

1 MetaConnect, a new platform for population viability modelling to assist decision makers in
2 conservation and urban planning

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1 Abstract:

2 In a context of global change, scientists and policy-makers require tools to address the issue
3 of biodiversity loss. Population viability analysis (PVA) has been the main tool to deal with
4 this problem. However, the tools developed during the 90s poorly integrate recent scientific
5 advances in landscape genetics and dispersal. We developed a flexible and modular modelling
6 platform for PVA that addresses many of the limitations of existing software. MetaConnect is
7 an individual-based, process-based and PVA-oriented modelling platform which could be
8 used as a research or a decision-making tool. Here, we present the core base modelling of
9 MetaConnect. We demonstrate its potential use through a case study illustrating the
10 platform's capability for performing integrated PVA including extinction probability
11 estimation, genetic differentiation and landscape connectivity analysis. We used MetaConnect
12 to assess the impact of infrastructure works on the natterjack toad metapopulation functioning.

13

14 Keywords:

15 Modelling platform, individual-based model, process-based model, decision-making tool,
16 dispersal, landscape genetics, landscape planning

1 Introduction:

2 In a context of rapid global change, habitat loss and habitat fragmentation have become the
3 major threats to biodiversity (IUCN 2013), and have been considered for some time as the
4 principal cause of species extinction (Dobson, Bradshaw & Baker 1997; Millenium
5 Ecosystem Assessment 2005). They have consequences from the ecosystem (Fahrig 2003;
6 Cardinale *et al.* 2012; de Mazancourt *et al.* 2013) to the genetic scale (Ingvarsson 2001;
7 Baguette *et al.* 2013) by modifying landscape patterns in a four-step process: reduction in
8 amount of habitat, increase in number of habitat patches, decrease patch sizes and increase in
9 patch isolation (Fahrig 2003). This alteration of landscape patterns has diverse effects on
10 population dynamics (e.g. Baguette *et al.* 2013). As patches become smaller, the size of the
11 population supported decreases; this can increase stochastic risk of extinction from
12 demographic processes (Legendre *et al.* 1999; Reed *et al.* 2002), but also from genetic
13 stochasticity: small populations are more subjected to risk of inbreeding and consanguinity
14 depression (Brook *et al.* 2002b), loss of genetic diversity and mutational accumulation (Rowe
15 & Beebee 2003), leading to the extinction vortex (Gilpin & Soulé 1986; Fagan & Holmes
16 2006). Moreover, by increasing inter-patch distances and therefore dispersal cost, habitat loss
17 and fragmentation decrease the probability of individuals moving between sub-populations.
18 This can hinder recolonization or the demographic rescue of patches where sub-populations
19 have become extinct, or declining, potentially leading to stochastic extinction of
20 metapopulations (Fahrig 2003). Furthermore, by reducing gene flow between sub-
21 populations, isolation can lead to genetic differentiation of sub-populations and impede
22 genetic rescue of highly inbred sub-populations (Ingvarsson 2001; Keller & Waller 2002;
23 Tallmon, Luikart & Waples 2004).

24 Historically, an ecological tool much used by scientists and conservation managers was
25 population viability analysis (PVA), which aims at estimating extinction or quasi-extinction

1 probability of a species (Boyce 1992; Legendre & Clobert 1995; Beissinger & Westphal
2 1998) and which was used to inform conservation programs (Southgate & Possingham 1995;
3 Ferriere *et al.* 1996; Letcher *et al.* 1998; Schtickzelle & Baguette 2004; Radchuk *et al.* 2013).
4 Most of the PVA models focused on species population dynamics (Lindenmayer *et al.* 1995;
5 Brook *et al.* 1999; Legendre *et al.* 1999), and offered limited flexibility regarding population
6 genetics (but see Lacy, Borbat & Pollak 2009) or metapopulation functioning (Reed *et al.*
7 2002; Pe'er *et al.* 2013). PVA is principally focused on demographic and genetic processes
8 and individual movement behaviour determining species persistence (Keller & Waller 2002;
9 Fahrig 2003; Piou & Prevost 2012; Frank & Baret 2013; Noel, Machon & Robert 2013).
10 Population genetics has made major advances during recent decades, and it is now possible to
11 identify at generation g those individuals that are offspring of individuals immigrating at
12 generation $g-1$; and assign these immigrants to their original population (Beerli & Felsenstein
13 2001). Besides, the rise of landscape genetics allows the assessment and quantification of how
14 landscape elements affect gene flow in a metapopulation (Manel *et al.* 2003; Manel &
15 Holderegger 2013). Integrating both population and landscape genetics approaches in models
16 of metapopulation functioning to support conservation managers' and policy makers' plans
17 should be highly valuable (Baguette *et al.* 2013; Pe'er *et al.* 2013).

18 The growth of a community of ecological modellers using individual-based models (IBMs)
19 rather than the mathematical approaches has led to the production of a huge number of models
20 (DeAngelis & Mooij 2005) and metrics (Moilanen & Nieminen 2002; Calabrese & Fagan
21 2004). Moreover, most such models were developed to answer specific questions, which
22 renders comparison between outputs difficult, if not impossible (DeAngelis & Mooij 2005;
23 Kindlmann & Burel 2008; Pe'er *et al.* 2013), and their application inefficient out of the
24 narrow context for which each was typically developed (Grimm *et al.* 2004; Kindlmann &
25 Burel 2008). Generic PVA modelling platforms built from IBM and process-based modelling

1 are lacking (but see Grimm *et al.* 2004; Lacy, Borbat & Pollak 2009; Bocedi *et al.* 2014) or do
2 not permit a sufficient level of flexibility (VORTEX is spatially implicit, RangeShifter and
3 MetaX have limited demographic modules) to deal with a large spectrum of conceptual
4 framework and ecological themes (DeAngelis & Mooij 2005; Evans, Norris & Benton 2012;
5 Evans *et al.* 2013; Purves *et al.* 2013).

6 Because PVA is a relevant basic decision-making tool (Brook *et al.* 2000; Brook *et al.* 2002a;
7 Pe'er *et al.* 2013), we developed MetaConnect, a generic PVA-based IBM following the
8 Beissinger & Westphal (1998) framework, which allows the design of a range of models from
9 very simple to highly detailed and which integrates demography and genetics in a spatially-
10 explicit context (Baguette *et al.* 2013). MetaConnect not only aims at performing traditional
11 PVAs based on demographic data, but also integrates the recent development of population
12 and landscape genetics, which allows the assessment of functional connectivity (*sensu* Taylor,
13 Fahrig & With 2006). We expect that this integrated modelling platform will be a useful tool
14 for scientists, conservation managers and policy makers. Here we present MetaConnect's core
15 base modelling, its validation (Appendix A) and present a case study demonstrating its use to
16 assess the impact of infrastructure development on the population viability, genetic
17 differentiation and functional connectivity of existing populations of the endangered
18 natterjack toad (*Epidalea calamita*).

19

20 Model

21 Model design

22

23 MetaConnect simulates metapopulation dynamics and genetics using the species life cycle
24 and life history traits, the landscape characteristics and their interactions. The simulations

1 allow inferring of individual dispersal and local and global extinction probabilities, genetic
2 diversity and genetic differentiation (from classical Fst analyses or as input files for the
3 Structure software (Pritchard, Stephens & Donnelly 2000)).

4 MetaConnect is an individual- and process-based model which means that:

- 5 • all individuals in the model are independent and behave in respect to their
6 phenotype.
- 7 • patterns emerging in the different outputs of the model are the products of flexible
8 and adjustable rules implemented in the model.

9 Model structure

10

11 *Landscape*

12

13 The landscape is imported as two shapefiles and then rasterized by MetaConnect.

- 14 • Patches: locates suitable habitats for the focal species. The carrying capacity
15 (individual/m²) can be assumed to be constant, or an optional shapefile of
16 carrying capacities can be provided.
- 17 • Costs: provides a coefficient (of rugosity) representing the ability of a given
18 species to move through each habitat type of the landscape. The higher the cost,
19 the harder to cross.

20

21 *Demography*

22

23 Population dynamics is represented by a succession of individual states linked by transitions.

24 The user builds the species life-cycle by assembling “bubbles” representing the individual

1 state and “arrows” representing transition rules between individual states (Figure 1, 2). The
2 “bubbles”, hereafter regarded as classes, correspond to age classes, sex or anything that can be
3 defined as a group of individuals with the same demographic characteristics. Density
4 dependence can be scramble or contest and designed as a part of transitions. The mating
5 system can be chosen from monogamy, polygamy, polyandry and/or polygyny (Legendre *et*
6 *al.* 1999). The demographic parameters (Table 1) can be patch-specific. Environmental
7 stochasticity has been included as random processes inducing normal variation around the
8 patch’s mean value of demographic parameters truncated to realistic values set by the user. As
9 an example, the fecundity parameter follows a Poisson distribution (demographic
10 stochasticity) with parameter λ equal to the average fecundity ($F \sim \mathcal{P}(\bar{F})$). The average
11 fecundity can vary from one patch to another and within simulation time steps following a
12 Gaussian distribution (Table 1).

13 Dispersal probability p_d is implemented by setting a proportion of individuals in a
14 given class leaving a patch. The density-dependent recruitment probability p_r is determined
15 by equation 1 where N_T can be a chosen combination of the number of individuals per class
16 (i.e. N_T could be the total population or the number of individual in a given class) (Caswell
17 2001).

18 Equation 1:

19 Contest:
$$p_r = \frac{1}{1 + kN_T}$$

20 Scramble:
$$p_r = e^{-kN_t}$$

21 Dispersal is age- and sex-dependent, and the process by which individuals disperse can be
22 chosen from three families of movement rules:

- 1 • Dispersal between patches is modelled by a probability for an individual to reach
2 another patch, ignoring rugosity coefficient. The probability of reaching a patch
3 can be equal between patches, depend on the Euclidean distance between patches’
4 centres, or be set manually.
- 5 • The interaction between individuals and their environment depends on rugosity
6 coefficients. This family comprises a random-walk (RW) and a correlated
7 random-walk rule (CRW). The CRW assumes a degree of directional persistence,
8 (i.e. movement direction at time $t+1$ depends on the direction taken at time t) and
9 not solely an environmental based one. Dispersing individuals benefit from a
10 “energy gauge” decreasing at each step of the (C)RW in respect of the cell cost
11 weighted by direction (1 for straight moves, $\sqrt{2}$ for diagonal moves).
- 12 • This family of rules assumes that individuals have knowledge of their
13 environment, and move by one of two methods. From a focal patch, the least cost
14 path (LCP) algorithm usually assumes that a single patch can be reached (Botea,
15 Müller & Schaeffer; Adriaensen *et al.* 2003; Pe'er & Kramer-Schadt 2008;
16 Barraquand, Inchausti & Bretagnolle 2009). Such an assumption is unrealistic,
17 and to relax it we implemented a multiple LCP movement rule, in which we
18 calculated all possible LCPs between the focal patch and all other patches (Urban
19 *et al.* 2009; Foltete, Clauzel & Vuidel 2012). Then, for reachable patches (i.e.
20 LCP length less than the maximum dispersal distance), the probability to reach a
21 patch is inversely weighted by the LCP length (number of map cells crossed) or
22 cumulative cost (total cost of all map cells crossed). We also adapted the
23 Stochastic Movement Simulator (SMS) (Palmer, Coulon & Travis 2011; Aben *et*
24 *al.* 2014; Palmer, Coulon & Travis 2014; Coulon *et al.* Submitted), which relaxes
25 the assumption of omniscience inherent in the LCP approach. With the SMS rule,

1 individuals make movement decisions based on the environment within a limited
2 perceptual range and a tendency to directional persistence similar to that in a
3 CRW. At each movement, the SMS algorithm calculates a movement probability
4 for each cell surrounding the current cell based on the rugosity coefficient of the
5 cells in the perceptual range (see Palmer, Coulon & Travis 2011 for details).

6 The dispersal event ends when the individual dies or reaches a patch different from his
7 original patch regardless of the arrival patch quality.

8

9 *Genetics*

10

11 Individuals are genetically tagged using neutral polymorphic loci. The number of loci and
12 number of alleles per locus can be specified by the user. A single mutation rate (a probability
13 of creating a new allele without possibility of reverse mutation) implemented in the model
14 allows the production of new alleles at each locus during simulations, and can be specified by
15 the user. Gene transmission is assumed to be Mendelian and siblings are assumed to have the
16 same father (randomly chosen from the female harem for polyandrous cases).

17

18 Model outputs

19

20 The model provides many forms of outputs based on focal species life history traits
21 and landscape maps, which are adaptable to various theoretical and applied contexts. The
22 outputs report the results at three levels at a frequency specified by the user, allowing
23 dynamic visualization of the simulations:

- 1 • Demography: population size is split into the classes and sexes implemented in
2 the model. The model derives extinction probability, colonization probability and
3 time to extinction and colonization. These indicators are calculated at the local
4 (patch) and global (metapopulation) scales.
- 5 • Dispersal: the model provides the number of individuals reaching a new patch or
6 dying during dispersal. Maps of cell occupancy are drawn from successful
7 dispersal events (number of individuals visiting each cell during the whole run).
- 8 • Genetics: genetic diversity and differentiation (F_{st} , F_{is} , F_{it} , H_e and H_o) at the
9 local and/or global scale applicable to each statistic.

10 All these outputs can be directly plotted using the MetaConnect project manager (figure 2) or
11 extracted as text files. In addition R (R Development Core Team 2005) has been incorporated
12 to the project manager, which allows direct analysis of the outputs.

13

14 Model sensitivity:

15

16 MetaConnect is a highly flexible and modular IBM, which means that dozens of variables can
17 be specified in various modelling contexts, rendering global sensitivity analyses impossible to
18 run (Cross & Beissinger 2001; Naujokaitis-Lewis *et al.* 2009; Pe'er *et al.* 2013). A thematic
19 sensitivity analysis will be presented in the MetaConnect user manual, in which sensitivity of
20 extinction probabilities, genetic structure and connectivity metrics will be analyzed in relation
21 to the appropriate model parameters and their relative contribution to the sensitivity estimate
22 (Cross & Beissinger 2001).

23

1 Case study: Changes in the metapopulation functioning of an existing natterjack
2 toad population under scenarios of economic development.

3

4 *MetaConnect* parameterization

5

6 We used a model designed with MetaConnect to determine the potential impact of the
7 development of an industrial area and a terrestrial transport infrastructure (high-speed
8 railway), both alone and together, on the population viability of *Epidalea calamita*
9 populations in south-western France close to Agen (44°11'36"N, 0°31'14"E) (figure 3).

10 Habitat patches were determined *a priori* based on expert assessment (figure 3). Preferences
11 for landscape elements were derived from those experimentally determined by Stevens et al.
12 (2006). *E. calamita* was assumed to disperse following the stochastic-movement-simulator
13 (SMS) assumptions (Palmer, Coulon & Travis 2011; Coulon *et al.* Submitted). MetaConnect
14 was parameterized with published values of life history traits (Stevens & Baguette 2008)
15 (Appendix B).

16 We analysed MetaConnect genetic outputs for all the patches containing more than 10
17 individuals at the end of each run of 100 time steps. This analysis was performed using
18 STRUCTURE (Pritchard, Stephens & Donnelly 2000) with an admixture model assuming that
19 the origin population of an individual is known and the allele frequencies are independent.
20 STRUCTURE runs were performed for a variable number of clusters between 1 and 7, and
21 with 10 iterations of 100000 steps (50000 burn-in and 50000 analysis steps to ensure model
22 convergence). This procedure was reproduced for each iteration of the simulation of a given
23 scenario. We determined the best number of genetic clusters following the Evanno method
24 (see Evanno, Regnaut & Goudet 2005) using STRUCTURE HARVESTER (Earl & Vonholdt

1 2012). We counted the assignation of a patch to a cluster for each MetaConnect run analysed
2 with STRUCTURE and tested the clustering robustness by performing a χ^2 test per patch.

3

4 Current metapopulation functioning

5

6 Within the study site, (10 km around the industrial area development), the *E. calamita*
7 population is not threatened (extinction probability $p_e = 0$) and we observed two main
8 dispersal corridors. The major corridor joins the north (quarry, patch 29 and 32) to the south
9 (motorway, patch 103) and is stopped by the motorway in its southern part and by the
10 Garonne River at its northern part. The minor corridor joins the quarry (east) to a pond (patch
11 34, west) (figure 4.A). Our focal area covers these two corridors (figure 3). Both corridors
12 incorporate stepping-stone sites (North-south: patches 50 and 67, east-west: patch 36) (figure
13 4.A). Within the focal area all the patches have a very low extinction probability (see figure
14 4), and except for patch 103, all patches are able to exchange individuals with all the others.
15 Indeed, only patch 103 is unable to provide individuals to patches 34, 36, 29 and 32 or to
16 receive individuals from patches 34 and 36.

17 The analysis of the genetic output suggests that currently the study site is divided into three
18 separate clusters (all cluster differentiation p.values<0.05). The first one is situated at the
19 north of the Garonne, the second between the Garonne and the motorway and the third at the
20 south of the motorway (figure 5.A).

21

1 Expected consequences of the industrial area and of the high-speed railway building

2

3 The industrial area development and the associated destruction of patch 67 leads to a
4 reduction of individual flow between patches to the north and south of the industrial area and
5 to a population size reduction within the southern patches (figure 6.B). Such a modification
6 would not threaten *E. calamita* persistence in the study site (all $p_e = 0$, figure 6.D). However,
7 dispersal would be more concentrated between patches 29, 32 and 50 due to the repelling
8 effect of the industrial area for *E. calamita* (figure 6.D). In addition, the reduction of dispersal
9 along the north-south axis should lead to a fourth genetic cluster in the western part of the
10 study sites (Figure 5.B).

11 The high-speed railway project will fragment the study site landscape. This would lead to the
12 reduction of patches 34 and 103 areas (since none of the newly created patches 45, 46 nor 112
13 could shelter a population (Respectively $p_e = 0.71, 0.71, 0.61$, figure 6.E)) inducing the
14 reduction of their sheltered population sizes (figure 6.C). In addition, dispersal along the
15 north-south corridor is reduced to the south of the patch 50 (figure 6.C). Moreover, the
16 connectivity along the north-south corridor is also decreased due to the population size
17 reduction of patches 71 and 103. The reduction of the patch population size and the change in
18 the connectivity along the north-south axis change the clustering outcome of these last
19 simulations. Indeed, if the Evanno method suggests that 2 clusters can be identified, the χ^2 test
20 shows that the assignation to a second cluster does not differ significantly from a random
21 assignation, suggesting that only a single cluster exists or that the cluster 1 (north of the
22 Garonne) is poorly differentiated from cluster 2 between the Garonne and the high-speed
23 railway (Figure 5.C).

24 Although the development of the industrial area and the building of the high-speed railway do
25 not directly threaten the *E. calamita* survival in the study site (all $p_e = 0$) (figure 6.F), it will

1 restrain the species' displacement capabilities and reduce the global population size
2 (respectively, average population size within the focal patches are 2907, 2635 and 2166
3 individuals). In addition, figure 8.F highlights the central role of patch 50 as a stepping-stone
4 patch, which allows the maintenance of connectivity between the north (patches 29 and 32)
5 and the south (patches 71 and 103). Such a map constitutes a powerful decision-making tool
6 in the new ecological context of compensatory measures which will be taken in the context of
7 large-scale landscape planning (Lanius, Kiss & Den Betsen 2013; Regnery, Couvet &
8 Kerbirou 2013).

9

1 Model limitations:

2 By its structure, MetaConnect allows the user to take into account most of the requirements
3 necessary for a complete and flexible PVA and decision-making tool (i.e. metapopulation
4 dynamics and genetics) (Grimm *et al.* 2004; Baguette *et al.* 2013; Pe'er *et al.* 2013).

5 Currently, its main limitation comes from the landscape representation. In MetaConnect the
6 landscape is represented using the patch-matrix approach, in which a cell is a suitable habitat
7 or not. This approach will not be fully unrealistic for many species (Clobert *et al.* 2001; Urban
8 *et al.* 2009; Pe'er *et al.* 2011). Furthermore, reproduction in the suitable habitat is assumed to
9 be panmictic which is usually not true because patch shape and structure isolate or aggregate
10 individuals within a patch and individual behaviour (territoriality, mating system,
11 cooperation,...) may aggregate or isolate individuals within a patch (Doebeli & Koella 1994;
12 Snyder & Chesson 2003; Ylonen, Pech & Davis 2003; Nonacs & Kapheim 2007). Further
13 development of MetaConnect toolboxes would allow tackling this limitation of intra-patch
14 spatial structuring by splitting individual use of space into daily movements and dispersal
15 events (Mueller & Fagan 2008; Roshier, Doerr & Doerr 2008; Pe'er *et al.* 2013).

16 A second limitation is the way genetic mutation is modelled. Currently, the mutation model is
17 very simple, just assuming that a new allele can occur at a given constant rate and that no
18 reverse mutations are possible. Further toolbox development would allow various methods for
19 modelling mutations to be incorporated (Willi, Van Buskirk & Hoffmann 2006; Neher 2013;
20 Wray 2013) and in addition would permit simulation of the action of the genotypes on the
21 individual phenotype (Montalvo *et al.* 1997; Mouquet *et al.* 2012; Moulherat *et al.*
22 submitted).

23

1 Conclusion: model application and perspectives

2 European regulation requires spatial planners to evaluate precisely the impacts of
3 developments on ecological network functioning. Baguette et al. (2013) recommended a
4 robust workflow in that direction. The procedure comprises performing an analysis of
5 metapopulation dynamics and dispersal over a landscape for each affected species to design
6 sound ecological network functioning. MetaConnect provides an important tool that moves in
7 this direction. Indeed, the user can easily build consensus networks for several species within
8 the same study site and under the same framework with standardized and comparable outputs.
9 However, such an approach does not yet incorporate the inter-specific interactions that could
10 greatly change population dynamics and dispersal (Caswell 2001; Clobert *et al.* 2013).
11 Further MetaConnect toolbox development will integrate basic inter-specific interactions such
12 as competition, predation and parasitism.

13 Application of graph-theoretic connectivity is increasing at an exponential rate in ecology and
14 conservation (Kindlmann & Burel 2008; Kadoya 2009; Moilanen 2011). In this framework,
15 graph nodes represent habitat patches and graph edges represent the connectivity between
16 patches (Urban & Keitt 2001). Whilst the mathematical background of graph theory is
17 promising to deal efficiently with the ecological connectivity (Urban & Keitt 2001), the
18 simplification made by modelling a metapopulation with a graph (Moilanen 2011) has the
19 potential to lead to limited interpretation and operational efficiency (Kadoya 2009; Moilanen
20 2011). Kadoya (2009) concluded that graph modelling of metapopulations provides little
21 congruence with connectivity inferred from population genetic structure and Moilanen (2011)
22 listed the limits of graph-theoretic connectivity in spatial ecology. With MetaConnect, as
23 shown in our case study (figure 6.A-C), we provide an efficient tool to define habitat patches
24 (nodes of a graph) with predictions of the demographic module and dispersal functionality
25 between patches (graph's edges) with dispersal assessed from dispersal simulation or derived

1 from genetic estimates applicable from local to national scales and grid-based data. However,
2 further development of MetaConnect and the development of a specific toolbox will allow
3 that the graph does not model the metapopulation functioning as such, but to be used as a
4 powerful analytical tool preventing the graph-theoretic connectivity analysis from biases
5 described by Moilanen (2011).

6 We conclude by highlighting the recent call for a new generation of models that begin to
7 provide predictive systems ecology (Evans, Norris & Benton 2012; Evans *et al.* 2013). This
8 call argued that, while in a few sub-disciplines such as dynamic vegetation modelling and
9 climate change modelling we have already developed a capacity for simulating complex
10 systems, typically we lack such a predictive modelling capability elsewhere in ecological and
11 evolutionary disciplines (Moorcroft, Hurtt & Pacala 2001; Evans, Norris & Benton 2012;
12 Hoban, Bertorelle & Gaggiotti 2012; Purves *et al.* 2013; Bocedi *et al.* 2014). The climate
13 modelling community and the dynamic vegetation modelling communities both possess
14 several models with which they can conduct inter-model comparisons, conduct cross-
15 validations, etc (Evans, Norris & Benton 2012; Pe'er *et al.* 2013). This is also now true of the
16 population genetics community, which has several software packages available (reviewed in
17 Hoban, Bertorelle & Gaggiotti 2012). We believe that MetaConnect, together with the
18 recently published software RangeShifter (Bocedi *et al.* 2014) and the integrative statistical
19 inferences procedure proposed by Pagel & Schurr (2012), begin to address this challenge to
20 develop complex systems models that can be used to inform policy in the sphere of spatial
21 and landscape ecology.

22

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7

8 Where to find MetaConnect

9 MetaConnect (IDDN.FR.001.430001.000.S.C.2012.000.20600) is developed in C++ by SM
10 and MM and runs exclusively in cloud-computing under UNIX. A Graphical User Interface
11 (GUI) developed in OpenGL insures the access to MetaConnect from multiple platforms
12 (currently available for Linux Centos7). MetaConnect is available for academic purposes
13 contacting the authors (SM).

14

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1 Table 1: Nomenclature of MetaConnect’s main parameters and variables.

Parameters and variables	Description	Distribution law of random variables
<i>Demographic characteristics</i>		
K	Carrying capacity*	
k	Total competition coefficient	
s_i	Survival of individual from class i	Bernoulli
F	Fecundity	Poisson
σ	Primary sex ratio	Bernoulli
<i>Mating system</i>		
Mating system	Mating system assumptions	
H_m	Male harem size	Poisson
H_f	Female harem size	Poisson
<i>Genetics</i>		
L	Number of loci	
A	Number of alleles per locus	
μ	Mutation rate	
<i>Dispersal</i>		
p_d	Dispersal probability	Bernoulli
Dispersal rule	Dispersal algorithm	
<i>Initialization and model parameterization</i>		
N_0	Initial number of individuals	
σ_0	Initial sex-ratio	
f_a	Initial class structure	
T	Time steps	
MC_l	Number of landscape random generations	
MC_d	Number of population dynamic simulations per landscape	

2

3 * The carrying capacity K is derived from the competition coefficient and the competition
4 assumption.

5

MetaConnect GUI v0.01β (201404301042)

File Style Tools Window

Others

Cartes

patch: map.patch

k: map.k

Structure

costs: map.cost

Patches

autodetect

Number of patches: 0

Centres

rbGraphCenter rbRandomCell rbMap

patch center:

Iterations

Matrice Leslie

$$\begin{pmatrix} (1 - dd)s_0F & s_0F \\ dds_1 & s_2 \end{pmatrix}$$

Properties

Age Ratio

Survival

Dispersal

Fecundity

CheckBox

CheckBox

	Males	Females
	0	7

Add Class Add Transition Generate Seq Del

A

B

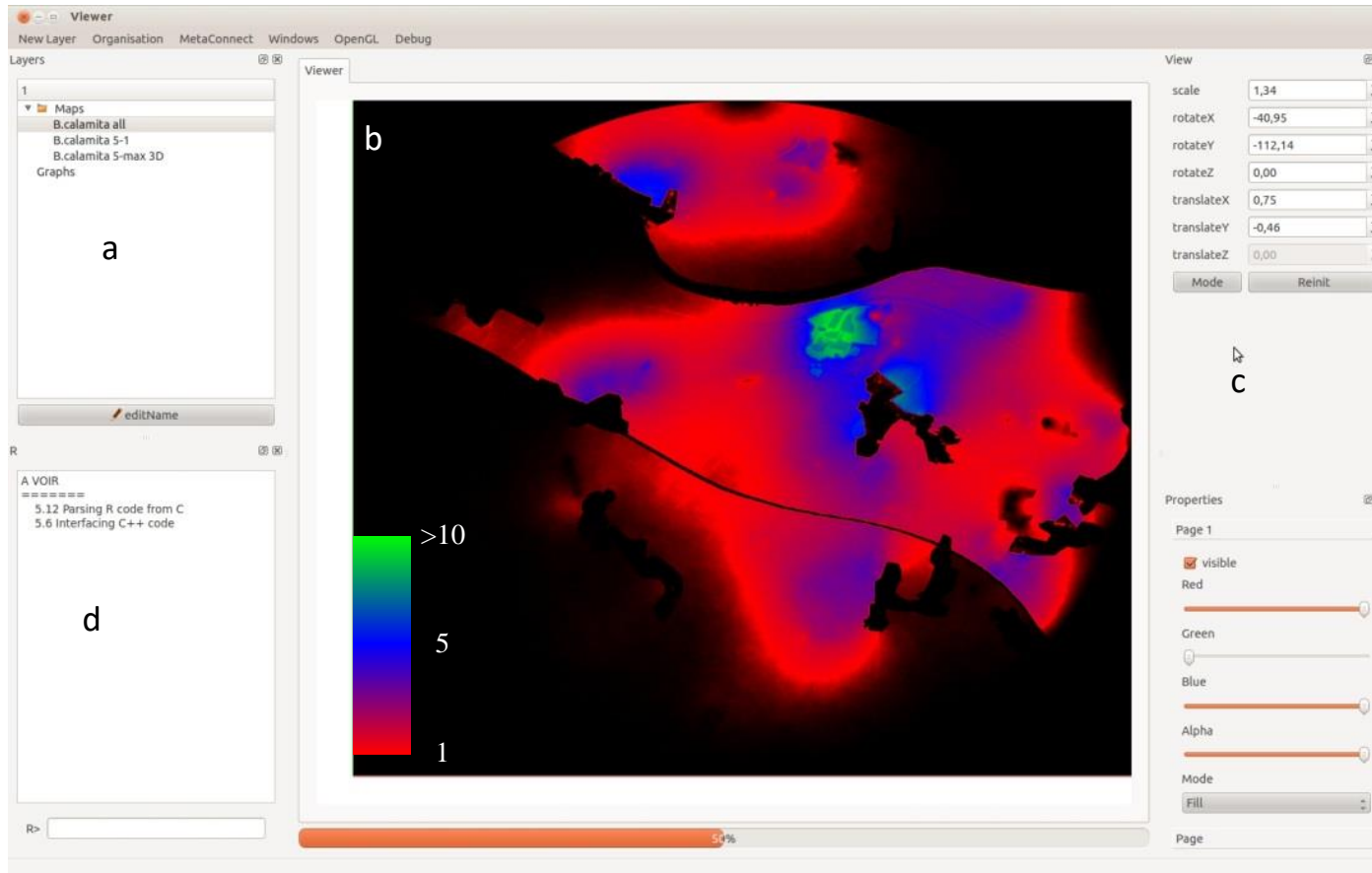
C

D

MetaConnect Sequence

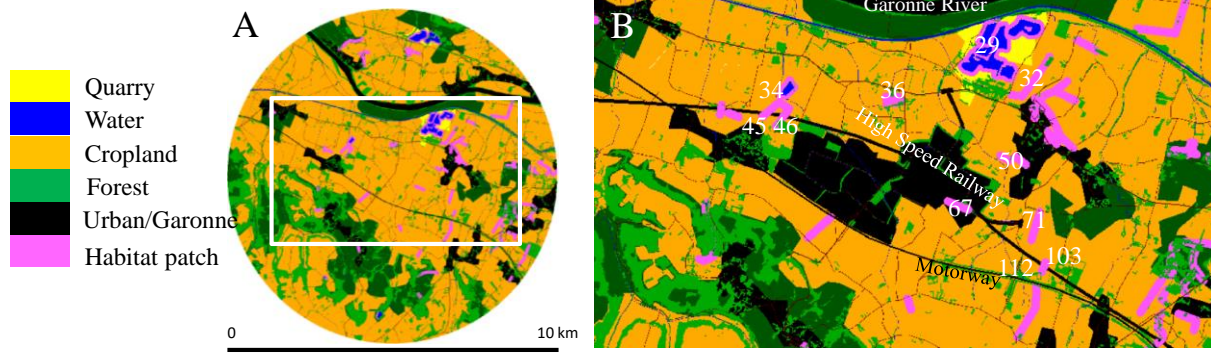
1

- 1 Figure 1: Screenshot example of the Legendre et al. (1999) passerine life cycle with two age-
- 2 class and two sexes that can be modelled with MetaConnect. The user defines the species life-
- 3 cycle as a combination of “bubbles” (add class) and “arrows” (add transition) (A). The species
- 4 life history traits are set up in the B section and the run setting is defined in the C. Then, the
- 5 MetaConnect workflow (D) and the Leslie matrix (E) are generated automatically.



1

2 Figure 2: *E. calamita* landscape use during dispersal (indiv./year) estimated with MetaConnect. Data to be displayed or analysed are selected in
 3 section *a* and displayed in *b* in two or three dimensions. Section *c* allows setting of the display options, and *d* is an R console to perform simple
 4 analysis.



1

2 Figure 3: Site of industrial and transport development in south western France close to Agen.

3 Panel A presents the complete study site used for MetaConnect simulations, rasterized to a

4 grid of 10m x 10m cells. Panel B shows enlarged the future development of an industrial area

5 and of a high-speed railway. Our analysis is focused on the patches numbered in white. Patch

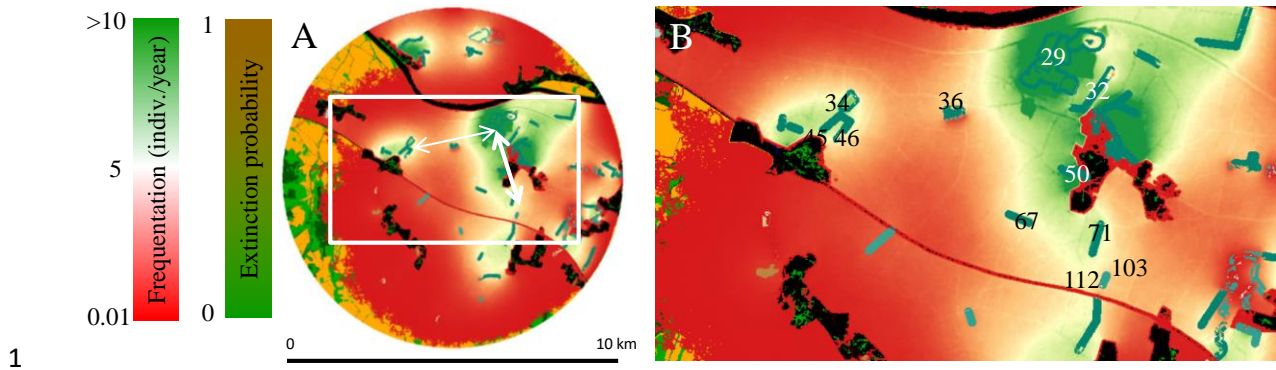
6 67 will be destroyed by the industrial area development. Patches 45, 46 and 112 do not

7 currently exist, but will appear with the building of the high-speed railway as a result of the

8 fragmentation of respectively patches 34 (split into 34, 45 and 46) and 103 (split into 103 and

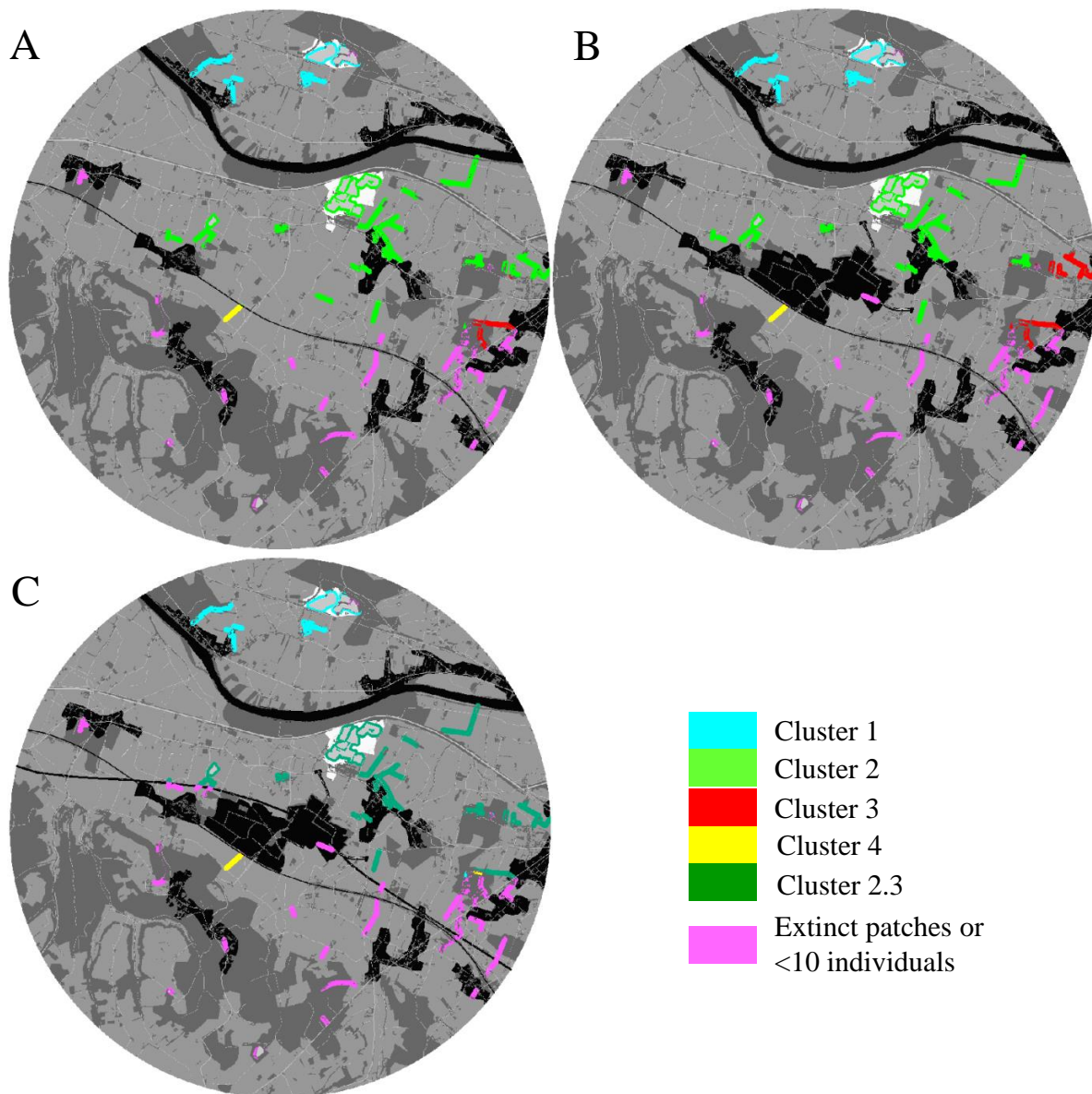
9 112).

10



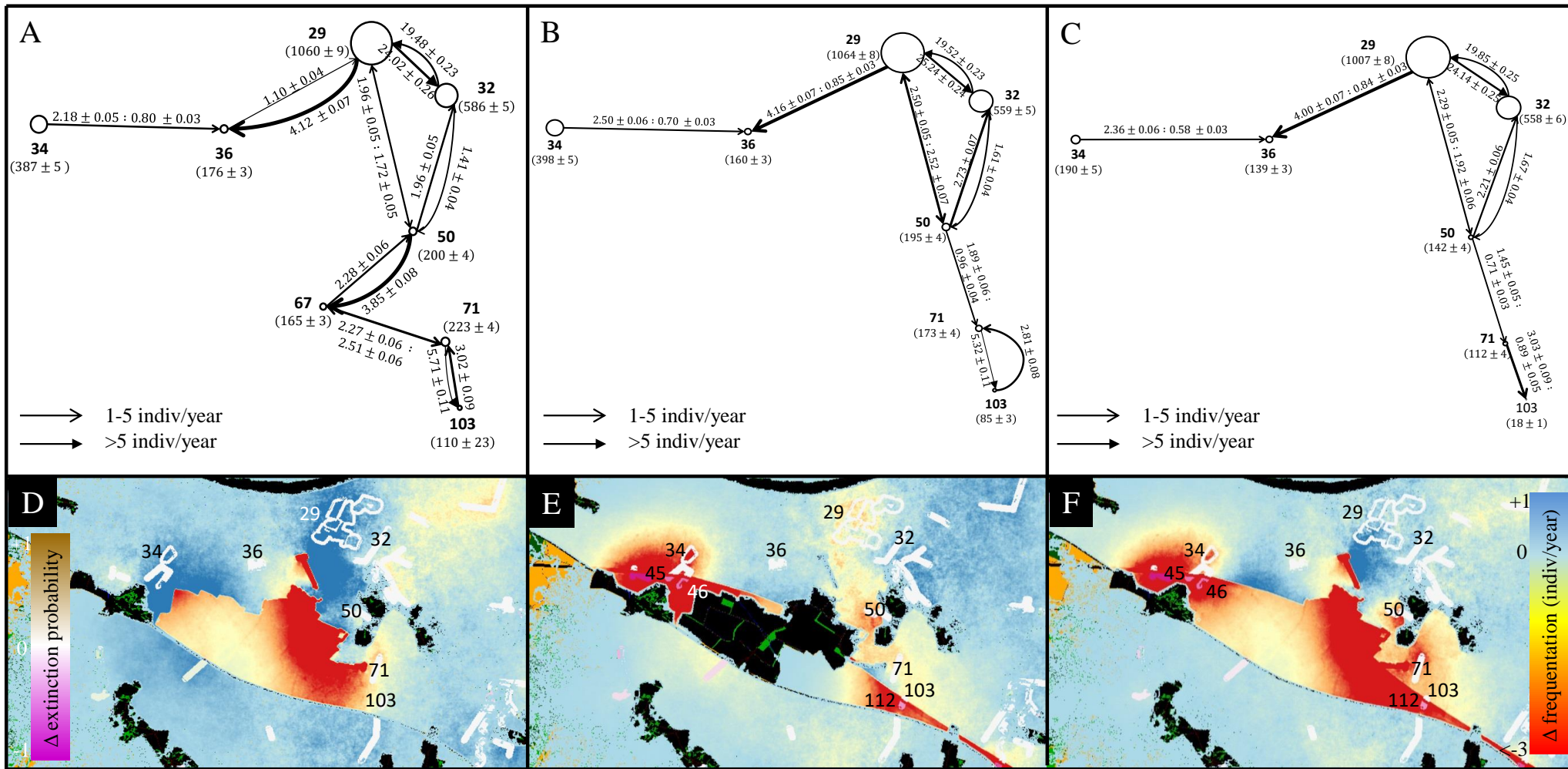
2 Figure 4: MetaConnect output layers of patch extinction probabilities and mean cell
3 frequentation during efficient dispersal events. At the global scale, dispersing individuals
4 follow two main corridors (white arrows in panel A): a major one along the north-south axis
5 and a minor one along the east-west axis.

6



1

2 Figure 5: Genetic clustering of the suitable patches for *E. calamita*. The development of the
3 industrial area (B) does not change the genetic structure of the *E. calamita* population from
4 the current situation (A). 4 clusters are identified and separated by the Garonne (isolating
5 clusters 1 and 2), a forest (barrier between cluster 2 and 3) and the motorway (separating
6 cluster 2 from 4). The addition of the high-speed railway (C) would modify the genetic
7 exchanges and only two clusters would be kept (cluster 1 and 4). The 2.3 cluster is neither
8 aggregated to the cluster 1 nor 4 (all p.values > 0.05) due to the reduction of the number of
9 individuals per patches and the change in the inter-patch genetic exchanges.



1 Figure 6: Graphical representation of the focal area metapopulation functioning derived from
2 MetaConnect outputs for the current situation (A) with the industrial area (B) and with both
3 the industrial area and the high-speed railway (C). Node sizes are proportional to patch
4 population sizes (mean \pm SE). Arrows represent dispersal intensity (mean \pm SE) and direction
5 (bidirectional arrows values correspond to smaller patch number to larger patch number flow:
6 larger patch number to smaller). Maps represent the change in extinction probabilities per
7 patch between scenario B and scenario A and similarly the change in cell occupancy during
8 efficient dispersal. Panel D corresponds to the metapopulation functioning variations after the
9 development of the industrial area. Panel E presents the variation between the situations after
10 the industrial area development and after the high-speed railway building. Panel F
11 summarizes the cumulative differences from the current metapopulation functioning to the
12 expected functioning after the development of the industrial area and the high-speed railway.
13