Package 'pedSimulate'

January 7, 2021

Title Pedigree, Genetic Merit and Phenotype Simulation

Version 0.1.1

Description Simulate pedigree, genetic merits and phenotypes with (non)random mating followed by (non)random selection with different patterns in males and females.
Bijma, P. & Rutten, M. (2002) <https://www.wur.nl/en/Research-Results/Chair-groups/Animal-Sciences/Animal-Breeding-and-Genomics-Group/Research/Software.htm>.

License GPL-3

LazyData true

URL <https://github.com/nilforooshan/pedSimulate>

BugReports <https://github.com/nilforooshan/pedSimulate/issues>

RoxygenNote 7.1.1

Encoding UTF-8

Repository CRAN

NeedsCompilation no

Author Mohammad Ali Nilforooshan [aut, cre]
(<https://orcid.org/0000-0003-0339-5442>)

Maintainer Mohammad Ali Nilforooshan <m.a.nilforooshan@gmail.com>

R topics documented:

---

pedSimulte-package   *Pedigree, genetic merit and phenotype simulation*

Description

An R package for simulating a pedigree with genetic merits and phenotypes, starting from a base population (generation 0). The pedigree depth and design can be chosen by the values provided to the arguments of the simulation function.

Details

Starting from a base population with equal number of males and females, next generations are simulated for a user-defined number of generations. The size of the base population is defined by the user. No selection (natural or artificial) and non-random mating is applied to this population. Natural (mortality) and artificial selection are applied to the next generations. Different selection patterns can be applied to males and females, including different proportion of selected individuals from selection candidates (after applying mortality) as parents of the next generation, random or merit-based selection, and generation overlap. Selected individuals are mated randomly using function `simulatePed`, or mated assortatively/disassortatively using function `assortative`. In assortative/disassortative mating, males and females are sorted for mating based on the criteria for which they have been selected for (can be different between males and females). Further choices, such as litter size, and avoiding fullsib matings and parent-progeny matings are provided. Performance and genetic merit of individuals are simulated using the basic rules of quantitative genetics. The performance (P) of an individual is influenced by genetic (A) and environmental (E) effects. Thus, P = A + E, and Var(P) = Var(A) + Var(E). The additive genetic merit (A) of an individual is the average of its parents' additive genetic merits '(PA = (A_{sire} + A_{dam})/2) plus the Mendelian Sampling term due to the sampling of alleles passed from the parent to the offspring. The Mendelian Sampling variance is half of Var(A) in the base population. Because there is no provided information for environmental effects, the environment effect is assigned to individuals from a normal distribution of random numbers (E ~ N(0, **I**Var(E))).

Author(s)

Mohammad Ali Nilforooshan <m.a.nilforooshan@gmail.com>

---

assortative   *Data simulation with assortative/disassortative matings*

Description

Simulate Pedigree, genetic merits and phenotypes with assortative/disassortative mating followed by non-random selection, differntly for males and females.

Usage

```
assortative(
  F0size,
  f.rate = 1,
  m.rate = 1,
  mort.rate = 0,
  littersize = 1,
  ngen,
  overlap.s = 0,
  overlap.d = 0,
  Va0,
  Ve,
  fsel = "P",
  msel = "P",
  negative = FALSE
)
```

Arguments

F0size	: Even number of founder animals. No mortality and selection in this generation, and matings are random in this generation.
f.rate	: Proportion of females selected as dams, default = 1.
m.rate	: Proportion of males (<= f.rate) selected as sires, default = 1.
mort.rate	: Mortality rate per generation, after the availability of phenotype (e.g., birth weight, weaning weight) and before the age of maturity (i.e., before mating), default = 0. Maximum mort.rate = 0.5.
littersize	: Litter size, default = 1.
ngen	: Number of generations to simulate.
overlap.s	: Number of generation overlaps for sires, default = 0 for no generation overlap.
overlap.d	: Number of generation overlaps for dams, default = 0 for no generation overlap.
Va0	: Additive genetic variance in the base generation (i.e., F0).
Ve	: Environment (plus residual) variance, set constant across generations.
fsel	: If "P" (default), selection on phenotypes or true breeding values if Ve = 0; if "PA", selection on true parent averages; redundant if f.rate = 1. "-P" and "-PA" work in opposite direction of "P" and "PA", respectively.
msel	: If "P" (default), selection on phenotypes or true breeding values if Ve = 0; if "PA", selection on true parent averages; redundant if m.rate = 1. "-P" and "-PA" work in opposite direction of "P" and "PA", respectively.
negative	: Assortative mating if TRUE (default) and disassortative mating if false. Males are sorted based on msel and females are sorted based on fsel.

Details

The output pedigree data.frame (ped) has 9 columns: ID, SIRE, DAM, SEX, GEN (generation number starting with 0 for the base generation), PA (parent average), MS (Mendelian Sampling), E (environment and residuals), and P (phenotype).

Value

ped : The output pedigree `data.frame`. Further information provided in **Details**.

Examples

```
ped = assortative(
    F0size = 100,
    f.rate = 0.8,
    m.rate = 0.5,
    mort.rate = 0.05,
    littersize = 2,
    ngen = 4,
    overlap.s = 1,
    overlap.d = 0,
    negative = FALSE,
    Va0 = 9,
    Ve = 36,
    fsel = "P",
    msel = "PA"
)
```

---

simulatePed   *Simulate pedigree, genetic merits and phenotypes*

Description

Simulate Pedigree, genetic merits and phenotypes with random mating followed by (non)random selection with different patterns in males and females.

Usage

```
simulatePed(
  F0size,
  f.rate = 1,
  m.rate = 1,
  mort.rate = 0,
  littersize = 1,
  ngen,
  overlap.s = 0,
  overlap.d = 0,
  fullsib = TRUE,
  parentprogeny = TRUE,
  Va0,
  Ve,
  fsel = "R",
  msel = "R"
)
```

Arguments

F0size	: Even number of founder animals. No mortality and selection in this generation.
f.rate	: Proportion of females selected as dams, default = 1.
m.rate	: Proportion of males (<= f.rate) selected as sires, default = 1.
mort.rate	: Mortality rate per generation, after the availability of phenotype (e.g., birth weight, weaning weight) and before the age of maturity (i.e., before mating), default = 0. Maximum mort.rate = 0.5.
littersize	: Litter size, default = 1.
ngen	: Number of generations to simulate.
overlap.s	: Number of generation overlaps for sires, default = 0 for no generation overlap.
overlap.d	: Number of generation overlaps for dams, default = 0 for no generation overlap.
fullsib	: If FALSE, avoid fullsib matings, default = TRUE. Further information provided in **Details**.
parentprogeny	: If FALSE, avoid parent-progeny matings, default = TRUE. Further information provided in **Details**.
Va0	: Additive genetic variance in the base generation (i.e., F0).
Ve	: Environment (plus residual) variance, set constant across generations.
fsel	: If ″R″ (default), random selection on females; if ″P″, selection on phenotypes or true breeding values if Ve = 0; if ″PA″, selection on true parent averages; redundant if f.rate = 1. ″-P″ and ″-PA″ work in opposite direction of ″P″ and ″PA″, respectively.
msel	: If ″R″ (default), random selection on males; if ″P″, selection on phenotypes or true breeding values if Ve = 0; if ″PA″, selection on true parent averages; redundant if m.rate = 1. ″-P″ and ″-PA″ work in opposite direction of ″P″ and ″PA″, respectively.

Details

fullsib = FALSE : Avoid fullsib matings in each generation by replacing the male mate (SIRE) with a random SIRE among the selected sires, until no fullsib mating is left. If due to a small population bottleneck there is any fullsib mating remained, it would be reported.

parentprogeny = FALSE : Avoid parent-progeny matings in each generation by replacing the male mate (SIRE) with a random SIRE among the selected sires, until no parent-progeny mating is left. If due to a small population bottleneck there is any parent-progeny mating remained, it would be reported.

The output pedigree data.frame (ped) has 9 columns: ID, SIRE, DAM, SEX, GEN (generation number starting with 0 for the base generation), PA (parent average), MS (Mendelian Sampling), E (environment and residuals), and P (phenotype).

Value

ped : The output pedigree data.frame. Further information provided in **Details**.

Examples

```
ped = simulatePed(
    F0size = 100,
    f.rate = 0.8,
    m.rate = 0.5,
    mort.rate = 0.05,
    littersize = 2,
    ngen = 4,
    overlap.s = 1,
    overlap.d = 0,
    fullsib = FALSE,
    parentprogeny = FALSE,
    Va0 = 9,
    Ve = 36,
    fsel = "P",
    msel = "PA"
)
```

Index