Package 'pedSimulate'

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Title Pedigree, Genetic Merit and Phenotype Simulation

Version 0.0.4

Description Simulate pedigree, genetic merits and phenotypes with random mating followed by (non)random selection with different patterns for males and females. Bijma, P. & Rutten, M. (2002) <https://pdfs.semanticscholar.org/ac22/e2961cc7797a121d956abd1ecbaddc017f87.pdf>.

License GPL-3

LazyData true

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

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

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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, and there is no natural or artificial selection 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 the 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. 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 (MS) due to the sampling of alleles passed from the parent to the offspring. The variance of MS is equal to 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))).

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simulatePed *Simulate pedigree, genetic merits and phenotypes*

Description

Simulate Pedigree, genetic merits and phenotypes with random mating followed by (non)random selection differntly for 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`.
`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`.

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"
)
```

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