Landsepi: List of assumptions and parameters

Stochastic, spatially-explicit, demo-genetic model simulating the spread and evolution of a plant pathogen in a heterogeneous landscape to assess resistance deployment strategies.

Assumptions:

In orange assumptions that can be relaxed with appropriate parameterization.

1. The spatial unit is the field, i.e. a piece of land delimited by boundaries and possibly cultivated with a crop. Such crop may be host or non-host, and the field is considered a homogeneous mixture of individuals (i.e. there is no intra-field structuration).

2. Host individuals are in one of these four categories: H (healthy), E (latent, i.e. infected but not infectious nor symptomatic), I (infectious and symptomatic), or R (removed, i.e. epidemiologically inactive).

3. A host 'individual' is an infection unit and may correspond to a given amount of plant tissue (where a local infection may develop, e.g. fungal lesion) or a whole plant (e.g. systemic viral infection). In the first case, plant growth increases the amount of available plant tissue (hence the number of individuals) during the cropping season. Plant growth is deterministic (logistic growth) and only healthy hosts (state H) contribute to plant growth (castrating pathogen).

4. The decreasing availability of healthy host tissues (as epidemics spread) makes pathogen infection less likely (i.e. density-dependence due to plant architecture).

5. Host are cultivated, thus there is no host reproduction, dispersal and natural death.

6. Environmental and climate conditions are constant, and host individuals of a given genotype are equally susceptible to disease from the first to the last day of every cropping season.

7. Crop yield depends on the average amount of producing host individuals during the cropping season and does not depend on the time of epidemic peak. Only healthy individuals (state H) contribute to crop yield.

8. Initially, the pathogen is not adapted to any source of resistance, and is only present on susceptible hosts (at state I).

9. Pathogen dispersal is isotropic (i.e. equally probable in every direction).

10. Pathogen reproduction is clonal.

11. Pathogenicity genes mutate independently from each other.

12. Pathogen adaptation to a given resistance gene consists in restoring the same aggressiveness component as the one targeted by the resistance gene.

13. If a fitness cost penalises pathogen adaptation to a given resistance gene, this cost is paid on hosts that do not carry this gene, and consists in a reduction in the same aggressiveness component as the one targeted by the resistance gene.

14. When there is a delay for activation of a given resistance gene (APR), the time to activation is the same for all hosts carrying this gene and located in the same field.

15. Variances of the durations of the latent and the infectious periods of the pathogen are not affected by plant resistance.

16. If there is sexual reproduction (or gene recombination), it occurs only between parental infections located in the same field and the same host genotype. The propagule production rate of a couple is the sum of the propagule production rates of the parents. The genotype of each daughter propagule is issued from random loci segregation between parental loci.

Parameter	Notation in article	Possible values	Default value	Meaning	Remarks
SIMULATION PARAMETERS					
Nyears	Y	$\mathbb{N}^*$	20	Number of cropping seasons (e.g. years)	
nTSpY	T	$\mathbb{N}^*$	120	Number of time steps per cropping season (e.g. days)	Duration of the epidemic season
seed		$\mathbb{N}$	12345	Seed for random number generator	
writeTXT		{TRUE ; FALSE}	TRUE	Whether or not outputs must be written in text files	
graphic		{TRUE ; FALSE}	TRUE	Whether or not graphics must be generated	
videoMP4		{TRUE ; FALSE}	FALSE	Whether or not a video must be generated	Works only if graphic=TRUE and epid_outputs="audpc" (or epid_outputs="all"). Requires ffmpeg library. Up to 9 different croptypes can be properly represented.
keepRawResults		{TRUE ; FALSE}	FALSE	Whether or not raw outputs (binary files) must be kept	Keeps 6 binary files (H, Hjuv, L, I, R, P) per simulated year
PATHOGEN PARAMETERS				Basic pathogen aggressiveness components on a susceptible host for a pathogen genotype not adapted to resistance	Parameters of random draws, thus every infection has its own values (stochastic variability)
infection_rate	e_{max}	[0 ; 1]	0.40	Maximal expected infection rate of a propagule on a healthy host	Given that the propagule landed on the host
propagule_prod_rate	r_{max}	$\mathbb{R}^+$	3.125	Maximal expected effective propagule production rate per timestep and per infectious host	Number of viable propagules that disperse and land on another host individual
latent_period_exp	γ_{min}	$\mathbb{R}^+$	10	Minimal expected latent period duration	(in time steps)
latent_period_var	γ_{var}	$\mathbb{R}^+$	9	Variance of the latent period duration	(in time steps)
infectious_period_exp	Υ_{max}	$\mathbb{R}^+$	24	Maximal expected infectious period duration	(in time steps)
infectious_period_var	Υ_{var}	$\mathbb{R}^+$	105	Variance of the infectious period duration	(in time steps)
survival_prob	λ	[0 ; 1]	10^{-4}	Off-season survival probability of a propagule	Bottleneck size
repro_sex_prob		[0 ; 1]	0	Probability for an infectious host to reproduce via sex	> 0 to allow sexual reproduction. Clonal reproduction is completely replaced by sexual reproduction in concerned host individuals
sigmoid_kappa	κ	$\mathbb{R}^+$	5.33	Kappa parameter of the sigmoid contamination function	$\kappa=0$ and $\sigma=1$ for linear relationship
sigmoid_sigma	σ	$\mathbb{R}^+$	3	Sigma parameter of the sigmoid contamination function	$\sigma=0$ to relax density-dependence assumption
sigmoid_plateau		[0 ; 1]	1	Plateau parameter of the sigmoid contamination function	
CROPTYPE PARAMETERS				Characteristics of the landscape and of each cultivated croptype	
GPKGLandscape				Landscape in shapefile format, containing spatial coordinates of every field	Buit-in simulated landscapes are available. Areas must be expressed in square meters.
aggreg		$\mathbb{R}^+$		Level of spatial aggregation of the landscape	Units relative to the maximal distance between two fields of the landscape: between 0 and 0.1 for fragmented landscape, 0.1 and 0.5 for balanced landscape, 0.5 and 3 for aggregated landscape, and above 3 for bloc planting

Parameter	Symbol	Range/Values	Default	Description	Notes
algo		{"exp"; "periodic"; "random"}		Algorithm used to control spatial aggregation in croptype allocation	Parameter "aggreg" is ignored for random allocation
croptypeName				Name of the croptype	
prop		[0 ; 1]		Proportion of the landscape surface cultivated with the croptype (cropping ratio)	A minimum of 1 field is allocated to each croptype
rotation_period		$\mathbb{N}$		Number of years before rotation of the landscape	There is no rotation if rotation_period=0 or rotation_period=Nyears
rotation_sequence		$\mathbb{N}$		Indices of cultivated croptypes for each period of the rotation sequence	There is no rotation if the list contains only one element
rotation_realloc		{TRUE ; FALSE}	FALSE	Whether or not a new random allocation of croptypes is performed when the landscape is rotated.	rotation_realloc=FALSE for static allocation ; rotation_realloc=TRUE for dynamic allocation
DISPERSAL PARAMETERS				Probability of dispersal from any field to any other field of the landscape	
disp_patho	μ	[0 ; 1]		Pathogen dispersal matrix	To compute from dispersal kernel via RCALI package. Dispersal matrices for rust pathogens are available for each built-in landscape. Identity matrix = no dispersal
disp_host		[0 ; 1]	I	Host dispersal matrix	Identity matrix (cultivated hosts do not disperse)
CULTIVAR PARAMETERS				Characteristics of each host genotype as if cultivated in pure crop	
cultivarName				Name of the cultivar	Avoid using spaces in cultivar names
initial_density	C^0	$\mathbb{R}^+$	0.1	Host density (in pure crop) per surface unit at the beginning of the cropping season	$C^0=0$ if the crop is not cultivated. $C^0 \leq C^{max}$
max_density	C^{max}	$\mathbb{R}^{+*}$	2	Maximum host density (in pure crop) per surface unit at the end of the cropping season	$C^0=C^{max}$ if individual hosts are whole plants or do not grow
growth_rate	δ	[0 ; 1]	0.10	Growth rate	$\delta=0$ if individual hosts are whole plants or do not grow
reproduction_rate		[0 ; 1]	0	Reproduction rate	(cultivated hosts do not reproduce)
death_rate		[0 ; 1]	0	Death rate	(cultivated hosts do not naturally die)
yield_H		$\mathbb{R}^+$	2.5	Yield in pure crop (in weight or volume unit / ha / cropping season) associated with the sanitary status 'H'	yield_H=0 if the crop is not a cash crop
yield_L		$\mathbb{R}^+$	0	Yield in pure crop (in weight or volume unit / ha / cropping season) associated with the sanitary status 'L'	yield_L>0 for non-castrating pathogen
yield_I		$\mathbb{R}^+$	0	Yield in pure crop (in weight or volume unit / ha / cropping season) associated with the sanitary status 'I'	yield_I>0 for tolerant cultivar
yield_R		$\mathbb{R}^+$	0	Yield in pure crop (in weight or volume unit / ha / cropping season) associated with the sanitary status 'R'	yield_R>0 for tolerant cultivar
production_cost		$\mathbb{R}^+$	225	Overall production costs in pure crop (in monetary units / ha / cropping season) including planting, amortization, wages, etc.	
market_value		$\mathbb{R}^+$	200	Market value of the product (in monetary units / weight or volume unit)	

GENE PARAMETERS				Characteristics of each plant resistance gene and of each corresponding pathogen pathogenicity gene	
geneName				Name of the resistance gene	
target_trait	w	{"IR" ; "LAT" ; "IP" ; "PR"}	"IR"	Aggressiveness component targeted by the resistance gene	IR=e_{max} ; LAT=γ_{min} ; IP=Y_{max} ; PR=r_{max}
efficiency	ρ	[0 ; 1]	1.00	Efficiency of the resistance gene (percentage of reduction of the targeted aggressiveness component: IR, 1/LAT, IP or PR)	ρ=1 for complete resistance, ρ<1 for partial resistance, ρ=0 for no resistance
time_to_activ_exp		$\mathbb{R}^+$	0	Expected delay to resistance activation (for APRs)	time_to_activ_exp>0 for APRs
time_to_activ_var		$\mathbb{R}^+$	0	Variance of the delay to resistance activation (for APRs)	time_to_activ_var=0 for deterministic activation at time_to_activ_exp
mutation_prob	τ	[0 ; 1]	10^{-7}	Probability for a pathogenicity gene to mutate	τ=0 for no evolution
Nlevels_aggressiveness	Q	$\mathbb{N}^*$	2	Number of adaptation levels related to each resistance gene (i.e. 1 + number of required mutations for a pathogenicity gene to fully adapt to the corresponding resistance gene)	Q=1 for no adaptation ; Q=2 for adaptation via a single mutation ; Q>2 for gradual adaptation to resistance. Careful, value of Q severely impacts computational time.
fitness_cost	θ	[0 ; 1]	0.50	maximal fitness penalty paid by a pathogen genotype fully adapted to the resistance gene on hosts that do not carry this gene	θ=0 for no fitness cost ; θ=1 for matching allele model
tradeoff_strength	β	$\mathbb{R}^{+*}$	1.0	Strength of the trade-off relationship between the level of aggressiveness hosts that do and do not carry the resistance gene	β=1 for linear trade-off ; β>1 for strong trade-off (cost higher than gain) ; β>1 for weak trade-off
INOCULUM PARAMETER				Initial conditions	
pI0	ϕ	[0 ; 1]	5.10^{-4}	Initial probability for the first host (usually parameterised as a susceptible cultivar) to be infectious (state I) at the beginning of the simulation	ϕ=0 for absence of disease. Note: if ϕ is too high the epidemic collapses before the end of the first season due to lack of healthy hosts to infect
OUTPUT PARAMETERS					
epid_outputs			"all"	Epidemiological and economic outputs to generate: "audpc" : Area Under Disease Progress Curve "gla_abs" : Absolute Green Leaf Area "gla_rel" : Relative Green Leaf Area "eco_cost" : total crop costs "eco_product" : total crop production "eco_benefit" : total crop benefits "eco_grossmargin" : Gross Margin (benefits - costs) "HLIR_dynamics", "H_dynamics", "IR_dynamics", etc. : Epidemic dynamics related to the specified sanitary status "all" : compute all these outputs "" : none of these outputs will be generated.	- AUDPC: average proportion of diseased hosts (status I + R) relative to the carrying capacity. - GLA$_{abs}$: average number of healthy hosts (status H) per time step and per square meter. - GLA$_{rel}$: average proportion of healthy hosts (status H) relative to the total number of existing hosts (H+L+I+R). - HLIR_dynamics: graphic only - Economic outputs in monetary units per hectare. - Gross margin = market_value * (yield – loss) – production_cost
evol_outputs			"all"	Evolutionary outputs to generate : "evol_patho" : Dynamics of pathogen genotype frequencies "evol_aggr" : Evolution of pathogen aggressiveness	For durability, several computations are performed for each pathogen genotype: - time to first appearance (as propagules);

			▪ "durability" : Durability of resistance genes ▪ "all" : compute all these outputs ▪ "" : none of these outputs will be generated.	- time to first true infection of a resistant host; - time when the number of infections of resistant hosts reaches thres_breakdown.
GLAnoDis	$\mathbb{R}^{+*}$	1.48315	Absolute Green Leaf Area in absence of disease	(used to compute economic outputs)
audpc100S	]0 ; 1]	0.38	AUDPC in a fully susceptible landscape	(used as reference value for graphics and video)
thres_breakdown	$\mathbb{N}*$	50,000	Threshold (i.e. number of infections) above which a pathogen genotype is unlikely to go extinct and resistance is considered broken down	Used to characterise the time to invasion of resistant hosts (several values are computed if several thresholds are given in a vector)