Package ‘SimPlus’

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Title Functions to enhance AlphaSimR

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Description Functions to enhance AlphaSimR

Depends R (>= 4.1)

License GPL-3

LazyData true

RoxygenNote 7.2.3

Encoding UTF-8

Imports utils, AlphaSimR, dplyr, polyBreedR, pedigree, data.table, COMA

Suggests knitr, rmarkdown, StageWise

VignetteBuilder knitr

R topics documented:

`sim_accuracy` *Estimate selection accuracy*

Description

Estimate selection accuracy

Usage

```
sim_accuracy(pop, SP, COMA.file, K.file = NULL, n.mate = 100, n.progeny = 50)
```

Arguments

`pop`	parental candidates, AlphaSimR Pop-class
`SP`	simulation parameters for AlphaSimR
`COMA.file`	COMA filename
`K.file`	kinship filename for COMA
`n.mate`	number of matings to sample
`n.progeny`	number of progeny per mating

Value

list of accuracies for OCS and OMA

`sim_load` *Load simulation files*

Description

Load simulation files

Usage

```
sim_load(rda.file, geno.file, pheno.file, ped.file)
```

Arguments

`rda.file`	R data filename
`geno.file`	genotype CSV file
`pheno.file`	phenotype CSV filename
`ped.file`	pedigree CSV filename

Value

list containing pop,SP,p.ref

`sim_mate` *Perform mating in AlphaSimR*

Description

Perform mating in AlphaSimR

Usage

```
sim_mate(pop, SP, matings, total.progeny, min.progeny)
```

Arguments

`pop`	parental candidates, AlphaSimR Pop-class
`SP`	simulation parameters for AlphaSimR
`matings`	data frame of mate allocations, with columns parent1, parent2, value
`total.progeny`	total progeny to generate
`min.progeny`	minimum progeny per mating

Details

Details

Value

list containing

progeny Pop-class of progeny

matings matings with additional column for mu

`sim_OCS` *Parent selection and mating by OCS in AlphaSimR*

Description

Parent selection and mating by OCS in AlphaSimR

Usage

```
sim_OCS(pop, SP, n.progeny, dF, COMA.file, K.file, solver = "ECOS")
```

Arguments

`pop`	parental candidates, AlphaSimR Pop-class
`SP`	simulation parameters for AlphaSimR
`n.progeny`	number of progeny to simulate
`dF`	target inbreeding rate
`COMA.file`	marker effect or pheno filename for COMA
`K.file`	kinship filename for COMA
`solver`	CVXR solver

Details

Auto detects whether COMA.file has marker effects or phenotype data based on the first column name.

Value

list containing

response named vector with realized dF, merit, Shannon diversity

oc data frame of optimal contributions for each individual

om data frame of optimal allocations for each mating

`sim_OMA` *Parent selection and mating by OMA in AlphaSimR*

Description

Parent selection and mating by OMA in AlphaSimR

Usage

```
sim_OMA(pop, SP, n.progeny, dF, COMA.file, K.file, max.parent, solver = "ECOS")
```

Arguments

`pop`	parental candidates, AlphaSimR Pop-class
`SP`	simulation parameters for AlphaSimR
`n.progeny`	number of progeny to simulate
`dF`	target inbreeding rate
`COMA.file`	geno filename for COMA
`K.file`	kinship filename for COMA
`max.parent`	maximum number of candidate parents for oma
`solver`	CVXR solver

Details

Argument `dF` is a numeric vector of length 2, for lower and upper bounds on inbreeding rate.

Parent pre-selection is done with `ocs` to satisfy the `max.parent` limit for `oma`.

Value

list containing

response named vector with realized dF, merit, Shannon diversity

oc data frame of optimal contributions for each individual

om data frame of optimal allocations for each mating

`sim_save` *Save simulation files*

Description

Save simulation files

Usage

```
sim_save(rda.file, pop, SP, geno.file, pheno.file, ped.file, p.ref)
```

Arguments

`rda.file`	R data filename
`pop`	variable of AlphaSimR Pop-class
`SP`	simulation parameters for AlphaSimR
`geno.file`	genotype CSV file
`pheno.file`	phenotype CSV filename
`ped.file`	pedigree CSV filename
`p.ref`	reference allele frequencies (for G.VR1)

`sim_StageWise` *Estimate marker effects by StageWise*

Description

Estimate marker effects by StageWise

Usage

```
sim_StageWise(
  geno.file,
  pheno.file,
  ploidy,
  COMA.file,
  gen.TP,
  asreml.workspace = "500mb"
)
```

Arguments

`geno.file`	TP genotype CSV filename
`pheno.file`	TP phenotype CSV filename
`ploidy`	ploidy
`COMA.file`	input filename for COMA
`gen.TP`	number of generations for TP (including current)
`asreml.workspace`	memory workspace

Details

Details

Value

list of dominance parameters

`update_K` *Update kinship file*

Description

Update kinship file

Usage

```
update_K(
  pop,
  SP,
  K.method,
  K.file,
  ped.file = NULL,
  p.ref = NULL,
  ibd.loci = 100,
  n.core = 1
)
```

Arguments

`pop`	variable of AlphaSimR Pop-class
`SP`	simulation parameters for AlphaSimR
`K.method`	kinship method: A, G, G.IBD
`K.file`	kinship CSV filename
`ped.file`	pedigree CSV filename
`p.ref`	reference pop allele frequencies for "G" method
`ibd.loci`	number of loci per chromosome for "G.IBD" method
`n.core`	number cores for "G.IBD" method

Details

Kinship is computed for selection candidates in `pop`. For `K.method`="A", argument `ped.file` is the three-column pedigree file. `K.method`="G" specifies VanRaden Method 1, and argument `p.ref` is the vector of reference allele frequencies. To reduce computing time for `K.method`="G.IBD", only `ibd.loci` are sampled per chromosome.

Value

average inbreeding coefficient of the population

`update_TP` *Update the Training Population (TP)*

Description

Update genotype, genotyped, and pedigree files for the TP

Usage

```
update_TP(pop, SP, geno.file, pheno.file, ped.file, gen.TP)
```

Arguments

`pop`	variable of AlphaSimR Pop-class
`SP`	simulation parameters for AlphaSimR
`geno.file`	genotype CSV file
`pheno.file`	phenotype CSV filename
`ped.file`	pedigree CSV filename
`gen.TP`	# generations recorded for the TP (including current)

Details

Pedigree file has three columns: id, mother, father. Phenotype file has three columns: id, value, gen. To start a new TP, use `gen.TP` = 0.

Value

vector of allele frequencies for pop if gen.TP==0, otherwise NULL

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