

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 a polygon, 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 polygon is considered a homogeneous mixture of host individuals (i.e. there is no intra-polygon structuration). A field may be composed of a single or several polygons.
2. Host individuals are in one of these four categories: H (healthy), E (exposed and 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 individuals (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 (i.e. sown/planted and harvested), 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. Components of a mixture are independent each other (i.e. there is neither plant-plant interaction nor competition for space, and harvests are segregated).
9. Crops may be treated with chemicals which reduce the pathogen infection rate (contact treatment). Treatment efficiency decreases with host growth (i.e. new biomass is not protected by treatments) and time (i.e. pesticide degradation). Crops to be treated and dates of chemical applications are fixed prior to simulations (thus they are independent from the epidemic dynamics) and are the same for all polygons cultivated with the crops to be treated.
10. The pathogen is haploid.
11. Initially, the pathogen is not adapted to any source of resistance, and is only present on susceptible hosts (at state I).
12. Pathogen dispersal is isotropic (i.e. equally probable in every direction).
13. Pathogen reproduction can be purely clonal, purely sexual, or mixed (alternation of clonal and sexual reproduction).
14. If there is sexual reproduction (or gene recombination), it occurs only between parental infections located in the same polygon and the same host genotype. At that scale, the pathogen population is panmictic (i.e. all pairs of parents have the same probability to occur). The propagule production rate of

evol_outputs			"all"	"all"	Evolutionary outputs to generate : <ul style="list-style-type: none"> ▪ "evol_patho" : dynamics of pathogen genotype frequencies ▪ "evol_patho_bi": pathogen genotype frequencies after the off-season (after bottleneck) ▪ "evol_aggr" : evolution of pathogen aggressiveness ▪ "durability" : durability of resistance genes ▪ "all" : compute all these outputs ▪ "" : none of these outputs will be generated. 	For durability, several computations are performed for each pathogen genotype: - time to first appearance (as propagules); - time to first true infection of a resistant host; - time when the number of infections of resistant hosts reaches thres_breakdown.
audpc100S		\mathbb{R}^{+*}	0.76	8.48	AUDPC in a fully susceptible landscape	(used as reference value for graphics and video)
thres_breakdown		\mathbb{N}^*	50,000	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)