Package ‘COMA’

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Title Convex Optimization of Mate Allocation

Version 0.19

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Description Convex Optimization of Mate Allocation

Depends R (>= 4.0)

License GPL-3

RoxygenNote 7.2.3

Encoding UTF-8

Imports ggplot2, CVXR, tidyr

Suggests knitr, rmarkdown, Rmosek

R topics documented:

`ocs` *Optimal Contribution Selection*

Description

Optimize the contribution of each individual to the next generation

Usage

```
ocs(dF, parents, ploidy, K, tol = 1e-06, dF.adapt = NULL, solver = "ECOS")
```

Arguments

`dF`	inbreeding rate
`parents`	input data frame (see Details)
`ploidy`	ploidy
`K`	kinship matrix
`tol`	tolerance, values below this set to 0
`dF.adapt`	see Details
`solver`	solver for CVXR (default is "ECOS")

Details

The first four columns of `parents` should be named as follows: id, merit, min, max. Min and max are real numbers between 0 and 1 specifying the minimum and maximum contribution for each parent. An optional fifth column named "female" is a logical TRUE/FALSE variable for species with separate sexes.

Additional columns can be used to specify constraints on linear combinations of the contributions. The values are the coefficients of the contribution variables, and the name of each column specifies the right-hand side of the constraint. Each name must begin with "lt","gt", or "eq", followed by a non-negative numeric value. For example, "lt0.5" means less than or equal to 0.5.

The average inbreeding coefficient of the current generation is based on all individuals in `K`, which may exceed the list of individuals in `parents`.

It is possible that no feasible solution exists for the specified `dF`. Argument `dF.adapt` can be used to automatically increase dF by dF.adapt$step up to dF.adapt$max.

Value

list containing

response data.frame with realized dF, merit, n.parent

oc data frame of optimal contributions

`oma` *Optimal Mate Allocation*

Description

Optimize the allocation for each mating

Usage

```
oma(
  dF,
  parents,
  matings,
  ploidy,
  K,
  tol = 1e-06,
  dF.adapt = NULL,
  solver = "ECOS"
)
```

Arguments

`dF`	inbreeding rate
`parents`	parents data frame (see Details)
`matings`	matings data frame (see Details)
`ploidy`	ploidy
`K`	kinship matrix
`tol`	tolerance, values below this set to 0
`dF.adapt`	see Details
`solver`	solver for CVXR (default is "ECOS")

Details

Originally, only an upper bound was placed on the average kinship of the progeny, according to `dF`. As of package v0.19, both lower and upper bounds are allowed by passing a vector of length 2. When a single number is supplied, it is interpreted as equal lower and upper bounds.

The first three columns of `parents` should be named "id", "min", "max", with an optional fourth column "female" to indicate sex in dioecious species. Additional columns can be used to specify constraints on linear combinations of the contributions. The values are the coefficients of the contribution variables, and the name of each column specifies the right-hand side of the constraint. Each name must begin with "lt","gt", or "eq", followed by a non-negative numeric value. For example, "lt0.5" means less than or equal to 0.5.

The data.frame `matings` has five columns: "female, male, merit, min, max" for dioecious species, or else "parent1, parent2, merit, min, max".

The average inbreeding coefficient of the current generation is based on all individuals in `K`, which may exceed the list of individuals in `parents`.

It is possible that no feasible solution exists for the specified `dF`. Argument `dF.adapt` can be used to automatically increase the upper bound by dF.adapt$step up to dF.adapt$max.

Value

list containing

response data.frame with realized dF, merit, n.parent, n.mate

oc data frame of optimal contributions for each individual

om data frame of optimal allocations for each mating

`plot_ribbon` *Ribbon Plot of Optimal Contributions*

Description

Ribbon Plot of Optimal Contributions

Usage

```
plot_ribbon(oc, min.c = 0.001)
```

Arguments

`oc`	named list of optimal contributions
`min.c`	minimum contribution for plotting

Details

The inbreeding rates are taken from the names of `oc`. Each element of `oc` should be a data frame with columns "id" and "value".

Value

ggplot2 object

`read_data` *Read data for OCS/OMA*

Description

Predicts merit for OCS/OMA

Usage

```
read_data(
  geno.file,
  kinship.file,
  ploidy,
  sex = NULL,
  matings = "none",
  standardize = FALSE,
  n.core = 1,
  partition = FALSE
)
```

Arguments

`geno.file`	file with marker effects and genotypes
`kinship.file`	file with kinship matrix
`ploidy`	even integer
`sex`	optional, data frame with columns id and female (T/F)
`matings`	see Details
`standardize`	T/F, standardize merit based on additive std. dev.
`n.core`	multi-core evaluation
`partition`	T/F, partition matings as MPA, MPD, MPH for dominance model

Details

The first column of `geno.file` is the marker name. The second column contains the additive effects for the breeding value parameterization, and (digenic) dominance effects (when available) should be in the third column with the header "dom". Subsequent columns contain the marker data for the population, coded as allele dosage, from 0 to ploidy. Missing marker data is imputed with the population mean.

The `kinship.file` should contain an N x N kinship matrix with id names in the first column and row.

There are several options for argument `matings`: (1) "none" = no matings; (2) "all" = all possible matings of the individuals in `geno.file` (excluding reciprocals); (3) a character vector of genotype ids to calculate all pairs of matings; (4) a 2-column data.frame of desired matings with header "female","male" for dioecious species (separate sexes) or "parent1","parent2" for hermaphrodites. Self-matings are included under options (2) and (3) for dioecious species but are easily removed in the output if desired.

Value

list containing

K	kinship matrix
parents	data frame of individual merits
matings	data frame of mating merits

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