

# Package ‘landsepi’

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**Description** A stochastic, spatially-explicit, demo-genetic model simulating the spread and evolution of a plant pathogen in a heterogeneous landscape to assess resistance deployment strategies. It is based on a spatial geometry for describing the landscape and allocation of different cultivars, a dispersal kernel for the dissemination of the pathogen, and a SEIR (‘Susceptible-Exposed-Infectious-Removed’) structure with a discrete time step. It provides a useful tool to assess the performance of a wide range of deployment options with respect to their epidemiological, evolutionary and economic outcomes. Loup Rimbaud, Julien Papaïx, Jean-François Rey, Luke G Barrett, Peter H Thrall (2018) <[doi:10.1371/journal.pcbi.1006067](https://doi.org/10.1371/journal.pcbi.1006067)>.

**URL** <https://csiro-inra.pages.biosp.inrae.fr/landsepi/>,  
<https://gitlab.paca.inrae.fr/CSIRO-INRA/landsepi>

**BugReports** <https://gitlab.paca.inrae.fr/CSIRO-INRA/landsepi/-/issues>

**License** GPL (>= 2) | file LICENSE

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**BuildVignettes** true

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**Collate** 'Math-Functions.R' 'RcppExports.R' 'graphics.R' 'AgriLand.R'  
 'Class-LandsepiParams.R' 'Cultivars\_List.R' 'GPKGTools.R'  
 'tools.R' 'Methods-LandsepiParams.R' 'demo\_landsepi.R'  
 'landsepi.R' 'output.R' 'runShiny.R' 'simul\_landsepi.R'

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**Suggests** testthat (>= 3.0.0), shiny, shinyjs, DT, knitr, rmarkdown

**VignetteBuilder** knitr

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landsepi-package      *Landscape Epidemiology and Evolution*

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## Description

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

## Details

Package: landsepi  
 Type: Package  
 Version: 1.3.0  
 Date: 2023-07-11  
 License: GPL (>=2)

The landsepi package implements a spatially explicit stochastic model able to assess the epidemiological, evolutionary and economic outcomes of strategies to deploy plant resistance to pathogens. It also helps investigate the effect of landscape organisation, the considered pathosystem and the epidemio-evolutionary context on the performance of a given strategy.

It is based on a spatial geometry for describing the landscape and allocation of different cultivars, a dispersal kernel for the dissemination of the pathogen, and a SEIR ('susceptible-exposed-infectious-removed', renamed HLIIR for 'healthy-latent-infectious-removed' to avoid confusions with 'susceptible host') structure with a discrete time step. It simulates the spread and evolution (via mutation, recombination through sexual reproduction, selection and drift) of a pathogen in a heterogeneous cropping landscape, across cropping seasons split by host harvests which impose potential bottlenecks to the pathogen.

The landscape is represented by a set of polygons where the pathogen can disperse (the basic spatial unit is an individual polygon; an agricultural field may be composed of a single or several polygons). *landsepi* includes built-in simulated landscapes (and associated dispersal matrices for rust pathogens, see below), but is it possible to use your own landscape (in shapefile format) and dispersal matrix.

A wide array of resistance deployment strategies can be simulated in landsepi: fields of the landscape are cultivated with different croptypes that can rotate through time; each croptype is composed of either a pure cultivar or a mixture; and each cultivar may carry one or several resistance genes. Thus, all combinations of rotations, mosaics, mixtures and pyramiding strategies are possible. Resistance genes affect several possible pathogen aggressiveness components: infection rate, durations of the latent period and the infectious period, and propagule production rate. Resistance may be complete (i.e. complete inhibition of the targeted aggressiveness component) or partial (i.e. the targeted aggressiveness component is only softened), and expressed from the beginning of the season, or later (to simulate Adult Plant Resistance (APR), also called Mature Plant Resistance). Cultivar allocation can be realised via an algorithm (`allocateCroptypeCultivars()`) but

it is possible to use your own cultivar allocation if it is included in the shapefile containing the landscape. Additionally, any cultivar may be treated with contact pesticides, which reduce the pathogen infection rate with an efficiency gradually decreasing with time and host growth.

To each resistance gene in the host (whether it may be a major gene or a QTL for quantitative resistance) is associated a pathogenicity gene in the pathogen. Through mutation of pathogenicity genes, the pathogen can restore its aggressiveness on resistance hosts and thus adapt to resistance (leading to sudden breakdown or gradual erosion of resistance genes). Pathogenicity genes may also be reassorted via sexual reproduction or gene recombination. Increased aggressiveness on a resistant host (i.e. adaptation to the corresponding resistance genes) can be penalised by a fitness cost on susceptible hosts, i.e. pathogen genotypes adapted to a resistance gene have a reduced aggressiveness on hosts that do not carry this gene. The relation between pathogen aggressiveness on susceptible and resistant hosts is defined by a trade-off relationship whose shape depends on the strength of the trade-off. Strong trade-off means that the gain in fitness on resistant hosts is smaller than the cost on susceptible hosts.

The package includes five examples of landscape structures and a default parameterisation to represent plant pathogens as typified by rusts of cereal crops (genus *Puccinia*, e.g. stripe rust, stem rust and leaf rust of wheat and barley). A parameterisation to downy mildew of grapevine (*Plasmopara viticola*) and black sigatoka of banana (*Pseudocercospora fijiensis*) are also available. The main function of the package is `runSimul()`. It can be parameterised to simulate various resistance deployment strategies using either the provided landscapes and parameters for cereal rusts, or landscapes and parameters set by the user. See `demo_landsepi()` for a demonstration, and our tutorials (`browseVignettes("landsepi")`) for details on how to use `landsepi`.

- Assumptions (in bold those 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. Cultivars 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)**. Cultivars to be treated and dates of chemical applications are fixed prior to simulations but only polygons where disease severity exceeds a given threshold (possibly 0) are treated.
9. Components of a mixture are independent each other (i.e. there is neither plant-plant interaction nor competition for space, and harvests are segregated). If one component is treated with a chemical, it does not affect other components.
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. **Boundaries of the landscape are reflective: propagules stay in the system as if it was closed.**
14. Pathogen reproduction can be purely clonal, purely sexual, or mixed (alternation of clonal and sexual reproduction).
15. 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 a parental pair is the sum of the propagule production rates of the parents. For a given parental pair, the genotype of each propagule is issued from random loci segregation of parental qualitative resistance genes. For each quantitative resistance gene, the value of each propagule trait is issued from a normal distribution around the average of the parental traits, following the infinitesimal model (Fisher 1919).
16. All types of propagules (i.e. clonal and sexual) share the same pathogenicity parameters (e.g. infection rate, latent period duration, etc.) but each of them has their own dispersal and survival abilities (see after).
17. At the end of each cropping season, pathogens experience a bottleneck representing the off-season and then propagules are produced (either via clonal or sexual reproduction). Clonal propagules are released during the following season only, either altogether at the first day of the season, or progressively (in that case the day of release of each propagule is sampled from a uniform distribution). Sexual propagules are gradually released during several of the following seasons (between-season release). The season of release of each propagule is sampled from an exponential distribution, truncated by a maximum viability limit. Then, the day of release in a given season is sampled from a uniform distribution (within-season release).
18. Pathogenicity genes mutate independently from each other.
19. **Pathogen adaptation to a given resistance gene consists in restoring the same aggressiveness component as the one targeted by the resistance gene.**
20. 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.
21. When there is a delay for activation of a given resistance gene (APR), the age of activation is the same for all hosts carrying this gene and located in the same polygon.
22. Variances of the durations of the latent and the infectious periods of the pathogen are not affected by plant resistance.

**Epidemiological outputs** The epidemiological outcome of a deployment strategy is evaluated using:

1. the area under the disease progress curve (AUDPC) to measure disease severity (i.e. the average number of diseased plant tissue -status I and R- per time step and square meter),
2. the relative area under the disease progress curve (AUDPCr) to measure the average proportion of diseased tissue (status I and R) relative to the total number of existing host individuals (H+L+I+R).
3. the Green Leaf Area (GLA) to measure the average amount of healthy plant tissue (status H) per time step and square meter,
4. the relative Green Leaf Area (GLAr) to measure the average proportion of healthy tissue (status H) relative to the total number of existing host individuals (H+L+I+R).
5. the yearly contribution of pathogen genotypes to LIR dynamics on every host as well as the whole landscape.

A set of graphics and a video showing epidemic dynamics can also be generated.

**Evolutionary outputs** The evolutionary outcome is assessed by measuring:

1. the dynamics of pathogen genotype frequencies,
2. the evolution of pathogen aggressiveness,
3. the durability of resistance genes. Durability can be estimated using the time until the pathogen reaches the three steps to adapt to plant resistance: (1) first appearance of adapted mutants, (2) initial migration to resistant hosts and infection, and (3) broader establishment in the resistant host population (i.e. the point at which extinction becomes unlikely).

**Economic outputs** The economic outcome of a simulation can be evaluated using:

1. the crop yield: yearly crop production (e.g. grains, fruits, wine) in weight (or volume) units per hectare (depends on the number of productive hosts and associated theoretical yield),
2. the crop products: yearly products generated from sales, in monetary units per hectare (depends on crop yield and market value),
3. the crop operational costs: yearly costs associated with crop planting (depends on initial host density and planting cost) and pesticide treatments (depends on the number of applications and the cost of a single application) in monetary units per hectare.
4. the margin, i.e. products - operational costs, in monetary units per hectare.

#### **Future versions:**

Future versions of the package will include in particular:

- Sets of pathogen parameters to simulate other pathosystems (e.g. Cucumber mosaic virus on pepper, potato virus Y on pepper).
- More flexible initial conditions (e.g. size, location and composition of pathogen inoculum at the beginning of the simulation).

#### **Dependencies:**

The package for compiling needs:

- g++

- libgsl2
- libgsl-dev

and the following R packages:

- Rcpp
- sp
- stats
- Matrix
- mvtnorm
- fields
- splancs
- sf
- DBI
- RSQLite
- foreach
- parallel
- doParallel
- deSolve

In addition, to generate videos the package will need ffmpeg.

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#### References

**When referencing the simulation model, please cite the following article::**

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 Computational Biology* 14(4):e1006067.

**When referencing the R package, please cite the following package::**

Rimbaud L., Papaix J. and Rey J.-F. (2018). landsepi: Landscape Epidemiology and Evolution. *R package*, url: <https://cran.r-project.org/package=landsepi>.



## See Also

Useful links:

- <https://csiro-inra.pages.biosp.inrae.fr/landsepi/>
- <https://gitlab.paca.inrae.fr/CSIRO-INRA/landsepi>
- Report bugs at <https://gitlab.paca.inrae.fr/CSIRO-INRA/landsepi/-/issues>

## Examples

```
## Not run:
library("landsepi")

## Run demonstrations (in 10-year simulations) for different deployment strategies:
demo_landsepi(strat = "MO") ## for a mosaic of cultivars
demo_landsepi(strat = "MI") ## for a mixture of cultivars
demo_landsepi(strat = "RO") ## for a rotation of cultivars
demo_landsepi(strat = "PY") ## for a pyramid of resistance genes

## End(Not run)
```

---

AgriLand

*Landscape allocation*

---

## Description

Generates a landscape composed of fields where croptypes are allocated with controlled proportions and spatio-temporal aggregation.

## Usage

```
AgriLand(
  landscape,
  Nyears,
  rotation_period = 0,
  rotation_sequence = list(c(0, 1, 2)),
  rotation_realloc = FALSE,
  prop = list(c(1/3, 1/3, 1/3)),
  aggreg = list(1),
  algo = "periodic",
  croptype_names = c(),
  graphic = FALSE,
  outputDir = "./"
)
```

**Arguments**

landscape	a spatialpolygon object containing field coordinates.
Nyears	an integer giving the number of simulated cropping seasons.
rotation_period	number of years before rotation of the landscape. There is no rotation if rotation_period=0 or rotation_period=Nyears.
rotation_sequence	a list, each element of the list contains indices of croptypes that are cultivated during a period given by "rotation_period". There is no change in cultivated croptypes if the list contains only one element (e.g. only one vector c(0,1,2), indicating cultivation of croptypes 0, 1 and 2).
rotation_realloc	a logical indicating if a new random allocation of croptypes is performed when the landscape is rotated (FALSE=static allocation, TRUE=dynamic allocation). Note that if rotation_realloc=FALSE, all elements of the list "rotation_sequence" must have the same length, and only the first element of the lists "prop" and "aggreg" will be used.
prop	a list of the same size as "rotation_sequence", each element of the list contains a vector of the proportions (in surface) associated with the croptypes in "rotation_sequence". A single vector can be given instead of a list if all elements of "rotation_sequence" are associated with the same proportions.
aggreg	a list of the same size as "rotation_sequence", each element of the list is a single double indicating the degree of aggregation of the landscape. This double must be greater or equal 0; the greater its value, the higher the degree of spatial aggregation (roughly, aggreg between 0 and 0.1 for fragmented landscapes, between 0.1 and 0.5 for balanced landscapes, between 0.5 and 3 for aggregated landscapes, and above 3 for highly aggregated landscapes). A single double can be given instead of a list if all elements of "rotation_sequence" are associated with the same level of aggregation.
algo	the algorithm used for the computation of the variance-covariance matrix of the multivariate normal distribution: "exp" for exponential function, "periodic" for periodic function, "random" for random draw (see details of function multiN). If algo="random", the parameter aggreg is not used. Algorithm "exp" is preferable for big landscapes.
croptype_names	a vector of croptype names (for legend in graphic).
graphic	a logical indicating if a graphic of the landscape must be generated (TRUE) or not (FALSE).
outputDir	a directory to save graphic

**Details**

An algorithm based on latent Gaussian fields is used to allocate two different croptypes across the simulated landscapes (e.g. a susceptible and a resistant cultivar, denoted as SC and RC, respectively). This algorithm allows the control of the proportions of each croptype in terms of surface coverage, and their level of spatial aggregation. A random vector of values is drawn from a multivariate normal distribution with expectation 0 and a variance-covariance matrix which depends

on the pairwise distances between the centroids of the fields. Next, the croptypes are allocated to different fields depending on whether each value drawn from the multivariate normal distribution is above or below a threshold. The proportion of each cultivar in the landscape is controlled by the value of this threshold. To allocate more than two croptypes, AgriLand uses sequentially this algorithm. For instance, the allocation of three croptypes (e.g. SC, RC1 and RC2) is performed as follows:

1. the allocation algorithm is run once to segregate the fields where the susceptible cultivar is grown, and
2. the two resistant cultivars (RC1 and RC2) are assigned to the remaining candidate fields by re-running the allocation algorithm.

### Value

a gpkg (shapefile) containing the landscape structure (i.e. coordinates of field boundaries), the area and composition (i.e. croptypes) in time (i.e. each year) for each field. A png graphic can be generated if `graphic=TRUE`.

### References

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 Computational Biology* 14(4):e1006067.

### See Also

[multiN](#), [periodic\\_cov](#), [allocateLandscapeCroptypes](#)

### Examples

```
## Not run:
data(landscapeTEST)
landscape <- get("landscapeTEST1")
set.seed(12345)
## Generate a mosaic of three croptypes in balanced proportions
## and high level of spatial aggregation
AgriLand(landscape,
  Nyears = 10,
  rotation_sequence = c(0, 1, 2), prop = rep(1 / 3, 3),
  aggreg = rep(10, 3), algo = "periodic",
  graphic = TRUE, outputDir = getwd()
)

## Generate a dynamic mosaic of two croptypes in unbalanced proportions
## and low level of spatial aggregation,
## the second croptype being replaced every 5 years without changing field allocation
AgriLand(landscape,
  Nyears = 20, rotation_period = 5, rotation_sequence = list(c(0, 1), c(0, 2)),
  prop = c(1 / 3, 2 / 3), aggreg = c(0.07, 0.07), algo = "periodic", graphic = TRUE,
  outputDir = getwd()
)
```

```

## Generate a dynamic mosaic of four croptypes in balanced proportions
## and medium level of spatial aggregation,
## with field allocation changing every year
Agriland(landscape,
  Nyears = 5, rotation_period = 1, rotation_realloc = TRUE,
  rotation_sequence = c(0, 1, 2, 3),
  prop = rep(1 / 4, 4), aggreg = 0.25, algo = "exp", graphic = TRUE, outputDir = getwd()
)

## End(Not run)

```

---

```
allocateCroptypeCultivars
```

*Allocate cultivars to one croptype*

---

### Description

Updates a given croptype by allocating cultivars composing it.

### Usage

```

allocateCroptypeCultivars(
  croptypes,
  croptypeName,
  cultivarsInCroptype,
  prop = NULL
)

```

### Arguments

croptypes	a dataframe containing all croptypes, initialised via <a href="#">loadCroptypes</a>
croptypeName	the name of the croptype to be allocated
cultivarsInCroptype	name of cultivars composing the croptype
prop	vector of proportions of each cultivar in the croptype. Default to balanced proportions.

### Value

a croptype data.frame updated for the concerned croptype.

### See Also

[setCroptypes](#), [setCultivars](#)

## Examples

```
## Not run:
simul_params <- createSimulParams()
cultivar1 <- loadCultivar(name = "Susceptible", type = "growingHost")
cultivar2 <- loadCultivar(name = "Resistant1", type = "growingHost")
cultivar3 <- loadCultivar(name = "Resistant2", type = "growingHost")
cultivars <- data.frame(rbind(cultivar1, cultivar2, cultivar3), stringsAsFactors = FALSE)
simul_params <- setCultivars(simul_params, cultivars)
croptypes <- loadCroptypes(simul_params, names = c("Susceptible crop", "Mixture"))
croptypes
croptypes <- allocateCroptypeCultivars(croptypes, "Susceptible crop", "Susceptible")
croptypes <- allocateCroptypeCultivars(croptypes, "Mixture", c("Resistant1", "Resistant2"))
croptypes

## End(Not run)
```

---

allocateCultivarGenes *Allocate genes to a cultivar*

---

## Description

Updates a LandsepiParams object with, for a given cultivar, the list of genes it carries

## Usage

```
allocateCultivarGenes(
  params,
  cultivarName,
  listGenesNames = c(""),
  force.clean = FALSE
)
```

## Arguments

params            a LandsepiParams object.  
cultivarName     the name of the cultivar to be allocated.  
listGenesNames   the names of the genes the cultivar carries  
force.clean      force to clean previous allocated genes to all cultivars

## Value

a LandsepiParams object

## See Also

[setGenes](#), [setCultivars](#)

**Examples**

```
## Not run:
simul_params <- createSimulParams()
gene1 <- loadGene(name = "MG 1", type = "majorGene")
gene2 <- loadGene(name = "MG 2", type = "majorGene")
genes <- data.frame(rbind(gene1, gene2), stringsAsFactors = FALSE)
simul_params <- setGenes(simul_params, genes)
cultivar1 <- loadCultivar(name = "Susceptible", type = "growingHost")
cultivar2 <- loadCultivar(name = "Resistant", type = "growingHost")
cultivars <- data.frame(rbind(cultivar1, cultivar2), stringsAsFactors = FALSE)
simul_params <- setCultivars(simul_params, cultivars)
simul_params <- allocateCultivarGenes(simul_params, "Resistant", c("MG 1", "MG 2"))
simul_params@CultivarsGenes

## End(Not run)
```

---

allocateLandscapeCroptypes

*Allocate croptypes to the landscape*

---

**Description**

Updates the landscape of a LandsepiParams object with croptype allocation in every field of the landscape and every year of simulation. Allocation is based on an algorithm which controls croptype proportions (in surface) and spatio-temporal aggregation.

**Usage**

```
allocateLandscapeCroptypes(
  params,
  rotation_period,
  rotation_sequence,
  rotation_realloc = FALSE,
  prop,
  aggreg,
  algo = "periodic",
  graphic = TRUE
)
```

**Arguments**

**params** a LandsepiParams Object.

**rotation\_period** number of years before rotation of the landscape. There is no rotation if rotation\_period=0 or rotation\_period=Nyears.

rotation_sequence	a list, each element of the list contains indices of croptypes that are cultivated during a period given by "rotation_period". There is no change in cultivated croptypes if the list contains only one element (e.g. only one vector c(0,1,2), indicating cultivation of croptypes 0, 1 and 2).
rotation_realloc	a logical indicating if a new random allocation of croptypes is performed when the landscape is rotated (FALSE=static allocation, TRUE=dynamic allocation). Note that if rotation_realloc=FALSE, all elements of the list "rotation_sequence" must have the same length, and only the first element of the lists "prop" and "aggreg" will be used.
prop	a list of the same size as "rotation_sequence", each element of the list contains a vector of the proportions (in surface) associated with the croptypes in "rotation_sequence". A single vector can be given instead of a list if all elements of "rotation_sequence" are associated with the same proportions.
aggreg	a list of the same size as "rotation_sequence", each element of the list is a single double indicating the degree of aggregation of the landscape. This double must be greater or equal 0; the greater its value, the higher the degree of spatial aggregation (roughly, aggreg between 0 and 0.1 for fragmented landscapes, between 0.1 and 0.5 for balanced landscapes, between 0.5 and 3 for aggregated landscapes, and above 3 for highly aggregated landscapes). A single double can be given instead of a list if all elements of "rotation_sequence" are associated with the same level of aggregation.
algo	the algorithm used for the computation of the variance-covariance matrix of the multivariate normal distribution: "exp" for exponential function, "periodic" for periodic function, "random" for random draw (see details of function multiN). If algo="random", the parameter aggreg is not used. Algorithm "exp" is preferable for big landscapes.
graphic	a logical indicating if graphics must be generated (TRUE) or not (FALSE).

## Details

An algorithm based on latent Gaussian fields is used to allocate two different croptypes across the simulated landscapes (e.g. a susceptible and a resistant cultivar, denoted as SC and RC, respectively). This algorithm allows the control of the proportions of each croptype in terms of surface coverage, and their level of spatial aggregation. A random vector of values is drawn from a multivariate normal distribution with expectation 0 and a variance-covariance matrix which depends on the pairwise distances between the centroids of the fields. Next, the croptypes are allocated to different fields depending on whether each value drawn from the multivariate normal distribution is above or below a threshold. The proportion of each cultivar in the landscape is controlled by the value of this threshold. To allocate more than two croptypes, AgriLand uses sequentially this algorithm. For instance, the allocation of three croptypes (e.g. SC, RC1 and RC2) is performed as follows:

1. the allocation algorithm is run once to segregate the fields where the susceptible cultivar is grown, and
2. the two resistant cultivars (RC1 and RC2) are assigned to the remaining candidate fields by re-running the allocation algorithm.

**Value**

a LandsepiParams object with Landscape updated with the layer "croptypeID". It contains croptype allocation in every field of the landscape for all years of simulation.

**Examples**

```
## Not run:
## Initialisation
simul_params <- createSimulParams(outputDir = getwd())
## Time parameters
simul_params <- setTime(simul_params, Nyears = 10, nTSpY = 120)
## Landscape
simul_params <- setLandscape(simul_params, loadLandscape(1))
## Cultivars
cultivar1 <- loadCultivar(name = "Susceptible", type = "growingHost")
cultivar2 <- loadCultivar(name = "Resistant1", type = "growingHost")
cultivar3 <- loadCultivar(name = "Resistant2", type = "growingHost")
cultivars <- data.frame(rbind(cultivar1, cultivar2, cultivar3), stringsAsFactors = FALSE)
simul_params <- setCultivars(simul_params, cultivars)
## Allocate cultivars to croptypes
croptypes <- loadCroptypes(simul_params, names = c("Susceptible crop"
, "Resistant crop 1"
, "Resistant crop 2"))
croptypes <- allocateCroptypeCultivars(croptypes, "Susceptible crop", "Susceptible")
croptypes <- allocateCroptypeCultivars(croptypes, "Resistant crop 1", "Resistant1")
croptypes <- allocateCroptypeCultivars(croptypes, "Resistant crop 2", "Resistant2")
simul_params <- setCroptypes(simul_params, croptypes)
## Allocate croptypes to landscape
rotation_sequence <- croptypes$croptypeID ## No rotation -> 1 rotation_sequence element
rotation_period <- 0 ## same croptypes every years
prop <- c(1 / 3, 1 / 3, 1 / 3) ## croptypes proportions
aggreg <- 10 ## aggregated landscape
simul_params <- allocateLandscapeCroptypes(simul_params, rotation_period = rotation_period,
rotation_sequence = rotation_sequence,
rotation_realloc = FALSE, prop = prop, aggreg = aggreg)
simul_params@Landscape

## End(Not run)
```

---

antideriv\_verhulst      *Antiderivative of the Verhulst logistic function*

---

**Description**

Give the antiderivative of the logistic function from the Verhulst model.

**Usage**

```
antideriv_verhulst(x, initial_density, max_density, growth_rate)
```



**Arguments**

x	timestep up to which antiderivative must be computed
initial_density	initial density
max_density	maximal density
growth_rate	growth rate

**Details**

The Verhulst model (used to simulate host growth) is defined by  $f(x) = \frac{max\_density}{1 + (max\_density/initial\_density)*exp(-growth\_rate*x)}$ . See [https://en.wikipedia.org/wiki/Logistic\\_function](https://en.wikipedia.org/wiki/Logistic_function) for details.

**Value**

An object of the same type as x containing the antiderivative of the input values.

**Examples**

```
antideriv_verhulst(119, 0.1, 2, 0.1) / 120
```

---

checkCroptypes	<i>Check croptypes</i>
----------------	------------------------

---

**Description**

checks croptypes validity

**Usage**

```
checkCroptypes(params)
```

**Arguments**

params            a LandsepiParams object.

**Value**

a boolean, TRUE if OK, FALSE otherwise

---

checkCultivars      *Check cultivars*

---

**Description**

check cultivars validity

**Usage**

checkCultivars(params)

**Arguments**

params              a LandsepiParams object.

**Value**

a boolean, TRUE if OK, FALSE otherwise

---

checkCultivarsGenes      *Check cultivars genes*

---

**Description**

Checks CultivarsGene data.frame validity

**Usage**

checkCultivarsGenes(params)

**Arguments**

params              a LandsepiParams object.

**Value**

a boolean, TRUE if OK, FALSE otherwise

---

checkDispersalHost      *Check host dispersal*

---

**Description**

Checks host dispersal matrix validity.

**Usage**

checkDispersalHost(params)

**Arguments**

params                  a LandsepiParams Object.

**Value**

a boolean TRUE if OK, FALSE otherwise

---

checkDispersalPathogen  
                                  *Check pathogen dispersal*

---

**Description**

Checks pathogen dispersal validity

**Usage**

checkDispersalPathogen(params)

**Arguments**

params                  a LandsepiParams Object.

**Value**

a boolean TRUE if OK, FALSE otherwise

---

checkGenes	<i>Check genes</i>
------------	--------------------

---

**Description**

checks Genes data.frame validity

**Usage**

```
checkGenes(params)
```

**Arguments**

params            a LandsepiParams object.

**Value**

a boolean, TRUE if OK, FALSE otherwise

---

checkInoculum	<i>Check inoculum</i>
---------------	-----------------------

---

**Description**

Checks inoculum validity.

**Usage**

```
checkInoculum(params)
```

**Arguments**

params            a LandsepiParams object.

**Value**

a boolean, TRUE if OK, FALSE otherwise

---

checkLandscape	<i>Check the landscape</i>
----------------	----------------------------

---

**Description**

Checks landscape validity

**Usage**

checkLandscape(params)

**Arguments**

params            a LandsepiParams Object.

**Value**

TRUE if Ok, FALSE otherwise

---

checkOutputs	<i>Check outputs</i>
--------------	----------------------

---

**Description**

Checks outputs validity.

**Usage**

checkOutputs(params)

**Arguments**

params            a LandsepiParams object.

**Value**

a boolean, TRUE if OK, FALSE otherwise

checkPathogen            *Check pathogen*

---

**Description**

Checks pathogen validity

**Usage**

checkPathogen(params)

**Arguments**

params            a LandsepiParams Object.

**Value**

a boolean, TRUE if OK, FALSE otherwise

---

checkSimulParams        *Check simulation parameters*

---

**Description**

Checks validity of a LandsepiParams object.

**Usage**

checkSimulParams(params)

**Arguments**

params            a LandsepiParams Object.

**Value**

TRUE if OK for simulation, FALSE otherwise

---

checkTime	<i>Check time</i>
-----------	-------------------

---

**Description**

Checks time parameters validity

**Usage**

checkTime(params)

**Arguments**

params            a LandsepiParams Object.

**Value**

a boolean TRUE if times are setted.

---

checkTreatment	<i>Check treatment</i>
----------------	------------------------

---

**Description**

Checks treatment validity

**Usage**

checkTreatment(params)

**Arguments**

params            a LandsepiParams Object.

**Value**

a boolean, TRUE if OK, FALSE otherwise

---

compute\_audpc100S      *Compute AUDPC in a single 100% susceptible field*

---

### Description

Compute AUDPC in a single field cultivated with a susceptible cultivar.

### Usage

```
compute_audpc100S(  
  disease = "rust",  
  hostType = "growingHost",  
  nTSpY = 120,  
  area = 1e+06,  
  seed = 12345  
)
```

### Arguments

disease	a disease name, among "rust" (default), "mildew" and "sigatoka"
hostType	cultivar type, among: "growingHost" (default), "nongrowingHost", "grapevine".
nTSpY	number to time steps per cropping season
area	area of the field (must be in square meters).
seed	an integer used as seed value (for random number generator).

### Details

audpc100S is the average AUDPC computed in a non-spatial simulation.

### Value

The AUDPC value (numeric)

### See Also

[loadOutputs](#)

### Examples

```
## Not run:  
compute_audpc100S("rust", "growingHost", area=1E6)  
compute_audpc100S("mildew", "grapevine", area=1E6)  
compute_audpc100S("sigatoka", "banana", area=1E6, nTSpY=182)  
  
## End(Not run)
```



---

createSimulParams      *Create a LandsepiParams object.*

---

### Description

Creates a default object of class LandsepiParams.

### Usage

```
createSimulParams(outputDir = "./")
```

### Arguments

outputDir      ouput directory for simulation (default: current directory)

### Details

Create a default object of class LandsepiParams used to store all simulation parameters. It also creates a subdirectory in outputDir using the date; this directory will contain all simulation outputs.

### Value

a LandsepiParams object initialised with the following context:

- random seed
- all pathogen parameters fixed at 0
- no between-field dispersal (neither pathogen nor host)
- no pathogen introduction
- no resistance gene
- no chemical treatment
- no output to generate.

### Examples

```
## Not run:  
createSimulParams()  
  
## End(Not run)
```

---

Cultivars_list	<i>Cultivars Type list</i>
----------------	----------------------------

---

**Description**

A set of configured cultivars types

**Usage**

Cultivars\_list

**Format**

A list of list indexed by type name

- cultivarName: cultivar names (cannot accept space),
- initial\_density: host densities (per square meter) at the beginning of the cropping season as if cultivated in pure crop,
- max\_density: maximum host densities (per square meter) at the end of the cropping season as if cultivated in pure crop,
- growth rate: host growth rates,
- reproduction rate: host reproduction rates,
- yield\_H: theoretical yield (in weight or volume units / ha / cropping season) associated with hosts in sanitary status H as if cultivated in pure crop,
- yield\_L: theoretical yield (in weight or volume units / ha / cropping season) associated with hosts in sanitary status L as if cultivated in pure crop,
- yield\_I: theoretical yield (in weight or volume units / ha / cropping season) associated with hosts in sanitary status I as if cultivated in pure crop,
- yield\_R: theoretical yield (in weight or volume units / ha / cropping season) associated with hosts in sanitary status R as if cultivated in pure crop,
- planting\_cost = planting costs (in monetary units / ha / cropping season) as if cultivated in pure crop,
- market\_value = market values of the production (in monetary units / weight or volume unit).

**Description**

run a simulation demonstration with landsepi

**Usage**

```
demo_landsepi(  
  seed = 5,  
  strat = "MO",  
  Nyears = 10,  
  nTSpY = 120,  
  videoMP4 = FALSE  
)
```

**Arguments**

seed	an interger used as seed for Random Number Generator.
strat	a string specifying the deployment strategy: "MO" for mosaic of resistant cultivars, "MI" for intra-fied mixtures, "RO" for cultivar rotations, and "PY" for resistance gene pyramiding in a cultivar.
Nyears	number of cropping seasons (years) to simulate.
nTSpY	number of time-steps (days) per cropping season.
videoMP4	a logical indicating if a video must be generated (TRUE, default) or not (FALSE).

**Details**

In these examples on rust fungi of cereal crops, 2 completely efficient resistance sources (typical of major resistance genes) are deployed in the landscape according to one of the following strategies:

- Mosaic: 3 pure crops (S + R1 + R2) with very high spatial aggregation.
- Mixture: 1 pure susceptible crop + 1 mixture of two resistant cultivars, with high aggregation.
- Rotation: 1 susceptible pure crop + 2 resistant crops in alternation every 2 years , with moderate aggregation.
- Pyramiding: 1 susceptible crop + 1 pyramided cultivar in a fragmented landscape (low aggregation).

**Value**

A set of text files, graphics and a video showing epidemic dynamics.

**See Also**

[runSimul](#), [runShinyApp](#)

## Examples

```
## Not run:
## Run demonstrations (in 10-year simulations) for different deployment strategies:
demo_landsepi(strat = "MO") ## for a mosaic of cultivars
demo_landsepi(strat = "MI") ## for a mixture of cultivars
demo_landsepi(strat = "RO") ## for a rotation of cultivars
demo_landsepi(strat = "PY") ## for a pyramid of resistance genes

## End(Not run)
```

---

 dispP

*Dispersal matrices for rust fungi of cereal crops.*


---

## Description

Five vectorised dispersal matrices of pathogens as typified by rust fungi of cereal crops (genus *Puccinia*), and associated with landscapes 1 to 5 (composed of 155, 154, 152, 153 and 156 fields, respectively).

## Usage

```
dispP_1
dispP_2
dispP_3
dispP_4
dispP_5
```

## Format

The format is: num [1:24025] 8.81e-01 9.53e-04 7.08e-10 1.59e-10 3.29e-06 ...

## Details

The pathogen dispersal matrix gives the probability for a pathogen in a field  $i$  (row) to migrate to field  $i'$  (column) through dispersal. It is computed based on a dispersal kernel and the euclidian distance between each point in fields  $i$  and  $i'$ , using the CaliFloPP algorithm (Bouvier et al. 2009). The dispersal kernel is an isotropic power-law function of equation:  $f(x) = ((b - 2) * (b - 1) / (2 * \pi * a^2)) * (1 + x/a)^{-b}$  with  $a=40$  a scale parameter and  $b=7$  related to the weight of the dispersal tail. The expected mean dispersal distance is given by  $2*a/(b-3)=20$  m.

## References

Bouvier A, Ki  u K, Adamczyk K, Monod H. Computation of the integrated flow of particles between polygons. *Environ. Model Softw.* 2009;24(7):843-9. doi: <http://dx.doi.org/10.1016/j.envsoft.2008.11.006>.

**Examples**

```
dispP_1
summary(dispP_1)
## maybe str(dispP_1) ; plot(dispP_1) ...
```

---

epid\_output

*Generation of epidemiological and economic model outputs*


---

**Description**

Generates epidemiological and economic outputs from model simulations.

**Usage**

```
epid_output(
  types = "all",
  time_param,
  Npatho,
  area,
  rotation,
  croptypes,
  cultivars_param,
  eco_param,
  treatment_param,
  pathogen_param,
  audpc100S = 0.76,
  writeTXT = TRUE,
  graphic = TRUE,
  path = getwd()
)
```

**Arguments**

types a character string (or a vector of character strings if several outputs are to be computed) specifying the type of outputs to generate (see details):

- "audpc": Area Under Disease Progress Curve
- "audpc\_rel": Relative Area Under Disease Progress Curve
- "gla": Green Leaf Area
- "gla\_rel": Relative Green Leaf Area
- "eco\_yield": Total crop yield
- "eco\_cost": Operational crop costs
- "eco\_product": Crop products
- "eco\_margin": Margin (products - operational costs)
- "contrib": contribution of pathogen genotypes to LIR dynamics

	<ul style="list-style-type: none"> <li>• "HLIR_dynamics", "H_dynamics", "L_dynamics", "IR_dynamics", "HLI_dynamics", etc.: Epidemic dynamics related to the specified sanitary status (H, L, I or R and all their combinations). Graphics only, works only if graphic=TRUE.</li> <li>• "all": compute all these outputs (default).</li> </ul>
time_param	list of simulation parameters: <ul style="list-style-type: none"> <li>• Nyears = number cropping seasons,</li> <li>• nTSpY = number of time-steps per cropping season.</li> </ul>
Npatho	number of pathogen genotypes.
area	a vector containing polygon areas (must be in square meters).
rotation	a dataframe containing for each field (rows) and year (columns, named "year_1", "year_2", etc.), the index of the cultivated croptype. Importantly, the matrix must contain 1 more column than the real number of simulated years.
croptypes	a dataframe with three columns named 'croptypeID' for croptype index, 'cultivarID' for cultivar index and 'proportion' for the proportion of the cultivar within the croptype.
cultivars_param	list of parameters associated with each host genotype (i.e. cultivars): <ul style="list-style-type: none"> <li>• name = vector of cultivar names,</li> <li>• initial_density = vector of host densities (per square meter) at the beginning of the cropping season as if cultivated in pure crop,</li> <li>• max_density = vector of maximum host densities (per square meter) at the end of the cropping season as if cultivated in pure crop,</li> <li>• cultivars_genes_list = a list containing, for each host genotype, the indices of carried resistance genes.</li> </ul>
eco_param	a list of economic parameters for each host genotype as if cultivated in pure crop: <ul style="list-style-type: none"> <li>• yield_perHa = a dataframe of 4 columns for the theoretical yield associated with hosts in sanitary status H, L, I and R, as if cultivated in pure crops, and one row per host genotype (yields are expressed in weight or volume units / ha / cropping season),</li> <li>• planting_cost_perHa = a vector of planting costs (in monetary units / ha / cropping season),</li> <li>• market_value = a vector of market values of the production (in monetary units / weight or volume unit).</li> </ul>
treatment_param	list of parameters related to pesticide treatments: <ul style="list-style-type: none"> <li>• treatment_degradation_rate = degradation rate (per time step) of chemical concentration,</li> <li>• treatment_efficiency = maximal efficiency of chemical treatments (i.e. fractional reduction of pathogen infection rate at the time of application),</li> <li>• treatment_timesteps = vector of time-steps corresponding to treatment application dates,</li> <li>• treatment_cultivars = vector of indices of the cultivars that receive treatments,</li> </ul>

	<ul style="list-style-type: none"> <li>• <code>treatment_cost</code> = cost of a single treatment application (monetary units/ha)</li> <li>• <code>treatment_application_threshold</code> = vector of thresholds (i.e. disease severity, one for each treated cultivar) above which the treatment is applied in a polygon</li> </ul>
<code>pathogen_param</code>	<p>a list of i. pathogen aggressiveness parameters on a susceptible host for a pathogen genotype not adapted to resistance and ii. sexual reproduction parameters:</p> <ul style="list-style-type: none"> <li>• <code>infection_rate</code> = maximal expected infection rate of a propagule on a healthy host,</li> <li>• <code>propagule_prod_rate</code> = maximal expected effective propagule production rate of an infectious host per time step,</li> <li>• <code>latent_period_mean</code> = minimal expected duration of the latent period,</li> <li>• <code>latent_period_var</code> = variance of the latent period duration,</li> <li>• <code>infectious_period_mean</code> = maximal expected duration of the infectious period,</li> <li>• <code>infectious_period_var</code> = variance of the infectious period duration,</li> <li>• <code>survival_prob</code> = probability for a propagule to survive the off-season,</li> <li>• <code>repro_sex_prob</code> = probability for an infectious host to reproduce via sex rather than via cloning,</li> <li>• <code>sigmoid_kappa</code> = kappa parameter of the sigmoid contamination function,</li> <li>• <code>sigmoid_sigma</code> = sigma parameter of the sigmoid contamination function,</li> <li>• <code>sigmoid_plateau</code> = plateau parameter of the sigmoid contamination function,</li> <li>• <code>sex_propagule_viability_limit</code> = maximum number of cropping seasons up to which a sexual propagule is viable</li> <li>• <code>sex_propagule_release_mean</code> = average number of seasons after which a sexual propagule is released,</li> <li>• <code>clonal_propagule_gradual_release</code> = whether or not clonal propagules surviving the bottleneck are gradually released along the following cropping season.</li> </ul>
<code>audpc100S</code>	the audpc in a fully susceptible landscape (used as reference value for graphics).
<code>writeTXT</code>	a logical indicating if the output is written in a text file (TRUE) or not (FALSE).
<code>graphic</code>	a logical indicating if a tiff graphic of the output is generated (only if more than one year is simulated).
<code>path</code>	path of text file (if <code>writeTXT</code> = TRUE) and tiff graphic (if <code>graphic</code> = TRUE) to be generated.

## Details

Outputs are computed every year for every cultivar as well as for the whole landscape.

**Epidemiological outputs.** The epidemiological impact of pathogen spread can be evaluated by different measures:

1. Area Under Disease Progress Curve (AUDPC): average number of diseased host individuals (status I + R) per time step and square meter.

2. Relative Area Under Disease Progress Curve (AUDPCr): average proportion of diseased host individuals (status I + R) relative to the total number of existing hosts (H+L+I+R).
3. Green Leaf Area (GLA): average number of healthy host individuals (status H) per time step and per square meter.
4. Relative Green Leaf Area (GLAr): average proportion of healthy host individuals (status H) relative to the total number of existing hosts (H+L+I+R).
5. Contribution of pathogen genotypes: for every year and every host (as well as for the whole landscape and the whole simulation duration), fraction of cumulative LIR infections attributed to each pathogen genotype.

**Economic outputs.** The economic outcome of a simulation can be evaluated using:

1. Crop yield: yearly crop yield (e.g. grains, fruits, wine) in weight (or volume) units per hectare (depends on the number of productive hosts and associated theoretical yield).
2. Crop products: yearly product generated from sales, in monetary units per hectare (depends on crop yield and market value). Note that when disease = "mildew" a price reduction between 0% and 5% is applied to the market value depending on disease severity.
3. Operational crop costs: yearly costs associated with crop planting (depends on initial host density and planting cost) and pesticide treatments (depends on the number of applications and the cost of a single application) in monetary units per hectare.
4. Crop margin, i.e. products - operational costs, in monetary units per hectare.

## Value

A list containing, for each required type of output, a matrix summarising the output for each year and cultivar (as well as the whole landscape). Each matrix can be written in a txt file (if writeTXT=TRUE), and illustrated in a graphic (if graphic=TRUE).

## References

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 Computational Biology* 14(4):e1006067.

## See Also

[evol\\_output](#)

## Examples

```
## Not run:
demo_landsepi()

## End(Not run)
```



---

evol\_output

*Generation of evolutionary model outputs*


---

### Description

Generates evolutionary outputs from model simulations.

### Usage

```
evol_output(
  types = "all",
  time_param,
  Npoly,
  cultivars_param,
  genes_param,
  thres_breakdown = 50000,
  writeTXT = TRUE,
  graphic = TRUE,
  path = getwd()
)
```

### Arguments

types	a character string (or a vector of character strings if several outputs are to be computed) specifying the type of outputs to generate (see details): <ul style="list-style-type: none"> <li>• "evol_patho": Evolution of pathogen genotypes</li> <li>• "evol_aggr": Evolution of pathogen aggressiveness (i.e. phenotype)</li> <li>• "durability": Durability of resistance genes</li> <li>• "all": compute all these outputs (default)</li> </ul>
time_param	list of simulation parameters: <ul style="list-style-type: none"> <li>• Nyears = number cropping seasons,</li> <li>• nTSpY = number of time-steps per cropping season.</li> </ul>
Npoly	number of fields in the landscape.
cultivars_param	list of parameters associated with each host genotype (i.e. cultivars) when cultivated in pure crops: <ul style="list-style-type: none"> <li>• name = vector of cultivar names,</li> <li>• cultivars_genes_list = a list containing, for each host genotype, the indices of carried resistance genes.</li> </ul>
genes_param	list of parameters associated with each resistance gene and with the evolution of each corresponding pathogenicity gene: <ul style="list-style-type: none"> <li>• name = vector of names of resistance genes,</li> </ul>

- Nlevels\_aggressiveness = vector containing the 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),

thres_breakdown	an integer (or vector of integers) giving the 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).
writeTXT	a logical indicating if the output is written in a text file (TRUE) or not (FALSE).
graphic	a logical indicating if graphics must be generated (TRUE) or not (FALSE).
path	a character string indicating the path of the repository where simulation output files are located and where .txt files and graphics will be generated.

### Details

For each pathogen genotype (evol\_patho) or phenotype (evol\_aggr, note that different pathogen genotypes may lead to the same phenotype on a resistant host), several computations are performed based on pathogen genotype frequencies:

- appearance: time to first appearance (as propagule);
- R\_infection: time to first true infection of a resistant host;
- R\_invasion: time to invasion, when the number of infections of resistant hosts reaches a threshold above which the genotype or phenotype is unlikely to go extinct.

The value Nyears + 1 time step is used if the genotype or phenotype never appeared/infected/invaded. Durability is defined as the time to invasion of completely adapted pathogen individuals.

### Value

A list containing, for each required type of output, a matrix summarising the output. Each matrix can be written in a txt file (if writeTXT=TRUE), and illustrated in a graphic (if graphic=TRUE).

### References

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 Computational Biology* 14(4):e1006067.

### See Also

[epid\\_output](#)

### Examples

```
## Not run:
demo_landsepi()

## End(Not run)
```

---

```
initialize, LandsepiParams-method
      LandsepiParams
```

---

### Description

Creates and initialises a LandsepiParams object with default parameters.

### Usage

```
## S4 method for signature 'LandsepiParams'
initialize(
  .Object,
  Landscape = st_sf(st_sfc()),
  Croptypes = data.frame(),
  Cultivars = data.frame(matrix(ncol = length(.cultivarsColNames), nrow = 0, dimnames =
    list(NULL, .cultivarsColNames))),
  CultivarsGenes = data.frame(),
  Genes = data.frame(matrix(ncol = length(.geneColNames), nrow = 0, dimnames = list(NULL,
    .geneColNames))),
  Pathogen = list(name = "no pathogen", survival_prob = 0, repro_sex_prob = 0,
    infection_rate = 0, propagule_prod_rate = 0, latent_period_mean = 0,
    latent_period_var = 0, infectious_period_mean = 0, infectious_period_var = 0,
    sigmoid_kappa = 0, sigmoid_sigma = 0, sigmoid_plateau = 1,
    sex_propagule_viability_limit = 0, sex_propagule_release_mean = 0,
    clonal_propagule_gradual_release = 0),
  ReproSexProb = vector(),
  PI0 = 0,
  DispHost = vector(),
  DispPathoClonal = vector(),
  DispPathoSex = vector(),
  Treatment = list(treatment_degradation_rate = 0.1, treatment_efficiency = 0,
    treatment_timesteps = vector(), treatment_cultivars = vector(), treatment_cost = 0,
    treatment_application_threshold = vector()),
  OutputDir = normalizePath(character(getwd())),
  OutputGPKG = "landsepi_landscape.gpkg",
  Outputs = list(epid_outputs = "", evol_outputs = "", thres_breakdown = NA, audpc100S =
    NA),
  TimeParam = list(Nyears = 0, nTSpY = 0),
  Seed = NULL,
  ...
)
```

### Arguments

.Object	a LandsepiParam object.
Landscape	a landscape as sf object.

Croptypes	a dataframe with three columns named 'croptypeID' for croptype index, 'cultivarID' for cultivar index and 'proportion' for the proportion of the cultivar within the croptype.
Cultivars	a dataframe of parameters associated with each host genotype (i.e. cultivars, lines) when cultivated in pure crops.
CultivarsGenes	a list containing, for each host genotype, the indices of carried resistance genes.
Genes	a data.frame of parameters associated with each resistance gene and with the evolution of each corresponding pathogenicity gene.
Pathogen	a list of pathogen aggressiveness parameters on a susceptible host for a pathogen genotype not adapted to resistance.
ReproSexProb	a vector of size $\text{TimeParam}\$nTSpY + 1$ (end of season) of the probabilities for an infectious host to reproduce via sex rather than via cloning at each time step (days).
PI0	initial probability for the first host (whose index is 0) to be infectious (i.e. state I) at the beginning of the simulation. Must be between 0 and 1.
DispHost	a vectorized matrix giving the probability of host dispersal from any field of the landscape to any other field
DispPathoClonal	a vectorized matrix giving the probability of pathogen dispersal from any field of the landscape to any other field.
DispPathoSex	a vectorized matrix giving the probability of pathogen dispersal from any field of the landscape to any other field (sexual propagule).
Treatment	a list of chemical treatment parameters (indices of treated cultivars, times of application, efficiency and degradation rate)
OutputDir	the directory for simulation outputs
OutputGPKG	the name of the output GPKG file containing parameters of the deployment strategy
Outputs	a list of outputs parameters.
TimeParam	a list of time parameters.
Seed	an integer used as seed value (for random number generator).
...	more options

---

 invlogit

*Inverse logit function*


---

### Description

Given a numeric object, return the invlogit of the values. Missing values (NAs) are allowed.

### Usage

```
invlogit(x)
```

**Arguments**

x                    a numeric object

**Details**

The invlogit is defined by  $\exp(x)/(1 + \exp(x))$ . Values in x of -Inf or Inf return invlogits of 0 or 1 respectively. Any NAs in the input will also be NAs in the output.

**Value**

An object of the same type as x containing the invlogits of the input values.

**Examples**

```
invlogit(10)
```

---

is.in.01	<i>is.in.01</i>
----------	-----------------

---

**Description**

Tests if a number or vector is in the interval [0,1]

**Usage**

```
is.in.01(x, exclude0 = FALSE)
```

**Arguments**

x                    a number or vector or matrix  
 exclude0           TRUE is 0 is excluded, FALSE otherwise (default)

**Value**

a logical of the same size as x

**Examples**

```
is.in.01(-5)
is.in.01(0)
is.in.01(1)
is.in.01(0, exclude0 = TRUE)
is.in.01(2.5)
is.in.01(matrix(5:13/10, nrow=3))
```

---

<code>is.positive</code>	<i>is.positive</i>
--------------------------	--------------------

---

**Description**

Tests if a number or vector is positive (including 0)

**Usage**

```
is.positive(x)
```

**Arguments**

`x` a number or vector or matrix

**Value**

a logical of the same size as `x`

**Examples**

```
is.positive(-5)
is.positive(10)
is.positive(2.5)
is.positive(matrix(1:9, nrow=3))
```

---

<code>is.strict.positive</code>	<i>is.strict.positive</i>
---------------------------------	---------------------------

---

**Description**

Tests if a number or vector is strictly positive (i.e. excluding 0)

**Usage**

```
is.strict.positive(x)
```

**Arguments**

`x` a number or vector or matrix

**Value**

a logical of the same size as `x`

**Examples**

```
is.strict.positive(-5)
is.strict.positive(10)
is.strict.positive(2.5)
is.strict.positive(matrix(1:9, nrow=3))
```

---

is.wholenumber	<i>is.wholenumber</i>
----------------	-----------------------

---

**Description**

Tests if a number or vector is a whole number

**Usage**

```
is.wholenumber(x, tol = .Machine$double.eps^0.5)
```

**Arguments**

x	a number or vector or matrix
tol	double tolerance

**Value**

a logical of the same format as x

**Examples**

```
is.wholenumber(-5)
is.wholenumber(10)
is.wholenumber(2.5)
is.wholenumber(matrix(1:9, nrow=3))
```

---

landscapeTEST	<i>Landscape</i>
---------------	------------------

---

**Description**

Five simulated landscapes, composed of 155, 154, 152, 153 and 156 fields, respectively.

**Usage**

```
landscapeTEST1
landscapeTEST2
landscapeTEST3
landscapeTEST4
landscapeTEST5
```

**Format**

Landscapes have been generated using a T-tessellation algorithm. The format is a formal class 'SpatialPolygons' [package "sp"].

**Details**

The landscape structure is simulated using a T-tessellation algorithm (Kiêu et al. 2013) in order to control specific features such as number, area and shape of the fields.

**References**

Kiêu K, Adamczyk-Chauvat K, Monod H, Stoica RS. A completely random T-tessellation model and Gibbsian extensions. *Spat. Stat.* 2013;6:118-38. doi: <http://dx.doi.org/10.1016/j.spasta.2013.09.003>.

**Examples**

```
library(sp)
library(landsepi)
landscapeTEST1
plot(landscapeTEST1)
```

---

LandsepiParams

*Class LandsepiParams*

---

**Description**

Landsepi simulation parameters

**Details**

An object of class LandsepiParams that can be created by calling [createSimulParams](#)

**Slots**

**Landscape** a landscape as sf object. See [loadLandscape](#)

**Croptypes** a dataframe with three columns named 'croptypeID' for croptype index, 'cultivarID' for cultivar index and 'proportion' for the proportion of the cultivar within the croptype. See [loadCroptypes](#), [setCroptypes](#) and [allocateCroptypeCultivars](#)

**Cultivars** a dataframe of parameters associated with each host genotype (i.e. cultivars, lines) when cultivated in pure crops. See [loadCultivar](#) and [setCultivars](#)

**CultivarsGenes** a list containing, for each host genotype, the indices of carried resistance genes. See [allocateCultivarGenes](#)

**Genes** a data.frame of parameters associated with each resistance gene and with the evolution of each corresponding pathogenicity gene. See [loadGene](#) and [setGenes](#)

**Pathogen** a list of i. pathogen aggressiveness parameters on a susceptible host for a pathogen genotype not adapted to resistance and ii. sexual reproduction parameters. See [loadPathogen](#) and [setPathogen](#)



- ReproSexProb** a vector of size `TimeParam$NtSpY + 1` (end of season) of the probabilities for an infectious host to reproduce via sex rather than via cloning at each step.
- PI0** initial probability for the first host (whose index is 0) to be infectious (i.e. state I) at the beginning of the simulation. Must be between 0 and 1. See [setInoculum](#)
- DispHost** a vectorized matrix giving the probability of host dispersal from any field of the landscape to any other field. See [loadDispersalHost](#) and [setDispersalHost](#)
- DispPathoClonal** a vectorized matrix giving the probability of pathogen dispersal (clonal propagules) from any field of the landscape to any other field. See [loadDispersalPathogen](#) and [setDispersalPathogen](#)
- DispPathoSex** a vectorized matrix giving the probability of pathogen dispersal (sexual propagules) from any field of the landscape to any other field. See [loadDispersalPathogen](#) and [setDispersalPathogen](#)
- Treatment** a list of parameters to simulate the effect of chemical treatments on the pathogen, see [loadTreatment](#) and [setTreatment](#)
- OutputDir** the directory for simulation outputs
- OutputGPKG** the name of the output GPKG file containing parameters of the deployment strategy
- Outputs** a list of outputs parameters. See [loadOutputs](#) and [setOutputs](#)
- TimeParam** a list of time parameters. See [setTime](#)
- Seed** an integer used as seed value (for random number generator). See [setTime](#)

---

loadCrootypes

*Load Crootypes*


---

## Description

Creates a data.frame containing croptype parameters and filled with 0

## Usage

```
loadCrootypes(params, croptypeIDs = NULL, names = NULL)
```

## Arguments

- |                          |   |
|--------------------------|---|
| <code>params</code>      | a LandsepiParams Object.  |
| <code>croptypeIDs</code> | a vector of indices of crootypes (must start at 0 and match with croptype IDs in the landscape) |
| <code>names</code>       | a vector containing the names of all crootypes  |

## Details

Crootypes need to be later updated with [allocateCrootypeCultivars](#). If neither croptypeIDs nor names are given, it will automatically generate 1 croptype per cultivar.

**Value**

a data.frame with croptype parameters

**See Also**

[setCroptypes](#)

**Examples**

```
## Not run:
simul_params <- createSimulParams()
cultivar1 <- loadCultivar(name = "Susceptible", type = "growingHost")
cultivar2 <- loadCultivar(name = "Resistant1", type = "growingHost")
cultivar3 <- loadCultivar(name = "Resistant2", type = "growingHost")
cultivars <- data.frame(rbind(cultivar1, cultivar2, cultivar3), stringsAsFactors = FALSE)
simul_params <- setCultivars(simul_params, cultivars)
croptypes <- loadCroptypes(simul_params, names = c("Susceptible crop", "Mixture"))
croptypes

## End(Not run)
```

---

loadCultivar

*Load a cultivar*

---

**Description**

create a data.frame containing cultivar parameters depending of his type

**Usage**

```
loadCultivar(name, type = "growingHost")
```

**Arguments**

name	a character string (without space) specifying the cultivar name.
type	the cultivar type, among: "growingHost" (default), "nongrowingHost", "grapevine", "banana" or "nonCrop".

**Details**

- "growingHost" is adapted to situations where the infection unit is a piece of leaf (e.g. where a fungal lesion can develop); the number of available infection units increasing during the season due to plant growth (as typified by cereal crops).
- "nongrowingHost" corresponds to situations where the infection unit is the whole plant (e.g. for viral systemic infection); thus the number of infection units is constant.
- "grapevine" corresponds to parameters for grapevine (including host growth).
- "banana" corresponds to parameters for banana (including host growth).
- "nonCrop" is not planted, does not cost anything and does not yield anything (e.g. forest, fallow).

**Value**

a dataframe of parameters associated with each host genotype (i.e. cultivars, lines) when cultivated in pure crops.

**See Also**

[setCultivars](#)

**Examples**

```
c1 <- loadCultivar("winterWheat", type = "growingHost")
c1
c2 <- loadCultivar("forest", type = "nonCrop")
c2
```

---

loadDispersalHost	<i>Load a host dispersal matrix</i>
-------------------	-------------------------------------

---

**Description**

It loads a vectorised diagonal matrix to simulate no host dispersal.

**Usage**

```
loadDispersalHost(params, type = "no")
```

**Arguments**

params	a LandsepiParams Object.
type	a character string specifying the type of dispersal ("no" for no dispersal)

**Details**

as the size of the matrix depends on the number of fields in the landscape, the landscape must be defined before calling loadDispersalHost.

**Value**

a vectorised dispersal matrix.

**See Also**

[setDispersalHost](#)

**Examples**

```
## Not run:
simul_params <- createSimulParams()
simul_params <- setLandscape(simul_params, loadLandscape(1))
d <- loadDispersalHost(simul_params)
d

## End(Not run)
```

---

loadDispersalPathogen *Load pathogen dispersal matrices*

---

**Description**

It loads one of the five built-in vectorised dispersal matrices of rust fungi associated with the five built-in landscapes. Landscape and DispersalPathogen ID must be the same. And set a vectorized identity matrix for sexual reproduction dispersal.

**Usage**

```
loadDispersalPathogen(id = 1)
```

**Arguments**

**id** a matrix ID between 1 to 5 (must match the ID of the landscape loaded with [loadLandscape](#)).

**Details**

*landsepi* includes built-in dispersal matrices to represent rust dispersal in the five built-in landscapes. These have been computed from a power-law dispersal kernel:  $g(d) = ((b - 2) * (b - 1) / (2 * \pi * a^2)) * (1 + d/a)^{-b}$  with  $a=40$  the scale parameter and  $b=7$  a parameter related to the width of the dispersal kernel. The expected mean dispersal distance is given by  $2*a/(b-3) = 20m$ .

**Value**

a vectorised dispersal matrix representing the dispersal of clonal propagules, and a vectorised dispersal identity matrix for sexual propagules. All by columns.

**See Also**

[dispP](#), [setDispersalPathogen](#)

**Examples**

```
d <- loadDispersalPathogen(1)
d
```

---

loadGene	<i>Load a gene</i>
----------	--------------------

---

### Description

Creates a data.frame containing parameters of a gene depending of his type

### Usage

```
loadGene(name, type = "majorGene")
```

### Arguments

name	name of the gene
type	type of the gene: "majorGene", "APR", "QTL" or "immunity" (default = "majorGene")

### Details

- "majorGene" means a completely efficient gene that can be broken down via a single pathogen mutation
- "APR" means a major gene that is active only after a delay of 30 days after planting
- "QTL" means a partial resistance (50% efficiency) that requires several pathogen mutations to be completely eroded
- "immunity" means a completely efficient resistance that the pathogen has no way to adapt (i.e. the cultivar is non-host).

For different scenarios, the data.frame can be manually updated later.

### Value

a data.frame with gene parameters

### See Also

[setGenes](#)

### Examples

```
gene1 <- loadGene(name = "MG 1", type = "majorGene")
gene1
gene2 <- loadGene(name = "Lr34", type = "APR")
gene2
```

---

loadLandscape	<i>Load a landscape</i>
---------------	-------------------------

---

**Description**

Lloads one of the five built-in landscapes simulated using a T-tesselation algorithm and composed of 155, 154, 152, 153 and 156 fields, respectively. Each landscape is identified by a numeric from 1 to 5.

**Usage**

```
loadLandscape(id = 1)
```

**Arguments**

id                    a landscape ID between 1 to 5 (default = 1)

**Value**

a landscape in sp format

**See Also**

[landscapeTEST](#), [setLandscape](#)

**Examples**

```
land <- loadLandscape(1)
length(land)
```

---

loadOutputs	<i>Load outputs</i>
-------------	---------------------

---

**Description**

Creates an output list

**Usage**

```
loadOutputs(epid_outputs = "all", evol_outputs = "all")
```

**Arguments**

- `epid_outputs` a character string (or a vector of character strings if several outputs are to be computed) specifying the type of epidemiological and economic outputs to generate (see details):
- "audpc" : Area Under Disease Progress Curve (average number of diseased host individuals per time step and square meter)
  - "audpc\_rel" : Relative Area Under Disease Progress Curve (average proportion of diseased host individuals relative to the total number of existing hosts)
  - "gla" : Green Leaf Area (average number of healthy host individuals per time step and square meter)
  - "gla\_rel" : Relative Green Leaf Area (average proportion of healthy host individuals relative to the total number of existing hosts)
  - "eco\_yield" : total crop yield (in weight or volume units per ha)
  - "eco\_cost" : operational crop costs (in monetary units per ha)
  - "eco\_product" : total crop products (in monetary units per ha)
  - "eco\_margin" : Margin (products - operational costs, in monetary units per ha)
  - "contrib": contribution of pathogen genotypes to LIR dynamics
  - "HLIR\_dynamics", "H\_dynamics", "L\_dynamics", "IR\_dynamics", "HLI\_dynamics", etc.: Epidemic dynamics related to the specified sanitary status (H, L, I or R and all their combinations). Graphics only, works only if `graphic=TRUE`.
  - "all" : compute all these outputs (default)
  - "" : none of these outputs will be generated.
- `evol_outputs` a character string (or a vector of character strings if several outputs are to be computed) specifying the type of evolutionary outputs to generate :
- "evol\_patho": Dynamics of pathogen genotype frequencies
  - "evol\_aggr": Evolution of pathogen aggressiveness
  - "durability": Durability of resistance genes
  - "all": compute all these outputs (default)
  - "": none of these outputs will be generated.

**Value**

a list of outputs and parameters for output generation

**See Also**

[setOutputs](#), [compute\\_audpc100S](#)

**Examples**

```
outputList <- loadOutputs(epid_outputs = "audpc", evol_outputs = "durability")
outputList
```

---

loadPathogen	<i>Load pathogen parameters</i>
--------------	---------------------------------

---

### Description

Loads default pathogen parameters for a specific disease

### Usage

```
loadPathogen(disease = "rust")
```

### Arguments

disease            a disease name, among "rust" (default), "mildew", "sigatoka" and "no pathogen"

### Details

Available diseases:

- "no pathogen"
- "rust" (genus *Puccinia*, e.g. stripe rust, stem rust and leaf rust of wheat and barley)
- "mildew" (*Plasmopara viticola*, downy mildew of grapevine)
- "sigatoka" (*Pseudocercospora fijiensis*, black sigatoka of banana) Note that when disease = "mildew" a price reduction between 0% and 5% is applied to the market value according to disease severity.

### Value

a list of pathogen parameters on a susceptible host for a pathogen genotype not adapted to resistance

### See Also

[setPathogen](#)

### Examples

```
basic_patho_params <- loadPathogen()
basic_patho_params
```



---

loadSimulParams	<i>Load simulation parameters</i>
-----------------	-----------------------------------

---

### Description

Loads a GPKG file from the output of a landsepi simulation.

### Usage

```
loadSimulParams(inputGPKG = "")
```

### Arguments

inputGPKG      name of the GPKG file.

### Details

See [saveDeploymentStrategy](#).

### Value

a LandsepiParams object.

---

loadTreatment	<i>Load treatment parameters</i>
---------------	----------------------------------

---

### Description

Loads the list of treatment parameters required by the model (initialised at 0 , i.e. absence of treatments)

### Usage

```
loadTreatment()
```

### Details

Chemical treatment is applied in a polygon only if disease severity (i.e.  $I/N$ ) in this polygon exceeds the threshold given by `treatment_application_threshold`. Treatment efficiency is maximum (i.e. equal to the parameter `treatment_efficiency`) at the time of treatment application (noted  $t^*$ ); then it decreases with time (i.e. natural pesticide degradation) and host growth (i.e. new biomass is not protected by treatments): protected by treatments):Efficiency of the treatment at time  $t$  after the application date is given by:  $efficiency(t) = treatment\_efficiency / (1 + exp(a - b * C(t)))$  with  $C(t) = C_1 * C_2$ :

- $C_1 = \exp(-\text{treatment\_degradation\_rate} * \Delta t)$  is the reduction of fungicide concentration due to time (e.g. natural degradation, volatilization, weathering), with  $\Delta t = t - t^*$  the timelag passed since the time of treatment application.
- $C_2 = \min(1, N(t^*)/N(t))$  is the reduction of fungicide concentration due to plant growth, since new plant tissue is not covered by fungicide.  $N(t^*)$  and  $N(t)$  being the number of host individuals at the time of treatment  $t^*$  and at time  $t$ , respectively.
- $a \in [3.5; 4.5]$  and  $b \in [8; 9]$  are shape parameters.

### Value

a list of treatment parameters:

- `treatment_degradation_rate` = degradation rate (per time step) of chemical concentration,
- `treatment_efficiency` = maximal efficiency of chemical treatments (i.e. fractional reduction of pathogen infection rate at the time of application),
- `treatment_timesteps` = vector of time steps corresponding to treatment application dates,
- `treatment_cultivars` = vector of indices of the cultivars that receive treatments,
- `treatment_cost` = cost of a single treatment application (monetary units/ha)
- `treatment_application_threshold` = vector of thresholds (i.e. disease severity, one for each treated cultivar) above which the treatment is applied in a polygon.

### See Also

[setTreatment](#)

### Examples

```
treat <- loadTreatment()
treat
```

---

logit

*Logit function*

---

### Description

Given a numeric object, return the logit of the values. Missing values (NAs) are allowed.

### Usage

```
logit(x)
```

### Arguments

`x` a numeric object containing values between 0 and 1

**Details**

The logit is defined by  $\log(x/(1-x))$ . Values in  $x$  of 0 or 1 return logits of  $-\text{Inf}$  or  $\text{Inf}$  respectively. Any NAs in the input will also be NAs in the output.

**Value**

An object of the same type as  $x$  containing the logits of the input values.

**Examples**

```
logit(0.5)
```

---

 model\_landsepi

*Model for Landscape Epidemiology & Evolution*


---

**Description**

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

**Usage**

```
model_landsepi(
  time_param,
  area_vector,
  rotation_matrix,
  croptypes_cultivars_prop,
  dispersal,
  inits,
  seed,
  cultivars_param,
  basic_patho_param,
  genes_param,
  treatment_param
)
```

**Arguments**

time_param	list of simulation parameters: <ul style="list-style-type: none"> <li>• Nyears = number cropping seasons,</li> <li>• nTSpY = number of time-steps per cropping season.</li> </ul>
area_vector	a vector containing areas of polygons (i.e. fields), in surface units.
rotation_matrix	a matrix containing for each field (rows) and year (columns, named "year_1", "year_2", etc.), the index of the cultivated croptype. Importantly, the matrix must contain 1 more column than the real number of simulated years.

croptypes_cultivars_prop	a matrix with three columns named 'croptypeID' for croptype index, 'cultivarID' for cultivar index and 'proportion' for the proportion of the cultivar within the croptype.
dispersal	list of dispersal parameters: <ul style="list-style-type: none"> <li>• disp_patho_clonal = vectorised dispersal matrix of the pathogen (clonal propagules),</li> <li>• disp_patho_sex = vectorised dispersal matrix of the pathogen (sexual propagules),</li> <li>• disp_host = vectorised dispersal matrix of the host.</li> </ul>
inits	list of initial conditions: <ul style="list-style-type: none"> <li>• pI0 = initial probability for the first host (whose index is 0) to be infectious (i.e. state I) at t=0.</li> </ul>
seed	seed (for random number generation).
cultivars_param	list of parameters associated with each host genotype (i.e. cultivars) when cultivated in pure crops: <ul style="list-style-type: none"> <li>• initial_density = vector of host densities (per surface unit) at the beginning of the cropping season,</li> <li>• max_density = vector of maximum host densities (per surface unit) at the end of the cropping season,</li> <li>• growth_rate = vector of host growth rates,</li> <li>• reproduction_rate = vector of host reproduction rates,</li> <li>• relative_yield_H = Yield of H individuals relative to H individuals (100%)</li> <li>• relative_yield_L = Yield of L individuals relative to H individuals</li> <li>• relative_yield_I = Yield of I individuals relative to H individuals</li> <li>• relative_yield_R = Yield of R individuals relative to H individuals</li> <li>• sigmoid_kappa_host = kappa parameter for the sigmoid invasion function (for host dispersal),</li> <li>• sigmoid_sigma_host = sigma parameter for the sigmoid invasion function (for host dispersal),</li> <li>• sigmoid_plateau_host = plateau parameter for the sigmoid invasion function (for host dispersal),</li> <li>• cultivars_genes_list = a list containing, for each host genotype, the indices of carried resistance genes,</li> </ul>
basic_patho_param	list of i. pathogen aggressiveness parameters on a susceptible host for a pathogen genotype not adapted to resistance and ii. sexual reproduction parameters: <ul style="list-style-type: none"> <li>• infection_rate = maximal expected infection rate of a propagule on a healthy host,</li> <li>• propagule_prod_rate = maximal expected reproduction_rate of an infectious host per timestep,</li> <li>• latent_period_mean = minimal expected duration of the latent period,</li> <li>• latent_period_var = variance of the latent period duration,</li> </ul>

- infectious\_period\_mean = maximal expected duration of the infectious period,
- infectious\_period\_var = variance of the infectious period duration,
- survival\_prob = probability for a propagule to survive the off-season,
- reproto\_sex\_prob = probability for an infectious host to reproduce via sex rather than via cloning,
- sigmoid\_kappa = kappa parameter of the sigmoid contamination function,
- sigmoid\_sigma = sigma parameter of the sigmoid contamination function,
- sigmoid\_plateau = plateau parameter of the sigmoid contamination function,
- sex\_propagule\_viability\_limit = maximum number of cropping seasons up to which a sexual propagule is viable
- sex\_propagule\_release\_mean = average number of cropping seasons after which a sexual propagule is released.
- clonal\_propagule\_gradual\_release = whether or not clonal propagules surviving the bottleneck are gradually released along the following cropping season.

genes\_param list of parameters associated with each resistance gene and with the evolution of each corresponding pathogenicity gene:

- target\_trait = vector of aggressiveness components (IR, LAT, IP, or PR) targeted by resistance genes,
- efficiency = vector of resistance gene efficiencies (percentage of reduction of the targeted aggressiveness component: IR, 1/LAT, IP and PR),
- age\_of\_activ\_mean = vector of expected delays to resistance activation (for APRs),
- age\_of\_activ\_var = vector of variances of the delay to resistance activation (for APRs),
- mutation\_prob = vector of mutation probabilities for pathogenicity genes (each of them corresponding to a resistance gene),
- Nlevels\_aggressiveness = vector of 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),
- adaptation\_cost = vector of adaptation penalties paid by pathogen genotypes fully adapted to the considered resistance genes on hosts that do not carry this gene,
- tradeoff\_strength = vector of strengths of the trade-off relationships between the level of aggressiveness on hosts that do and do not carry the resistance genes.

treatment\_param

list of parameters related to pesticide treatments:

- treatment\_degradation\_rate = degradation rate (per time step) of chemical concentration,
- treatment\_efficiency = maximal efficiency of chemical treatments (i.e. fractional reduction of pathogen infection rate at the time of application),

- treatment\_timesteps = vector of time-steps corresponding to treatment application dates,
- treatment\_cultivars = vector of indices of the cultivars that receive treatments,
- treatment\_cost = cost of a single treatment application (monetary units/ha),
- treatment\_application\_threshold = vector of thresholds (i.e. disease severity, one for each treated cultivar) above which the treatment is applied

## Details

See ?landsepi for details on the model and assumptions. Briefly, the model is stochastic, spatially explicit (the basic spatial unit is an individual field), based on a SEIR ('susceptible-exposed-infectious-removed', renamed HLIR for 'healthy-latent-infectious-removed' to avoid confusions with 'susceptible host') structure with a discrete time step. It simulates the spread and evolution (via mutation, recombination through sexual reproduction, selection and drift) of a pathogen in a heterogeneous cropping landscape, across cropping seasons split by host harvests which impose potential bottlenecks to the pathogen. A wide array of resistance deployment strategies (possibly including chemical treatments) can be simulated.

## Value

A set of binary files is generated for every year of simulation and every compartment:

- H: healthy hosts,
- Hjuv: juvenile healthy hosts (for host reproduction),
- L: latently infected hosts,
- I: infectious hosts,
- R: removed hosts,
- P: propagules.

Each file indicates for every time-step the number of individuals in each field, and when appropriate for each host and pathogen genotypes). Additionally, a binary file called TFI is generated and gives the Treatment Frequency Indicator (expressed as the number of treatment applications per polygon).

## References

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 Computational Biology* 14(4):e1006067.

## Examples

```
## Not run:
#### Spatially-implicit simulation with 2 patches (S + R) during 3 years ####

## Simulation parameters
time_param <- list(Nyears=3, nTSpY=120)
Npoly=2
Npatho=2
```

```

area <- c(100000, 100000)
cultivars <- as.list(rbind(loadCultivar(name="Susceptible", type="growingHost")
, loadCultivar(name="Resistant", type="growingHost")))
names(cultivars)[names(cultivars)=="cultivarName"] <- "name"
cultivars <- c(cultivars, list(sigmoid_kappa_host=0.002, sigmoid_sigma_host=1.001,
  sigmoid_plateau_host=1, cultivars_genes_list=list(numeric(0),0)))
rotation <- data.frame(year_1=c(0,1), year_2=c(0,1), year_3=c(0,1), year_4=c(0,1))
croptypes_cultivars_prop <- data.frame(croptypeID=c(0,1), cultivarID=c(0,1), proportion=c(1,1))
genes <- as.list(loadGene(name="MG", type="majorGene"))

## run simulation
model_landsepi(seed=1,
  time_param = time_param,
  basic_patho_param = loadPathogen(disease = "rust"),
  inits = list(pI0=0.01), area_vector = area,
  dispersal = list(dispatho_clonal=c(0.99,0.01,0.01,0.99),
  disp_patho_sex=c(1,0,0,1),
  disp_host=c(1,0,0,1)),
  rotation_matrix = as.matrix(rotation),
  croptypes_cultivars_prop = as.matrix(croptypes_cultivars_prop),
  cultivars_param = cultivars, genes_param = genes)

## Compute outputs
eco_param <- list(yield_perHa = cbind(H = as.numeric(cultivars$yield_H),
  L = as.numeric(cultivars$yield_L),
  I = as.numeric(cultivars$yield_I),
  R = as.numeric(cultivars$yield_R)),
  planting_cost_perHa = as.numeric(cultivars$planting_cost),
  market_value = as.numeric(cultivars$market_value))

evol_res <- evol_output(, time_param, Npoly, cultivars, genes)
epid_output(, time_param, Npatho, area, rotation
, croptypes_cultivars_prop, cultivars, eco_param)

#### 1-year simulation of a rust epidemic in pure susceptible crop in a single 1-km2 patch ####
## Simulation and pathogen parameters
time_param <- list(Nyears=1, nTSpY=120)
area <- c(1E6)
basic_patho_param = loadPathogen(disease = "rust")
## croptypes, cultivars and genes
rotation <- data.frame(year_1=c(0), year_2=c(0))
croptypes_cultivars_prop <- data.frame(croptypeID=c(0), cultivarID=c(0), proportion=c(1))
cultivars <- as.list(rbind(loadCultivar(name="Susceptible", type="growingHost")))
names(cultivars)[names(cultivars)=="cultivarName"] <- "name"
yield0 <- cultivars$yield_H + as.numeric(cultivars$yield_H==0)
cultivars <- c(cultivars, list(relative_yield_H = as.numeric(cultivars$yield_H / yield0)
  , relative_yield_L = as.numeric(cultivars$yield_L / yield0)
  , relative_yield_I = as.numeric(cultivars$yield_I / yield0)
  , relative_yield_R = as.numeric(cultivars$yield_R / yield0)
  , sigmoid_kappa_host=0.002, sigmoid_sigma_host=1.001, sigmoid_plateau_host=1

```

```

    , cultivars_genes_list=list(numeric(0)))
genes <- list(geneName = character(0) , adaptation_cost = numeric(0)
  , mutation_prob = numeric(0)
  , efficiency = numeric(0) , tradeoff_strength = numeric(0)
  , Nlevels_aggressiveness = numeric(0)
  , age_of_activ_mean = numeric(0) , age_of_activ_var = numeric(0)
  , target_trait = character(0)
  , recombination_sd = numeric(0))
treatment=list(treatment_degradation_rate=0.1
  , treatment_efficiency=0
  , treatment_timesteps=logical(0)
  , treatment_cultivars=logical(0)
  , treatment_cost=0
  , treatment_application_threshold = logical(0))

## run simulation
model_landsepi(seed=1, time_param = time_param
  , basic_patho_param = basic_patho_param
  , inits = list(pI0=5E-4), area_vector = area
  , dispersal = list(dispatho_clonal=c(1), disp_patho_sex=c(1), disp_host=c(1))
  , rotation_matrix = as.matrix(rotation)
  , treatment_param = treatment
  , croptypes_cultivars_prop = as.matrix(croptypes_cultivars_prop)
  , cultivars_param = cultivars, genes_param = genes)

## End(Not run)

```

---

multiN

*Allocation of cultivars*


---

## Description

Algorithm based on latent Gaussian fields to allocate two different types of crops across a landscape.

## Usage

```
multiN(d, area, prop, range = 0, algo = "random")
```

## Arguments

d	a symmetric matrix of the pairwise distances between the centroids of the fields of the landscape.
area	vector containing field areas.
prop	proportion of landscape surface covered by the second type of crop.
range	range of spatial autocorrelation between fields (must be greater or equal 0). The greater the value of range, the higher the degree of spatial aggregation (roughly, range between 0 and 0.1 for fragmented landscapes, between 0.1 and 0.5 for balanced landscapes, between 0.5 and 3 for aggregated landscapes, and above 3 for highly aggregated landscapes).



**algo** the algorithm used for the computation of the variance-covariance matrix of the multivariate normal distribution: "exp" for exponential function, "periodic" for periodic function, "random" for random draw (see details). If algo="random", the parameter range is ignored.

### Details

This algorithm allows the control of the proportions of each type of crop in terms of surface coverage, and their level of spatial aggregation. A random vector of values is drawn from a multivariate normal distribution with expectation 0 and a variance-covariance matrix which depends on the pairwise distances between the centroids of the fields. Two different functions allow the computation of the variance-covariance matrix to allocate crops with more or less spatial aggregation (depending on the value of the range parameter). The exponential function codes for an exponential decay of the spatial autocorrelation as distance between fields increases. The periodic function codes for a periodic fluctuation of the spatial autocorrelation as distance between fields increases. Alternatively, a normal distribution can be used for a random allocation of the types of crops. Next, the two types of crops are allocated to different fields depending on whether the value drawn from the multivariate normal distribution is above or below a threshold. The proportion of each type of crop in the landscape is controlled by the value of this threshold (parameter prop).

### Value

A dataframe containing the index of each field (column 1) and the index (0 or 1) of the type of crop grown on these fields (column 2).

### See Also

[AgriLand](#), [allocateLandscapeCroptypes](#)

### Examples

```
## Not run:
d <- matrix(rpois(100, 100), nrow = 10)
d <- d + t(d) ## ensures that d is symmetric
area <- data.frame(id = 1:10, area = 10)
multiN(d, area, prop = 0.5, range = 0.5, algo = "periodic")

## End(Not run)
```

---

periodic\_cov

*Periodic covariance function*

---

### Description

Periodic function used to compute the variance-covariance matrix of the fields of the landscape.

### Usage

```
periodic_cov(d, range, phi = 1)
```

**Arguments**

d	a numeric object containing pairwise distances between the centroids of the fields
range	range (half-period of oscillations)
phi	amplitude of the oscillations

**Details**

The periodic covariance is defined by  $\exp(-2 * \sin(d * \pi / (2 * range))^2 / \phi^2)$ . It is used to generate highly fragmented or highly aggregated landscapes.

**Value**

An object of the same type as d.

**See Also**

[multiN](#)

**Examples**

```
periodic_cov(10, range = 5)
```

---

plotland

*Plotting the landscape*

---

**Description**

Plots a landscape with colors or hatched lines to represent different types of fields

**Usage**

```
plotland(
  landscape,
  COL = rep(0, length(landscape)),
  DENS = rep(0, length(landscape)),
  ANGLE = rep(30, length(landscape)),
  COL.LEG = unique(COL),
  DENS.LEG = unique(DENS),
  ANGLE.LEG = unique(ANGLE),
  TITLE = "",
  SUBTITLE = "",
  LEGEND1 = rep("", length(COL.LEG)),
  LEGEND2 = rep("", length(COL.LEG)),
  TITLE.LEG2 = ""
)
```

**Arguments**

landscape	a spatialpolygon object containing field coordinates
COL	vector containing the color of each field
DENS	vector containing the density of hatched lines for each field
ANGLE	vector containing the angle of hatched lines for each field
COL.LEG	vector containing the colors in the first legend
DENS.LEG	vector containing the density of hatched lines in the second legend
ANGLE.LEG	vector containing the angle of hatched lines in the second legend
TITLE	title of the graphic
SUBTITLE	subtitle of the graphic
LEGEND1	labels in the first legend (colors)
LEGEND2	labels in the second legend (hatched lines)
TITLE.LEG2	title for the second legend

**Examples**

```
## Not run:
## Draw a landscape with various colours
landscapeTEST1
plotland(landscapeTEST1,
  COL = 1:length(landscapeTEST1),
  DENS = rep(0, length(landscapeTEST1)), ANGLE = rep(30, length(landscapeTEST1))
)
## End(Not run)
```

---

plot_allocation	<i>Plotting allocation of croptypes in a landscape</i>
-----------------	--

---

**Description**

Plots croptype allocation in the landscape at a given year of the simulation

**Usage**

```
plot_allocation(
  landscape,
  year,
  croptype_names = c(),
  title = "",
  subtitle = "",
  filename = "landscape.png"
)
```

**Arguments**

landscape	a SpatialPolygonsDataFrame
year	year to be plotted
croptype_names	croptype names (for legend)
title	title of the graphic
subtitle	subtitle of the graphic
filename	name of the .png file to be generated

**Value**

a png file.

**See Also**

[plotland](#)

**Examples**

```
## Not run:
landscape <- landscapeTEST1
croptypes <- data.frame(sample.int(3, length(landscape), replace = TRUE))
allocation <- SpatialPolygonsDataFrame(landscape, croptypes, match.ID = TRUE)
plot_allocation(allocation, 1,
  title = "Simulated landscape", subtitle = "Year 1",
  filename = paste(getwd(), "/landscape.png", sep = "")
)

## End(Not run)
```

---

plot_freqPatho	<i>Plotting pathotype frequencies</i>
----------------	---------------------------------------

---

**Description**

Plots in a .tiff file the dynamics of pathotype frequencies with respect to pathogen adaptation to a specific resistance gene.

**Usage**

```
plot_freqPatho(
  name_gene,
  Nlevels_aggressiveness,
  I_aggrProp,
  nTS,
  Nyears,
  nTSpY
)
```

**Arguments**

name\_gene        a string specifying the name of the gene under investigation  
 Nlevels\_aggressiveness        number of pathotypes with respect to the gene under investigation  
 I\_aggrProp        a matrix giving the frequency of every pathotype (rows) for every time-step (columns)  
 nTS                number of simulated time-steps  
 Nyears            number of simulated cropping seasons  
 nTSpY             number of time-steps per cropping season

**Examples**

```

## Not run:
freqMatrix <- matrix(0, nrow = 2, ncol = 100)
freqMatrix[2, 26:100] <- (26:100) / 100
freqMatrix[1, ] <- 1 - freqMatrix[2, ]
plot_freqPatho(
  index_gene = 1,
  Nlevels_aggressiveness = 2,
  freqMatrix,
  nTS = 100,
  Nyears = 10,
  nTSpY = 10
)

## End(Not run)

```

---

price\_reduction        *Price reduction function*

---

**Description**

Give the price reduction rate associated with the infection on the (grapevine) fruits

**Usage**

```

price_reduction(
  I_host,
  N_host,
  Nhost,
  Nyears,
  nTSpY,
  severity_thresh = 0.075,
  price_penalty = 0.3
)

```

**Arguments**

I_host	number of infected individuals for each cultivar and timestep
N_host	total number of individuals for each cultivar and timestep
Nhost	total number of cultivars considered in the simulation
Nyears	number of simulated cropping seasons
nTSpY	number of timesteps (e.g. days) per cropping season
severity_thresh	disease severity threshold above which the price reduction is applied
price_penalty	percentage of price reduction

**Value**

A matrix with the price reduction rate per cultivar and per year of simulation

**References**

Savary, S., Delbac, L., Rochas, A., Taisant, G., & Willocquet, L. (2009). Analysis of nonlinear relationships in dual epidemics, and its application to the management of grapevine downy and powdery mildews. *Phytopathology*, 99(8), 930-942.

---

*print*

*print*

---

**Description**

Prints a LandsepiParams object.

**Usage**

```
## S4 method for signature 'LandsepiParams'
print(x, ...)
```

**Arguments**

x	a LandsepiParams object
...	print options

---

resetCultivarsGenes     *Reset cultivars genes*

---

**Description**

Resets the lists of genes carried by all cultivars

**Usage**

```
resetCultivarsGenes(params)
```

**Arguments**

params             a LandsepiParams object.

**Value**

a LandsepiParams object

---

runShinyApp             *runShinyApp*

---

**Description**

Launches landsepi shiny application into browser

**Usage**

```
runShinyApp()
```

**Details**

R packages needed to run the shiny app : `install.packages(c("shiny","DT", "shinyjs", "gridExtra", "png", "grid", "future", "promises", "tools"))`

---

runSimul	<i>Run a simulation</i>
----------	-------------------------

---

### Description

Runs a simulation with `landsepi`, a stochastic, spatially-explicit, demo-genetic model simulating the spread and evolution of a pathogen in a heterogeneous landscape and generating a wide range of epidemiological, evolutionary and economic outputs.

### Usage

```
runSimul(
  params,
  graphic = TRUE,
  writeTXT = TRUE,
  videoMP4 = FALSE,
  keepRawResults = FALSE
)
```

### Arguments

<code>params</code>	a <code>LandsepiParams</code> Object containing all simulation parameters. Must be initialised with <code>createSimulParams</code> and updated using <code>set*()</code> methods (see vignettes for details).
<code>graphic</code>	a logical indicating if graphics must be generated (TRUE, default) or not (FALSE).
<code>writeTXT</code>	a logical indicating if outputs must be written in text files (TRUE, default) or not (FALSE).
<code>videoMP4</code>	a logical indicating if a video must be generated (TRUE) or not (FALSE, default). Works only if <code>graphic=TRUE</code> and <code>audpc_rel</code> is computed.
<code>keepRawResults</code>	a logical indicating if binary files must be kept after the end of the simulation (default=FALSE). Careful, many files may be generated if <code>keepRawResults=TRUE</code> .

### Details

See `?landsepi` for details on the model, assumptions and outputs, and our vignettes for tutorials (`browseVignettes("landsepi")`). The function runs the model simulation using a `LandsepiParams` object. Briefly, the model is stochastic, spatially explicit (the basic spatial unit is an individual field), based on a SEIR ('susceptible-exposed-infectious-removed', renamed HLIR for 'healthy-latent-infectious-removed' to avoid confusions with 'susceptible host') structure with a discrete time step. It simulates the spread and evolution (via mutation, recombination through sexual reproduction, selection and drift) of a pathogen in a heterogeneous cropping landscape, across cropping seasons split by host harvests which impose potential bottlenecks to the pathogen. A wide array of resistance deployment strategies (possibly including chemical treatments) can be simulated and evaluated using several possible outputs to assess the epidemiological, evolutionary and economic performance of deployment strategies.



**Value**

A list containing all required outputs. A set of text files, graphics and a video showing epidemic dynamics can be generated. If `keepRawResults=TRUE`, a set of binary files is generated for every year of simulation and every compartment:

- H: healthy hosts,
- Hjuv: juvenile healthy hosts (for host reproduction),
- L: latently infected hosts,
- I: infectious hosts,
- R: removed hosts,
- P: propagules.

Each file indicates for every time step the number of individuals in each field, and when appropriate for each host and pathogen genotype. Additionally, a binary file called TFI is generated and gives the Treatment Frequency Indicator (expressed as the number of treatment applications per polygon).

**References**

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 Computational Biology* 14(4):e1006067.

**See Also**

[demo\\_landsepi](#)

**Examples**

```
## Not run:
### Here is an example of simulation of a mosaic of three cultivars (S + R1 + R2). See our
## tutorials for more examples.
## Initialisation
simul_params <- createSimulParams(outputDir = getwd())
## Seed & Time parameters
simul_params <- setSeed(simul_params, seed = 1)
simul_params <- setTime(simul_params, Nyears = 10, nTSpY = 120)
## Pathogen & inoculum parameters
simul_params <- setPathogen(simul_params, loadPathogen("rust"))
simul_params <- setInoculum(simul_params, 5e-4)
## Landscape & dispersal
simul_params <- setLandscape(simul_params, loadLandscape(1))
simul_params <- setDispersalPathogen(simul_params, loadDispersalPathogen[[1]])
## Genes
gene1 <- loadGene(name = "MG 1", type = "majorGene")
gene2 <- loadGene(name = "MG 2", type = "majorGene")
genes <- data.frame(rbind(gene1, gene2), stringsAsFactors = FALSE)
simul_params <- setGenes(simul_params, genes)
## Cultivars
cultivar1 <- loadCultivar(name = "Susceptible", type = "growingHost")
cultivar2 <- loadCultivar(name = "Resistant1", type = "growingHost")
```

```

cultivar3 <- loadCultivar(name = "Resistant2", type = "growingHost")
cultivars <- data.frame(rbind(cultivar1, cultivar2, cultivar3), stringsAsFactors = FALSE)
simul_params <- setCultivars(simul_params, cultivars)
## Allocate genes to cultivars
simul_params <- allocateCultivarGenes(simul_params, "Resistant1", c("MG 1"))
simul_params <- allocateCultivarGenes(simul_params, "Resistant2", c("MG 2"))
## Allocate cultivars to croptypes
croptypes <- loadCroptypes(simul_params, names = c("Susceptible crop"
, "Resistant crop 1"
, "Resistant crop 2"))
croptypes <- allocateCroptypeCultivars(croptypes, "Susceptible crop", "Susceptible")
croptypes <- allocateCroptypeCultivars(croptypes, "Resistant crop 1", "Resistant1")
croptypes <- allocateCroptypeCultivars(croptypes, "Resistant crop 2", "Resistant2")
simul_params <- setCroptypes(simul_params, croptypes)
## Allocate croptypes to landscape
rotation_sequence <- croptypes$croptypeID ## No rotation -> 1 rotation_sequence element
rotation_period <- 0 ## same croptypes every years
prop <- c(1 / 3, 1 / 3, 1 / 3) ## croptypes proportions
aggreg <- 10 ## aggregated landscape
simul_params <- allocateLandscapeCroptypes(simul_params, rotation_period = rotation_period,
rotation_sequence = rotation_sequence,
rotation_realloc = FALSE, prop = prop, aggreg = aggreg)
## list of outputs to be generated
simul_params <- setOutputs(simul_params, loadOutputs())
## Check simulation parameters
checkSimulParams(simul_params)
## Save deployment strategy into GPKG file
simul_params <- saveDeploymentStrategy(simul_params)
## Run simulation
runSimul(simul_params)

### Simulation of rust epidemics in a 1-km^2 patch cultivated with a susceptible wheat cultivar
seed=10
Nyears=5
disease="rust"
hostType="growingHost"
simul_params <- createSimulParams(outputDir = getwd())

## Seed and time parameters
simul_params <- setSeed(simul_params, seed)
simul_params <- setTime(simul_params, Nyears, nTSpY=120)

simul_params <- setPathogen(simul_params, loadPathogen(disease))
myLand <- Polygons(list(Polygon(matrix(c(0,0,1,1,0,1,1,0)*1000, nrow=4))), "ID1")
myLand <- SpatialPolygons(list(myLand))
simul_params <- setLandscape(simul_params, myLand)

## Simulation, pathogen, landscape and dispersal parameters
simul_params <- setInoculum(simul_params, 5e-4)
simul_params <- setDispersalPathogen(simul_params, c(1))

## Cultivars
simul_params <- setCultivars(simul_params, loadCultivar(name = "Susceptible", type = hostType))

```

```

## Croptypes
croptype <- data.frame(croptypeID = 0, croptypeName = c("Fully susceptible crop"), Susceptible = 1)
simul_params <- setCroptypes(simul_params, croptype)
simul_params <- allocateLandscapeCroptypes(simul_params,
rotation_period = 0, rotation_sequence = list(c(0)),
rotation_realloc = FALSE, prop = 1, aggreg = 1)

## list of outputs to be generated
outputlist <- loadOutputs(epid_outputs = "all", evol_outputs = "")
simul_params <- setOutputs(simul_params, outputlist)

## Check, save and run simulation
checkSimulParams(simul_params)
runSimul(simul_params, graphic = TRUE)

## End(Not run)

```

---

saveDeploymentStrategy

*Save landscape and deployment strategy*


---

## Description

Generates a GPKG file containing the landscape and all parameters of the deployment strategy

## Usage

```

saveDeploymentStrategy(
  params,
  outputGPKG = "landsepi_landscape.gpkg",
  overwrite = FALSE
)

```

## Arguments

params	a LandsepiParams Object.
outputGPKG	name of the GPKG output (default: "landsepi_landscape.gpkg") to be generated.
overwrite	a boolean specifying if existing files can be overwritten (TRUE) or not (FALSE, default).

## Details

The function generates a GPKG file in the simulation path. The GPKG file contains all input parameters needed to restore the landscape (sf object) and deployment strategy (croptypes, cultivars and genes).

**Value**

an updated LandsepiParams object.

**Examples**

```
## Not run:
## Initialisation
simul_params <- createSimulParams(outputDir = getwd())
## Time parameters
simul_params <- setTime(simul_params, Nyears = 10, nTSpY = 120)
## Landscape
simul_params <- setLandscape(simul_params, loadLandscape(1))
## Genes
gene1 <- loadGene(name = "MG 1", type = "majorGene")
gene2 <- loadGene(name = "MG 2", type = "majorGene")
genes <- data.frame(rbind(gene1, gene2), stringsAsFactors = FALSE)
simul_params <- setGenes(simul_params, genes)
## Cultivars
cultivar1 <- loadCultivar(name = "Susceptible", type = "growingHost")
cultivar2 <- loadCultivar(name = "Resistant1", type = "growingHost")
cultivar3 <- loadCultivar(name = "Resistant2", type = "growingHost")
cultivars <- data.frame(rbind(cultivar1, cultivar2, cultivar3), stringsAsFactors = FALSE)
simul_params <- setCultivars(simul_params, cultivars)
## Allocate genes to cultivars
simul_params <- allocateCultivarGenes(simul_params, "Resistant1", c("MG 1"))
simul_params <- allocateCultivarGenes(simul_params, "Resistant2", c("MG 2"))
## Allocate cultivars to croptypes
croptypes <- loadCroptypes(simul_params, names = c("Susceptible crop"
, "Resistant crop 1"
, "Resistant crop 2"))
croptypes <- allocateCroptypeCultivars(croptypes, "Susceptible crop", "Susceptible")
croptypes <- allocateCroptypeCultivars(croptypes, "Resistant crop 1", "Resistant1")
croptypes <- allocateCroptypeCultivars(croptypes, "Resistant crop 2", "Resistant2")
simul_params <- setCroptypes(simul_params, croptypes)
## Allocate croptypes to landscape
rotation_sequence <- croptypes$croptypeID ## No rotation -> 1 rotation_sequence element
rotation_period <- 0 ## same croptypes every years
prop <- c(1 / 3, 1 / 3, 1 / 3) ## croptypes proportions
aggreg <- 10 ## aggregated landscape
simul_params <- allocateLandscapeCroptypes(simul_params, rotation_period = rotation_period,
rotation_sequence = rotation_sequence,
rotation_realloc = FALSE, prop = prop, aggregr = aggregr)
## Save into a GPKG file
simul_params <- saveDeploymentStrategy(simul_params)

## End(Not run)
```

**Description**

Updates a LandsepiParams object with croptypes and their composition with regard to cultivar proportions

**Usage**

```
setCroptypes(params, dfCroptypes)
```

**Arguments**

params            a LandsepiParams Object.  
dfCroptypes       a data.frame containing cultivar proportions in each croptype (see details). It can be generated manually, or initialised with [loadCroptypes](#) and later updated with [allocateCroptypeCultivars](#).

**Details**

The data.frame for cultivar allocations into croptypes must take this format (example):

croptypeID	croptypeName	cultivarName1	cultivarName2	...
0	"cropt1"	1	0	...
1	"cropt2"	0.5	0.5	...

croptypeIDs must start at 0 and match with values from landscape "croptypeID" layer with feature year\_X. Cultivars names have to match cultivar names in the cultivars data.frame.

**Value**

a LandsepiParams object

**See Also**

[loadCroptypes](#)

**Examples**

```
## Not run:
simul_params <- createSimulParams()
cultivar1 <- loadCultivar(name = "Susceptible", type = "growingHost")
cultivar2 <- loadCultivar(name = "Resistant1", type = "growingHost")
cultivar3 <- loadCultivar(name = "Resistant2", type = "growingHost")
cultivars <- data.frame(rbind(cultivar1, cultivar2, cultivar3), stringsAsFactors = FALSE)
simul_params <- setCultivars(simul_params, cultivars)
croptypes <- loadCroptypes(simul_params, names = c("Susceptible crop", "Mixture"))
croptypes <- allocateCroptypeCultivars(croptypes, "Susceptible crop", "Susceptible")
croptypes <- allocateCroptypeCultivars(croptypes, "Mixture", c("Resistant1", "Resistant2"))
simul_params <- setCroptypes(simul_params, croptypes)
simul_params@Croptypes
```

```
## End(Not run)
```

---

setCultivars	<i>Set cultivars</i>
--------------	----------------------

---

### Description

Updates a LandsepiParams object with cultivars parameters

### Usage

```
setCultivars(params, dfCultivars)
```

### Arguments

params	a landsepiParams object.
dfCultivars	a data.frame defining the cultivars (see details). It can be generated manually or, alternatively, via <a href="#">loadCultivar</a> .

### Details

dfCultivars is a dataframe of parameters associated with each host genotype (i.e. cultivars, lines) when cultivated in pure crops. Columns of the dataframe are:

- cultivarName: cultivar names (cannot accept space),
- initial\_density: host densities (per square meter) at the beginning of the cropping season as if cultivated in pure crop,
- max\_density: maximum host densities (per square meter) at the end of the cropping season as if cultivated in pure crop,
- growth rate: host growth rates,
- reproduction rate: host reproduction rates,
- yield\_H: theoretical yield (in weight or volume units / ha / cropping season) associated with hosts in sanitary status H as if cultivated in pure crop,
- yield\_L: theoretical yield (in weight or volume units / ha / cropping season) associated with hosts in sanitary status L as if cultivated in pure crop,
- yield\_I: theoretical yield (in weight or volume units / ha / cropping season) associated with hosts in sanitary status I as if cultivated in pure crop,
- yield\_R: theoretical yield (in weight or volume units / ha / cropping season) associated with hosts in sanitary status R as if cultivated in pure crop,
- planting\_cost = planting costs (in monetary units / ha / cropping season) as if cultivated in pure crop,
- market\_value = market values of the production (in monetary units / weight or volume unit).

The data.frame must be defined as follow (example):

cultivarName	initial_density	max_density	growth_rate	reproduction_rate	yield_H	yield_L	yield_I	yield_R
Susceptible	0.1	2.0	0.1	0.0	2.5	0.0	0.0	0.0
Resistant1	0.1	2.0	0.1	0.0	2.5	0.0	0.0	0.0
Resistant2	0.1	2.0	0.1	0.0	2.5	0.0	0.0	0.0

**Value**

a LandsepiParams object

**See Also**

[loadCultivar](#)

**Examples**

```
## Not run:
simul_params <- createSimulParams()
cultivar1 <- loadCultivar(name = "Susceptible", type = "growingHost")
cultivar2 <- loadCultivar(name = "Resistant", type = "growingHost")
cultivars <- data.frame(rbind(cultivar1, cultivar2), stringsAsFactors = FALSE)
simul_params <- setCultivars(simul_params, cultivars)
simul_params@Cultivars

## End(Not run)
```

---

setDispersalHost	<i>Set host dispersal</i>
------------------	---------------------------

---

**Description**

Updates a LandsepiParams object with a host dispersal matrix.

**Usage**

```
setDispersalHost(params, mat)
```

**Arguments**

params	a LandsepiParams Object.
mat	a square matrix giving the probability of host dispersal from any field of the landscape to any other field. It can be generated manually, or, alternatively, via <a href="#">loadDispersalHost</a> . The size of the matrix must match the number of fields in the landscape.

**Details**

the dispersal matrix gives the probability for a host individual in a field *i* (row) to migrate to field *j* (column) through dispersal. If the host is a cultivated plant: seeds are harvested and do not disperse. Thus the dispersal matrix is the identity matrix.

**Value**

a LandsepiParam object.

**See Also**

[loadDispersalHost](#)

**Examples**

```
## Not run:
simul_params <- createSimulParams()
simul_params <- setLandscape(simul_params, loadLandscape(1))
d <- loadDispersalHost(simul_params)
simul_params <- setDispersalHost(simul_params, d)
simul_params@DispHost

## End(Not run)
```

---

setDispersalPathogen *Set pathogen dispersal*

---

**Description**

Updates a LandsepiParams object with a pathogen dispersal matrix.

**Usage**

```
setDispersalPathogen(params, mat_clonal, mat_sex = NULL)
```

**Arguments**

params	a LandsepiParams Object.
mat_clonal	a square matrix giving the probability of pathogen dispersal (clonal propagules) from any field of the landscape to any other field. It can be generated manually, or, alternatively, via <a href="#">loadDispersalPathogen</a> . The size of the matrix must match the number of fields in the landscape, and lines of the matrix may sum to 1 (reflecting boundaries) or be <1 (absorbing boundaries).
mat_sex	a square matrix giving the probability of pathogen dispersal (sexual propagules) from any field of the landscape to any other field (default identity matrix) . It can be generated manually, or, alternatively, via <a href="#">loadDispersalPathogen</a> . The size of the matrix must match the number of fields in the landscape, and lines of the matrix may sum to 1 (reflecting boundaries) or be <1 (absorbing boundaries).



## Details

See tutorial (vignettes) on how to use your own landscape and compute your own pathogen dispersal kernel. The dispersal matrix is a square matrix whose size is the number of fields in the landscape and whose elements are, for each line  $i$  and each column  $i'$  the probability that propagules migrate from field  $i$  to field  $i'$ . Lines of the matrix can be normalised to sum to 1 (reflective boundaries); otherwise propagules dispersing outside the landscape are lost (absorbing boundaries).

## Value

a LandsepiParam object.

## See Also

[loadDispersalPathogen](#)

## Examples

```
## Not run:
simul_params <- createSimulParams()
simul_params <- setLandscape(simul_params, loadLandscape(1))
d <- loadDispersalPathogen(1)
simul_params <- setDispersalPathogen(simul_params, d[[1]], d[[2]])
simul_params@DispPathoClonal

## End(Not run)
```

---

setGenes	<i>Set genes</i>
----------	------------------

---

## Description

Updates a LandsepiParams object with parameters associated with resistance genes and pathogen adaptation.

## Usage

```
setGenes(params, dfGenes)
```

## Arguments

params	a LandsepiParams object
dfGenes	a data.frame containing gene parameters. It can be defined manually, or, alternatively, with <a href="#">loadGene</a> .

## Details

dfGenes is a data.frame of parameters associated with each resistance gene and with the evolution of each corresponding pathogenicity gene. Columns of the dataframe are:

- geneName: names of resistance genes,
- target\_trait: aggressiveness components ("IR", "LAT", "IP", or "PR") targeted by resistance genes,
- efficiency: resistance gene efficiencies, i.e. the percentage of reduction of the targeted aggressiveness component (IR, 1/LAT, IP and PR),
- age\_of\_activ\_mean: expected delays to resistance activation (for APRs),
- age\_of\_activ\_var: variances of the delay to resistance activation (for APRs),
- mutation\_prob: mutation probabilities for pathogenicity genes (each of them corresponding to a resistance gene),
- Nlevels\_aggressiveness: 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),
- adaptation\_cost: fitness penalties paid by pathogen genotypes fully adapted to the considered resistance genes on host that do not carry these genes,
- tradeoff\_strength: strengths of the trade-off relationships between the level of aggressiveness on hosts that do and do not carry the resistance genes.
- recombination\_sd: standard deviation of the normal distribution used for recombination of quantitative traits during sexual reproduction (infinitesimal model)

The data.frame must be defined as follow (example):

geneName	efficiency	age_of_activ_mean	age_of_activ_var	mutation_prob	Nlevels_aggressiveness	adaptation_cos
MG1	1	0	0	1e-07	2	0.5
QTL1	0.5	0	0	0.0001	10	0.74

## Value

a LandsepiParams object.

## See Also

[loadGene](#)

## Examples

```
## Not run:
simul_params <- createSimulParams()
gene1 <- loadGene(name = "MG 1", type = "majorGene")
gene2 <- loadGene(name = "MG 2", type = "majorGene")
genes <- data.frame(rbind(gene1, gene2), stringsAsFactors = FALSE)
simul_params <- setGenes(simul_params, genes)
simul_params@Genes
```

```
## End(Not run)
```

---

setInoculum	<i>Set inoculum</i>
-------------	---------------------

---

### Description

Updates a LandsepiParams object with the initial probability for the first host (whose index is 0) to be infectious (i.e. state I) at the beginning of the simulation.

### Usage

```
setInoculum(params, val = 5e-04)
```

### Arguments

params	a LandsepiParams object.
val	a numeric value (default = 5e-4). Must be between 0 and 1.

### Value

a LandsepiParams object

### Examples

```
## Not run:  
simul_params <- createSimulParams()  
simul_params <- setInoculum(simul_params, 1E-3)  
simul_params@PI0  
  
## End(Not run)
```

---

setLandscape	<i>Set the landscape</i>
--------------	--------------------------

---

### Description

Updates a LandsepiParams object with a sp or sf object as landscape.

### Usage

```
setLandscape(params, land)
```

**Arguments**

params            a LandsepiParams Object.  
 land             a landscape as sp or sf object

**Details**

The landscape should be a sp or sf object. Built-in landscape are available using [loadLandscape](#). See our tutorial (vignettes) for details on how to use your own landscape. If the landscape contains only polygons, croptypes can be allocated later using [allocateLandscapeCroptypes](#). Otherwise the landscape has to contain a data.frame specifying for every year, the index of the croptype cultivated in each polygon. Each features has a field identified by "year\_XX" (XX <- seq(1:Nyears+1)) and containing the croptype ID.

Features/fields	year_1	year_2	... year_Nyears+1
polygons1	13	10	13
polygonsX	2	1	2

**Value**

a LandsepiParams object.

**See Also**

[loadLandscape](#)

**Examples**

```
## Not run:
simul_params <- createSimulParams()
simul_params <- setLandscape(simul_params, loadLandscape(1))
simul_params@Landscape

## End(Not run)
```

---

setOutputs

*Set outputs*

---

**Description**

Updates a LandsepiParams object with a list of output parameters.

**Usage**

```
setOutputs(params, output_list)
```

## Arguments

params	a LandsepiParams object.
output_list	a list of outputs to be generated and parameters for output generation. It can be generated manually or, alternatively, via <a href="#">loadOutputs</a> . This list is composed of: <ul style="list-style-type: none"> <li>• epid_outputs = epidemiological outputs to compute (see details)</li> <li>• evol_outputs = evolutionary outputs to compute (see details)</li> <li>• thres_breakdown = an integer (or vector of integers) giving the threshold (i.e. number of infections) above which a pathogen genotype is unlikely to go extinct, used to characterise the time to invasion of resistant hosts (several values are computed if several thresholds are given in a vector).</li> <li>• audpc100S = the audpc in a fully susceptible landscape (used as reference value for graphics).</li> </ul>

## Details

"epid\_outputs" is a character string (or a vector of character strings if several outputs are to be computed) specifying the type of epidemiological and economic outputs to generate:

- "audpc" : Area Under Disease Progress Curve (average number of diseased host individuals per time step and square meter)
- "audpc\_rel" : Relative Area Under Disease Progress Curve (average proportion of diseased host individuals relative to the total number of existing hosts)
- "gla" : Green Leaf Area (average number of healthy host individuals per square meter)
- "gla\_rel" : Relative Green Leaf Area (average proportion of healthy host individuals relative to the total number of existing hosts)
- "eco\_yield" : total crop yield (in weight or volume units per ha)
- "eco\_cost" : operational crop costs (in monetary units per ha)
- "eco\_product" : total crop products (in monetary units per ha)
- "eco\_margin" : Margin (products - costs, in monetary units per ha)
- "contrib": contribution of pathogen genotypes to LIR dynamics
- "HLIR\_dynamics", "H\_dynamics", "L\_dynamics", "IR\_dynamics", "HLI\_dynamics", etc.: Epidemic dynamics related to the specified sanitary status (H, L, I or R and all their combinations). Graphics only, works only if graphic=TRUE.
- "all" : compute all these outputs (default)
- "" : none of these outputs will be generated.

"evol\_outputs" is a character string (or a vector of character strings if several outputs are to be computed) specifying the type of evolutionary outputs to generate :

- "evol\_patho": Dynamics of pathogen genotype frequencies
- "evol\_aggr": Evolution of pathogen aggressiveness
- "durability": Durability of resistance genes
- "all": compute all these outputs (default)
- "" : none of these outputs will be generated.

**Value**

a LandsepiParams object.

**See Also**

[loadOutputs](#)

**Examples**

```
## Not run:
simul_params <- createSimulParams()
simul_params <- setOutputs(simul_params, loadOutputs())
simul_params@Outputs

## End(Not run)
```

---

setPathogen

*Set the pathogen*

---

**Description**

Updates a LandsepiParams object with pathogen parameters

**Usage**

```
setPathogen(params, patho_params)
```

**Arguments**

params	a LandsepiParams Object.
patho_params	a list of pathogen aggressiveness parameters on a susceptible host for a pathogen genotype not adapted to resistance: <ul style="list-style-type: none"> <li>infection_rate = maximal expected infection rate of a propagule on a healthy host,</li> <li>propagule_prod_rate = maximal expected effective propagule production rate of an infectious host per time step,</li> <li>latent_period_mean = minimal expected duration of the latent period,</li> <li>latent_period_var = variance of the latent period duration,</li> <li>infectious_period_mean = maximal expected duration of the infectious period,</li> <li>infectious_period_var = variance of the infectious period duration,</li> <li>survival_prob = probability for a propagule to survive the off-season,</li> <li>repro_sex_prob = probability for an infectious host to reproduce via sex rather than via cloning,</li> <li>sigmoid_kappa = kappa parameter of the sigmoid contamination function,</li> <li>sigmoid_sigma = sigma parameter of the sigmoid contamination function,</li> </ul>

- sigmoid\_plateau = plateau parameter of the sigmoid contamination function,
- sex\_propagule\_viability\_limit = maximum number of cropping seasons up to which a sexual propagule is viable
- sex\_propagule\_release\_mean = average number of seasons after which a sexual propagule is released.
- clonal\_propagule\_gradual\_release = whether or not clonal propagules surviving the bottleneck are gradually released along the following cropping season.

It can be generated manually, or, alternatively, via [loadPathogen](#).

### Details

a set of parameters representative of rust fungi, downy mildew or black sigatoka can be loaded via [loadPathogen](#).

### Value

a LandsepiParams object

### See Also

[loadPathogen](#)

### Examples

```
## Not run:
simul_params <- createSimulParams()
simul_params <- setPathogen(simul_params, loadPathogen())
simul_params@Pathogen

## End(Not run)
```

---

setReproSexProb

*Set the vector of probabilities of sexual reproduction*

---

### Description

set the probabilities for an infectious host to reproduce via sex rather than via cloning at every time step.

### Usage

```
setReproSexProb(params, vec)
```

**Arguments**

params            a LandsepiParams object  
 vec                a vector of size TimeParam\$nTSpY +1 (season end) with the probabilities for  
 an infectious host to reproduce via sex rather than via cloning at each time step.

**Value**

a LandsepiParams object updated

**Examples**

```
## Not run:
simul_params <- createSimulParams()
simul_params <- setTime(simul_params, Nyears=10, nTSpY=120)
repro_sex_probs <- c(rep(0.0, 120), 1.0)
simul_params <- setReproSexProb(simul_params, repro_sex_probs)
simul_params@ReproSexProb

## End(Not run)
```

---

 setSeed

*Set the seed*


---

**Description**

Updates a LandsepiParams object with a seed value for random number generator

**Usage**

```
setSeed(params, seed)
```

**Arguments**

params            a LandsepiParams Object.  
 seed              an integer used as seed value (for random number generator).

**Value**

a LandsepiParams object.

**Examples**

```
## Not run:
simul_params <- createSimulParams()
simul_params <- setSeed(simul_params, 100)
simul_params@Seed

## End(Not run)
```



---

setSeedValue	<i>setSeedValue</i>
--------------	---------------------

---

**Description**

Set RNG seed to seed value if not NULL, otherwise set it to timestamps value

**Usage**

```
setSeedValue(seed = NULL)
```

**Arguments**

seed                    an interger as seed value or NULL

**Details**

Sets seed for "Mersenne-Twister" algorithm using Inversion generation

**Value**

the new seed value for RNG

**Examples**

```
setSeedValue(seed = 10)
```

---

setTime	<i>Set time parameters</i>
---------	----------------------------

---

**Description**

Updates a LandsepiParams object with time parameters : Nyears and nTSpY

**Usage**

```
setTime(params, Nyears, nTSpY)
```

**Arguments**

params                    a LandsepiParams Object.  
 Nyears                    an integer giving the number of cropping seasons (e.g. years) to simulate.  
 nTSpY                    an integer giving the number of time steps per cropping season (e.g. days).

**Value**

a LandsepiParams object.

**Examples**

```
## Not run:
simul_params <- createSimulParams()
simul_params <- setTime(simul_params, Nyears=10, nTSpY=120)
simul_params@TimeParam

## End(Not run)
```

---

setTreatment	<i>Set chemical treatments</i>
--------------	--------------------------------

---

**Description**

Updates a LandsepiParams object with treatment parameters

**Usage**

```
setTreatment(params, treatment_params)
```

**Arguments**

params            a LandsepiParams Object.

treatment\_params

list of parameters related to pesticide treatments:

- treatment\_degradation\_rate = degradation rate (per time step) of chemical concentration,
- treatment\_efficiency = maximal efficiency of chemical treatments (i.e. fractional reduction of pathogen infection rate at the time of application),
- treatment\_timesteps = vector of time steps corresponding to treatment application dates,
- treatment\_cultivars = vector of indices of the cultivars that receive treatments,
- treatment\_cost = cost of a single treatment application (monetary units/ha)
- treatment\_application\_threshold = vector of thresholds (i.e. disease severity, one for each treated cultivar) above which the treatment is applied in a polygon.

**Details**

Chemical treatment is applied in a polygon only if disease severity (i.e.  $I/N$ ) in this polygon exceeds the threshold given by `treatment_application_threshold`. Treatment efficiency is maximum (i.e. equal to the parameter `treatment_efficiency`) at the time of treatment application (noted  $t^*$ ); then it decreases with time (i.e. natural pesticide degradation) and host growth (i.e. new biomass is not protected by treatments): protected by treatments): Efficiency of the treatment at time  $t$  after the application date is given by:  $efficiency(t) = treatment\_efficiency / (1 + exp(a - b * C(t)))$  with  $C(t) = C_1 * C_2$ :

- $C_1 = \exp(-\text{treatment\_degradation\_rate} * \Delta t)$  is the reduction of fungicide concentration due to time (e.g. natural degradation, volatilization, weathering), with  $\Delta t = t - t^*$  the timelag passed since the time of treatment application.
- $C_2 = \min(1, N(t^*)/N(t))$  is the reduction of fungicide concentration due to plant growth, since new plant tissue is not covered by fungicide.  $N(t^*)$  and  $N(t)$  being the number of host individuals a the time of treatment  $t^*$  and at time  $t$ , respectively.
- $a \in [3.5; 4.5]$  and  $b \in [8; 9]$  are shape parameters.

An empty list of treatments (i.e. absence of application) can be loaded using [loadPathogen](#).

### Value

a LandsepiParams object

### See Also

[loadTreatment](#)

### Examples

```
## Not run:
t <- loadTreatment()
simul_params <- setTreatment(simul_params, t)
simul_params@Treatment

## End(Not run)
```

---

show

*show*

---

### Description

Shows a LandsepiParams object.

### Usage

```
## S4 method for signature 'LandsepiParams'
show(object)
```

### Arguments

object            a LandsepiParams object

---

simul_landsepi	<i>Simulation with input parameters as data.frames.</i>
----------------	---

---

## Description

Stochastic, spatially-explicit, demo-genetic model simulating the spread and evolution of a pathogen in a heterogeneous landscape and generating a wide range of epidemiological, evolutionary and economic outputs.

## Usage

```
simul_landsepi(
  seed = 12345,
  time_param = list(Nyears = 5, nTSpY = 120),
  croptype_names = c("Susceptible crop"),
  croptypes_cultivars_prop = data.frame(croptypeID = 0, cultivarID = 0, proportion = 1),
  cultivars = data.frame(cultivarName = "Susceptible", initial_density = 0.1, max_density =
    2, growth_rate = 0.1, reproduction_rate = 0, yield_H = 2.5, yield_L = 0, yield_I =
    0, yield_R = 0, planting_cost = 225, market_value = 200),
  cultivars_genes_list = list(numeric(0)),
  genes = data.frame(geneName = character(0), mutation_prob = numeric(0), efficiency =
    numeric(0), tradeoff_strength = numeric(0), Nlevels_aggressiveness = numeric(0),
    adaptation_cost = numeric(0), age_of_activ_mean = numeric(0), age_of_activ_var =
    numeric(0), target_trait = character(0), recombination_sd = numeric(0)),
  landscape = NULL,
  area = 1e+06,
  rotation = data.frame(year_1 = c(0), year_2 = c(0), year_3 = c(0), year_4 = c(0),
    year_5 = c(0), year_6 = c(0)),
  basic_patho_param = list(name = "rust", survival_prob = 1e-04, repro_sex_prob = 0,
    infection_rate = 0.4, propagule_prod_rate = 3.125, latent_period_mean = 10,
    latent_period_var = 9, infectious_period_mean = 24, infectious_period_var = 105,
    sigmoid_kappa = 5.333, sigmoid_sigma = 3, sigmoid_plateau = 1,
    sex_propagule_viability_limit = 1, sex_propagule_release_mean = 1,
    clonal_propagule_gradual_release = 0),
  repro_sex_prob = rep(0, time_param$nTSpY + 1),
  disp_patho_clonal = c(1),
  disp_patho_sex = c(1),
  disp_host = c(1),
  treatment = list(treatment_degradation_rate = 0.1, treatment_efficiency = 0,
    treatment_timesteps = logical(0), treatment_cultivars = logical(0), treatment_cost =
    0, treatment_application_threshold = logical(0)),
  pI0 = 5e-04,
  epid_outputs = "all",
  evol_outputs = "all",
  thres_breakdown = 50000,
  audpc100S = 0.76,
  writeTXT = TRUE,
```

```

    graphic = TRUE,
    videoMP4 = FALSE,
    keepRawResults = FALSE
  )

```

## Arguments

- seed** an integer used as seed value (for random number generator).
- time\_param** a list of simulation parameters:
- Nyears = number cropping seasons,
  - nTSpY = number of time-steps per cropping season.
- croptype\_names** a vector of croptypes names.
- croptypes\_cultivars\_prop** a dataframe with three columns named 'croptypeID' for croptype index, 'cultivarID' for cultivar index and 'proportion' for the proportion of the cultivar within the croptype.
- cultivars** a dataframe of parameters associated with each host genotype (i.e. cultivars) when cultivated in pure crops. Columns of the dataframe are:
- cultivarName: cultivar names,
  - initial\_density: host densities (per square meter) at the beginning of the cropping season as if cultivated in pure crop,
  - max\_density: maximum host densities (per square meter) at the end of the cropping season as if cultivated in pure crop,
  - growth\_rate: host growth rates,
  - reproduction\_rate: host reproduction rates,
  - yield\_H: theoretical yield (in weight or volume units / ha / cropping season) associated with hosts in sanitary status H as if cultivated in pure crop,
  - yield\_L: theoretical yield (in weight or volume units / ha / cropping season) associated with hosts in sanitary status L as if cultivated in pure crop,
  - yield\_I: theoretical yield (in weight or volume units / ha / cropping season) associated with hosts in sanitary status I as if cultivated in pure crop,
  - yield\_R: theoretical yield (in weight or volume units / ha / cropping season) associated with hosts in sanitary status R as if cultivated in pure crop,
  - planting\_cost = planting costs (in monetary units / ha / cropping season) as if cultivated in pure crop,
  - market\_value = market values of the production (in monetary units / weight or volume unit).
- cultivars\_genes\_list** a list containing, for each host genotype, the indices of carried resistance genes.
- genes** a data.frame of parameters associated with each resistance gene and with the evolution of each corresponding pathogenicity gene. Columns of the dataframe are:
- geneName: names of resistance genes,
  - target\_trait: aggressiveness components (IR, LAT, IP, or PR) targeted by resistance genes,

- efficiency: resistance gene efficiencies (percentage of reduction of targeted aggressiveness components: IR, 1/LAT, IP and PR),
  - age\_of\_activ\_mean: expected delays to resistance activation (for APRs),
  - age\_of\_activ\_var: variances of the delay to resistance activation (for APRs),
  - mutation\_prob: mutation probabilities for pathogenicity genes (each of them corresponding to a resistance gene),
  - Nlevels\_aggressiveness: 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),
  - adaptation\_cost: fitness penalties paid by pathogen genotypes fully adapted to the considered resistance genes on host that do not carry the resistance genes,
  - tradeoff\_strength: strengths of the trade-off relationships between the level of aggressiveness on hosts that do and do not carry the resistance genes.
  - recombination\_sd: standard deviation of the normal distribution used for recombination of quantitative traits during sexual reproduction (infinitesimal model)
- landscape a sp object containing the landscape (required only if videoMP4=TRUE).
- area a vector containing polygon areas (must be in square meters).
- rotation a dataframe containing for each field (rows) and year (columns, named "year\_1", "year\_2", etc.), the index of the cultivated croptype. Importantly, the matrix must contain 1 more column than the real number of simulated years.
- basic\_patho\_param a list of i. pathogen aggressiveness parameters on a susceptible host for a pathogen genotype not adapted to resistance and ii. sexual reproduction parameters:
- infection\_rate = maximal expected infection rate of a propagule on a healthy host,
  - propagule\_prod\_rate = maximal expected effective propagule production rate of an infectious host per time step,
  - latent\_period\_mean = minimal expected duration of the latent period,
  - latent\_period\_var = variance of the latent period duration,
  - infectious\_period\_mean = maximal expected duration of the infectious period,
  - infectious\_period\_var = variance of the infectious period duration,
  - survival\_prob = probability for a propagule to survive the off-season,
  - repro\_sex\_prob = probability for an infectious host to reproduce via sex rather than via cloning,
  - sigmoid\_kappa = kappa parameter of the sigmoid contamination function,
  - sigmoid\_sigma = sigma parameter of the sigmoid contamination function,
  - sigmoid\_plateau = plateau parameter of the sigmoid contamination function,
  - sex\_propagule\_viability\_limit = maximum number of cropping seasons up to which a sexual propagule is viable

	<ul style="list-style-type: none"> <li>• <code>sex_propagule_release_mean</code> = average number of seasons after which a sexual propagule is released,</li> <li>• <code>clonal_propagule_gradual_release</code> = Whether or not clonal propagules surviving the bottleneck are gradually released along the following cropping season.</li> </ul>
<code>repro_sex_prob</code>	a vector of size <code>time_param\$nSTpY+1</code> giving the probability for an infectious host to reproduce via sex rather than via cloning for every time step,
<code>disp_patho_clonal</code>	a vectorized matrix giving the probability of pathogen dispersal from any field of the landscape to any other field.
<code>disp_patho_sex</code>	a vectorized matrix giving the probability of pathogen dispersal for sexual propagules from any field of the landscape to any other field.
<code>disp_host</code>	a vectorized matrix giving the probability of host dispersal from any field of the landscape to any other field
<code>treatment</code>	list of parameters related to pesticide treatments: <ul style="list-style-type: none"> <li>• <code>treatment_degradation_rate</code> = degradation rate (per time step) of chemical concentration,</li> <li>• <code>treatment_efficiency</code> = maximal efficiency of chemical treatments (i.e. fractional reduction of pathogen infection rate at the time of application),</li> <li>• <code>treatment_timesteps</code> = vector of time-steps corresponding to treatment application dates,</li> <li>• <code>treatment_cultivars</code> = vector of indices of the cultivars that receive treatments,</li> <li>• <code>treatment_cost</code> = cost of a single treatment application (monetary units/ha)</li> <li>• <code>treatment_application_threshold</code> = vector of thresholds (i.e. disease severity, one for each treated cultivar) above which the treatment is applied in a polygon</li> </ul>
<code>pI0</code>	initial probability for the first host (whose index is 0) to be infectious (i.e. state I) at the beginning of the simulation. Must be between 0 and 1.
<code>epid_outputs</code>	a character string (or a vector of character strings if several outputs are to be computed) specifying the type of epidemiological and economic outputs to generate (see details): <ul style="list-style-type: none"> <li>• <code>"audpc"</code> : Area Under Disease Progress Curve (average number of diseased host individuals per time step and square meter)</li> <li>• <code>"audpc_rel"</code> : Relative Area Under Disease Progress Curve (average proportion of diseased host individuals relative to the total number of existing hosts)</li> <li>• <code>"gla"</code> : Green Leaf Area (average number of healthy host individuals per time step and square meter)</li> <li>• <code>"gla_rel"</code> : Relative Green Leaf Area (average proportion of healthy host individuals relative to the total number of existing hosts)</li> <li>• <code>"eco_yield"</code> : total crop yield (in weight or volume units per ha)</li> <li>• <code>"eco_cost"</code> : operational crop costs (in monetary units per ha)</li> <li>• <code>"eco_product"</code> : total crop products (in monetary units per ha)</li> </ul>

	<ul style="list-style-type: none"> <li>• "eco_margin" : Margin (products - operational costs, in monetary units per ha)</li> <li>• "contrib": contribution of pathogen genotypes to LIR dynamics</li> <li>• "HLIR_dynamics", "H_dynamics", "L_dynamics", "IR_dynamics", "HLI_dynamics", etc.: Epidemic dynamics related to the specified sanitary status (H, L, I or R and all their combinations). Graphics only, works only if graphic=TRUE.</li> <li>• "all" : compute all these outputs (default)</li> <li>• "" : none of these outputs will be generated.</li> </ul>
evol_outputs	<p>a character string (or a vector of character strings if several outputs are to be computed) specifying the type of evolutionary outputs to generate :</p> <ul style="list-style-type: none"> <li>• "evol_patho": Dynamics of pathogen genotype frequencies</li> <li>• "evol_aggr": Evolution of pathogen aggressiveness</li> <li>• "durability": Durability of resistance genes</li> <li>• "all": compute all these outputs (default)</li> <li>• "": none of these outputs will be generated.</li> </ul>
thres_breakdown	<p>an integer (or vector of integers) giving the threshold (i.e. number of infections) above which a pathogen genotype is unlikely to go extinct, used to characterise the time to invasion of resistant hosts (several values are computed if several thresholds are given in a vector).</p>
audpc100S	<p>the audpc in a fully susceptible landscape (used as reference value for graphics).</p>
writeTXT	<p>a logical indicating if outputs must be written in text files (TRUE, default) or not (FALSE).</p>
graphic	<p>a logical indicating if graphics must be generated (TRUE, default) or not (FALSE).</p>
videoMP4	<p>a logical indicating if a video must be generated (TRUE) or not (FALSE, default). Works only if graphic=TRUE and epid_outputs="audpc_rel" (or epid_outputs="all").</p>
keepRawResults	<p>a logical indicating if binary files must be kept after the end of the simulation (default=FALSE). Careful, many files may be generated if keepRawResults=TRUE.</p>

## Details

See ?landsepi for details on the model and assumptions. Briefly, the model is stochastic, spatially explicit (the basic spatial unit is an individual field), based on a SEIR ('susceptible-exposed-infectious-removed', renamed HLIR for 'healthy-latent-infectious-removed' to avoid confusions with 'susceptible host') structure with a discrete time step. It simulates the spread and evolution (via mutation, recombination through sexual reproduction, selection and drift) of a pathogen in a heterogeneous cropping landscape, across cropping seasons split by host harvests which impose potential bottlenecks to the pathogen. A wide array of resistance deployment strategies (possibly including chemical treatments) can be simulated and evaluated using several possible outputs to assess the epidemiological, evolutionary and economic performance of deployment strategies (See ?epid\_output and ?evol\_output for details).



**Value**

A list containing all outputs that have been required via "epid\_outputs" and "evol\_outputs". A set of text files, graphics and a video showing epidemic dynamics can be generated. If keepRawResults=TRUE, a set of binary files is generated for every year of simulation and every compartment:

- H: healthy hosts,
- Hjuv: juvenile healthy hosts (for host reproduction),
- L: latently infected hosts,
- I: infectious hosts,
- R: removed hosts,
- P: propagules.

Each file indicates for every time-step the number of individuals in each field, and when appropriate for each host and pathogen genotype. Additionally, a binary file called TFI is generated and gives the Treatment Frequency Indicator (expressed as the number of treatment applications per polygon).

**References**

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 Computational Biology* 14(4):e1006067.

**See Also**

[model\\_landsepi](#), [epid\\_output](#), [evol\\_output](#), [video](#), [runSimul](#)

**Examples**

```
## Not run:
#### Spatially-implicit simulation with a single 1-km^2 patch 100% cultivated
# with a susceptible cultivar

simul_landsepi()

#### Spatially-implicit simulation with 2 patches (S + R) during 3 years ####

## Simulation parameters
time_param <- list(Nyears = 3, nTSpY = 120)
area <- c(100000, 100000)
rotation <- data.frame(year_1 = c(0, 1), year_2 = c(0, 1), year_3 = c(0, 1), year_4 = c(0, 1))
croptype_names <- c("Susceptible crop", "Resistant crop")
croptypes_cultivars_prop <- data.frame(
  croptypeID = c(0, 1),
  cultivarID = c(0, 1),
  proportion = c(1, 1)
)
cultivars <- rbind(
  loadCultivar(name = "Susceptible", type = "growingHost"),
  loadCultivar(name = "Resistant", type = "growingHost")
)
```

```

genes <- loadGene(name = "MG", type = "majorGene")
cultivars_genes_list <- list(numeric(0), 0)

## Run simulation
simul_landsepi(
  seed = 12345, time_param, croptype_names, croptypes_cultivars_prop, cultivars,
  cultivars_genes_list, genes, landscape = NULL, area, rotation,
  basic_patho_param = loadPathogen(disease = "rust"),
  repro_sex_prob = rep(0, time_param$nTSpY+1),
  disp_patho_clonal = c(0.99, 0.01, 0.01, 0.99),
  disp_patho_sex = c(0.99, 0.01, 0.01, 0.99),
  disp_host = c(1, 0, 0, 1),
  pI0 = 5e-4
)

#### Spatially-explicit simulation with built-in landscape during 10 years ####
# Generate a mosaic of four croptypes in balanced proportions
# and medium level of spatial aggregation

## Simulation and Landscape parameters
Nyears <- 10
landscape <- loadLandscape(1)
Npoly <- length(landscape)
library(sf)
area <- st_area(st_as_sf(landscape))
rotation <- AgriLand(landscape, Nyears,
  rotation_period = 1, rotation_realloc = FALSE,
  rotation_sequence = c(0, 1, 2, 3),
  prop = rep(1 / 4, 4), aggreg = 0.5, graphic = TRUE, outputDir = getwd())
)
rotation <- data.frame(rotation)[, 1:(Nyears + 1)]
croptype_names <- c("Susceptible crop"
, "Resistant crop 1"
, "Resistant crop 2"
, "Resistant crop 3")
croptypes_cultivars_prop <- data.frame(croptypeID = c(0, 1, 2, 3), cultivarID = c(0, 1, 2, 3),
  proportion = c(1, 1, 1, 1))
cultivars <- data.frame(rbind(
  loadCultivar(name = "Susceptible", type = "growingHost"),
  loadCultivar(name = "Resistant1", type = "growingHost"),
  loadCultivar(name = "Resistant2", type = "growingHost"),
  loadCultivar(name = "Resistant3", type = "growingHost")
), stringsAsFactors = FALSE)
genes <- data.frame(rbind(
  loadGene(name = "MG 1", type = "majorGene"),
  loadGene(name = "MG 2", type = "majorGene"),
  loadGene(name = "MG 3", type = "majorGene")
), stringsAsFactors = FALSE)
cultivars_genes_list <- list(numeric(0), 0, 1, 2)

## Run simulation
simul_landsepi(

```

```

seed = 12345, time_param = list(Nyears = Nyears, nTSpY = 120),
croptype_names, croptypes_cultivars_prop, cultivars,
cultivars_genes_list, genes, landscape, area, rotation,
basic_patho_param = loadPathogen(disease = "rust"),
repro_sex_prob = rep(0, 120+1),
disp_patho_clonal = loadDispersalPathogen(1)[[1]],
disp_patho_sex = as.numeric(diag(Npoly)),
disp_host = as.numeric(diag(Npoly)),
pI0 = 5e-4
)

## End(Not run)

```

---

summary

*summary*


---

### Description

Prints the summary of a LandsepiParams object.

### Usage

```
## S4 method for signature 'LandsepiParams'
summary(object)
```

### Arguments

object            a LandsepiParams object.

---

switch_patho_to_aggr	<i>Switch from index of genotype to indices of aggressiveness on different components</i>
----------------------	---

---

### Description

Finds the level of aggressiveness on different components (targeted by different resistance genes) from the index of a given pathogen genotype

### Usage

```
switch_patho_to_aggr(index_patho, Ngenes, Nlevels_aggressiveness)
```

### Arguments

index_patho	index of pathogen genotype
Ngenes	number of resistance genes
Nlevels_aggressiveness	vector of the number of adaptation levels related to each resistance gene

**Value**

a vector containing the indices of aggressiveness on the different components targeted by the resistance genes

**Examples**

```
switch_patho_to_aggr(5, 3, c(2, 2, 3))
```

---

 video

*Generation of a video*


---

**Description**

Generates a video showing the epidemic dynamics on a map representing the cropping landscape. (requires ffmpeg library).

**Usage**

```
video(
  audpc,
  time_param,
  Npatho,
  landscape,
  area,
  rotation,
  croptypes,
  croptype_names = c(),
  cultivars_param,
  keyDates = NULL,
  nMapPY = 10,
  path = getwd()
)
```

**Arguments**

audpc	A dataframe containing audpc outputs (generated through epid_output). 1 line per year and 1 column per cultivar, with an additional column for the average audpc in the landscape.
time_param	list of simulation parameters: <ul style="list-style-type: none"> <li>• Nyears = number cropping seasons,</li> <li>• nTSpY = number of time-steps per cropping season.</li> </ul>
Npatho	number of pathogen genotypes.
landscape	a sp object containing the landscape.
area	a vector containing polygon areas (must be in square meters).

rotation	a dataframe containing for each field (rows) and year (columns, named "year_1", "year_2", etc.), the index of the cultivated croptype. Importantly, the matrix must contain 1 more column than the real number of simulated years.
croptypes	a dataframe with three columns named 'croptypeID' for croptype index, 'cultivarID' for cultivar index and 'proportion' for the proportion of the cultivar within the croptype.
croptype_names	a vector of croptype names (for legend).
cultivars_param	a list of parameters associated with each host genotype (i.e. cultivars) when cultivated in pure crops: <ul style="list-style-type: none"> <li>• name = vector of cultivar names,</li> <li>• max_density = vector of maximum host densities (per square meter) at the end of the cropping season as if cultivated in pure crops,</li> <li>• cultivars_genes_list = a list containing, for each host genotype, the indices of carried resistance genes.</li> </ul>
keyDates	a vector of times (in time steps) where to draw vertical lines in the AUDPC graphic. Usually used to delimit durabilities of the resistance genes. No line is drawn if keyDates=NULL (default).
nMapPY	an integer specifying the number of epidemic maps per year to generate.
path	path where binary files are located and where the video will be generated.

### Details

The left panel shows the year-after-year dynamics of AUDPC, for each cultivar as well as the global average. The right panel illustrates the landscape, where fields are hatched depending on the cultivated croptype, and coloured depending on the prevalence of the disease. Note that up to 9 different croptypes can be represented properly in the right panel.

### Value

A video file of format webM

### Examples

```
## Not run:
demo_landsepi()

## End(Not run)
```

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