The drm Package

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Title Regression and association models for repeated categorical data

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Description Likelihood-based marginal regression and association modelling for repeated, or otherwise clustered, categorical responses using dependence ratio as a measure of the association

Depends R(>= 1.0)

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URL http://www.helsinki.fi/~jtjokine/drm

R topics documented:

- Time ................................................................. 2
- cluster ......................................................... 2
- depratio ..................................................... 3
- drm-internal .................................................. 4
- drm .............................................................. 4
- getass.drm .................................................... 10
- madras ....................................................... 13
- marijuana ..................................................... 14
- movie ......................................................... 14
- obese .......................................................... 15
- profiles.drm ................................................... 16
- wheeze ....................................................... 17

Index 19
**Time**

*Identify ordering of the responses*

**Description**

This is a special function used in the `drm` or `depratio` syntax. It identifies the ordering in correlated groups of observations, and is used on the right hand side of a formula.

**Usage**

```r
Time(x)
```

**Arguments**

- `x` A factor, or numeric variable.

**Details**

The function’s only action is semantic, to mark a variable as the Time indicator.

**See Also**

`drm`, `depratio`, `cluster`

**Examples**

```r
formula(wheeze~cluster(id)+Time(age))
```

---

**cluster**

*Identify clusters*

**Description**

This is a special function used in the `drm` or `depratio` syntax. It identifies correlated groups of observations, and is used on the right hand side of a formula.

**Usage**

```r
cluster(x)
```

**Arguments**

- `x` A character, factor, or numeric variable.

**Details**

The function’s only action is semantic, to mark a variable as the cluster indicator.
depratio

Value

x

See Also
drm, depratio, Time

Examples

formula(wheeze~cluster(id))

depratio                Empirical estimates of the dependence ratios

Description

Calculates the observed values of the adjacent dependence ratios from the data.

Usage

depratio(formula, data, subset, ord = 2, boot.ci = FALSE, n.boot = NULL, ci.width=0.95)

Arguments

formula  the syntax is of form y~cluster(id)+Time(time), where id denotes the
          cluster indicator, and Time denotes the order along which the adjacent depen-
          dence ratios will be calculated.
data      optional data frame containing the variables in the formula
subset    an optional vector specifying a subset of observations from the data
ord       order of the dependence ratios to be calculated. The default is 2
boot.ci   logical argument specifying whether bootstrap confidence intervals will be cal-
          culated for the empirical dependence ratio estimates
n.boot    number of bootstrap replicates
ci.width  width of the confidence interval. Default is 0.95

Value

An object of class depratio. Generic functions print and plot are also available.
An object of class depratio is a list containing at least the following two components:

tau       matrix of the observed dependence ratios
freq      matrix of the frequencies of events for the numerator of the observed dependence ratios
See Also
drm, cluster, Time

Examples

```r
## calculate and plot the observed 2nd order dependence ratios
## for the marijuana data:
data(marijuana)
dr.male <- depratio(y~cluster(id)+Time(age), data=marijuana,
    subset=sex=="male")
dr.male
plot(dr.male)

## confirm that the 1st order Markov assumption is adequate
## for the madras data:
data(madras)

dr2 <- depratio(symptom~cluster(id)+Time(month), data=madras)
dr3 <- depratio(symptom~cluster(id)+Time(month), ord=3, data=madras)
dr <- rbind(dr2$tau[-length(dr2$tau)]*dr2$tau[-1], dr3$tau)

matplot(1:ncol(dr), t(dr))
```

---

### drm - internal

**Internal drm functions**

**Description**

Internal drm functions

**Details**

These are internal drm functions and are not to be called by the user.

---

### drm

**Combined regression and association models for clustered categorical responses**

**Description**

`drm` fits a combined regression and association model for longitudinal or otherwise clustered categorical responses using dependence ratio as a measure of the association.
Usage

drm(formula, family=binomial, data=sys.parent(), weights, offset,
subset=NULL, na.action, start=NULL, link="cum", dep="I", Ncond=TRUE,
Lclass=2, dropout=FALSE, drop.x=NULL, save.profiles=TRUE, pmatrix=NULL,
print.level=2, iterlim=200, ...)

Arguments

formula a formula expression as for other regression models. In addition the cluster
term has to be specified in the expression by `cluster()` and if using temporal
association structure the temporal term has to be specified by `Time()`. See
examples below and the documentation of `lm` and `formula` for further details.

family a description of the link function to be used in the model for a binary response.
Default is logit link. See `family` for details. For an ordinal response, link is
defined for the cumulative probabilities when `link`-argument is set to "cum". See
`link` below.

data an optional data frame containing the variables in the model.

weights an optional vector of weights to be used in the fitting process. Only equal
weights within cluster are allowed.

offset this can be used to specify an a priori known component to be included in the
linear predictor during fitting.

subset an optional vector specifying a subset of observations to be used in the fitting
process.

na.action a function which indicates what should happen when the data contain NAs. The
default is `na.include` after which the analysis assumes missing data mecha-
nism at random (MAR) if `dropout=FALSE`, and not at random if `dropout=
TRUE`. See `dropout` below.

start an optional vector of starting values for the parameters. If not specified by the
user, the starting values are estimated from `glm`-procedure assuming indepen-
dence

link this can be used to specify alternative link functions for nominal and ordinal
responses. By default "cum", after which the link is specified through `family`
= `binomial(link=?)` for the cumulative probabilities. Alternative links
include adjacent category logit "acl" and baseline category logit "bcl" (baseline
category being the last category). For "bcl", the regression parameters are esti-
mated for each logit level. For a binary response, this argument is ignored.

dep dep defines the association structure. The default is independence "I". Other
singular options are for the exchangeable association: Necessary factor "N",
Latent categorical factor "L", Latent Beta-distributed propensity "B" (binary re-
sponse), Latent Dirichlet-distributed propensities "D" (multicategorical response),
and for the temporal association: first order Markov "M", and second order
Markov "M2" (binary response). By default, Markov structure for the adjacent
2-way dependence ratios is assumed to be stationary. Superpositions of these
structures can be imposed, such as "NL", "NB", "ND", "NM", "LM", "NLM", "NM2".
See [3-7] for further details. Parameter restrictions, covariates and functional
forms for the association parameters can also be specified. In that case the dep-argument must be a list. See examples below. For the interpretation of the association parameters, see the documentation of the support function `getass.drm`.

Ncond logical argument defining whether the regression model is marginal or conditional when the association is "N". The default is TRUE, i.e. the regression estimation is conditional on N=1. If covariates are used for the "N"-association, it is advisable to set Ncond=FALSE, since otherwise the interpretation of the regression parameters is less clear.

Lclass Number of latent classes in the population when the association is "L". Default is 2. Available only for binary response. Note that in the current implementation, the conditional probabilities are not calculated for Lclass>2. For checking the validity of the model, the user needs to check whether the estimated conditional probabilities fall within 0 and 1. See example in `getass.drm` for parameter interpretation and how to calculate the conditional probabilities.

dropout logical argument. For monotone missing patterns in longitudinal studies, this argument allows to impose a selection model (see [8] for details) on top of regression and association model to investigate the sensitivity of the results due to missingness. The model formula notation is: logit(hz(drop.cur)) = (Intercept)d+response.cur+response.prev, where response.cur denotes the effect of current, possibly missing response value and response.prev denotes the effect of previous response value. MCAR, MAR and MNAR-models can be specified by imposing restrictions on selection model parameters in dep-argument as for the association parameters. See dep above and examples below. If the response is a factor, the effect of the factor levels are estimated contrasting to the lowest level.

drop.x an optional covariate vector for the selection model. The covariate’s previous value (notation: covariate.prev) is used in the selection model.

save.profiles logical argument defining whether the fitted values of all possible profiles is saved. If FALSE, only the indicator vector (-1 for a negative, 1 for a positive profile) over all units will be saved. If the cluster size is large, using save.profiles=TRUE may result to a very large object.

pmatrix a character object specifying the name of the matrix for all possible profiles, created using `profiles.drm`. If the cluster size is large, this speeds up the estimation in case several models are fitted. See examples below.

print.level level of printing during numerical optimisation. The default is 2. See `nlm` for further details.

iterlim maximum iteration limit for the numerical maximisation. See `nlm` for further details.

... other arguments passed to `nlm`, e.g. controlling the convergence. See `nlm` for further details.

Details

drm gives maximum likelihood estimates for the combined regression and association model by decomposing a joint probability of responses in a cluster to univariate marginal or cumulative probabilities and dependence ratios of all orders. See [1] and [5] for further details. The dimensionality
of the association part is reduced by imposing a model for the association structure with dep-
argument. See getass.drm and [3-7] for details. Furthermore, a selection model can be added
on top of regression and association model. See examples below and [5] and [8] for details.

Value

drm returns an object of class drm. The function summary (i.e., summary.drm) can be used to
obtain or print a summary of the results. The generic accessor function coefficients can be
used to extract coefficients.

An object of class drm is a list containing at least the following components:

coefficients a named vector of regression, and possibly association and selection model co-
efficients.
cov.scaled a variance-covariance matrix of the parameter estimates.
fitted.marginals the fitted values for the univariate means, obtained by transforming the linear
predictors by the inverse of the link function.
fitted.conditionals in case of "L"-structure, the fitted values for the conditional univariate means,
otherwise NULL. Not yet implemented for Lclass>2; see also getass.drm
fitted.profiles the fitted response profile probabilities within each cluster, calculated by using
the maximum likelihood estimates from the model. See also save.profiles
above
deviance minus twice the maximised log-likelihood.
aic Akaike’s Information Criterion, minus twice the maximised log-likelihood plus
twice the number of coefficients. Not available if the likelihood is weighted with
the dropout probabilities.
niter the number of iterations that nlm used.
code convergence code from nlm. See nlm for details.
call the matched call.
terms the ‘terms’ object used.

WARNING

The maximum likelihood estimates may sometimes lead to negative fitted probabilities. In this case,
both generic print-methods warn about this. In this case, the model is considered to be wrongly
specified and model specification should be changed.

Author(s)

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## References


## See Also

`getass.drm`, `nlm`, `cluster`, `Time profiles.drm`, `depratio`

## Examples

```r
# Examples for binary responses
# Wheeze among Steubenville (see [3]):
# Latent Beta-distributed propensity
data(wheeze)
fit1 <- drm(wheeze~I(age>9)+smoking+cluster(id), data=wheeze, dep="B", print=0)

# Obesity among Muscatine children (see [2]):
# Analysis for completers: M2 for girls
data(obese)
fit2 <- drm(obese~age+cluster(id)+Time(year), subset=sex=="female",
            dep="M2", data=obese)

# Not run:
# Muscatine children continued (see [3]):
# LM for boys and girls separately
fit3 <- drm(obese~age+cluster(id)+Time(age), subset=sex=="male",
            dep="LM", data=obese)
fit4 <- drm(obese~age+cluster(id)+Time(age), subset=sex=="female",
            dep="LM", data=obese)
# End(Not run)
```

```
## Examples for ordinal responses

Latent Dirichlet propensities with baseline category link.

```r
options(contrasts = c("contr.treatment","contr.treatment"))
fit5 <- drm(y~critic+cluster(movie), data=movie, dep="D", link="bcl")
```

Longitudinal dataset on teenage marijuana use (see [6]):

Superposition of structures N, L and M for the girls.

```r
fit6 <- drm(y~age+cluster(id)+Time(age), data=marijuana, 
            subset=sex=="female", dep=list("NLM", ~kappa1==1, 
            ~kappa2==0, ~tau12==1, ~tau21==1, ~tau11==tau22))
```

Parameter restrictions with functions using M-structure for the boys.

Plot the second order dependence ratios:

```r
plot(depratio(y~cluster(id)+Time(age), data=marijuana, 
            subset=sex=="male"))
```

## Covariates for the association (see [7]):

```r
data(madras)
```

Plot empirical 2nd order dependence ratios with bootstrap CI's

```r
tau.madras <- depratio(symptom~cluster(id)+Time(month), data=madras, 
            boot.ci = TRUE, n.boot = 1000)
plot(tau.madras, log="y", ylim=c(1,40), plot.ci=TRUE)
```

Create matrix for profiles:

```r
W.madras <- profiles.drm(n.categories=2, n.repetitions=12, "M")
```

Create four-level covariate, combining age and sex:

```r
madras$age.sex <- factor(paste(madras$age,madras$sex,sep="."))
```

## Dropout model on top of regression & association

```r
fit8 <- drm(symptom~age+sex+month+month:age+month:sex+cluster(id)+Time(month),
            data=madras, Ncond=FALSE, save.profiles=FALSE, pmatrix="W.madras", 
            dep=list("NM",nu~nu:age.sex, 
            tau~function(a0=0,a1=0) 1+a0*c(0:10)), print=2)
```
## Continue with the madras data.

### Fit a model without the dropout model:
```
fit9 <- drm(symptom~age+sex+month+month:age+month:sex+cluster(id)+Time(month),
            data=madras, save.profiles=FALSE, pmatrix="W.madras", print=0,
            dep=list("NM", tau~function(a0=0,a1=0) 1+a0*exp(a1*c(0:10))))
```

### A dropout model assuming MCAR for the thought disorders:
```
mcar <- drm(symptom~age+sex+month+month:age+month:sex+cluster(id)+Time(month),
            data=madras, save.profiles=FALSE, pmatrix="W.madras",
            dep=list("NM", tau~function(a0=0,a1=0) 1+a0*exp(a1*c(0:10)),
                     ~symptom.cur==0,~symptom.prev==0),
            dropout=TRUE, start=c(coef(fit9), -4))
```

### A dropout model assuming MAR; including sex as a covariate:
```
mnr <- drm(symptom~age+sex+month+month:age+month:sex+cluster(id)+Time(month),
            data=madras, save.profiles=FALSE, pmatrix="W.madras",
            dep=list("NM", tau~function(a0=0,a1=0) 1+a0*exp(a1*c(0:10)),
                     ~symptom.cur==0), dropout=TRUE, drop.x=sex,
            start=c(coef(mcar),0,0))
```

### A dropout model assuming MNAR and sex as a covariate:
```
mnar <- drm(symptom~age+sex+month+month:age+month:sex+cluster(id)+Time(month),
            data=madras, save.profiles=FALSE, pmatrix="W.madras",
            dep=list("NM", tau~function(a0=0,a1=0) 1+a0*exp(a1*c(0:10))),
            dropout=TRUE, drop.x=sex, start=c(coef(mcar),0,0,0))
```

### Print out coefficients and std.errors:
```
coef(summary(mnar))
```
```
# End (Not run)
```

std.error of `symptom.cur' all over the place; too few dropouts
### for a comprehensive evaluation of the dropout mechanism

---

**getass.drm**

**Support function for drm: specification of the association model**

**Description**

A support function called by `drm` that parses from the argument `dep` the covariates and functional forms for the association model. This function should not be used directly by the user.

**Details**

In the argument `dep`, the user needs to specify the covariates and functional forms on the association parameters. The following list describes the notation and concise interpretation of the association parameters. For more details, see the reference below.
nu For "N"-structure: the proportion of susceptibles in the population, i.e. proportion of units that can have a value greater than the smallest category. Covariates can be specified. See examples below.

nu1, nu2, ..., nuk For "L"-structure: the proportion in the population in the latent class 1, 2, ..., k. The proportion in the latent class 0 can be obtained by calculating 1-nu1-nu2-... Note that for binary responses, the number of latent classes can be specified with an argument Lclass (Default 2). Covariates can be specified. See examples below.

kappa (binary response) For "L"-structure with Lclass=2 (default), the success probability in the latent class 0 divided by the success probability in the latent class 1, i.e. kappa = pr(Y=1|L=0)/pr(Y=1|L=1). Covariates can be specified; examples below.

kappa0, kappa1, ..., kappak-1 (binary response) For "L"-structure with Lclass=k+1: the success probabilities in the latent class 0, 1, ..., k-1 divided by the success probability in the latent class k. For example, kappa0 = pr(Y=1|L=0)/pr(Y=1|L=k). Covariates can be specified. See examples below.

kappa1, kappa2, ..., kappak-1 (multicategorical response with k levels) For "L"-structure with two latent classes (i.e. Lclass=2): the category probabilities in categories 1, 2, ..., k-1 in the latent class 0 divided by the corresponding probabilities in the latent class 1. For example, kappa2 = pr(Y=2|L=0)/pr(Y=2|L=1). The smallest response value is regarded as the baseline, denoted by 0

xi1, xi0 (binary response) For "B"-structure: the shape parameters of the Beta-distribution (sometimes also noted as xi1=p and xi0=q). Covariates can be specified. See examples below.

xi0, xi1, ..., xik (multicategorical response) For "D"-structure: the shape parameters of the Dirichlet distribution

tau (binary responses) For "M"-structure: adjacent second order dependence ratio. If the number of repeated measurements is greater than two, the adjacent tau's are assumed to be equal (i.e. stationarity of the dependence ratios). In order to specify equalities or functional forms (i.e. non-stationary overlapping dependence ratios), see examples below.

tau12, tau13, tau123 (binary responses) For "M2"-structure: adjacent second order dependence ratio (tau12), adjacent third order dependence ratio (tau123) and the second order dependence ratio between first and third response (tau13). If the number of repeated measurements is greater than three, the tau's are assumed to be equal (i.e. stationarity of the dependence ratios). Equalities and functional forms can be specified. See examples below.

tau11, tau12, ..., tau21, tau22, ..., taukk (multicategorical responses) For "M"-structure: adjacent second order dependence ratios for categories 1, 2, ..., k, where the smallest response value is regarded as the baseline, denoted by 0. Equalities and functional forms can be specified as for the binary "M"-structures above. See examples below.

References


See Also

drm
Examples

```r
### Example of functional forms:
## non-stationary second order Markov structure
## initial values of the dependence ratios are set to 1.
## Not run:
data(wheeze)
assoc <- list("M2",
  tau12 ~ function(a78=1, a89=1, a910=1)c(a78, a89, a910),
  tau123 ~ function(a789=1, a8910=1)c(a789, a8910),
  tau13 ~ function(a79=1, a810=1)c(a79, a810))
fit1 <- drm(wheeze~I(age>9)+smoking+cluster(id)+Time(age),
  data=wheeze, dep=assoc, print=0)
### Example of other parameter restrictions:
## fixing parameters to a known value: ~tau12==1, ~tau21==1
## setting parameters to equal: ~tau11==tau22
data(marijuana)
assoc <- list("M", ~tau12==1, ~tau21==1, ~tau11==tau22)
fit2 <- drm(y~age+cluster(id)+Time(age), data=marijuana,
  subset=sex="female", dep=assoc, print=0)
## setting all parameters to equal:
assoc <- list("M", ~tau11==tau12, ~tau11==tau21, ~tau11==tau22)
fit3 <- drm(y~age+cluster(id)+Time(age), data=marijuana,
  subset=sex="female", dep=assoc, print=0)
## End(Not run)
### Example of covariates for the association parameters:
## allow the probabilities within the latent class
## vary by sex. Note: covariate needs to be a factor.
data(obese)
assoc <- list("L", kappa ~ kappa:factor(sex))
fit4 <- drm(obese~age+cluster(id)+Time(age), data=obese,
  dep=assoc, print=0)
### Example how to derive conditional probabilities from marginals
## Fit a model with three latent classes:
data(wheeze)
latent3 <- drm(wheeze~I(age>9)+smoking+cluster(id),data=wheeze,
  dep="L",Lclass=3, print=0)
## calculate conditional probabilities:
## pr(Y=1|L=2) = pr(Y=1)/(nu2+kappa1*nu1+kappa0*(1-nu1-nu2))
## pr(Y=1|L=1) = kappa1*pr(Y=1|L=2)
## pr(Y=1|L=0) = kappa0*pr(Y=1|L=2)
est <- coef(latent3)
p02 <- latent3$fitted.marginals/
  (est["nu2"]+est["kappa1"]*est["nu1"]+
```
est["kappa0"]*(1-est["nu1"]-est["nu2"]))
psi1 <- psi2*est["kappa1"]
psi0 <- psi2*est["kappa0"]

## check the model validity, i.e. require that 0 < psi_i <1:
range(cbind(psi0,psi1,psi2))

### madras

#### Madras Longitudinal Schizophrenia Study

**Description**

Monthly records of presence/absence of psychiatric symptom ‘thought disorder’ of 86 patients over the first year after initial hospitalisation for disease.

**Usage**

data(madras)

**Format**

A data frame with 1032 observations on the following 5 variables.

- **id** identification number of a patient
- **symptom** response ‘thought disorder’: 0 = absent, 1 = present
- **month** month since hospitalisation
- **age** age indicator: 0 = less than 20 years, 1 = 20 or over
- **sex** sex indicator: 0 = male, 1 = female

**Source**


http://faculty.washington.edu/heagerty/Books/AnalysisLongitudinal/datasets.html

**References**

marijuana Longitudinal data set on teenage marijuana use

Description
This data set is from US National Youth Survey reporting a repeated questionnaire on marijuana use of 237 teenagers yearly from ages 13 to 17 on an ordinal scale.

Usage
data(marijuana)

Format
This data frame contains the following columns:

- id identification number of a teenager.
- y marijuana response, 1: never; 2: less than once a month; 3: more than once a month.
- sex a factor with levels female male
- age age as a factor with levels 13 14 15 16 17

Source

References

movie Movie reviews from a Variety magazine

Description
This dataset contains reviews of 93 movies by four critics in the Variety magazine from April 1995 through March 1997.

Usage
data(movie)
### Format

This data frame contains the following columns:

- **movie**: Identification number of a movie.
- **y**: Review response, 1: Positive; 2: Mixture of positive and negative; 3: Negative.
- **critic**: An ordered factor: critics with levels `medved < siskel < ebert < lyons`.

### Source


### References


---

#### obese

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
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<tbody>
<tr>
<td><strong>Obesity among Muscatine children</strong></td>
<td></td>
</tr>
</tbody>
</table>

### Description

Data of the completers concerning the presence or absence of obesity in five age cohorts in Muscatine, Ohio, measured repeatedly in 1977, 1979 and 1981.

### Usage

```r
data(obese)
```

### Format

A data frame with 5310 observations on the following 5 variables.

- **id**: Identification number of a child
- **obese**: A binary indicator of obesity
- **sex**: A factor with levels `male female`
- **year**: Year of measurement
- **age**: A factor indicating age cohorts from `{5,7}` to `{17,19}`

### Source


http://www.biostat.harvard.edu/fitzmaur/ala/obesity.txt
profiles.drm

Creates a support matrix for ‘drm’ for profile probability calculation

Description

Creates a support matrix for the calculation of all possible profile probabilities using the ML estimates obtained from drm.

Usage

profiles.drm(n.categories, n.repetitions, structure = "exchangeable")

Arguments

n.categories Number of response variable categories
n.repetitions Number of response repetitions within a cluster
structure Association structure indicator of the model to be fitted: "exchangeable" if the structure is exchangeable, otherwise either "M" or "M2"

Details

Creation of this support object is useful if the cluster size is large and if several models are fitted to the same dataset. Avoids creating the same matrix over and over again for each model fit. See examples for drm.

Value

If structure="exchangeable", returns a matrix with row and column size equal to n.categories to the power of n.repetitions. For temporal structures "M" and "M2", the result is an array.

See Also

drm

References


wheeze

Examples

```r
## use marijuana-data
data(marijuana)

## create matrix for profiles:
W.mari <- profiles.drm(3, 5, "M")

## fit the model using W.mari:
fit <- drm(y~age+cluster(id)+Time(age), data=marijuana,
           subset=sex=="male",pmatrix="W.mari", save.profiles=FALSE,
           dep=list("M",tau12~function(a=1,b=0) a+b*c(0:3),
                    tau21~function(a=1,b=0) a+b*c(0:3)),print=0)

## a speedy way of saving the profile probabilities to the object:
fit <- drm(y~age+cluster(id)+Time(age), data=marijuana,
           subset=sex=="male",pmatrix="W.mari", save.profiles=TRUE,
           dep=list("M",tau12~function(a=1,b=0) a+b*c(0:3),
                    tau21~function(a=1,b=0) a+b*c(0:3)),print=0,
           start=coef(fit))
```

wheeze

Wheeze among Steubenville children

Description

wheeze is a longitudinal dataset reporting the presence and absence of wheeze at ages 7, 8, 9 and 10 among 537 Steubenville children.

Usage

data(wheeze)

Format

This data frame contains the following columns:

- **id** identification number of a child.
- **wheeze** a binary indicator of the presence of wheeze.
- **age** a numeric vector of age from 7 to 10.
- **smoking** a binary indicator of mother’s smoking status at baseline.

Source

References

Index

*Topic arith
  depratio, 3

*Topic array
  profiles.drm, 16

*Topic datasets
  madras, 12
  marijuana, 13
  movie, 14
  obese, 15
  wheeze, 17

*Topic misc
  cluster, 2
  drm-internal, 4
  Time, 1

*Topic models
  drm, 4

*Topic utilities
  getass.drm, 10

Cluster, 2, 2, 3, 8

depratio, 2, 3, 8

drm, 2, 3, 4, 10, 11, 16

drm-internal

getass.drm, 5–8, 10

getpath.drm (drm-internal), 4

kronecker.drm (drm-internal), 4

kronecker.drm (drm-internal), 4

loglikd.drm (drm-internal), 4

logliks.drm (drm-internal), 4

madras, 12

marijuana, 13

movie, 14

na.include (drm-internal), 4

nlm, 6, 8

obese, 15

plot.depratio (depratio), 3

print.depratio (depratio), 3

print.drm (drm), 4

print.summary.drm (drm), 4

profiles.drm, 6, 8, 16

strata (drm-internal), 4

summary.drm (drm), 4

Time, 1, 2, 3, 8

untangle.specials (drm-internal),

wheeze, 17

19