

Modelling plant resistance deployment: the R package *landsepi*

The R package *landsepi* provides a general modelling framework to help compare plant resistance deployment strategies and understand the impact of epidemiological, evolutionary and genetic factors for a wide range of pathosystems.

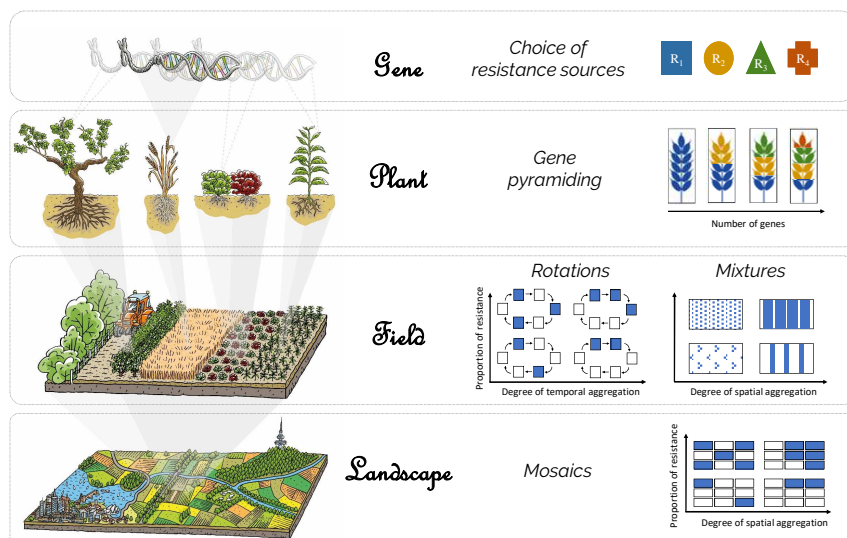


Strategies to improve plant resistance management rely on careful selection of resistance sources and their combination at various spatio-temporal scales.

In *landsepi*, the landscape is a **dynamic mosaic of fields** cultivated with **croptypes**. Each croptype is composed of either a pure cultivar or a mixture; and each **cultivar** may carry one or several **resistance genes**. Each resistance gene targets one or several **pathogenicity traits**, with complete or partial **efficiency**, and may be expressed from the beginning of the season or later (e.g. APR gene). The pathogen adapts to these genes (restoring its pathogenicity), possibly associated with a **fitness cost**.

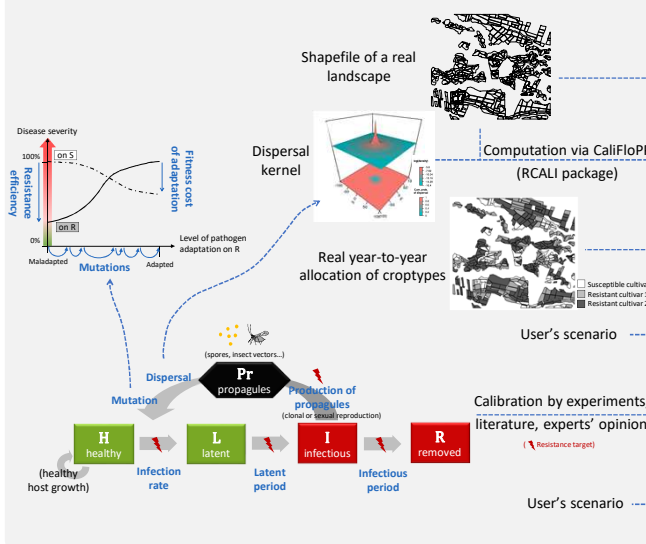
The model is based on a **spatial geometry** for describing the heterogeneous landscape and allocating different cultivars, a **dispersal kernel** for the dissemination of the pathogen, and a **stochastic SEIR** ('Susceptible-Exposed-Infectious-Removed') structure with a discrete time step for the description of the host-pathogen interaction. Cropping seasons are split by host harvests which impose potential **bottlenecks** to the pathogen. The model accounts for pathogen evolution (via **mutation**, **sexual reproduction**, **selection** and **drift**) and provides **epidemiological, evolutionary and economic outputs** to assess the performance of the simulated strategies.

The package also includes a **shiny interface** for pedagogical purposes.



Adapted from Rimbaud L., Fabre F., Papaix J., Moury B., Lannou C., Barrett L. and Thrall P. (2021). Models of plant resistance deployment. *Annual Review of Phytopathology* 59 (in press)

User's parameterisation



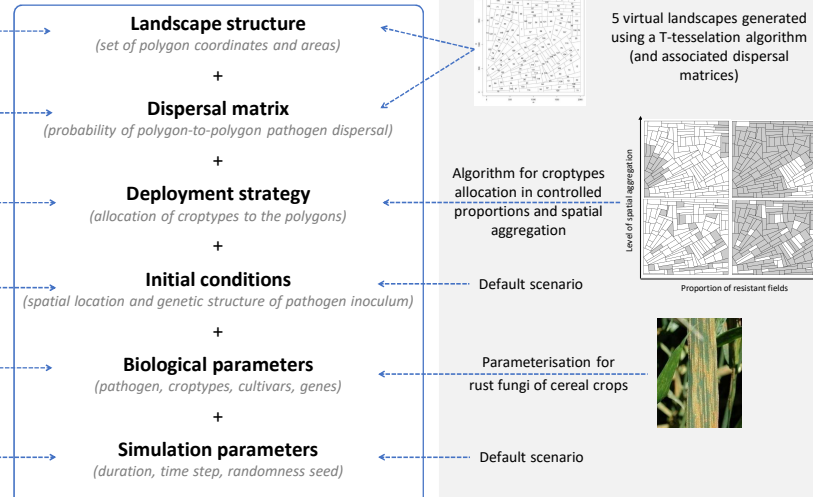
Spatial unit: The spatial unit is a polygon. An agricultural field (i.e. a piece of land cultivated by the same croptype) may be composed of a single or several polygons.

Individual: 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.

R package
 ### R package ###
 ### {landsepi} ###






Built-in objects and functions



Average computational time: 30 seconds (for a 30-year simulation with 3 cultivars and 2 major resistance genes)

Computation of specific outputs from raw results

Outputs

-  **Evolutionary: Resistance durability**
 ability to limit pathogen evolution and delay resistance breakdown
 (Pathotype and genotype frequencies, Time to resistance breakdown)
-  **Epidemiological: Disease control**
 ability to reduce disease impact
 (AUDPC, GLA)
-  **Economic: Cost efficiency**
 ability to overcompensate epidemic losses and management costs
 (Yield, Product, Operational cost, Margin)

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PUBLICATIONS

- Rimbaud L., Fabre F., Papaix J., Moury B., Lannou C., Barrett L. G. and Thrall P. H. (2021). Models of plant resistance deployment. *Annu. Rev. Phytopathol.* 59(1):in press.
- Rimbaud L., Papaix J., Rey J.-F., Barrett L. G. and Thrall P. H. (2018). Assessing the durability and efficiency of landscape-based strategies to deploy plant resistance to pathogens. *PLoS Comput. Biol.* 14:e1006067.
- Rimbaud L., Papaix J., Barrett L. G., Burdon J. J. and Thrall P. H. (2018). Mosaics, mixtures, rotations or pyramiding: What is the optimal strategy to deploy major gene resistance? *Evol. Appl.* 11:1791-1810.

LINKS

Homepage: <https://csi-ro-inra.pages.biosp.inrae.fr/landsepi/>
 Web app: https://shiny.biosp.inrae.fr/app_direct/landsepi/
 R package: <https://cran.r-project.org/web/packages/landsepi/index.html>

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