Package 'hypr'

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Type Package

Title Hypothesis Matrix Translation

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BugReports https://github.com/mmrabe/hypr/issues

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Description Translation between experimental null hypotheses, hypothesis matrices, and contrast matrices as used in linear regression models. The package is based on the method described in Schad, Vasishth, Hohenstein, and Kliegl (2019) <doi:10.1016/j.jml.2019.104038> and Rabe, Vasishth, Hohenstein, Kliegl, and Schad (2020) <doi:10.21105/joss.02134>.

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Collate 'equations.R' 'hypr.R'

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R topics documented:

  `+,hypr,hypr-method`   *Combining hypr objects by addition or interaction*

Description

You can combine one or more `hypr` objects, i.e. combine their hypothesis to a single `hypr` object, by adding them with the + or * operators.

Usage

```
## S4 method for signature 'hypr,hypr'
e1 + e2

## S4 method for signature 'hypr,hypr'
e1 * e2

## S4 method for signature 'hypr,hypr'
e1 & e2

## S4 method for signature 'hypr,hypr'
e1 / e2
```

Arguments

  e1, e2   hypr objects to concatenate

Value

The combined `hypr` object

Functions

- `*,hypr,hypr-method`: Interaction of `e1` and `e2`

- `&,hypr,hypr-method`: Interaction and main contrasts of `e1` and `e2`

- `/,hypr,hypr-method`: Nesting levels of `e2` within `e1`

Examples

```
(h1 <- hypr(a~i, b~i)) # a hypr object of two treatments

(h2 <- hypr(i~0)) # an intercept-only hypr object

hc <- h1 + h2

hc

interaction <- h1 & h2

interaction_and_main <- h1 * h2
```

---

cmat   *Retrieve or set contrast matrix*

Description

Use these functions to retrieve or set a hypr object's contrast matrix. If used for updating, the hypothesis matrix and equations are derived automatically.

Usage

```
cmat(x, add_intercept = FALSE, remove_intercept = FALSE, as_fractions = TRUE)

cmat(x, add_intercept = FALSE, remove_intercept = FALSE) <- value

contr.hypothesis(
  ...,
  add_intercept = FALSE,
  remove_intercept = NULL,
  as_fractions = FALSE
)

## S4 replacement method for signature 'ANY,ANY,hypr'
contrasts(x, how.many) <- value

## S4 replacement method for signature 'ANY,ANY,hypr_cmat'
contrasts(x, how.many) <- value

contr.hypothesis(
  x,
  add_intercept = NULL,
  remove_intercept = FALSE,
  as_fractions = FALSE
) <- value
```

Arguments

x	A hypr object
add_intercept	Add additional intercept column to contrast matrix
remove_intercept	
	If TRUE, tries to find an intercept column (all codes equal) and removes it from the matrix. If NULL, does the same but does not throw an exception if no intercept is found. FALSE explicitly disables this functionality. A numeric argument explicitly identifies the index of the column to be removed.
as_fractions	Should the returned matrix be formatted as fractions (using MASS::as.fractions())?
value	contrast matrix
...	A list of hypothesis equations for which to retrieve a contrast matrix
how.many	see stats::contrasts()

Details

Basic specification of contrasts in R is accomplished with basic R functions stats::contrasts() and stats::C() (Chambers & Hastie, 1992). Other relevant packages for this topic are multcomp (Bretz et al., 2010), contrast (Kuhn et al., 2016), and, including also various vignettes, emmeans (Lenth, 2019).

Value

A matrix of contrast codes with contrasts as columns and levels as rows.

Functions

- cmat<-: Set contrast matrix
- contr.hypothesis: Retrieve contrast matrix with sensible intercept default to override factor contrasts
- contrasts<-,ANY,ANY,hypr-method: Update factor contrasts
- contrasts<-,ANY,ANY,hypr_cmat-method: Update factor contrasts
- contr.hypothesis<-: Update contrast matrix with sensible intercept default

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical models*. Chapter 2 of *Statistical Models* in S eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

Frank Bretz, Torsten Hothorn and Peter Westfall (2010), *Multiple Comparisons Using R*, CRC Press, Boca Raton.

Max Kuhn, contributions from Steve Weston, Jed Wing, James Forester and Thorn Thaler (2016). *contrast: A Collection of Contrast Methods*. R package version 0.21. https://CRAN.R-project.org/package=contrast

Lenth, R. (2019). *emmeans: Estimated Marginal Means, aka Least-Squares Means*. R package version 1.4.1. https://CRAN.R-project.org/package=emmeans

See Also

hypr

Examples

```
h <- hypr(mu1~0, mu2~mu1)
cmat(h) # retrieve the contrast matrix

contr.hypothesis(h) # by default without intercept (removes first column)
contr.hypothesis(mu1~0, mu2~mu1)
```

---

conversions	*Shorthand versions for simple hypothesis translation*

Description

These functions can be used to translate between null hypothesis equations, hypothesis matrices, and contrast matrices without defining a hypr object. Note that some of these functions do generate a hypr object internally but they never return one.

Usage

```
eqs2hmat(
  eqs,
  levels = NULL,
  order_levels = missing(levels),
  as_fractions = TRUE
)

eqs2cmat(eqs, as_fractions = TRUE)

hmat2cmat(hmat, as_fractions = TRUE)

cmat2hmat(cmat, as_fractions = TRUE)

hmat2eqs(hmat, as_fractions = TRUE)

cmat2eqs(cmat, as_fractions = TRUE)
```

Arguments

eqs	A list of equations
levels	(optional) A character vector of variables to be expected (if not provided, automatically generated from all terms occurring in the equations list)

order_levels	(optional) Whether to alphabetically order appearance of levels (rows in transposed hypothesis matrix or contrast matrix). Default is TRUE if levels were not explicitly provided.
as_fractions	(optional) Whether to output matrix using fractions formatting (via `MASS::as.fractions`). Defaults to TRUE.
hmat	Hypothesis matrix
cmat	Contrast matrix

Value

A list of equations (hmat2eqs and cmat2eqs), a contrast matrix (hmat2cmat, eqs2cmat), or a hypothesis matrix (cmat2hmat, eqs2hmat).

Functions

- eqs2hmat: Convert null hypothesis equations to hypothesis matrix
- eqs2cmat: Convert null hypothesis equations to contrast matrix
- hmat2cmat: Convert hypothesis matrix to contrast matrix
- cmat2hmat: Convert contrast matrix to hypothesis matrix
- hmat2eqs: Convert hypothesis matrix to null hypothesis equations
- cmat2eqs: Convert contrast matrix to null hypothesis equations

Examples

```
# The following examples are based on a 2-level treatment contrast (i.e., baseline and treatment).
hypotheses <- list(baseline = mu1~0, treatment = mu2~mu1)
hypothesis_matrix <- matrix(
  c(c(1, -1), c(0, 1)), ncol = 2, dimnames = list(c("baseline","treatment"), c("mu1", "mu2")))
contrast_matrix <- matrix(
  c(c(1, 1), c(0, 1)), ncol = 2, dimnames = list(c("mu1","mu2"), c("baseline", "treatment")))

# Convert a list of null hypothesis equations to ...
# ... a hypothesis matrix:
eqs2hmat(hypotheses)
# ... a contrast matrix:
eqs2cmat(hypotheses)

# Convert a hypothesis matrix to...
# ... a list of null hypothesis equations:
hmat2eqs(hypothesis_matrix)
# ... a contrast matrix:
hmat2cmat(hypothesis_matrix)

# Convert a contrast matrix to...
# ... a list of null hypothesis equations:
cmat2eqs(contrast_matrix)
# ... a hypothesis matrix:
cmat2hmat(contrast_matrix)
```

```
# Are all functions returning the expected results?
stopifnot(all.equal(eqs2hmat(hypotheses, as_fractions = FALSE), hypothesis_matrix))
stopifnot(all.equal(eqs2cmat(hypotheses, as_fractions = FALSE), contrast_matrix))
stopifnot(all.equal(hmat2cmat(hypothesis_matrix, as_fractions = FALSE), contrast_matrix))
stopifnot(all.equal(cmat2hmat(contrast_matrix, as_fractions = FALSE), hypothesis_matrix))
```

---

formula<-	*Manipulate the formulas of an S4 object*

Description

This is a generic function for setting an S4 object's formulas.

Usage

```
formula(x, ...) <- value
```

Arguments

x	The object to manipulate
...	Additional arguments passed on to the method
value	The new formula

---

ginv2	*Enhanced generalized inverse function*

Description

This function is a wrapper for `MASS::ginv` and calculates the generalized inverse of x.

Usage

```
ginv2(x, as_fractions = TRUE)
```

Arguments

x	The original matrix
as_fractions	Whether to format the matrix as fractions (MASS package)

Details

In addition to `MASS::ginv`, this function rounds values, formats the matrix as fractions and copies dimension names from the original matrix.

Value

Generalized inverse of x

See Also

[ginv](#)

Examples

```
h <- hypr(mu1~0, mu2~mu1)
hmat(h)

ginv2(hmat(h))
cmat(h)

# cmat is effectively the generalized inverse of hmat
stopifnot(all.equal(ginv2(hmat(h)), cmat(h), check.attributes = FALSE))
```

---

hmat *Retrieve and set hypothesis matrix*

Description

Use these functions to retrieve or set a hypr object's hypothesis matrix. If used for updating, the contrast matrix and equations are derived automatically.

Usage

```
hmat(x, as_fractions = TRUE)

thmat(x, as_fractions = TRUE)

hmat(x) <- value

thmat(x) <- value
```

Arguments

x	A hypr object
as_fractions	Whether to format matrix as fractions (via [MASS::as.fractions](#))
value	Hypothesis matrix

Value

Hypothesis matrix of x

Functions

- `thmat`: Retrieve transposed hypothesis matrix
- `hmat<-`: Set hypothesis matrix
- `thmat<-`: Set transposed hypothesis matrix

Examples

```
h <- hypr(mu1~0, mu2~mu1)

# To retrieve the hypothesis matrix of `h`:
hmat(h)

# To retrieve the transposed hypothesis matrix of `h`:
thmat(h)

# Setting the hypothesis matrix of `h`:
hmat(h) <- matrix(c(1,-1,0,1), ncol=2, dimnames=list(NULL, c("mu1","mu2")))
h

h2 <- hypr() # an empty hypr object
thmat(h2) <- matrix(c(1,0,-1,1), ncol=2, dimnames=list(c("mu1","mu2"), NULL))
h2

# `h` and `h2` should be identical:
stopifnot(all.equal(hmat(h), hmat(h2)))
stopifnot(all.equal(cmat(h), cmat(h2)))
```

---

hypr   *Create a hypr object*

Description

Use this function to create hypr objects from null hypothesis equations. Each argument should be one equation. For example, a null hypothesis for the grand mean (GM), often used as the intercept, is usually coded as mu~0.

Usage

```
hypr(..., levels = NULL, order_levels = missing(levels))
```

Arguments

`...`	A list of null hypothesis equations
`levels`	(Optional) A list of terms/levels to use. If supplied, matrix rows/columns will be in this order. An error will be thrown if an equation contains a level that is not in this vector.

order_levels   (Optional) Whether to order the rows/columns of the hypothesis/contrast matrices alphabetically. Default is TRUE if levels were not explicitly provided.

Details

You may call the function without any arguments. In that case, an empty hypr object is returned. This is useful if you want to derive equations from a known hypothesis matrix or contrast matrix.

Basic specification of contrasts in R is accomplished with basic R functions stats::contrasts() and stats::C() (Chambers & Hastie, 1992). Other relevant packages for this topic are multcomp (Bretz et al., 2010), contrast (Kuhn et al., 2016), and, including also various vignettes, emmeans (Lenth, 2019).

Value

A hypr object

References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical models*. Chapter 2 of *Statistical Models* in S eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

Frank Bretz, Torsten Hothorn and Peter Westfall (2010), *Multiple Comparisons Using R*, CRC Press, Boca Raton.

Max Kuhn, contributions from Steve Weston, Jed Wing, James Forester and Thorn Thaler (2016). *contrast: A Collection of Contrast Methods*. R package version 0.21. https://CRAN.R-project.org/package=contrast

Lenth, R. (2019). *emmeans: Estimated Marginal Means, aka Least-Squares Means*. R package version 1.4.1. https://CRAN.R-project.org/package=emmeans

See Also

contrasts and C for basic specification of contrasts in R, S4 class hypr, cmat, contr.hypothesis for retrieval of contrast matrices from hypr objects

Examples

```
# Create an empty hypr object (no hypotheses):
h <- hypr()

# Treatment contrast:
h <- hypr(mu1~0, mu2~mu1, mu3~mu1, mu4~mu1)

# Identical version:
h <- hypr(~mu1, ~mu2-mu1, ~mu3-mu1, ~mu4-mu1)

contr.hypothesis(h)


# Generate a dataset
set.seed(123)
```

```
M <- c(mu1 = 10, mu2 = 20, mu3 = 10, mu4 = 40) # condition means
N <- 5 # number of observations per condition
SD <- 10 # residual SD
simdat <- do.call(rbind, lapply(names(M), function(x) {
  data.frame(X = x, DV = as.numeric(MASS::mvrnorm(N, unname(M[x]), SD^2, empirical = TRUE)))
}))
simdat$X <- factor(simdat$X, levels=levels(h))
simdat

# Check agreement of hypothesis levels and factor levels
stopifnot(levels(h) == levels(simdat$X))

# Linear regression
contrasts(simdat$X) <- contr.hypothesis(h)

round(coef(summary(lm(DV ~ X, data=simdat))),3)
```

---

hypr-class   *S4 class "hypr" and its methods*

Description

A hypr object contains equations, a hypothesis matrix and a contrast matrix, all of which are related to each other. See below for methods.

Usage

```
## S4 method for signature 'hypr'
show(object)

## S4 method for signature 'hypr'
levels(x)

## S4 method for signature 'hypr'
names(x)

## S4 replacement method for signature 'hypr'
names(x) <- value

## S4 replacement method for signature 'hypr'
levels(x) <- value

## S4 method for signature 'hypr'
formula(x, ...)

## S4 replacement method for signature 'hypr'
formula(x, ...) <- value
```

Arguments

`object, x`	a hypr object
`value`	New value (`list` of equations for `formula`, `character` vector for `levels` and `names`)
`...`	(ignored)

Details

To generate a hypr object, use the hypr function.

Value

A character vector of level names

A character vector of contrast names

A `list` of null hypothesis equations

Methods (by generic)

- `show`: Show summary of hypr object, including contrast equations, the (transposed) hypothesis matrix and the derived contrast matrix.
- `levels`: Retrieve the levels (variable names) used in a `hypr` object
- `names`: Retrieve the contrast names used in a `hypr` object
- `names<-`: Set the contrast names used in a `hypr` object
- `levels<-`: Set the levels used in a `hypr` object
- `formula`: Retrieve a hypr object's null hypothesis equations.
- `formula<-`: Modify a hypr object's null hypothesis equations

Slots

`eqs` List of null hypotheses

`hmat` Hypothesis matrix

`cmat` Contrast matrix

See Also

hypr, cmat, hmat

Examples

```
# Equations and matrices in a hypr object are always congruent
# Therefore creating a hypr object h and then copying ...
h <- hypr(mu1~0, mu2~mu1)

# ... its equations, ...
h2 <- hypr()
formula(h2) <- formula(h)
```

```
# ... its hypothesis matrix, ...
h3 <- hypr()
hmat(h3) <- hmat(h)

# ... or its contast matrix ...
h4 <- hypr()
cmat(h4) <- cmat(h)

# ... over to another hypr object is the same as copying the object:
h5 <- h

# check that hypr objects are equal by comparing hmat() and cmat()
stopifnot(all.equal(hmat(h), hmat(h2)))
stopifnot(all.equal(cmat(h), cmat(h2)))
stopifnot(all.equal(hmat(h), hmat(h3)))
stopifnot(all.equal(cmat(h), cmat(h3)))
stopifnot(all.equal(hmat(h), hmat(h4)))
stopifnot(all.equal(cmat(h), cmat(h4)))
stopifnot(all.equal(hmat(h), hmat(h5)))
stopifnot(all.equal(cmat(h), cmat(h5)))


h <- hypr(mu1~0, mu2~mu1)
formula(h)

h2 <- hypr()
formula(h2) <- formula(h)
h2
formula(h2)

# After updating, matrices should be equal
stopifnot(all.equal(hmat(h), hmat(h2)))
stopifnot(all.equal(cmat(h), cmat(h2)))
```

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