



HAL
open science

Modelling plant resistance deployment: the R package landsepi

Loup Rimbaud, Julien Papaïx, Jean-François Rey, Jean-Loup Gaussen, Marta Zafarroni

► To cite this version:

Loup Rimbaud, Julien Papaïx, Jean-François Rey, Jean-Loup Gaussen, Marta Zafarroni. Modelling plant resistance deployment: the R package landsepi. 18. Rencontres de virologie végétale (RVV2021), Sep 2021, Aussois, France. hal-03368375

HAL Id: hal-03368375

<https://hal.inrae.fr/hal-03368375>

Submitted on 6 Oct 2021

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial - NoDerivatives 4.0
International License

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.

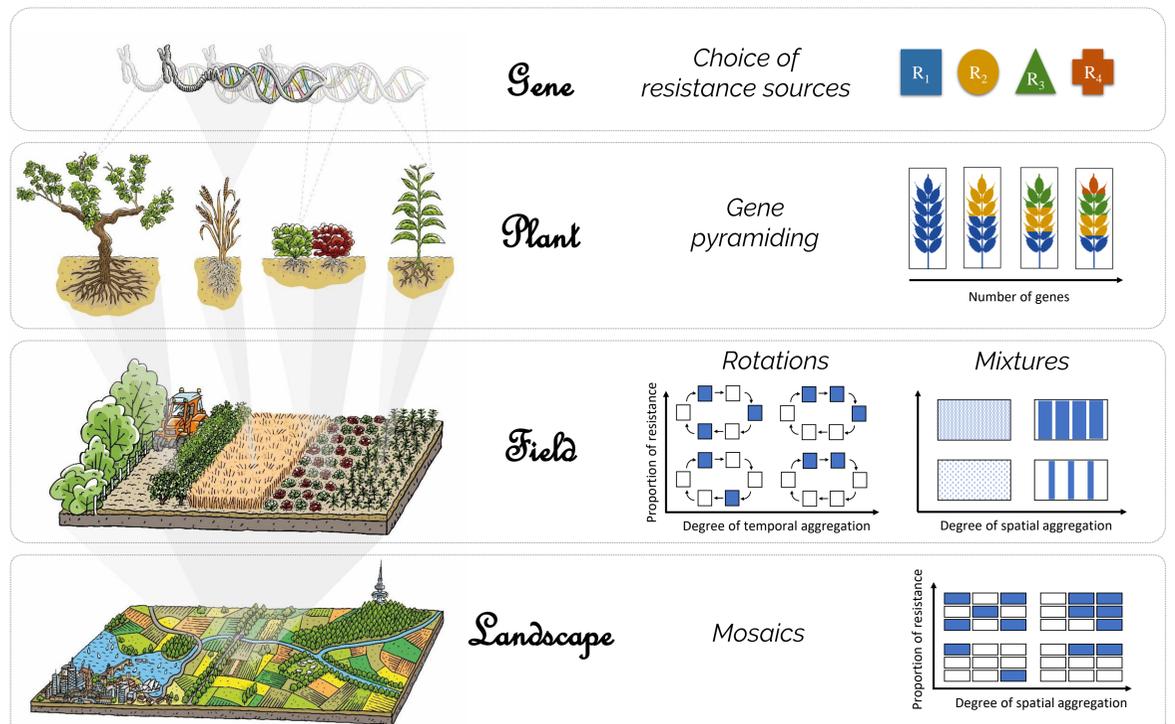


Strategies to improve plant resistance management rely on careful selection of resistance sources and their combination at various spatio-temporal scales.

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 may adapt to these genes (restoring its pathogenicity), possibly associated with a **fitness cost**.

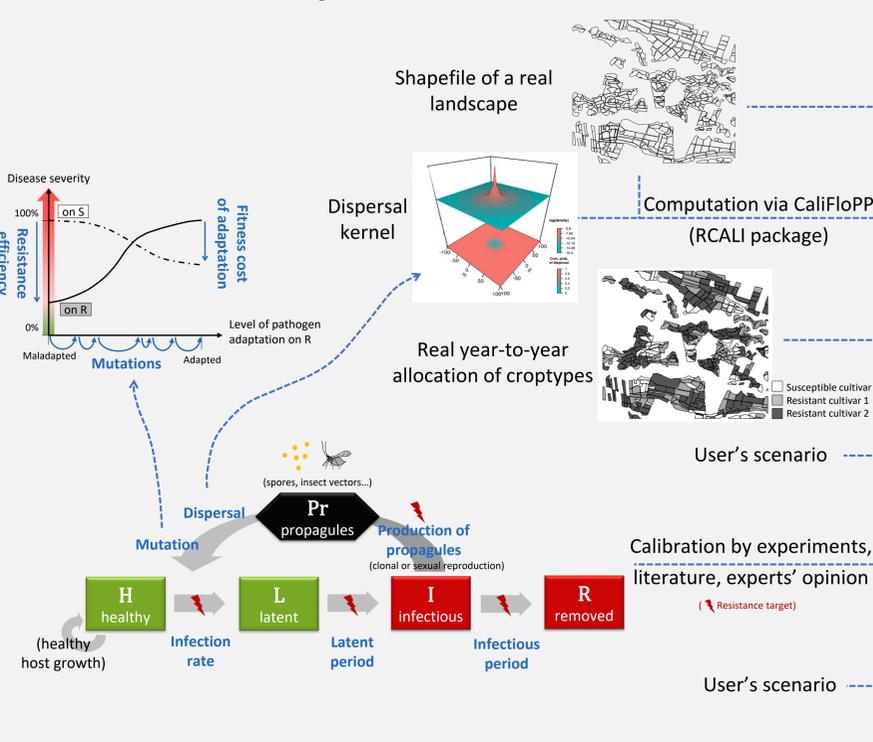
The model is based on a **spatial geometry** for describing the heterogeneous landscape and allocating different cultivars, a **dispersal kernel** for the dissemination of the pathogen, and a **stochastic SEIR** ('Susceptible-Exposed-Infectious-Removed') structure with a discrete time step for the description 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(1):125-152.

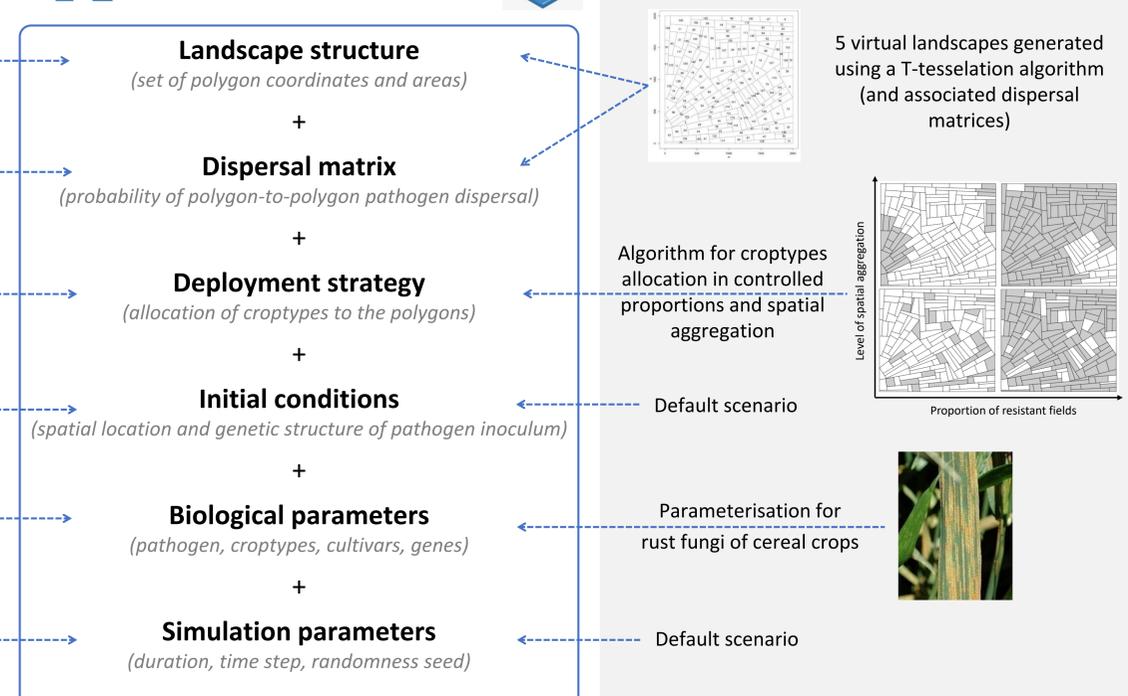
User's parameterisation




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)

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)

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>

CONTACT DETAILS

1 INRAE – Pathologie Végétale, 84140, Montfavet, France.
 2 INRAE – BioSP, 84914, Avignon, France.
 3 INRAE – SAVE, 33882 Villenave d'Ornon, France.
loup.rimbaud@inrae.fr

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):125-152.
- 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.

ACKNOWLEDGEMENTS

This work benefited from ANR project "Archiv" (2019-2022, grant n°ANR-18-CE32-0004-01), AFB Ecophyto II-Leviers Territoriaux Project "Médée" (2020-2022), GRDC grant CSP00192 and the CSIRO/INRA linkage program