

# Package ‘MethComp’

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**Title** Functions for analysis of agreement in method comparison studies.

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**Description** Methods (standard and advanced) for analysis of agreement between measurement methods.

**License** GPL (>= 2)

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abconv	<i>Derive linear conversion coefficients from a set of indeterminate coefficients</i>
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## Description

If a method comparison model is defined as  $y_{mi} = \alpha_m + \beta_m \mu_i$ ,  $m = 1, 2$   $y_{mi} = \alpha_m + \beta_m \mu_i$ ,  $m=1,2$  the coefficients of the linear conversion from method 1 to 2 are computed as:  $\alpha_{2|1} = -\alpha_2 - \alpha_1 \beta_2 / \beta_1$   $\alpha_{2|1} = -\alpha_2 - \alpha_1 \beta_2 / \beta_1$   $\beta_{2|1} = \beta_2 / \beta_1$  Moreover the the point where the linear conversion function intersects the identity line is computed too.. The function is designed to work on numerical vectors of posterior samples from BUGS output.

**Usage**

```
abconv( a1, b1 = 1:4, a2 = NULL, b2 = NULL,
        col.names = c("alpha.2.1", "beta.2.1", "id.2.1") )
```

**Arguments**

a1	Numerical vector of intercepts for first method. Alternatively a dataframe where the vectors are selected from.
b1	Numerical vector of slopes for first method. If a1 is a dataframe, b1 is assumed to be a numerical vector of length 4 pointing to the columns of a1 with the intercepts and slopes.
a2	Numerical vector of intercepts for second method.
b2	Numerical vector of slopes for second method.
col.names	Names for the resulting three vectors.

**Value**

A dataframe with three columns: intercept and slope for the conversion from method 1 to method 2, and the value where the conversion is the identity.

**Author(s)**

Bendix Carstensen, Steno Diabetes Center, <http://BendixCarstensen.com>

**References**

B Carstensen: Comparing and predicting between several methods of measurement, Biostatistics, 5, pp 399-413, 2004

**See Also**

[BA.plot](#), [MCMcmc](#)

**Examples**

```
abconv( 0.3, 0.9, 0.8, 0.8 )
```

---

AltReg

---

*Estimate in a method comparison model with replicates*


---

**Description**

Estimates in the general model for method comparison studies with replicate measurements by each method, allowing for a linear relationship between methods, using the method of alternating regressions.

**Usage**

```
AltReg( data,
        linked = FALSE,
        IxR = linked,
        MxI = TRUE,
        varMxI = FALSE,
        eps = 0.001,
        maxiter = 50,
        trace = FALSE,
        sd.lim = 0.01,
        Transform = NULL,
        trans.tol = 1e-6 )
```

**Arguments**

data	Data frame with the data in long format, (or a <a href="#">Meth</a> object) i.e. it must have columns meth, item, repl and y
linked	Logical. Are the replicates linked across methods? If true, a random item by repl is included in the model, otherwise not.
IxR	Logical, alias for linked.
MxI	Logical, should the method by item effect (matrix effect) be in the model?
varMxI	Logical, should the method by item effect have method-specific variances. Ignored if only two methods are compared. See details.
eps	Convergence criterion, the test is the max of the relative change since last iteration in both mean and variance parameters.
maxiter	Maximal number of iterations.
trace	Should a trace of the iterations be printed? If TRUE iteration number, convergence criterion and current estimates of means and sds are printed.
sd.lim	Estimated standard deviations below sd.lim are disregarded in the evaluation of convergence. See details.
Transform	A character string, or a list of two functions, each other's inverse. The measurements are transformed by this before analysis. Possibilities are: "exp", "log", "logit", "pctlogit" (transforms percentages by the logit), "sqrt", "sq" (square), "c1l" (complementary log-minus-log), "l1" (log-minus-log). For further details see <a href="#">choose.trans</a> .
trans.tol	The tolerance used to check whether the supplied transformation and its inverse combine to the identity. Only used if Transform is a list of two functions.

**Details**

When fitting a model with both IxR and MxI interactions it may become very unstable to have different variances of the MxI random effects for each method, and hence the default option is to have a constant MxI variance across methods. On the other hand it may be grossly inadequate to assume these variances to be identical.

If only two methods are compared, it is not possible to separate different variances of the MxI effect, and hence the varMxI is ignored in this case.

The model fitted is formulated as:

$$y_{mir} = \alpha_m + \beta_m(\mu_i + a_{ir} + c_{mi}) + e_{mir}$$

and the relevant parameters to report are the estimates sds of  $a_{ir}$  and  $c_{mi}$  multiplied with the corresponding  $\beta_m$ . Therefore, different values of the variances for MxI and IxR are reported also when varMxI==FALSE. Note that varMxI==FALSE is the default and that this is the opposite of the default in [BA.est](#).

## Value

An object of class `c("MethComp", "AltReg")`, which is a list with three elements:

Conv	A 3-way array with the 2 first dimensions named "To:" and "From:", with methods as levels. The third dimension is classified by the linear parameters "alpha", "beta", and "sd".
VarComp	A matrix with methods as rows and variance components as columns. Entries are the estimated standard deviations.
data	The original data used in the analysis, with untransformed measurements (ys). This is needed for plotting purposes.

Moreover, if a transformation was applied before analysis, an attribute "Transform" is present; a list with two elements `trans` and `inv`, both of which are functions, the first the transform, the last the inverse.

## Author(s)

Bendix Carstensen, Steno Diabetes Center, <bxcc@steno.dk>, <http://BendixCarstensen.com>.

## References

B Carstensen: Comparing and predicting between several methods of measurement. *Biostatistics* (2004), 5, 3, pp. 399–413.

## See Also

[BA.est](#), [DA.reg](#), [Meth.sim](#), [MethComp](#)

## Examples

```
data( ox )
ox <- Meth( ox )
## Not run:
ox.AR <- AltReg( ox, linked=TRUE, trace=TRUE, Transform="pctlogit" )
str( ox.AR )
ox.AR
# plot the resulting conversion between methods
plot(ox.AR,pl.type="conv",axlim=c(20,100),points=TRUE,xaxs="i",yaxs="i",pch=16)
# - or the rotated plot
```

```
plot(ox.AR,pl.type="BA",xlim=c(20,100),points=TRUE,xaxs="i",yaxs="i",pch=16)
## End(Not run)
```

---

Ancona

---

*Data from a rating experiment of recorgnizing point counts.*


---

## Description

At the course "Statsitcal Analysis of Method Comparison Studies" ai the SISMEC conference in Ancona, on 28 September 2011, the participants on the course were used as raters of ten pictures of points. Pitures were shown 3 times each to the participants, and they assessed the number of points in each.

## Usage

```
data(Ancona)
```

## Format

A data frame with 510 observations on the following 4 variables.

`rater` a factor with 17 levels

`item` a numeric vector indicating the pictures shown. The value is the actual number of points.

`repl` a numeric vector, replicate number

`score` a numeric vector, the number of points in `item`

## Source

The course "Statsitcal Analysis of Method Comparison Studies" ai the SISMEC conference in Ancona, on 28 September 2011.

## Examples

```
library( MethComp )
data( Ancona )
Anc <- Meth( Ancona, 1, 2, 3, 4 )
```

## Description

A variance component model is fitted to method comparison data with replicate measurements in each method by item stratum. The purpose is to simplify the construction of a correct Bland-Altman-plot when replicate measurements are available, and to give the REML-estimates of the relevant variance components.

## Usage

```
BA.est( data, linked=TRUE, IxR=has.repl(data),
        MxI=has.repl(data),
        corMxI=FALSE,
        varMxI=TRUE,
        IxR.pr=FALSE,
        bias=TRUE, alpha=0.05,
        Transform = NULL,
        trans.tol = 1e-6,
        random.raters = FALSE,
        lmecontrol = lmeControl(msMaxIter=300),
        weightfunction = c("mean", "median")
)
## S3 method for class 'BA.est'
bias( obj, ref=1, ... )
VC.est( data,
        IxR = has.repl(data), linked = IxR,
        MxI = has.repl(data), matrix = MxI,
        corMxI = FALSE,
        varMxI = TRUE,
        bias = TRUE,
        print = FALSE,
        random.raters = FALSE,
        lmecontrol = lmeControl(msMaxIter=300)
)
```

## Arguments

data	A <a href="#">Meth</a> object representing method comparison data with replicate measurements, i.e. with columns meth, item, repl and y.
linked	Logical. Are replicates linked within item across methods?
IxR	Logical. Should an item by repl interaction be included in the model. This is needed when the replicates are linked within item across methods, so it is just another name for the linked argument. If linked= is given, this is ignored.

MxI	Logical. Should the method by item interaction (matrix effect) be included in the model.
matrix	Logical. Alias for MxI.
corMxI	Logical. Should the method by item interaction allow coorelated effects within item. Ignored if only two methods are compared.
varMxI	Logical. Should the method by item interaction have a variance that varies between methods. Ignored if only two methods are compared.
IxR.pr	Logical. Should the item by repl interaction variation be included in the prediction standard deviation?
bias	Logical. Should a systematic bias between methods be estimated? If FALSE no bias between methods are assumed, i.e. $\alpha_m = 0, m = 1, \dots, M$ .
alpha	Numerical. Significance level. By default the value 2 is used when computing prediction intervals, otherwise the $1 - \alpha/2$ t-quantile is used. The number of d.f. is taken as the number of units minus the number of items minus the number of methods minus 1 ( $I - M - 1$ ).
Transform	Transformation applied to data (y) before analysis. See <a href="#">check.trans</a> for possible values.
trans.tol	Numerical. The tolerance used to check whether the supplied transformation and its inverse combine to the identity.
random.raters	Logical. Should methods/raters be considered as random. Defaults to FALSE which corresponds to a fixed effect of methods/raters.
lmecontrol	A list of control parameters passed on to lme.
weightfunction	Function to weigh variance components for random raters. Defaults to mean but can also be median.
obj	A BA.est object from which to extract the biases between methods.
ref	Numeric or character. The reference method for the biases: the method with bias 0.
print	Logical. Should the estimated bias and variance components be printed?
...	Further arguments passed on. Currently ignored.

## Details

The model fitted is:

$$y = \alpha_m + \mu_i + c_{mi} + a_{ir} + e_{mir}, \quad \text{var}(c_{mi}) = \tau_m^2, \quad \text{var}(a_{ir}) = \omega^2, \quad \text{var}(e_{mir}) = \sigma_m^2,$$

We can only fit separate variances for the  $\tau_s$  if more than two methods are compared (i.e.  $nM > 2$ ), hence varMxI is ignored when  $nM == 2$ .

The function VC.est is the workhorse; BA.est just calls it. VC.est figures out which model to fit by lme, extracts results and returns estimates. VC.est is also used as part of the fitting algorithm in AltReg, where each iteration step requires fit of this model. The function VC.est is actually just a wrapper for the functions VC.est.fixed that handles the case with fixed methods (usually 2 or three) i.e. the classical method comparison problem, and VC.est.random that handles the situation where "methods" are merely a random sample of raters from some population of raters; and therefore are regarded as random.



**Value**

BA.est returns an object of class `c("MethComp", "BA.est")`, a list with four elements `Conv`, `VarComp`, `LoA`, `RepCoef`; `VC.est` returns (invisibly!) a list with elements `Bias`, `VarComp`, `Mu`, `RanEff`. These list components are:

Conv	3-dimensional array with dimensions "To", "From" and unnamed. The first two dimensions have the methods compared as levels, the last one <code>c("alpha", "beta", "sd.pred", "LoA: lo")</code> . It represents the mean conversions between methods and the prediction standard deviation. Where "To" and "From" take the same value the value of the "sd" component is $\sqrt{2}$ times the residual variation for the method. If <code>IxR.pr=TRUE</code> the variation between replicates are included too, i.e. $\sqrt{2(\sigma_m^2 + \omega^2)}$ <code>sqrt[2(sigma_m^2+omega^2)]</code> .
VarComp	A matrix of variance components (on the SD scale) with methods as rows and variance components "IxR", "MxI" and "res" as columns.
LoA	Four-column matrix with mean difference, lower and upper limit of agreement and prediction SD. Each row in the matrix represents a pair of methods.
RepCoef	Two-column matrix of repeatability SDs and repeatability coefficients. The SDs are the standard deviation of the difference between two measurements by the same method on the item under identical circumstances; the repeatability coefficient the numerical extent of the prediction interval for this difference, i.e. $2\sqrt{2}$ times the sd.
Mu	Estimates of the item-specific parameters.
RanEff	Estimates of the random effects from the model (BLUPS). This is a (possibly empty) list with possible elements named <code>MxI</code> and <code>IxR</code> according to whether these random effects are in the model.

The returned object has an attribute, `Transform` with the transformation applied to data before analysis, and its inverse — see [choose.trans](#).

**Author(s)**

Bendix Carstensen

**References**

Carstensen, Simpson & Gurrin: Statistical models for assessing agreement in method comparison studies with replicate measurements, The International Journal of Biostatistics: Vol. 4 : Iss. 1, Article 16. <http://www.bepress.com/ijb/vol4/iss1/16>.

**See Also**

[BA.plot](#), [perm.repl](#)

**Examples**

```
data( ox )
ox <- Meth( ox )
summary( ox )
```

```

BA.est( ox )
BA.est( ox, linked=FALSE )
BA.est( ox, linked=TRUE, Transform="pctlogit" )
## Not run:
data( sbp )
BA.est( sbp )
BA.est( sbp, linked=FALSE )
# Check what you get from VC.est
str( VC.est( sbp ) )
## End(Not run)

```

---

BA.plot

*Bland-Altman plot of differences versus averages.*


---

### Description

For two vectors of equal length representing measurements of the same quantity by two different methods, the differences are plotted versus the average. The limits of agreement (prediction limits for the differences) are plotted, optionally a regression of differences of means is given too. Works with [Meth](#) and [MethComp](#) objects too.

### Usage

```

BA.plot( y1, y2, meth.names = NULL,
         wh.comp = 1:2,
         pl.type = "BA",
         dif.type = "const",
         sd.type = "const",
         model = if( inherits(y1,"Meth") & has.repl(y1) ) "exch"
           else NULL,
         eqax = FALSE,
         axlim = if( is.data.frame(y1) ) range(y1$y) else range(c(y1,y2)),
         diflim = NULL,
         grid = TRUE,
         N.grid = 10,
         col.grid = grey(0.9),
         points = TRUE,
         col.points = "black",
         cex.points = 1,
         pch.points = 16,
         lwd = c(3,1,1),
         col.lines = "blue",
         repl.conn = FALSE,
         col.conn = "gray",
         lwd.conn = 1,
         xlab = NULL,
         ylab = NULL,
         eqn = FALSE,

```

```

col.eqn = col.lines,
font.eqn = 2,
digits = 2,
Transform = if( mult ) "log" else NULL,
      mult = FALSE,
      alpha = NULL,
      ... )

```

## Arguments

y1	Numerical vector of measurements by 1st method. Can also be a <a href="#">Meth</a> or a <a href="#">MethComp</a> object, see details.
y2	Numerical vector of measurements by 2nd method. Must of same length as x. Ignored if a <a href="#">Meth</a> or a <a href="#">MethComp</a> objects is given for y1.
meth.names	Label for the method names.
wh.comp	Which methods should be compared. Either numerical or character.
pl.type	What type of plot should be made, "BA" for differences versus averages, "conv" for method 1 versus method 2.
dif.type	How should difference depend on the averages. "const" or "lin".
sd.type	How should the standard deviation depend on the averages. "const" or "lin".
model	Should a variance component model be used to compute the limits of agreement? If NULL a simple analysis is made; other possibilities are "exch" or "linked" for exchangeable or linked replicates.
eqax	Should the axes be identical? If a Bland-Altman plot is drawn, the axis for the differences will have the same extent as the axis for the averages, but centered on 0 (see diflim).
axlim	The limits of the axes.
diflim	The limits of the difference axis.
grid	Should a grid be drawn? If numeric it indicates the places where the grid is drawn.
N.grid	How many grid-lines should be drawn.
col.grid	What should be the color of the grid?
points	Logical. Should the observed points be drawn?
col.points	What color should they have?
cex.points	How large should they be?
pch.points	What plot character for the points
lwd	Numerical vector of 3, giving the width of the conversion line (mean difference) and the limits of agreement.
col.lines	What color should the lines have.
repl.conn	Should replicate measurements be connected (within items)?
col.conn	Color of connecting lines.

lwd.conn	Width of connecting lines.
xlab	x-axis label.
ylab	y-axis label.
eqn	Logical. Should the equations linking the methods be shown on the plot? If a Bland-Altman plot is made, both the equations linking the methods and the equation for the differences versus the averages are shown.
col.eqn	Color for equations
font.eqn	Font for equations
digits	How many digits after the decimal point should be used when showing the equations.
Transform	Transformation applied to data prior to analysis. Plots are made on the original scale after back-transformation.
mult	Logical. If TRUE, ratios of measurement instead of differences will be plotted in the Bland-Altman plot on a logarithmic axis, and limits of agreement will be given on this scale? This gives the same analysis as using Transform="log", but a different plot. Using another transformation than the log is accommodated, but no LoA is shown on the axis.
alpha	1 minus the confidence level. If NULL a multiplier of 2 is used for constructing prediction limits, otherwise a t-quantile with d.f. equal th number of items minus 1.
...	Further parameters passed on to <a href="#">plot.MethComp</a>

### Details

A plot of the relationship between the methods is produced; either a Bland-Altman plot of the differences versus averages, or a 45 degree rotation as a conversion between the methods. If model=NULL a simple regression of averages on differences is made by calling DA.reg, and the specified conversion plotted.

### Value

An object of class [MethComp](#) and either DA.reg (if model=NULL) or BA.est (if model is character).

### Author(s)

Bendix Carstensen <bxc@steno.dk>, <http://BendixCarstensen.com>.

### References

- JM Bland and DG Altman: Statistical methods for assessing agreement between two methods of clinical measurement, Lancet, i, 1986, pp. 307-310.
- JM Bland and DG Altman. Measuring agreement in method comparison studies. Statistical Methods in Medical Research, 8:136-160, 1999.
- B Carstensen: Comparing methods of measurement: Extending the LoA by regression. Stat Med. 2010 Feb 10;29(3):401-10.

**See Also**

[BA.est](#), [DA.reg](#), [MCMcmc](#).

**Examples**

```
data( ox )
ox <- Meth( ox )
# The simplest possible Bland-Altman plot
BA.plot( ox )

## With bells and whistles, comparing the naive and model
par( mfrow=c(2,2) )
BA.plot( ox, model=NULL, repl.conn=TRUE, col.lines="blue",
         axlim=c(0,100), diflim=c(-50,50), xaxs="i", yaxs="i",
         las=1, eqn=TRUE, dif.type="lin", pl.type="BA", sd.type="lin",
         grid=1:9*10, digits=3, font.eqn=1)
par(new=TRUE)
BA.plot( ox, model="linked", repl.conn=TRUE, col.lines="red",
         axlim=c(0,100), diflim=c(-50,50), xaxs="i", yaxs="i",
         las=1, eqn=FALSE, dif.type="lin", pl.type="BA", sd.type="lin",
         grid=1:0*10, digits=3)
BA.plot( ox, model=NULL, repl.conn=TRUE, col.lines="blue",
         axlim=c(0,100), diflim=c(-50,50), xaxs="i", yaxs="i",
         las=1, eqn=TRUE, dif.type="lin", pl.type="conv", sd.type="lin",
         grid=1:9*10, digits=3, font.eqn=1)
par(new=TRUE)
BA.plot( ox, model="linked", repl.conn=TRUE, col.lines="red",
         axlim=c(0,100), diflim=c(-50,50), xaxs="i", yaxs="i",
         las=1, eqn=FALSE, dif.type="lin", pl.type="conv", sd.type="lin",
         grid=1:9*10, digits=3)
# The same again, but now logit-transformed
BA.plot( ox, model=NULL, repl.conn=TRUE, col.lines="blue",
         axlim=c(0,100), diflim=c(-50,50), xaxs="i", yaxs="i",
         las=1, eqn=TRUE, dif.type="lin", pl.type="BA", sd.type="lin",
         grid=1:9*10, digits=3, font.eqn=1, Transform="pctlogit")
par(new=TRUE)
BA.plot( ox, model="linked", repl.conn=TRUE, col.lines="red",
         axlim=c(0,100), diflim=c(-50,50), xaxs="i", yaxs="i",
         las=1, eqn=FALSE, dif.type="lin", pl.type="BA", sd.type="lin",
         grid=1:0*10, digits=3, Transform="pctlogit")
BA.plot( ox, model=NULL, repl.conn=TRUE, col.lines="blue",
         axlim=c(0,100), diflim=c(-50,50), xaxs="i", yaxs="i",
         las=1, eqn=TRUE, dif.type="lin", pl.type="conv", sd.type="lin",
         grid=1:9*10, digits=3, font.eqn=1, Transform="pctlogit")
par(new=TRUE)
BA.plot( ox, model="linked", repl.conn=TRUE, col.lines="red",
         axlim=c(0,100), diflim=c(-50,50), xaxs="i", yaxs="i",
         las=1, eqn=FALSE, dif.type="lin", pl.type="conv", sd.type="lin",
         grid=1:9*10, digits=3, Transform="pctlogit")
```

BlandAltman

*Bland-Altman plot of differences versus averages. Deprecated, formerly known as BA.plot, likely to disappear from the package.*

## Description

For two vectors of equal length representing measurements of the same quantity by two different methods, the differences are plotted versus the average. The limits of agreement (prediction limits for the differences) are plotted, optionally a regression of differences of means is given too.

## Usage

```
BlandAltman(x, y,
            x.name = NULL,
            y.name = NULL,
            maintit = "",
            cex = 1,
            pch = 16,
            col.points = "black",
            col.lines = "blue",
            limx = NULL,
            limy = NULL,
            ymax = NULL,
            eqax = FALSE,
            xlab = NULL,
            ylab = NULL,
            print = TRUE,
            reg.line = FALSE,
            digits = 2,
            mult = FALSE,
            alpha,
            ... )
AB.plot( y1, y2,
        meth.names = NULL,
        mean.repl = FALSE,
        conn.repl = !mean.repl,
        lwd.conn = 1,
        col.conn = "black",
        comp.levels = 2:1,
        ... )
```

## Arguments

x	Numerical vector of measurements by 1st method.
y	Numerical vector of measurements by 2nd method. Must of same length as x.
x.name	Label for the 1st method (x).

<code>y.name</code>	Label for the 2nd method (y).
<code>maintit</code>	Main title for the plot
<code>cex</code>	Character expansion for the points.
<code>pch</code>	Plot symbol for points.
<code>col.points</code>	Color for the points.
<code>col.lines</code>	Color for the lines indicating limits of agreement.
<code>limx</code>	x-axis limits.
<code>limy</code>	y-axis limits.
<code>ymax</code>	Scalar. The y-axis will extend from -ymax to +ymax.
<code>eqax</code>	Logical. Should the range on x- and y- axes be the same?
<code>xlab</code>	x-axis label.
<code>ylab</code>	y-axis label.
<code>print</code>	Logical: Should the limits of agreement and the c.i.s of these be printed?
<code>reg.line</code>	If TRUE, the regression line of x-y on (x+y)/2 is drawn. If numerical the regression equation is printed with the given number of digits after the decimal points.
<code>digits</code>	How many decimal places should be used when printing limits of agreement? Used both for the printing of results and for annotation of the plot.
<code>mult</code>	Logical. Should data be log-transformed and reporting be on a multiplicative scale?
<code>alpha</code>	1 minus confidence level used when computing confidence intervals and limits of agreement, i.e. the $t(1-\alpha/2)$ quantile is used. If not supplied the standard value of 2 is used for computing LoA.
<code>y1</code>	Measurements by method 1. Alternatively a <a href="#">Meth</a> object or a dataframe with columns <code>meth</code> , <code>item</code> , <code>y</code> , and possibly <code>repl</code> .
<code>y2</code>	Corresponding measurements by method 2. Ignored if <code>y1</code> is a dataframe.
<code>meth.names</code>	Names for the two methods. Used for annotation of the plot. If not supplied and <code>y1</code> is a dataframe names are derived from the factor level names of <code>meth</code> .
<code>mean.repl</code>	Logical. If there are replicate measurements by each method should the means by <code>item</code> and <code>meth</code> be formed before further ado. WARNING: This will give too narrow limits of agreement.
<code>conn.repl</code>	Logical. Should replicates from the same item be connected?
<code>lwd.conn</code>	Line width of connecting lines
<code>col.conn</code>	Color of connecting lines
<code>comp.levels</code>	Levels of the <code>meth</code> factor to compare. May be used to switch the order of the methods compared by specifying <code>comp.meth=2:1</code> .
<code>...</code>	Further arguments passed on from <code>BA.plot</code> to <code>BlandAltman</code> and possibly further to the plot function. The arguments passed to <a href="#">BlandAltman</a> are used for fine-tuning the appearance of the plot.

**Value**

An object of class `BA.check`; list with 3 elements:

<code>LoA</code>	A vector of length 3 with Limits of Agreement.
<code>p.value</code>	P-values for three hypotheses: 1) Constant variance - this is the test of 0 slope in the regression of absolute residuals on averages. 2) Constant difference - this is the test of 0 slope in the regression of differences on averages. 3) Difference equal to 0 - this is usually a lame thing to use.
<code>reg.res</code>	A $3 \times 4$ matrix with (in the first row) the results from regressing the averages on the means, and in the two other rows the derived relationships between methods. In each line the intercept ( <code>alpha</code> ), slope ( <code>beta</code> ), the prediction standard deviation ( <code>pr.sd</code> ) and half the width of the prediction interval ( <code>pr.int</code> ).

**Author(s)**

Bendix Carstensen <bxc@steno.dk>, <http://BendixCarstensen.com>.

**References**

JM Bland and DG Altman: Statistical methods for assessing agreement between two methods of clinical measurement, *Lancet*, i, 1986, pp. 307-310.

JM Bland and DG Altman. Measuring agreement in method comparison studies. *Statistical Methods in Medical Research*, 8:136-160, 1999.

B Carstensen: Comparing methods of measurement: Extending the LoA by regression. *Stat Med*. 2010 Feb 10;29(3):401-10.

**See Also**

[BA.plot](#), [MCmcmc](#).

**Examples**

```
data( ox )
par( mfrow=c(1,2) )
# Wrong to use mean over replicates
mtab <- with( ox, tapply( y, list(item, meth), mean ) )
CO <- mtab[, "CO"]
pulse <- mtab[, "pulse"]
BlandAltman( CO, pulse )

# (almost) Right to use replicates singly
par( mfrow=c(1,1) )
oxw <- to.wide( ox )
CO <- oxw[, "CO"]
pulse <- oxw[, "pulse"]
BlandAltman( CO, pulse, mult=TRUE )
BlandAltman( CO, pulse, eqax=TRUE )

data( plvol )
```



```
BA.plot( plvol )
BA.plot( plvol, reg.line=TRUE )
BA.plot( plvol, reg.line=2 )
```

---

bothlines

*Add regression lines to a plot*


---

## Description

Add the regression lines of  $y$  on  $x$  AND  $x$  on  $y$  to the plot. Optionally add the line obtained by allowing errors in both variables (Deming regression).

## Usage

```
bothlines(x, y, Dem = FALSE, sdr = 1, col = "black", ...)
```

## Arguments

<code>x</code>	Numeric vector
<code>y</code>	Numeric vector
<code>Dem</code>	Logical. Should the Deming regression line be added too?
<code>sdr</code>	Numeric. The assumed ratio of standard deviations used in the Deming regression.
<code>col</code>	Colour of the lines. Can be a vector of up to 3 elements, one for each line.
<code>...</code>	Additional arguments passed on to <a href="#">abline</a> , which does the actual plotting.

## Value

None.

## Author(s)

Bendix Carstensen, Steno Diabetes Center, <http://BendixCarstensen.com>

## See Also

[abline](#).

## Examples

```
data( ox )
oxw <- to.wide(ox)
attach( oxw )
plot( CO, pulse )
abline(0,1)
bothlines( CO, pulse, Dem=TRUE, col=rainbow(3), lwd=2 )
plot( CO, pulse, pch=16 )
abline(0,1, col=gray(0.7), lwd=2)
bothlines( CO, pulse, Dem=TRUE, col=c(rep("transparent",2),"black"), lwd=2 )
```

cardiac

*Measurement of cardiac output by two different methods.***Description**

For each subject cardiac output is measured repeatedly (three to six times) by impedance cardiography (IC) and radionuclide ventriculography (RV).

**Usage**

```
data(cardiac)
```

**Format**

A data frame with 120 observations on the following 4 variables.

`meth` a factor with levels IC RV  
`item` a numeric vector giving the item number.  
`repl` a numeric vector with replicate number.  
`y` the measuremnts of cardiac output.

**Details**

It is not entirely clear from the source whether the replicates are exchangeable within (method,item) or whether they represent pairs of measurements. From the description it looks as if replicates are linked between methods, but in the paper they are treated as if they were not.

**Source**

The dataset is adapted from table 4 in: JM Bland and DG Altman: Measuring agreement in method comparison studies. Statistical Methods in Medical Research, 8:136-160, 1999. Originally supplied to Bland & Altman by Dr LS Bowling, see: Bowling LS, Sageman WS, O'Connor SM, Cole R, Amundson DE. Lack of agreement between measurement of ejection fraction by impedance cardiography versus radionuclide ventriculography. Critical Care Medicine 1993; 21: 1523-27.

**Examples**

```
data(cardiac)
cardiac <- Meth(cardiac)
summary(cardiac)
# Visually check exchangeability
plot( cardiac )
plot( perm.repl( cardiac ) )
BA.est(cardiac)
# Run MCmcmc using BRugs for an insufficient amount of iterations
## Not run: card.mi.ir <- MCmcmc( cardiac,
                                beta=FALSE, random=c("mi","ir"),
                                n.iter=100, trace=T )
```

```
print( card.mi.ir )  
## End(Not run)
```

---

CardOutput

*Measurements of Cardiac output.*

---

## Description

Two different ways of measuring cardiac output and oxygen saturation in 15 critically ill persons.

## Usage

```
data(CardOutput)
```

## Format

A data frame with 15 observations on the following 8 variables.

Age Patient age

Diag Diagnosis, a factor with levels sepsis, cardiogenic, hypothermia

V02 Oxygen consumption

Svo2 Mixed venous O2 saturation

Scvo2 Central venous oxygen saturation

TCO Thermodilution-derived cardiac output

FCO Fick-derived cardiac output.

Sex Sex, a factor with levels F, M

## Source

Avi A. Weinbroum, Philippe Biderman, Dror Soffer, Joseph M. Klausner & Oded Szold:

Reliability of cardiac output calculation by the fick principle and central venous oxygen saturation in emergency conditions.

Journal of Clinical Monitoring and Computing (2008) 22: 361-366

## Examples

```
data(CardOutput)
```

check.MCmcmc

---

*Functions to graphically assess the convergence of the MCMC-simulation in a MCmcmc object*


---

## Description

These functions display traces, posterior densities and autocorrelation functions for the relevant subset of the parameters in a MCmcmc object.

## Usage

```
## S3 method for class 'MCmcmc'
trace( obj, what = "sd",
      scales = c("same", "free"),
      layout = "col",
      aspect = "fill", ...)
```

```
## S3 method for class 'MCmcmc'
post( obj, what = "sd",
      check = TRUE,
      scales = "same",
      layout = "row",
      lwd = 2,
      col,
      plot.points = FALSE,
      aspect = "fill", ... )
```

```
## S3 method for class 'MCmcmc'
pairs( x, what = "sd",
      subset,
      col = NULL,
      pch = 16,
      cex = 0.2,
      scales = "free", ... )
```

## Arguments

obj	A MCmcmc object.
x	A MCmcmc object.
what	Character indicating what parameters to plot. Possible values are "sd" or "var" which gives plots for the variance components (on the sd. scale), "beta" or "slope", which gives plots for slope parameters and "alpha" or "int", which gives plots for the intercept parameters.

scales	Character vector of length two, with possible values "same" or "free", indicating whether x- and y-axes of the plots should be constrained to be the same across panels. For pairs only the first element is used to decide whether all panels should have the same axes.
layout	Character. If "col" parameters are displayed columnwise by method, if "row" they are displayed row-wise.
aspect	How should the panels be scaled. Default ("fill") is to make a panels take up as much place as possible.
check	Logical. Should the density plots be separate for each chain (in order to check convergence) or should the chains be merged.
lwd	Width of the lines used for plotting of the posterior densities.
col	Color of the lines points used for plotting of the posterior densities.
plot.points	Logical. Should a rug with actual data points be plotted beneath the density.
pch	Plot symbol for the points.
subset	Character or numerical indicating the columns of the posterior that should be plotted by pairs.
cex	Plot character size for points in pairs.
...	Further arguments passed on to the <a href="#">Lattice</a> function called: trace calls <a href="#">xyplot</a> from the coda package, post calls <a href="#">densityplot</a> from the coda package, pairs calls <a href="#">pairs</a> from the graphics package.

### Details

A Lattice plot is returned, which means that it must be printed when these functions are called in a batch program or inside another function or for-loop.

trace plots traces of the sampled chains, post plots posterior densities of the parameters and pairs plots a scatter-plot matrix of bivariate marginal posterior distributions.

### Value

A [Lattice](#) plot.

### Author(s)

Bendix Carstensen, Steno Diabetes Center, <bx@steno.dk>, <http://BendixCarstensen.com>.

### See Also

[MCmcmc](#), [plot.MCmcmc](#), [ox.MC](#), [sbp.MC](#)

### Examples

```
# Load a provided MCmcmc object
data( ox.MC )
trace.MCmcmc( ox.MC, what="beta" )
pairs.MCmcmc( ox.MC, what="sd" )
```

---

choose.trans

*Functions to handle transformations of measurement results.*


---

## Description

Choose a function and inverse based on a text string; check whether two functions actually are each others inverse.

## Usage

```
choose.trans( tr )
check.trans( trans, y, trans.tol = 1e-05 )
```

## Arguments

tr	A character string, or a list of two functions, they should be each other's inverse. Names of the list are ignored.
trans	A list of two functions, each other's inverse.
y	Vector of numerical values where the functions should be each other's inverse.
trans.tol	Numerical constant indication how precise the evaluation should be.

## Value

choose.trans returns a named list with two elements "trans" and "inv", both functions which are each other's inverse. This is intended to be stored as an attribute "Transform" with the resulting object and used in plotting and reporting. All results will be on the transformed scale. If the tr argument to choose.trans is a character constant, the appropriate named list of two functions will be generated. Possibilities are: "exp", "log", "logit", "pctlogit" (transforms percentages by the logit), "sqrt", "sq" (square), "clogit" (complementary log-minus-log), "llogit" (log-minus-log). If there is no match NULL is returned, which will correspond to no transformation.

check.trans returns nothing.

## Author(s)

Bendix Carstensen, Steno Diabetes Center, <http://www.biostat.ku.dk/~bxc>.

## Examples

```
choose.trans( "logit" )
```

---

corr.measures	<i>Correlation measures for method comparison studies. Please don't use them!</i>
---------------	---

---

### Description

Computes correlation, mean squared difference, concordance correlation coefficient and the association coefficient. middle and ends are useful utilities for illustrating the shortcomings of the association measures, see the example.

### Usage

```
corr.measures(x, y)
middle(w, rm = 1/3)
ends(w, rm = 1/3)
```

### Arguments

x	vector of measurements by one method.
y	vector of measurements by another method.
w	numerical vector.
rm	fraction of data to remove.

### Details

These measures are all flawed since they are based on the correlation in various guises. They fail to address the relevant problem of AGREEMENT. It is recommended NOT to use them. The example gives an example, illustrating what happens when increasingly large chunks of data in the middle are removed.

### Value

corr.measures return a vector with 4 elements. middle and ends return a logical vector pointing to the middle or the ends of the w after removing a fraction of rm from data.

### Author(s)

Bendix Carstensen, Steno Diabetes Center, <http://BendixCarstensen.com>

### References

Shortly...

### See Also

[MCmcmc](#).

### Examples

```

cbind( zz <- 1:15, middle(zz), ends(zz) )
data( sbp )
bp <- subset( sbp, repl==1 & meth!="J" )
bp <- Meth( bp )
summary( bp )
plot( bp )
bw <- to.wide( bp )
with( bw, corr.measures( R, S ) )
# See how it gets better with less and less data:
summ.corr <-
rbind(
  with( subset( bw, middle( R+S, 0.6 ) ), corr.measures( R, S ) ),
  with( subset( bw, middle( R+S, 0.4 ) ), corr.measures( R, S ) ),
  with(      bw      , corr.measures( R, S ) ),
  with( subset( bw, ends( R+S, 0.3 ) ), corr.measures( R, S ) ),
  with( subset( bw, ends( R+S, 0.4 ) ), corr.measures( R, S ) ),
  with( subset( bw, ends( R+S, 0.6 ) ), corr.measures( R, S ) ),
  with( subset( bw, ends( R+S, 0.8 ) ), corr.measures( R, S ) ) )
rownames( summ.corr ) <- c("middle 40%",
                          "middle 60%",
                          "total",
                          "outer 70%",
                          "outer 60%",
                          "outer 40%",
                          "outer 20%")

summ.corr

```

---

DA.reg

---

*Make a regression of differences on averages*


---

### Description

For each pair of methods in data, a regression of the differences on the averages between methods is made and a linear relationship between methods with prediction standard deviations is derived.

### Usage

```

DA.reg(data,
  Transform = NULL,
  trans.tol = 1e-6,
  print = TRUE,
  random.raters = FALSE,
  DA.slope = TRUE )
DA2y( a=0, b=0, s=NA )
y2DA( A=0, B=1, S=NA )

```



## Arguments

data	A <a href="#">Meth</a> object. May also be a data frame with columns meth, item and y.
Transform	A character string, or a list of two functions, each other's inverse. The measurements are transformed by this before analysis. Possibilities are: "exp", "log", "logit", "pctlogit" (transforms percentages by the logit), "sqrt", "sq" (square), "c1l" (complementary log-minus-log), "l1" (log-minus-log). For further details see <a href="#">choose.trans</a> .
trans.tol	The tolerance used to check whether the supplied transformation and its inverse combine to the identity. Only used if Transform is a list of two functions.
print	Should the results be printed?
random.raters	If methods really are a random selection of raters, neither intercept nor slope different from 0 are sensible, so if this is TRUE, intercept and slope in the regression of difference on averages are fixed to 0. Meaning that we are essentially looking at the raw differences as residuals.
DA.slope	If this is TRUE, a slope of the differences in the averages is estimated, otherwise the relationship is assumed constant.
a	Intercept in the linear relation of the differences $y_1 - y_2$ to the averages $(y_1 + y_2)/2$ . If a vector of length > 1, this is used instead of a, b and s, and b and s are ignored.
b	Slope in the linear relation of the differences to the averages.
s	SD from the regression of the differences in the averages. Can be NA.
A	Intercept in the linear relation of $y_1$ on $y_2$ .
B	Slope in the linear relation of $y_1$ on $y_2$ .
S	SD for the linear relation of $y_1$ on $y_2$ . Can be NA.

## Details

If the input object contains replicate measurements these are taken as separate items in the order they appear in the dataset.

The functions DA2y and y2DA are convenience functions that convert the estimates of intercept, slope and sd from the regression of  $D = y_1 - y_2$  on  $A = (y_1 + y_2)/2$ , back and forth to the resulting intercept, slope and sd in the relationship between  $y_1$  and  $y_2$ , cf. Carstensen (2010), equation 6.

DA2y takes intercept(a), slope(b) and sd(s) from the relationship  $(y_1 - y_2) = a + b((y_1 + y_2)/2) + e$  with  $sd(e) = s$ , and returns a two by 3 matrix with columns "int", "slope", "sd" and rows "y1|2", "y2|1".

y2DA takes intercept(A), slope(B) and sd(S) from the relationship  $y_1 = A + B y_2 + E$  with  $sd(E) = E$ , and returns a vector of length 3 with names "int(t-f)", "slope(t-f)", "sd(t-f)", where t refers to "to" ( $y_1$  and f to "from"  $y_2$ ).

## Value

DA.reg returns a [MethComp](#) object, i.e. a list with three components, Conv, VarComp, and data. Conv is a three-dimensional array, with dimensions To, From (both with levels equal to the methods in data) and an unnamed dimension with levels "alpha", "beta", "sd.pred", "beta=1", referring to the linear relationship of To to From, "int(t-f)", "slope(t-f)", "sd(t-f)", referring to the

regression of the differences on the averages, and "int(sd)", "slope(sd)", and "s.d.=K", referring to the regression of the absolute residuals on the averages, and LoA-lo, LoA-hi, the limits of agreement.

Converting from method  $l$  to method  $k$  using

$$y_{k|l} = \alpha + \beta y_l$$

with prediction standard deviation  $\sigma$ , just requires the entries `[k,l,c("alpha","beta","sd.pred")]`, if we assume the s.d. is constant.

The next entry is the p-values for the hypothesis  $\beta = 1$ , intercept and slope of the SD of the differences as a linear function of the average and finally p-value of the hypothesis that standard errors are constant over the range. The latter three are derived by regressing the absolute values of the residuals on the averages, and can be used to produce LoA where the s.d. increases (or decreases) by the mean, using the function DA2y.

The VarComp element of the list is NULL, and only present for compatibility with the print method for MethComp objects.

The data element is the input dataframe. The measurements in y are left un-transformed, even if data are transformed (i.e. if the Transform attribute of the object is non-null).

DA2y returns a 2 by 3 matrix with rownames `c("y1|2","y2|1")` and columnnames `c("int","slope","sd")`, calculated under the assumption that the differences were formed as `D <- y1 - y2`.

y2DA returns a 3-component vector with names `c("DA-int","DA-slope","DA-sd")`, referring to differences `D=y1-y2` as a linear function of `A=(y1+y2)/2`.

### Author(s)

Bendix Carstensen, Steno Diabetes Center, bxc\$steno.dk, <http://BendixCarstensen.com/MethComp>

### References

B. Carstensen: Comparing methods of measurement: Extending the LoA by regression. Stat Med, 29:401-410, 2010.

### Examples

```
data( milk )
DA.reg( milk )
data( sbp )
print( DA.reg(sbp), digits=3 )
# Slope, intercept : y1 = 0.7 + 1.2*y2 (0.4)
A <- c(0.7,1.2,0.4)
( y2DA( A ) )
( DA2y( y2DA( A ) ) )
```

Deming

*Regression with errors in both variables (Deming regression)***Description**

The function makes a regression of y on x, assuming that both x and y are measured with error. This problem only has an analytical solution if the ratio of the variances is known, hence this is required as an input parameter.

**Usage**

```
Deming(x, y, vr = sdr^2, sdr = sqrt(vr),
      boot = FALSE, keep.boot = FALSE, alpha = 0.05)
```

**Arguments**

x	numerical variable.
y	numerical variable.
vr	The assumed known ratio of the (residual) variance of the ys relative to that of the xs. Defaults to 1.
sdr	do. for standard deviations. Defaults to 1. vr takes precedence if both are given.
boot	Should bootstrap estimates of standard errors of parameters be done? If boot==TRUE, 1000 bootstrap samples are done, if boot is numeric, boot samples are made.
keep.boot	Should the 4-column matrix of bootstrap samples be returned? If TRUE, the summary is printed, but the matrix is returned invisibly. Ignored if boot=FALSE
alpha	What significance level should be used when displaying confidence intervals?

**Details**

The formal model underlying the procedure is based on a so called functional relationship:

$$x_i = \xi_i + e_{1i}, \quad y_i = \alpha + \beta\xi_i + e_{2i}$$

with  $\text{var}(e_{1i}) = \sigma$ ,  $\text{var}(e_{2i}) = \lambda\sigma$ , where  $\lambda$  is the known variance ratio.

The estimates of the residual variance is based on a weighting of the sum of squared deviations in both directions, divided by  $n - 2$ . The ML estimate would use  $2n$  instead, but in the model we actually estimate  $n + 2$  parameters —  $\alpha, \beta$  and the  $n \xi$ s.

This is not in Peter Sprent's book (see references).

**Value**

If `boot==FALSE` a named vector with components `Intercept`, `Slope`, `sigma.x`, `sigma.y`, where `x` and `y` are substituted by the variable names.

If `boot==TRUE` a matrix with rows `Intercept`, `Slope`, `sigma.x`, `sigma.y`, and columns giving the estimates, the bootstrap standard error and the bootstrap estimate and c.i. as the 0.5,  $\alpha/2$  and  $1-\alpha/2$  quantiles of the sample.

If `keep.boot==TRUE` this summary is printed, but a matrix with columns `Intercept`, `Slope`, `sigma.x`, `sigma.y` and `boot` rows is returned.

**Author(s)**

Bendix Carstensen, Steno Diabetes Center, <bx@steno.dk>, <http://BendixCarstensen.com>.

**References**

Peter Sprent: Models in Regression, Methuen & Co., London 1969, ch.3.4.

WE Deming: Statistical adjustment of data, New York: Wiley, 1943. [This is a reference taken from a reference list — I never saw the book myself].

**See Also**

[MCmcmc](#)

**Examples**

```
# 'True' values
M <- runif(100,0,5)
# Measurements:
x <- M + rnorm(100)
y <- 2 + 3 * M + rnorm(100,sd=2)
# Deming regression with equal variances, variance ratio 2.
Deming(x,y)
Deming(x,y,vr=2)
Deming(x,y,boot=TRUE)
bb <- Deming(x,y,boot=TRUE,keep.boot=TRUE)
str(bb)
# Plot data with the two classical regression lines
plot(x,y)
abline(lm(y~x))
ir <- coef(lm(x~y))
abline(-ir[1]/ir[2],1/ir[2])
abline(Deming(x,y,sdr=2)[1:2],col="red")
abline(Deming(x,y,sdr=10)[1:2],col="blue")
# Comparing classical regression and "Deming extreme"
summary(lm(y~x))
Deming(x,y,vr=1000000)
```

---

Enzyme	<i>Enzyme activity data</i>
--------	-----------------------------

---

**Description**

Three measurement of enzyme activity on 24 patients. The measurements is of the enzymes sucrase and alkaline phosphatase. The interest is to compare the 'homogenate' and 'pellet' methods.

**Usage**

```
data(Enzyme)
```

**Format**

A data frame with 72 observations on the following 3 variables.

`meth` a factor with levels SucHom SucPel Alkphos, representing three different measurements, i.e. homogenate and pellet values of sucrase, as well as homogenate values of alkaline.

`item` a numeric vector, the person ID for the 24 patients

`y` a numeric vector, the measurements on the enzyme activity.

**Source**

R. L. Carter; Restricted Maximum Likelihood Estimation of Bias and Reliability in the Comparison of Several Measuring Methods; Biometrics, Dec., 1981, Vol. 37, No. 4, pp. 733-741.

**Examples**

```
data(Enzyme)
Enzyme <- Meth( Enzyme )
summary( Enzyme )
# plot( Enzyme )
```

---

fat	<i>Measurements of subcutaneous and visceral fat</i>
-----	--

---

**Description**

43 persons had Subcutaneous and Visceral fat thickness measured at Steno Diabetes Center in 2006 by two observers; all measurements were done three times. The interest is to compare the measurements by the two observers. Persons are items, observers are methods, the three replicates are exchangeable within (person,observer)=(item,method)

**Usage**

```
data(fat)
```

**Format**

A data frame with 258 observations on the following 6 variables.

Id Person id.

Obs Observers, a factor with levels KL and SL.

Rep Replicate — exchangeable within person and observer.

Sub Subcutaneous fat measured in cm.

Vic Visceral fat measured in cm.

**Examples**

```
data(fat)
str(fat)
vic <- Meth( fat, meth=2, item=1, repl="Rep", y="Vic" )
str(vic)
BA.est( vic, linked=FALSE )
```

---

glucose

*Glucose measurements by different methods*

---

**Description**

74 persons in 5 centres in Finland had blood glucose measured by 11 different methods, based on 4 different types of blood. Each person had blood sampled at 0, 30, 60 and 120 min after a 75 g glucose load.

**Usage**

```
data(glucose)
```

**Format**

A data frame with 1302 observations on the following 6 variables.

meth Method of measurement. A factor with 11 levels: n.plas1 n.plas2 h.cap h.blood h.plas h.serum m.plas m.serum o.cap s.serum k.plas.

type Type of blood sample. A factor with 4 levels: blood plasma serum capil

item Person id.

time Time of blood sampling. Minutes since glucose load.

cent Center of sampling. Except for the two first methods, n.plas1 and n.plas2, samples were analyzed at the centres too

y Glucose measurement in mmol/l.

**Source**

The study was conducted at the National Public Health Institute in Helsinki by Jaana Lindstrom.

## References

B Carstensen, J Lindstrom, J Sundvall, K Borch-Johnsen<sup>1</sup>, J Tuomilehto & the DPS Study Group: Measurement of Blood Glucose: Comparison between different Types of Specimens. Annals of Clinical Biochemistry, to appear.

## Examples

```
data( glucose )
str( glucose )
# Use only plasma and serum as methods and make a Bland-Altman plot
gluc <- subset( glucose, type %in% c("plasma","serum") )
gluc$meth <- gluc$type
gluc$repl <- gluc$time
BA.plot( gluc )
```

---

hba.MC

*A MCmcmc object from the hba1c data*

---

## Description

This object is included for illustrative purposes. It is a result of a 5-hour run using MCmcmc, with `n.iter=100000`.

## Usage

```
data(hba.MC)
```

## Format

The format is a [MCmcmc](#) object.

## Details

The data are the venous measurements from the [hba1c](#) dataset, using the day of analysis as replicate. Measurements are taken to be linked within replicate (=day of analysis).

## Examples

```
data(hba.MC)
attr(hba.MC,"mcmc.par")
# print.MCmcmc(hba.MC)
# One of the chains is really fishy (it's the first one)
# trace.MCmcmc(hba.MC)
# trace.MCmcmc(hba.MC,"beta")
# Try to have a look, excluding the first chain
# hba.MCsub <- subset.MCmcmc(hba.MC,chains=-1)
# trace.MCmcmc(hba.MCsub)
# trace.MCmcmc(hba.MCsub,"beta")
```

```
# A MCMC object also has class mcmc.list, so we can use the
# coda functions for convergence diagnostics:
# acfplot( subset.MCMC(hba.MC, subset="sigma"))
```

hba1c

*Measurements of HbA1c from Steno Diabetes Center***Description**

Three analysers (machines) for determination of HbA1c (glycosylated haemoglobin) were tested on samples from 38 individuals. Each had drawn a venous and capillary blood sample. These were analysed on five different days.

**Usage**

```
data(hba1c)
```

**Format**

A data frame with 835 observations on the following 6 variables.

`dev` Type of machine used. A factor with levels BR.V2, BR.VC and Tosoh.

`type` Type of blood analysed (capillary or venous). A factor with levels Cap Ven

`item` Person-id. A numeric vector

`d.samp` Day of sampling.

`d.ana` Day of laboratory analysis.

`y` The measured value of HbA1c.

**Details**

In the terminology of method comparison studies, `methods` is the cross-classification of `dev` and `type`, and `replicate` is `d.ana`. It may be of interest to look at the effect of time between `d.ana` and `d.samp`, i.e. the time between sampling and analysis.

**Source**

Bendix Carstensen, Steno Diabetes Center.

**References**

These data were analysed as example in: Carstensen: Comparing and predicting between several methods of measurement, *Biostatistics* 5, pp. 399–413, 2004.



## Examples

```
data(hba1c)
str(hba1c)
hb1 <- with( hba1c,
             Meth( meth = interaction(dev,type),
                   item = item,
                   repl = d.ana-d.samp,
                   y = y, print=TRUE ) )
```

---

MCmcmc

---

*Fit a model for method comparison studies using WinBUGS*


---

## Description

A model linking each of a number of methods of measurement linearly to the "true" value is set up in BUGS and run via the function `bugs` from the R2WinBUGS package.

## Usage

```
MCmcmc( data,
        bias = "linear",
        IxR = has.repl(data), linked = IxR,
        MxI = TRUE,          matrix = MxI,
        varMxI = nlevels(factor(data$meth)) > 2,
        n.chains = 4,
        n.iter = 2000,
        n.burnin = n.iter/2,
        n.thin = ceiling((n.iter-n.burnin)/1000),
        bugs.directory = getOption("bugs.directory"),
        debug = FALSE,
        bugs.code.file = "model.txt",
        clearWD = TRUE,
        code.only = FALSE,
        ini.mult = 2,
        list.ini = TRUE,
        org = FALSE,
        program = "JAGS",
        Transform = NULL,
        trans.tol = 1e-6,
        ... )
## S3 method for class 'MCmcmc'
summary( object, alpha=0.05, ... )
## S3 method for class 'MCmcmc'
print( x, digits=3, alpha=0.05, ... )
## S3 method for class 'MCmcmc'
subset( x, subset=NULL, allow.repl=FALSE, chains=NULL, ... )
## S3 method for class 'MCmcmc'
```

```
mcmc( x, ... )
```

### Arguments

<code>data</code>	Data frame with variables <code>meth</code> , <code>item</code> , <code>repl</code> and <code>y</code> , possibly a <a href="#">Meth</a> object. <code>y</code> represents a measurement on an <code>item</code> (typically patient or sample) by method <code>meth</code> , in replicate <code>repl</code> .
<code>bias</code>	Character. Indicating how the bias between methods should be modelled. Possible values are "none", "constant", "linear" and "proportional". Only the first three letters are significant. Case insensitive.
<code>IxR</code>	Logical. Are the replicates linked across methods, i.e. should a random <code>item</code> by <code>repl</code> be included in the model.
<code>linked</code>	Logical, alias for <code>IxR</code> .
<code>MxI</code>	Logical, should a <code>meth</code> by <code>item</code> effect be included in the model?
<code>matrix</code>	Logical, alias for <code>MxI</code> .
<code>varMxI</code>	Logical, should the method by item effect have method-specific variances. Ignored if only two methods are compared.
<code>n.chains</code>	How many chains should be run by WinBUGS — passed on to <code>bugs</code> .
<code>n.iter</code>	How many total iterations — passed on to <code>bugs</code> .
<code>n.burnin</code>	How many of these should be burn-in — passed on to <code>bugs</code> .
<code>n.thin</code>	How many should be sampled — passed on to <code>bugs</code> .
<code>bugs.directory</code>	Where is WinBUGS ( $\geq 1.4$ ) installed — passed on to <code>bugs</code> . The default is to use a parameter from <code>options()</code> . If you use this routinely, this is most conveniently set in your <code>.Rprofile</code> file.
<code>debug</code>	Should WinBUGS remain open after running — passed on to <code>bugs</code> .
<code>clearWD</code>	Should the working directory be cleared for junk files after the running of WinBUGS — passed on to <code>bugs</code> .
<code>bugs.code.file</code>	Where should the bugs code go?
<code>code.only</code>	Should MCmcmc just create a bugs code file and a set of inits? See the <code>list.ini</code> argument.
<code>ini.mult</code>	Numeric. What factor should be used to randomly perturb the initial values for the variance components, see below in details.
<code>list.ini</code>	List of lists of starting values for the chains, or logical indicating whether starting values should be generated. If TRUE (the default), the function <a href="#">VC.est</a> will be used to generate initial values for the chains. <code>list.ini</code> is a list of length <code>n.chains</code> . Each element of which is a list with the following vectors as elements: <code>mu</code> - length I <code>alpha</code> - length M <code>beta</code> - length M <code>sigma.mi</code> - length M - if M is 2 then length 1

	sigma.ir - length 1
	sigma.mi - length M
	sigma.res - length M
	If code.only==TRUE, list.ini indicates whether a list of initial values is returned (invisibly) or not. If code.only==FALSE, list.ini==FALSE is ignored.
org	Logical. Should the posterior of the original model parameters be returned too? If TRUE, the MCmcmc object will have an attribute, original, with the posterior of the parameters in the model actually simulated.
program	Which program should be used for the MCMC simulation. Possible values are "BRugs", "openbugs", "ob" (openBUGS/BRugs), "winbugs", "wb" (WinBUGS), "jags" (JAGS). Case insensitive. Defaults to "JAGS" since: 1) JAGS is available on all platforms and 2) JAGS seems to be faster than BRugs on (some) windows machines.
Transform	Transformation of data (y) before analysis. See <a href="#">choose.trans</a> .
trans.tol	The tolerance used to check whether the supplied transformation and its inverse combine to the identity.
...	Additional arguments passed on to <a href="#">bugs</a> .
object	An MCmcmc object
alpha	1 minus the the confidence level
x	An MCmcmc object
digits	Number of digits after the decimal point when printing.
subset	Numerical, character or list giving the variables to keep. If numerical, the variables in the MCmcmc object with these numbers are selected. If character, each element of the character vector is "grep"ed against the variable names, and the matches are selected to the subset. If a list each element is used in turn, numerical and character elements can be mixed.
allow.repl	Should duplicate columns be allowed in the result?
chains	Numerical vector giving the number of the chains to keep.

## Details

The model set up for an observation  $y_{mir}$  is:

$$y_{mir} = \alpha_m + \beta_m(\mu_i + b_{ir} + c_{mi}) + e_{mir}$$

where  $b_{ir}$  is a random item by repl interaction (included if "ir" %in% random) and  $c_{mi}$  is a random meth by item interaction (included if "mi" %in% random). The  $\mu_i$ 's are parameters in the model but are not monitored — only the  $\alpha$ s,  $\beta$ s and the variances of  $b_{ir}$ ,  $c_{mi}$  and  $e_{mir}$  are monitored and returned. The estimated parameters are only determined up to a linear transformation of the  $\mu$ s, but the linear functions linking methods are invariant. The identifiable conversion parameters are:

$$\alpha_{m \cdot k} = \alpha_m - \alpha_k \beta_m / \beta_k, \quad \beta_{m \cdot k} = \beta_m / \beta_k$$

The posteriors of these are derived and included in the posterior, which also will contain the posterior of the variance components (the SDs, that is). Furthermore, the posterior of the point

where the conversion lines intersects the identity as well as the prediction SDs between any pairs of methods are included.

The function `summary.MCmcmc` method gives estimates of the conversion parameters that are consistent. Clearly,

$$\text{median}(\beta_{1.2}) = 1/\text{median}(\beta_{2.1})$$

because the inverse is a monotone transformation, but there is no guarantee that

$$\text{median}(\alpha_{1.2}) = \text{median}(-\alpha_{2.1}/\beta_{2.1})$$

and hence no guarantee that the parameters derived as posterior medians produce conversion lines that are the same in both directions. Therefore, `summary.MCmcmc` computes the estimate for  $\alpha_{2.1}$  as

$$(\text{median}(\alpha_{1.2}) - \text{median}(\alpha_{2.1})/\text{median}(\beta_{2.1}))/2$$

and the estimate of  $\alpha_{1.2}$  correspondingly. The resulting parameter estimates defines the same lines.

## Value

If `code.only==FALSE`, an object of class `MCmcmc` which is a `mcmc.list` object of the relevant parameters, i.e. the posteriors of the conversion parameters and the variance components transformed to the scales of each of the methods.

Furthermore, the object have the following attributes:

<code>random</code>	Character vector indicating which random effects ("ir","mi") were included in the model.
<code>methods</code>	Character vector with the method names.
<code>data</code>	The data frame used in the analysis. This is used in <code>plot.MCmcmc</code> when plotting points.
<code>mcmc.par</code>	A list giving the number of chains etc. used to generate the object.
<code>original</code>	If <code>org=TRUE</code> , an <code>mcmc.list</code> object with the posterior of the original model parameters, i.e. the variance components and the unidentifiable mean parameters.
<code>Transform</code>	The transformation used to the measurements before the analysis.

If `code.only==TRUE`, a list containing the initial values is generated.

## Author(s)

Bendix Carstensen, Steno Diabetes Center, <http://BendixCarstensen.com>, Lyle Gurrin, University of Melbourne, <http://www.epi.unimelb.edu.au/about/staff/gurrin-lyle>.

## References

B Carstensen: Comparing and predicting between several methods of measurement, *Biostatistics*, 5, pp 399-413, 2004

## See Also

[BA.plot](#), [plot.MCmcmc](#), [print.MCmcmc](#), [check.MCmcmc](#)

**Examples**

```

data( ox )
str( ox )
ox <- Meth( ox )
# Writes the BUGS program to your console
MCMcmc( ox, MI=TRUE, IR=TRUE, code.only=TRUE, bugs.code.file="" )

### What is written here is not necessarily correct on your machine.
# ox.MC <- MCMcmc( ox, MI=TRUE, IR=TRUE, n.iter=100, program="JAGS" )
# ox.MC <- MCMcmc( ox, MI=TRUE, IR=TRUE, n.iter=100 )
# data( ox.MC )
# str( ox.MC )
# print( ox.MC )

```

Meth

*Create a Meth object representing a method comparison study***Description**

Creates a dataframe with columns meth, item, (repl) and y.

**Usage**

```

Meth( data=NULL,
      meth="meth", item="item", repl=NULL, y="y",
      print=!is.null(data), keep.vars=!is.null(data) )
## S3 method for class 'Meth'
summary( object, ... )
## S3 method for class 'Meth'
plot(x, which = NULL,
     col.LoA = "blue", col.pt = "black", cex.name = 2,
     var.range,
     diff.range,
     var.names = FALSE,
     pch = 16,
     cex = 0.7,
     Transform,
     ... )
## S3 method for class 'Meth'
mean(x, na.rm=TRUE, simplify=TRUE, ... )
## S3 method for class 'Meth'
sort(x, ... )
## S3 method for class 'Meth'
subset(x, ... )
## S3 method for class 'Meth'
sample( x,
        how = "random",

```

```

      N = if( how=="items" ) nlevels( x$item ) else nrow(x),
      ... )
## S3 method for class 'Meth'
transform('_data', ... )

```

### Arguments

<code>data</code>	A dataframe.
<code>meth</code>	Vector of methods, numeric, character or factor. Can also be a number or character referring to a column in data.
<code>item</code>	Vector of items, numeric, character or factor. Can also be a number or character referring to a column in data.
<code>repl</code>	Vector of replicate numbers, numeric, character or factor. Can also be a number or character referring to a column in data.
<code>y</code>	Vector of measurements. Can also be a character or numerical vector pointing to columns in data which contains the measurements by different methods or a dataframe with columns representing measurements by different methods. In this case the argument <code>meth</code> is ignored, and the names of the columns are taken as method names.
<code>print</code>	Logical: Should a summary result be printed?
<code>keep.vars</code>	Logical. Should the remaining variables from the dataframe <code>data</code> be transferred to the <code>Meth</code> object.
<code>object</code>	A <code>Meth</code> object.
<code>x</code>	A <code>Meth</code> object.
<code>which</code>	A vector of indices or names of methods to plot. If <code>NULL</code> all methods in the object are plotted.
<code>col.LoA</code>	What color should be used for the limits of agreement.
<code>col.pt</code>	What color should be used for the points.
<code>cex.name</code>	Character expansion factor for plotting method names
<code>var.range</code>	The range of both axes in the scatter plot and the x-axis in the Bland-Altman plot be?
<code>diff.range</code>	The range of yaxis in the Bland-Altman plot. Defaults to a range as the x-axis, but centered around 0.
<code>var.names</code>	If logical: should the individual panels be labelled with the variable names?. If character, then the values of the character will be used to label the methods.
<code>pch</code>	Plot character for points.
<code>cex</code>	Plot character expansion for points.
<code>Transform</code>	Transformation used to the measurements prior to plotting. Function or character, see <a href="#">choose.trans</a> for possible values.
<code>na.rm</code>	Logical. Should NAs be removed before calculations?
<code>simplify</code>	Should a <code>Meth</code> object with one row per ( <code>meth,item</code> ) be returned?
<code>how</code>	Character. What sampling strategy should be used, one of "random", "linked" or "item". Only the first letter is significant. See details for explanation.

<code>N</code>	How many observations should be sampled?
<code>_data</code>	A <code>Meth</code> object.
<code>...</code>	Ignored by the <code>Meth</code> and the <code>summary</code> and <code>sample</code> functions. In the <code>plot</code> function, parameters passed on to both the panel function plotting methods against each other, as well as to those plotting differences against means.

## Details

In order to perform analyses of method comparisons it is convenient to have a dataframe with classifying factors, `meth`, `item`, and possibly `repl` and the response variable `y`. This function creates such a dataframe, and gives it a class, `Meth`, for which there is a number of methods: `summary` - `tabulation`, `plot` - plotting and a couple of analysis methods.

If there are replicates in the values of `item` it is assumed that those observations represent replicate measurements and different replicate numbers are given to those.

`sample.Meth` samples a `Meth` object with replacement. If `how=="random"`, a random sample of the rows are sampled, the existing values of `meth`, `item` and `y` are kept but new replicate numbers are generated. If `how=="linked"`, a random sample of the linked observations (i.e. observations with identical `item` and `repl` values) are sampled with replacement and replicate numbers are kept. If `how=="item"`, items are sampled with replacement, and their observations are included the sampled number of times.

## Value

The `Meth` function returns a `Meth` object which is a dataframe with columns `meth`, `item`, (`repl`) and `y`. `summary.Meth` returns a table classified by method and no. of replicate measurements, extended with columns of the total number of items, total number of observations and the range of the measurements.

The `mean.Meth` returns a `Meth` object where means have been computed over replicates, and put in a variable `mean.y`. If `simplify=TRUE`, a smaller `Meth` object will be returned with only one row per (`meth`,`item`), and the means in the variable `y`. This is useful if the definition of a particular measurement method is the mean of a specified number of replicate measurements. The functions `mean.Meth`, `median.Meth`, `max.Meth`, and `min.Meth` behaves similarly, whereas `sort.Meth` just sorts the replicates within each (`meth`,`item`), and puts the results in a variable `sort.y` added `Meth` object.

The `subset.Meth` returns a subset of the `Meth` rows. If a subset of the methods is selected, the new `meth` variable will have levels equal to the actually present levels of `meth` in the new `Meth` object. This is not the case if subsetting is done using `"["`.

## Author(s)

Bendix Carstensen, <bxc@steno.dk>

## Examples

```
data(fat)
# Different ways of selecting columns and generating replicate numbers
Sub1 <- Meth(fat, meth=2, item=1, repl=3, y=4, print=TRUE)
Sub2 <- Meth(fat, 2, 1, 3, 4, print=TRUE)
```

```

Sub3 <- Meth(fat, meth="Obs", item="Id", repl="Rep", y="Sub", print=TRUE)
summary( Sub3 )
plot( Sub3 )

# Use observation in different columns as methods
data( CardOutput )
head( CardOutput )
sv <- Meth( CardOutput, y=c("Svo2", "Scvo2") )
# Note that replicates are generated if a non-unique item-id is used
sv <- Meth( CardOutput, y=c("Svo2", "Scvo2"), item="Age" )
str( sv )
# A summary is not created if the the first argument (data=) is not used:
sv <- Meth( y=CardOutput[,c("Svo2", "Scvo2")], item=CardOutput$V02 )
summary(sv)

# Sample items
ssv <- sample.Meth( sv, how="item", N=8 )

# More than two methods
data( sbp )
plot( Meth( sbp ) )
# Creating non-unique replicate numbers per (meth,item) creates a warning:
data( hba1c )
hb1 <- with( hba1c,
             Meth( meth=dev, item=item, repl=d.ana-d.samp, y=y, print=TRUE ) )
hb2 <- with( subset(hba1c, type=="Cap"),
             Meth( meth=dev, item=item, repl=d.ana-d.samp, y=y, print=TRUE ) )

```

Meth.sim

*Simulate a dataframe containing replicate measurements on the same items using different methods.*

## Description

Simulates a dataframe representing data from a method comparison study. It is returned as a [Meth](#) object.

## Usage

```

Meth.sim( Ni = 100,
          Nm = 2,
          Nr = 3,
          nr = Nr,
          alpha = rep(0, Nm),
          beta = rep(1, Nm),
          mu.range = c(0, 100),
          sigma.mi = rep(5, Nm),
          sigma.ir = 2.5,

```



```
sigma.mir = rep(5,Nm),
  m.thin = 1,
  i.thin = 1 )
```

## Arguments

Ni	The number of items (patient, animal, sample, unit etc.)
Nm	The number of methods of measurement.
Nr	The (maximal) number of replicate measurements for each (item,method) pair.
nr	The minimal number of replicate measurements for each (item,method) pair. If $nr < Nr$ , the number of replicates for each (meth,item) pair is uniformly distributed on the points $nr:Nr$ , otherwise $nr$ is ignored. Different number of replicates is only meaningful if replicates are not linked, hence $nr$ is also ignored when $\text{sigma.ir} > 0$ .
alpha	A vector of method-specific intercepts for the linear equation relating the "true" underlying item mean measurement to the mean measurement on each method.
beta	A vector of method-specific slopes for the linear equation relating the "true" underlying item mean measurement to the mean measurement on each method.
mu.range	The range across items of the "true" mean measurement. Item means are uniformly spaced across the range. If a vector length $Ni$ is given, the values of that vector will be used as "true" means.
sigma.mi	A vector of method-specific standard deviations for a method by item random effect. Some or all components can be zero.
sigma.ir	Method-specific standard deviations for the item by replicate random effect.
sigma.mir	A vector of method-specific residual standard deviations for a method by item by replicate random effect (residual variation). All components must be greater than zero.
m.thin	Fraction of the observations from each method to keep.
i.thin	Fraction of the observations from each item to keep. If both $m.thin$ and $i.thin$ are given the thinning is by their componentwise product.

## Details

Data are simulated according to the following model for an observation  $y_{mir}$ :

$$y_{mir} = \alpha_m + \beta_m(\mu_i + b_{ir} + c_{mi}) + e_{mir}$$

where  $b_{ir}$  is a random item by repl interaction (with standard deviation for method  $m$  the corresponding component of the vector  $\sigma_{ir}$ ),  $c_{mi}$  is a random meth by item interaction (with standard deviation for method  $m$  the corresponding component of the vector  $\sigma_{mi}$ ) and  $e_{mir}$  is a residual error term (with standard deviation for method  $m$  the corresponding component of the vector  $\sigma_{mir}$ ). The  $\mu_i$ 's are uniformly spaced in a range specified by  $\text{mu.range}$ .

## Value

A **Meth** object, i.e. dataframe with columns `meth`, `item`, `repl` and `y`, representing results from a method comparison study.

**Author(s)**

Lyle Gurrin, University of Melbourne, <http://www.epi.unimelb.edu.au/about/staff/gurrin-lyle>  
 Bendix Carstensen, Steno Diabetes Center, <http://BendixCarstensen.com>

**See Also**

[summary.Meth](#), [plot.Meth](#), [MCMcmc](#)

**Examples**

```
Meth.sim( Ni=4, Nr=3 )
xx <- Meth.sim( Nm=3, Nr=5, nr=2, alpha=1:3, beta=c(0.7,0.9,1.2), m.thin=0.7 )
summary( xx )
plot( xx )
```

---

MethComp

*Summarize conversion equations and prediction intervals between methods.*

---

**Description**

Takes the results from [BA.est](#), [DA.reg](#), [AltReg](#) or [MCMcmc](#) and returns a MethComp object, suitable for displaying the relationship between methods in print or graphic form.

**Usage**

```
MethComp(obj)
## S3 method for class 'MethComp'
print(x, digits=3, ... )
## S3 method for class 'MethComp'
plot(x,
      wh.comp = 1:2,
      pl.type = "conv",
      dif.type = "lin",
      sd.type = "const",
      axlim = range(x$data$y, na.rm=TRUE),
      diflim = axlim-mean(axlim),
      points = FALSE,
      repl.conn = FALSE,
      col.conn = "gray",
      lwd.conn = 1,
      grid = TRUE,
      N.grid = 10,
      col.grid = grey(0.9),
      lwd = c(3,1,1),
      col.lines = "black",
```

```

col.points = "black",
pch.points = 16,
  eqn = is.null(attr(x,"Transform")),
col.eqn = col.lines,
font.eqn = 2,
  digits = 2,
  mult = FALSE,
  alpha = NULL,
  ... )
## S3 method for class 'MethComp'
lines(x,
      wh.comp = getOption("MethComp.wh.comp"),
      pl.type = getOption("MethComp.pl.type"),
      dif.type = getOption("MethComp.dif.type"),
      sd.type = getOption("MethComp.sd.type"),
      col.lines = "black",
      lwd = c(3,1,1),
      digits = 3,
      mult = FALSE,
      alpha = NULL,
      ... )
## S3 method for class 'MethComp'
points(x,
      wh.comp = getOption("MethComp.wh.comp"),
      pl.type = getOption("MethComp.pl.type"),
      col.points = "black",
      pch.points = 16,
      repl.conn = FALSE,
      col.conn = "gray",
      lwd.conn = 1,
      mult = FALSE,
      ... )

```

### Arguments

<code>obj</code>	A MethComp or <a href="#">MCMcmc</a> object.
<code>x</code>	A MethComp object.
<code>wh.comp</code>	Numeric or character of length 2. Which two methods should be plotted.
<code>pl.type</code>	Character. If "conv" it will be a plot of two methods against each other, otherwise it will be a plot of the 1st minus the 2nd versus the average; a Bland-Altman type plot.
<code>dif.type</code>	Character. If "lin" (the default) a linear relationship between methods is allowed. Otherwise a constant difference is assumed and LoA can be indicated on the plot.
<code>sd.type</code>	Should the estimated dependence of the SD (from <a href="#">DA.reg</a> be used when plotting prediction limits?
<code>axlim</code>	The extent of the axes of the measurements.

<code>diflim</code>	The extent of the axis of the differences.
<code>points</code>	Logical. Should the points be included in the plot.
<code>repl.conn</code>	Logical. Should replicate measurements be connected; this assumes linked replicates.
<code>col.conn</code>	Color of the lines connecting replicates.
<code>lwd.conn</code>	Width of the connection lines.
<code>grid</code>	Should there be a grid? If numerical, gridlines are drawn at these locations.
<code>N.grid</code>	Numeric. How many gridlines? If a vector of length>1, it will be taken as the position of the gridlines.
<code>col.grid</code>	Color of the gridlines.
<code>col.lines</code>	Color of the conversion lines.
<code>lwd</code>	Numerical vector of length 3. Width of the conversion line and the prediction limits.
<code>pch.points</code>	Plot character for points.
<code>col.points</code>	Color of the points.
<code>eqn</code>	Logical. Should the conversion equation be printed on the plot.
<code>col.eqn</code>	Color of the conversion formula
<code>font.eqn</code>	font for the conversion formula
<code>digits</code>	The number of digits after the decimal point in the conversion formulae.
<code>mult</code>	Logical. Should ratios be plotted on a log-scale instead of differences on a linear scale? See description of the argument for <a href="#">BA.plot</a> .
<code>alpha</code>	1 minus the confidence level for the prediction interval. If not given, the prediction interval is constructed as plus/minus twice the SD.
<code>...</code>	Further arguments.

## Details

Using `MethComp` on the results from [BA.est](#) or [AltReg](#) is not necessary, as these two functions already return objects of class `MethComp`.

`plot.MethComp` plots the conversion function with prediction limits; always using the original scale of measurements. It also sets the options "`MethComp.wh.cmp`" indicating which two methods are plotted and "`MethComp.pl.type`" indicating whether a plot of methods against each other or a Bland-Altman type plot of differences versus averages. By default the conversion lines are plotted.

`lines.MethComp` and `points.MethComp` adds conversion lines with prediction limits and points to a plot.

## Value

`MethComp` returns a `MethComp` object, which is a list with three elements, `Conv`, a three-way array giving the linear conversion equations between methods, `VarComp`, a two-way array classified by methods and variance components and `data`, a copy of the original [Meth](#) object supplied — see the description under [BA.est](#).

A MethComp object has an attribute Transform, which is either NULL, or a named list with elements trans and inv, both of which are functions. The first is the transformation applied to measurements before analysis; the results are all given on the transformed scale. The second is the inverse transformation; this is only used when plotting the resulting relationship between methods.

The methods print, plot, lines and points return nothing.

### Author(s)

Bendix Carstensen, Steno Diabetes Center, <bxc@steno.dk>.

### See Also

[BA.est](#) [AltReg](#) [MCmcmc](#)

### Examples

```
data( ox )
BA.ox <- BA.est( ox, linked=TRUE )
print( BA.ox )
## Not run:
AR.ox <- AltReg( ox, linked=TRUE )
print( AR.ox )
plot( AR.ox )
## End(Not run)
```

---

milk

*Measurement of fat content of human milk by two different methods.*

---

### Description

Fat content of human milk determined by measurement of glycerol released by enzymic hydrolysis of triglycerides (Trig) and measurement by the Standard Gerber method (Gerber). Units are (g/100 ml).

### Usage

```
data(milk)
```

### Format

A data frame with 90 observations on the following 3 variables.

meth a factor with levels Gerber Trig

item sample id

y a numeric vector

## Source

The dataset is adapted from table 3 in: JM Bland and DG Altman: Measuring agreement in method comparison studies. *Statistical Methods in Medical Research*, 8:136-160, 1999. See: Lucas A, Hudson GJ, Simpson P, Cole TJ, Baker BA. An automated enzymic micromethod for the measurement of fat in human milk. *Journal of Dairy Research* 1987; 54: 487-92.

## Examples

```
data(milk)
str(milk)
milk <- Meth(milk)
plot(milk)
abline(0,1)
```

---

 ox

---

*Measurement of oxygen saturation in blood*


---

## Description

61 children had their blood oxygen content measured at the Children's Hospital in Melbourne, either with a chemical method analysing gases in the blood (CO) or by a pulse oximeter measuring transcutaneously (pulse). Replicates are linked between methods; i.e. replicate 1 for each of the two methods are done at the same time. However, replicate measurements were taken in quick succession so the pairs of measurements are exchangeable within person.

## Usage

```
data(ox)
```

## Format

A data frame with 354 observations on the following 4 variables.

meth Measurement methods, factor with levels CO, pulse

item Id for the child

repl Replicate of measurements. There were 3 measurements for most children, 4 had only 2 replicates with each method, one only 1

y Oxygen saturation in percent.

## Examples

```
data(ox)
str(ox)
ox <- Meth(ox)
with( ox, table(table(item)) )
summary( ox )
# The effect of basing LoA on means over replicates:
```

```
par( mfrow=c(1,2), mar=c(4,4,1,4) )
BA.plot(      ox , diflim=c(-20,20), axlim=c(20,100), repl.conn=TRUE )
BA.plot( mean(ox), diflim=c(-20,20), axlim=c(20,100) )
```

---

ox.MC

*A MCmcmc object from the oximetry data.*


---

## Description

This object is included for illustrative purposes. It is a result of using [MCmcmc](#), with `n.iter=20000`.

## Usage

```
data(ox.MC)
```

## Format

The format is a [MCmcmc](#) object.

## Details

The data are the [ox](#) dataset, where measurements are linked within replicate (=day of analysis).

## Examples

```
data(ox.MC)
attr(ox.MC,"mcmc.par")
## Not run:
print.MCmcmc(ox.MC)
trace.MCmcmc(ox.MC)
trace.MCmcmc(ox.MC,"beta")
post.MCmcmc(ox.MC)
post.MCmcmc(ox.MC,"beta")
## End(Not run)
# A MCmcmc object also has class mcmc.list, so we can use the
# coda functions for convergence diagnostics:
## Not run: acfplot( subset.MCmcmc(ox.MC, subset="sigma"))
```

PBreg

*Passing-Bablok regression***Description**

Implementation of the Passing-Bablok's procedure for assessing of the equality of measurements by two different analytical methods.

**Usage**

```
PBreg(x, y=NULL, conf.level=0.05, wh.meth=1:2)
## S3 method for class 'PBreg'
print(x,...)
```

**Arguments**

x	a <a href="#">Meth</a> object, alternatively a numeric vector of measurements by method A, or a data frame of exactly two columns, first column with measurements by method A, second column with measurements by method B.
y	a numeric vector of measurements by method B - must be of the same length as x. If not provided, x must be the <a href="#">Meth</a> object or a data frame of exactly 2 columns.
conf.level	confidence level for calculation of confidence boundaries - 0.05 is the default.
wh.meth	Which of the methods from the Meth object are used in the regression.
...	other parameters, currently ignored.

**Details**

This is an implementation of the original Passing-Bablok procedure of fitting unbiased linear regression line to data in the method comparison studies. It calculates the unbiased slope and intercept, along with their confidence intervals. However, the tests for linearity is not yet fully implemented.

It doesn't matter which results are assigned to "Method A" and "Method B", however the "Method A" results will be plotted on the x-axis by the plot method.

**Value**

PBreg returns an object of class "PBreg", for which the print, predict and plot methods are defined.

An object of class "PBreg" is a list composed of the following elements:

coefficients	a matrix of 3 columns and 2 rows, containing the estimates of the intercept and slope, along with their confidence boundaries.
residuals	defined as in the "lm" class, as the response minus the fitted value.
fitted.values	the fitted values.
model	the model data frame used.



n	a vector of two values: the number of observations read, and the number of observations used.
S	A vector of all slope estimates.
I	A vector of all intercept estimates.
adj	A vector of fit parameters, where $S_s$ is the number of estimated slopes ( $\text{length}(S)$ ), $K$ is the offset for slopes $<(-1)$ , $M1$ and $M2$ are the locations of confidence boundaries in $S$ , and $l$ and $L$ are the numbers of points above and below the fitted line, used in cusum calculation.
cusum	A vector of cumulative sums of residuals sorted by the D-rank.
Di	A vector of D-ranks.

### Note

Please note that this method can become very computationally intensive for larger numbers of observations. One can expect a reasonable computation times for datasets with fewer than 100 observations.

### Author(s)

Michal J. Figurski <mfigrs@gmail.com>

### References

Passing, H. and Bablok, W. (1983), A New Biometrical Procedure for Testing the Equality of Measurements from Two Different Analytical Methods. *Journal of Clinical Chemistry and Clinical Biochemistry*, Vol 21, 709–720

### See Also

[plot.PBreg](#), [predict.PBreg](#), [Deming](#).

### Examples

```
## Model data frame generation
a <- data.frame(x=seq(1, 30)+rnorm(mean=0, sd=1, n=30),
               y=seq(1, 30)*rnorm(mean=1, sd=0.4, n=30))

## Call to PBreg
x <- PBreg(a)
print(x)

par(mfrow=c(2,2))
plot(x, s=1:4)

## A real data example
data(milk)
milk <- Meth(milk)
summary(milk)
PBmilk <- PBreg(milk)
```

```
par(mfrow=c(2,2))
plot(PBmilk, s=1:4)
```

PEFR

*Peak Expiratory Flow Rate (PEFR) measurements with Wright peak flow and mini Wright peak flow meter.*

### Description

Measurement of PEFR with Wright peak flow and mini Wright peak flow meter on 17 individuals.

### Usage

```
data(PEFR)
```

### Format

A data frame with 68 observations on the following 3 variables.

`meth` a factor with levels `Wright` and `Mini`, representing measurements by a Wright peak flow meter and a mini Wright meter respectively, in random order.

`item` Numeric vector, the person ID.

`y` Numeric vector, the measurements, i.e. PEFR for the two measurements with a Wright peak flow meter and a mini Wright meter respectively. The measurement unit is l/min.

`repl` Numeric vector, replicate number. Replicates are exchangeable within item.

### Source

J. M. Bland and D. G. Altman (1986) Statistical Methods for Assessing Agreement Between Two Methods of Clinical Measurement, *Lancet*. 1986 Feb 8;1(8476):307-10.

### Examples

```
data(PEFR)
PEFR <- Meth(PEFR)
summary(PEFR)
plot(PEFR)
plot(perm.repl(PEFR))
```

---

perm.repl	<i>Manipulate the replicate numbering within (item,method)</i>
-----------	--

---

## Description

Replicate numbers are generated within (item,method) in a dataframe representing a method comparison study. The function assumes that observations are in the correct order within each (item,method), i.e. if replicate observations are non-exchangeable within method, linked observations are assumed to be in the same order within each (item,method).

## Usage

```
make.repl( data )  
has.repl( data )  
perm.repl( data )
```

## Arguments

data                    A [Meth](#) object or a data frame with columns meth, item and y.

## Details

make.repl just adds replicate numbers in the order of the data.frame rows. perm.repl is designed to explore the effect of permuting the replicates within (item,method). If replicates are truly exchangeable within methods, the inference should be independent of this permutation.

## Value

make.repl returns a dataframe with a column, repl added or replaced, whereas has.repl returns a logical indicating wheter a combination of (meth,item) wioth more that one valid y- value.

perm.repl returns a dataframe of class [Meth](#) where the rows (i.e. replicates) are randomly permuted within (meth,item), and subsequently ordered by (meth,item,repl).

## Author(s)

Bendix Carstensen, Steno Diabetes Center, <http://www.biostat.ku.dk/~bxc>

## See Also

[perm.repl](#)

## Examples

```
data(ox)
xx <- subset( ox, item<4 )[-3]
cbind( xx, make.repl(xx) )
cbind( make.repl(xx), perm.repl(xx) )
data( ox )
xx <- subset( ox, item<4 )
cbind( xx, perm.repl(xx) )
# Replicates are linked in the oximetry dataset, so randomly permuting
# them clearly inflates the limits of agreement:
par( mfrow=c(1,2), mar=c(4,4,1,4) )
BA.plot(      ox , ymax=30, digits=1 )
BA.plot( perm.repl(ox), ymax=30, digits=1 )
```

---

plot.MCmcmc

---

*Plot estimated conversion lines and formulae.*


---

## Description

Plots the pairwise conversion formulae between methods from a [MCmcmc](#) object.

## Usage

```
## S3 method for class 'MCmcmc'
plot( x,
      axlim = range( attr(x,"data")$y, na.rm=TRUE ),
      wh.cmp,
      lwd.line = c(3,1), col.line = rep("black",2), lty.line=rep(1,2),
      eqn = TRUE, digits = 2,
      grid = FALSE, col.grid=gray(0.8),
      points = FALSE,
      col.pts = "black", pch.pts = 16, cex.pts = 0.8,
      ... )
```

## Arguments

x	A <a href="#">MCmcmc</a> object
axlim	The limits for the axes in the panels
wh.cmp	Numeric vector or vector of method names. Which of the methods should be included in the plot?
lwd.line	Numerical vector of length 2. The width of the conversion line and the prediction limits. If the second values is 0, no prediction limits are drawn.
col.line	Numerical vector of length 2. The color of the conversion line and the prediction limits.

lty.line	Numerical vector of length 2. The line types of the conversion line and the prediction limits.
eqn	Should the conversion equations be printed on the plot?. Defaults to TRUE.
digits	How many digits after the decimal point should be used when printing the conversion equations.
grid	Should a grid be drawn? If a numerical vector is given, the grid is drawn at those values.
col.grid	What color should the grid have?
points	Logical or character. Should the points be plotted. If TRUE or "repl" paired values of single replicates are plotted. If "perm", replicates are randomly permuted within (item, method) before plotting. If "mean", means across replicates within item, method are formed and plotted.
col.pts	What color should the observation have.
pch.pts	What plotting symbol should be used.
cex.pts	What scaling should be used for the plot symbols.
...	Parameters to pass on. Currently not used.

### Value

Nothing. The lower part of a (M-1) by (M-1) matrix of plots is drawn, showing the pairwise conversion lines. In the corners of each is given the two conversion equations together with the prediction standard error.

### See Also

[MCmcmc](#), [print.MCmcmc](#)

### Examples

```
## Not run: data( hba1c )
## Not run: str( hba1c )
## Not run: hba1c <- transform( subset( hba1c, type=="Ven" ),
                             meth = dev,
                             repl = d.ana )

## End(Not run)
## Not run: hb.res <- MCmcmc( hba1c, n.iter=50 )
## Not run: data( hba.MC )
## Not run: str( hba.MC )
## Not run: par( ask=TRUE )
## Not run: plot( hba.MC )
## Not run: plot( hba.MC, pl.obs=TRUE )
```

plot.PBreg

*Passing-Bablok regression - plot method***Description**

A plot method for the "PBreg" class object, that is a result of Passing-Bablok regression.

**Usage**

```
## S3 method for class 'PBreg'
plot(x,
      pch=21, bg="#2200aa33",
      xlim=c(0, max(x$model)), ylim=c(0, max(x$model)),
      xlab=x$meths[1], ylab=x$meths[2], subtype=1, colors =
      list(CI = "#ccaaff50", fit = "blue", ref = "#99999955",
      bars = "gray", dens = "#8866aaa0", ref2 = c("#1222bb99",
      "#bb221299")), ...)
```

**Arguments**

x	an object of class "PBreg"
pch	Which plotting character should be used for the points.
bg	Background colour for the plotting character.
xlim	Limits for the x-axis.
ylim	Limits for the y-axis.
xlab	Label on the x-axis.
ylab	Label on the y-axis.
subtype	a numeric value or vector, that selects the desired plot subtype. Subtype <b>1</b> is an x-y plot of raw data with regression line and confidence boundaries for the fit as a shaded area. This is the default. Subtype <b>2</b> is a ranked residuals plot. Subtype <b>3</b> is the "Cusum" plot useful for assessing linearity of the fit. Plot subtypes 1 through 3 are standard plots from the 1983 paper by Passing and Bablok - see the reference. Plot subtype <b>4</b> is a histogram (with overlaid density line) of the individual slopes. The range of this plot is limited to 5 x IQR for better visibility.
colors	A list of 6 elements allowing customization of colors of various plot elements. For plot subtype 1: "CI" is the color of the shaded confidence interval area; and "fit" is the color of fit line. For plot subtypes 2 & 3: "ref" is the color of the horizontal reference line. For plot subtype 4: "bars" is the bar background color, "dens" is the color of the density line, and "ref2" is a vector of two colors for lines indicating the median and confidence limits.
...	other parameters as in "plot", some of which are pre-defined for improved appearance. This affects only the subtype 1 plot.

**Author(s)**

Michal J. Figurski <mfigrs@gmail.com>

**References**

Passing, H. and Bablok, W. (1983), A New Biometrical Procedure for Testing the Equality of Measurements from Two Different Analytical Methods. *Journal of Clinical Chemistry and Clinical Biochemistry*, Vol 21, 709–720

**See Also**

[PBreg](#), [Deming](#).

**Examples**

```
## Model data frame generation
a <- data.frame(x=seq(1, 30)+rnorm(mean=0, sd=1, n=30),
               y=seq(1, 30)*rnorm(mean=1, sd=0.4, n=30))

## Call to PBreg
x <- PBreg(a)
print(x)
par(mfrow=c(2,2))
plot(x, s=1:4)

## Or the same using "Meth" object
a <- Meth(a, y=1:2)
x <- PBreg(a)
print(x)
par(mfrow=c(2,2))
plot(x, s=1:4)
```

---

plot.VarComp

---

*Plot the a posteriori densities for variance components*


---

**Description**

When a method comparison model is fitted and stored in a [MCMcmc](#) object, then the posterior distributions of the variance components are plotted, in separate displays for method.

**Usage**

```
## S3 method for class 'VarComp'
plot( x,
      which,
      lwd.line = rep(2, 4),
      col.line = c("red", "green", "blue", "black"),
      lty.line = rep(1, 4),
```

```

      grid = TRUE,
col.grid = gray(0.8),
      rug = TRUE,
      probs = c(5, 50, 95),
      tot.var = FALSE,
      same.ax = TRUE,
meth.names = TRUE,
      VC.names = "first",
      ... )

```

### Arguments

<code>x</code>	A MCmcmc object.
<code>which</code>	For which of the compared methods should the plot be made?
<code>lwd.line</code>	Line width for drawing the density.
<code>col.line</code>	Color for drawing the densities.
<code>lty.line</code>	Line type for drawing the densities.
<code>grid</code>	Logical. Should a vertical grid be set up? If numeric it is set up at the values specified. If <code>same.ax</code> , the range of the grid is taken to be the extent of the x-axis for all plots.
<code>col.grid</code>	The color of the grid.
<code>rug</code>	Should a small rug at the bottom show posterior quantiles?
<code>probs</code>	Numeric vector with numbers in the range from 0 to 100, indicating the posterior percentiles to be shown in the rug.
<code>tot.var</code>	Should the posterior of the total variance also be shown?
<code>same.ax</code>	Should the same axes be used for all methods?
<code>meth.names</code>	Should the names of the methods be put on the plots?
<code>VC.names</code>	Should the names of the variance components be put on the first plot ("first"), the last ("last"), all ("all") or none ("none"). Only the first letter is needed.
<code>...</code>	Parameters passed on the <a href="#">density</a> function that does the smoothing of the posterior samples.

### Details

The function generates a series of plots, one for each method compared in the MCmcmc object supplied (or those chosen by `which=`). Therefore the user must take care to set `mfrow` or `mfcol` to capture all the plots.

### Value

A list with one element for each method. Each element of this is a list of densities, i.e. of objects of class `density`, one for each variance component.



**Author(s)**

Bendix Carstensen, [www.biostat.ku.dk/~bxc](http://www.biostat.ku.dk/~bxc)

**See Also**

[plot.MCmcmc](#), [MCmcmc](#), [check.MCmcmc](#)

**Examples**

```
data( ox.MC )
par( mfrow=c(2,1) )
plot.VarComp( ox.MC, grid=c(0,15) )
```

---

plvol

*Measurements of plasma volume measured by two different methods.*

---

**Description**

For each subject (*item*) the plasma volume is expressed as a percentage of the expected value for normal individuals. Two alternative sets of normal values are used, named Nadler and Hurley respectively.

**Usage**

```
data(plvol)
```

**Format**

A data frame with 198 observations on the following 3 variables.

*meth* a factor with levels Hurley and Nadler

*item* a numeric vector

*y* a numeric vector

**Source**

The dataset is adapted from table 2 in: JM Bland and DG Altman: Measuring agreement in method comparison studies. *Statistical Methods in Medical Research*, 8:136-160, 1999. Originally supplied to Bland & Altman by C Dore, see: Cotes PM, Dore CJ, Liu Yin JA, Lewis SM, Messinezy M, Pearson TC, Reid C. Determination of serum immunoreactive erythropoietin in the investigation of erythrocytosis. *New England Journal of Medicine* 1986; 315: 283-87.

**Examples**

```
data(plvol)
str(plvol)
plot( y[meth=="Nadler"]~y[meth=="Hurley"],data=plvol,
      xlab="Plasma volume (Hurley) (pct)",
      ylab="Plasma volume (Nadler) (pct)" )
abline(0,1)
par( mar=c(4,4,1,4) )
BA.plot(plvol)
```

---

predict.PBreg	<i>Passing-Bablok regression - predict method</i>
---------------	---

---

**Description**

A predict method for the "PBreg" class object, that is a result of Passing-Bablok regression.

**Usage**

```
## S3 method for class 'PBreg'
predict(object, newdata = object$model$x, interval="confidence",
        level=0.95,...)
```

**Arguments**

object	an object of class "PBreg"
newdata	an optional vector of new values of x to make predictions for. If omitted, the fitted values will be used.
interval	type of interval calculation - either confidence or none. The former is the default.
level	tolerance/confidence level.
...	Not used.

**Value**

If interval is "confidence" this function returns a data frame with three columns: "fit", "lwr" and "upr" - similarly to predict.lm.

If interval is "none" a vector of predicted values is returned.

**Author(s)**

Michal J. Figurski <mfigrs@gmail.com>

**References**

Passing, H. and Bablok, W. (1983), A New Biometrical Procedure for Testing the Equality of Measurements from Two Different Analytical Methods. *Journal of Clinical Chemistry and Clinical Biochemistry*, Vol 21, 709–720

**See Also**

[PBreg](#), [Deming](#).

**Examples**

```
## Model data frame generation
a <- data.frame(x=seq(1, 30)+rnorm(mean=0, sd=1, n=30),
               y=seq(1, 30)*rnorm(mean=1, sd=0.4, n=30))

## Call to PBreg
x <- PBreg(a)
print(x)
predict(x, interval="none")

## Or the same using "Meth" object
a <- Meth(a, y=1:2)
x <- PBreg(a)
print(x)
predict(x)
```

---

rainman

---

*Perception of points in a swarm*


---

**Description**

Five raters were asked to guess the number of points in a swarm for 10 different figures (which - unknown to the raters - were each repeated three times).

**Usage**

```
data(rainman)
```

**Format**

A data frame with 30 observations on the following 6 variables.

SAND The true number of points in the swarm. Each picture is replicated thrice

ME Ratings from judge 1

TM Ratings from judge 2

AJ Ratings from judge 3

BM Ratings from judge 4

LO Ratings from judge 5

**Details**

The raters had approximately 10 seconds to judge each picture, and they thought it were 30 different pictures. Before starting the experiment they were shown 6 (unrelated) pictures and were told the number of points in each of those pictures. The SAND column contains the picture id (which is also the true number of points in the swarm).

## Source

Collected by Claus Ekstrom.

## Examples

```
library(MethComp)
data( rainman )
str( rainman )
RM <- Meth( rainman, item=1, y=2:6 )
head( RM )
BA.est( RM, linked=FALSE )
library(lme4)
mf <- lmer( y ~ meth + item + (1|MI),
            data = transform( RM, MI=interaction(meth,item) ) )
summary( mf )
mr <- lmer( y ~ (1|meth) + (1|item) + (1|MI),
            data = transform( RM, MI=interaction(meth,item) ) )
summary( mr )

#
# Point swarms were generated by the following program
#
## Not run:
set.seed(2) # Original
npoints <- sample(4:30)*4
nplots <- 10
pdf(file="swarms.pdf", onefile=TRUE)

s1 <- sample(npoints[1:nplots])
print(s1)
for (i in 1:nplots) {
  n <- s1[i]
  set.seed(n)
  x <- runif(n)
  y <- runif(n)
  plot(x,y, xlim=c(-.15, 1.15), ylim=c(-.15, 1.15), pch=20, axes=F,
        xlab="", ylab="")
}
s1 <- sample(npoints[1:nplots])
print(s1)
for (i in 1:nplots) {
  n <- s1[i]
  set.seed(n)
  x <- runif(n)
  y <- runif(n)
  plot(y,x, xlim=c(-.15, 1.15), ylim=c(-.15, 1.15), pch=20, axes=F,
        xlab="", ylab="")
}
s1 <- sample(npoints[1:nplots])
print(s1)
for (i in 1:nplots) {
  n <- s1[i]
```

```

set.seed(n)
x <- runif(n)
y <- runif(n)
plot(-x,y, xlim=c(-1.15, .15), ylim=c(-.15, 1.15), pch=20, axes=F,
      xlab="", ylab="")
}
dev.off()

## End(Not run)

```

sbp

*Systolic blood pressure measured by three different methods.***Description**

For each subject (*item*) there are three replicate measurements by three methods (two observers, J and R and the automatic machine, S). The replicates are linked within (*method,item*).

**Usage**

```
data(sbp)
```

**Format**

A data frame with 765 observations on the following 4 variables:

*meth* Methods, a factor with levels J(observer 1), R(observer 2) and S(machine)

*item* Person id, numeric.

*repl* Replicate number, a numeric vector

*y* Systolic blood pressure measurement, a numeric vector

**Source**

The dataset is adapted from table 1 in: JM Bland and DG Altman: Measuring agreement in method comparison studies. *Statistical Methods in Medical Research*, 8:136-160, 1999. Originally supplied to Bland & Altman by E. O'Brien, see: Altman DG, Bland JM. The analysis of blood pressure data. In O'Brien E, O'Malley K eds. *Blood pressure measurement*. Amsterdam: Elsevier, 1991: 287-314.

**See Also**

[sbp.MC](#)

**Examples**

```

data(sbp)
par( mfrow=c(2,2), mar=c(4,4,1,4) )
BA.plot( sbp, comp=1:2 )
BA.plot( sbp, comp=2:3 )
BA.plot( sbp, comp=c(1,3) )
## Not run: BA.est( sbp, linked=TRUE )

```

---

sbp.MC

*A MCmcmc object from the sbp data*


---

## Description

This object is included for illustrative purposes. It is a result of using [MCmcmc](#), with `n.iter=100000` on the dataset [sbp](#) from this package.

## Usage

```
data(sbp.MC)
```

## Format

The format is a [MCmcmc](#) object.

## Details

The basic data are measurements of systolic blood pressure from the [sbp](#) dataset. Measurements are taken to be linked within replicate. The code used to generate the object was:

```
library(MethComp)
data( sbp )
spb <- Meth( sbp )
sbp.MC <- MCmcmc( sbp, linked=TRUE, n.iter=100000, program="JAGS" ) )
```

## Examples

```
data(sbp.MC)
# How was the data generated
attr(sbp.MC, "mcmc.par")

# Traceplots
trace.MCmcmc(sbp.MC)
trace.MCmcmc(sbp.MC, "beta")

# A MCmcmc object also has class mcmc.list, so we can use the
# standard coda functions for convergence diagnostics:
acfplot( subset.MCmcmc(sbp.MC, subset="sigma") )

# Have a look at the correlation between the 9 variance parameters
pairs.MCmcmc( sbp.MC )

# Have a look at whether the MxI variance components are the same between methods:
## Not run:
pairs.MCmcmc( sbp.MC, subset=c("mi"), eq=TRUE,
              panel=function(x,y,...)
                {
```

```

        abline(0,1)
        abline(v=median(x),h=median(y),col="gray")
        points(x,y,...)
    }
)
## End(Not run)

```

---

scint

*Relative renal function by Scintigraphy*


---

### Description

Measurements of the relative kidney function (=renal function) for 111 patients. The percentage of the total renal function present in the left kidney is determined by one reference method, DMSA (static) and by one of two dynamic methods, DTPA or EC.

### Usage

```
data(scint)
```

### Format

A data frame with 222 observations on the following 5 variables:

**meth** Measurement method, a factor with levels DMSA, DTPA, EC.

**item** Patient identification.

**y** Percentage of total kidney function in the left kidney.

**age** Age of the patient.

**sex** Sex of the patient, a factor with levels F, M.

### Source

F. C. Domingues, G. Y. Fujikawa, H. Decker, G. Alonso, J. C. Pereira, P. S. Duarte: Comparison of Relative Renal Function Measured with Either 99mTc-DTPA or 99mTc-EC Dynamic Scintigraphies with that Measured with 99mTc-DMSA Static Scintigraphy. International Braz J Urol Vol. 32 (4): 405-409, 2006

### Examples

```

data(scint)
str(scint)
# Make a Bland-Altman plot for each of the possible comparisons:
par(mfrow=c(1,2),mgp=c(3,1,0)/1.6,mar=c(3,3,1,3))
BA.plot(scint,comp.levels=c(1,2),ymax=15,digits=1,cex=2)
BA.plot(scint,comp.levels=c(1,3),ymax=15,digits=1,cex=2)

```

---

TDI	<i>Compute Lin's Total deviation index</i>
-----	--

---

### Description

This index calculates a value such that a certain fraction of difference between methods will be numerically smaller than this.

### Usage

```
TDI( y1, y2, p = 0.05, boot = 1000, alpha = 0.05 )
```

### Arguments

y1	Measurements by one method.
y2	Measurements by the other method
p	The fraction of items with differences numerically exceeding the TDI
boot	If numerical, this is the number of bootstraps. If FALSE no confidence interval for the TDI is produced.
alpha	1 - confidence degree.

### Details

If boot==FALSE a single number, the TDI is returned. If boot is a number, the median and the 1-alpha/2 central interval based on boot resamples are returned too, in a named vector of length 4.

### Value

A list with 3 components. The names of the list are preceeded by the criterion percentage, i.e. the percentage of the population that the TDI is devised to catch.

TDI	The numerically computed value for the TDI. If boot is numeric, a vector of median and a bootstrap c.i. is appended.
TDI	The approximate value of the TDI
Limits of Agreement	Limits of agreement

### Note

The TDI is a measure which essentially is a number K such that the interval [-K,K] contains the limits of agreement.

### Author(s)

Bendix Carstensen, bxc@steno.dk



## References

LI Lin: Total deviation index for measuring individual agreement with applications in laboratory performance and bioequivalence, *Statistics in Medicine*, 19, 255-270 (2000)

## See Also

[BA.plot](#), [corr.measures](#)

## Examples

```
data(plvol)
pw <- to.wide(plvol)
with(pw, TDI(Hurley, Nadler))
```

---

to.wide

*Functions to convert between long and wide representations of data.*

---

## Description

These functions are merely wrappers for [reshape](#). Given the complicated syntax of reshape and the particularly simple structure of this problem, the functions facilitate the conversion enormously.

## Usage

```
to.wide( data, warn=TRUE )
to.long( data, vars )
```

## Arguments

data	A <a href="#">Meth</a> object.
warn	Logical. Should a warning be printed when replicates are taken as items?
vars	The variables representing measurements by different methods. Either a character vector of names, or a numerical vector with the number of the variables in the dataframe.

## Details

If data represents method comparisons with exchangeable replicates within method, the transformation to wide format does not necessarily make sense. Also recognizes a

## Value

A dataframe.

## Author(s)

Bendix Carstensen, Steno Diabetes Center, <http://BendixCarstensen.com>

**See Also**

[perm.repl](#)

**Examples**

```
data( milk )
str( milk )
mw <- to.wide( milk )
str( mw )
( mw <- subset( mw, as.integer(item) < 3 ) )
to.long( mw, 3:4 )
```

---

VitCap

*Merits of two instruments designed to measure certain aspects of human lung function (Vital Capacity)*

---

**Description**

Measurement on certain aspects of human lung capacity for 72 patients on 4 instrument-operative combination, i.e. two different instruments and two different users, a skilled one and a new one.

**Usage**

```
data(VitCap)
```

**Format**

A data frame with 288 observations on the following 5 variables.

**meth** a factor with levels StNew, StSkil, ExpNew and ExpSkil, representing the instrument by user combinations. See below.

**item** a numeric vector, the person ID, i.e. the 72 patients

**y** a numeric vector, the measurements, i.e. vital capacity.

**user** a factor with levels New Skil, for the new user and the skilled user

**instrument** a factor with levels Exp and St, for the experimental instrument and the standard one.

**Source**

V. D. Barnett, Simultaneous Pairwise Linear Structural Relationships, Biometrics, Mar. 1969, Vol. 25, No. 1, pp. 129-142.

**Examples**

```
data(VitCap)
Vcap <- Meth( VitCap )
str( Vcap )
plot( Vcap )
```

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