Package ‘lmDiallel’

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Title Linear Fixed/Mixed Effects Models for Diallel Crosses

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Depends R (>= 3.5.0)

Imports multcomp, plyr, sommer, enhancer, tidyr

Description Several service functions to be used to analyse datasets obtained from diallel experiments within the frame of linear models in R, as described in Onofri et al (2020) <DOI:10.1007/s00122-020-03716-8>.

URL `https://www.statforbiology.com/lmDiallel/`

NeedsCompilation no

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Contents

`blockMatrixDiagonal` *Creates block diagonal matrix. It is used internally.*

Description

This function takes a list of matrices and creates a block diagonal matrix. It is used to fit multi-environment diallel models

Usage

```
blockMatrixDiagonal(matList)
```

Arguments

`matList`	It is a list of matrices to be combined

Value

Returns a matrix object

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theoretical Applied Genetics (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
a <- matrix(1:16, 8, 2)
b <- matrix(1:9, 3, 3)
c <- list(a, b)
blockMatrixDiagonal(c)
```

`DD` *Dominant Deviation effect*

Description

DD effect to fit Hayman2 model with `lm` function

Usage

```
DD(P1, P2, type = "fix", data)
```

Arguments

`P1`	`a variable for the first parent`
`P2`	`a variable for the second parent`
`type`	`a variable for model selection. May be "fix" (fixed model) or "random" (random model).`
`data`	`a 'data.frame' where to look for explanatory variables`

Details

a design matrix of n-1 parentals

Value

A design matrix for the DD effect

Author(s)

Andrea Onofri, Niccolo' Terzaroli , Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("hayman54")
contrasts(hayman54$Block) <- "contr.sum"
dMod <- lm(Ftime ~ Block + GCA(Par1, Par2) + MDD(Par1, Par2) +
             DD(Par1, Par2) + SCA(Par1, Par2) +
             RGCA(Par1, Par2) + RSCA(Par1, Par2), data = hayman54)
summary(dMod)
```

`diallelMET` *Factitious dataset for Diallel analysis*

Description

Multi-environment half-diallel dataset with six parentals, in five blocks and ten environments; the dataset is factitious and was obtained by Monte Carlo simulation.

Usage

```
data("diallelMET")
```

Format

A data.frame with 1050 observations on the following 5 variables.

`Env`	environment, a factor with 10 levels
`Block`	block, a factor with 5 levels
`Par1`	male parent, a factor with 6 levels
`Par2`	female parent, a factor with 6 levels
`Yield`	yield, a numeric vector

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

Source

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("diallelMET")
```

`diallelMod-methods` *Functions to retreive full list of genetical effects*

Description

Diallel model parameters are estimated under a set of restrictions and, therefore, the methods 'coef' and 'summary' do not return the full list of genetical parameters. Therefore, the 'glht.diallelMod' method can be used, which works by way of a series of helper functions, providing the necessary contrast matrices.

Usage

```
## S3 method for class 'diallelMod'
glht(model, linfct, ...)
```

Arguments

`model`	a model object (OPTIONAL)
`linfct`	a diellel.eff() function
`...`	Other optional arguments

Details

...

Value

`summary` Returns the full list of genetical parameters

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
library(lmDiallel)
library(multcomp)

# Data with replicates
data("hayman54")

fit <- lm.diallel(Ftime ~ Par1 + Par2, data = hayman54,
                  fct = "HAYMAN1")
summary(fit)
anova(fit)
gh <- glht(linfct = diallel.eff(fit))
```

`expand.diallel` *Create a Data Frame from All Combinations of Parentals*

Description

This is a modification of the 'expand.grid()' function working specifically with diallel experiments. It creates a data frame from all combinations of the supplied vector of parents, depending on the mating scheme.

Usage

```
expand.diallel(pars, mating = 1)
```

Arguments

`pars`	`pars` a vector of parentals
`mating`	The type of mating scheme. 1: full diallel experiment; 2: no reciprocals; 3: no selfs; 4: no reciprocals and no selfs

Value

returns a data.frame object

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
pars <- LETTERS[1:4]
expand.diallel(pars, mating = 3)
```

GCA *General Combining Ability effect*

Description

GCA effect to fit Hayman1 & 2 and Griffing 1 & 2 models with `lm` function

Usage

```
GCA(P1,P2,type = "fix", data)
```

Arguments

`P1`	`a variable for the first parent`
`P2`	`a variable for the second parent`
`type`	`a variable for model selection. May be "fix" (fixed model) or "random" (random model).`
`data`	`a 'data.frame' where to look for explanatory variables`

Details

a design matrix of n-1 parentals

Value

A design matrix for the GCA effect

Author(s)

Andrea Onofri, Niccolo' Terzaroli , Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("hayman54")
contrasts(hayman54$Block) <- "contr.sum"
dMod<-lm(Ftime ~ Block + GCA(Par1,Par2)
         + tSCA(Par1, Par2) + RGCA(Par1, Par2)
         + RSCA(Par1,Par2), data = hayman54)
anova(dMod)
```

`GCAC` *General Combining Ability without considering the selfed parents*

Description

Design matrix for GCAC, useful to fit Gardner & Eberhart model 3 (GE3) with `lm` function

Usage

```
GCAC(P1,P2,type = "fix", data)
```

Arguments

`P1`	a variable for the first parent
`P2`	a variable for the second parent
`type`	a variable for model selection. May be "fix" (fixed model) or "random" (random model).
`data`	a 'data.frame' where to look for explanatory variables

Details

a design matrix of n-1 parentals

Value

A design matrix for the GCAC effect

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("hayman54")
GCAC(Par1,Par2, data=hayman54)
```

`griffing56` *Griffing's dataset for diallel analysis*

Description

Data for a diallel in maize, with no selfs and no selfed parents. Data are the means of several replicates.

Usage

```
data("griffing56")
```

Format

A data.frame with 36 observations on the following 5 variables

`Par1`	male parent, a factor with 8 levels
`Par2`	female parent, a factor with 8 levels
`Yield`	Maize Yield
`Cob`	Cob weight
`Shelled`	Shelled corn weight

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

Source

Griffing, B., 1956. Concept of general and specific combining ability in relation to diallel crossing systems. Australian Journal of Biological Science 9, 463–493.

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("griffing56")
dMod2 <- lm.diallel(Yield ~ Par1 + Par2,
                    data = griffing56, fct = "GRIFFING4")
anova(dMod2, MSE = 21.05, dfr = 2558)
summary(dMod2, MSE = 21.05, dfr = 2558)
```

`H.BAR` *Average heterosis effect*

Description

H.BAR effect to fit GE2 and GE3 models with `lm` function

Usage

```
H.BAR(P1, P2, type = "fix", data)
```

Arguments

`P1`	a variable for the first parent
`P2`	a variable for the second parent
`type`	a variable for model selection. May be "fix" (fixed model) or "random" (random model).
`data`	a 'data.frame' where to look for explanatory variables

Value

A design matrix for the H.BAR effect

Author(s)

Andrea Onofri, Niccolo' Terzaroli , Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("zhang05")
dMod <- lm(Yield ~ Env/Block + H.BAR(Par1, Par2) + VEi(Par1, Par2) +
                  Hi(Par1, Par2) + SCA(Par1, Par2) +
                  H.BAR(Par1, Par2):Env + VEi(Par1, Par2):Env +
                  Hi(Par1, Par2):Env + SCA(Par1, Par2):Env, data = zhang05)
anova(dMod)
```

`hayman54` *Hayman dataset for diallel analysis*

Description

Data for a diallel in tobacco with 2 reps

Usage

```
data(hayman54)
```

Format

A data.frame with 128 observations on the following 4 variables

`Block`	block, a factor with 2 levels
`Par1`	male parent, a factor with 8 levels
`Par2`	female parent, a factor with 8 levels
`Ftime`	mean flowering time (days), a numeric vector

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

Source

B. I. Hayman (1954a). The Analysis of Variance of Diallel Tables. Biometrics, 10, 235-244. Table 5, page 241. http://doi.org/10.2307/3001877

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("hayman54")

contrasts(hayman54$Block) <- c("contr.sum")
dMod <- lm(Ftime ~ Block  + GCA(Par1, Par2)
             + tSCA(Par1, Par2) + RGCA(Par1, Par2)
             + RSCA(Par1, Par2), data = hayman54)
anova(dMod)
#or
dMod2 <- lm.diallel(Ftime ~ Par1 + Par2, Block = Block,
                  data = hayman54,
                  fct = "HAYMAN1")
anova(dMod2)
```

`Hi` *Average heterosis effect*

Description

H.i effect to fit GE2 Model with `lm` function

Usage

```
Hi(P1, P2, type = "fix", data)
```

Arguments

`P1`	a variable for the first parent
`P2`	a variable for the second parent
`type`	a variable for model selection. May be "fix" (fixed model) or "random" (random model).
`data`	a 'data.frame' where to look for explanatory variables

Details

a design matrix of n-1 parentals

Value

A design matrix for the Hi effect

Author(s)

Andrea Onofri, Niccolo' Terzaroli , Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("zhang05")
dMod <- lm(Yield ~ Env/Block + H.BAR(Par1, Par2) + VEi(Par1, Par2) +
                  Hi(Par1, Par2) + SCA(Par1, Par2) +
                  H.BAR(Par1, Par2):Env + VEi(Par1, Par2):Env +
                  Hi(Par1, Par2):Env + SCA(Par1, Par2):Env, data = zhang05)
anova(dMod)
```

`int.matrix` *Utilities for fitting diallel models.*

Description

These functions are used internally by the package, but they can also called from the outside, to fit specific needs

Usage

```
int.matrix(Xa, Xb)
checkScheme(P1, P2)
emm.diallel(obj)
```

Arguments

`Xa`	Incidence matrix of genetic effects
`Xb`	Incidence matrix for an external factor
`P1`	A vector with parentals
`P2`	A vector with parentals
`obj`	A glht object

Details

The function ’int.matrix()’ produces the incidence matrix for the interaction between two main effects; ’Xa’ and ’Xb’ are two incidence matrices for two main effects. The function ’checkScheme()’ takes two vectors containing the codings for parentals (P1 and P2), retrieves the mating scheme and detects whether there are missing crosses. The function ’emm.diallel()’ is used with multi-environment diallel experiments to obtain the expected marginal means for genetic effects across environments.

Value

The function ’int.matrix()’ returns an incidence matrix. The function ’checkScheme()’ returns a list, containing the main traits of the mating scheme. The function ’emm.diallel()’ retrns a data.frame with the marginal means, standard errors and t-test statistics.

Note

No further notes

Author(s)

Andrea Onofri

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data(griffing56)
head(griffing56)
checkScheme(griffing56$Par1, griffing56$Par2)
```

`lm.diallel` *Fitting diallel linear models*

Description

Wrapper function for lm.fit and diallel models. It can be used to carry out several powerful methods for linear models, such as 'summary()', anova() or 'glht()' in the 'multcomp' package.

Usage

```
lm.diallel(formula, Block, Env, fct = "GRIFFING2", data)
```

Arguments

`formula`	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted.'formula' uses the regular R syntax to specify the response variable and the two variables for parentals `(e.g., Yield ~ Par1 + Par2)`
`Block`	used to specify an optional variable coding for blocks
`Env`	used to specify an optional variable coding for environments
`fct`	a string variable coding for the selected model. 8 main diallel models: Hayman's model 1 (="HAYMAN1"), Hayman's model 2 (="HAYMAN2"), Griffing's model 1 (="GRIFFING1"), Griffing's model 2 (="GRIFFING2"), Griffing's model 3 (="GRIFFING3"), Griffing's model 4 (="GRIFFING4"), Gardner-Eberhart model 2 (="GE2") and Gardner-Eberhart model 3 (="GE3"). The strings "GE2r" and "GE3r" can be used to specify the 'enhanced' GE2 and GE3 models, including the effect of reciprocals (REC).
`data`	a 'data.frame' where to look for explanatory variables

Details

Notations for the 8 models

Model name in 'lm.diallel()'	Model notation in 'lm()'
HAYMAN1	Y ~ GCA(Par1, Par2) + tSCA(Par1, Par2) + RGCA(Par1, Par2) + RSCA(Par1, Par2)
GRIFFING1	Y ~ GCA(Par1, Par2) + tSCA(Par1, Par2) + REC(Par1, Par2)

GRIFFING2	Y ~ GCA(Par1, Par2) + tSCA(Par1, Par2)
HAYMAN2	Y ~ GCA(Par1, Par2) + MDD(Par1, Par2) + DD(Par1, Par2) + SCA(Par1, Par2) + RGCA(Par1,
GE2	Y ~ H.BAR(Par1, Par2) + VE.i(Par1, Par2) + H.i(Par1, Par2) + SCA(Par1, Par2)
GE3	Y ~ H.BAR(Par1, Par2) + SP(Par1, Par2) + GCAC(Par1, Par2) + SCA(Par1, Par2)
GE2r	Y ~ H.BAR(Par1, Par2) + VE.i(Par1, Par2) + H.i(Par1, Par2) + SCA(Par1, Par2) + RGCA(Par1
GE3r	Y ~ H.BAR(Par1, Par2) + SP(Par1, Par2) + GCAC(Par1, Par2) + SCA(Par1, Par2) + RGCA(Pa

Value

lm.diallel returns an object of class c("diallel", "lm"), that is a list containing at least the following components:

`coefficients` a named vector of coefficients

`residuals` the residuals, that is response minus fitted values

`fitted.values` the fitted mean values

`rank` the numeric rank of the fitted linear models

`weights` (only for weighted fits) the specified weights

`df.residual` the residual degrees of freedom

`call` the matched call

`terms` the terms object used

`contrasts` (only where relevant) the contrasts used

`xlevels` (only where relevant) a record of the levels of the factors used in fitting

`call` the matched call

`offset` the offset used (missing if none were used)

`y` if requested, the response used

`x` if requested, the model matrix used

`model` if requested (the default), the model frame used

`na.action` (where relevant) information returned by model.frame on the special handling of NAs

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("hayman54")
dMod <- lm.diallel(Ftime ~ Par1 + Par2, Block = Block,
                   data = hayman54,
                   fct = "HAYMAN1")
anova(dMod)
```

```
#or
data("zhang05")
contrasts(zhang05$Block) <- c("contr.sum")
dMod2 <- lm.diallel(Yield ~ Par1 + Par2, Env = Env, Block = Block,
            data = zhang05, fct = "GE2")

#or
data("lonnquist61")
dMod3 <- lm.diallel(Yield ~ Par1 + Par2,
                  data = lonnquist61,
                  fct = "GE2")
summary(dMod3, MSE = 7.10, dfr = 60)
anova(dMod3, MSE = 7.10, dfr = 60)
```

`lmDiallel-methods` *Methods for diallel model fitting*

Description

The object returned by the 'lm.diallel()' function is of classes 'lm' and 'diallel'. Specific methods were devised to explore the 'diallel' object.

Usage

```
## S3 method for class 'diallel'
summary(object, MSE, dfr, ...)
## S3 method for class 'diallel'
vcov(object, MSE, ...)
## S3 method for class 'diallel'
anova(object, MSE, dfr, type = 1, ...)
## S3 method for class 'diallel'
model.matrix(object, ...)
```

Arguments

`object`	an object of class diallel.
`MSE`	Mean Square Error, when it cannot be derived from model fit
`dfr`	Residual degrees of freedom, when they cannot be derived from model fit
`type`	It is used to select between Type I (sequential) or Type III (marginal) F tests in ANOVA
`...`	Other optional arguments

Details

To be defined

Value

`vcov.diallel`: a variance-covariance matrix `summary.diallel`: a data.frame of estimated parameters with standard errors `anova.diallel`: an ANOVA table `predict.diallel`: a vector of predictions from a diallel model `model.matrix.diallel`: a design matrix for the fitted diallel model

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
library(lmDiallel)
library(multcomp)
# Data with replicates
data("hayman54")

fit <- lm.diallel(Ftime ~ Par1 + Par2, data = hayman54,
                  fct = "HAYMAN1")
summary(fit)
anova(fit)
gh <- glht(linfct = diallel.eff(fit), adjust = "none")
```

`lonnquist61` *Half diallel of maize dataset*

Description

Diallel experiment with six maize varieties and no reciprocals. The data here are means adjusted for block effects.

Usage

```
data("lonnquist61")
```

Format

A data.frame with 21 observations on the following 3 variables.

`Par1`	male parent, a factor with 6 levels
`Par2`	female parent, a factor with 6 levels
`Yield`	mean across blocks, a numeric vector

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

Source

J. H. Lonnquist, C. O. Gardner. (1961) Heterosis in Intervarietal Crosses in Maize and Its Implication in Breeding Procedures. Crop Science, 1, 179-183. Table 1.

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Mohring, Melchinger, Piepho. (2011). REML-Based Diallel Analysis. Crop Science, 51, 470-478. http://doi.org/10.2135/cropsci2010.05.0272

C. O. Gardner and S. A. Eberhart. 1966. Analysis and Interpretation of the Variety Cross Diallel and Related Populations. Biometrics, 22, 439-452. http://doi.org/10.2307/2528181

Examples

```
data("lonnquist61")
dMod <- lm(Yield ~ H.BAR(Par1, Par2) + VEi(Par1, Par2) +
             Hi(Par1, Par2) + SCA(Par1, Par2),
                  data = lonnquist61)
summary.diallel(dMod, MSE = 7.10, dfr = 60)
anova.diallel(dMod, MSE = 7.10, dfr = 60)
```

`matBlock` *Design matrix for blocks*

Description

It creates a disign matrix for block effects (with sum-to-zero constraint). It is used internally

Usage

```
matBlock(formula)
```

Arguments

`formula`	a formula containing the block variables

Value

A design matrix for the block effect

Author(s)

Andrea Onofri, Niccolo’ Terzaroli, Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("hayman54")
matBlock(~hayman54$Block)
```

`MDD` *Mean Dominance Deviation effect*

Description

It relates to the difference between the average yield of selfed parents and the average yield of crosses. DD effect to fit Hayman2 model with `lm` function

Usage

```
MDD(P1, P2, type = "fix", data)
```

Arguments

P1	a variable for the first parent
P2	a variable for the second parent
type	a variable for the model
data	a 'data.frame' where to look for explanatory variables

Value

A design matrix for the MDD effect

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("hayman54")
MDD(Par1, Par2, data = hayman54)
```

`mmer.diallel` *Fitting random diallel linear models*

Description

Wrapper function for the function 'mmer()' in the 'sommer' package. It can be used to fit random diallel models and retreive variance components for main effects.

Usage

```
mmer.diallel(formula, Block, Env, fct, data, type = "all")
```

Arguments

`formula`	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted.'formula' uses the regular R syntax to specify the response variable and the two variables for parentals (`e.g., Yield ~ Par1 + Par2`)
`Block`	used to specify an optional variable coding for blocks
`Env`	used to specify an optional variable coding for environments
`data`	a 'data.frame' where to look for explanatory variables
`fct`	a string variable coding for the selected model. 8 main diallel models: Hayman's model 1 (="HAYMAN1"), Hayman's model 2 (="HAYMAN2"), Griffing's model 1 (="GRIFFING1"), Griffing's model 2 (="GRIFFING2"), Griffing's model 3 (="GRIFFING3"), Griffing's model 4 (="GRIFFING4"), Gardner-Eberhart model 2 (="GE2") and Gardner-Eberhart model 3 (="GE3"). The strings "GE2r" and "GE3r" can be used to specify the 'enhanced' GE2 and GE3 models, including the effect of reciprocals (REC).
`type`	a string variable coding for the selected model. It is only used for multi-environment experiments and it is equal to "all" when both the environment and genetical effects are random or "environment" when the environment is random and genetical effects are fixed.

Value

Returns a data frame of variance components with standard errors

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

References

Covarrubias-Pazaran, G., 2016. Genome-Assisted Prediction of Quantitative Traits Using the R Package sommer. PLOS ONE 11, e0156744. https://doi.org/10.1371/journal.pone.0156744

Examples

```
data("hayman54")
rMod <- mmer.diallel(Ftime ~ Par1 + Par2, Block = Block,
                     data = hayman54,
                     fct = "HAYMAN1")
rMod
```

`model.matrixDiallel` *Incidence matrices for Diallel model parametrisation*

Description

`model.matrixDiallel` is useful to build design matrices, according to the user-defined (or default) parameterisation for `lm` function. It shares the same syntax of the `lm.diallel` function.

Arguments

`formula`	an object of class "formula" (or one that can be coerced to that class): a symbolic description of the model to be fitted.'formula' uses the regular R syntax to specify the response variable and the two variables for parentals (`e.g., Yield ~ Par1 + Par2`)
`Block`	used to specify an optional variable coding for blocks
`Env`	used to specify an optional variable coding for environments
`data`	a 'data.frame' where to look for explanatory variables
`fct`	a string variable coding for the selected model. 6 main diallel models: Hayman's model 1 (="HAYMAN1"), Hayman's model 2 (="HAYMAN2"), Griffing's model 1 (="GRIFFING1"), Griffing's model 2 (="GRIFFING2"), Gardner-Eberhart model 2 (="GE2") and Gardner-Eberhart model 3 (="GE3"). The strings "GE2r" and "GE3r" can be used to specify the 'enhanced' GE2 and GE3 models, including the effect of reciprocals (REC).

Details

model.matrixDiallel creates a design matrix for a diallel model, as specified in the 'fct' argument.

Value

The design matrix for a diallel model as specified in the 'fct' argument.

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("diallelMET")
ModMat <- model.matrixDiallel(Yield ~ Par1 + Par2,
                   Env, Block, fct= "GE3",
                   data = diallelMET)
```

`REC` *Reciprocal Effect not parted into RGCA and RSCA*

Description

Build incidence matrix to fit reciprocal effects in Griffing's model 1, 2, 4 (REC) and 3 (REC.G3) with `lm` function

Usage

```
REC(P1, P2, type = "fix", data)
```

Arguments

`P1`	a variable for the first parent
`P2`	a variable for the second parent
`type`	a variable for model selection. May be "fix" (fixed model) or "random" (random model).
`data`	a 'data.frame' where to look for explanatory variables

Details

a design matrix of n-1 parentals

Value

A design matrix for the reciprocal (REC) effect

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("hayman54")
dMod<-lm(Ftime~ Block + GCA(Par1,Par2)
         +tSCA(Par1, Par2)+REC(Par1, Par2)
         , data = hayman54)
anova(dMod)
```

`RGCA` *Reciprocal General Combining Ability*

Description

RGCA effect to fit Hayman1 & 2 models with `lm` function

Usage

```
RGCA(P1,P2,type = "fix", data)
```

Arguments

`P1`	a variable for the first parent
`P2`	a variable for the second parent
`type`	a variable for model selection. May be "fix" (fixed model) or "random" (random model).
`data`	a 'data.frame' where to look for explanatory variables

Details

a design matrix of n-1 parentals

Value

A design matrix for the RGCA effect

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("hayman54")
dMod<-lm(Ftime~ Block + GCA(Par1,Par2)
         + tSCA(Par1, Par2) + RGCA(Par1, Par2)
         + RSCA(Par1,Par2), data = hayman54)
anova(dMod)
```

`RSCA` *Reciprocal Specific Combining Ability*

Description

RSCA effect to fit Hayman 1 & 2 models with `lm` function

Usage

```
RSCA(P1,P2,type = "fix",data)
```

Arguments

`P1`	a variable for the first parent
`P2`	a variable for the second parent
`type`	a variable for model selection. May be "fix" (fixed model) or "random" (random model).
`data`	a 'data.frame' where to look for explanatory variables

Details

a design matrix of all possible combinations between parentals with no selfs and no reciprocals

Value

A design matrix for the RSCA effect

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("hayman54")
dMod<-lm(Ftime~ Block + GCA(Par1,Par2)
         + tSCA(Par1, Par2) + RGCA(Par1, Par2)
         + RSCA(Par1,Par2), data = hayman54)
anova(dMod)
```

SCA *Specific Combining Ability*

Description

SCA effect to fit Hayman2, Griffing3 (SCA.G3), GE2 and GE3 (SCA.GE) models with `lm` function

Usage

```
SCA(P1, P2, type = "fix", data)
SCA.G3(P1, P2,  type = "fix", data)
```

Arguments

`P1`	a variable for the first parent
`P2`	a variable for the second parent
`type`	a variable for model selection. May be "fix" (fixed model) or "random" (random model).
`data`	a 'data.frame' where to look for explanatory variables

Details

a design matrix of all possible combinations between parentals with no selfs and no reciprocals

Value

A design matrix for the SCA effect

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("zhang05")
dMod <- lm(Yield ~ Env/Block + H.BAR(Par1, Par2) + VEi(Par1, Par2) +
                   Hi(Par1, Par2) + SCA(Par1, Par2) +
                   H.BAR(Par1, Par2):Env + VEi(Par1, Par2):Env +
                   Hi(Par1, Par2):Env + SCA(Par1, Par2):Env, data = zhang05)
anova(dMod)
```

`SP` *Selfed Parents effect*

Description

SP effect to fit GE3 model with `lm` function

Usage

```
SP(P1, P2, type = "fix", data)
```

Arguments

`P1`	`a variable for the first parent`
`P2`	`a variable for the second parent`
`type`	`a variable for model selection. May be "fix" (fixed model) or "random" (random model).`
`data`	`a 'data.frame' where to look for explanatory variables`

Details

a design matrix of n-1 parentals

Value

A design matrix for the SP effect

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("hayman54")
SP(Par1,Par2, data=hayman54)
```

`tSCA` *Total Specific Combining Ability*

Description

Total SCA to fit Hayman1, Griffing1 and Griffing2 models with `lm` function

Usage

```
tSCA(P1,P2,type = "fix", data)
```

Arguments

P1	a variable for the first parent
P2	a variable for the second parent
type	a variable for model selection. May be "fix" (fixed model) or "random" (random model).
data	a 'data.frame' where to look for explanatory variables

Details

a design matrix of all possible combinations between parentals with selfs but no reciprocals

Value

A design matrix for the tSCA effect

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("hayman54")
dMod<-lm(Ftime~ Block + GCA(Par1,Par2)
         + tSCA(Par1, Par2) + RGCA(Par1, Par2)
         + RSCA(Par1,Par2), data = hayman54)
anova(dMod)
```

`VEi` *Variety Effect*

Description

VE.i effect to fit GE2 model with `lm` function

Usage

```
VEi(P1, P2, type = "fix", data)
```

Arguments

`P1`	a variable for the first parent
`P2`	a variable for the second parent
`type`	a variable for model selection. May be "fix" (fixed model) or "random" (random model).
`data`	a 'data.frame' where to look for explanatory variables

Details

a design matrix of n-1 parentals

Value

A design matrix for the VEi effect

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("zhang05")
dMod <- lm(Yield ~ Env/Block + H.BAR(Par1, Par2) + VEi(Par1, Par2) +
                   Hi(Par1, Par2) + SCA(Par1, Par2) +
                   H.BAR(Par1, Par2):Env + VEi(Par1, Par2):Env +
                   Hi(Par1, Par2):Env + SCA(Par1, Par2):Env, data = zhang05)
anova(dMod)
```

`zhang05` *Data for diallel analysis from Zhang (2005)*

Description

Data collected in XXX with 5 parents, 2 reps and 2 environments

Usage

```
data("zhang05")
```

Format

A data.frame with 60 observations on the following 6 variables.

`Par1` male parent, a factor with 5 levels

`Par2` female parent, a factor with 5 levels

`Block` block, a factor with 2 levels

`Combination` combination between environment and block, an integer vector

`Env` environment, a factor with 2 levels

`Yield` yield, a numeric vector

Author(s)

Andrea Onofri, Niccolo' Terzaroli, Luigi Russi

Source

Zhang, Y., Kang, M.S. and Lamkey, K.R. (2005), DIALLEL-SAS05: A Comprehensive Program for Griffing's and Gardner&Eberhart Analyses. Agron. J., 97: 1097-1106. https://doi.org/10.2134/agronj2004.0260

References

Onofri, A., Terzaroli, N. & Russi, L. Linear models for diallel crosses: a review with R functions. Theor Appl Genet (2020). https://doi.org/10.1007/s00122-020-03716-8

Examples

```
data("zhang05")
contrasts(zhang05$Block) <- c("contr.sum")
contrasts(zhang05$Env) <- c("contr.sum")
dMod <- lm(Yield ~ Env/Block + H.BAR(Par1, Par2) + VEi(Par1, Par2) +
                  Hi(Par1, Par2) + SCA(Par1, Par2) +
                  H.BAR(Par1, Par2):Env + GCA(Par1, Par2):Env +
                  Hi(Par1, Par2):Env + SCA(Par1, Par2):Env, data = zhang05)
anova(dMod)
#or
```

```
dMod2 <- lm(Yield ~ Env/Block + H.BAR(Par1, Par2) + VEi(Par1, Par2) +
                   Hi(Par1, Par2) + SCA(Par1, Par2), data = zhang05)
summary(dMod2)$coefficients
```

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