

# Package ‘COMA’

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**Title** Convex Optimization of Mate Allocation

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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

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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

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oma

*Optimal Mate Allocation*

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### 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" 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`.

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

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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

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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

<code>geno.file</code>	file with marker effects and genotypes
<code>kinship.file</code>	NULL
<code>ploidy</code>	even integer
<code>sex</code>	optional, data frame with columns id and female (T/F)
<code>matings</code>	see Details
<code>standardize</code>	T/F, standardize merit in parental candidates
<code>n.core</code>	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 2-column data.frame of desired matings with header "female", "male" for dioecious species or else "parent1", "parent2". Self-matings are included under options (2) and (3) but can be easily removed in the output.

## Value

list containing

**K** genomic kinship matrix

**parents** data frame of individual merits

**matings** data frame of mating merits

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