Article

Central to landscape ecology is the idea that landscape patterns and processes are scale dependent (Wiens, 1989). Multiple spatial scale approaches are thus recommended to obtain a thorough picture of landscape effects on the genetic structure of populations (Pflüger & Balkenhol, 2014; Wagner & Fortin, 2013), with recent research documenting how multiple scale analysis supports distinct and scale dependent landscape effects (e.g. Angelone, Kienast, & Holderegger, 2011; Dionne, Caron, Dodson, & Bernatchez, 2008; Hand et al., 2016; Millette & Keyghobadi, 2015). However, most studies still evaluate landscape – genetic relationships at a single spatial scale (Manel & Holderegger, 2013; Waits, Cushman, & Spear, 2016), which might result in the lack of a particular landscape effect because of limited scale and/or inferential power. An additional difficulty is that landscape genetic inferences made at one scale are difficult to extrapolate to another scale and may lead to erroneous management recommendations (Dudaniec et al., 2013). For example, Murphy, Evans, & Storfer (2010) showed that the landscape variables in association with genetic structure of the western toad (*Anaxyrus boreas*) were different when they considered several scales (or hierarchical levels, i.e. within or between genetic clusters). Within clusters, significant landscape variables corresponded to localized processes (e.g. growing season precipitation) whereas connectivity between clusters was explained by more general, broad-scale metrics (e.g. topography). Only the proportion of impervious surfaces (including roads) was significant both within and between clusters, showing the effect of fragmentation at different scales. Different hierarchical levels of analysis can be used, but so far most landscape genetic studies have focused on pairwise distance analysis (i.e. matrix quality effect between population pairs), so that the effects of overall landscape or local environmental conditions are most often ignored (DiLeo & Wagner, 2016).

Analysis at the overall landscape scale is rare because it requires replicated landscapes and

Accepted Article

integrating these landscapes into a single analysis. Consideration of the overall landscape scale provides an opportunity to assess the intensity of gene flow and to compare it among landscapes, using metrics of landscape composition and configuration. The degree of homogeneity among landscapes can be assessed and associated with specific effects on the overall genetic structure. Moreover, it provides clues to interpret potential overall landscape effects, e.g. urban green spaces or green waste management, which may influence the probability of passive dispersal events and lead to overall population homogenization.

At a finer spatial scale, local conditions such as habitat amount and habitat spatial structure (respectively linked to resource availability and fragmentation) play a major role in population ecology (DiLeo & Wagner, 2016). For example, local conditions can influence population size (and consequently genetic drift) and dispersal through density-dependent processes (Baguette & Van Dyck, 2007; Dahirel, Vardakis, Ansart, & Madec, 2016; Pflüger & Balkenhol, 2014).

Pairwise  $F_{ST}$  approaches classically compare genetic differentiation indices to different scenarios testing the effects of matrix quality on dispersal success (Pflüger & Balkenhol, 2014). The simplest scenario is the isolation-by-distance model (IBD), which refers to limited dispersal across space based on Euclidean distances between populations. Based on functional connectivity concepts, isolation-by-resistance (IBR) models hypothesize that low resistant areas exchange a greater number of individuals (McRae, 2006). The classically used resistance-based models are least-cost-path (LCP, Adriaensen et al., 2003) and circuit-theory- (CT-) based analyses (McRae, Dickson, Keitt, & Shah, 2008). The different scenarios

based on these two models can vary according to the resistance value sets, habitat types, and environmental conditions, which support assessing of their relative performances (e.g. Braaker et al., 2017; Dupont, Torres-Leguizamon, René-Corail, & Mathieu, 2017; Fenderson et al., 2014).

The effects of landscape fragmentation vary depending on organism mobility (Concepción, Moretti, Altermatt, Nobis, & Obrist, 2015). Low-mobility organisms can survive in relatively small habitat patches (Braaker, Ghazoul, Obrist, & Moretti, 2014). However, they tend to be intensively affected by fragmentation (and habitat loss, Öckinger et al., 2010; Piano et al., 2017) when they move among distant habitat patches to disperse or move away from disturbances. Despite their low degree of mobility, organisms such as terrestrial Gastropods can persist and are largely spread across urban landscapes (Barbato, Benocci, Caruso, & Manganelli, 2017). The garden snail *Cornu aspersum* (Gastropoda, Helicidae, formerly *Helix aspersa*) is a widespread, synanthropic species (Ansart, Madec, & Guiller, 2009; Barbato et al., 2017; Kerney, Cameron, & Bertrand, 2006). It has poor mobility (a maximum of 10-50 meters per month during activity periods, Dahirel, Vardakis, et al., 2016; Dan, 1978) due to the extremely high cost associated with movement, in energy (foot muscle contraction) and water (mucus production, Denny, 1980). *C. aspersum* lives in aggregated colonies connected by low ongoing gene flow. Spatial distances between populations strongly influence genetic differentiation (Arnaud, 2003; Arnaud et al., 1999; Selander & Kaufman, 1975). Moreover, snails are very sensitive to the type of substrate they are moving through, so their movements can be facilitated by road verges and hedgerows (Arnaud, 2003), while roads drastically limit them (Baur & Baur, 1990).

We used methodological approaches which aim at identifying the diversity of landscape effects on dispersal, based on landscape replication and multi-scale analyses. Landscape composition and configuration were characterized in each landscape and local environments, and functional connectivity scenarios were applied between population pairs. Resistance-based models (LCP and CT analyses) were compared in association with different sets of resistance values varying in distribution functions. For each scale, population differentiation was quantified using landscape, population, and pairwise  $F_{ST}$ , respectively. Based on a replicated study design, the effects of overall landscape, local environment, and functional connectivity were assessed across and among twelve distinct urban landscapes. We expected the amount of favorable habitats (i.e. vegetation) to decrease population divergence whereas unfavorable land cover (roads, buildings) would increase it through fragmentation and barrier effects. We also expected IBR scenarios to better explain population structure than simple IBD models as snails have restricted dispersal capacities and are sensitive to landscape composition.

## Materials and methods

### Study sites and sampling design

The sampled sites were located in 3 different French urban agglomerations: Angers (Long-Term Ecological Research site [LTER] Zone Atelier Loire - 47°28'N, 0°33'W), Rennes (LTER Zone Atelier Armorique - 48°06'N, 1°40'W), and Lens (50°25'N, 2°49'W). In each urban agglomeration, we selected 4 landscape windows, named "landscapes". The 12 landscapes measured 1.3 km in diameter (SD=0.3 – Fig. 1) with land cover consisting of 43% (SD=12) of green infrastructures (wooded and herbaceous areas), while all the other surfaces were artificial (buildings, roads, asphalt surfaces, detailed in Fig. 2).

In each of the 12 landscapes, 10 snail populations were collected. *C. aspersum* discrete colonies have been estimated as panmictic units of 25 - 70 m in diameter (Arnaud et al., 1999; Madec, 1989; Selander & Kaufman, 1975). In this study, a population referred to individuals spatially aggregated across a maximum distance of 50m. Populations were on average 580 m (SD = 125) apart in each landscape. We sampled 21 individuals (SD = 3) in each population. Sampling took place from June to October 2015 in Angers and Rennes, and from April to November 2014 in Lens. Snails were found on lawns, at the base of hedgerows, along walls or sidewalks. A total of 2,600 snails was sampled.

#### Genetic data

DNA extraction, locus amplification and genotyping were performed as described in Arnaud, Madec, Guiller, & Deunff (2003) and Guiller, Arnaud, Vautrin, & Solignac (2000), with slight modifications. Garden snails were genotyped at seven microsatellite loci (Table S1).

Total genomic DNA was extracted from foot muscle tissue (of fresh snails) mixed with 500  $\mu$ L of 10% Chelex-100 suspension preheated to 60°C and 15  $\mu$ L of Proteinase K (10 mg/mL). Samples were incubated overnight at 55°C. Then they were mixed twice at 100°C for 15 minutes.

The seven microsatellite loci were multiplexed in three distinct PCR reactions ([Ha6, Ha8], [Ha2, Ha10, Ha11], [Ha14, Ha16]). PCR amplifications were carried out in a total volume of 15  $\mu$ L containing 7  $\mu$ L of MyTaq™ Mix (Bioline), 0.5  $\mu$ L of each primer (0.2  $\mu$ M concentration), 1.25  $\mu$ L of extracted DNA sample, and completed with sterilized water.

Cycling was performed with one 5-min step at 94°C, 35 cycles of 30 s at 94°C, 30 s at 51.4°C for [Ha6, Ha8] and [Ha14, Ha16] loci or at 54 °C for [Ha2, Ha10, Ha11], 30 s at 72°C, and one final 5-min step at 72°C before incubation at 4°C. Prior to genotyping with an ABI 3130 XL

automated DNA sequencer (Applied Biosystems), 1.25  $\mu\text{L}$  of amplified DNA were mixed with 0.25  $\mu\text{L}$  of GeneScan™ 500 ROX™ dye size standard (Applied Biosystems) and 10  $\mu\text{L}$  of Hi-Di™ Formamide for 5 min at 95°C.

Alleles were scored using GeneMapper 4.1 (Applied Biosystems). Genotypic linkage disequilibrium and departures from Hardy Weinberg (HW) equilibrium were tested in each population using Fstat 2.9 (Goudet, 2001). Genotypic (linkage) disequilibrium was altogether non-significant (except for one test in LF1 – adjusted p-value <0.05), so all markers were considered as independent. Significant departures from HW equilibrium (adjusted p-value <0.05) were found in 10% of the 834 tests, with two loci showing the greatest deviations from HW equilibrium in Rennes landscapes (Ha16 and Ha11 - Table S2). We suspected null alleles, whose frequencies were mostly low (mean = 0.067; SD = 0.064, Table S3), but occasionally reached >0.2 in Rennes landscapes. We thus computed landscape  $F_{ST}$ , population  $F_{ST}$ , and pairwise  $F_{ST}$  values by correcting for the presence of null alleles with an expectation maximization method using FreeNA software (Chapuis & Estoup, 2007). Landscape  $F_{ST}$  was estimated including all sampled populations in each landscape. Population-specific  $F_{ST}$  was estimated between the focal population and all other populations in each landscape, reflecting the genetic differentiation of a population as compared to all other populations (Gaggiotti & Foll, 2010; Pflüger & Balkenhol, 2014). Pairwise  $F_{ST}$  was estimated between population pairs in each landscape. Allele frequencies and heterozygosities were computed with R (R Core Team, 2015) and hierfstat R package (Goudet & Jombart, 2015). Mean expected heterozygosity ranged from 0.69 to 0.85 (depending on landscape). The mean number of alleles was 7.7, and ranged between 5.7 and 10.3 (Table 2).

## Landscape metrics and connectivity map modeling

For each city, a high resolution ( $5 \times 5$  m) land cover map was produced from GIS Data from the National Geographic Institute of France (BD TOPO (c) IGN - 2010). The maps distinguished 6 land cover classes: building, wooded areas, herbaceous areas, water bodies, transport infrastructures (roads and railways), and other impervious asphalt surfaces (e.g. parking lots, sidewalks – Fig. 1, Fig. 2, and Table 1). We computed simple landscape metrics applied to each land cover class (except water surfaces, which were rare) using two spatial pattern analysis programs, Fragstat v.4 (Mcgarigal, Cushman, Neel, & Ene, 2002) and Chloé2012 (Boussard & Baudry, 2014). The percentage of landscape occupied by each characterized landscape composition (PLAND) and the mean area of patches for each land cover class (AREA (MN)) reported the landscape fragmentation level. As *Cornu aspersum* can detect boundaries between land cover types during exploration (Dahirel, Séguret, Ansart, & Madec, 2016), we quantified another fragmentation metric that was the proportion of borders combining two different specified adjacent land cover classes (RATE COUPLE, Fig. S1). These 20 landscape metrics (i.e. 5 land cover classes each for PLAND and AREA metrics, 10 combinations for RATE COUPLE) were computed at the landscape (the 12 landscapes - 1.3 km diameter) and population scales, with a buffer radius of 70 m around each population location, corresponding to the estimated panmictic unit size for the population scale (Fig. 1).

Regarding pairwise  $F_{ST}$  analysis, landscape connectivity was estimated with two different resistance-based models. These models are based on landscape resistance values that reflect the energetic cost for an individual to move, its willingness to move, and/or the risk of moving across each habitat class (Zeller, McGarigal, & Whiteley, 2012). Populations are linked to each other across resistance maps (on which resistance values are applied to each

land cover class) by different algorithms, searching for optimal (less resistant) pathways. Least-cost-path (LCP) analyses predict the optimal path with the lowest cumulated resistance, whereas circuit-theory- (CT-) based models integrate all available pathways (McRae et al., 2008). To determine resistance values, hierarchization of land cover classes was adapted from the 4-level fuzzy coding system used by Falkner, Obrdlík, Castella, & Speight (2001) to describe the degree of association of molluscan species to habitat types. Herbaceous areas were the most favorable habitat. Wooded and impervious areas were less favorable, followed by transport infrastructure. Building and water bodies were the least permeable areas (Table 1). Resistance-based model performance is known to vary with the transformation function applied to resistance values (Chardon, Adriaensen, & Matthysen, 2003; Rayfield, Fortin, & Fall, 2010). We created three sets of resistance values varying in transformation function: linear, exponential, and logarithmic functions, bounded from 1 to 100 (Table 1). LCP lengths were extracted with Graphab software (Foltête, Clauzel, & Vuidel, 2012) and cumulated resistance (from CT-based analysis) with Circuitscape (McRae et al., 2008). Geographic Euclidean distances were also computed (ArcGIS, ESRI, and R-package g-distance, van Etten, 2017). All Euclidean and resistance distances were log-transformed and used in distinct regression analyses.

#### Statistical analyses

We first described the overall genetic structure of our data set by means of a hierarchical analysis of molecular variance using the R package hierfstat (Goudet & Jombart, 2015).

At the landscape scale, we tested whether landscape  $F_{ST}$  was related to any landscape metrics with linear models by frequentist hypothesis testing (F statistics in ANOVA). Because of the small sample size (12 landscapes), landscape metrics were tested one after the other

in the linear model.

For both population and pairwise  $F_{ST}$  analyses, the whole dataset (i.e. the 120 populations and 574 pairs included in the 12 landscapes) was used in linear mixed models integrating landscape identity as a random factor. Despite the hierarchical sampling design, landscape identity could not be nested within the three cities because of model overfitting considerations. The number of levels would be too small (four landscapes) per random factor (city; Bolker et al., 2009).

At the population scale, the relation between population  $F_{ST}$  and local landscape metrics was analyzed in two steps. First, we used automated model selection (R package MuMin, Bartoń, 2016) to compare additive mixed models that included a maximum of 10 variables (the number of 20 landscape metrics was too large for our sample size: 12×10 populations, Forstmeier, Wagenmakers, & Parker, 2017). We retained all variables included in models that were within 2 AICc units from the best model (Burnham & Anderson, 2002) and computed the model-averaged importance of these variables. Then, we focused on landscape-specific effects by analyzing models built with each of the retained variables (fixed factor) and including a random slope to the random factor (Bates, Mächler, Bolker, & Walker, 2014). Random effect variations were highlighted by likelihood ratio tests (LRT) by comparing models with and without random slopes (see Jaffé et al., 2016).

Pairwise  $F_{ST}$  (standardized with a logit function, Rousset, 1997) were used as the dependent variable, and resistance-based (least-cost lengths or cumulated resistances) or Euclidean distances were used as the independent variable in linear mixed models (random intercept and slope). Linear mixed models were compared based on their AICc values (J. B. Johnson & Omland, 2004; Row, Knick, Oyler-McCance, Loughheed, & Fedy, 2017). The correlation structure of the maximum likelihood population effect (MLPE, Clarke, Rothery, & Raybould,

2002; Jaffé et al., 2016; Peterman, Connette, Semlitsch, & Eggert, 2014; Van Strien, Keller, & Holderegger, 2012) was added to the pairwise  $F_{ST}$  models. MLPE parameterization accounted for the covariate structure of allelic frequencies between populations in each landscape, corresponding to the proportion of the variance linked to the correlation between pairwise distances. The R package nmle (Pinheiro, Bates, DebRoy, Sarkar, & R-core Team, 2016) was used with corMLPE R function (<https://github.com/nspope/corMLPE>). The contribution of landscape-specific effects was highlighted by LRT, comparing models with and without a random slope (Jaffé et al., 2016).

Moreover, landscape-specific effects were analyzed by linear models computed for each landscape (as classically done in non-replicated landscape studies – e.g. Dupont, Torres-Leguizamon, René-Corail, & Mathieu, 2017). This one-by-one landscape approach was applied to population and pairwise  $F_{ST}$  analyses. Metrics were separately tested in each model by hypothesis testing (F statistics in ANOVA). Focusing on population  $F_{ST}$ , we tried to determine why some landscape metrics were relevant as fixed factors in the whole dataset linear mixed model whereas they performed satisfactorily only in a few landscapes when landscapes were analyzed separately. We compared landscape metric values with permutation tests between the group of landscapes with relevant metrics and the group of remaining landscapes (see Short Bull et al., 2011).

## Results

### Landscape $F_{ST}$

Landscape  $F_{ST}$  values varied among landscapes (range: 0.035- 0.15; Fig. 3, Table 2; see also the Supplementary text for a global overview of the genetic structure across cities, landscapes and populations and Fig. S2). The percentage of transport infrastructure was the only landscape metric (from a total of 20) with a significant relationship with landscape  $F_{ST}$  (slope estimate (SE) = -0.011 (0.004); F value = 8.2 on 1 and 10 DF; p-value = 0.017;  $R^2$  = 0.43 – Fig. 3). Globally, populations were genetically more differentiated when landscapes comprised a low percentage of transport infrastructure (mainly roads).

### Population $F_{ST}$

Model selection retained three metrics included in models within 2 AICc units from the best model. Population  $F_{ST}$  values were positively correlated with the average surface of buildings (AREA building), the proportion of wooded/transport infrastructure borders (RATE COUPLE w/t) and wooded/impervious borders (RATE COUPLE w/i – Table 3). We focused on models associating one of the three retained metrics as a fixed factor and the landscape random factor with random intercept and slope. Variability among landscapes (random effects) was detected for these three models (LRT and random estimate ranges – Table 3). When each landscape was analyzed separately, the links between population  $F_{ST}$  and landscape metrics were not consistent across landscapes (fixed factor p-value <0.05 in less than three landscapes out of the 12 landscapes for each of the 20 landscape metrics: PLAND, AREA, RATE\_COUPLE for each land cover class). Only the average surface of buildings (AREA

Accepted Article

building) and proportion of wooded/ transport infrastructure borders (RATE COUPLE w/t) were positively related with population  $F_{ST}$  in 3 different landscapes ([AF2, AF4, RF2] and [LF2, RF2, RF3], respectively). We tested whether the non-significance of the average surface of buildings in some landscapes was linked with a reduced surface occupied by buildings, which may have been non-limiting for individual dispersal. AREA building was higher in the group of significant landscapes (mean (SD) = 437 (288) sq.m vs. mean (SD) = 315 (297) sq.m – permutation test,  $p = 0.04$ ). No difference was detected for RATE COUPLE w/t values.

#### Pairwise $F_{ST}$

Regarding pairwise analysis with the whole dataset (landscapes as a random factor), several models had lower AICc values than the null model (i.e. without any fixed factor – Table 4). These models included Euclidean distances or LCP distances for exponential, linear and logarithmic distributions of resistance values, and CT distances for all distributions of resistance values. Among those, three models equally outperformed the model with Euclidean distances: two models with LCP distances (logarithmic and exponential distributions) and one model with CT distances (exponential distribution - Table 4). We focused on the Euclidean distance model (i.e. the isolation by distance [IBD] model) to study variability among landscape random effects because among satisfactory models it was the most parsimonious model (regarding its intrinsic simplicity relative to resistance-based models). The likelihood ratio test of this IBD model with or without a random slope was significant (LR = 7.98;  $p = 0.018$ ). The magnitude of the landscape-specific IBD effect varied across landscapes. The mean IBD slope for all landscapes (fixed effect estimate) was 0.010,

while landscape-specific IBD slopes (random effect estimates) ranged from -0.010 (AF2) to 0.014 (LF1, Fig. 4). When landscapes were analyzed separately (one linear model per landscape), null models (without any fixed effect) had the lowest AICc values in 11 landscapes. Only landscape LF3 had LCP distance models (all distributions of resistance values) better than the null model ( $\Delta AICc > 2$ ).

## Discussion

We studied the population genetic structure of the garden snail (*Cornu aspersum*), an organism with restricted dispersal, across 12 fragmented urban landscapes. We aimed to generalize our results across landscapes and highlight the diversity of relationships between landscape and genetic patterns, by means of landscape replication and multi-scale analyses. Three different scales of analysis yielded diverse relationships between landscape structure, composition, functional connectivity, and population differentiation. We showed at the landscape scale that transport infrastructures decreased genetic differentiation, suggesting these infrastructures facilitate passive dispersal events across cityscapes in the land snail. At the population scale, building surfaces, the proportion of borders combining wooded areas and roads or wooded areas and impervious surfaces increased genetic differentiation. These local factors may reduce (short) active dispersal movements. We also documented isolation by distance and isolation by resistance for the species in urban matrices. Relationships between genetic differentiation and landscape characteristics were highly variable among landscapes, supporting the necessity to replicate landscapes.

## Landscape structure and scales

At the landscape scale, populations were genetically more differentiated when roads were in low proportion. Roads are mainly recognized to act as barriers to dispersal (Balkenhol & Waits, 2009; M. T. J. Johnson & Munshi-South, 2017). However, in our case, no barrier effect was detected at the landscape scale. Instead, we detected a positive effect of roads on gene flow, meaning that roads were not only permeable but also facilitated gene flow. The potential role of roads as dispersal corridors has already been documented in the alpine newt (*Ichthyosaura alpestris*, Prunier et al., 2014) and is often linked with road verge effects. Gene flow can be favored by the presence of vegetated road verges known to facilitate animal dispersal (Holderegger & Di Giulio, 2010) and favor snail dispersal movements (Arnaud, 2003; Baur & Baur, 1990). Another interpretation could be that roads increase events of passive dispersal. Snails have a great potential for passive dispersal associated with human activities (e.g. Aubry, Labaune, Magnin, Roche, & Kiss, 2006): some of their biological traits favor passive dispersal events, such as easily transported dormant stages or human-associated habitat requirements (Medley, Jenkins, & Hoffman, 2015).

At the local environment scale, populations located close to large (enough) building areas were genetically different from the others. Based on these results, buildings can be considered as local fragmenting elements that impede gene exchange between the focal population and the others, and limit population size. Despite the wide acceptance that buildings fragment cityscapes, this effect has rarely been precisely identified (but see Beninde et al., 2016) and is more often included in a general effect attributed to urban infrastructure (associated with roads and impervious areas, e.g. Davis et al., 2010; Delaney,

Riley, & Fisher, 2010; Munshi-South et al., 2016; Ruiz-González et al., 2014; Watts, Rouquette, Saccheri, Kemp, & Thompson, 2004). The amount of borders associating wooded areas and roads or wooded and impervious areas was related to increased population differentiation, and by consequence showed a barrier effect. Wooded areas are not an optimal habitat for *Cornu aspersum* (Falkner et al., 2001) or other land snails (Rosin, Lesicki, Kwieciński, Skórka, & Tryjanowski, 2017). At this local scale, the proximity of wooded areas to roads (or other impervious areas) resulted in fragmented wooded patches and may have decreased habitat quality. A typical case was street trees associated with asphalt, covering the ground under the tree canopy (e.g. Fernández-Juricic, 2000). We could also hypothesize that garden snails present in these wooded/road borders ran higher risks of mortality due to the negative effects of roads (e.g. crushing, dehydration, pollution, Balkenhol & Waits, 2009; Forman, 2003).

Landscape- and population-related analyses extracted different significant landscape effects, adding to the scale-dependent effects that have been documented in a few studies (Angelone et al., 2011; Keller, Holderegger, & van Strien, 2013; Razgour et al., 2014; Worthington Wilmer et al., 2008). An intriguing result of our study was that roads had contrasting effects depending on scale, facilitating dispersal at large distances and impeding it at shorter distances. Scale-dependent effects are easily understood when accounting for different dispersal mechanisms, such as passive and active dispersal (Worthington Wilmer et al., 2008). These authors have documented that passive and active dispersal can be influenced by different landscape features in an aquatic snail. We suggest here that the same landscape feature can have contrasting effects depending on the dispersal

mechanism, with roads increasing passive dispersal but impeding active dispersal in the land snail. Our results also show that extrapolation across spatial scales can be misleading, and we encourage the study of multiple scales in landscape genetic studies (Keller et al., 2013).

#### Relevance of resistance-based models

IBD was validated as expected for a species with limited and highly costly dispersal movements (Bohonak, 1999). Few resistance-based models outperformed the IBD model (LCP associated with logarithmic and exponential resistance value distribution and CT with exponential distribution). It was difficult to determine which distribution of resistance values performed best. Basically, the difference between distributions was the classification of intermediate-quality habitat classes, considered as rather favorable and similar to a secondary habitat (exponential distribution) or largely costly and risky (logarithmic distribution). The exponential distribution has been illustrated as a better distribution to apply to resistance values (e.g. Braaker, Moretti, et al., 2014; Driezen, Adriaensen, Rondinini, Doncaster, & Matthysen, 2007; Trainor, Walters, Morris, Sexton, & Moody, 2013). However, the best transformation may depend on the type of biological data used to calculate resistance values (e.g. genetic distance or daily movement, Braaker et al., 2017). In our study, LCP and CT performed equally well with the exponential distribution, and it was not possible to resolve competing assumptions (e.g. single or multiple optimal paths). Circuit-theory-based analysis is commonly highlighted as more informative than LCP about gene flow (Coulon et al., 2004; Garrido-Garduño, Téllez-Valdés, Manel, & Vázquez-Domínguez, 2016; La Point, Gallery, Wikelski, & Kays, 2013; McRae et al., 2008), but comparisons have seldom been made in urban landscapes. Urban landscape characteristics

could lead to different relative performance between LCP and CT-based models. Highly contrasted land cover, restricted habitat, or high landscape fragmentation may indeed reduce the number of potential pathways and movement success probability and thereby limit the added value of CT analysis.

#### Landscape replication

We showed that single landscape analyses led to various (sometimes opposite) conclusions about the effects of landscape on genetic structure. Gathering several landscape data in linear mixed models increased statistical power and provided more robust conclusions: for example, we validated the IBD model and identified landscape characteristics that influence dispersal that would not have been detected otherwise. Moreover, the mixed model offered the opportunity to study specific effects of landscape through random effect analysis.

However, this opportunity to study the whole dataset of replicated landscapes with a mixed model seems to be rarely used (Castillo et al., 2016; Short Bull et al., 2011; Villemey et al., 2016; but see Jaffé et al., 2016, who did not replicate landscapes but species).

The correspondence between our general conclusions and landscape-specific contributions (single landscape analyses) was not straightforward. For example, at the population  $F_{ST}$  scale, landscape metrics that were significant in at least 3 landscapes were also significant in the analysis of the whole dataset. Variability in landscape-specific results illustrates the difficulty of generalizing results from single-landscape studies. Several arguments can be advanced to explain this variability across landscapes (Richardson et al., 2016). First,

landscapes influence organisms in a heterogeneous way (e.g. Short Bull et al., 2011). In the case of the garden snail, the average surface occupied by buildings was a significant and positive predictor of population differentiation only in the three landscapes in which building surface was the highest. Second, statistical power may be too low to detect and quantify landscape effects when analyzing single landscapes (Jaquiéry, Broquet, Hirzel, Yearsley, & Perrin, 2011). For example, analyses of pairwise distances in single landscape sorted the null model as the best one although a highly significant IBD was found when analyzing the whole dataset. Disentangling the relative importance of these and other factors on the differences expressed across landscapes is an interesting topic linked to replicated study designs that would deserve further investigations.

#### Genetic differentiation using $F_{ST}$

$F_{ST}$  is a robust metric widely used to describe population genetic structure (Holsinger & Weir, 2009) and indirectly measures effective dispersal (successful gene flow) across evolutionary time scales (Broquet & Petit, 2009). It is important to keep in mind that patterns of genetic differentiation result from a dynamic equilibrium between drift and dispersal, which are forces with opposite effects on population divergence. Genetic drift induces lower genetic differentiation between large populations compared to small ones independently of dispersal rate (Jaquiéry et al., 2011). However, the contribution of genetic drift is rarely determined (but see Prunier, Dubut, Chikhi, & Blanchet, 2015). Moreover, certain amount of time is required to reach an equilibrium after a landscape transformation or a disturbance. This time lag is difficult to assess because it depends on multiple demographic and landscape factors (Epps & Keyghobadi, 2015). A time lag between

landscape and genetic patterns may be frequent in urban landscapes due to high rates of area transformation and disturbance (Ramalho & Hobbs, 2012).

We studied three different scales separately with three  $F_{ST}$  computing variations (landscape, population, and pairwise  $F_{ST}$ ). It could be interesting to integrate data from each scale analysis into one model to quantify the relative contribution of each scale. The use of gravity models may be promising in explaining gene flow as a function of landscape predictors measured at both population and pairwise levels (DiLeo & Wagner, 2016; Murphy, Dezzani, Pilliod, & Storfer, 2010; Pflüger & Balkenhol, 2014).

#### Conclusion

We used landscape replication to highlight the effects of landscape composition, configuration and connectivity models on genetic differentiation of garden snail populations. Replication gave access to robust conclusions about the overall effects of landscape on population structure by linear mixed model analysis and the consideration of different scales of analysis. Relationships between landscape and genetic structure were also partly landscape- and scale-dependent.

#### Acknowledgements

We thank Stephane Dreano (UMR 6061, IGDR, Rennes) for technical help; Hervé Daniel, Arnaud Cochard, Guillaume Pain, Romain Georges and all students for their participation to snail collection. We also thank Maxime Dahirel, Marc Bélisle, and the anonymous reviewers for their helpful comments on the manuscript. Financial support was provided by the French

Nord-Pas-de-Calais and Bretagne regions (CORBAM project) and the French LTER “zones ateliers” network.

#### References

- Adriaenssens, F., Chardon, J. P., De Blust, G., Swinnen, E., Villalba, S., Gulinck, H., & Matthysen, E. (2003). The application of ‘least-cost’ modelling as a functional landscape model. *Landscape and Urban Planning*, *64*(4), 233–247. doi:10.1016/S0169-2046(02)00242-6
- Angelone, S., Kienast, F., & Holderegger, R. (2011). Where movement happens: scale-dependent landscape effects on genetic differentiation in the European tree frog. *Ecography*, *34*(5), 714–722. doi:10.1111/j.1600-0587.2010.06494.x
- Ansart, A., Madec, L., & Guiller, A. (2009). *Cornu aspersum* (common garden snail). Retrieved January 25, 2017, from <http://www.cabi.org/isc/datasheet/26821>
- Arnaud, J. F. (2003). Metapopulation genetic structure and migration pathways in the land snail *Helix aspersa*: influence of landscape heterogeneity. *Landscape Ecology*, *18*(3), 333–346. doi:10.1023/A:1024409116214
- Arnaud, J. F., Madec, L., Bellido, A., & Guiller, A. (1999). Microspatial genetic structure in the land snail *Helix aspersa* (Gastropoda: Helicidae). *Heredity*, *83*(2), 110–119. doi:10.1046/j.1365-2540.1999.00565.x
- Arnaud, J. F., Madec, L., Guiller, A., & Deunff, J. (2003). Population genetic structure in a human-disturbed environment: a case study in the land snail *Helix aspersa* (Gastropoda: Pulmonata). *Heredity*, *90*(6), 451–458. doi:10.1038/sj.hdy.6800256
- Aubry, S., Labaune, C., Magnin, F., Roche, P., & Kiss, L. (2006). Active and passive dispersal of an invading land snail in Mediterranean France. *Journal of Animal Ecology*, *75*(3), 802–813. doi:10.1111/j.1365-2656.2006.01100.x
- Baguette, M., Blanchet, S., Legrand, D., Stevens, V. M., & Turlure, C. (2013). Individual dispersal, landscape connectivity and ecological networks. *Biological Reviews*, *88*(2), 310–326.

doi:10.1111/brv.12000

Baguette, M., & Van Dyck, H. (2007). Landscape connectivity and animal behavior: functional grain as a key determinant for dispersal. *Landscape Ecology*, *22*(8), 1117–1129.

doi:10.1007/s10980-007-9108-4

Balkenhol, N., & Waits, L. P. (2009). Molecular road ecology: exploring the potential of genetics for investigating transportation impacts on wildlife. *Molecular Ecology*, *18*(20), 4151–4164.

doi:10.1111/j.1365-294X.2009.04322.x

Barbato, D., Benocci, A., Caruso, T., & Manganelli, G. (2017). The role of dispersal and local environment in urban land snail assemblages: an example of three cities in Central Italy.

*Urban Ecosystems*, 1–13. doi:10.1007/s11252-017-0643-8

Bartoń, K. (2016). MuMIn: Multi-Model Inference (Version 1.15.6). Retrieved from <https://cran.r-project.org/web/packages/MuMIn/index.html>

Bates, D., Mächler, M., Bolker, B., & Walker, S. (2014). Fitting linear mixed-effects models using lme4. *ArXiv:1406.5823 [Stat]*. Retrieved from <http://arxiv.org/abs/1406.5823>

Baur, A., & Baur, B. (1990). Are roads barriers to dispersal in the land snail *Arianta arbustorum*?

*Canadian Journal of Zoology*, *68*(3), 613–617. doi:10.1139/z90-091

Beninde, J., Feldmeier, S., Werner, M., Peroverde, D., Schulte, U., Hochkirch, A., & Veith, M. (2016). Cityscape genetics: structural vs. functional connectivity of an urban lizard population.

*Molecular Ecology*, *25*(20), 4984–5000. doi:10.1111/mec.13810

Bohonak, A. J. (1999). Dispersal, Gene Flow, and Population Structure. *The Quarterly Review of Biology*, *74*(1), 21–45. doi:10.1086/392950

Bolker, B. M., Brooks, M. E., Clark, C. J., Geange, S. W., Poulsen, J. R., Stevens, M. H. H., & White, J.-S.

S. (2009). Generalized linear mixed models: a practical guide for ecology and evolution.

*Trends in Ecology & Evolution*, *24*(3), 127–135. doi:10.1016/j.tree.2008.10.008

Boussard, H., & Baudry, J. (2014). *Chloe212 : a software for landscape pattern analysis*. Retrieved from <http://www.rennes.inra.fr/sad/Outils-Produits/Outils-informatiques/Chloe>

- Braaker, S., Ghazoul, J., Obrist, M. K., & Moretti, M. (2014). Habitat connectivity shapes urban arthropod communities: the key role of green roofs. *Ecology*, *95*(4), 1010–1021. doi:10.1890/13-0705.1
- Braaker, S., Kormann, U., Bontadina, F., & Obrist, M. K. (2017). Prediction of genetic connectivity in urban ecosystems by combining detailed movement data, genetic data and multi-path modelling. *Landscape and Urban Planning*, *160*, 107–114. doi:10.1016/j.landurbplan.2016.12.011
- Braaker, S., Moretti, M., Boesch, R., Ghazoul, J., Obrist, M. K., & Bontadina, F. (2014). Assessing habitat connectivity for ground-dwelling animals in an urban environment. *Ecological Applications*, *24*(7), 1583–1595. doi:10.1890/13-1088.1
- Broquet, T., & Petit, E. J. (2009). Molecular estimation of dispersal for ecology and population genetics. *Annual Review of Ecology, Evolution, and Systematics*, *40*, 193–216.
- Burnham, K. P., & Anderson, D. R. (2002). *Model Selection and Multimodel Inference: A Practical Information-Theoretic Approach*. Springer Science & Business Media.
- Cadenasso, M. L., Pickett, S. T. A., & Schwarz, K. (2007). Spatial heterogeneity in urban ecosystems: reconceptualizing land cover and a framework for classification. *Frontiers in Ecology and the Environment*, *5*(2), 80–88. doi:10.1890/1540-9295(2007)5[80:SHIUER]2.0.CO;2
- Castillo, J. A., Epps, C. W., Jeffress, M. R., Ray, C., Rodhouse, T. J., & Schwalm, D. (2016). Replicated landscape genetic and network analyses reveal wide variation in functional connectivity for American pikas. *Ecological Applications*, *26*(6), 1660–1676. doi:10.1890/15-1452.1
- Chapuis, M.-P., & Estoup, A. (2007). Microsatellite Null Alleles and Estimation of Population Differentiation. *Molecular Biology and Evolution*, *24*(3), 621–631. doi:10.1093/molbev/msl191
- Chardon, J. P., Adriaensen, F., & Matthysen, E. (2003). Incorporating landscape elements into a connectivity measure: a case study for the Speckled wood butterfly (*Pararge aegeria* L.). *Landscape Ecology*, *18*(6), 561–573. doi:10.1023/A:1026062530600

- Clarke, R. T., Rothery, P., & Raybould, A. F. (2002). Confidence limits for regression relationships between distance matrices: Estimating gene flow with distance. *Journal of Agricultural, Biological, and Environmental Statistics*, 7(3), 361. doi:10.1198/108571102320
- Concepción, E. D., Moretti, M., Altermatt, F., Nobis, M. P., & Obrist, M. K. (2015). Impacts of urbanisation on biodiversity: the role of species mobility, degree of specialisation and spatial scale. *Oikos*, 124(12), 1571–1582. doi:10.1111/oik.02166
- Coulon, A., Cosson, J. F., Angibault, J. M., Cargnelutti, B., Galan, M., Morellet, N., ... Hewison, A. J. M. (2004). Landscape connectivity influences gene flow in a roe deer population inhabiting a fragmented landscape: an individual-based approach. *Molecular Ecology*, 13(9), 2841–2850. doi:10.1111/j.1365-294X.2004.02253.x
- Dahirel, M., Séguret, A., Ansart, A., & Madec, L. (2016). Dispersal-related traits of the snail *Cornu aspersum* along an urbanisation gradient: maintenance of mobility across life stages despite high costs. *Urban Ecosystems*, 19(4), 1847–1859. doi:10.1007/s11252-016-0564-y
- Dahirel, M., Vardakis, M., Ansart, A., & Madec, L. (2016). Density-dependence across dispersal stages in a hermaphrodite land snail: insights from discrete choice models. *Oecologia*, 181(4), 1117–1128. doi:10.1007/s00442-016-3636-z
- Dan, N. (1978). *Studies on the growth and ecology of Helix aspersa Müller*. University of Manchester, Manchester.
- Davis, E. S., Murray, T. E., Fitzpatrick, Ú., Brown, M. J. F., & Paxton, R. J. (2010). Landscape effects on extremely fragmented populations of a rare solitary bee, *Colletes floralis*. *Molecular Ecology*, 19(22), 4922–4935. doi:10.1111/j.1365-294X.2010.04868.x
- Delaney, K. S., Riley, S. P. D., & Fisher, R. N. (2010). A Rapid, Strong, and Convergent Genetic Response to Urban Habitat Fragmentation in Four Divergent and Widespread Vertebrates. *PLOS ONE*, 5(9), e12767. doi:10.1371/journal.pone.0012767
- Denny, M. (1980). Locomotion: The Cost of Gastropod Crawling. *Science*, 208(4449), 1288–1290. doi:10.1126/science.208.4449.1288

- DiLeo, M. F., & Wagner, H. H. (2016). A Landscape Ecologist's Agenda for Landscape Genetics. *Current Landscape Ecology Reports*, 1(3), 115–126. doi:10.1007/s40823-016-0013-x
- Dionne, M., Caron, F., Dodson, J. J., & Bernatchez, L. (2008). Landscape genetics and hierarchical genetic structure in Atlantic salmon: the interaction of gene flow and local adaptation. *Molecular Ecology*, 17(10), 2382–2396. doi:10.1111/j.1365-294X.2008.03771.x
- Driezen, K., Adriaensen, F., Rondinini, C., Doncaster, C. P., & Matthysen, E. (2007). Evaluating least-cost model predictions with empirical dispersal data: A case-study using radiotracking data of hedgehogs (*Erinaceus europaeus*). *Ecological Modelling*, 209(2–4), 314–322. doi:10.1016/j.ecolmodel.2007.07.002
- Dudaniec, R. Y., Rhodes, J. R., Worthington Wilmer, J., Lyons, M., Lee, K. E., McAlpine, C. A., & Carrick, F. N. (2013). Using multilevel models to identify drivers of landscape-genetic structure among management areas. *Molecular Ecology*, 22(14), 3752–3765. doi:10.1111/mec.12359
- Dupont, L., Torres-Leguizamon, M., René-Corail, P., & Mathieu, J. (2017). Landscape features impact connectivity between soil populations: a comparative study of gene flow in earthworms. *Molecular Ecology*, 26(12), 3128–3140. doi:10.1111/mec.14102
- Epps, C. W., & Keyghobadi, N. (2015). Landscape genetics in a changing world: disentangling historical and contemporary influences and inferring change. *Molecular Ecology*, 24(24), 6021–6040. doi:10.1111/mec.13454
- Falkner, G., Obrdlík, P., Castella, E., & Speight, C. C. (2001). *Shelled gastropoda of western Europe*. München: Friedrich-Held-Gesellschaft.
- Fenderson, L. E., Kovach, A. I., Litvaitis, J. A., O'Brien, K. M., Boland, K. M., & Jakubas, W. J. (2014). A multiscale analysis of gene flow for the New England cottontail, an imperiled habitat specialist in a fragmented landscape. *Ecology and Evolution*, 4(10), 1853–1875. doi:10.1002/ece3.1068
- Fernández-Juricic, E. (2000). Avifaunal Use of Wooded Streets in an Urban Landscape. *Conservation*

*Biology*, 14(2), 513–521. doi:10.1046/j.1523-1739.2000.98600.x

Foltête, J.-C., Clauzel, C., & Vuidel, G. (2012). A software tool dedicated to the modelling of landscape networks. *Environmental Modelling & Software*, 38, 316–327.

doi:10.1016/j.envsoft.2012.07.002

Forman, R. T. T. (2003). *Road Ecology: Science and Solutions*. Island Press.

Forman, R. T. T. (2014). *Urban Ecology: Science of Cities*. Cambridge University Press.

Forstmeier, W., Wagenmakers, E.-J., & Parker, T. H. (2017). Detecting and avoiding likely false-positive findings – a practical guide. *Biological Reviews*, 92(4), 1941–1968.

doi:10.1111/brv.12315

Gaggiotti, O. E., & Foll, M. (2010). Quantifying population structure using the F-model. *Molecular Ecology Resources*, 10(5), 821–830. doi:10.1111/j.1755-0998.2010.02873.x

Garrido-Garduño, T., Téllez-Valdés, O., Manel, S., & Vázquez-Domínguez, E. (2016). Role of habitat heterogeneity and landscape connectivity in shaping gene flow and spatial population structure of a dominant rodent species in a tropical dry forest. *Journal of Zoology*, 298(4), 293–302. doi:10.1111/jzo.12307

Goudet, J. (2001). *FSTAT, a program to estimate and test gene diversities and fixation indices (version 2.9.3)*.

Goudet, J. (2005). hierfstat, a package for r to compute and test hierarchical F-statistics. *Molecular Ecology Notes*, 5(1), 184–186. doi:10.1111/j.1471-8286.2004.00828.x

Goudet, J., & Jombart, T. (2015). hierfstat: Estimation and Tests of Hierarchical F-Statistics (Version 0.04-22). Retrieved from <https://cran.r-project.org/web/packages/hierfstat/index.html>

Grimm, N. B., Faeth, S. H., Golubiewski, N. E., Redman, C. L., Wu, J., Bai, X., & Briggs, J. M. (2008). Global change and the ecology of cities. *Science*, 319(5864), 756–760.

doi:10.1126/science.1150195

Groffman, P. M., Avolio, M., Cavender-Bares, J., Bettez, N. D., Grove, J. M., Hall, S. J., ... others.

(2017). Ecological homogenization of residential macrosystems. *Nature Ecology & Evolution*,

1(7), s41559–017.

- Guiller, A., Arnaud, J.-F., Vautrin, D., & Solignac, M. (2000). Highly polymorphic microsatellite markers in the landsnail *Helix aspersa* (Mollusca Gastropoda). *Molecular Ecology*, *9*(8), 1191–1193. doi:10.1046/j.1365-294x.2000.00954-13.x
- Hand, B. K., Muhlfeld, C. C., Wade, A. A., Kovach, R. P., Whited, D. C., Narum, S. R., ... Luikart, G. (2016). Climate variables explain neutral and adaptive variation within salmonid metapopulations: the importance of replication in landscape genetics. *Molecular Ecology*, *25*(3), 689–705. doi:10.1111/mec.13517
- Holderegger, R., & Di Giulio, M. (2010). The genetic effects of roads: A review of empirical evidence. *Basic and Applied Ecology*, *11*(6), 522–531. doi:10.1016/j.baae.2010.06.006
- Holderegger, R., & Wagner, H. H. (2008). Landscape Genetics. *BioScience*, *58*(3), 199–207. doi:10.1641/B580306
- Holsinger, K. E., & Weir, B. S. (2009). Genetics in geographically structured populations: defining, estimating and interpreting FST. *Nature Reviews Genetics*, *10*(9), 639–650. doi:10.1038/nrg2611
- Jaffé, R., Pope, N., Acosta, A. L., Alves, D. A., Arias, M. C., De la Rúa, P., ... Carvalheiro, L. G. (2016). Beekeeping practices and geographic distance, not land use, drive gene flow across tropical bees. *Molecular Ecology*, *25*(21), 5345–5358. doi:10.1111/mec.13852
- Jaquiéry, J., Broquet, T., Hirzel, A. H., Yearsley, J., & Perrin, N. (2011). Inferring landscape effects on dispersal from genetic distances: how far can we go? *Molecular Ecology*, *20*(4), 692–705. doi:10.1111/j.1365-294X.2010.04966.x
- Johnson, J. B., & Omland, K. S. (2004). Model selection in ecology and evolution. *Trends in Ecology & Evolution*, *19*(2), 101–108. doi:10.1016/j.tree.2003.10.013
- Johnson, M. T. J., & Munshi-South, J. (2017). Evolution of life in urban environments. *Science*, *358*(6363), eaam8327. doi:10.1126/science.aam8327
- Keller, D., Holderegger, R., & van Strien, M. J. (2013). Spatial scale affects landscape genetic analysis

- of a wetland grasshopper. *Molecular Ecology*, 22(9), 2467–2482. doi:10.1111/mec.12265
- Kerney, M.-P., Cameron, R.-A.-D., & Bertrand, A. (2006). *Guide des escargots et limaces d'Europe*. Paris: Delachaux et Niestlé.
- Keyghobadi, N. (2007). The genetic implications of habitat fragmentation for animals. *Canadian Journal of Zoology*, 85(10), 1049–1064. doi:10.1139/Z07-095
- La Point, S., Balkenhol, N., Hale, J., Sadler, J., & van der Ree, R. (2015). Ecological connectivity research in urban areas. *Functional Ecology*, 29(7), 868–878. doi:10.1111/1365-2435.12489
- La Point, S., Gallery, P., Wikelski, M., & Kays, R. (2013). Animal behavior, cost-based corridor models, and real corridors. *Landscape Ecology*, 28(8), 1615–1630. doi:10.1007/s10980-013-9910-0
- Lee, J. S., Ruell, E. W., Boydston, E. E., Lyren, L. M., Alonso, R. S., Troyer, J. L., ... VandeWOUDE, S. U. E. (2012). Gene flow and pathogen transmission among bobcats (*Lynx rufus*) in a fragmented urban landscape. *Molecular Ecology*, 21. doi:10.1111/j.1365-294X.2012.05493.x
- Madec, L. (1989). *Etude de la différenciation de quelques populations géographiquement séparées de l'espèce Helix Aspersa Müller(mollusque gastéropode pulmoné): aspects morphologiques, écophysiologiques et biochimiques*. University of Rennes I. Retrieved from <http://cat.inist.fr/?aModele=afficheN&cpsid=6832234>
- Manel, S., & Holderegger, R. (2013). Ten years of landscape genetics. *Trends in Ecology & Evolution*, 28(10), 614–621. doi:10.1016/j.tree.2013.05.012
- Manel, S., Schwartz, M. K., Luikart, G., & Taberlet, P. (2003). Landscape genetics: combining landscape ecology and population genetics. *Trends in Ecology & Evolution*, 18(4), 189–197. doi:10.1016/S0169-5347(03)00008-9
- Mcgarigal, K., Cushman, S., Neel, M., & Ene, E. (2002). FRAGSTATS: Spatial Pattern Analysis Program for Categorical Maps. Retrieved from <http://www.umass.edu/landeco/research/fragstats/fragstats.html>
- McKinney, M. L. (2006). Urbanization as a major cause of biotic homogenization. *Biological Conservation*, 127(3), 247–260. doi:10.1016/j.biocon.2005.09.005

- McRae, B. H. (2006). Isolation by Resistance. *Evolution*, *60*(8), 1551–1561. doi:10.1111/j.0014-3820.2006.tb00500.x
- McRae, B. H., Dickson, B. G., Keitt, T. H., & Shah, V. B. (2008). Using circuit theory to model connectivity in ecology, evolution, and conservation. *Ecology*, *89*(10), 2712–2724. doi:10.1890/07-1861.1
- Medley, K. A., Jenkins, D. G., & Hoffman, E. A. (2015). Human-aided and natural dispersal drive gene flow across the range of an invasive mosquito. *Molecular Ecology*, *24*(2), 284–295. doi:10.1111/mec.12925
- Millette, K. L., & Keyghobadi, N. (2015). The relative influence of habitat amount and configuration on genetic structure across multiple spatial scales. *Ecology and Evolution*, *5*(1), 73–86. doi:10.1002/ece3.1325
- Munshi-South, J. (2012). Urban landscape genetics: canopy cover predicts gene flow between white-footed mouse (*Peromyscus leucopus*) populations in New York City. *Molecular Ecology*, *21*(6), 1360–1378. doi:10.1111/j.1365-294X.2012.05476.x
- Munshi-South, J., & Kharchenko, K. (2010). Rapid, pervasive genetic differentiation of urban white-footed mouse (*Peromyscus leucopus*) populations in New York City. *Molecular Ecology*, *19*(19), 4242–4254. doi:10.1111/j.1365-294X.2010.04816.x
- Munshi-South, J., Zolnik, C. P., & Harris, S. E. (2016). Population genomics of the Anthropocene: urbanization is negatively associated with genome-wide variation in white-footed mouse populations. *Evolutionary Applications*, *9*(4), 546–564. doi:10.1111/eva.12357
- Murphy, M. A., Dezzani, R., Pilliod, D. S., & Storfer, A. (2010). Landscape genetics of high mountain frog metapopulations. *Molecular Ecology*, *19*(17), 3634–3649. doi:10.1111/j.1365-294X.2010.04723.x
- Murphy, M. A., Evans, J. S., & Storfer, A. (2010). Quantifying *Bufo boreas* connectivity in Yellowstone National Park with landscape genetics. *Ecology*, *91*(1), 252–261. doi:10.1890/08-0879.1
- Öckinger, E., Schweiger, O., Crist, T. O., Debinski, D. M., Krauss, J., Kuussaari, M., ... others. (2010).

Life-history traits predict species responses to habitat area and isolation: a cross-continental synthesis. *Ecology Letters*, 13(8), 969–979.

Parris, K. M. (2016). *Ecology of Urban Environments*. John Wiley & Sons.

Peterman, W. E., Connette, G. M., Semlitsch, R. D., & Eggert, L. S. (2014). Ecological resistance surfaces predict fine-scale genetic differentiation in a terrestrial woodland salamander. *Molecular Ecology*, 23(10), 2402–2413. doi:10.1111/mec.12747

Pflüger, F. J., & Balkenhol, N. (2014). A plea for simultaneously considering matrix quality and local environmental conditions when analysing landscape impacts on effective dispersal. *Molecular Ecology*, 23(9), 2146–2156. doi:10.1111/mec.12712

Piano, E., De Wolf, K., Bona, F., Bonte, D., Bowler, D. E., Isaia, M., ... Hendrickx, F. (2017). Urbanization drives community shifts towards thermophilic and dispersive species at local and landscape scales. *Global Change Biology*, 23(7), 2554–2564. doi:10.1111/gcb.13606

Pinheiro, J., Bates, D., DebRoy, S., Sarkar, D., & R-core Team. (2016). nlme: Linear and Nonlinear Mixed Effects Models (Version 3.1-128). Retrieved from <https://cran.r-project.org/web/packages/nlme/index.html>

Prunier, J. G., Dubut, V., Chikhi, L., & Blanchet, S. (2015). Isolation-by-Drift: Quantifying the Respective Contributions of Genetic Drift and Gene Flow in Shaping Spatial Patterns of Genetic Differentiation. *BioRxiv*, 031633. doi:10.1101/031633

Prunier, J. G., Kaufmann, B., Lena, J.-P., Fenet, S., Pompanon, F., & Joly, P. (2014). A 40-year-old divided highway does not prevent gene flow in the alpine newt *Ichthyosaura alpestris*. *Conservation Genetics*, 15(2), 453–468.

R Core Team. (2015). R: A language and environment for statistical computing (Version 3.2). Vienna, Austria: R Foundation for Statistical Computing. Retrieved from <http://www.R-project.org/>

Ramalho, C. E., & Hobbs, R. J. (2012). Time for a change: dynamic urban ecology. *Trends in Ecology & Evolution*, 27(3), 179–188. doi:10.1016/j.tree.2011.10.008

Rayfield, B., Fortin, M.-J., & Fall, A. (2010). The sensitivity of least-cost habitat graphs to relative cost

- surface values. *Landscape Ecology*, 25(4), 519–532. doi:10.1007/s10980-009-9436-7
- Razgour, O., Rebelo, H., Puechmaille, S. J., Juste, J., Ibáñez, C., Kiefer, A., ... Jones, G. (2014). Scale-dependent effects of landscape variables on gene flow and population structure in bats. *Diversity and Distributions*, 20(10), 1173–1185. doi:10.1111/ddi.12200
- Richardson, J. L., Brady, S. P., Wang, I. J., & Spear, S. F. (2016). Navigating the pitfalls and promise of landscape genetics. *Molecular Ecology*, 25(4), 849–863. doi:10.1111/mec.13527
- Rosin, Z. M., Lesicki, A., Kwieciński, Z., Skórka, P., & Tryjanowski, P. (2017). Land snails benefit from human alterations in rural landscapes and habitats. *Ecosphere*, 8(7), n/a-n/a. doi:10.1002/ecs2.1874
- Rousset, F. (1997). Genetic Differentiation and Estimation of Gene Flow from F-Statistics Under Isolation by Distance. *Genetics*, 145(4), 1219–1228.
- Row, J. R., Knick, S. T., Oyler-McCance, S. J., Loughheed, S. C., & Fedy, B. C. (2017). Developing approaches for linear mixed modeling in landscape genetics through landscape-directed dispersal simulations. *Ecology and Evolution*, 7(11), 3751–3761. doi:10.1002/ece3.2825
- Ruiz-González, A., Gurrutxaga, M., Cushman, S. A., Madeira, M. J., Randi, E., & Gómez-Moliner, B. J. (2014). Landscape Genetics for the Empirical Assessment of Resistance Surfaces: The European Pine Marten (*Martes martes*) as a Target-Species of a Regional Ecological Network. *PLOS ONE*, 9(10), e110552. doi:10.1371/journal.pone.0110552
- Segelbacher, G., Cushman, S. A., Epperson, B. K., Fortin, M.-J., Francois, O., Hardy, O. J., ... Manel, S. (2010). Applications of landscape genetics in conservation biology: concepts and challenges. *Conservation Genetics*, 11(2), 375–385. doi:10.1007/s10592-009-0044-5
- Selander, R. K., & Kaufman, D. W. (1975). Genetic Structure of Populations of the Brown Snail (*Helix aspersa*). I. Microgeographic Variation. *Evolution*, 29(3), 385–401. doi:10.2307/2407252
- Short Bull, R. A., Cushman, S. A., Mace, R., Chilton, T., Kendall, K. C., Landguth, E. L., ... Luikart, G. (2011). Why replication is important in landscape genetics: American black bear in the Rocky Mountains. *Molecular Ecology*, 20(6), 1092–1107. doi:10.1111/j.1365-294X.2010.04944.x

- Storfer, A., Murphy, M. A., Spear, S. F., Holderegger, R., & Waits, L. P. (2010). Landscape genetics: where are we now? *Molecular Ecology*, *19*(17), 3496–3514. doi:10.1111/j.1365-294X.2010.04691.x
- Taylor, P. D., Fahrig, L., Henein, K., & Merriam, G. (1993). Connectivity is a vital element of landscape structure. *Oikos*, *68*(3), 571–573. doi:10.2307/3544927
- Taylor, P. D., Fahrig, L., & With, K. A. (2006). Landscape connectivity: a return to the basics. In K. R. Crooks & M. Sanjayan (Eds.), *Connectivity conservation* (pp. 29–43). Cambridge University Press.
- Trainor, A. M., Walters, J. R., Morris, W. F., Sexton, J., & Moody, A. (2013). Empirical estimation of dispersal resistance surfaces: a case study with red-cockaded woodpeckers. *Landscape Ecology*, *28*(4), 755–767. doi:10.1007/s10980-013-9861-5
- United Nations. (2015). World Urbanization Prospects: The 2014 Revision. *Department of Economic and Social Affairs, Population Division*.
- van Etten, J. (2017). R Package gdistance: Distances and Routes on Geographical Grids. *Journal of Statistical Software*, *76*(13), 1–21. doi:10.18637/jss.v076.i13
- Van Strien, M. J., Keller, D., & Holderegger, R. (2012). A new analytical approach to landscape genetic modelling: least-cost transect analysis and linear mixed models. *Molecular Ecology*, *21*(16), 4010–4023. doi:10.1111/j.1365-294X.2012.05687.x
- Villemey, A., Peterman, W. E., Richard, M., Ouin, A., Halder, I. van, Stevens, V. M., ... Archaux, F. (2016). Butterfly dispersal in farmland: a replicated landscape genetics study on the meadow brown butterfly (*Maniola jurtina*). *Landscape Ecology*, *31*(7), 1629–1641. doi:10.1007/s10980-016-0348-z
- Wagner, H. H., & Fortin, M.-J. (2013). A conceptual framework for the spatial analysis of landscape genetic data. *Conservation Genetics*, *14*(2), 253–261. doi:10.1007/s10592-012-0391-5
- Waits, L. P., Cushman, S. A., & Spear, S. F. (2016). Applications of landscape genetics to connectivity research in terrestrial animals. In N. Balkenhol, S. A. Cushman, A. T. Storfer, & L. P. Waits

(Eds.), *Landscape Genetics: Concepts, Methods, Applications* (pp. 199–219). Wiley-Blackwell.

Watts, P. C., Rouquette, J. R., Saccheri, I. J., Kemp, S. J., & Thompson, D. J. (2004). Molecular and ecological evidence for small-scale isolation by distance in an endangered damselfly, *Coenagrion mercuriale*. *Molecular Ecology*, *13*(10), 2931–2945. doi:10.1111/j.1365-294X.2004.02300.x

Wiens, J. A. (1989). Spatial Scaling in Ecology. *Functional Ecology*, *3*(4), 385–397.

Worthington Wilmer, J., Elkin, C., Wilcox, C., Murray, L., Niejalke, D., & Possingham, H. (2008). The influence of multiple dispersal mechanisms and landscape structure on population clustering and connectivity in fragmented artesian spring snail populations. *Molecular Ecology*, *17*(16), 3733–3751. doi:10.1111/j.1365-294X.2008.03861.x

Zeller, K. A., McGarigal, K., & Whiteley, A. R. (2012). Estimating landscape resistance to movement: a review. *Landscape Ecology*, *27*(6), 777–797. doi:10.1007/s10980-012-9737-0

#### Data accessibility

The datasets with *C. aspersum* microsatellite genotypes are available from the Dryad Digital Repository: <http://doi.org/10.5061/dryad.p9f13>

#### Authors' Contributions

E.J.P., A.E., L.M. initiated and designed the study. M.B., A.E., P.P., L.M., V.B., E.J.P. collected the data, and M.C.M, A.G., M.B., P.P. performed molecular analyses. J.N. and V.B. provided maps. M.B. and P.P. conducted connectivity and landscape genetics analyses. M.B. performed statistical analyses and wrote the manuscript, supervised by E.J.P., A.E. and L.M..

## Tables and Figures

Table 1: Habitat classes, description, hierarchization (Hier) and resistance value sets; Exp : exponential, Log: logarithmic, Lin: linear

Habitat class	Description	Hier	Exp	Log	Lin
<b>Herbaceous</b>	Garden, lawn, grassland, ruderal area, herbaceous plant, bush, hedge, isolated trees	1	1	1	1
<b>Wooded</b>	Grove, tree, wood	2	13	50	33
<b>Impervious</b>	Asphalt surfaces other than roads, parking lots, sidewalks	2	13	50	33
<b>Transport infrastructure</b>	Road, railway	3	37	80	67
<b>Building</b>	Building, construction site	4	100	100	100
<b>Water</b>	Canal, ditch, pond	4	100	100	100

Table 2: Genetic statistics for each landscape: Number of sampled individuals (Tot nb), Mean Fis, mean observed heterozygosities (Ho), mean expected heterozygosities (He), mean number of alleles per locus, landscape FST ( $F_{STG}$ ).

Study area	Tot nb	Mean Fis	Ho	He	Mean allele nb	$F_{STG}$
<b>AF1</b>	224	0.047	0.803	0.843	10.20	0.048
<b>AF2</b>	229	0.091	0.775	0.852	10.33	0.041
<b>AF3</b>	211	0.124	0.736	0.840	9.73	0.035
<b>AF4</b>	212	0.104	0.750	0.838	9.25	0.052
<b>LF1</b>	198	0.103	0.622	0.693	5.88	0.124
<b>LF2</b>	210	0.080	0.669	0.727	5.88	0.116

<b>LF3</b>	174	0.076	0.701	0.759	6.24	0.098
<b>LF4</b>	191	0.065	0.717	0.766	6.68	0.059
<b>RF1</b>	235	0.219	0.596	0.764	8.14	0.081
<b>RF2</b>	233	0.250	0.548	0.731	7.13	0.151
<b>RF3</b>	232	0.289	0.529	0.743	6.94	0.115
<b>RF4</b>	244	0.293	0.509	0.720	5.71	0.110
<b>Grand mean</b>	216	0.145	0.663	0.773	7.68	0.086

Table 3: Population  $F_{ST}$  analysis, regressions summarized according to landscape metrics associated with model-averaged importance, fixed estimate, standard error and range of the random estimates from random slope models; LRT ratio and level of significance, p-value: \*\*\*<0.001; \*<0.05.

<b>Landscape metrics</b>	<b>Model-averaged importance</b>	<b>Fixed estimate</b>	<b>Fixed SE</b>	<b>Random estimate range</b>	<b>LRT</b>
<b>RATE COUPLE wooded/ impervious</b>	0.74	0.63	0.32	[-0.68; 0.88]	4.7 *
<b>RATE COUPLE wooded / transport infr.</b>	0.56	0.61	0.49	[-1.82; 2.78]	24.4 ***
<b>AREA building</b>	0.51	0.27	0.17	[-0.53; 1.13]	30.1 ***

Table 4: Pairwise  $F_{ST}$  analyses with distances as a fixed factor, fixed estimate and standard error, AICc, and  $\Delta AICc$ . Distances were extracted from least-cost-path (LCP) or circuit-theory (CT) analyses based on different distributions of resistance values: exponential (exp), logarithmic (log), linear (lin), and Euclidean distance (Euc)

Distance	Fixed estimate	Fixed SE	AICc	$\Delta AICc$
LCP.log	0.0094	0.0035	-2287.6	0
CT.exp	0.0272	0.0090	-2287.1	0.5
LCP.exp	0.0096	0.0032	-2286.9	0.7
Euc	0.0099	0.0035	-2284.3	3.3
LCP.lin	0.0091	0.0032	-2284.1	3.5
CT.lin	0.0223	0.0074	-2283.0	4.6
CT.log	0.0203	0.0068	-2281.4	6.2
null	NA	NA	-2270.5	17.1

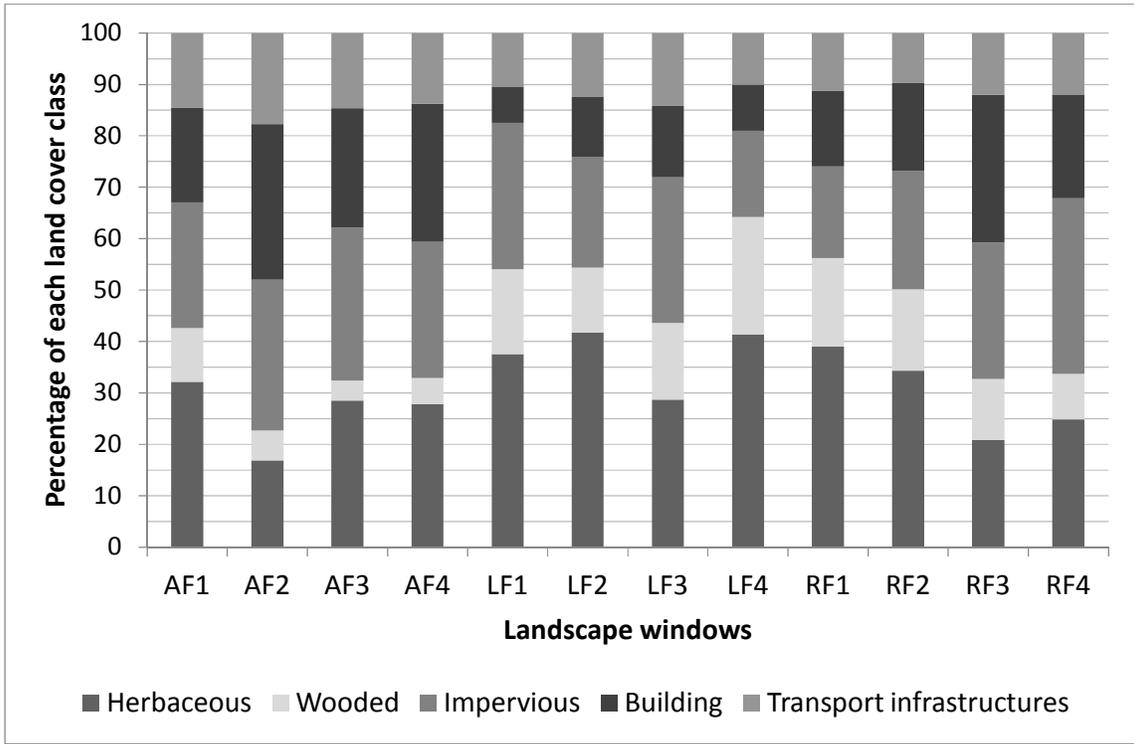


Figure 2: Percentage of each land cover class in the 12 landscapes. AF: Angers, LF: Lens, RF: Rennes.

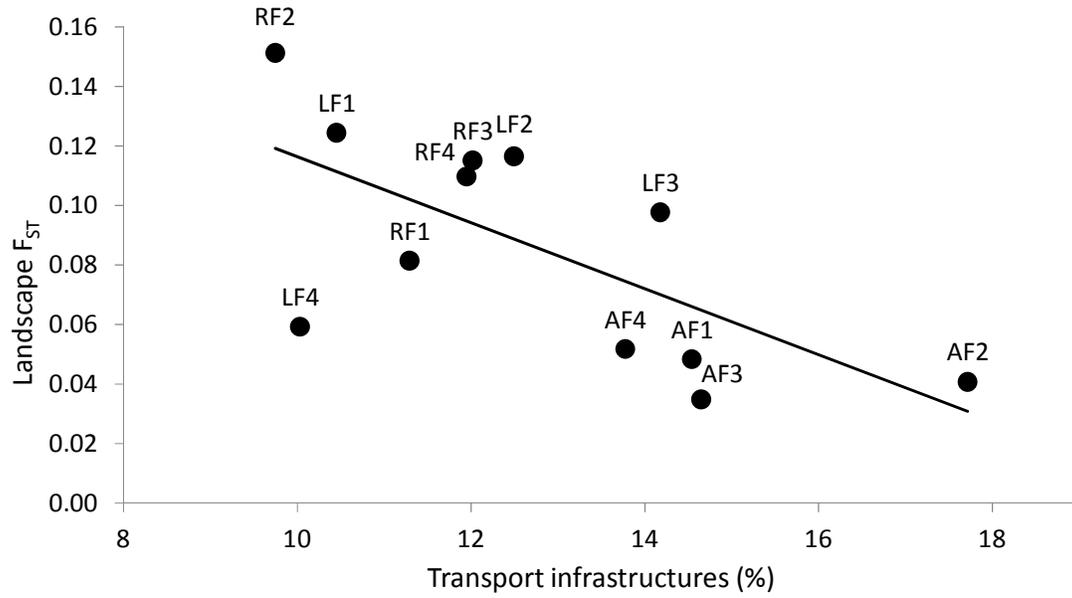


Figure 3: Landscape  $F_{ST}$  and percentage of surfaces occupied by transport infrastructures in each landscape; linear regression (line):  $R^2 = 0.43$ ; slope estimate = -0.011

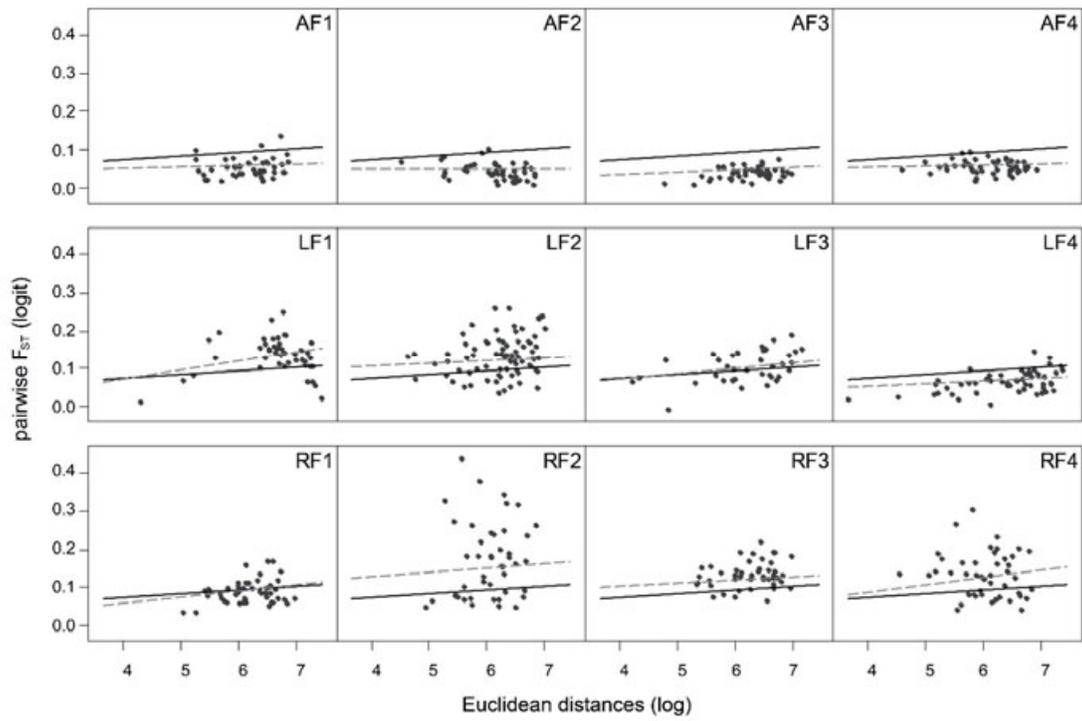


Figure 4: Isolation by Euclidean distance (IBD) in the 12 landscapes, fixed effect (black line) and landscape-specific random effect (grey dotted lines).