

# Package ‘PopIn’

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**Type** Package

**Title** impact of linear Infrastructures on Populations

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**Description** Includes functions to compute dispersal variance, population growth rate in favorable habitats, the maximum linear infrastructure density and the minimum size of a habitat patch delimited by linear infrastructures beyond which populations cannot persist, a spatially-implicit stochastic age-structured model and a spatially-explicit individual-based model of population dynamics.

This package can be used to assess the impact of linear infrastructures in general - such as roads, railways, wind farms, power lines, water channels -, on populations, although the functions and models included were initially developed for studying the impact of roads.

**License** GPL (>= 2)

**LinkingTo** Rcpp

**Imports** Rcpp, plyr

**RoxygenNote** 6.0.1

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** yes

**Encoding** UTF-8

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agemodel	<i>A spatially-implicit, age-structured, stochastic model to evaluate the impact of direct mortality caused by infrastructures on populations and their risk of extinction</i>
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## Description

Simulates the time evolution of a population with and without infrastructure driven mortality, enabling its study under different infrastructure mortality rates and carrying capacities, including its probability of extinction, and taking into account the specificities of the life history of the species. See "Details"

## Usage

```
agemodel(n.rep, param = "", file = "")
```

## Arguments

n.rep	The number of replicates to be run
param	<p>A list with the model parameter values. See also "examples". The parameters are the following:</p> <ol style="list-style-type: none"> <li>1. years: the total number of years for which the simulation runs</li> <li>2. transient1: number of years; ensures that the age classes stabilize</li> <li>3. transient2: number of years; this period is used to estimate the average population size without infrastructure mortality (which is applied after transient2)</li> <li>4. transient3: number of years; ensures that the population "stabilizes" after infrastructure driven mortality starts being applied; only if the population survives until the end of transient3 then information is collected</li> <li>5. a: parameter of the Beverton-Holt relationship; used when n.rep = 1</li> <li>6. b: parameter of the Beverton-Holt relationship; used when n.rep = 1</li> <li>7. a.val: the values that "a" will take; this parameter is used when n.rep &gt; 1</li> <li>8. f.mort: the fraction of the population killed by infrastructures per year; this parameter is used when n.rep = 1</li> <li>9. f.values: the values that the fraction of the population killed by infrastructures per year takes; this parameter is used when n.rep &gt; 1</li> <li>10. n.ages: the number of age classes, i.e., the maximum number of years an individual can live</li> <li>11. min.age: the age at maturity, that is, the minimum age at which an animal can reproduce (in months)</li> <li>12. repr.period: the reproduction interval for a female (in months)</li> <li>13. months.of.recruitment: the months where animals reproduce</li> <li>14. prob.recr.month.m: in those months where the population can reproduce, the mean proportion that reproduces (logit scale)</li> <li>15. prob.recr.month.sd: in those months where the population can reproduce, the standard deviation of the proportion that reproduces (logit scale)</li> <li>16. prop.recr.age.m: the mean proportion per age that reproduces (linear scale)</li> <li>17. prop.recr.age.sd: the standard deviation of the proportion per age that reproduces (linear scale)</li> </ol>

	18. clutch.size.m: the mean number of eggs per clutch (mean litter size; mean number of offspring)
	19. clutch.size.sd: the standard deviation of the number of eggs per clutch
	20. jsmm: the mean of juvenile survival rate for males
	21. jssdm: the standard deviation of juvenile survival rate for males
	22. jsmf: the mean of juvenile survival rate for females
	23. jssdf: the standard deviation of juvenile survival rate for females
	24. ysmm: the mean of yearling survival rate for males
	25. yssdm: the standard deviation of yearling survival rate for males
	26. ysmf: the mean of yearling survival rate for females
	27. yssdf: the standard deviation of yearling survival rate for females
	28. asmm: the mean of adult survival rate for males
	29. assdm: the standard deviation of adult survival rate for males
	30. asmf: the mean of adult survival rate for females
	31. assdf: the standard deviation of adult survival rate for females
	32. plotTF: draws plots with results if set to TRUE
	33. writeTF: creates a directory containing files with results if set to TRUE
	34. dirname.basic: the name of the directory where the files with results are stored when writeTF = TRUE and when n.rep = 1
	35. dirname.rep: the name of the directory where the files with results are stored when writeTF = TRUE and n.rep > 1
file	A file with the model parameter values. See above and default file provided with the package (pam.txt)

## Details

The function takes as inputs the number of replicates (n.rep) and a list or a file with the remaining parameter values. If both a list and a file are given, an error message is returned. The package provides default parameter values using a file ("pam.txt").

Density dependence is introduced between the number of recruits and the number of eggs, thus the values of parameters a and b (Beverton-Holt relationship) should be chosen so that the number of recruits is always smaller than the number of eggs (i.e., a is smaller than or equal to b).

## Value

The function return the names of and the values used for the parameters. See "arguments" for the description of each parameter and "examples". When plotTF = T, plots are created; when writeTF = T, a directory is created which includes files with results (see below).

WHEN plotTF = T, FOUR PLOTS ARE CREATED:

1. When n.rep = 1

1.1. Plots 1 and 2: Time evolution of the simulated number of individuals during the years that the simulation runs, in January, and in December.

1.2. Plot 3: Number of individuals killed by infrastructures per year from the time when such mortality is applied until the end of the simulation.

1.3. Plots 4 and 5: Histogram of the logarithm of the simulated number of individuals killed per year during the infrastructure driven mortality regime, and a plot with the same data in double logarithmic scales.

2. When n.rep > 1

# the plots show the results of the simulations for different values of a.val, and several values of f.values:

- 2.1. Plot a: Number of animals at the first month of recruitment.
- 2.2. Plot b: Number of animals killed per year.
- 2.3. Plot c: Probability of extinction.
- 2.4. Plot d: Time to extinction (years).

WHEN writeTF = T, A DIRECTORY IS CREATED WHICH INCLUDES THE FILES:

1. When n.rep = 1

1.1. pop\_size\_jan: the time evolution of the simulated number of individuals in the population for the month of January, during the years that the simulation runs. The first column corresponds to the years and the second column corresponds to the number of individuals in the population in January, in each of the years.

1.2. pop\_size\_dec: the time evolution of the simulated number of individuals in the population for the month of December, during the years that the simulation runs. The first column corresponds to the years and the second column corresponds to the number of individuals in the population in December, in each of the years.

1.3. n\_killed: the number of individuals killed by infrastructures per year from the time when such mortality is applied until the end of the simulation. The first column corresponds to the years and the second column corresponds to the number of individuals killed by infrastructures in each year.

2. When n.rep > 1

2.1. a\_values: values taken by a

2.2. f\_values: values taken by the fraction of the population to be killed by infrastructures per year

2.3. population size before infrastructure mortality is applied (after the age classes have stabilized), for each value of a.val, averaged across replicates and f.values:

2.3.1. before recruitment (January):

2.3.1.1. n\_annual\_median: median population size

2.3.1.2. n\_annual\_sd: standard deviation of the population size

2.3.1.3. n\_annual\_mean: mean population size

2.3.1.4. n\_annual\_max: maximum population size

2.3.1.5. n\_annual\_min: minimum population size

2.3.2. after recruitment (December):

2.3.2.1. n\_annual\_recr\_median: median population size

2.3.2.2. n\_annual\_recr\_sd: standard deviation of the population size

2.3.2.3. n\_annual\_recr\_mean: mean population size

2.3.2.4. n\_annual\_recr\_max: maximum population size

2.3.2.5. n\_annual\_recr\_min: minimum population size

2.4. absolute maximum and minimum population size before infrastructure mortality is applied (after the age classes have stabilized), for each value of a.val:

2.4.1. before recruitment (January):

2.4.1.1. n\_annual\_max\_max: absolute maximum population size

2.4.1.2. n\_annual\_min\_min: absolute minimum population size

2.4.2. after recruitment (December):

- 2.4.2.1. n\_annual\_recr\_max\_max: absolute maximum population size
- 2.4.2.2. n\_annual\_recr\_min\_min: absolute minimum population size
- 2.5. population size after infrastructure mortality is applied, for the populations that persisted to the end of the simulation, for each combination of values of (a.val, f.values), averaged across replicates:
  - 2.5.1. before recruitment (January):
    - 2.5.1.1. n\_annual\_m\_median: median population size
    - 2.5.1.2. n\_annual\_m\_sd: standard deviation of the population size
    - 2.5.1.3. n\_annual\_m\_mean: mean population size
    - 2.5.1.4. n\_annual\_m\_max: maximum population size
    - 2.5.1.5. n\_annual\_m\_min: minimum population size
  - 2.5.2. after recruitment (December):
    - 2.5.2.1. n\_annual\_recr\_m\_median: median population size
    - 2.5.2.2. n\_annual\_recr\_m\_sd: standard deviation of the population size
    - 2.5.2.3. n\_annual\_recr\_m\_mean: mean population size
    - 2.5.2.4. n\_annual\_recr\_m\_max: maximum population size
    - 2.5.2.5. n\_annual\_recr\_m\_min: minimum population size
- 2.6. absolute maximum and minimum population size after infrastructure mortality is applied, for the populations that persisted to the end of the simulation, for each combination of values of (a.val, f.values):
  - 2.6.1. before recruitment (January):
    - 2.6.1.1. n\_annual\_m\_max\_max: absolute maximum population size
    - 2.6.1.2. n\_annual\_m\_min\_min: absolute minimum population size
  - 2.6.2. after recruitment (December):
    - 2.6.2.1. n\_annual\_recr\_m\_max\_max: maximum population size
    - 2.6.2.2. n\_annual\_recr\_m\_min\_min: minimum population size
- 2.7. number of individuals killed by infrastructures for the populations that persisted to the end of the simulation, for each combination of values of (a.val, f.values), averaged across replicates:
  - 2.7.1. n\_killed\_median: median number of individuals killed by infrastructures
  - 2.7.2. n\_killed\_sd: standard deviation
  - 2.7.3. n\_killed\_mean: mean
  - 2.7.4. n\_killed\_max: maximum
  - 2.7.5. n\_killed\_min: minimum
- 2.8. absolute maximum and minimum number of individuals killed by infrastructures for the populations that persisted to the end of the simulation, for each combination of values of (a.val, f.values):
  - 2.8.1. n\_killed\_max\_max: absolute maximum
  - 2.8.2. n\_killed\_min\_min: absolute minimum
- 2.9. f\_mort\_12: fraction of the population killed by infrastructures in December for the different combinations of values of (a.val, f.values)
- 2.10. results for the populations that went extinct, for the different combinations of values of (a.val, f.values)
  - 2.10.1. prob\_ext: probability of population extinction

- 2.10.2. mean\_t: mean time to extinction
- 2.10.3. median\_t: median time to extinction
- 2.10.4. sd\_t: standard deviation of the time to extinction
- 2.10.5. max\_t: maximum time to extinction
- 2.10.6. min\_t: minimum time to extinction

### Author(s)

Ana Ceia-Hasse, Luís Borda-de-Água, Henrique M. Pereira

### References

Borda-de-Água L, Grilo C, Pereira HM. 2014. Ecological Modelling 276: 29-37

### Examples

```
# Run agemodel with default parameter values:
# uses default file provided with the package

agemodel(1,,) # agemodel(n.rep = 1, param = "", file = "")

agemodel(2,,) # agemodel(n.rep = 2, param = "", file = "")

# Use with your own parameter values, e.g.:
# agemodel(n.rep = 1, param = mylist_1rep)
# agemodel(n.rep = 2, param = mylist_2rep)

# mylist_1rep = list(
#   years = 320, transient1 = 120, transient2 = 100, transient3 = 50,
#   f.mort = 0.05, a = 5, b = 5,
#   n.ages = 17, min.age = 37, repr.period = 18,
#   months.of.recruitment = c("May", "June", "July", "August"),
#   prob.recr.month.m = c(100,100,100,100,100,100,100,100,100,100,100,100),
#   prob.recr.month.sd = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0),
#   prop.recr.age.m = rep(1, 17), prop.recr.age.sd = rep(0, 17),
#   clutch.size.m = 2.3, clutch.size.sd = 1,
#   jsdm = 0.86, jssdm = 0.09, jsfm = 0.86, jssdf = 0.06,
#   ysdm = 0.62, yssdm = 0.06, ysfm = 0.62, yssdf = 0.06,
#   asdm = 0.47, assdm = 0.05, asfm = 0.47, assdf = 0.05,
#   plotTF = T, writeTF = T, dirname.basic = "agemodel_1rep")

# mylist_2rep = list(
#   years = 320, transient1 = 120, transient2 = 100, transient3 = 50,
#   f.values = seq(0.1, 0.9, 0.1), a.val = seq(1, 5, 1),
#   n.ages = 17, min.age = 37, repr.period = 18,
#   months.of.recruitment = c("May", "June", "July", "August"),
#   prob.recr.month.m = c(100,100,100,100,100,100,100,100,100,100,100,100),
#   prob.recr.month.sd = c(0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0),
#   prop.recr.age.m = rep(1, 17), prop.recr.age.sd = rep(0, 17),
#   clutch.size.m = 2.3, clutch.size.sd = 1,
#   jsdm = 0.86, jssdm = 0.09, jsfm = 0.86, jssdf = 0.06,
#   ysdm = 0.62, yssdm = 0.06, ysfm = 0.62, yssdf = 0.06,
#   asdm = 0.47, assdm = 0.05, asfm = 0.47, assdf = 0.05,
#   plotTF = T, writeTF = T, dirname.rep = "agemodel_2rep")
```

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indmodel	<i>Simulate source-sink population dynamics using a spatially-explicit individual-based model</i>
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---

## Description

Simulates population dynamics in landscapes with different types of habitat that have different habitat qualities (sources and sinks), including landscapes fragmented by linear infrastructures, using a spatially-explicit individual-based model that keeps track of the features of the landscape and of the population

## Usage

```
indmodel(land_r = "", param = "", file = "")
```

## Arguments

land_r	A matrix that corresponds to the landscape
param	<p>A list with the model parameter values. See also "examples". The parameters are the following:</p> <ol style="list-style-type: none"> <li>1. n_rep: the number of replicates to be run</li> <li>2. hab_aff: the affinity of the species for each type of habitat in the landscape, in increasing order; e.g., if there are two types of habitat in the landscape matrix, "0" and "1" (corresponding to lower and higher quality habitats, respectively), and the affinity is 0.1 for the lower quality habitat ("0") and 0.9 for the higher quality habitat ("1"), then hab_aff = c(0.1, 0.9)</li> <li>3. n_steps: the number of steps in the simulation</li> <li>4. init_population: the population size at the start of the simulation</li> <li>5. hr_size: the size (number of cells) of the home range</li> <li>6. birth_rate: the maximum number of female juveniles produced by a breeding female (maximum fecundity)</li> <li>7. breeding_age: the age at which individuals start breeding</li> <li>8. survival: the probability of survival</li> <li>9. distance_weight: a higher distance weight corresponds to a higher contribution of cells closer to the home range centroid (thus the optimal home range shape is as close to a circle as possible)</li> <li>10. dispersal_distance: the distance (number of cells) that an individual has to disperse in order to settle a home range</li> <li>11. dispersal_mode: the dispersal mode; case 0: global dispersal; case 1: local dispersal, habitat search in a local kernel; case 2: local dispersal, random walk</li> <li>12. sink_avoidance: the probability that an individual avoids dispersing through cells that correspond to sink habitat</li> <li>13. neigh_avoidance: the probability that an individual avoids dispersing through cells that are already occupied</li> <li>14. sink_mortality: the probability that an individual dies while dispersing through cells that correspond to sink habitat</li> <li>15. plotYN: draws plots with results if set to TRUE</li> <li>16. writeYN: creates a directory containing files with results if set to TRUE</li> </ol>

	17. <code>dir_name</code> : the name of the directory where files storing the results are saved
	18. <code>file_name</code> : the name of the file that will store, for each replicate: the values of the parameters, the landscape used, and for each time step: the position of each individual in the landscape ( <code>hrmaphist</code> ), the age of each individual ( <code>ageshist</code> ), and the population size ( <code>popsiz</code> )
<code>file</code>	A file with the model parameter values. See above and default file provided with the package ( <code>pim.txt</code> )

## Details

The function provides a default landscape and default parameter values using a file ("`pim.txt`"). It can read a list or a file with the parameter values, but if both a list and a file are given, an error message is returned.

## Value

<code>\$popsiz_av_end</code>	The population size (number of individuals) at the end of the simulation, averaged across all replicates
<code>\$prob_ext</code>	The probability of population extinction (the number of populations that went extinct divided by the total number of replicates)
<code>\$prob_persist</code>	The probability of population persistence (the number of populations that persisted divided by the total number of replicates (or <code>1-prob_ext</code> ))
<code>\$time_ext_av</code>	The average time to extinction (number of time steps it took for a population to go extinct, averaged across the replicates in which populations went extinct)
<code>\$popsizematrix</code>	A matrix with the population size at each time step of the simulation (columns), for each replicate (lines)
<code>\$popsiz_av_time_step</code>	The population size (number of individuals) at each time step of the simulation, averaged across all replicates

When `plotYN = T`, a plot is created showing the population size at each time step, averaged across all replicates.

## Author(s)

Ana Ceia-Hasse, Luís Borda-de-Água, Henrique M. Pereira

## Examples

```
# Run indmodel with default parameter values:

indmodel() # indmodel(land_r = "", param = "", file = "")
# uses default landscape and default file with parameter values

# Use with your own landscape and/or parameter values, e.g.:
# indmodel(param = list(
#   n_rep = 2, hab_aff = c(0.0, 1.0), n_steps = 200, init_population = 10,
#   hr_size = 1, birth_rate = 2.0, breeding_age = 1, survival = 0.4,
#   distance_weight = 0.001, dispersal_distance = 5.0, dispersal_mode = 2,
#   sink_avoidance = 0.1, neigh_avoidance = 1.0, sink_mortality = 0.9,
#   plotYN = "TRUE", writeYN = "TRUE",
#   dir_name = "Res_mylist", file_name = "indmodel_rep"))
```



---

`mlid`*Calculate maximum linear infrastructure density*

---

**Description**

Calculates the maximum linear infrastructure density above which a population cannot persist

**Usage**

```
mlid(r1 = 0.4631507, r0 = -(1/16)*10^3, li.width = 0.01)
```

**Arguments**

<code>r1</code>	rate of population growth in favourable habitats
<code>r0</code>	rate of population decay in unfavourable habitats
<code>li.width</code>	the width of the linear infrastructure (km)

**Details**

`r0` corresponds to the rate of population decay due to direct mortality occurring when individuals cross the linear infrastructure (e.g., roadkills due to wildlife-vehicle collisions)

**Value**

<code>Dmax</code>	The maximum linear infrastructure density above which a population cannot persist
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**Author(s)**

Ana Ceia-Hasse, Luís Borda-de-Água, Henrique M. Pereira

**References**

Borda-de-Água L, Navarro L, Gavinhos C, Pereira HM. 2011. Landscape Ecology 26: 253-265.  
Ceia-Hasse A, Borda-de-Água L, Grilo C, Pereira HM. 2017. Global Ecology and Biogeography 26: 592-600.

**Examples**

```
# Run mlid with default parameter values:  
  
mlid()  
# mlid(r1 = 0.4631507, r0 = -(1/16)*10^3, li.width = 0.01)  
# Dmax = 0.7355901 km/km2  
# r1 and r0 values for Puma concolor
```

mps

*Calculate minimum patch size***Description**

Calculates the minimum patch size below which a population cannot persist

**Usage**

```
mps(r1 = 0.4631507, sigma2 = 285.6852, alpha = 1)
```

**Arguments**

r1	rate of population growth in favourable habitat patches
sigma2	dispersal variance (of the dispersal distance of an individual)
alpha	ratio of the largest to the smallest side of a rectangular habitat patch (in the case of a square, alpha = 1)

**Details**

Calculates the minimum size of a favourable habitat patch delimited by linear infrastructures such that the population size remains constant or increases

**Value**

Lmin	The minimum size of the smallest side of a rectangular patch (i.e., the smallest distance between linear infrastructures) below which a population cannot persist
Amin	The minimum area of a patch below which a population cannot persist

**Author(s)**

Ana Ceia-Hasse, Luís Borda-de-Água, Henrique M. Pereira

**References**

Borda-de-Água L, Navarro L, Gavinhos C, Pereira HM. 2011. Landscape Ecology 26: 253-265.  
 Ceia-Hasse A, Borda-de-Água L, Grilo C, Pereira HM. 2017. Global Ecology and Biogeography 26: 592-600.

**Examples**

```
# Run mps with default parameter values:

mps()
# mps(r1 = 0.4631507, sigma2 = 285.6852, alpha = 1)
# Lmin = 78.02479 km
# Amin = 6087.867 km2
# r1 and sigma2 values for Puma concolor
```

r1

*Calculate population growth rate in favourable habitats***Description**

Calculates the growth rate of a population in favourable habitats

**Usage**

```
r1(b = 1.75, B = 2.75, s = (1 - (1/16)), maxage = 80)
```

**Arguments**

b	0.5*litter size
B	breeding age
s	survival rate
maxage	maximum age

**Details**

"survival rate" (s) can be computed from mortality rate (u) ( $s = 1 - u$ ) or from mean life span (mls) ( $s = 1 - (1/mls)$ )

"maxage" can be computed from mean life span (mls) ( $maxage = 5 * mls$ )

**Value**

population growth rate in favourable habitats

**Author(s)**

Ana Ceia-Hasse, Luís Borda-de-Água, Henrique M. Pereira

**References**

Pereira HM, Daily GC, Roughgarden J. 2004. Ecological Applications 14: 730-742.

Pereira HM, Daily GC. 2006. Ecology 87: 1877-1885.

Ceia-Hasse A, Borda-de-Água L, Grilo C, Pereira HM. 2017. Global Ecology and Biogeography 26: 592-600.

**Examples**

```
# Run r1 with default parameter values:
```

```
r1()
# r1(b = 1.75, B = 2.75, s = (1 - (1/16)), maxage = 80)
# default values for Puma concolor (Pereira and Daily 2006)
# [1] 0.4631507
```

sigma2

*Calculate dispersal variance***Description**

Calculates the dispersal variance of the dispersal distance of an individual

**Usage**

```
sigma2(sigma_median = 7*sqrt(129.89), u = 1/16)
```

**Arguments**

sigma_median	dispersal median (km/generation)
u	mortality rate (per year)

**Details**

"u" was obtained from mean life span (mls) ( $u = 1/\text{mls}$ )

"sigma\_median" was obtained from home range (HR; km<sup>2</sup>) ( $\text{sigma\_median} = 7 \cdot \sqrt{\text{HR}}$ ) (mammals; Bowman et al. 2002. Ecology 83: 2049-2055);  $\text{sigma\_median} = 12 \cdot \sqrt{\text{HR}}$  (birds; Bowman 2003. Canadian Journal of Zoology 81: 195-202))

**Value**

dispersal variance (km<sup>2</sup>/year)

**Author(s)**

Ana Ceia-Hasse, Luís Borda-de-Água, Henrique M. Pereira

**References**

Pereira HM, Daily GC. 2006. Ecology 87: 1877-1885.

Ceia-Hasse A, Borda-de-Água L, Grilo C, Pereira HM. 2017. Global Ecology and Biogeography 26: 592-600.

**Examples**

```
# Run sigma2 with default parameter values:

sigma2()
# sigma2(sigma_median = 7*sqrt(129.89), u = 1/16)
# default values for Puma concolor (Jones et al. 2009. Ecology 90: 2648, Pereira and Daily 2006)
# [1] 285.6852
```

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