Package 'SimPlus'

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Title Functions to enhance AlphaSimR

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Author Jeffrey B. Endelman

Maintainer Jeffrey Endelman <endelman@wisc.edu>

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:

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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

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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

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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

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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

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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

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

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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)

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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

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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.VR, G.IBD
K.file	kinship CSV filename
ped.file	pedigree CSV filename
p.ref	reference pop allele frequencies for "VR" 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. For K.method="G.VR", 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

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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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