# Modelling plant resistance deployment: the R package *landsepi*

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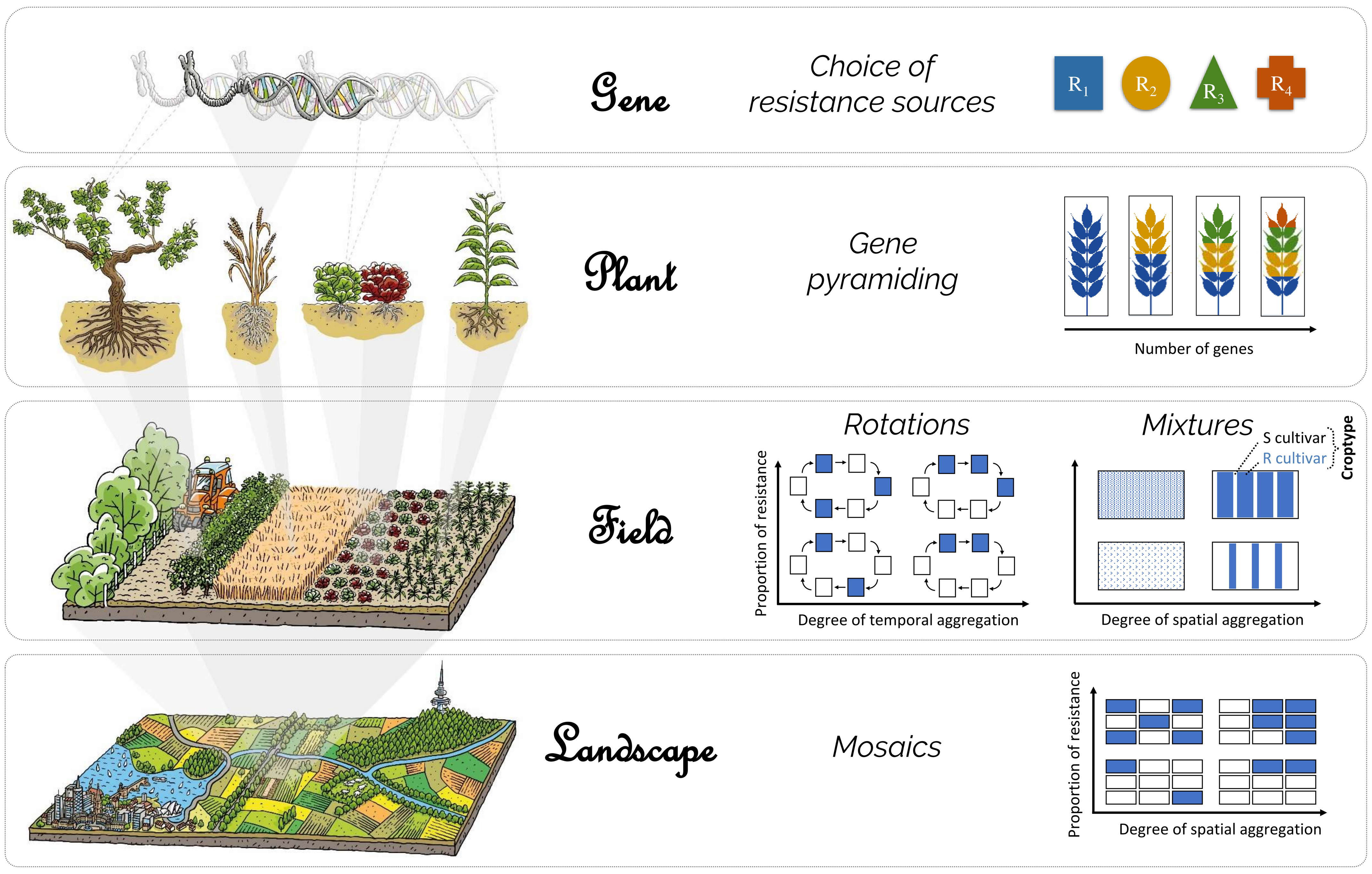
The R package *landsepi* provides a general modelling framework to help compare plant resistance deployment strategies and understand the impact of epidemiological, evolutionary and genetic factors for a wide range of pathosystems.

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 may adapt to these genes (restoring its pathogenicity), possibly associated with a **fitness cost**. Additionally, any cultivar may be treated with contact pesticides, which reduce the pathogen infection rate with an efficiency gradually decreasing with host growth.

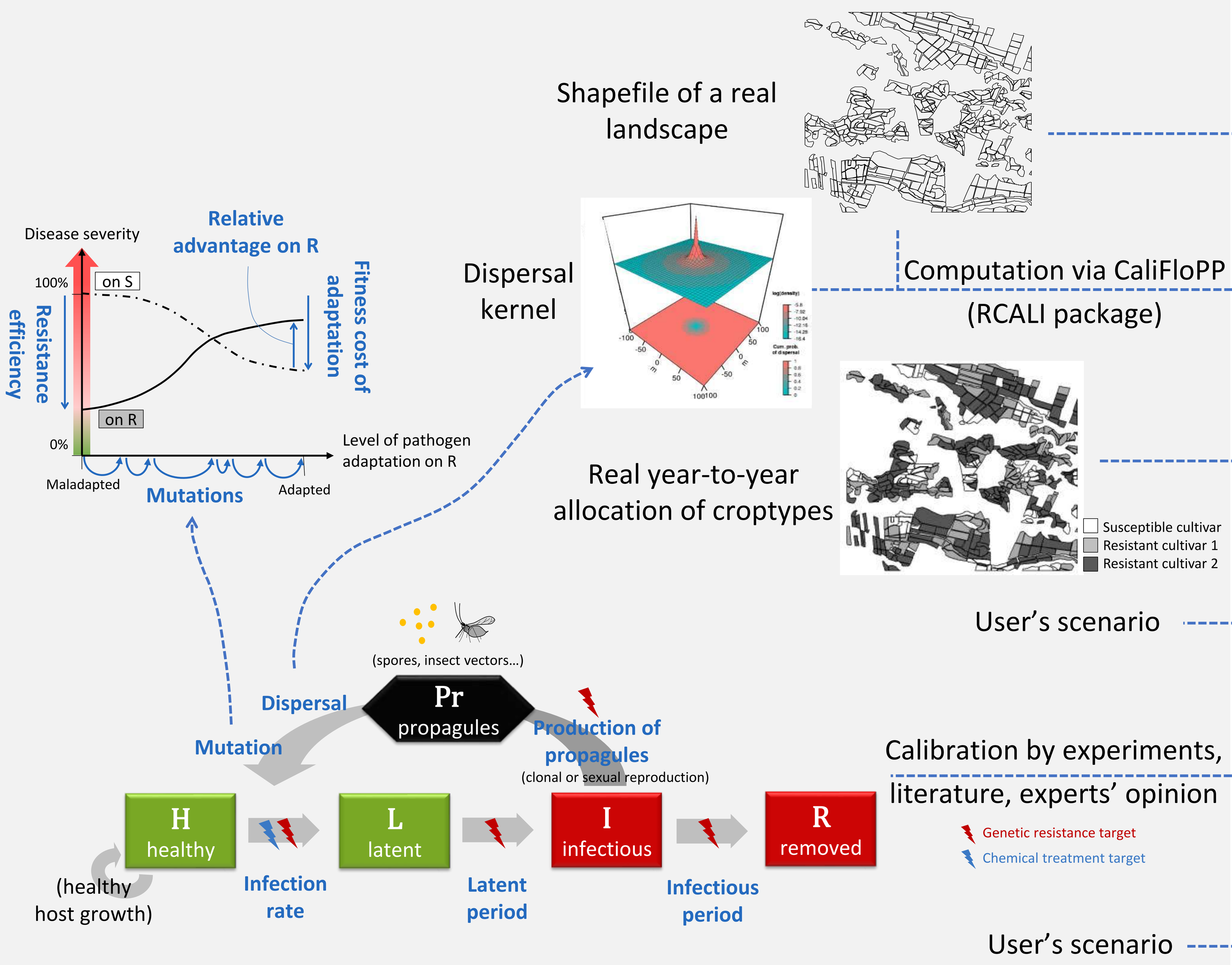
The model is based on a **spatial geometry** for describing the heterogeneous landscape and allocating different cultivars, **dispersal kernels** for the dissemination of the pathogen, and a **stochastic SEIR** ('Susceptible-Exposed-Infectious-Removed') structure with a discrete time step for the description 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**, **recombination** via 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., Papaïx J., Moury B., Lannou C., Barrett L. and Thrall P. (2021). Models of plant resistance deployment. *Annual Review of Phytopathology* 59(1):125-152.

## User's parameterisation




### R package {landsepi}

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**Landscape structure**
*(set of polygon coordinates and areas)*

\+

**Dispersal matrix**
*(probability of polygon-to-polygon pathogen dispersal)*

\+

**Deployment strategy**
*(allocation of croptypes to the polygons)*

\+

**Initial conditions**
*(spatial location and genetic structure of pathogen inoculum)*

\+

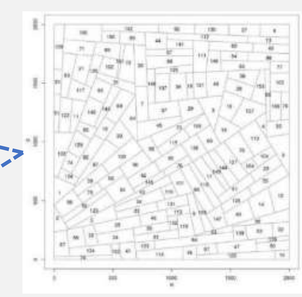
**Biological parameters**
*(pathogen, croptypes, cultivars, genes)*

\+

**Simulation parameters**
*(duration, time step, randomness seed)*

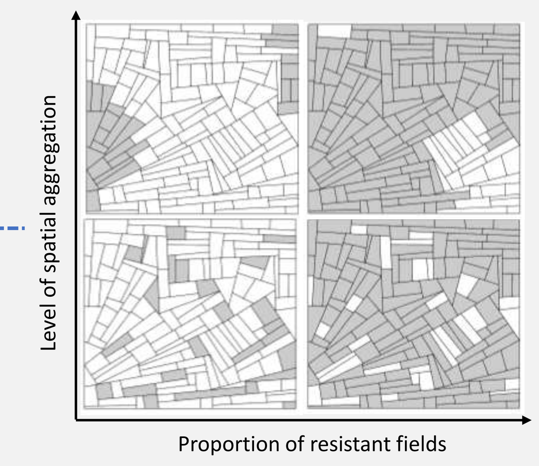
Average computational time: 30 seconds (for a 30-year simulation with 3 cultivars and 2 major resistance genes)

## Built-in objects and functions



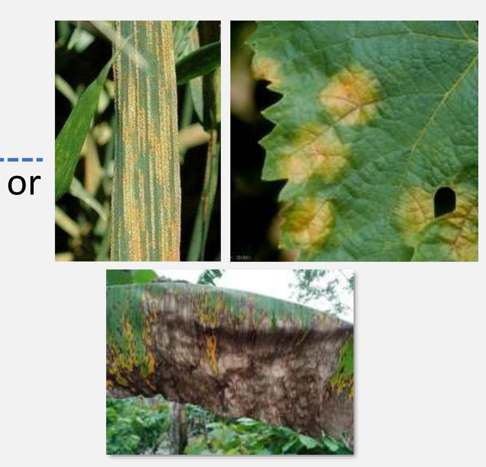
5 virtual landscapes generated using a T-tesselation algorithm (and associated dispersal matrices)

Algorithm for croptypes allocation in controlled proportions and spatial aggregation




Default scenario

Parameterisation for rust fungi of cereal crops, downy mildew of grapevine, or black sigatoka of banana



Default scenario

**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.

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


1. Rimbaud L., Fabre F., Papaïx J., Moury B., Lannou C., Barrett L. G. and Thrall P. H. (2021). Models of plant resistance deployment. *Annu. Rev. Phytopathol.* 59:125-152.
2. Rimbaud L., Papaïx 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.
3. Rimbaud L., Papaïx 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.
4. Rimbaud L., Papaïx J., Rey J.-F., Moury B., Barrett L.G. and Thrall P.H. (2023). Durable resistance or efficient disease control? Adult Plant Resistance (APR) genes at the heart of the dilemma. *Peer Community J.* 3:e43.
5. Zaffaroni M., Rimbaud L., Rey J.-F., Papaïx J. and Fabre F. (accepted with minor revision). Effects of pathogen sexual reproduction on the evolutionary and epidemiological control provided by deployment strategies for two major resistance genes in agricultural landscapes. *Evol. Appl.* doi: 10.1101/2023.02.02.526796.


## LINKS

Homepage: https://csiro-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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## ACKNOWLEDGEMENTS


This work benefited from ANR project "ArchiV" (2019–2023, grant n°ANR-18-CE32-0004-01), AFB Ecophyto II-Leviers Territoriaux Project "Médée" (2020–2023), GRDC grant CSP00192 and the CSIRO/INRA linkage program