

Package ‘COMA’

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Title Convex Optimization of Mate Allocation
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Description Convex Optimization of Mate Allocation
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Suggests knitr, rmarkdown

R topics documented:

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ocs	<i>Optimal Contribution Selection</i>
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Description

Optimize the contribution of each individual to the next generation

Usage

```
ocs(dF, parents, ploidy, K, min.c = 0, dF.adapt = NULL, solver = "ECOS")
```

Arguments

dF	inbreeding rate
parents	input data frame (see Details)
ploidy	ploidy
K	kinship matrix
min.c	minimum contribution
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`.

After optimization, contributions less than `min.c` are set equal to zero, and the remainder are renormalized. The realized inbreeding rate can exceed the specified limit after applying this threshold. It is also possible that no feasible solution exists for the specified dF. In either case, argument `dF.adapt` can be used to find other solutions. It is a list with two named components: `step`, `max`. The software increases the dF limit by `dF.adapt$step` up to the smaller of `dF.adapt$max` or the realized value under the original dF, in an attempt to find a solution with less inbreeding.

Value

list containing

response named vector with realized dF, merit, Shannon diversity for parents

oc data frame of optimal contributions

oma

Optimal Mate Allocation

Description

Optimize the allocation for each mating

Usage

```
oma(
  dF,
  parents,
  matings,
  ploidy,
  K,
  min.a = 0,
  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
min.a	minimum allocation
dF.adapt	see Details
solver	solver for CVXR (default is "ECOS")

Details

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.

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

After optimization, allocations less than `min.a` are set equal to zero, and the remainder are renormalized. The realized inbreeding rate can exceed the specified limit after applying this threshold. It is also possible that no feasible solution exists for the specified `dF`. In either case, argument `dF.adapt` can be used to find other solutions. It is a list with two named components: `step`, `max`. The software increases the `dF` limit by `dF.adapt$step` up to the smaller of `dF.adapt$max` or the realized value under the original `dF`, in an attempt to find a solution with less inbreeding.

Value

list containing

response named vector with realized dF, merit, Shannon diversity for parents

oc data frame of optimal contributions for each individual

om data frame of optimal allocations for each mating

plot_ribbon	<i>Ribbon Plot of Optimal Contributions</i>
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Description

Ribbon Plot of Optimal Contributions

Usage

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

Arguments

oc	named list of optimal contributions/allocations
min.c	minimum contribution/allocation 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	<i>Read data for OCS/OMA</i>
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Description

Constructs the kinship matrix and predicts merit for OCS/OMA

Usage

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

Arguments

geno.file	file with marker effects and genotypes
kinship.file	NULL
ploidy	even integer
sex	optional, data frame with columns id and female (T/F)
matings	see Details
standardize	T/F, standardize merit in parental candidates
n.core	multi-core evaluation

Details

The first column of `geno.file` is marker name. The second column contains the additive effects for the breeding value parameterization, and (digenic) dominance effects should be in the third column with the header "dom". When `kinship.file=NULL`, the software assumes the following column "p.ref" contains allele frequencies for the reference population to control genomic inbreeding. Subsequent columns contain the marker data for the population, coded as allele dosage, from 0 to ploidy.

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 data.frame of desired matings with 2 columns: female, male.

Value

list containing

K genomic kinship matrix

parents data frame of individual merits

matings data frame of mating merits

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