Extinction Dynamics Model description

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Summary

Even if the number of species extinctions caused by habitat perturbation depends mostly on the relative magnitude of the perturbation, extinctions can also be both accelerated and delayed by eco-evolutionary processes happening at different levels of the community. As long as these extinctions have not happened, an extinction debt exists. The debt is paid as extinctions happen. However, conservation measures can decrease the actual size of the debt by re-establishing habitat conditions or eco-evolutionary processes that promote population rescue from otherwise deterministic extinction. To elucidate the relative importance of these processes, we build an individual-based model to simulate and characterize community response to different kinds of habitat perturbation at different ecological levels (population genetics, species diversity and network change).

Motivation

The model is designed to elucidate how eco-evolutionary processes triggered by the perturbation of a plant-insect metacommunity relate to the resulting extinctions. More specifically, we are interested at ecological (e.g. dispersal capacity, reproductive strategy, species interactions) and evolutionary (e.g. evolutionary rescue, genetic drift) processes delaying or accelerating extinctions.

Questions

With this model, we aim at answering the following questions:

1. What are the long term consequences of habitat fragmentation and climate change for species survival and interactions?

Hypotheses:

- Predictions of extinction debts that only consider isolated abiotic perturbations (habitat fragmentation or climate change) yield understimations, because abiotic perturbations also cause biotic perturbations (pollination loss) as a secondary effect.

- The time necessary to achieve equilibrium decreases in scenarios of dynamical perturbation (multiple events of smaller perturbations over time) in comparison to static perturbation (one single event of larger magnitude).

2. What is the impact of the payment of extinction debts on interaction networks?

Hypothesis: Plants and insects have different dynamics of extinction, which will affect network structure and extinction dynamics differently. The extinction debt takes longer to be paid when insects go extinct first because plants have longer relaxation times.

3. How do microevolutionary dynamics affect the payment of extinction debts?

Hypothesis: Habitat fragmentation allows evolutionary rescue. At the same time, isolation increases the risk of extinction. Therefore, that exists an threshold of population size and isolation that allows the metacommunity to survive despite the total amount of habitat lost (through fragmentation).

Use and applicability

The model is suited for theoretical explorations of eco-evolutionary dynamics and to inform conservation policy.

Model description

Summary: This is a complete version of the model description presented in @FigueiredoEDMODD.

Overview

Purpose

The model simulates the effects of abiotic and biotic perturbations on i) plant species richness and population dynamics, ii) community trait space, and iii) interaction networks of plant-insect (meta)community.

Entities, state variables and scales

The model simulates the life cycle of plants in a landscape. Plant individuals are characterized by state variables listed in Table 1, which are used as parameters values in the simulation of the individual's life cycle (detailed in the next section, Process overview and scheduling).

The landscape is represented as a grid of cells. Each grid cell has an area of 1 m² and represents either suitable or unsuitable habitat (Table 1). The configuration of these cells in the grid generates landscapes that can be composed of a single or multiple patch(es) of suitable habitat. The later are inserted in a matrix of unsuitable habitat. Upon initialization, all grid cells are suitable and can, therefore, be occupied. Upon landscape perturbation (loss of habitat area or fragmentation), a new landscape configuration is loaded (following user definitions) and all plants located in unsuitable cells are killed (details in the Disturbances submodel description). Temperature is a global variable in the model (all patches are subjected to the same temperature). The temperature is used to calculate the biological rates of the organisms being simulated (details in the Submodels section). The model runs on weekly discrete time-steps. The species to be included in the simulation, the landscape configuration, the regime of perturbation (type of perturbation, time of occurrence and magnitude) and total duration of the simulation are determined by the user-defined experimental design (details in the Input and Disturbance submodel sections).

Table 1: Entities and their respective state variables in the model. Variables marked with (*) are species-specific and do not evolve thoughout the simulation. Variables marked with (**) can evolve, as described in

the Microevolution section. The criteria regarding the selection and attribution of the respective values is described in the sections listed below.

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require(knitr)
knitr::kable(statevars_table,
             align = c('l', 'l', 'l', 'l'))
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Scope	State variable	Value (Unit)	References and section of ODD d
Plant	Individual tag	-	-
	Species	species name	Krauss et al. (2010)
	Developmental stage	"seed", "juvenile" or "adult"	Seed germination and establishm
	Age	(weeks)	-
	Vegetative biomass of leaves	(g)	Resource allocation section
	Vegetative biomass of stem	(g)	Resource allocation section
	Vegetative biomass of roots	(g)	Resource allocation section
	Reproductive biomass	(g)	Resource allocation section
	Pollination status	"true" or "false"	Pollination and sexual reproducti
	Dispersal kernel *	"short", "medium, or "long"	Vittoz & engler (2007), LEDA tr
	Clonal ability *	"true" or "false"	LEDA traitbase (Kleyer et al. 20
	Seed mass **	species-specific (g)	LEDA traitbase (Kleyer et al. 20
	Maximal biomass compartment size **	species-specific (g)	Weiss et al. (2014); details in the
	Life span **	species-specific (weeks)	LEDA traitbase (Kleyer et al. 20
	Age of first flowering **	species-specific (weeks)	LEDA traitbase (Kleyer et al. 20
	Beginning of flowering season **	species-specific (week of year)	BiolFlor database (Kühn and Klc
	End of flowering season **	species-specific (week of year)	BiolFlor database (Kühn and Klc
	Beginning of sowing season **	species-specific (week of year)	BiolFlor database (Kühn and Klc
	End of flowering season**	species-specific (week of year)	BiolFlor database (Kühn and Klc
	Maximal number of seeds (weekly) **	species-specific (weeks)	LEDA traitbase (Kleyer et al. 20
	Seed-bank duration **	species-specific (weeks)	LEDA traitbase (Kleyer et al. 20
	Normalization constant of biomass growth	Species-specific (1/week-)	LEDA traitbase (Kleyer et al. 20
Landscape	Suitability	"true" or "false"	User-defined

Normalization constants of metabolic rates of germination and mortality, environmental temperature and carrying-capacity are global parameters of the model. In other words, all individuals have the same values for the constants controlling germination and mortality (callibration of all normalization constants is detailed in the [Metabolic biological rates][Metabolic biological rates] section of [Data evaluation][Data evaluation]). Similarly, all grid-cells have the same temperature, and the same carrying-capacity of plant biomass (detailled in the [Environmental characteristics][Environmental characteristics] section of [Data evaluation][Data evaluation]).

Process overview and scheduling

At each time-step, each individual goes through its life cycle processes, which vary according to the life history strategy determined by the individual's traits and current developmental stage (Table 1), *i.e.*, seeds, juveniles and adults go through different processes.
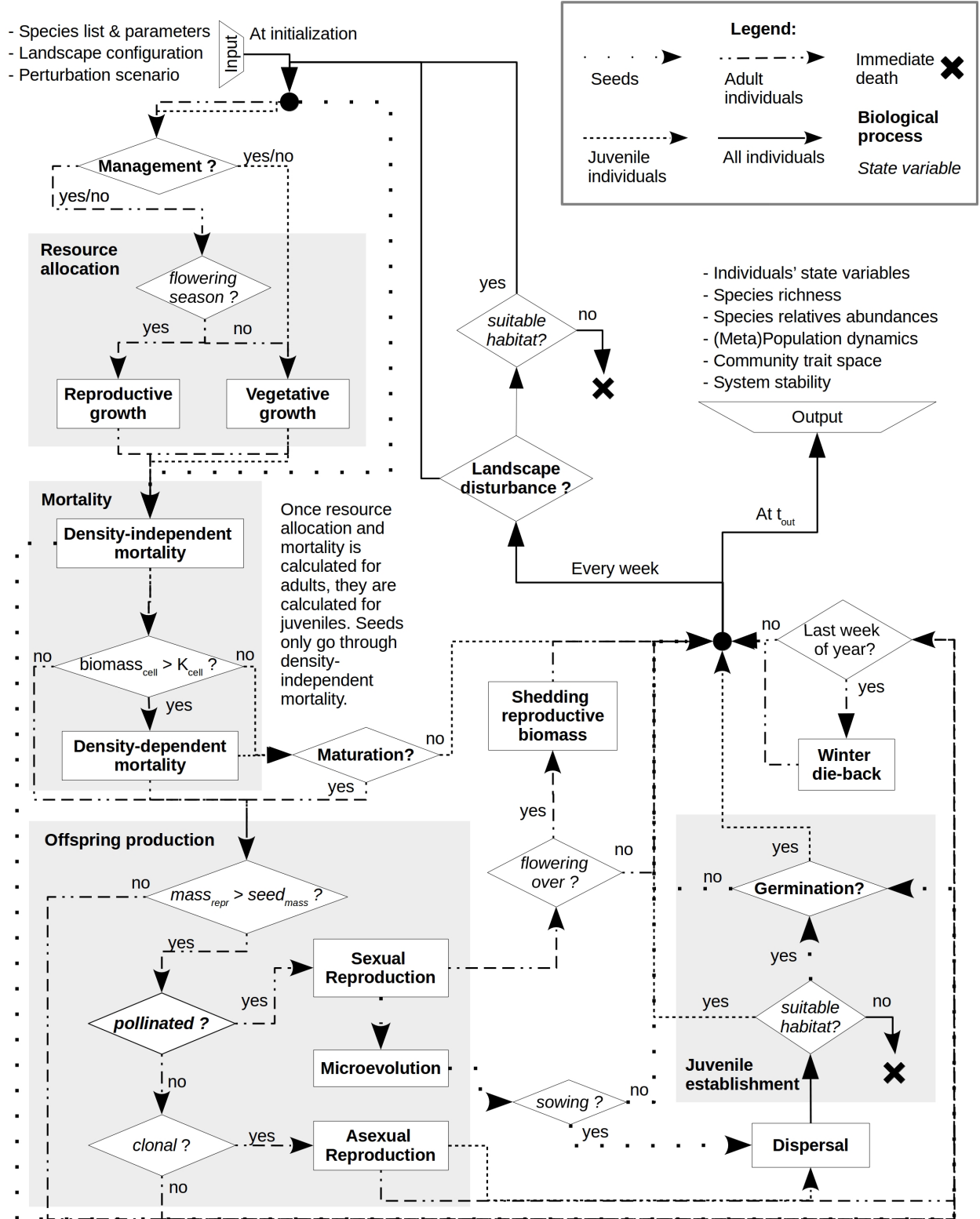
Figure 1: Flowchart of the processes simulated by the model for each individual plant. The biological processes differ between individuals according to state variables such as stage (as identified by the line type), or phenology (e.g.flowering season). The circumstances where state variables control the The outcome of certain biological processes, namely pollination, maturation, germination, or excesive growth ($biomass_{cell} > K_{cell}$ refers to

the biomass production being over the landscape carrying capacity) can also determine the course of an individual's life cycle.

The processes simulated in the model are the following (scheduling is depicted in Figure 1):

Management: Annualy, at most once a year, between August and September, the effects of management (mowing or grazing) are simulated as the reduction of above-ground biomass of juvenile and adult plants that are big enough to be affected.

Resource allocation: Whole organism biomass production is calculated according to metabolic theory of ecology [@Ernest et al. 2004; @Brownetal2004]. The total production is allocated to **vegetative** or **reproductive growth** according to an individual's developmental stage and phenology, following the dynamic energy budget theory (@Kooijman et al.). Juveniles can only accumulate vegetative biomass. During their species-specific reproductive season, adults allocate biomass production to reproductive structures if they have reached a species-specific minimal size. Otherwise, adults grow their vegetative structures.

Mortality: The probability of **density-independent mortality** is calculated for each individual according to the metabolic theory of ecology (@Brownetal2004, details in the Submodels section 3.3) **Density-dependent mortality** is calculated for plants occupying the same grid cell, once the cell's total vegetative biomass reaches the cell's carrying capacity. A species maximal biomass in a given cell corresponds to an amount of the cell's carrying capacity proportional to the species relative fitness. Resource allocation and mortality are calculated in sequence, first for adults, and then for juveniles.

Maturation of juveniles: Regardless of species or size, juvenile individuals become adults once they reach their age of first flowering.

Offspring production: Offspring production encompasses **pollination** and **sexual**, and **assexual reproduction**. Pollination is implicitly simulated as pollination service, *i.e.*, a plant is to sexually produce offspring only if it has been pollinated. Plants can be pollinated if they have enough reproductive biomass to produce at least one seed. If a plant is not pollinated, but is a clonal species, it can produce clones. **Microevolution** is simulated upon sexual reproduction. Clones are exact copies of their mother plants. The phenology of flowering, seed release, maximal seed production and clonality are species-specific traits (Table 1).

Shedding: At the end of flowering season adult plants lose all their reproductive biomass. At the last week of the year, adults loose all of the biomass allocated to *leaves*, and 50% of the biomass allocated to *stem* (Table 1), due to winter die-back.

Seed dispersal: Seeds can be dispersed at short (0.1-100 m), medium- (100-500 m), and long-distances (1-10km; details under [Dispersal submodel description and data evaluation][Dispersal kernels]). The phenology of seed release and the seed dispersal syndrome are species-specific traits (Table 1).

Juvenile establishment: Juvenile establishment is only possible in grid-cells labeled "suitable". Seeds or clones that fall outside patches of habitat (or outside the landscape) are considered to be dead and discarded from the simulation. The probability of **seed germination** is calculated for each individual, according to the metabolic theory of ecology @Brownetal2004. If a seed is successful, it turn into an juvenile.

Design concepts

Basic design principles

The basic principle of the model is to capture how habitat change affects the individual, population and community levels of an ecosystem and how those processes contribute to the size of extinction debts and relaxation times. For its ability to scale individual level effects to community level patterns, the metabolic theory of ecology (@Brownetal2004) was chosen as the guiding principle for calculating biological rates.

Emergence

Metapopulation and metacommunity dynamics arise from the local population dynamics and from species-specific dispersal abilities. Population dynamics results from individual biological demographic rates (biomass growth - both vegetative and reproductive biomass, germination, and mortality) that are calculated according to the metabolic theory of ecology (@Brownetal2004). Competition emerges from individuals occupying the same grid cell having high mortality rate once biomass production reaches the landscape carrying capacity. Consequently, coexistence arises from each population of a species having a relative carrying-capacity (K_c) in the grid-cell. Once it is reached, the species total biomass in the cell is decreased by killing individuals (details in Mortality).

Interactions

Organisms interact with the environment because all vital rates depend on local temperature, as determined by the metabolic theory of ecology (@Brownetal2004, further details under Submodels section). Plants also compete for space (each species has a relative carrying-capacity in the landscape) and pollination services.

Stochasticity

Reproduction, seed dispersal, germination and density-independent mortality are stochastic processes. The probability distribution used in each process is specified in their respective submodel description. Density-dependent mortality is deterministic for small individuals of species going over their carrying capacity.

Observations

To keep track of extinction arising at different ecological levels (individual, population or community), the model outputs all state variables of each individual being simulated (Table 1) at user-defined intervals. From these outputs, the model readily summarizes species diversity, abundance and trait composition changes over time. Other analysis can be derived by the user with the same file.

Details

Initialization

Simulations are defined by the landscape configuration, the species pool, the climatic conditions (temperature) and the type of disturbance. Landscape configuration determines which grid cells constitute suitable habitat and can, therefore, be occupied. Initial temperature (temperature is a global variable of the model) is read from an input file and updated at every time step (the file contains a time-series of weekly temperatures). Individuals are created according to the list of species list given as input. Upon initialization, each individual is randomly placed in the landscape, receives an individual identification number. The individual's grid location is recorded because it is relevant for the calculation of density-dependent mortality (detailed in the [Density-dependent mortality section][Density-dependent mortality]). Upon initialization, an individual's trait value (v) of seed number, seed bank duration, life span and age of first flowering are initialized as $v \sim \mathsf{Unif}(v_{min}, v_{max})$, where v_{min} and v_{max} are given in the species list input file. Trait values regarding minimal and maximal biomass, flower and seed phenology, dispersability, clonality, are read from a single value each, given the same input file. Individuals that are initialized as seeds are one week old. Individuals that are initialized as juveniles have the same biomass as seeds, since they are considered young seedlings, with four weeks old (recently germinated). Adults are initialized with 75% of the species maximum adult biomass and have the age of first flower of the species. Individual's maximal mass, age of first flowering, life span, and flower and seed phenology can evolve through sexual reproduction (complete list of traits and their evolvability in Table 1)

Input

Since simulation scenarios are user-defined, input files must be provided accordingly. A basic experimental design must define: a. Landscape configuration: a.1. A raster file defining landscape configuration (binary values coding habitat availability). a.2. If the landscape is disturbed, similar files should be provided, specifying the new configuration after perturbation b. Species list and trait values: The list of the species to be initialized, their respective minimum and maximum trait values and initial abundance must be given for initialization of the organisms. Details on the species and trait values data used to develop the model under [Data evaluation][Data evaluation]. c. Simulation configuration: i. Duration: Total duration of simulation, in weeks. Simulations always start on the first date given in the temperature time series (details immediately below). Default duration is 52 weeks (one year). ii. Time series of temperature variation: a table of the regional temperature values (all fragments get the same temperature, in °C) for each week of simulation. Details on the time-series data used to develop the model under [Environmental characteristcs in Data evaluation][Data evaluation]. iii. Pollination availability: availabilty of pollination services and its disturbance, if it is simulated. The loss of pollination services can be general (all species lose it equally) or specific (the group of species losing pollination is determined by the experimental design). The intensity of pollination loss is also user-defined. iv. Type, time and magnitude of environmental disturbance: Specification of whether temperature change, area loss or fragmentation should be simulated. For simulating temperature change, the time series should contain the temperature values to be simulated. For simulating area loss or fragmentation, the time of occurrence of disturbance (number of weeks after the beginning of simulation) and the proportion of area to be lost or a new landscape configuration must be given (further details under the Disturbance submodel description).

Submodels

All biological rates (biomass growth, reproduction, germination, and mortality - both density-dependent and independent) are calculated according to the metabolic theory of ecology (@Brownetal2004):

$$B = b_0 . m^\alpha . e^{\frac{-E}{k.T}}$$

where B is the metabolic rate, b_0 is a taxon and stage-specific proportionality constant rate (Brown et al., 2004), m is the individual's body mass, α is the allometric exponent (¾ for individual biomass production and - ¼ for germination and mortality rates, following @Brownetal2004), $E = 8.62e - 5eV/K$ is the activation energy, $k = 0.63eV$ is the Boltzmann constant (@Brown&SiblyChapter2) and T is the local temperature. The proportionality constant b_0 is specifically calculated for each biological rate in order to generate realistic values (details in [Metabolic biological rates section][Metabolic biological rates] of [Data evaluation][Data evaluation]). Biological rates are converted into individual probabilities following

$$p = 1 - e^{-B}$$

Management

following the regime reported for Göttingen by Kormann et al. 2015).

Resource allocation

Biomass growth is calculated as

$$mass_{t+1} = mass_t + B_{growth} \times (mass_{max} - mass_t)$$

where $mass_{max}$ refers to the species total maximal biomass (vegetative and reproductive), and B_{growth} is the rate of growth, derived from a Richards curve parameterized according to the species minimal and maximal sizes, and age of first flowering (details under [Biomass growth rates][Biomass growth rates]). At each time step, biomass production is allocated to vegetative or reproductive structures, depending on the

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individual developmental stage, size and flowering phenology. The reproductive allocation is the proportion of surplus energy allocated to reproduction (@Wenk & Falster 2015). The reproduction allocation schedule allows mapping productivity into different plant structures (vegetative and reproductive), which sustain different food webs (@Wenk&Falster2015), impacting plants population dynamics differently (pollination and herbivory, for example, eg. @Sauveetal). Hence, adult individuals allocate biomass to reproductive structures according to species-specific phenology, *i.e.* each species has a *flowering season* during which biomass production is stored as reproductive biomass. Adults weighing less than 50% of the species maximal body mass do not allocate to reproduction, only to vegetative structures, even during their reproductive season. When growing vegetative structures, biomass production is equally devided into the three structures (*leaves*, *stem* and *roots*).

Mortality

Biomass growth and mortality are calculated in sequence, separately for adults and juveniles(Figure 1). Only density-independent mortality is calculated for seeds.

Density-independent mortality is calculated for all individuals (except seeds that are still attached to the mother plant), at each time-step. Mortality rate, B_{mort}, and probability, p_{mort}, are calculated according to the metabolic theory of ecology (Eq.1 and 2). The mortality normalization constants, b_{0mort} are the same for all species, but vary according to the developmental stage of the individual. For juveniles and adults, $b_{0mort} = 1.11324 \times 10^9$ was derived from a study of allometric relationships of plant life history traits condicted by @Marbàetal. For seeds, $b_{0mort} = 1.6699 \times 10^{10}$, which yields probability of mortality of 93% for the smaller seeds, at the highest temperature. The realization of mortality is randomly drawn from a Bernoulli distribution for each individual, with probability p_{mort}. Details on the callibration of these parameters values are described under [Mortality rates][Mortality rates]. Adult individuals that are older than their maximal lifespan are killed deterministically.

Resource competition is implicitly modeled and arises as **density-dependent mortality**, which is calculated once the total standing biomass in a grid-cell(vegetative and reproductive), $biomass_{cell}$, is higher than its carrying-capacity ($K = 3.5T/ha$, downscaled to the grid-cell size of $1m^2$ yields $K_{cell} = 350g$). Then, individuals of the species that have grown past their relative relative carrying-capacity in the cell, $K_{cell_{sp}}$, are ranked by size and the smaller ones are killed first until the species-specific vegetative biomass in the cell $m_{cell_{sp}}$ is smaller than the species' $K_{cell_{sp}}$. A species' relative carrying-capacity in the cell is calculated as

$$K_{cell_{sp}}(t) = \frac{f_{sp}(t)}{\sum_{i=1}^{spp_{cell}} f_{sp_i}(t)} \times K_{cell}$$

where $f_{sp}(t)$ if the species' absolute fitness value at time t, and spp_{cell} is the number of species in the cell. Species fitness is calculated with a Gaussian function $g(x) = ae^{\frac{-(x-b)^2}{2c^2}}$ applied to the mean annual temperature of the current year, $\mu_{annual}(t)$. The parameters controlling the function are the curve's peak value a, to which we assign maximal fitness value $f_{max} = 1$; the value of b, for which $f(b) = a = f_{max}$, which we assign to the mean of annual mean temperatures of the species geographical distribution μ_{dist}; and the standard deviation c, to which we assign $\frac{max_{dist} - min_{dist}}{6}$, where min_{dist} and max_{dist} are minimum and the maximum annual mean temperatures of the species geographical distribution, respectively. The reasoning behind the our decision to assign this values and the data used to calculate them are described in the [Niche partitioning section][Niche partitioning] of [Data evaluation][Data evaluation]. The fitness of a species is, then:

$$f_{sp}(\mu_{annual}(t)) = f_{max} \times e^{\frac{-(\mu_{annual}(t) - \mu_{dist})^2}{2 \times (\frac{max_{dist} - min_{dist}}{6})^2}}$$

Offspring production

Only adult individuals with reproductive structures (biomass allocated to reproduction) have the potential to reproduce. The production of offspring will depend on the amount of reproductive biomass, the availability of pollination services (for pollination-dependent species) and the species's capacity of clonal reproduction (pollination-independent species).

Pollination and sexual reproduction

The occurrence of pollination is a stochastic process that depends on the availability of pollination services, which is determined by the experimental design.

The base number of reproducing individuals is calculated according to weekly pollination availability. From all the plants with reproductive biomass, the number of effectively pollinated plants is drawn from a Binomial distribution

$$n_{poll} \sim \mathsf{Binom}(n = n_p \times n_o, \pi = 0.5)$$

where n_p is the number of plants with enough reproductive biomass, $n_o \sim \mathsf{Unif}(10^{-4}, 10^{-2})$ is the proportion of occupied flowers (@Fishman&Hadany2010), and $\pi = 0.6$ accounts for pollination efficiency (@Kingetal2013 reports 40% of visitors are not effective pollinators). The availability of pollination is determined by the pollination scenario. Under the independent scenario, the number of pollinated plants is calculated as above, independent of the species. In the scenario of "equal" pollination loss, the number of pollinated plants (still species-independent) is a proportion (value between 0-1) defined by the input file (see details in the Input section). Under the random scenario, a given number of species can be defined to lose pollination according to a fixed proportion. Under the specific scenario, a given list of species loses pollination, again according to a fixed proportion provided by the user. In all the scenarios it is possible to define the proportion of lost pollination at different time-steps (see details in the Input section) Five percent of the biomass allocated in reproductive compartiment is used to produce seeds by plants that have been effectively pollinated (@Weissetal.2014). The actual amount of seed is limited by the species weekly maximal number of seeds, i.e even if the plant has enough biomass to produce more than its maximum, it will not (the species weekly maximal number of seeds is given as input to the model - seed details in the Inputs and in [Seed number secion][Seed number] of [Data evaluation][Data evaluation]). The trait values of the new individuals are calculated according to a simplified model of phenotypical change of a population under panmixia (described in the Microevolution submodel). After offspring production, the mother-plant loses biomass from its reproductive compartment equivalent to the number of seeds produced.

Asexual reproduction

A clonal plant that has not been pollinated has 50% probability of generating a ramet. The clone is initialized as a juvenile, in the same grid cell as the mother-plant, weighing 10% of the species total maximal biomass. In the same way as with the sexual reproduction, the mother-plant looses biomass from its reproductive structures equivalent to the size of the clone produced. The clone inherits the same trait values as its mother-plant Table 1.

Microevolution

Offspring inherits its traits values according to the type of reproduction it is generated from. Clonal individuals inherent the same set of traits as the mother-plant. Sexual reproduction follows a random mating model, where the new trait value v of evolvable traits ([table1][table1]) is calculated according to the formula:

$$v = \frac{v_{mother} + v_{mother}}{2} + \mathsf{Normal}(0, |\frac{(v_{mother} - v_{father})}{6}|)$$

where v_{mother} is the trait value of the individual originating the seed and v_{father} is the trait value of a conspecific individual randomly chosen in the population. By using $\frac{(v_{mother} - v_{father})}{6}$, the introduced variability in trait hereditability is limited to the difference between the parent's values. The resulting trait value, however, is limited by the species minimal and maximal values, v_{min} and v_{max}, given as input.

Seed dispersal

During the reproductive season, seeds are produced, but not necessarily dispersed. Seed dispersal happens one week after the end of the flowering season, which is a species-specific trait. The model simulates kernel-based dispersal. Kernel parameters characterize the distribution of distances achieved by the species

mode of dispersal. In this application of the model, species dispersal modes were retrieved from the @LEDAtraitbase and the assignemnt of dispersal kernel to dispersal syndrome is described in the [Dispersal mode section][Dispersal mode]. The model simulates three dispersal kernels:

Table 2: Dispersal kernels simulated in the model and the range of values generated by each.

Dispersal kernel	Function (parameter values)	Min. and max. distances
Short-distance	Inverse Gaussian ($\mu = 1$, $\lambda = 0.2$) $\times$ 4	0.1-100 m
Medium-distance	Inverse Gaussian ($\mu = 0.2$, $\lambda = 3$) $\times$ 1000	100-500 m
Long-distance	Inverse Gaussian ($\mu = 1000$, $\lambda = 100$)	1-10 km

Dispersal is simulated by drawing a random radian angle θ (0-2*π) with Uniform probability and drawing the dispersal distance $dist_{disp}$ from the species' dispersal kernel. If the species presents dispersal syndromes that are assigned to different dispersal kernels, one of them is randomly drawn from an Uniform probability distribution before drawing $dist_{disp}$. The new location is calculated as

$$(x_{new}, y_{new}) = (x + cos\theta \times dist_{disp}, y + sin\theta \times dist_{disp})$$

where (x, y) is the individual's current location (cartesian coordinates of the cell in the landscape).

Seed germination and seedling establishment

If a seeds is dispersed and falls on an unavailable grid cell, it dies immediately. Otherwise, its germination rate, B_{germ}, and probability, p_{germ} are calculated according to the metabolic theory of ecology, with a global normalization constant parameterized as described in the [Germination rate section][Germination rate] of [Data evaluation][Data evaluation].

The realization of germination is randomly drawn from a Bernoulli distribution, with probability p_{germ}. If germination happens, the new seedling is identified as a juvenile individual. Seeds that do not germinate remain in the seed bank.

Maturation of juveniles

Juvenile individuals become adults once they reach their age of first flowering.

Disturbances

The model can simulate scenarios of temperature change, loss of habitat area (with or without fragmentation) and loss of pollinators. These scenarios are defined independently from each other, which allows the combination of different perturbations into a single scenario. Each type of disturbance is simulated as follows:

Temperature change

The model is dependent on a temperature time series being input (to calculate the rates of biological processes), therefore, temperature change can be simulated by providing a time series that characterizes the temperature change for the duration of the simulation.

Area loss (without fragmentation)

The simulation scenario must define a proportion of habitat to be lost at a given timestep. Then, the corresponding number contiguous grid cells are marked as 'unsuitable' and all individuals occupying this cells are immediately killed (as will be any seeds dispersing into these cells in the remaining of the simulation). It

is also possible to simulate area loss if a raster file describing a new configuration of habitat suitability of the original area is provided (associated with a time-step when it should be loaded). Cells are amarked as "unsuitable" according to raster configuration and local individuals are killed.

Fragmentation

Habitat fragmentation can only be simulated via raster files. Similarly to area loss, cells are marked as unsuitable according to the description contained in the raster file and individuals in the area are killed. Several episodes of area loss or fragmentation can be simulated if several proportions or raster files describing loss are provided, associated with different time-steps.

Pollinator loss

Loss of pollinators can be defined according to its i) *specificity*, *i.e*, which species are affected, ii) *intensity*, *i.e.*, the proportion of flowers still being pollinated and iii) *regime*, *i.e*, whether loss is permanent or ocasional.