

Package ‘PBImisc’

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Type Package

Title A set of datasets used in my classes or in the book „Modele liniowe i mieszane w R, wraz z przykladami w analizie danych”

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Description A set of datasets prepared as a support for my classes or the book „Modele liniowe i mieszane w R, wraz z przykladami w analizie danych”

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License GPL (>= 2)

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LazyData yes

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PBImisc-package	<i>PBI misc</i>
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Description

A set of datasets used in my classes or in the book „Modele liniowe i mieszane w R, wraz z przykladami w analizie danych”

Details

Package: PBImisc
 Type: Package
 Version: 0.999
 Date: 2013-07-25
 License: GPL-2

General Description

A set of datasets some of them are my original ones, some are taken from other packages of literature.

Author(s)

Przemyslaw Biecek

Maintainer: You should complain to Przemyslaw Biecek <przemyslaw.biecek@gmail.com>

References

Przemyslaw Biecek „Modele liniowe i mieszane w R, wraz z przykladami w analizie danych” 2011, Wydawnictwo PWN

Examples

```
# here you will find some examples  
#
```

AML	<i>Acute myeloid leukemia AML study</i>
-----	---

Description

This dataset bases on blood samples for patients with Acute myeloid leukemia.

Usage

```
data(AML)
```

Format

```
data.frame with 66 obs. and 5 variables  
  
Mutation Factor w/ 4 levels CBFbeta, FLT3, None, Other  
CD14.control CD14 level in the control group  
CD14.D3 CD14 level after D3 treatment  
CD14.1906 CD14 level after D3 homolog 1906 treatment  
CD14.2191 CD14 level after D3 homolog 2191 treatment
```

Details

Mutation - mutated gene that causes leucemia, one of following CBFbeta, FLT3, None, Other
CD14.control, CD14.D3, CD14.1906, CD14.2191 - effects in vitamin D3 or its homologues

Source

Artificial dataset generated to be consistent with Ewa M. study

Examples

```
library(lattice)  
data(AML)  
AML2 = reshape(AML, direction="long", varying=colnames(AML)[2:5])  
bwplot(CD14~time|Mutation, AML2)  
interaction.plot(AML2$time,AML2$Mutation, AML2$CD14)
```

apartments

Apartment prices in Warsaw in years 2007-2009

Description

Dataset downloaded from website <http://www.oferty.net/>. Dataset contains offer and transactional prices for apartments sold in in Warsaw in years 2007-2009.

Usage

```
data(apartments)
```

Format

data.frame with 973 obs. and 16 variables

year data year of the transaction

month data month of the transaction

surface apartment area in m2

city city (all transactions are from Warsaw)

district district in which the apartment is located, factor with 28 levels

street street in which the apartment is located

n.rooms number of rooms

floor floor

construction.date the construction year

type ownership rights

offer.price price in the offer

transaction.price declared price in the transaction

m2.price price per m2

condition apartment condition, factor with 5 levels

lat, lon latitude and longitude coordinates for district center

Details

This and other related dataset you may find here <http://www.oferty.net/>.

Source

website <http://www.oferty.net/>

Examples

```

data(apartments)
library(lattice)
xyplot(m2.price~construction.date|district, apartments, type=c("g","p"))

#
# apartments2 = na.omit(apartments[,c(13,1,3,5,7,8,9,10,14,15,16)])
# wsp = (bincombinations(10)==1)[-1,]
# params = matrix(0, nrow(wsp), 3)
# for (i in 1:nrow(wsp)) {
#   model = lm(m2.price~., data=apartments2[,c(TRUE,wsp[i,])])
#   params[i,1] = AIC(model, k=log(nrow(apartments2)))
#   params[i,2] = model$rank
#   params[i,3] = summary(model)$adj.r.squared
# }
# plot(params[,2], params[,3], xlab="no. of regressors", ylab="adj R^2")
#

```

boxplotpp

boxplot plus plus

Description

boxplotpp

Usage

```

boxplotpp(x, xname=seq(1:ncol(x)), utitle="", addLines=TRUE,
          color = ifelse(addLines, "white", "lightgrey"), ...)

boxplotInTime(x, xname, additional=T, color = ifelse(additional,
  "white", "lightgrey"), main="", ylim=range(unlist(x),na.rm=T), ...,
  points = dim(x)[2], at = 1:points)

```

Arguments

x	TODO
xname	TODO
utitle	TODO
addLines	TODO
color	TODO
additional	TODO
main	TODO
points	TODO
at	TODO
ylim	TODO
...	TODO

Details

TODO

Value

TODO

Author(s)

Przemyslaw Biecek

Examples

```
#TODO
```

corn

A datasets relatead to gene expression in corn

Description

Dataset from the book „Modele liniowe i mieszane w R, wraz z przykladami w analizie danych”.

Usage

```
data(corn)
```

Format

data.frame with 5339 obs. and 36 variables

A dataset with expression of 5339 genes. Each column corresponds to a single experiment. Column name codes the setup of experiment. For example DH.C.1 is related to line DH in the condition C and it is a first technical replicate of this set of conditions.

Note that a noise injection was added to this data, in order to obtain the original dataset please contact with the package maintainer.

Details

Dataset from the book „Modele liniowe i mieszane w R, wraz z przykladami w analizie danych”.

Used as an example of modeling of data from expression microarrays with the use of models with mixed effects.

Examples

```
## Not run:

require(lme4)

names <- colnames(corn)
X <- t(matrix(unlist(strsplit(names, "."), fixed=T), 3, 36))
X <- data.frame(X)
colnames(X) <- c("spec", "temp", "plant")

summary(X)

y <- corn[4662,]
lmer(y~spec*temp + (1|plant:spec:temp), data=X)

## End(Not run)
```

dementia

A set of datasets related to dementia

Description

Dataset from the book „Modele liniowe i mieszane w R, wraz z przykladami w analizie danych”.

Usage

```
data(dementia)
```

Format

data.frame with 1000 obs. and 4 variables

demscore score of dementia

age age, a factor with two levels

sex sex, a factor with two levels

study a source of data, a factor with 10 levels

Details

Dataset from the book „Modele liniowe i mieszane w R, wraz z przykladami w analizie danych”.

Used as an example of mixed modeling in meta analysis.

Examples

```
## Not run:
require(lme4)
modelFullI <- lmer(demscore~age*sex+(age*sex|study), data=dementia,
                  REML=FALSE)
summary(modelFullI)

## End(Not run)
```

Drosophila

Drosophila datasets and QTL mapping study

Description

Two datasets with genotypes and phenotypes for backcrossed Drosophilas.

Usage

```
data(Drosophila)
```

Format

Two datasets with genotypes and phenotypes for backcrossed Drosophilas.

The set of 41 markers describes genotypes while 5 variables describe phenotypes. See references for more details.

bm A data.frame with 370 obs. and 46 variables, first 41 are genotypes of gene markers, last five describes genotypes

bs A data.frame with 402 obs. and 46 variables, first 41 are genotypes of gene markers, last five describes genotypes

chr Factor w/ 4 levels CBFbeta, FLT3, None, Other

pos Markers position on chromosom in centimorgnas

Details

The phonotype pc1 is nicely described by genotype in both backcrossed datasets.

Source

Genetic Architecture of a Morphological Shape Difference Between Two Drosophila Species Zhao-Bang Zenga, Jianjun Liu, Lynn F. Stamb, Chen-Hung Kao, John M. Mercer, Cathy C. Laurie Genetics, Vol. 154, 299-310, January 2000

Examples

```

data(Drosophila)
library(lattice)
# calculate log likelihoods
pval1 = numeric(41)
for (i in 1:41) {
  y = Drosophila$bm$pc1
  x = factor(Drosophila$bm[,i])
  pval1[i] = logLik(lm(y~x))
}
# loglikelihood plot
xyplot(pval1~pos|chr, data=Drosophila, type=c("p","l"),
       pch=19, ylab="log likelihood")

```

 ecap

Epidemiology of Allergic Disease in Poland

Description

This dataset touch one particular aspect from ECAP dataset. The original dataset is much more richer.

Usage

```
data(ecap)
```

Format

data.frame with 2102 obs. and 9 variables

city, district City and district, city is a factor with nine levels, the district effect is nested in the city effect

sex Sex

weight,height Weight and height

house.surface Surface of house in which the pearson live

PNIF Peak Nasal Inspiratory Flow

age Age of the pearson

allergenes Number of allergens

Details

PNIF stands for Peak Nasal Inspiratory Flow

Source

Artificial dataset generated to be consistent with ECAP (Epidemiologia Chorob Alergicznych w Polsce) study <http://www.ecap.pl/>

Examples

```
data(ecap)
library(lattice)
xyplot(PNIF~age|city, data=ecap, type=c("p","g","smooth"))
```

eden

European day hospital evaluation

Description

This dataset bases on original study of European day hospital evaluation

Artificial dataset (subset from real dataset with some random modifications). Do not use it for derivation of real conclusions.

Usage

```
data(eden)
```

Format

data.frame with 642 obs. and 12 variables

mdid Medical doctor id, there are 24 different MDs which examine patients

center City in which the examination takes place

BPRS.Maniac, BPRS.Negative, BPRS.Positive, BPRS.Depression BPRS stands for Brief Psychiatric Rating Scale, scores are averaged in four subscales

BPRS.Average Average from 24 questions

MANSA Scale which measures Quality of Life (Manchester Short Assessment of Quality of Life)

sex Sex

children Number of childs

years.of.education Number of years of education

day Hospitalization mode, day or stationary

Details

This dataset touch one particular aspect from EDEN dataset. The original dataset is much more richer.

Source

Artificial dataset generated to be consistent with Joanna R. study.

Bases on European day hospital evaluation, <http://www.edenstudy.com/>

Examples

```
data(eden)
library(lattice)
xyplot(BPRS.Average~MANSA|center, data=eden, type=c("p","g","smooth"))
```

elastase

Relation between graft function and elastase

Description

Relation between graft function and elastase from nephrology study.

Usage

```
data(elastase)
```

Format

data.frame with 54 obs. and 5 variables

sex, age, weight Patient's sex, age and weight

elastase Elastase concentration

GFR Patient's GFR (glomerular filtration rate)

Details

Artificial dataset (real one with some random modifications). Do not use it for medical reasoning.

Source

Artificial dataset generated to be consistent with Malgorzata L. study

Examples

```
data(elastase)
library(lattice)
xyplot(GFR~elastase, data=elastase, type=c("p","r","g"))
```

endometriosis	<i>Endometriosis study</i>
---------------	----------------------------

Description

How the endometriosis affects concentration of alpha and beta factors in the blood.

Usage

```
data(endometriosis)
```

Format

data.frame with 165 obs. and 4 variables

disease disease, blood samples were taken from women with endometriosis or from healthy ones

phase phase in the menstrual cycle as the examination day (proliferative or secretory)

alpha.factor, beta.factor concentration of alpha and beta factors in blood

Details

Dataset used as example of ANCOVA

Source

Artificial dataset generated to be consistent with Ula S. study

Examples

```
data(endometriosis)
library(lattice)
xyplot(log(alpha.factor)~log(beta.factor)|disease*phase,
        data=endometriosis, type=c("p", "r"))
summary(aov(alpha.factor~beta.factor*disease*phase, data=endometriosis))
```

eunomia	<i>European Evaluation of Coercion in Psychiatry and Harmonisation of Best Clinical Practise</i>
---------	--

Description

This dataset touch one particular aspect from EUNOMIA dataset. The original dataset is much more richer.

Usage

```
data(eunomia)
```

Format

data.frame with 2008 obs. and 15 variables

CENTRE13 Center in which the patient is hospitalized, factor with 13 levels

SUBJECT Patients ID

GENDER, AGE, NUM.HOSP Gender, age and number of hospitalizations of given patient

CAT.T1, CAT.T2, CAT.T3 Clients Scale for Assessment of Treatment, short assessment, which measures the impact of COPD on a patients life, measured in times: T1, T2 and T3

BPRS.T1, BPRS.T2, BPRS.T3 Average score for Brief Psychiatric Rating Scale, measured in times: T1, T2 and T3

MANSA.T1, MANSA.T2, MANSA.T3 Scale which measures Quality of Life (Manchester Short Assessment of Quality of Life), measured in times: T1, T2 and T3

ICD10 International Statistical Classification of Diseases and Related Health Problems 10th Revision (ICD-10)

Details

Artificial dataset generated to be consistent with Eunomia study (European Evaluation of Coercion in Psychiatry and Harmonisation of Best Clinical Practise)

Source

Artificial dataset generated to be consistent with Joanna R. study.

Eunomia dataset, <http://www.eunomia-study.net/>

Examples

```
data(eunomia)
library(lattice)
bwplot(CENTRE13~BPRS.T1, data=eunomia)
xyplot(BPRS.T1~MANSA.T1|CENTRE13, data=eunomia, type=c("p","g","smooth"))
```

 flu

Numbers of flu occurrences in the 10 years period in the Poland.

Description

Data from National Institute of Hygiene reports. Each row correspond to one record from NIH institute.

Usage

```
data(flu)
```

Format

data.frame with 6384 obs. and 11 variables

region Region for which given report was taken. A factor with 16 levels

inception.no Number of flu occurrences in given region for given report period (one or two weeks)

inception.no Number of flu occurrences in given region for given report period (one or two weeks)

inception.rate Number of flu occurrences normalized to 100k people

inception.no.0-14, inception.no.15+, inception.rate.0-14, inception.rate.15+ Absolute and normalized numbers of flu occurrences calculated for age group 0-14 or 15+

date Date of given report

date.id Report id, there is 38 reports per year

latitude, longitude Geographical coordinates for region

Details

Dataset used during the third edition of WZUR conference, see <http://www.biecek.pl/WZUR3/wzurDane.html> for more information.

Source

Reports from National Institute of Public Health - National Institute of Hygiene, see: <http://www.pzh.gov.pl>

More information: <http://www.biecek.pl/WZUR3/wzurDane.html>

Examples

```
data(flu)
library(ggplot2)
subflu = flu[flu$region=="Mazowieckie", ]
# linear scale
qplot(date, inception.rate, data=subflu, geom="line")+scale_y_sqrt() +theme_bw()

# polar coordinates
qplot(1 + date.id*12/38, inception.rate, data=subflu, geom="path", xlab="month")+
  scale_y_sqrt()+geom_smooth(span=0.1, se=FALSE, size=2, col="red") +
  coord_polar() +theme_bw()
```

genomes

724 bacterial genomes data

Description

Few parameters gathered for 724 bacterial species.

Usage

```
data(genomes)
```

Format

data.frame with 724 obs. and 7 variables
organism Organism name, unique value for every row
group Group, a factor with 22 levels
size Genome size in Mbp
CG GC content for genome sequence
habitat, temp.group, temperature Where does this bacteria live?

Details

This dataset is prepared by Pawel M., data are taken from NCBI repository.
See <http://www.ncbi.nlm.nih.gov/> for more details

Source

Pawel M. study

Examples

```
data(genomes)
library(ggplot2)
# is this relation linear ?
qplot(size,GC, data=genomes) + theme_bw()
# or linear in log scales?
qplot(size,GC, data=genomes, log="xy") + theme_bw()
```

heights

Husband and Wife heights

Description

A dataset from „A modern approach to regression with R”. Simon J. Sheather 2009 . Paired heights for husbands and wives.

Usage

```
data(heights)
```

Format

data.frame with 96 obs. and 2 variables
Husband, Wife Height of husband and wife.

Details

The dataset from „A modern approach to regression with R”. Simon J. Sheather 2009

Source

A modern approach to regression with R. Simon J. Sheather 2009

Examples

```
data(heights)
plot(Husband~Wife, data=heights, pch=19)
abline(lm(Husband~Wife, data=heights), col="red")
abline(lm(Husband~Wife-1, data=heights), col="blue")
```

histpp

hist plus plus

Description

histpp

Usage

```
histpp(x, xname="", utitle="")
```

Arguments

x	TODO
xname	TODO
utitle	TODO

Details

TODO

Value

TODO

Author(s)

Przemyslaw Biecek

References

TODO

Examples

```
# TODO
```

kidney

Graft function after kidney transplantation

Description

Artificial dataset (subset from real dataset with some random modifications)

Usage

```
data(kidney)
```

Format

data.frame with 334 obs. and 16 variables

recipient.age, donor.age Age of donor and recipient

CIT Cold ischemia time

discrepancy.AB, discrepancy.DR discrepancies in AB and DR antibodies

therapy scheme of immunosuppression

diabetes diabetes

bp1.drugs number of drugs for blood pressure lowering

MDRD7, MDRD30, MDRD3, MDRD6, MDRD12, MDRD24, MDRD36, MDRD60 MDRD (Modification of Diet in Renal Disease) as a estimator of glomerular filtration rate (GFR) from serum creatinine, measured 7, 30 days and 3, 6, 12, 24, 36 and 60 months after kidney transplantation

Details

Example of longitudinal study, note that graft for all patients survives 5 years after kidney transplantation.

Source

Artificial dataset generated to be consistent with Maria M. study

Examples

```
data(kidney)
boxplotInTime(kidney[,9:16], colnames(kidney[,9:16]), additional=TRUE)
```

Likelihood displacements

Log-likelihood displacements for single observation and single grouping variable

Description

Functions for log-likelihood displacements for each observation or each level of given factor

Usage

```
recalculateLogLik(model, fixef = fixef(model), vcor = VarCorr(model))
groupDisp(formula, data, var)
obsDisp(formula, data, inds=1:nrow(data))
```

Arguments

model	a mixed model of the class mer,
fixef, vcor	model parameters log-likelihood evaluation, if not provided then the estimates extracted from the 'model' parameter will be used
formula	a model formula that will be passes to the nlme function
data	a data frame
var	a name of grouping variable (factor) for which the group log-likelihood displacement will be performed
inds	indexes of observations for which observation log-likelihood displacement will be performed

Details

Likelihood displacement is defined as a difference of likelihoods calculated on full dataset for two models with different sets of parameters. The first model is a model with ML estimates obtained for full dataset, while the second model is a model with ML estimates obtained on dataset without a selected observation or group of observations.

Likelihood displacements are used in model diagnostic.

Note that these functions reestimate coefficients in a set of model may be a time consuming.

The function `recalculateLogLik()` calculated a log-likelihood for model defined by the object `model` and model parameters defined in following function arguments.

The functions `groupDisp()` and `obsDisp()` calculates how the log-likelihood will decrease if selected groups or selected observations will not be used for parameter estimates. Note that log-likelihood is calculated on full dataset.

Author(s)

Przemyslaw Biecek

Examples

```
data(eunomia)
require(lme4)
set.seed(1313)
eunomias <- eunomia[sample(1:2000,100),]
groupDisp(formula = BPRS.T2~ (1|CENTRE13), data=eunomias, var="CENTRE13")

obsDisp(formula = BPRS.T2~ (1|CENTRE13), data=eunomias, inds = 1:10)

obsDisp(formula = BPRS.T2~ (1|CENTRE13), data=eunomias)
```

milk

Milk yield data

Description

Milk yield data for 10 unrelated cows

Usage

```
data(milk)
```

Format

data.frame with 40 obs. and 2 variables

cow cow id, a factor with 10 levels

milk.amount milk amount in kgs per week

Details

Weekly milk yield amount for 10 cows. For every cow 5 measurements are taken.

Examples

```
data(milk)
library(lattice)
# change the order of levels
milk$cow = reorder(milk$cow, milk$milk.amount, mean)
#plot it
dotplot(cow~milk.amount, data=milk)
```

`milkgene`*Mutation in BTN3A1 gene and milk yield*

Description

It is known that BTN3A1 (Butyrophilin subfamily 3 member A1) has a crucial function in the secretion of lipids into milk. Does the SNP mutation in it change the average milk yield?

Usage

```
data(milkgene)
```

Format

data.frame with 1000 obs. and 5 variables

cow.id cow id, there is 465 cows in this study

btn3a1 btn3a1 genotype, a factor with two levels

lactation for some cows there are milk yields for four lactations for other only for the first one

milk, fat milk and fat amount in kgs per lactation

Details

Milk and fat yields for 465 cows. For every cow also the genotype of btn3a1 is measured.

Source

Artificial dataset generated to be consistent with Joanna Sz. study

Examples

```
data(milkgene)
library(lattice)
xyplot(milk~fat, data=milkgene)
bwplot(milk~lactation, data=milkgene)
```

musculus	<i>A dataset related to mice musculus growth which depends on diet and genetic structure</i>
----------	--

Description

Dataset from the book „Modele liniowe i mieszane w R, wraz z przykladami w analizie danych”.

Usage

```
data(musculus)
```

Format

data.frame with 30 obs. and 10 variables

id an individual id

dadid id of father, 0 for founders

momid id of mother, 0 for founders

sex sex

sigma maximal stress

diet diet, D1 or D2

k1 resilience coefficient in point 1

k2 resilience coefficient in point 2

E1 Younga module in point 1

E2 Younga module in point 2

Details

Dataset from the book „Modele liniowe i mieszane w R, wraz z przykladami w analizie danych”.

Used as an example of model with mixed effects where random effects have know dependency structure, here related to the kinship coefficient.

Examples

```
## Not run:
require(kinship2)
pedmus <- pedigree(musculus$id, musculus$dadid, musculus$momid, musculus$sex)
plot(pedmus, affected=musculus$diet)

fam <- makefamid(musculus$id, musculus$dadid, musculus$momid)
kmatrix <- makekinship(fam, musculus$id, musculus$dadid, musculus$momid)
kmatrix[1:5,1:15]

## End(Not run)
```

Plot results from post hoc testing

A function for visual representation of pairwise testing (both for pairwise.t.test and pairwise.wilcox.test)

Description

Plot sets of groups in which means or medians are not significantly different.

On the vertical axis the means are marked. Then in a greedy fashion means that are not significantly different are linked by a line.

Usage

```
plotPairwiseTests(p.vals, means, alpha=0.05, digits=3, mar=c(2,10,3,1), ...)
```

Arguments

<code>p.vals</code>	A slot \$p.value from the object returned by pairwise.*.test function
<code>means</code>	A vector of means or medians corresponding to p.vals object (the order of groups should be the same in both objects)
<code>alpha</code>	A threshold for p.value
<code>digits</code>	Number of significant digits to be plotted with means.
<code>mar</code>	Figure margins, left margin should be large enough to handle names of groups
<code>...</code>	These arguments are passed to the plot function.

Author(s)

Przemyslaw Biecek

Examples

```
data(iris)
tmp1 <- pairwise.wilcox.test(iris$Sepal.Width, iris$Species)
tmp2 <- tapply(iris$Sepal.Width, iris$Species, median, na.rm=TRUE)
plotPairwiseTests(tmp1$p.value, tmp2, alpha=0.001)
```

schizophrenia	<i>Genetic background of schizophrenia</i>
---------------	--

Description

Dataset with genotypes and phenotypes for 98 patients with schizophrenia disorder.

Usage

```
data(schizophrenia)
```

Format

data.frame with 98 obs. and 9 variables

Nfkb, CD28, IFN Genotypes for SNP mutations in selected three genes

Dikeos.manic, Dikeos.reality.distortion, Dikeos.depression, Dikeos.disorganization, Dikeos.negative
Dikeos scores for schizophrenia measured in five domains

Dikeos.sum Sum of Dikeos scores

Details

Alleles for two SNPs in genes: Nuclear Factor-Kappa Beta (Nfkb) and Cluster of Differentiation 28 (CD28) were examined as well as mental health described by five scales (see Dikeos 2008 for more details).

Source

Artificial dataset generated to be consistent with Dorota F. study

Examples

```
data(schizophrenia)
attach(schizophrenia)
interaction.plot(CD28, Nfkb, Dikeos.sum)
interaction.plot(Nfkb, CD28, Dikeos.sum)
model.tables(aov(Dikeos.sum~Nfkb*CD28))
```

SejmSenat

SejmSenat

Description

Changes in word usage in consecutive Sejm and Senate cadencies

Usage

```
data(SejmSenat)
```

Format

contingency matrix with 973 27 rows and 8 columns

Sejm. I, Sejm. II, Sejm. III, Sejm. IV, summary of records from four Sejm cadencies

Senat. II, Senat. III, Senat. IV, Senat. V, summary of records from four Senate cadencies

adj, adja, adjp, adv, aglt, bedzie,conj, depr, fin, ger, ign, imps, impt, inf, interp,num, pact, pant, pcon, ppas, pra
word modes

Details

Word usage statistics generated from Sejm and Senat records

Source

The IPI PAN Corpus webpage <http://korpus.pl/>

Examples

```
data(SejmSenat)
library(ca)
# can you see some patterns?
plot(ca(SejmSenat[-15,]), mass =c(TRUE,TRUE), arrows =c(FALSE,TRUE))
```

vaccination

Effective dose study

Description

What is the minimal dose that is effective?

Usage

```
data(vaccination)
```


Format

data.frame with 100 obs. and 2 variables

response a reaction effect

dose a dose that was applied

Details

Responses for different doses of treatment.

Source

Artificial dataset generated to be consistent with Karolina P. study

Examples

```
data(vaccination)
library(lattice)
bwplot(response~dose, data=vaccination)
```

YXZ

Artificial dataset which shows the differences between tests type I and III (sequential vs. marginal)

Description

Artificial dataset, shows inconsistency for test type I and III

Usage

```
data(YXZ)
```

Format

data.frame with 100 obs. and 3 variables

X, Z explanatory variables

Y response variable

Details

See the example, results for statistical tests are inconsistent due to correlation between X and Z variables

Source

Artificial dataset, generated by PBI

Examples

```
attach(YXZ)
summary(lm(Y~X+Z))
anova(lm(Y~Z+X))
anova(lm(Y~X))
anova(lm(Y~Z))
```

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