

# Package ‘SimPlus’

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**Title** Functions to enhance AlphaSimR  
**Version** 0.04  
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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

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sim_accuracy	<i>Estimate selection accuracy</i>
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**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	<i>Load simulation files</i>
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**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	<i>Perform mating in AlphaSimR</i>
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### 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	<i>Parent selection and mating by OCS in AlphaSimR</i>
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### 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	<i>Parent selection and mating by OMA in AlphaSimR</i>
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**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	<i>Save simulation files</i>
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**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	<i>Estimate marker effects by StageWise</i>
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**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**

none

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update_K	<i>Update kinship file</i>
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**Description**

Update kinship file

**Usage**

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

**Arguments**

pop	variable of AlphaSimR Pop-class
SP	simulation parameters for AlphaSimR
K.method	kinship method: A, G.VR1, G.IBD
K.file	kinship CSV filename
ped.file	pedigree CSV filename
p.ref	reference pop allele frequencies for "VR1" 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.VR1", 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

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*Update the Training Population (TP)*

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**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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