

Package ‘miceadds’

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Type Package

Title Some Additional Multiple Imputation Functions, Especially for
'mice'

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Description Contains some auxiliary functions for multiple
imputation which complements existing functionality
in R.

In addition to some utility functions, main features
include plausible value imputation, multilevel
imputation functions (arbitrary number of levels,
hierarchical and non-hierarchical datasets),
imputation using partial least squares (PLS) for
high dimensional predictors, and nested multiple
imputation.

Depends R (>= 3.0), mice (>= 3.0.0)

Imports CDM (>= 5.8-5), coda, graphics, lme4, MASS, methods, mitools,
mvtnorm, Rcpp, sirt, stats, TAM (>= 2.9-13), utils

LinkingTo Rcpp, RcppArmadillo

Suggests Amelia, BIFIEsurvey, blme, car, foreign, grouped, haven,
inline, jomo, MBESS, MCMCglmm, mitml, multiwayvcov, numDeriv,
pan, sjlabelled

URL <https://github.com/alexanderrobitzsch/miceadds>,
<https://sites.google.com/site/alexanderrobitzsch2/software>

License GPL (>= 2)

BugReports <https://github.com/alexanderrobitzsch/miceadds/issues?state=open>

NeedsCompilation yes

Repository CRAN

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Description

Contains some auxiliary functions for multiple imputation which complements existing functionality in R. In addition to some utility functions, main features include plausible value imputation, multilevel imputation functions (arbitrary number of levels, hierarchical and non-hierarchical datasets), imputation using partial least squares (PLS) for high dimensional predictors, and nested multiple imputation.

Details

- The **miceadds** package contains some functionality for imputation of multilevel data. The function `mice.impute.ml.lmer` is a general function for imputing multilevel data with hierarchical or cross-classified structures for variables at an arbitrary level. This imputation method uses the `lme4::lmer` function in the **lme4** package. The imputation method `mice.impute.2lonly.function` conducts an imputation for a variable at a higher level for already defined imputation methods in the **mice** package. Two-level imputation is available in several functions in the **mice** package (`mice::mice.impute.2l.pan`, `mice::mice.impute.2l.norm`) as well in **micemd** and **hmi** packages. The **miceadds** package contains additional imputation methods for two-level datasets: `mice.impute.2l.continuous` for normally distributed data, `mice.impute.2l.pmm` for predictive mean matching in multilevel models and `mice.impute.2l.binary` for binary data.
- In addition to the usual `mice` imputation function which employs parallel chains, the function `mice.1chain` does multiple imputation from a single chain.
- Nested multiple imputation can be conducted with `mice.nmi`. The function `NMIcombine` conducts statistical inference for nested multiply imputed datasets.
- Imputation based on partial least squares regression is implemented in `mice.impute.pls`.
- Unidimensional plausible value imputation for latent variables (or variables with measurement error) in the **mice** sequential imputation framework can be applied by using the method `mice.impute.plausible.values`.
- The **miceadds** package also includes some functions R utility functions (e.g. `write.pssp`, `ma.scale2`).
- Imputations for questionnaire items can be accomplished by two-way imputation (`tw.imputation`).

Author(s)

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See Also

See other R packages for conducting multiple imputation: **mice**, **Amelia**, **pan**, **mi**, **norm**, **norm2**, **BaBooN**, **VIM**, ...

Some links to internet sites related to missing data:

<http://missingdata.lshtm.ac.uk/>

<http://www.stefvanbuuren.nl/mi/>

<http://www.bristol.ac.uk/cmm/software/realcom/>

Examples

```
##
## :::::::::::::::::::::::::::::::::::::::::::::
## :: miceadds 0.11-69 (2013-12-01) ::
## :::::::::::::::::::::::::::::::::::::::::::::
##
## ----- mice at work -----
##
##          (\-.
##          /  _> .-----
##          /  _)= |'-----'|
##          /  _/  |0  0  o|
##          \-._(____)- | o 0 . o |
##          \-----/
##
##
##
##
##          oo__
##          <;____)-----
##          "  "
##
##          oo__
##          <;____)-----
##          "  "
##
##          oo__
##          <;____)-----
##          "  "
```

```
complete.miceadds
```

```
Creates Imputed Dataset from a mids.nmi or mids.1chain Object
```

Description

Creates imputed dataset from a `mids.nmi` or `mids.1chain` object.

Usage

```
complete.mids.nmi( x, action=c(1,1) )
```

```
complete.mids.1chain( x, action=1 )
```

Arguments

`x` Object of class `mids.nmi` (for `complete.mids.nmi`) or `mids.1chain` (for `complete.mids.1chain`)

`action` A vector of length two indicating to indices of between and within imputed dataset for `complete.mids.nmi` and an integer for the index of imputed dataset for `complete.mids.1chain`.

See Also

See also the corresponding `mice::complete` function and `mitml::mitmlComplete`.

Imputation methods: `mice.nmi`, `mice.1chain`

Examples

```
## Not run:
#####
# EXAMPLE 1: Nested multiple imputation and dataset extraction for TIMSS data
#####

library(BIFIEsurvey)
data(data.timss2, package="BIFIEsurvey" )
datlist <- data.timss2

# remove first four variables
M <- length(datlist)
for (ll in 1:M){
  datlist[[ll]] <- datlist[[ll]][, -c(1:4) ]
}

#####
# (1) nested multiple imputation using mice
imp1 <- miceadds::mice.nmi( datlist, m=4, maxit=3 )
summary(imp1)

#####
# (2) nested multiple imputation using mice.1chain
imp2 <- miceadds::mice.nmi( datlist, Nimp=4, burnin=10, iter=22, type="mice.1chain")
summary(imp2)

#####
# extract dataset for third original dataset the second within imputation
dat32a <- miceadds::complete.mids.nmi( imp1, action=c(3,2) )
dat32b <- miceadds::complete.mids.nmi( imp2, action=c(3,2) )

#####
# EXAMPLE 2: Imputation from one chain and extracting dataset for nhanes data
#####

library(mice)
data(nhanes, package="mice")

# nhanes data in one chain
```

```
imp1 <- miceadds::mice.1chain( nhanes, burnin=5, iter=40, Nimp=4,
                             method=rep("norm", 4) )

# extract first imputed dataset
dati1 <- miceadds::complete.mids.1chain( imp1, action=1 )

## End(Not run)
```

crlrem

R Utilities: Removing CF Line Endings

Description

This function removes CF line endings from a text file and writes the processed file in the working directory.

Usage

```
crlrem( filename1, filename2 )
```

Arguments

filename1	Name of the original file (possibly with CF line endings)
filename2	Name of the processed file (without CF line endings)

Author(s)

This is code by Dirk Eddelbuettel copied from <https://stat.ethz.ch/pipermail/r-devel/2010-September/058480.html>

Examples

```
## Not run:
filename1 <- "rm.arraymult__0.02.cpp"
filename2 <- "rm.arraymult__0.03.cpp"
crlrem( filename1, filename2 )
## End(Not run)
```

cxxfunction.copy *R Utilities: Copy of an Rcpp File*

Description

Copies the **Rcpp** function into the working directory.

Usage

```
cxxfunction.copy(cppfct, name)
```

Arguments

cppfct	Rcpp function
name	Name of the output Rcpp function to be generated

References

Eddelbuettel, D. & Francois, R. (2011). Rcpp: Seamless R and C++ integration. *Journal of Statistical Software*, 40(8), 1-18.

See Also

[inline::cxxfunction](#)

Examples

```
## Not run:
#####
# EXAMPLE 1: Rcpp code logistic distribution
#####

library(Rcpp)
library(inline)

# define Rcpp file
code1 <- "
  // input array A
  Rcpp::NumericMatrix AA(A);
  // Rcpp::IntegerVector dimAA(dimA);
  int nrows=AA.nrow();
  int ncolumns=AA.ncol();
  Rcpp::NumericMatrix Alogis(nrows,ncolumns) ;
  // compute logistic distribution
  for (int ii=0; ii<nrows; ii++){
    Rcpp::NumericVector h1=AA.row(ii) ;
    Rcpp::NumericVector res=plogis( h1 ) ;
    for (int jj=0;jj<ncolumns;jj++){
      Alogis(ii,jj)=res[jj] ;
    }
  }
"
```



```

    }
  }
  return( wrap(Alogis) );
"
# compile Rcpp code
fct_rcpp <- inline::cxxfunction( signature( A="matrix" ), code1,
                               plugin="Rcpp", verbose=TRUE )
# copy function and save it as object 'calclogis'
name <- "calclogis" # name of the function
cxxfunction.copy( cppfct=fct_rcpp, name=name )
# function is available as object named as name
Reval( paste0( name, " <- fct_rcpp " ) )
# test function
m1 <- outer( seq( -2, 2, len=10 ), seq(-1.5,1.5,len=4) )
calclogis(m1)

## End(Not run)

```

data.allison

Datasets from Allison's Missing Data Book

Description

Datasets from Allison's missing data book (Allison 2002).

Usage

```

data(data.allison.gssexp)
data(data.allison.hip)
data(data.allison.usnews)

```

Format

- Data data.allison.gssexp:


```

'data.frame':  2991 obs. of  14 variables:
 $ AGE      : num  33 59 NA 59 21 22 40 25 41 45 ...
 $ EDUC     : num  12 12 12 8 13 15 9 12 12 12 ...
 $ FEMALE   : num  1 0 1 0 1 1 1 0 1 1 ...
 $ SPANKING: num  1 1 2 2 NA 1 3 1 1 NA ...
 $ INCOM    : num  11.2 NA 16.2 18.8 13.8 ...
 $ NOCHILD  : num  0 0 0 0 1 1 0 0 0 0 ...
 $ NODOUBT  : num  NA NA NA 1 NA NA 1 NA NA 1 ...
 $ NEVMAR   : num  0 0 0 0 1 1 0 1 0 0 ...
 $ DIVSEP   : num  1 0 0 0 0 0 0 0 0 1 ...
 $ WIDOW    : num  0 0 0 0 0 0 1 0 1 0 ...
 $ BLACK    : num  1 1 1 0 1 1 0 1 1 1 ...
 $ EAST     : num  1 1 1 1 1 1 1 1 1 1 ...
 $ MIDWEST  : num  0 0 0 0 0 0 0 0 0 0 ...

```

```
$ SOUTH : num 0 0 0 0 0 0 0 0 0 ...
```

- Data data.allison.hip:

```
'data.frame': 880 obs. of 7 variables:
 $ SID : num 1 1 1 1 2 2 2 2 9 9 ...
 $ WAVE: num 1 2 3 4 1 2 3 4 1 2 ...
 $ ADL : num 3 2 3 3 3 1 2 1 3 3 ...
 $ PAIN: num 0 5 0 0 0 1 5 NA 0 NA ...
 $ SRH : num 2 4 2 2 4 1 1 2 2 3 ...
 $ WALK: num 1 0 0 0 0 0 0 0 1 NA ...
 $ CESD: num 9 28 31 11.6 NA ...
```

- Data data.allison.usnews:

```
'data.frame': 1302 obs. of 7 variables:
 $ CSAT : num 972 961 NA 881 NA ...
 $ ACT : num 20 22 NA 20 17 20 21 NA 24 26 ...
 $ STUFAC : num 11.9 10 9.5 13.7 14.3 32.8 18.9 18.7 16.7 14 ...
 $ GRADRAT: num 15 NA 39 NA 40 55 51 15 69 72 ...
 $ RMBRD : num 4.12 3.59 4.76 5.12 2.55 ...
 $ PRIVATE: num 1 0 0 0 0 1 0 0 0 1 ...
 $ LENROLL: num 4.01 6.83 4.49 7.06 6.89 ...
```

Source

The datasets are available from <http://www.ats.ucla.edu/stat/examples/md/>.

References

Allison, P. D. (2002). *Missing data*. Newbury Park, CA: Sage.

Examples

```
## Not run:
#####
# EXAMPLE 1: Hip dataset | Imputation using a wide format
#####

# at first, the hip dataset is 'melted' for imputation

data(data.allison.hip)
## head(data.allison.hip)
## SID WAVE ADL PAIN SRH WALK CESD
## 1 1 1 3 0 2 1 9.000
## 2 1 2 2 5 4 0 28.000
## 3 1 3 3 0 2 0 31.000
## 4 1 4 3 0 2 0 11.579
## 5 2 1 3 0 4 0 NA
## 6 2 2 1 1 1 0 2.222
```

```

library(reshape)
hip.wide <- reshape::reshape(data.allison.hip, idvar="SID", timevar="WAVE",
                             direction="wide")
## > head(hip.wide, 2)
##   SID ADL.1 PAIN.1 SRH.1 WALK.1 CESD.1 ADL.2 PAIN.2 SRH.2 WALK.2 CESD.2 ADL.3
## 1 1 3 0 2 1 9 2 5 4 0 28.000 3
## 5 2 3 0 4 0 NA 1 1 1 0 2.222 2
##   PAIN.3 SRH.3 WALK.3 CESD.3 ADL.4 PAIN.4 SRH.4 WALK.4 CESD.4
## 1 0 2 0 31 3 0 2 0 11.579
## 5 5 1 0 12 1 NA 2 0 NA

# imputation of the hip wide dataset
imp <- mice::mice( as.matrix( hip.wide[, -1] ), m=5, maxit=3 )
summary(imp)

## End(Not run)

```

data.enders

Datasets from Enders' Missing Data Book

Description

Datasets from Enders' missing data book (2010).

Usage

```

data(data.enders.depression)
data(data.enders.eatingattitudes)
data(data.enders.employee)

```

Format

- Dataset `data.enders.depression`:


```

'data.frame': 280 obs. of 8 variables:
 $ txgroup: int 0 0 0 0 0 0 0 0 0 ...
 $ dep1 : int 46 49 40 47 33 44 45 53 40 55 ...
 $ dep2 : int 44 42 28 47 33 41 43 35 43 45 ...
 $ dep3 : int 26 29 31 NA 34 34 34 35 35 36 ...
 $ r2 : int 0 0 0 0 0 0 0 0 0 ...
 $ r3 : int 0 0 0 1 0 0 0 0 0 ...
 $ pattern: int 3 3 3 2 3 3 3 3 3 ...
 $ dropout: int 0 0 0 1 0 0 0 0 0 ...

```
- Dataset `data.enders.eatingattitudes`:


```

'data.frame': 400 obs. of 14 variables:
 $ id : num 1 2 3 4 5 6 7 8 9 10 ...
 $ eat1 : num 4 6 3 3 3 4 5 4 4 6 ...
 $ eat2 : num 4 5 3 3 2 5 4 3 7 5 ...

```

```

$ eat10: num  4 6 2 4 3 4 4 4 6 5 ...
$ eat11: num  4 6 2 3 3 5 4 4 5 5 ...
$ eat12: num  4 6 3 4 3 4 4 4 4 6 ...
$ eat14: num  4 7 2 4 3 4 4 4 6 6 ...
$ eat24: num  3 6 3 3 3 4 4 4 4 5 ...
$ eat3  : num  4 5 3 3 4 4 3 6 4 5 ...
$ eat18: num  5 6 3 5 4 5 3 6 4 6 ...
$ eat21: num  4 5 2 4 4 4 3 5 4 5 ...
$ bmi   : num  18.9 26 18.3 18.2 24.4 ...
$ wsb   : num  9 13 6 5 10 7 11 8 10 12 ...
$ anx   : num  11 19 8 14 7 11 12 12 14 12 ..

```

- Dataset data.enders.employee:

```

'data.frame':  480 obs. of  9 variables:
 $ id      : num  1 2 3 4 5 6 7 8 9 10 ...
 $ age     : num  40 53 46 37 44 39 33 43 35 37 ...
 $ tenure  : num  10 14 10 8 9 10 7 9 9 10 ...
 $ female  : num  1 1 1 1 1 1 1 1 1 1 ...
 $ wbeing  : num  8 6 NA 7 NA 7 NA 7 7 5 ...
 $ jobsat  : num  8 5 7 NA 5 NA 5 NA 7 6 ...
 $ jobperf : num  6 5 7 5 5 7 7 7 7 6 ...
 $ turnover: num  0 0 0 0 0 0 0 0 1 0 ...
 $ iq      : num  106 93 107 94 107 118 103 106 108 97 ...

```

Source

The datasets were downloaded from <http://www.appliedmissingdata.com/book-examples.html>.

References

Enders, C. K. (2010). *Applied missing data analysis*. Guilford Press.

data.graham

Datasets from Grahams Missing Data Book

Description

Datasets from Grahams missing data book (2012).

Usage

```

data(data.graham.ex3)
data(data.graham.ex6)
data(data.graham.ex8a)
data(data.graham.ex8b)
data(data.graham.ex8c)

```

Format

- Dataset data.graham.ex3:


```
'data.frame': 2756 obs. of 20 variables:
 $ school : int 1 1 1 1 1 1 1 1 1 1 ...
 $ alc7 : int 1 1 1 7 3 6 1 5 4 3 ...
 $ rskreb71: int 1 3 1 2 1 NA 1 2 1 2 ...
 $ rskreb72: int NA NA NA NA NA NA NA NA 3 2 3 ...
 $ rskreb73: int NA NA NA NA NA NA NA NA 2 1 2 ...
 $ rskreb74: int NA NA NA NA NA NA NA NA 3 2 4 ...
 $ likepa71: int 4 2 3 3 2 NA 1 4 3 3 ...
 $ likepa72: int 5 2 4 2 2 NA 5 3 3 2 ...
 $ likepa73: int 4 1 3 3 2 NA 1 3 2 3 ...
 $ likepa74: int 5 3 1 5 4 4 3 4 3 2 ...
 $ likepa75: int 4 4 4 4 3 3 4 4 3 3 ...
 $ posatt71: int 1 1 1 1 1 2 1 NA NA NA ...
 $ posatt72: int 1 2 1 1 1 2 4 NA NA NA ...
 $ posatt73: int 1 1 1 1 1 2 1 NA NA NA ...
 $ alc8 : int 1 8 4 8 5 7 1 3 5 3 ...
 $ rskreb81: int 1 4 1 2 2 3 2 3 1 4 ...
 $ rskreb82: int NA NA NA NA NA NA NA NA 3 1 4 ...
 $ rskreb83: int NA NA NA NA NA NA NA NA 2 1 2 ...
 $ rskreb84: int NA NA NA NA NA NA NA NA 3 2 4 ...
 $ alc9 : int 3 NA 7 NA 5 7 NA 6 6 7 ...
```
- Dataset data.graham.ex6:


```
'data.frame': 2756 obs. of 9 variables:
 $ school : int 1 1 1 1 1 1 1 1 1 1 ...
 $ program : int 0 0 0 0 0 0 0 0 0 0 ...
 $ alc7 : int 1 1 1 7 3 6 1 5 4 3 ...
 $ riskreb7: int 1 3 1 2 1 NA 1 2 1 2 ...
 $ likepar7: int 4 2 3 3 2 NA 1 4 3 3 ...
 $ posatt7 : int 1 1 1 1 1 2 1 NA NA NA ...
 $ alc8 : int 1 8 4 8 5 7 1 3 5 3 ...
 $ riskreb8: int 1 4 1 2 2 3 2 3 1 4 ...
 $ alc9 : int 3 NA 7 NA 5 7 NA 6 6 7 ...
```
- Dataset data.graham.ex8a:


```
'data.frame': 1023 obs. of 20 variables:
 $ skill1 : int 28 29 27 29 29 NA NA NA 29 NA ...
 $ skill2 : int NA NA 29 29 NA NA NA NA NA 21 ...
 $ skill3 : int NA NA 29 29 29 NA 28 10 29 25 ...
 $ skill4 : int NA 29 25 29 29 28 29 NA NA NA ...
 $ skill5 : int 29 29 28 28 29 NA 29 10 NA 25 ...
 $ iplanV1: int 14 18 15 17 16 NA NA NA 18 NA ...
 $ iplanV2: int NA NA 17 16 NA NA NA NA NA 16 ...
 $ iplanV3: int NA NA 16 18 18 NA 17 1 18 16 ...
 $ iplanV4: int NA 18 14 18 14 6 18 NA NA NA ...
```

```

$ iplanV5: int 13 18 12 18 18 NA 18 3 NA 5 ...
$ planA1 : int 1 0 2 8 3 NA NA NA 7 NA ...
$ planA2 : int NA NA 0 4 NA NA NA NA NA 6 ...
$ planA3 : int NA NA 1 4 7 NA 2 0 1 7 ...
$ planA4 : int NA 8 0 4 6 0 0 NA NA NA ...
$ planA5 : int 0 7 1 5 7 NA 2 0 NA 6 ...
$ planV1 : int NA NA NA NA NA NA NA NA NA NA ...
$ planV2 : int NA NA NA NA NA NA NA NA NA 1 ...
$ planV3 : int NA NA 1 NA NA NA NA 0 NA 1 ...
$ planV4 : int NA NA NA NA 2 NA NA NA NA ...
$ planV5 : int 2 NA 2 NA NA NA NA 0 NA NA ...

```

- Dataset data.graham.ex8b:

```

'data.frame': 2570 obs. of 6 variables:
$ rskreb71: int 1 3 1 2 1 NA 1 2 1 2 ...
$ rskreb72: int NA NA NA NA NA NA NA 3 2 3 ...
$ posatt71: int 1 1 1 1 1 2 1 NA NA NA ...
$ posatt72: int 1 2 1 1 1 2 4 NA NA NA ...
$ posatt73: int 1 1 1 1 1 2 1 NA NA NA ...
$ posatt : int 3 4 3 3 3 6 6 NA NA NA ...

```

- Dataset data.graham.ex8c:

```

'data.frame': 2756 obs. of 16 variables:
$ s1 : int 1 1 1 1 1 1 1 1 1 1 ...
$ s2 : int 0 0 0 0 0 0 0 0 0 0 ...
$ s3 : int 0 0 0 0 0 0 0 0 0 0 ...
$ s4 : int 0 0 0 0 0 0 0 0 0 0 ...
$ s5 : int 0 0 0 0 0 0 0 0 0 0 ...
$ s6 : int 0 0 0 0 0 0 0 0 0 0 ...
$ s7 : int 0 0 0 0 0 0 0 0 0 0 ...
$ s8 : int 0 0 0 0 0 0 0 0 0 0 ...
$ s9 : int 0 0 0 0 0 0 0 0 0 0 ...
$ s10 : int 0 0 0 0 0 0 0 0 0 0 ...
$ s11 : int 0 0 0 0 0 0 0 0 0 0 ...
$ xalc7 : int 1 1 1 7 3 6 1 5 4 3 ...
$ rskreb72: int NA NA NA NA NA NA NA 3 2 3 ...
$ likepa71: int 4 2 3 3 2 NA 1 4 3 3 ...
$ posatt71: int 1 1 1 1 1 2 1 NA NA NA ...
$ alc8 : int 1 8 4 8 5 7 1 3 5 3 ...

```

Source

The datasets were downloaded from <http://methodology.psu.edu/pubs/books/missing>.

References

Graham, J. W. (2012). *Missing data*. New York: Springer.

Examples

```

## Not run:
library(mitools)
library(mice)
library(Amelia)
library(jomo)

#####
# EXAMPLE 1: data.graham.8a | Imputation under multivariate normal model
#####

data(data.graham.ex8a)
dat <- data.graham.ex8a
dat <- dat[,1:10]
vars <- colnames(dat)
V <- length(vars)
# remove persons with completely missing data
dat <- dat[ rowMeans( is.na(dat) ) < 1, ]
summary(dat)

# some descriptive statistics
psych::describe(dat)

#####
# imputation under a multivariate normal model
M <- 7 # number of imputations

#----- mice package
# define imputation method
impM <- rep("norm", V)
names(impM) <- vars
# mice imputation
imp1a <- mice::mice( dat, method=impM, m=M, maxit=4 )
summary(imp1a)
# convert into a list of datasets
datlist1a <- miceadds::mids2datlist(imp1a)

#----- Amelia package
imp1b <- Amelia::amelia( dat, m=M )
summary(imp1b)
datlist1b <- imp1b$imputations

#----- jomo package
imp1c <- jomo::jomo1con(Y=dat, nburn=100, nbetween=10, nimp=M)
str(imp1c)
# convert into a list of datasets
datlist1c <- miceadds::jomo2datlist(imp1c)

# alternatively one can use the jomo wrapper function
imp1c1 <- jomo::jomo(Y=dat, nburn=100, nbetween=10, nimp=M)

#####

```

```

# EXAMPLE 2: data.graham.8b | Imputation with categorical variables
#####

data(data.graham.ex8b)
dat <- data.graham.ex8b
vars <- colnames(dat)
V <- length(vars)

# descriptive statistics
psych::describe(dat)

#####
# imputation in mice using predictive mean matching
imp1a <- mice::mice( dat, m=5, maxit=10)
datlist1a <- mitools::imputationList( miceadds::mids2datlist(imp1a) )
print(datlist1a)

#####
# imputation in jomo treating all variables as categorical

# Note that variables must have values from 1 to N
# use categorize function from sirt package here
dat.categ <- sirt::categorize( dat, categorical=colnames(dat), lowest=1 )
dat0 <- dat.categ$data

# imputation in jomo treating all variables as categorical
Y_numcat <- apply( dat0, 2, max, na.rm=TRUE )
imp1b <- jomo::jomo1cat(Y.cat=dat0, Y.numcat=Y_numcat, nburn=100,
                      nbetween=10, nimp=5)

# recode original categories
datlist1b <- sirt::decategorize( imp1b, categ_design=dat.categ$categ_design )
# convert into a list of datasets
datlist1b <- miceadds::jomo2datlist(datlist1b)
datlist1b <- mitools::imputationList( datlist1b )

# Alternatively, jomo can be used but categorical variables must be
# declared as factors
dat <- dat0
# define two variables as factors
vars <- miceadds::scan.vec(" rskreb71 rskreb72")
for (vv in vars){
  dat[, vv] <- as.factor( dat[,vv] )
}
# use jomo
imp1b1 <- jomo::jomo(Y=dat, nburn=30, nbetween=10, nimp=5)

#####
# compare frequency tables for both imputation packages
fun_prop <- function( variable ){
  t1 <- table(variable)
  t1 / sum(t1)
}

```



```

# variable rskreb71
res1a <- with( datlist1a, fun_prop(rskreb71) )
res1b <- with( datlist1b, fun_prop(rskreb71) )
summary( miceadds::NMIcombine(qhat=res1a, NMI=FALSE ) )
summary( miceadds::NMIcombine(qhat=res1b, NMI=FALSE ) )

# variable posatt
res2a <- with( datlist1a, fun_prop(posatt) )
res2b <- with( datlist1b, fun_prop(posatt) )
summary( miceadds::NMIcombine(qhat=res2a, NMI=FALSE ) )
summary( miceadds::NMIcombine(qhat=res2b, NMI=FALSE ) )

## End(Not run)

```

data.internet

Dataset Internet

Description

Dataset with items corresponding to internet attitudes.

Usage

```
data(data.internet)
```

Format

A data frame with 281 observations on the following 22 variables.

The format of the dataset is

```

'data.frame':  281 obs. of  22 variables:
 $ IN1 : num  1 5 2 3 1 3 2 3 2 1 ...
 $ IN2 : num  4 3 2 7 7 4 4 7 4 3 ...
 $ IN3 : num  4 5 4 2 1 2 5 2 2 4 ...
 [...]
 $ IN20: num  3 2 2 3 3 4 2 7 2 2 ...
 $ IN21: num  3 3 6 5 4 4 5 5 6 5 ...
 $ IN22: num  3 4 2 5 3 5 3 7 3 5 ...

```

Details

The following text is copied from <http://people.few.eur.nl/groenen/Data/index.htm>

The data set is based on a questionnaire on attitudes towards the Internet. It consists of evaluations of 22 statements about the Internet by 281 students at Erasmus University Rotterdam. These data were gathered around 2002 before the wide availability of broadband Internet access in the Netherlands. The statements were evaluated using a seven-point Likert scale, ranging from 1 (completely disagree) to 7 (completely agree).

We would like to thank Peter Verhoef for making these data available.

Each variable (statement) is coded as follows:

1. Completely disagree
2. Disagree
3. Slightly disagree
4. Neutral
5. Slightly agree
6. Agree
7. Completely agree

Internet items:

1. Paying using Internet is safe
2. Surfing the Internet is easy
3. Internet is unreliable
4. Internet is slow
5. Internet is user-friendly
6. Internet is the future's means of communication
7. Internet is addictive
8. Internet is fast
9. Sending personal data using the Internet is unsafe
10. The prices of Internet subscriptions are high
11. Internet offers many possibilities for abuse
12. The costs of surfing are high
13. Internet offers unbounded opportunities
14. Internet phone costs are high
15. The content of web sites should be regulated
16. Internet is easy to use
17. I like surfing
18. I often speak with friends about the Internet
19. I like to be informed of important new things
20. I always attempt new things on the Internet first
21. I regularly visit websites recommended by others
22. I know much about the Internet

Source

Peter Verhoef

<http://people.few.eur.nl/groenen/Data/index.htm>

Examples

```
data(data.internet)
# missing proportions
colMeans( is.na(data.internet) )
```

data.largescale	<i>Large-scale Dataset for Testing Purposes (Many Cases, Few Variables)</i>
-----------------	---

Description

Large-scale dataset with many cases and few variables included for testing purposes.

Usage

```
data(data.largescale)
```

Format

A data frame with 14000 observations on the following 13 variables. The format is

```
'data.frame': 14000 obs. of 13 variables:
 $ id: num 1e+07 1e+07 1e+07 1e+07 1e+07 ...
 $ D1: num 0 0 0 0 1 0 0 0 0 0 ...
 $ D2: num 0 0 0 1 0 1 0 1 0 0 ...
 $ D3: num 0 0 0 0 0 0 0 0 0 0 ...
 $ D4: num 0 0 0 1 0 0 0 1 0 0 ...
 $ D5: num 0 0 0 0 0 1 0 0 0 0 ...
 $ v1: num 118 117 94 106 86 117 96 96 82 95 ...
 $ v2: num 101 101 86 101 65 94 72 75 70 99 ...
 $ v3: num 0 0 0 0 0 1 0 0 0 0 ...
 $ v4: num 3 NA 3 5 2 5 5 5 4 2 ...
 $ v5: num 0 NA 0 0 0 1 0 0 0 0 ...
 $ v6: num 3 3 3 4 NA 1 3 3 2 3 ...
 $ v7: num 51 36 14 47 22 17 13 37 47 38 ...
```

data.ma	<i>Example Datasets for miceadds Package</i>
---------	---

Description

Example datasets for **miceadds** package.

Usage

```
data(data.ma01)
data(data.ma02)
data(data.ma03)
data(data.ma04)
data(data.ma05)
```

```
data(data.ma06)
data(data.ma07)
data(data.ma08)
```

Format

- Dataset data.ma01:

Dataset with students nested within school and student weights (studwgt). The format is

```
'data.frame': 4073 obs. of 11 variables:
 $ idstud : num 1e+07 1e+07 1e+07 1e+07 1e+07 ...
 $ idschool: num 1001 1001 1001 1001 1001 ...
 $ studwgt : num 6.05 6.05 5.27 5.27 6.05 ...
 $ math : int 594 605 616 524 685 387 536 594 387 562 ...
 $ read : int 647 651 539 551 689 502 503 597 580 576 ...
 $ migrant : int 0 0 0 1 0 0 1 0 0 0 ...
 $ books : int 6 6 5 2 6 3 4 6 6 5 ...
 $ hisei : int NA 77 69 45 66 53 43 NA 64 50 ...
 $ paredu : int 3 7 7 2 7 3 4 NA 7 3 ...
 $ female : int 1 1 0 0 1 1 0 0 1 1 ...
 $ urban : num 1 1 1 1 1 1 1 1 1 1 ...
```

- Dataset data.ma02:

10 multiply imputed datasets of incomplete data data.ma01. The format is

List of 10

```
$ : 'data.frame': 4073 obs. of 11 variables:
$ : 'data.frame': 4073 obs. of 11 variables:
$ : 'data.frame': 4073 obs. of 11 variables:
$ : 'data.frame': 4073 obs. of 11 variables:
$ : 'data.frame': 4073 obs. of 11 variables:
$ : 'data.frame': 4073 obs. of 11 variables:
$ : 'data.frame': 4073 obs. of 11 variables:
$ : 'data.frame': 4073 obs. of 11 variables:
$ : 'data.frame': 4073 obs. of 11 variables:
$ : 'data.frame': 4073 obs. of 11 variables:
```

- Dataset data.ma03:

This dataset contains one variable math_EAP for which a conditional posterior distribution with EAP and its associated standard deviation is available.

```
'data.frame': 120 obs. of 8 variables:
 $ idstud : int 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 ...
 $ female : int 0 1 1 1 1 0 1 1 1 1 ...
 $ migrant : int 1 1 0 1 1 0 0 0 1 0 ...
 $ hisei : int 44 NA 26 NA 32 60 31 NA 34 26 ...
 $ educ : int NA 2 NA 1 4 NA 2 NA 2 NA ...
 $ read_wle : num 74.8 78.1 103.2 81.2 119.2 ...
 $ math_EAP : num 337 342 264 285 420 ...
 $ math_SEEAP: num 28 29.5 28.6 28.5 27.5 ...
```

- Dataset data.ma04:

This dataset contains two hypothetical scales A and B and single variables V5, V6 and V7.

```
'data.frame':  281 obs. of  13 variables:
 $ group: int  1 1 1 1 1 1 1 1 1 1 ...
 $ A1  : int  2 2 2 1 1 3 3 NA 2 1 ...
 $ A2  : int  2 2 2 3 1 2 4 4 4 4 ...
 $ A3  : int  2 3 3 4 1 3 2 2 2 4 ...
 $ A4  : int  3 4 6 4 7 5 3 5 5 1 ...
 $ V5  : int  2 2 5 5 4 3 4 1 3 4 ...
 $ V6  : int  2 5 5 1 1 3 2 2 2 4 ...
 $ V7  : int  6 NA 4 5 6 2 5 5 6 7 ...
 $ B1  : int  7 NA 6 4 5 2 5 7 3 7 ...
 $ B2  : int  6 NA NA 6 3 3 4 6 6 7 ...
 $ B3  : int  7 NA 7 4 3 4 3 7 5 NA ...
 $ B4  : int  4 5 6 5 4 3 4 5 2 1 ...
 $ B5  : int  7 NA 7 4 4 3 5 7 5 4 ...
```

- Dataset data.ma05:

This is a two-level dataset with students nested within classes. Variables at the student level are Dscore, Mscore, denote, manote, misei and migrant. Variables at the class level are sprengel and groesse.

```
'data.frame':  1673 obs. of  10 variables:
 $ idstud  : int  100110001 100110002 100110003 100110004 100110005 ...
 $ idclass : int  1001 1001 1001 1001 1001 1001 1001 1001 1001 1001 ...
 $ Dscore  : int  NA 558 643 611 518 552 NA 534 409 543 ...
 $ Mscore  : int  404 563 569 621 653 651 510 NA 517 566 ...
 $ denote  : int  NA 1 1 1 3 2 3 2 3 2 ...
 $ manote  : int  NA 1 1 1 1 1 2 2 2 1 ...
 $ misei   : int  NA 51 NA 38 NA 50 53 53 38 NA ...
 $ migrant : int  NA 0 0 NA 0 0 0 0 0 NA ...
 $ sprengel: int  0 0 0 0 0 0 0 0 0 ...
 $ groesse : int  25 25 25 25 25 25 25 25 25 ...
```

- Dataset data.ma06:

This is a dataset in which the variable FC is only available with grouped values (coarse data or interval data).

```
'data.frame':  198 obs. of  7 variables:
 $ id      : num  1001 1002 1003 1004 1005 ...
 $ A1     : int  14 7 10 15 0 5 9 6 8 0 ...
 $ A2     : int  5 6 4 8 2 5 4 0 7 0 ...
 $ Edu    : int  4 3 1 5 5 1 NA 1 5 3 ...
 $ FC     : int  3 2 2 2 2 NA NA 2 2 NA ...
 $ FC_low: num  10 5 5 5 5 0 0 5 5 0 ...
 $ FC_upp: num  15 10 10 10 10 100 100 10 10 100 ...
```

- Dataset data.ma07:

This is a three-level dataset in which the variable FC is only available with grouped values (coarse data or interval data).

```
'data.frame': 1600 obs. of 9 variables:
 $ id3: num 1001 1001 1001 1001 1001 ...
 $ id2: num 101 101 101 101 101 101 101 101 101 ...
 $ id1: int 1 2 3 4 5 6 7 8 9 10 ...
 $ x1 : num 0.91 1.88 NA 1.52 0.93 0.51 2.11 0.99 2.42 NA ...
 $ x2 : num -0.58 1.12 0.87 -0.01 -0.14 0.48 1.85 -0.9 0.93 0.63 ...
 $ y1 : num 1.66 1.66 1.66 1.66 1.66 1.66 1.66 1.66 1.66 1.66 ...
 $ y2 : num 0.96 0.96 0.96 0.96 0.96 0.96 0.96 0.96 0.96 0.96 ...
 $ z1 : num -0.53 -0.53 -0.53 -0.53 -0.53 -0.53 -0.53 -0.53 -0.53 ...
 $ z2 : num 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 0.42 ...
```

- Dataset data.ma08:

List with several vector of strings containing descriptive data from published articles. See [string_to_matrix](#) for converting these strings into matrices.

List of 4

```
$ mat1: chr [1:6] "1. T1_mental_health" ...
$ mat2: chr [1:16] "1. Exp voc-T1 -" ...
$ mat3: chr [1:12] "1. TOWRE age 7\t-\t\t\t\t\t\t\t" ...
$ mat4: chr [1:18] "1. Vocab. age 7\t-\t\t\t\t\t\t\t" ...
```

data.smallscale	<i>Small-Scale Dataset for Testing Purposes (Moderate Number of Cases, Many Variables)</i>
-----------------	--

Description

Small-scale dataset for testing purposes (moderate number of cases, many variables)

Usage

```
data(data.smallscale)
```

Format

A data frame with 675 observations on the following 164 variables. The format is

```
'data.frame': 675 obs. of 164 variables:
 $ v1 : num 3 3 2 3 3 0 1 0 3 NA ...
 $ v2 : num 3 0 1 3 0 0 0 3 2 NA ...
 $ v3 : num 0 0 2 3 2 0 1 0 0 NA ...
 $ v4 : num 1 3 3 3 NA 0 0 0 3 NA ...
 $ v5 : num 0 0 3 3 0 0 3 1 3 3 ...
 $ v6 : num 8 8 9 8 9 9 9 8 9 9 ...
 [...]
```

datlist2mids	<i>Converting a List of Multiply Imputed Data Sets into a mids Object</i>
--------------	---

Description

This function converts a list of multiply imputed data sets to a `mice::mids` object.

Usage

```
datlist2mids(dat.list, progress=FALSE)
datlist2mids(dat.list, progress=FALSE)
```

Arguments

<code>dat.list</code>	List of multiply imputed data sets or an object of class <code>imputationList</code> (see <code>mitools::imputationList</code>)
<code>progress</code>	An optional logical indicating whether conversion process be displayed

Value

An object of class `mids`

See Also

See `mice::as.mids` for converting a multiply imputed dataset in long format into a `mids` object.

Examples

```
#####
# EXAMPLE 1: Imputation of NHANES data using Amelia package
#####

library(mice)
library(Amelia)

data(nhanes, package="mice")
set.seed(566) # fix random seed

# impute 10 datasets using Amelia
a.out <- Amelia::amelia(x=nhanes, m=10)
# plot of observed and imputed data
plot(a.out)

# convert list of multiply imputed datasets into a mids object
a.mids <- miceadds::datlist2mids( a.out$imputations )

# linear regression: apply mice functionality lm.mids
mod <- with( a.mids, stats::lm( bmi ~ age ) )
summary( mice::pool( mod ) )
```

```

##               est      se      t      df      Pr(>|t|)      lo 95
## (Intercept) 30.624652 2.626886 11.658158 8.406608 1.767631e-06 24.617664
## age         -2.280607 1.323355 -1.723352 8.917910 1.192288e-01 -5.278451
##               hi 95 nmis      fmi      lambda
## (Intercept) 36.6316392  NA 0.5791956 0.4897257
## age         0.7172368    0 0.5549945 0.4652567

## Not run:
# fit linear regression model in Zelig
library(Zelig)
mod2 <- Zelig::zelig( bmi ~ age, model="ls", data=a.out, cite=FALSE)
summary(mod2)
## Model: Combined Imputations
##               Estimate Std.Error z value Pr(>|z|)
## (Intercept)   30.625     2.627  11.658  0.00000 ***
## age           -2.281     1.323  -1.723  0.08482
## ---
## Signif. codes:  '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# fit linear regression using mitools package
library(mitools)
datimp <- mitools::imputationList(a.out$imputations)
mod3 <- with( datimp, stats::lm( bmi ~ age ) )
summary( mitools::MIcombine( mod3 ) )
## Multiple imputation results:
##       with(datimp, stats::lm(bmi ~ age))
##       MIcombine.default(mod3)
##               results      se      (lower      upper) missInfo
## (Intercept) 30.624652 2.626886 25.304594 35.9447092      51
## age         -2.280607 1.323355 -4.952051  0.3908368      49

## End(Not run)

```

datlist_create

Creates Objects of Class datlist or nested.datlist

Description

Creates objects of class `datlist` or `nested.datlist`.

The functions `nested.datlist2datlist` and `datlist2nested.datlist` provide list conversions for imputed datasets.

Usage

```
datlist_create(datasets)
```

```
nested.datlist_create(datasets)
```

```
## S3 method for class 'datlist'
```



```

print(x, ...)

## S3 method for class 'nested.datlist'
print(x, ...)

nested.datlist2datlist(datlist)

datlist2nested.datlist(datlist, Nimp)

```

Arguments

datasets	For datlist_create: List of datasets, objects of class <code>imputationList</code> , <code>mids</code> , <code>mids.lchain</code> , For nested.datlist_create: nested list of datasets, <code>NestedImputationList</code> , <code>mids.nmi</code>
x	Object of classes <code>datlist</code> or <code>nested.datlist</code>
datlist	Object of classes <code>datlist</code> , <code>imputationList</code> , <code>nested.datlist</code> or <code>NestedImputationList</code> .
Nimp	Vector of length 2 containing numbers of between and within imputations.
...	Further arguments to be passed

Value

Object of class `datlist` or `nested.datlist`

Examples

```

## Not run:
## The function datlist_create is currently defined as
function (datasets)
{
  class(datasets) <- "datlist"
  return(datasets)
}

#####
# EXAMPLE 1: Create object of class datlist
#####

library(BIFIEsurvey)
data(data.timss2, package="BIFIEsurvey" )
datlist <- data.timss2

# class datlist
obj1 <- miceadds::datlist_create(data.timss2)

#####
# EXAMPLE 2: Multiply imputed datasets: Different object classes
#####

library(mice)

```

```

data(nhanes2, package="mice")
set.seed(990)

# nhanes2 data imputation
imp1 <- miceadds::mice.1chain( nhanes2, burnin=5, iter=25, Nimp=5 )
# object of class datlist
imp2 <- miceadds::mids2datlist(imp1)
# alternatively, one can use datlist_create
imp2b <- miceadds::datlist_create(imp1)
# object of class imputationList
imp3 <- mitools::imputationList(imp2)
# retransform object in class datlist
imp2c <- miceadds::datlist_create(imp3)
str(imp2c)

#####
# EXAMPLE 3: Nested multiply imputed datasets
#####

library(BIFIEsurvey)
data(data.timss2, package="BIFIEsurvey" )
datlist <- data.timss2
  # list of 5 datasets containing 5 plausible values

#** define imputation method and predictor matrix
data <- datlist[[1]]
V <- ncol(data)
# variables
vars <- colnames(data)
# variables not used for imputation
vars_unused <- miceadds::scan.vec("IDSTUD TOTWGT JKZONE JKREP" )

#- define imputation method
impMethod <- rep("norm", V )
names(impMethod) <- vars
impMethod[ vars_unused ] <- ""

#- define predictor matrix
predM <- matrix( 1, V, V )
colnames(predM) <- rownames(predM) <- vars
diag(predM) <- 0
predM[, vars_unused ] <- 0

# object of class nmi
imp1 <- miceadds::mice.nmi( datlist, method=impMethod, predictorMatrix=predM,
  m=4, maxit=3 )
# object of class nested.datlist
imp2 <- miceadds::mids2datlist(imp1)
# object of class NestedImputationList
imp3 <- miceadds::NestedImputationList(imp2)
# redefine class nested.datlist
imp4 <- miceadds::nested.datlist_create(imp3)

```

```
#####
# EXAMPLE 4: Conversions between nested lists of datasets and lists of datasets
#####

library(BIFIEsurvey)
data(data.timss4, package="BIFIEsurvey" )
datlist <- data.timss4

# object of class nested.datlist
datlist1a <- miceadds::nested.datlist_create(datlist)
# object of class NestedImputationList
datlist1b <- miceadds::NestedImputationList(datlist)

# conversion to datlist
datlist2a <- miceadds::nested.datlist2datlist(datlist1a) # class datlist
datlist2b <- miceadds::nested.datlist2datlist(datlist1b) # class imputationList

# convert into a nested list with 2 between nests and 10 within nests
datlist3a <- miceadds::datlist2nested.datlist(datlist2a, Nimp=c(2,10) )
datlist3b <- miceadds::datlist2nested.datlist(datlist2b, Nimp=c(4,5) )

## End(Not run)
```

draw.pv.ctt

Plausible Value Imputation Using a Known Measurement Error Variance (Based on Classical Test Theory)

Description

This function provides unidimensional plausible value imputation with a known measurement error variance or classical test theory (Mislevy, 1991). The reliability of the scale is estimated by Cronbach's Alpha or can be provided by the user.

Usage

```
draw.pv.ctt(y, dat.scale=NULL, x=NULL, samp.pars=TRUE,
            alpha=NULL, sig.e=NULL, var.e=NULL, true.var=NULL)
```

Arguments

y	Vector of scale scores if y should not be used.
dat.scale	Matrix of item responses
x	Matrix of covariates
samp.pars	An optional logical indicating whether scale parameters (reliability or measurement error standard deviation) should be sampled
alpha	Reliability estimate of the scale. The default of NULL means that Cronbach's alpha will be used as a reliability estimate.

sig.e	Optional vector of the standard deviation of the error. Note that it is <i>not</i> the error variance.
var.e	Optional vector of the variance of the error.
true.var	True score variance

Details

The linear model is assumed for drawing plausible values of a variable Y contaminated by measurement error. Assuming $Y = \theta + e$ and a linear regression model for θ

$$\theta = \mathbf{X}\beta + \epsilon$$

(plausible value) imputations from the posterior distribution $P(\theta|Y, \mathbf{X})$ are drawn. See Mislevy (1991) for details.

Value

A vector with plausible values

Note

Plausible value imputation is also labeled as multiple overimputation (Blackwell, Honaker & King, 2011).

References

Blackwell, M., Honaker, J., & King, G. (2011). *Multiple overimputation: A unified approach to measurement error and missing data*. Technical Report.

Mislevy, R. J. (1991). Randomization-based inference about latent variables from complex samples. *Psychometrika*, 56, 177-196.

See Also

See also [sirt::plausible.value.imputation.raschtype](#) for plausible value imputation.

Plausible value imputations can be conducted in **mice** using the imputation method [mice.impute.plausible.values](#).

Plausible values can be drawn in **Amelia** by specifying observation-level priors, see [Amelia::moPrep](#) and [Amelia::amelia](#).

Examples

```
#####
# SIMULATED EXAMPLE 1: Scale scores
#####

set.seed(899)
n <- 5000      # number of students
x <- round( stats::runif( n, 0,1 ) )
y <- stats::rnorm(n)
# simulate true score theta
```

```

theta <- .6 + .4*x + .5 * y + stats::rnorm(n)
# simulate observed score by adding measurement error
sig.e <- rep( sqrt(.40), n )
theta_obs <- theta + stats::rnorm( n, sd=sig.e)

# calculate alpha
( alpha <- stats::var( theta ) / stats::var( theta_obs ) )
# [1] 0.7424108
#=> Ordinarily, sig.e or alpha will be known, assumed or estimated by using items,
#   replications or an appropriate measurement model.

# create matrix of predictors
X <- as.matrix( cbind(x, y ) )

# plausible value imputation with scale score
imp1 <- miceadds::draw.pv.ctt( y=theta_obs, x=X, sig.e=sig.e )
# check results
stats::lm( imp1 ~ x + y )

# imputation with alpha as an input
imp2 <- miceadds::draw.pv.ctt( y=theta_obs, x=X, alpha=.74 )
stats::lm( imp2 ~ x + y )

## Not run:
#-- plausible value imputation in Amelia package
library(Amelia)

# define data frame
dat <- data.frame( "x"=x, "y"=y, "theta"=theta_obs )
# generate observation-level priors for theta
priors <- cbind( 1:n, 3, theta_obs, sig.e )
# 3 indicates column index for theta
overimp <- priors[,1:2]
# run Amelia
imp <- Amelia::amelia( dat, priors=priors, overimp=overimp, m=10)
# create object of class datlist and evaluate results
datlist <- miceadds::datlist_create( imp$imputations )
withPool_MI( with( datlist, stats::var(theta) ) )
stats::var(theta) # compare with true variance
mod <- with( datlist, stats::lm( theta ~ x + y ) )
mitools::MIcombine(mod)

## End(Not run)

```

filename_split

Some Functionality for Strings and File Names

Description

The function `filename_split` splits a file name into parts.

The function `string_extract_part` extracts a part of a string.

The function `string_to_matrix` converts a string into a matrix.

Usage

```
filename_split(file_name, file_sep="__", file_ext=".")
filename_split_vec( file_names, file_sep="__", file_ext=".")

string_extract_part( vec, part=1, sep="__", remove_empty=TRUE )

string_to_matrix(x, rownames=NULL, col_elim=NULL, as_numeric=FALSE,
                diag_val=NULL, extend=FALSE, split=" ")
```

Arguments

<code>file_name</code>	File name
<code>file_names</code>	File names
<code>file_sep</code>	Separator within file name
<code>file_ext</code>	Separator for file extension
<code>vec</code>	Vector with strings
<code>part</code>	Integer indicating the part of the string to be selected
<code>sep</code>	String separator
<code>remove_empty</code>	Logical indicating whether empty entries (" ") should be removed.
<code>x</code>	String vector
<code>rownames</code>	Column index for row names
<code>col_elim</code>	Indices for elimination of columns
<code>as_numeric</code>	Logical indicating whether numeric conversion is requested
<code>diag_val</code>	Optional values for inclusion in diagonal of matrix
<code>extend</code>	Optional indicating whether numeric matrix should be extended to become a symmetric matrix
<code>split</code>	String used for splitting

Value

List with components of the file name (see Examples).

See Also

[files_move](#)

Examples

```
#####
# EXAMPLE 1: Demonstration example for filename_split
#####

# file name
file_name <- "pisa_all_waves_invariant_items_DATA_ITEMS_RENAMED__DESCRIPTIVES__2016-10-12_1000.csv"

# apply function
miceadds::filename_split( file_name )
## $file_name
## [1] "pisa_all_waves_invariant_items_DATA_ITEMS_RENAMED__DESCRIPTIVES__2016-10-12_1000.csv"
## $stem
## [1] "pisa_all_waves_invariant_items_DATA_ITEMS_RENAMED__DESCRIPTIVES"
## $suffix
## [1] "2016-10-12_1000"
## $ext
## [1] "csv"
## $main
## [1] "pisa_all_waves_invariant_items_DATA_ITEMS_RENAMED__DESCRIPTIVES.csv"

#####
# EXAMPLE 2: Example string_extract_part
#####

vec <- c("ertu_DES", "ztu_DATA", "guzeuue745_ghshgk34__INFO", "zzu78347834_ghghwuz")

miceadds::string_extract_part( vec=vec, part=1, sep="__" )
miceadds::string_extract_part( vec=vec, part=2, sep="__" )
## > miceadds::string_extract_part( vec=vec, part=1, sep="__" )
## [1] "ertu" "ztu" "guzeuue745_ghshgk34"
## [4] "zzu78347834_ghghwuz"
## > miceadds::string_extract_part( vec=vec, part=2, sep="__" )
## [1] "DES" "DATA" "INFO" NA

#####
# EXAMPLE 3: Reading descriptive information from published articles
#####

## Not run:
data(data.ma08)
library(stringr)

#**** reading correlations (I)
dat <- data.ma08$mat1
miceadds::string_to_matrix(dat, rownames=2, col_elim=c(1,2))

#**** reading correlations including some processing (II)
dat0 <- data.ma08$mat2
dat <- dat0[1:14]

# substitute "*"

```

```

dat <- gsub(" ", "", dat, fixed=TRUE )

# replace blanks in variable names
s1 <- stringr::str_locate(dat, "[A-z] [A-z]")
start <- s1[, "start"] + 1
for (ss in 1:length(start) ){
  if ( ! is.na( start[ss] ) ){
    substring( dat[ss], start[ss], start[ss] ) <- "_"
  }
}

# character matrix
miceadds::string_to_matrix(dat)
# numeric matrix containing correlations
miceadds::string_to_matrix(dat, rownames=2, col_elim=c(1,2), as_numeric=TRUE, diag_val=1,
  extend=TRUE )
*** reading means and SDs
miceadds::string_to_matrix(dat0[ c(15,16)], rownames=1, col_elim=c(1), as_numeric=TRUE )

**** reading correlations (III)
dat <- data.ma08$mat3
dat <- gsub(" age ", "_age_", dat, fixed=TRUE )
miceadds::string_to_matrix(dat, rownames=2, col_elim=c(1,2), as_numeric=TRUE, diag_val=1,
  extend=TRUE )

**** reading correlations (IV)
dat <- data.ma08$mat4 <- dat0

# remove spaces in variable names
dat <- gsub(" age ", "_age_", dat, fixed=TRUE )
s1 <- stringr::str_locate_all(dat, "[A-z,.] [A-z]")
NL <- length(dat)
for (ss in 1:NL ){
  NR <- nrow(s1[[ss]])
  if (NR>1){
    start <- s1[[ss]][2,1]+1
    if ( ! is.na( start ) ){
      substring( dat[ss], start, start ) <- "_"
    }
  }
}

miceadds::string_to_matrix(dat, rownames=2, col_elim=c(1,2), as_numeric=TRUE, diag_val=1,
  extend=TRUE )

## End(Not run)

```


Description

Moves older (defined in alphanumeric order) files from one directory to another directory.

Usage

```
files_move(path1, path2, file_sep="__", pattern=NULL)
```

Arguments

path1	Original directory
path2	Target directory in which the files should be moved
file_sep	Separator for files
pattern	Pattern in file names to be searched for

See Also

[filename_split](#)

Examples

```
## Not run:
#####
# EXAMPLE 1: Move older files in '__ARCHIVE' directory
#####

# specify path
path1 <- "p:/IPN/Projects/PISA/Trend_2015/2__Data/All_Waves/"
# specify target directory which is an archive
path2 <- file.path( path1, "__ARCHIVE" )
# move files
files_move( path1, path2 )

## End(Not run)
```

Description

These functions slightly extend the usage of grep but it is extended to a vector argument.

Usage

```
grep.vec(pattern.vec, x, operator="AND")
grepvec( pattern.vec, x, operator="AND", value=FALSE)
grep_leading( pattern, x, value=FALSE )
grepvec_leading( patternvec, x, value=FALSE )
```

Arguments

pattern.vec	String which should be looked for in vector x
x	A character vector
operator	An optional string. The default argument "AND" searches all entries in x which contain all elements of pattern.vec. If operator is different from the default, then the "OR" logic applies, i.e. the functions searches for vector entries which contain at least one of the strings in pattern.vec.
pattern	String
patternvec	Vector of strings
value	Logical indicating whether indices or values are requested

Examples

```
#####
# EXAMPLE 1: Toy example
#####

vec <- c("abcd", "bcde", "aefd", "cdf" )
# search for entries in vec with contain 'a' and 'f'
# -> operator="AND"
grep.vec( pattern.vec=c("a","f"), x=vec )
## $x
## [1] "aefd"
## $index.x
## [1] 3

grepvec( pattern.vec=c("a","f"), x=vec, value=TRUE)
grepvec( pattern.vec=c("a","f"), x=vec, value=FALSE)

# search for entries in vec which contain 'a' or 'f'
grep.vec( pattern.vec=c("a","f"), x=vec, operator="OR")
## $x
## [1] "abcd" "aefd" "cdf"
## $index.x
## [1] 1 3 4
```

Description

Calculates some groupwise descriptive statistics.

Usage

```
GroupMean(data, group, weights=NULL, extend=FALSE)
```

```
GroupSum(data, group, weights=NULL, extend=FALSE)
```

```
GroupSD(data, group, weights=NULL, extend=FALSE)
```

```
# group mean of a variable  
gm(y, cluster)
```

```
# centering within clusters  
cwc(y, cluster)
```

Arguments

data	A numeric data frame
group	A vector of group identifiers
weights	An optional vector of sample weights
extend	Optional logical indicating whether the group means (or sums) should be extended to the original dimensions of the dataset.
y	Variable
cluster	Cluster identifier

Value

A data frame or a vector with groupwise calculated statistics

See Also

[mitml::clusterMeans](#)

[base::rowsum](#), [stats::aggregate](#), [stats::ave](#)

Examples

```
#####
# EXAMPLE 1: Group means and SDs data.ma02
#####

data(data.ma02, package="miceadds" )
dat <- data.ma02[[1]] # select first dataset

#--- group means for read and math
GroupMean( dat[, c("read","math") ], group=dat$idschool )
# using rowsum
a1 <- base::rowsum( dat[, c("read","math") ], dat$idschool )
a2 <- base::rowsum( 1+0*dat[, c("read","math") ], dat$idschool )
(a1/a2)[1:10,]
# using aggregate
stats::aggregate( dat[, c("read","math") ], list(dat$idschool), mean )[1:10,]

#--- extend group means to original dataset
GroupMean( dat[, c("read","math") ], group=dat$idschool, extend=TRUE )
# using ave
stats::ave( dat[, "read" ], dat$idschool )
stats::ave( dat[, "read" ], dat$idschool, FUN=mean )

## Not run:
#--- group standard deviations
GroupSD( dat[, c("read","math") ], group=dat$idschool)[1:10,]
# using aggregate
stats::aggregate( dat[, c("read","math") ], list(dat$idschool), sd )[1:10,]

#####
# EXAMPLE 2: Calculating group means and group mean centering
#####

data(data.ma07, package="miceadds")
dat <- data.ma07

# compute group means
miceadds::gm( dat$x1, dat$id2 )
# centering within clusters
miceadds::cwc( dat$x1, dat$id2 )

# evaluate formula with model.matrix
X <- model.matrix( ~ I( miceadds::cwc(x1, id2) ) + I( miceadds::gm(x1,id2) ), data=dat )
head(X)

## End(Not run)
```

Description

This function includes an index variable to a data frame in the first column.

Usage

```
index.dataframe(data, systime=FALSE)
```

Arguments

data	Data frame
systime	Should system time be included in the second column of the data frame?

Examples

```
dfr <- matrix( 2*1:12-3, 4,3 )
colnames(dfr) <- paste0("X",1:ncol(dfr))
index.dataframe( dfr)
##      index X1 X2 X3
##  1      1 -1  7 15
##  2      2  1  9 17
##  3      3  3 11 19
##  4      4  4 13 21
index.dataframe( dfr, systime=TRUE)
##      index      file_created X1 X2 X3
##  1      1  2013-08-22 10:26:28 -1  7 15
##  2      2  2013-08-22 10:26:28  1  9 17
##  3      3  2013-08-22 10:26:28  3 11 19
##  4      4  2013-08-22 10:26:28  5 13 21
```

in_CI

*Indicator Function for Analyzing Coverage***Description**

Indicator function for analyzing coverage. The output indicates whether a value lies within a computed confidence interval.

Usage

```
in_CI(est, se, true, level=0.95, df=Inf)
```

Arguments

est	Vector of estimates
se	Vector of standard errors
true	Vector of true parameters
level	Confidence level
df	Degrees of freedom for t distribution. The default corresponds to the normal distribution.

Value

Logical vector

Examples

```
#####
# EXAMPLE 1: Toy example
#####

#-- simulate estimates and standard errors
set.seed(987)
n <- 10
est <- stats::rnorm( n, sd=1)
se <- stats::runif( n, 0, .7 )
level <- .95
true <- 0

#-- apply coverage function
in_ci <- miceadds::in_CI( est, se, true)
#-- check correctness
cbind( est, se, true, in_ci )
```

jomo2datlist

*Converts a **jomo** Data Frame in Long Format into a List of Datasets or an Object of Class mids*

Description

Converts a **jomo** data frame in long format into a list of datasets or an object of class mids.

Usage

```
jomo2datlist(jomo.dataframe, variable="Imputation")
jomo2mids(jomo.dataframe, variable="Imputation")
```

Arguments

jomo.dataframe Data frame generated in **jomo** package
 variable Variable name for imputation index

Value

List of multiply imputed datasets

See Also

See the **jomo** package.

Examples

```
#####
# EXAMPLE 1: Dataset nhanes | jomo imputation and conversion into a data list
#####

data( nhanes, package="mice")
dat <- nhanes

# impute under multivariate normal model in jomo
imp1 <- jomo::jomo1con(Y=dat, nburn=100, nbetween=10, nimp=5)
# convert into a list of datasets
datlist1 <- miceadds::jomo2datlist(imp1)
# convert into mids object
datlist2 <- miceadds::jomo2datlist(imp1)
```

kernelpls.fit2

Kernel PLS Regression

Description

Fits a PLS regression model with the kernel algorithm (Dayal & Macgregor, 1997).

Usage

```
kernelpls.fit2(X, Y, ncomp)

## S3 method for class 'kernelpls.fit2'
predict(object,X, ...)
```

Arguments

X	Matrix of regressors
Y	Vector of a univariate outcome
ncomp	Number of components to be extracted
object	Object of class kernelpls.fit2
...	Further arguments to be passed

Value

The same list as in {pls::kernelpls.fit} is produced.
In addition, R^2 measures are contained in R2.

Author(s)

This code is a **Rcpp** translation of the original pls::kernelpls.fit function from the **pls** package (see Mevik & Wehrens, 2007).

References

Dayal, B., & Macgregor, J. F. (1997). Improved PLS algorithms. *Journal of Chemometrics*, 11, 73-85.

Mevik, B. H., & Wehrens, R. (2007). The **pls** package: Principal component and partial least squares regression in R. *Journal of Statistical Software*, 18, 1-24.

See Also

See the **pls** package for further estimation algorithms.

Examples

```
#####
# SIMULATED EXAMPLE 1: 300 cases on 100 variables
#####
set.seed(789)

N <- 300      # number of cases
p <- 100      # number of predictors
rho1 <- .6    # correlations between predictors

# simulate data
Sigma <- base::diag(1-rho1,p) + rho1
X <- mvtnorm::rmvnorm( N, sigma=Sigma )
beta <- base::seq( 0, 1, len=p )
y <- ( X %%% beta )[,1] + stats::rnorm( N, sd=.6 )
Y <- base::matrix(y,nrow=N, ncol=1 )

# PLS regression
res <- miceadds::kernelpls.fit2( X=X, Y=Y, ncomp=20 )

# predict new scores
Xpred <- predict( res, X=X[1:10,] )

## Not run:
#####
# EXAMPLE 2: Dataset yarn from pls package
#####

# use kernelpls.fit from pls package
library(pls)
data(yarn,package="pls")
mod1 <- pls::kernelpls.fit( X=yarn$NIR, Y=yarn$density, ncomp=10 )
# use kernelpls.fit2 from miceadds package
Y <- base::matrix( yarn$density, ncol=1 )
mod2 <- miceadds::kernelpls.fit2( X=yarn$NIR, Y=Y, ncomp=10 )

## End(Not run)
```

library_install	<i>R Utilities: Loading a Package or Installation of a Package if Necessary</i>
-----------------	---

Description

Loads packages specified in vector pkg. If some packages are not yet installed, they will be automatically installed by this function using [install.packages](#).

Usage

```
library_install( pkg, ... )
```

Arguments

pkg	Vector with package names
...	Further arguments to be passed to install.packages

Examples

```
## Not run:
# try to load packages PP and MCMCglm
library_install( pkg=c("PP", "MCMCglm") )

## End(Not run)
```

lm.cluster	<i>Cluster Robust Standard Errors for Linear Models and General Linear Models</i>
------------	---

Description

Computes cluster robust standard errors for linear models ([stats::lm](#)) and general linear models ([stats::glm](#)) using the [multiwayvcov::cluster.vcov](#) function in the **multiwayvcov** package.

Usage

```
lm.cluster(data, formula, cluster, ...)
```

```
glm.cluster(data, formula, cluster, ...)
```

```
## S3 method for class 'lm.cluster'
summary(object,...)
## S3 method for class 'glm.cluster'
summary(object,...)
```

```
## S3 method for class 'lm.cluster'
coef(object,...)
## S3 method for class 'glm.cluster'
coef(object,...)

## S3 method for class 'lm.cluster'
vcov(object,...)
## S3 method for class 'glm.cluster'
vcov(object,...)
```

Arguments

data	Data frame
formula	An R formula
cluster	Variable name for cluster variable contained in data or a vector with cluster identifiers
...	Further arguments to be passed to <code>stats::lm</code> and <code>stats::glm</code>
object	Object of class <code>lm.cluster</code> or <code>glm.cluster</code>

Value

List with following entries

lm_res	Value of <code>stats::lm</code>
glm_res	Value of <code>stats::glm</code>
vcov	Covariance matrix of parameter estimates

See Also

[stats::lm](#), [stats::glm](#), [multiwayvcov::cluster.vcov](#)

Examples

```
#####
# EXAMPLE 1: Cluster robust standard errors data.ma01
#####

data(data.ma01)
dat <- data.ma01

### Model 1: Linear regression
mod1 <- miceadds::lm.cluster( data=dat, formula=read ~ hisei + female,
                             cluster="idschool" )

coef(mod1)
vcov(mod1)
summary(mod1)

# estimate Model 1, but cluster is provided as a vector
mod1b <- miceadds::lm.cluster( data=dat, formula=read ~ hisei + female,
```

```

                                cluster=dat$idschool)
summary(mod1b)

#### Model 2: Logistic regression
dat$highmath <- 1 * ( dat$math > 600 ) # create dummy variable
mod2 <- miceadds::glm.cluster( data=dat, formula=highmath ~ hisei + female,
                              cluster="idschool", family="binomial")

coef(mod2)
vcov(mod2)
summary(mod2)

## Not run:
#####
# EXAMPLE 2: Cluster robust standard errors for multiply imputed datasets
#####

library(mitools)
data(data.ma05)
dat <- data.ma05

# imputation of the dataset: use six imputations
resp <- dat[, - c(1:2) ]
imp <- mice::mice( resp, method="norm", maxit=3, m=6 )
datlist <- miceadds::mids2datlist( imp )

# linear regression with cluster robust standard errors
mod <- lapply( datlist, FUN=function(data){
  miceadds::lm.cluster( data=data, formula=denote ~ migrant+ misei,
                        cluster=dat$idclass )
} )

# extract parameters and covariance matrix
betas <- lapply( mod, FUN=function(rr){ coef(rr) } )
vars <- lapply( mod, FUN=function(rr){ vcov(rr) } )
# conduct statistical inference
summary( miceadds::pool_mi( qhat=betas, u=vars ) )

#----- compute global F-test for hypothesis that all predictors have zero coefficient values
library(mitml)
Nimp <- 6 # number of imputations
np <- length(betas[[1]]) # number of parameters
beta_names <- names(betas[[1]])
# define vector of parameters for which constraints should be tested
constraints <- beta_names[-1]
# create input for mitml::testConstraints function
qhat <- matrix( unlist(betas), ncol=Nimp)
rownames(qhat) <- beta_names
uhat <- array( unlist(vars), dim=c(np,np,Nimp))
dimnames(uhat) <- list( beta_names, beta_names, NULL )
# compute global F-test
Ftest <- mitml::testConstraints( qhat=betas, uhat=vars, constraints=constraints )
print(Ftest)

## End(Not run)

```

lmer_vcov	<i>Statistical Inference for Fixed and Random Structure for Fitted Models in lme4</i>
-----------	--

Description

The function `lmer_vcov` conducts statistical inference for fixed coefficients and standard deviations and correlations of random effects structure of models fitted in the **lme4** package.

The function `lmer_pool` applies the Rubin formula for inference for fitted **lme4** models for multiply imputed datasets.

Usage

```
lmer_vcov(object, level=.95, use_reml=FALSE, ...)
```

```
## S3 method for class 'lmer_vcov'
summary(object, digits=4, file=NULL, ...)
## S3 method for class 'lmer_vcov'
coef(object, ...)
## S3 method for class 'lmer_vcov'
vcov(object, ...)
```

```
lmer_vcov2(object, level=.95, ...)
```

```
lmer_pool( models, level=.95, ...)
## S3 method for class 'lmer_pool'
summary(object, digits=4, file=NULL, ...)
```

```
lmer_pool2( models, level=.95, ...)
```

Arguments

<code>object</code>	Fitted object in lme4
<code>level</code>	Confidence level
<code>use_reml</code>	Logical indicating whether REML estimates should be used for variance components (if provided)
<code>digits</code>	Number of digits used for rounding in summary
<code>file</code>	Optional file name for sinking output
<code>models</code>	List of models fitted in lme4 for a multiply imputed dataset
<code>...</code>	Further arguments to be passed

Value

List with several entries:

par_summary	Parameter summary
coef	Estimated parameters
vcov	Covariance matrix of estimates
...	Further values

Author(s)

Function originally from Ben Bolker, <http://rpubs.com/bbolker/varwald>

See Also

[lme4::lmer](#), [mitml::testEstimates](#)

Examples

```
## Not run:
#####
# EXAMPLE 1: Single model fitted in lme4
#####

library(lme4)
data(data.ma01, package="miceadds")
dat <- na.omit(data.ma01)

#* fit multilevel model
formula <- math ~ hisei + miceadds::gm( books, idschool ) + ( 1 + books | idschool )
mod1 <- lme4::lmer( formula, data=dat, REML=FALSE)
summary(mod1)

#* statistical inference
res1 <- miceadds::lmer_vcov( mod1 )
summary(res1)
coef(res1)
vcov(res1)

#####
# EXAMPLE 2: lme4 model for multiply imputed dataset
#####

library(lme4)
data(data.ma02, package="miceadds")
datlist <- miceadds::datlist_create(data.ma02)

#** fit lme4 model for all imputed datasets
formula <- math ~ hisei + miceadds::gm( books, idschool ) + ( 1 | idschool )
models <- list()
M <- length(datlist)
for (mm in 1:M){
```

```

    models[[mm]] <- lme4::lmer( formula, data=datlist[[mm]], REML=FALSE)
  }

  *** statistical inference
  res1 <- miceadds::lmer_pool(models)
  summary(res1)

  ## End(Not run)

```

load.data

*R Utilities: Loading/Reading Data Files using **miceadds*****Description**

This function is a wrapper function for loading or reading data frames or matrices.

Usage

```
load.data( filename, type="Rdata", path=getwd(), spss.default=TRUE, ...)
```

Arguments

filename	Name of the data file (matrix or data frame). This can also be a part of the file name and the most recent file is loaded. filename can also be a vector which strings and a file is loaded which contains all the specified strings.
type	The type of file in which the data frame or matrix should be loaded. This can be Rdata (for R binary format, using load.Rdata2), csv (using utils::read.csv2), csv2 (using utils::read.csv), table (using utils::read.table ; the dataset must have the file extension dat or txt) or sav (using foreign::read.spss).
path	Directory from which the dataset should be loaded. It can also be set to NULL if the absolute path is already included in filename.
spss.default	Optional logical which is only applied for type="sav" indicating whether the arguments to <code>.data.frame=TRUE</code> and <code>use.value.labels=FALSE</code> are used.
...	Further arguments to be passed to <code>load.Rdata2</code> , <code>read.csv2</code> , <code>read.csv</code> , <code>read.table</code> or <code>foreign::read.spss</code> .

See Also

See also [load.Rdata](#) for loading R data frames.

See [save.Rdata](#) and [save.data](#) for saving/writing R data frames.

Examples

```

## Not run:
# load a data frame in the file "data_s3.Rdata" and save this
# as the object "dat.s3"
dat.s3 <- miceadds::load.data( filename="data_s3.Rdata", type="Rdata" )

## End(Not run)

```

Description

These functions loads a Rdata object saved as a data frame or a matrix in the current R environment. The function `load.Rdata` saves the loaded object in the global environment while `load.Rdata2` loads the object only specified environments. Hence, usage of `load.Rdata2` instead of `load.Rdata` is recommended.

Usage

```
load.Rdata(filename, objname)

load.Rdata2(filename, path=getwd())
```

Arguments

<code>filename</code>	Rdata file (matrix or data frame)
<code>objname</code>	Object name. This object will be a global variable in R.
<code>path</code>	Directory from which the dataset should be loaded

See Also

See also [save.Rdata](#) for saving data frames in a Rdata format.

See also: [base::load](#), [base::save](#)

Examples

```
## Not run:
# load a data frame in the file "data_s3.Rdata" and save this
# as the object "dat.s3"
load.Rdata( filename="data_s3.Rdata", "dat.s3" )
head(dat.s3)

# Alternatively one can use the function
dat.s3 <- miceadds::load.Rdata2( filename="data_s3.Rdata")

## End(Not run)
```

ma.scale2

*Standardization of a Matrix***Description**

This function performs a z-standardization for a numeric matrix. Note that in a case of a zero standard deviation all matrix entries are divided by a small number such that no NaNs occur.

Usage

```
ma.scale2(x, missings=FALSE)
```

Arguments

x	A numeric matrix in which missing values are permitted
missings	A logical indicating whether missings occur (or could occur) in the dataset

Value

A matrix

See Also

[base::scale](#)

Examples

```
#####
# EXAMPLE 1: z-standardization data.internet
#####

data(data.internet)
dat <- data.internet

# z-standardize all variables in this dataset
zdat <- miceadds::ma.scale2( dat, missings=TRUE )

## Not run:
#####
# SIMULATED EXAMPLE 2: Speed comparison for many cases and many variables
#####

set.seed(9786)
# 3000 cases, 200 variables
N <- 3000
p <- 200
# simulate some data
x <- matrix( stats::rnorm( N*p ), N, p )
x <- round( x, 2 )
```



```

# compare computation times for 10 replications
B <- 10
  s1 <- Sys.time()      # scale in R
for (bb in 1:B){
  res <- scale(x)
} ; s2 <- Sys.time() ; d1 <- s2-s1

  s1 <- Sys.time()      # scale in miceadds
for (bb in 1:B){
  res1 <- miceadds::ma.scale2(x)
} ; s2 <- Sys.time() ; d2 <- s2-s1

# scale in miceadds with missing handling
s1 <- Sys.time()
for (bb in 1:B){
  res1 <- miceadds::ma.scale2(x,missings=TRUE)
} ; s2 <- Sys.time() ; d3 <- s2-s1
d1      # scale in R
d2      # scale in miceadds (no missing handling)
d3      # scale in miceadds (with missing handling)
## > d1      # scale in R
## Time difference of 1.622431 secs
## > d2      # scale in miceadds (no missing handling)
## Time difference of 0.156003 secs
## > d3      # scale in miceadds (with missing handling)
## Time difference of 0.2028039 secs

## End(Not run)

```

ma.wtd.statNA

*Some Multivariate Descriptive Statistics for Weighted Data in
miceadds*

Description

Some multivariate descriptive statistics for weighted datasets in **miceadds**. A list of (nested) multiply imputed data sets is also allowed as input.

Usage

```
ma.wtd.meanNA(data, weights=NULL, vars=NULL )
```

```
ma.wtd.sdNA(data, weights=NULL, vars=NULL, method="unbiased" )
```

```
ma.wtd.covNA(data, weights=NULL, vars=NULL, method="unbiased" )
```

```
ma.wtd.corNA(data, weights=NULL, vars=NULL, method="unbiased" )
```

```
ma.wtd.skewnessNA(data, weights=NULL, vars=NULL, method="unbiased" )
```

```
ma.wtd.curtosisNA(data, weights=NULL, vars=NULL, method="unbiased" )
```

```
ma.wtd.quantileNA( data, weights=NULL, vars=NULL, type=7,
  probs=seq(0,1,.25) )
```

Arguments

data	Numeric data vector or data frame or objects of one of the classes <code>datlist</code> , <code>imputationList</code> , <code>mids</code> , <code>mids.1chain</code> , <code>nested.datlist</code> , <code>NestedImputationList</code> or <code>BIFIEdata</code> .
weights	Optional vector of sampling weights
vars	Optional vector of variable names
method	Computation method for covariances. These amount to choosing the divisor $(n-1)$ (<code>method="unbiased"</code>) instead of n (<code>method="ML"</code>). See stats::cov.wt for further details.
type	Quantile type. This specification follows TAM::weighted_quantile
probs	Vector of probabilities used for calculation of quantiles.

Details

Contrary to ordinary R practice, missing values are ignored in the calculation of descriptive statistics.

<code>ma.wtd.meanNA</code>	weighted means
<code>ma.wtd.sdNA</code>	weighted standard deviations
<code>ma.wtd.covNA</code>	weighted covariance matrix
<code>ma.wtd.corNA</code>	weighted correlation matrix
<code>ma.wtd.skewnessNA</code>	weighted skewness
<code>ma.wtd.curtosisNA</code>	weighted (excess) kurtosis

Value

A vector or a matrix depending on the requested statistic.

Note

If data is of class `BIFIEdata` and no weights are specified, sample weights are extracted from the `BIFIEdata` object.

See Also

Some functions for weighted statistics: [stats::weighted.mean](#), [stats::cov.wt](#), `{Hmisc::wtd.var}`, [TAM::weighted_quantile](#), ...

See [micombine.cor](#) for statistical inference of correlation coefficients.

Examples

```
#####
# EXAMPLE 1: Weighted statistics for a single dataset data.ma01
#####

data(data.ma01)
dat <- as.matrix(data.ma01[,-c(1:3)])

# weighted mean
ma.wtd.meanNA( dat, weights=data.ma01$studwgt )

# weighted SD
ma.wtd.sdNA( dat, weights=data.ma01$studwgt )

# weighted covariance for selected variables
ma.wtd.covNA( dat, weights=data.ma01$studwgt, vars=c("books","hisei") )

# weighted correlation
ma.wtd.corNA( dat, weights=data.ma01$studwgt )

# weighted curtosis
ma.wtd.skewnessNA( dat[, "books"], weights=data.ma01$studwgt )
# compare with result in TAM
TAM::weighted_skewness( x=dat[, "books"], w=data.ma01$studwgt )

# weighted curtosis
ma.wtd.curtosisNA( dat, weights=data.ma01$studwgt, vars=c("books","hisei") )
# result in TAM
TAM::weighted_curtosis( dat[, "books"], w=data.ma01$studwgt )
TAM::weighted_curtosis( dat[, "hisei"], w=data.ma01$studwgt )

## Not run:
#####
# EXAMPLE 2: Weighted statistics multiply imputed dataset
#####

library(mitools)
data(data.ma05)
dat <- data.ma05

# do imputations
resp <- dat[, - c(1:2) ]
# object of class mids
imp <- mice::mice( resp, method="norm", maxit=3, m=5 )
# object of class datlist
datlist <- miceadds::mids2datlist( imp )
# object of class imputationList
implist <- mitools::imputationList(datlist)

# weighted means
ma.wtd.meanNA(datlist)
ma.wtd.meanNA(implist)
```

```

ma.wtd.meanNA(imp)

# weighted quantiles
ma.wtd.quantileNA( implist, weights=data.ma05$studwgt, vars=c("manote","Dscore"))

#####
# EXAMPLE 3: Weighted statistics nested multiply imputed dataset
#####

library(BIFIEsurvey)
data(data.timss2, package="BIFIEsurvey" )
datlist <- data.timss2 # list of 5 datasets containing 5 plausible values

#** define imputation method and predictor matrix
data <- datlist[[1]]
V <- ncol(data)
# variables
vars <- colnames(data)
# variables not used for imputation
vars_unused <- miceadds::scan.vec("IDSTUD TOTWGT JKZONE JKREP" )
#- define imputation method
impMethod <- rep("norm", V )
names(impMethod) <- vars
impMethod[ vars_unused ] <- ""
#- define predictor matrix
predM <- matrix( 1, V, V )
colnames(predM) <- rownames(predM) <- vars
diag(predM) <- 0
predM[, vars_unused ] <- 0

# object of class mids.nmi
imp1 <- miceadds::mice.nmi( datlist, method=impMethod, predictorMatrix=predM,
                           m=4, maxit=3 )
# object of class nested.datlist
datlist <- miceadds::mids2datlist(imp1)
# object of class NestedImputationList
imp2 <- miceadds::NestedImputationList(datlist)

# weighted correlations
vars <- c("books","ASMMAT","likesc")
ma.wtd.corNA( datlist, vars=vars )
ma.wtd.corNA( imp2, vars=vars )
ma.wtd.corNA( imp1, vars=vars )

#####
# EXAMPLE 4: Multiply imputed datasets in BIFIEdata format
#####

library(BIFIEsurvey)
data(data.timss1, package="BIFIEsurvey")
data(data.timssrep, package="BIFIEsurvey")

# create BIFIEdata object

```

```

bdat <- BIFIEsurvey::BIFIE.data( data.list=data.timss1, wgt=data.timss1[[1]]$TOTWGT,
                               wgtrep=data.timssrep[, -1 ] )
summary(bdat)
# create BIFIEdata object in a compact way
bdat2 <- BIFIEsurvey::BIFIE.data( data.list=data.timss1, wgt=data.timss1[[1]]$TOTWGT,
                               wgtrep=data.timssrep[, -1 ], cdata=TRUE)
summary(bdat2)

# compute skewness
ma.wtd.skewnessNA( bdat, vars=c("ASMMAT", "books" ) )
ma.wtd.skewnessNA( bdat2, vars=c("ASMMAT", "books" ) )

#####
# EXAMPLE 5: Nested multiply imputed datasets in BIFIEdata format
#####

data(data.timss4, package="BIFIEsurvey")
data(data.timssrep, package="BIFIEsurvey")

# nested imputed dataset, save it in compact format
bdat <- BIFIE.data( data.list=data.timss4, wgt=data.timss4[[1]][[1]]$TOTWGT,
                   wgtrep=data.timssrep[, -1 ], NMI=TRUE, cdata=TRUE )
summary(bdat)
# skewness
ma.wtd.skewnessNA( bdat, vars=c("ASMMAT", "books" ) )

## End(Not run)

```

ma_lme4_formula

*Utility Functions for Working with **lme4** Formula Objects*

Description

Utility functions for working with **lme4** formula objects. The function `ma_lme4_formula_terms` decomposes an **lme4** formula into several parts for further processing.

Usage

```
ma_lme4_formula_terms(formula)
```

```
ma_lme4_formula_design_matrices(formula, data, start_index=0, formula_terms=NULL,
                                only_design_matrices=FALSE)
```

Arguments

<code>formula</code>	An R formula object
<code>data</code>	Data frame
<code>start_index</code>	Starting index for cluster identifiers

formula_terms Optional argument with processed formula terms using the function ma_lme4_formula_terms
 only_design_matrices Logical indicating whether only design matrices should be created

Value

List with several entries

Examples

```
#####
# EXAMPLE 1: Splitting a lme4 formula
#####

*** formula for a multilevel model
formula <- y ~ I( miceadds::cwc(x, idcluster)) + z + I(z^2) + I( miceadds::gm(x, idcluster) ) + w +
  ( x + I(x^2) | idcluster) + (0 + w | idcluster) +
  ( 0 + I(as.factor(f)) | idcluster)
miceadds::ma_lme4_formula_terms(formula)

*** formula for a single level model
formula2 <- y ~ I( miceadds::cwc(x, idcluster)) + z + I(z^2) + I( miceadds::gm(x, idcluster) ) + w
miceadds::ma_lme4_formula_terms(formula2)

#####
# EXAMPLE 2: Design matrices for multilevel model
#####

data(data.ma07, package="miceadds")
dat <- data.ma07

formula <- x1 ~ x2 + I( miceadds::gm( x2, id2)) + I( miceadds::gm( x2, id3)) + y1 + z1 +
  ( x2 | id2:id3 ) + ( 1 | id3 ) + ( 0 + x2 | id3 )
res <- miceadds::ma_lme4_formula_design_matrices(formula, data=dat)
str(res)
```

ma_rmvnorm

Simulating Normally Distributed Data

Description

Some functions for normally distributed data.

The function ma_rmvnorm is like mvtnorm::rmvnorm, but allows for a covariance matrix sigma which can have zero variances.

Usage

```
ma_rmvnorm(n, mu=NULL, sigma, eps=1e-10)
```

Arguments

n	Sample size
mu	Mean vector
sigma	Covariance matrix
eps	Trimming constant for zero variances

Value

Matrix of simulated values

See Also

[MASS::mvrnorm](#)

Examples

```
#####
# EXAMPLE 1: Two-dimensional simulation with zero variance at dimension 1
#####

sigma <- matrix( c(0,0,0,1), nrow=2, ncol=2)
miceadds::ma_rmvnorm( n=10, sigma=sigma )
```

mi.anova	<i>Analysis of Variance for Multiply Imputed Data Sets (Using the D_2 Statistic)</i>
----------	---

Description

This function combines F values from analysis of variance using the D_2 statistic which is based on combining χ^2 statistics (see Allison, 2001, Grund, Luedtke & Robitzsch, 2016; [micombine.F](#), [micombine.chisquare](#)).

Usage

```
mi.anova(mi.res, formula, type=2)
```

Arguments

mi.res	Object of class mids or mids.1chain
formula	Formula for lm function. Note that this can be also a string.
type	Type for ANOVA calculations. For type=3, the car::Anova function from the car package is used.

Value

A list with the following entries:

r.squared	Explained variance R^2
anova.table	ANOVA table

References

Allison, P. D. (2002). *Missing data*. Newbury Park, CA: Sage.

Grund, S., Luedtke, O., & Robitzsch, A. (2016). Pooling ANOVA results from multiply imputed datasets: A simulation study. *Methodology*, 12, 75-88.

See Also

This function uses `micombine.F` and `micombine.chisquare`.

See `mice::pool.compare` and `mitml::testModels` for model comparisons based on the D_1 statistic. The D_2 statistic is also included in `mitml::testConstraints`.

The D_1 , D_2 and D_3 statistics are also included in the **mice** package in functions `mice::D1`, `mice::D2` and `mice::D3`.

Examples

```
#####
# EXAMPLE 1: nhanes2 data | two-way ANOVA
#####

library(mice)
library(car)
data(nhanes2, package="mice")
set.seed(9090)

# nhanes data in one chain and 8 imputed datasets
mi.res <- miceadds::mice.lchain( nhanes2, burnin=4, iter=20, Nimp=8 )
# 2-way analysis of variance (type 2)
an2a <- miceadds::mi.anova(mi.res=mi.res, formula="bmi ~ age * chl" )
# 2-way analysis of variance (type 3)
an2b <- miceadds::mi.anova(mi.res=mi.res, formula="bmi ~ age * chl", type=3)

#***** analysis based on first imputed dataset

# extract first dataset
dat1 <- mice::complete( mi.res$mids )

# type 2 ANOVA
lm1 <- stats::lm( bmi ~ age * chl, data=dat1 )
summary( stats::aov( lm1 ) )
# type 3 ANOVA
lm2 <- stats::lm( bmi ~ age * chl, data=dat1, contrasts=list(age=contr.sum))
car::Anova( lm2, type=3)
```

mice.1chain

Multiple Imputation by Chained Equations using One Chain

Description

This function modifies the `mice::mice` function to multiply impute a dataset using a long chain instead of multiple parallel chains which is the approach employed in `mice::mice`.

Usage

```
mice.1chain(data, burnin=10, iter=20, Nimp=10, method=NULL,
            where=NULL, visitSequence=NULL, blots=NULL, post=NULL,
            defaultMethod=c("pmm", "logreg", "polyreg", "polr"),
            printFlag=TRUE, seed=NA, data.init=NULL, ...)
```

```
## S3 method for class 'mids.1chain'
summary(object, ...)
```

```
## S3 method for class 'mids.1chain'
print(x, ...)
```

```
## S3 method for class 'mids.1chain'
plot(x, plot.burnin=FALSE, ask=TRUE, ...)
```

Arguments

<code>data</code>	Numeric matrix
<code>burnin</code>	Number of burn-in iterations
<code>iter</code>	Total number of imputations (larger than burnin)
<code>Nimp</code>	Number of imputations
<code>method</code>	See <code>mice::mice</code>
<code>where</code>	See <code>mice::mice</code>
<code>visitSequence</code>	See <code>mice::mice</code>
<code>blots</code>	See <code>mice::mice</code>
<code>post</code>	See <code>mice::mice</code>
<code>defaultMethod</code>	See <code>mice::mice</code>
<code>printFlag</code>	See <code>mice::mice</code>
<code>seed</code>	See <code>mice::mice</code>
<code>data.init</code>	See <code>mice::mice</code>
<code>object</code>	Object of class <code>mids.1chain</code>
<code>x</code>	Object of class <code>mids.1chain</code>
<code>plot.burnin</code>	An optional logical indicating whether burnin iterations should be included in the traceplot
<code>ask</code>	An optional logical indicating a user request for viewing next plot
<code>...</code>	See <code>mice::mice</code>

Value

A list with following entries

midsobj	Objects of class mids
datlist	List of multiply imputed datasets
datalong	Original and imputed dataset in the long format
implist	List of mids objects for every imputation
chainMpar	Trace of means for all imputed variables
chainVarpar	Trace of variances for all imputed variables

Note

Multiple imputation can also be used for determining causal effects (see Example 3; Schafer & Kang, 2008).

See Also

[mice::mice](#)

Examples

```
#####
# EXAMPLE 1: One chain nhanes data
#####

library(mice)
data(nhanes, package="mice")
set.seed(9090)

# nhanes data in one chain
imp.mi1 <- miceadds::mice.1chain( nhanes, burnin=5, iter=40, Nimp=4,
                                method=rep("norm", 4) )
summary(imp.mi1)          # summary of mids.1chain
## Not run:
plot( imp.mi1 ) # trace plot excluding burnin iterations
plot( imp.mi1, plot.burnin=TRUE ) # trace plot including burnin iterations

# select mids object
imp.mi2 <- imp.mi1$midsobj
summary(imp.mi2)        # summary of mids

# apply mice functionality lm.mids
mod <- with( imp.mi2, stats::lm( bmi ~ age ) )
summary( mice::pool( mod ) )

#####
# EXAMPLE 2: One chain (mixed data: numeric and factor)
#####

library(mice)
```

```

data(nhanes2, package="mice")
set.seed(9090)

# nhanes2 data in one chain
imp.mi1 <- miceadds::mice.lchain( nhanes2, burnin=5, iter=25, Nimp=5 )
# summary
summary( imp.mi1$midsobj )

#####
# EXAMPLE 3: Multiple imputation with counterfactuals for estimating
# causal effects (average treatment effects)
# Schafer, J. L., & Kang, J. (2008). Average causal effects from nonrandomized
# studies: a practical guide and simulated example.
# Psychological Methods, 13, 279-313.
#####

data(data.ma01)
dat <- data.ma01[, 4:11]

# define counterfactuals for reading score for students with and
# without migrational background
dat$read.migrant1 <- ifelse( paste(dat$migrant)==1, dat$read, NA )
dat$read.migrant0 <- ifelse( paste(dat$migrant)==0, dat$read, NA )

# define imputation method
impmethod <- rep("pls", ncol(dat) )
names(impmethod) <- colnames(dat)

# define predictor matrix
pm <- 4*(1 - diag( ncol(dat) ) ) # 4 - use all interactions
rownames(pm) <- colnames(pm) <- colnames(dat)
pm[ c( "read.migrant0", "read.migrant1"), ] <- 0
# do not use counterfactuals for 'read' as a predictor
pm[, "read.migrant0"] <- 0
pm[, "read.migrant1"] <- 0
# define control variables for creation of counterfactuals
pm[ c( "read.migrant0", "read.migrant1"), c("hisei","paredu","female","books") ] <- 4
## > pm
##          math read migrant books hisei paredu female urban read.migrant1 read.migrant0
## math          0  4      4      4      4      4      4      4          0          0
## read          4  0      4      4      4      4      4      4          0          0
## migrant       4  4      0      4      4      4      4      4          0          0
## books         4  4      4      0      4      4      4      4          0          0
## hisei         4  4      4      4      0      4      4      4          0          0
## paredu        4  4      4      4      4      0      4      4          0          0
## female        4  4      4      4      4      4      0      4          0          0
## urban         4  4      4      4      4      4      4      0          0          0
## read.migrant1 0  0      0      4      4      4      4      0          0          0
## read.migrant0 0  0      0      4      4      4      4      0          0          0

# imputation using mice function and PLS imputation with
# predictive mean matching method 'pmm6'
imp <- mice::mice( dat, method=impmethod, predictorMatrix=pm,

```

```

maxit=4, m=5, pls.impMethod="pmm5" )

#### Model 1: Raw score difference
mod1 <- with( imp, stats::lm( read ~ migrant ) )
smod1 <- summary( mice::pool(mod1) )
## > smod1
##           est    se      t    df Pr(>|t|)  lo 95  hi 95 nmis   fmi lambda
## (Intercept) 510.21 1.460 349.37 358.26      0 507.34 513.09  NA 0.1053 0.1004
## migrant     -43.38 3.757 -11.55  62.78      0 -50.89 -35.87  404 0.2726 0.2498

#### Model 2: ANCOVA - regression adjustment
mod2 <- with( imp, stats::lm( read ~ migrant + hisei + paredu + female + books ) )
smod2 <- summary( mice::pool(mod2) )
## > smod2
##           est    se      t    df Pr(>|t|)  lo 95  hi 95 nmis   fmi lambda
## (Intercept) 385.1506 4.12027 93.477 3778.66 0.000e+00 377.0725 393.229  NA 0.008678 0.008153
## migrant     -29.1899 3.30263 -8.838  87.46 9.237e-14 -35.7537 -22.626  404 0.228363 0.210917
## hisei         0.9401 0.08749 10.745 160.51 0.000e+00  0.7673  1.113  733 0.164478 0.154132
## paredu        2.9305 0.79081  3.706  41.34 6.190e-04  1.3338  4.527  672 0.339961 0.308780
## female       38.1719 2.26499 16.853 1531.31 0.000e+00 33.7291 42.615  0 0.041093 0.039841
## books       14.0113 0.88953 15.751 154.71 0.000e+00 12.2541 15.768 423 0.167812 0.157123

#### Model 3a: Estimation using counterfactuals
mod3a <- with( imp, stats::lm( I( read.migrant1 - read.migrant0 ) ~ 1 ) )
smod3a <- summary( mice::pool(mod3a) )
## > smod3a
##           est    se      t    df Pr(>|t|)  lo 95  hi 95 nmis   fmi lambda
## (Intercept) -22.54 7.498 -3.007  4.315  0.03602 -42.77 -2.311  NA 0.9652 0.9521

#### Model 3b: Like Model 3a but using student weights
mod3b <- with( imp, stats::lm( I( read.migrant1 - read.migrant0 ) ~ 1,
                               weights=data.ma01$studwgt ) )
smod3b <- summary( mice::pool(mod3b) )
## > smod3b
##           est    se      t    df Pr(>|t|)  lo 95  hi 95 nmis   fmi lambda
## (Intercept) -21.88 7.605 -2.877  4.3  0.04142 -42.43 -1.336  NA 0.9662 0.9535

#### Model 4: Average treatment effect on the treated (ATT, migrants)
#           and non-treated (ATN, non-migrants)
mod4 <- with( imp, stats::lm( I( read.migrant1 - read.migrant0 ) ~ 0 + as.factor( migrant ) ) )
smod4 <- summary( mice::pool(mod4) )
## > smod4
##           est    se      t    df Pr(>|t|)  lo 95  hi 95 nmis   fmi lambda
## as.factor(migrant)0 -23.13 8.664 -2.669  4.27 0.052182 -46.59  0.3416  NA 0.9682 0.9562
## as.factor(migrant)1 -19.95 5.198 -3.837 19.57 0.001063 -30.81 -9.0884  NA 0.4988 0.4501
# ATN=-23.13 and ATT=-19.95

## End(Not run)

```

```
mice.impute.2l.contextual.pmm
```

Imputation by Predictive Mean Matching or Normal Linear Regression with Contextual Variables

Description

This imputation method imputes a variable using linear regression with predictive mean matching as the imputation method. Including a contextual effects means that an aggregated variable at a cluster level is included as a further covariate.

Usage

```
mice.impute.2l.contextual.pmm(y, ry, x, type, imputationWeights=NULL,
  interactions=NULL, quadratics=NULL, pls.facs=NULL, ...)

mice.impute.2l.contextual.norm(y, ry, x, type, ridge=10^(-5),
  imputationWeights=NULL, interactions=NULL, quadratics=NULL, pls.facs=NULL, ...)
```

Arguments

y	Incomplete data vector of length n
ry	Vector of missing data pattern (FALSE – missing, TRUE – observed)
x	Matrix (n x p) of complete covariates.
type	Type of predictor variables. type=-2 refers to the cluster variable, type=2 denotes a variable for which also a contextual effect is included and type=1 denotes all other variables which are included as 'ordinary' predictors.
imputationWeights	Optional vector of sample weights
interactions	Vector of variable names used for creating interactions
quadratics	Vector of variable names used for creating quadratic terms
pls.facs	Number of factors used in partial least dimension reduction (if requested)
...	Further arguments to be passed
ridge	Ridge parameter in the diagonal of $X'X$

Value

A vector of length `nmis=sum(!ry)` with imputed values.

See Also

For imputations at level 2 variables see [mice::mice.impute.2lonly.norm](#) and [mice::mice.impute.2lonly.pmm](#).

Examples

```

## Not run:
#####
# EXAMPLE 1: Sequential hierarchical imputation for data.ma05 dataset
#####

data(data.ma05)
dat <- data.ma05

# define predictor matrix
predM <- mice::make.predictorMatrix(data=dat)
# exclude student IDs
predM[, "idstud"] <- 0
# define idclass as the cluster variable (type=-2)
predM[, "idclass" ] <- -2

# initialize with norm method
impMethod <- mice::make.method(data=dat)
names(impMethod) <- names( imp0$method )
impMethod[ c("idstud","idclass")] <- ""

#*****
# STUDENT LEVEL (Level 1)

# Use a random slope model for Dscore and Mscore as the imputation method.
# Here, variance homogeneity of residuals is assumed (contrary to
# the 2l.norm imputation method in the mice package).
impMethod[ c("Dscore", "Mscore") ] <- "2l.pan"
predM[ c("Dscore","Mscore"), "misei" ] <- 2 # random slopes on 'misei'
predM[, "idclass" ] <- -2

# For imputing 'manote' and 'denote' use contextual effects (i.e. cluser means)
# of variables 'misei' and 'migrant'
impMethod[ c("denote", "manote") ] <- "2l.contextual.pmm"
predM[ c("denote", "manote"), c("misei","migrant")] <- 2

# Use no cluster variable 'idclass' for imputation of 'misei'
impMethod[ "misei" ] <- "norm"
predM[ "misei", "idclass" ] <- 0 # use no multilevel imputation model

# Variable migrant: contextual effects of Dscore and misei
impMethod[ "migrant" ] <- "2l.contextual.pmm"
predM[ "migrant", c("Dscore", "misei" ) ] <- 2
predM[ "migrant", "idclass" ] <- -2

#****
# CLASS LEVEL (Level 2)
# impute 'sprengel' and 'groesse' at the level of classes
impMethod[ "sprengel" ] <- "2lonly.pmm"
impMethod[ "groesse" ] <- "2lonly.norm"
predM[ c("sprengel","groesse"), "idclass" ] <- -2

```

```

# do imputation
imp <- mice::mice( dat, predictorMatrix=predM, m=3, maxit=4,
                  imputationMethod=impMethod, paniter=100)
summary(imp)

##### imputation model 2 with PLS dimension reduction

# define some interaction effects
interactions <- list( manote=c("migrant", "misei") )
# number of PLS factors (5 factors)
pls.facs <- list( manote=5 )

# do imputation
imp2 <- mice::mice( dat, predictorMatrix=predM, interactions=interactions,
                   pls.facs=pls.facs, method=impMethod, paniter=100)
summary(imp2)

## End(Not run)

```

```
mice.impute.2l.latentgroupmean.ml
```

Imputation of Latent and Manifest Group Means for Multilevel Data

Description

The imputation method `2l.latentgroupmean` imputes a latent group mean assuming an infinite population of subjects within a group (Grund, Luedtke & Robitzsch, 2018; see also Luedtke, Marsh, Robitzsch, Trautwein, Asparouhov & Muthen, 2008 or Croon & van Veldhoven, 2007). Therefore, unreliability of group means when treating subjects as indicators is taken into account.

The imputation method `mice.impute.2l.groupmean` just imputes (i.e. computes) the manifest group mean. See also [mice::mice.impute.2lonly.mean](#).

The imputation method `mice.impute.2l.groupmean.elim` computes the group mean eliminating the subject under study from the calculation. Therefore, this imputation method will lead to different values of individuals within the same group.

Usage

```
mice.impute.2l.latentgroupmean.ml(y, ry, x, type, pls.facs=NULL,
                                 imputationWeights=NULL, interactions=NULL, quadratics=NULL,
                                 EAP=FALSE, ...)
```

```
mice.impute.2l.latentgroupmean.mcmc(y, ry, x, type, pls.facs=NULL,
                                    imputationWeights=NULL, interactions=NULL, quadratics=NULL,
                                    mcmc.burnin=100, mcmc.adapt=100, mcmc.iter=1000, draw.fixed=TRUE, EAP=FALSE, ...)
```

```
mice.impute.2l.groupmean(y, ry, x, type, grmeanwarning=TRUE, ...)
```

```
mice.impute.2l.groupmean.elim(y, ry, x, type, ...)
```

Arguments

y	Incomplete data vector of length n
ry	Vector of missing data pattern (FALSE – missing, TRUE – observed)
x	Matrix (n x p) of complete covariates.
type	Type of predictor variables. type=-2 refers to the cluster variable, type=2 denotes a variable for which also a (latent) group mean should be calculated. Predictors with type=1 denote all other variables.
pls.facs	Number of factors used for PLS regression (optional).
imputationWeights	Optional vector of sample weights.
interactions	Vector of variable names used for creating interactions
quadratics	Vector of variable names used for creating quadratic terms
draw.fixed	Optional logical indicating whether parameters for fixed effects should be sampled.
EAP	Logical indicating whether EAPs should be used for imputation. The default FALSE corresponds to sampling from the posterior distribution.
mcmc.burnin	Number of MCMC burn-in iterations.
mcmc.adapt	Number of MCMC iterations in adaptation phase.
mcmc.iter	Total number of MCMC iterations.
grmeanwarning	An optional logical indicating whether some group means cannot be calculated.
...	Further arguments to be passed.

Details

The imputation of the latent group mean uses the `lme4::lmer` function of the **lme4** package for `mice.impute.2l.latentgroupmean.ml` and the `MCMCglmm::MCMCglmm` function of the **MCMCglmm** package for `mice.impute.2l.latentgroupmean.ml`. Latent group mean imputation also follows Mislevy (1991).

Value

A vector of length y containing imputed group means.

References

- Croon, M. A., & van Veldhoven, M. J. (2007). Predicting group-level outcome variables from variables measured at the individual level: a latent variable multilevel model. *Psychological Methods, 12*, 45-57.
- Grund, S., Luedtke, O., & Robitzsch, A. (2018). Multiple imputation of missing data at level 2: A comparison of fully conditional and joint modeling in multilevel designs. *Journal of Educational and Behavioral Statistics, 43*(3), 316-353.
- Luedtke, O., Marsh, H. W., Robitzsch, A., Trautwein, U., Asparouhov, T., & Muthen, B. (2008). The multilevel latent covariate model: a new, more reliable approach to group-level effects in contextual studies. *Psychological Methods, 13*, 203-229.
- Mislevy, R. J. (1991). Randomization-based inference about latent variables from complex samples. *Psychometrika, 56*, 177-196.

See Also

[mice::mice.impute.2lonly.mean](#)

Examples

```
## Not run:
#####
# EXAMPLE 1: Two-level imputation data.ma05 dataset with imputation
#           of a latent group mean
#####

data(data.ma05)
dat <- data.ma05

# include manifest group mean for 'Mscore'
dat$M.Mscore <- NA
# include latent group group for 'Mscore'
dat$LM.Mscore <- NA #=> LM: latent group mean

# define predictor matrix
predM <- mice::make.predictorMatrix(data=dat)
# exclude student ISs
predM[, "idstud"] <- 0
# idclass is the cluster identifier
predM[, "idclass" ] <- -2

# define imputation methods
impMethod <- mice::make.method(data=dat)
# initialize with norm
impMethod <- rep( "norm", length(impMethod) )
names(impMethod) <- names( imp$method )
impMethod[ c("idstud","idclass")] <- ""

#*****
# STUDENT LEVEL (Level 1)

# Use a random slope model for Dscore and Mscore as the imputation method.
# Here, variance homogeneity of residuals is assumed (contrary to
# the 2l.norm imputation method in the mice package).
impMethod[ c("Dscore", "Mscore") ] <- "2l.pan"
predM[ c("Dscore","Mscore"), "misei" ] <- 2 # random slopes on 'misei'
predM[, "idclass" ] <- -2

# For imputing 'manote' and 'denote' use contextual effects (i.e. cluster means)
# of variables 'misei' and 'migrant'
impMethod[ c("denote", "manote") ] <- "2l.contextual.pmm"
predM[ c("denote", "manote"), c("misei","migrant")] <- 2

# Use no cluster variable 'idclass' for imputation of 'misei'
impMethod[ "misei" ] <- "norm"
predM[ "misei", "idclass" ] <- 0 # use no multilevel imputation model
```

```

# Variable migrant: contextual effects of Dscore and misei
impMethod[ "migrant" ] <- "2l.contextual.pmm"
predM[ "migrant", c("Dscore", "misei" ) ] <- 2
predM[ "migrant", "idclass" ] <- -2

#****
# CLASS LEVEL (Level 2)
# impute 'sprengel' and 'groesse' at the level of classes
impMethod[ "sprengel" ] <- "2lonly.pmm2"
impMethod[ "groesse" ] <- "2lonly.norm2"
predM[ c("sprengel", "groesse"), "idclass" ] <- -2

# manifest group mean for Mscore
impMethod[ "M.Mscore" ] <- "2l.groupmean"
# latent group mean for Mscore
impMethod[ "LM.Mscore" ] <- "2l.latentgroupmean.ml"
predM[ "M.Mscore", "Mscore" ] <- 2

# covariates for latent group mean of 'Mscore'
predM[ "LM.Mscore", "Mscore" ] <- 2
predM[ "LM.Mscore", c( "Dscore", "sprengel" ) ] <- 1

# do imputations
imp <- mice::mice( dat, predictorMatrix=predM, m=3, maxit=4,
                  method=impMethod, allow.na=TRUE, pan.iter=100)

## End(Not run)

```

mice.impute.2lonly.function

Imputation at Level 2 (in miceadds)

Description

The imputation method `mice.impute.2lonly.function` is a general imputation function for level 2 imputation which allow any defined imputation function at level 1 in **mice**.

Usage

```
mice.impute.2lonly.function(y, ry, x, type, imputationFunction,
                           cluster_var, ...)
```

Arguments

<code>y</code>	Incomplete data vector of length <code>n</code>
<code>ry</code>	Vector of missing data pattern (FALSE=missing, TRUE=observed)
<code>x</code>	Matrix (<code>n x p</code>) of complete covariates. Only numeric variables are permitted for usage of this function.

type	Cluster identifier can be specified by -2 for aggregation. However, we recommend to use the argument <code>cluster_var</code> for specifying the cluster variable at Level 2. Predictors must be specified by 1.
imputationFunction	Imputation function for mice . Any imputation method which is defined at level 1 can be used for level 2 imputation.
cluster_var	Cluster identifier for Level 2 units
...	Other named arguments.

Value

A vector of length `nmis` with imputations.

See Also

See `mice::mice.impute.2lonly.norm` and the `mice::mice.impute.2lonly.pmm` function.

See also the **jomo** package (`jomo::jomo2`) for joint multilevel imputation of level 1 and level 2 variables.

Examples

```
## Not run:
#####
# EXAMPLE 1: Imputation of level 2 variables
#####

#**** Simulate some data
# x,y ... level 1 variables
# v,w ... level 2 variables

set.seed(987)
G <- 250      # number of groups
n <- 20      # number of persons
beta <- .3   # regression coefficient
rho <- .30   # residual intraclass correlation
rho.miss <- .10 # correlation with missing response
missrate <- .50 # missing proportion
y1 <- rep( stats::rnorm( G, sd=sqrt(rho)), each=n ) + stats::rnorm(G*n, sd=sqrt(1-rho))
w <- rep( round( stats::rnorm(G ), 2 ), each=n )
v <- rep( round( stats::runif( G, 0, 3 ) ), each=n )
x <- stats::rnorm( G*n )
y <- y1 + beta * x + .2 * w + .1 * v
dfr0 <- dfr <- data.frame( "group"=rep(1:G, each=n ), "x"=x, "y"=y,
                           "w"=w, "v"=v )
dfr[ rho.miss * x + stats::rnorm( G*n, sd=sqrt( 1 - rho.miss ) ) <
      stats::qnorm(missrate), y" ] <- NA
dfr[ rep( stats::rnorm(G), each=n ) < stats::qnorm(missrate), "w" ] <- NA
dfr[ rep( stats::rnorm(G), each=n ) < stats::qnorm(missrate), "v" ] <- NA

#* initial predictor matrix and imputation methods
predM <- mice::make.predictorMatrix(data=dat)
```

```

impM <- mice::make.method(data=dat)

#...
# multilevel imputation
predM1 <- predM
predM1[c("w","v","y"),"group"] <- c(0,0,-2)
predM1["y","x"] <- 1      # fixed x effects imputation
impM1 <- impM
impM1[c("y","w","v")] <- c("2l.continuous", "2lonly.function", "2lonly.function" )
# define imputation functions
imputationFunction <- list( "w"="sample", "v"="pmm5" )
# define cluster variable
cluster_var <- list( "w"="group", "v"="group" )

# impute
imp1 <- mice::mice( as.matrix(dfr), m=1, predictorMatrix=predM1, method=impM1, maxit=5,
                   imputationFunction=imputationFunction, cluster_var=cluster_var )

## End(Not run)

```

mice.impute.bygroup *Groupwise Imputation Function*

Description

The function `mice.impute.bygroup` performs groupwise imputation for arbitrary imputation methods defined in **mice**.

Usage

```
mice.impute.bygroup(y, ry, x, group, imputationFunction, ...)
```

Arguments

<code>y</code>	Incomplete data vector of length <code>n</code>
<code>ry</code>	Vector of missing data pattern (FALSE – missing, TRUE – observed)
<code>x</code>	Matrix (<code>n x p</code>) of complete covariates.
<code>group</code>	Name of grouping variable
<code>imputationFunction</code>	Imputation method for mice
<code>...</code>	More arguments to be passed to imputation function

Value

Vector of imputed values

Examples

```
## Not run:
#####
# EXAMPLE 1: Cluster-specific imputation for some variables
#####

library(mice)
data( data.ma01, package="miceadds")
dat <- data.ma01

# use sub-dataset
dat <- dat[ dat$idschool <=1006, ]
V <- ncol(dat)
# create initial predictor matrix and imputation methods
predictorMatrix <- matrix( 1, nrow=V, ncol=V)
diag(predictorMatrix) <- 0
rownames(predictorMatrix) <- colnames(predictorMatrix) <- colnames(dat)
predictorMatrix[, c("idstud", "studwgt", "urban" ) ] <- 0
method <- rep("norm", V)
names(method) <- colnames(dat)

*** groupwise imputation of variable books
method["books"] <- "bygroup"
# specify name of the grouping variable ('idschool') and imputation method ('norm')
group <- list( "books"="idschool" )
imputationFunction <- list("books"="norm" )

*** conduct multiple imputation in mice
imp <- mice::mice( dat, method=method, predictorMatrix=predictorMatrix,
                  m=1, maxit=1, group=group, imputationFunction=imputationFunction )

#####
# EXAMPLE 2: Group-wise multilevel imputation '2l.pan'
#####

library(mice)
data( data.ma01, package="miceadds" )
dat <- data.ma01

# select data
dat <- dat[, c("idschool", "hisei", "books", "female" ) ]
V <- ncol(dat)
dat <- dat[ ! is.na( dat$books), ]
# define factor variable

dat$books <- as.factor(dat$books)
# create initial predictor matrix and imputation methods
predictorMatrix <- matrix( 0, nrow=V, ncol=V)
rownames(predictorMatrix) <- colnames(predictorMatrix) <- colnames(dat)
predictorMatrix["idschool", ] <- 0
predictorMatrix[ "hisei", "idschool" ] <- -2
predictorMatrix[ "hisei", c("books", "female" ) ] <- 1
```

```

method <- rep("", V)
names(method) <- colnames(dat)
method["hisei"] <- "bygroup"
group <- list( "hisei"="female" )
imputationFunction <- list("hisei"="2l.pan" )

*** conduct multiple imputation in mice
imp <- mice::mice( dat, method=method, predictorMatrix=predictorMatrix,
                  m=1, maxit=1, group=group, imputationFunction=imputationFunction )
str(imp)

## End(Not run)

```

mice.impute.eap

Imputation of a Variable with a Known Posterior Distribution

Description

This function imputes values of a variable for which the mean and the standard deviation of the posterior distribution is known.

Usage

```
mice.impute.eap(y, ry, x, eap, ...)
```

Arguments

y	Incomplete data vector of length n
ry	Vector of missing data pattern (FALSE – missing, TRUE – observed)
x	Matrix (n x p) of complete covariates.
eap	List with means and standard deviations of the posterior distribution (see Examples). If for multiple variables posterior distributions are known, then it is a list named in which each list entry is named according th variable to be imputed and each list entry contains the variable's EAP and standard deviation of the EAP.
...	Further arguments to be passed

Value

A vector of length `nmis=sum(!ry)` with imputed values.

Examples

```

## Not run:
#####
# EXAMPLE 1: Imputation based on known posterior distribution
#####

data(data.ma03)

```

```

dat <- data.ma03

# definiere variable 'math_PV' as the plausible value imputation of math
dat$math_PV <- NA
vars <- colnames(dat)
dat1 <- as.matrix( dat[,vars] )

# define imputation methods
impmethod <- rep( "pmm", length(vars) )
names(impmethod) <- vars
# define plausible value imputation based on EAP and SEEAP for 'math_PV'
impmethod[ "math_PV" ] <- "eap"
eap <- list( "math_PV"=list( "M"=dat$math_EAP, "SE"=dat$math_SEEAP ) )
# define predictor matrix
pM <- 1 - diag(1,length(vars))
rownames(pM) <- colnames(pM) <- vars
pM[,c("idstud","math_EAP", "math_SEEAP") ] <- 0
  # remove some variables from imputation model

# imputation using three parallel chains
imp1 <- mice::mice( dat1, m=3, maxit=5, imputationMethod=impmethod,
  predictorMatrix=pM, allow.na=TRUE, eap=eap )
summary(imp1)  # summary

# imputation using one long chain
imp2 <- miceadds::mice.1chain( dat1, burnin=10, iter=20, Nimp=3,
  imputationMethod=impmethod, predictorMatrix=pM, allow.na=TRUE, eap=eap)
summary(imp2)  # summary

## End(Not run)

```

mice.impute.grouped *Imputation of a Variable with Grouped Values*

Description

Imputes a variable with continuous values whose original values are only available as grouped values.

Usage

```
mice.impute.grouped(y, ry, x, low=NULL, upp=NULL, ...)
```

Arguments

y	Incomplete data vector of length n
ry	Vector of missing data pattern (FALSE – missing, TRUE – observed)
x	Matrix (n x p) of complete covariates.
low	Vector with lower bound of grouping interval

upp Vector with upper bound of grouping interval
 ... Further arguments to be passed

Value

A vector of length `nmis=sum(!ry)` with imputed values.

See Also

This function uses the `grouped::grouped` function in the **grouped** package.

Examples

```
## Not run:
#####
# EXAMPLE 1: Imputation of grouped data
#####

data(data.ma06)
data <- data.ma06

# define the variable "FC_imp" which should contain the variables to be imputed
data$FC_imp <- NA
V <- ncol(data)
# variables not to be used for imputation
vars_elim <- c("id", "FC", "FC_low", "FC_upp")

# define imputation methods
impM <- rep("norm", V)
names(impM) <- colnames(data)
impM[ vars_elim ] <- ""
impM[ "FC_imp" ] <- "grouped"

# define predictor matrix
predM <- 1 - diag( 0, V)
rownames(predM) <- colnames(predM) <- colnames(data)
predM[vars_elim, ] <- 0
predM[,vars_elim] <- 0

# define lower and upper boundaries of the grouping intervals
low <- list("FC_imp"=data$FC_low )
upp <- list("FC_imp"=data$FC_upp )

# perform imputation
imp <- mice::mice( data, method=impM, predictorMatrix=predM,
                 m=1, maxit=3, allow.na=TRUE, low=low, upp=upp)
head( mice::complete(imp))

## End(Not run)
```

mice.impute.hotDeck *Imputation of a Variable Using Probabilistic Hot Deck Imputation*

Description

Imputes a variable under a random draw from a pool of donors defined by a distance function. Uncertainty with respect to the creation of donor pools is introduced by drawing a Bootstrap sample (approximate Bayesian Bootstrap, ABB) from observations with complete data (see Andridge & Little, 2010).

Usage

```
mice.impute.hotDeck(y, ry, x, donors=5, method="Mahalanobis", ...)
```

Arguments

y	Incomplete data vector of length n
ry	Vector of missing data pattern (FALSE – missing, TRUE – observed)
x	Matrix (n x p) of complete covariates.
donors	Number of donors used for random sampling of nearest neighbors in imputation
method	Method used for computation of weights in distance function. Options are the Mahalanobis metric (method="Mahalanobis"), weighted by correlations of covariates with the outcome (method="cor") and weighting by linear regression coefficients (method="lm").
...	Further arguments to be passed

Value

A vector of length `nmis=sum(!ry)` with imputed values.

References

Andridge, R. R., & Little, R. J. A. (2010). A review of hot deck imputation for survey non-response. *International Statistical Review*, 78, 40-64.

See Also

See also the packages **hot.deck** and **HotDeckImputation**.

Examples

```
## Not run:
#####
# EXAMPLE 1: Hot deck imputation NHANES dataset
#####

data(nhanes, package="mice")
```

```

dat <- nhanes

**** prepare imputation method
vars <- colnames(dat)
V <- length(vars)
impMethod <- rep("hotDeck", V)
method <- "cor"

**** imputation in mice
imp <- mice::mice( data=as.matrix(dat), m=1, method=impMethod, method=method )
summary(imp)

## End(Not run)

```

mice.impute.ml.lmer *Multilevel Imputation Using lme4*

Description

This function is a general imputation function based on the linear mixed effects model as implemented in `lme4::lmer`. The imputation model can be hierarchical or non-hierarchical and can be written in a general form $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \sum_{v=1}^V \mathbf{Z}_v \mathbf{u}_v$ for V multivariate random effects. While predictors can be selected by specifying the rows in the predictor matrix in `mice::mice` (i.e., modification of type), the level of random effects can be specified with `levels_id` and random slopes can be selected with `random_slopes`.

The function `mice.impute.ml.lmer` allows the imputation of variables at arbitrary levels. The corresponding level can be specified with `levels_id`. All predictor variables are aggregated to the corresponding level of the variable to be imputed.

Several strategies for the specification of the design matrix \mathbf{X} are accommodated. By default, predictors at a lower level are automatically aggregated to the higher level and included as further predictors to maintain the multilevel structure in the data (Grund, Luedtke & Robitzsch, 2018; Enders, Mistler & Keller, 2016; argument `aggregate_automatically=TRUE`). Further, interactions and quadratic effects can be defined by respective arguments `interactions` and `quadratics`. The dimension of the matrix of predictors can be reduced by applying partial least squares regression, see [mice.impute.pls](#).

The function now only allows continuous data (`model="continuous"`), ordinal data (`model="pmm"`) or binary data (`model="pmm"` or `model="binary"`). Nominal variables with missing values cannot (yet) be handled.

Usage

```

mice.impute.ml.lmer(y, ry, x, type, levels_id, variables_levels=NULL,
  random_slopes=NULL, aggregate_automatically=TRUE, intercept=TRUE,
  groupcenter.slope=FALSE, draw.fixed=TRUE, random.effects.shrinkage=1e-06,
  glmer.warnings=TRUE, model="continuous", donors=3, match_sampled_pars=FALSE,
  blme_use=FALSE, blme_args=NULL, pls.facs=0, interactions=NULL,
  quadratics=NULL, min.int.cor=0, min.all.cor=0, pls.print.progress=FALSE, ...)

```

Arguments

<code>y</code>	Incomplete data vector of length <code>n</code>
<code>ry</code>	Vector of missing data pattern (FALSE – missing, TRUE – observed)
<code>x</code>	Matrix ($n \times p$) of complete predictors.
<code>type</code>	Predictor variables associated with fixed effects.
<code>levels_id</code>	Specification of the level identifiers (see Examples)
<code>variables_levels</code>	Specification of the level of variables (see Examples)
<code>random_slopes</code>	Specification of random slopes (see Examples)
<code>aggregate_automatically</code>	Logical indicating whether aggregated effects at higher levels are automatically included.
<code>intercept</code>	Optional logical indicating whether the intercept should be included.
<code>groupcenter.slope</code>	Optional logical indicating whether covariates should be centered around group means
<code>draw.fixed</code>	Optional logical indicating whether fixed effects parameter should be randomly drawn
<code>random.effects.shrinkage</code>	Shrinkage parameter for stabilizing the covariance matrix of random effects
<code>glmer.warnings</code>	Optional logical indicating whether warnings from <code>glmer</code> should be displayed
<code>model</code>	Type of model. Can be "continuous" for normally distributed data, "binary" for dichotomous data specifying a logistic mixed effects model and "pmm" for predictive mean matching.
<code>donors</code>	Number of donors used for predictive mean matching
<code>match_sampled_pars</code>	Logical indicating whether values of nearest neighbors should also be sampled in pmm imputation.
<code>blme_use</code>	Logical indicating whether the blme package should be used.
<code>blme_args</code>	(Prior) Arguments for blme , see <code>blme::blmer</code> and <code>blme::bmerDist-class</code> .
<code>pls.fac</code>	Number of factors used in PLS dimension reduction
<code>interactions</code>	Specification of predictors with interaction effects
<code>quadratics</code>	Specification of predictors with quadratic effects
<code>min.int.cor</code>	Minimum absolute value of correlation with outcome for interaction effects to be retained
<code>min.all.cor</code>	Minimum absolute value of correlation with outcome for predictors to be retained
<code>pls.print.progress</code>	Logical indicating whether progress of algorithm should be displayed
<code>...</code>	Further arguments to be passed

Value

Vector of imputed values

References

Enders, C. K., Mistler, S. A., & Keller, B. T. (2016). Multilevel multiple imputation: A review and evaluation of joint modeling and chained equations imputation. *Psychological Methods*, 21(2), 222-240.

Grund, S., Luedtke, O., & Robitzsch, A. (2018). Multiple imputation of multilevel data in organizational research. *Organizational Research Methods*, 21(1), 111-149.

See Also

See [mice.impute.2l.continuous](#) for two-level imputation in **mice** and for several links to other packages which enable multilevel imputation.

Examples

```
## Not run:
#####
# EXAMPLE 1: Imputation of three-level data with normally distributed residuals
#####

data(data.ma07, package="miceadds")
dat <- data.ma07

# variables at level 1 (identifier id1): x1 (some missings), x2 (complete)
# variables at level 2 (identifier id2): y1 (some missings), y2 (complete)
# variables at level 3 (identifier id3): z1 (some missings), z2 (complete)

#####
# Imputation model 1

#----- specify levels of variables (only relevant for variables
#       with missing values)
variables_levels <- miceadds::mice_impute_create_type_vector( colnames(dat), value="")
# leave variables at lowest level blank (i.e., "")
variables_levels[ c("y1","y2") ] <- "id2"
variables_levels[ c("z1","z2") ] <- "id3"

#----- specify predictor matrix
predmat <- mice::make.predictorMatrix(data=dat)
predmat[ , c("id2", "id3") ] <- 0
# set -2 for cluster identifier for level 3 variable z1
# because "2lonly" function is used
predmat[ "z1", "id3" ] <- -2

#----- specify imputation methods
method <- mice::make.method(data=dat)
method[c("x1","y1")] <- "ml.lmer"
method[c("z1")] <- "2lonly.norm"
```

```

#----- specify hierarchical structure of imputation models
levels_id <- list()
#** hierarchical structure for variable x1
levels_id[["x1"]] <- c("id2", "id3")
#** hierarchical structure for variable y1
levels_id[["y1"]] <- c("id3")

#----- specify random slopes
random_slopes <- list()
#** random slopes for variable x1
random_slopes[["x1"]] <- list( "id2"=c("x2"), "id3"=c("y1") )
# if no random slopes should be specified, the corresponding entry can be left empty
# and only a random intercept is used in the imputation model

#----- imputation in mice
imp1 <- mice::mice( dat, maxit=10, m=5, method=method,
  predictorMatrix=predmat, levels_id=levels_id, random_slopes=random_slopes,
  variables_levels=variables_levels )
summary(imp1)

#*****
# Imputation model 2

#----- impute x1 with predictive mean matching and y1 with normally distributed residuals
model <- list( x1="pmm", y1="continuous" )

#----- assume only random intercepts
random_slopes <- NULL

#---- create interactions with z2 for all predictors in imputation models for x1 and y1
interactions <- list( "x1"=z2, "y1"=z2)

#----- imputation in mice
imp2 <- mice::mice( dat, method=method, predictorMatrix=predmat,
  levels_id=levels_id, random_slopes=random_slopes,
  variables_levels=variables_levels, model=model, interactions=interactions)
summary(imp2)

## End(Not run)

```

mice.impute.plausible.values

*Plausible Value Imputation using Classical Test Theory and Based on
Individual Likelihood*

Description

This imputation function performs unidimensional plausible value imputation if (subject-wise) measurement errors or the reliability of the scale is known (Mislevy, 1991; see also Asparouhov &

Muthen, 2010; Blackwell, Honaker & King, 2011, 2017a, 2017b). The function also allows the input of an individual likelihood obtained by fitting an item response model.

Usage

```
mice.impute.plausible.values(y, ry, x, type, alpha=NULL,
  alpha.se=0, scale.values=NULL, sig.e.miss=1e+06,
  like=NULL, theta=NULL, normal.approx=NULL,
  pviter=15, imputationWeights=rep(1, length(y)), plausible.value.print=TRUE,
  pls.facs=NULL, interactions=NULL, quadratics=NULL, extract_data=TRUE,
  control_latreg=list( progress=FALSE, ridge=1e-5 ), ...)
```

Arguments

<code>y</code>	Incomplete data vector of length <code>n</code>
<code>ry</code>	Vector of missing data pattern (FALSE – missing, TRUE – observed)
<code>x</code>	Matrix ($n \times p$) of complete covariates.
<code>type</code>	Type of predictor variables. <code>type=3</code> refers to items belonging to a scale to be imputed. A cluster (grouping) variable is defined by <code>type=-2</code> . If for some predictors, the cluster means should also be included as predictors, then specify <code>type=2</code> (see Imputation Model 3 of Example 1).
<code>alpha</code>	A known reliability estimate. An optional standard error of the estimate can be provided in <code>alpha.se</code>
<code>alpha.se</code>	Optional numeric value of the standard error of the alpha reliability estimate if in every iteration a new reliability should be sampled.
<code>scale.values</code>	A list consisting of scale values of scale values and its corresponding standard errors (see Example 1).
<code>sig.e.miss</code>	A standard error of measurement for cases with missing values on a scale
<code>like</code>	Individual likelihood evaluated at <code>theta</code>
<code>theta</code>	Grid of unidimensional latent variable
<code>normal.approx</code>	Logical indicating whether the individual posterior should be approximated by a normal distribution
<code>pviter</code>	Number of iterations in each imputation which should be run until the plausible values are drawn
<code>imputationWeights</code>	Optional vector of sample weights
<code>plausible.value.print</code>	An optional logical indicating whether some information about the plausible value imputation should be printed at the console
<code>pls.facs</code>	Number of PLS factors if PLS dimension reduction is used
<code>interactions</code>	Vector of variable names used for creating interactions
<code>quadratics</code>	Vector of variable names used for creating quadratic terms
<code>extract_data</code>	Logical indicating whether input data should be extracted from parent environment within <code>mice::mice</code> routine
<code>control_latreg</code>	Control arguments for <code>TAM::tam.latreg</code>
<code>...</code>	Further objects to be passed

Details

The linear model is assumed for drawing plausible values of a variable Y contaminated by measurement error. Assuming $Y = \theta + e$ and a linear regression model for θ

$$\theta = \mathbf{X}\beta + \epsilon$$

(plausible value) imputations from the posterior distribution $P(\theta|Y, \mathbf{X})$ are drawn. See Mislevy (1991) for details.

Value

A vector of length `nrow(x)` containing imputed plausible values.

Note

Plausible value imputation is also known as multiple overimputation (Blackwell, Honaker & King, 2016a, 2016b) which is implemented in the **Amelia** package, see `Amelia::moPrep` and `Amelia::amelia`.

References

Asparouhov, T., & Muthen, B. (2010). *Plausible values for latent variables using Mplus*. Technical Report. <https://www.statmodel.com/papers.shtml>

Blackwell, M., Honaker, J., & King, G. (2011). *Multiple overimputation: A unified approach to measurement error and missing data*. Technical Report.

Blackwell, M., Honaker, J., & King, G. (2017a). A unified approach to measurement error and missing data: Overview and applications. *Sociological Methods & Research*, 46(3), 303-341.

Blackwell, M., Honaker, J., & King, G. (2017b). A unified approach to measurement error and missing data: Details and extensions. *Sociological Methods & Research*, 46(3), 342-369.

Mislevy, R. J. (1991). Randomization-based inference about latent variables from complex samples. *Psychometrika*, 56, 177-196.

See Also

See `TAM::tam.latreg` for fitting latent regression models.

Examples

```
## Not run:
#####
# EXAMPLE 1: Plausible value imputation for data.ma04 | 2 scales
#####

data(data.ma04, package="miceadds")
dat <- data.ma04

# Scale 1 consists of items A1,...,A4
# Scale 2 consists of items B1,...,B5
dat$scale1 <- NA
dat$scale2 <- NA
```

```

*** inits imputation method and predictor matrix
res <- miceadds::mice_inits(dat, ignore=c("group") )
predM <- res$predictorMatrix
impMethod <- res$method
impMethod <- gsub("pmm", "norm", impMethod )

# look at missing proportions
colSums( is.na(dat) )

# redefine imputation methods for plausible value imputation
impMethod[ "scale1" ] <- "plausible.values"
predM[ "scale1", ] <- 1
predM[ "scale1", c("A1", "A2", "A3", "A4" ) ] <- 3
  # items corresponding to a scale should be declared by a 3 in the predictor matrix
impMethod[ "scale2" ] <- "plausible.values"
predM[,"scale2" ] <- 0
predM[ "scale2", c("A2","A3","A4","V6","V7") ] <- 1
diag(predM) <- 0

# use imputed scale values as predictors for V5, V6 and V7
predM[ c("V5","V6","V7"), c("scale1","scale2" ) ] <- 1
# exclude for V5, V6 and V7 the items of scales A and B as predictors
predM[ c("V5","V6","V7"), c( paste0("A",2:4), paste0("B",1:5) ) ] <- 0
# exclude 'group' as a predictor
predM[,"group"] <- 0

# look at imputation method and predictor matrix
impMethod
predM

#-----
# Parameter for imputation
***
# scale 1 (A1,...,A4)
# known Cronbach's Alpha
alpha <- NULL
alpha <- list( "scale1"=.8 )
alpha.se <- list( "scale1"=.05 ) # sample alpha with a standard deviation of .05

***
# scale 2 (B1,...,B5)
# means and SE's of scale scores are assumed to be known
M.scale2 <- rowMeans( dat[, paste("B",1:5,sep="") ] )
# M.scale2[ is.na( m1) ] <- mean( M.scale2, na.rm=TRUE )
SE.scale2 <- rep( sqrt( stats::var(M.scale2,na.rm=T)*(1-.8) ), nrow(dat) )
#=> heterogeneous measurement errors are allowed
scale.values <- list( "scale2"=list( "M"=M.scale2, "SE"=SE.scale2 ) )

*** Imputation Model 1: Imputation four using parallel chains
imp1 <- mice::mice( dat, predictorMatrix=predM, m=4, maxit=5,
  alpha.se=alpha.se, method=impMethod, allow.na=TRUE, alpha=alpha,
  scale.values=scale.values )

```



```

summary(imp1)

# extract first imputed dataset
dat11 <- mice::complete( imp, 1 )

#### Imputation Model 2: Imputation using one long chain
imp2 <- miceadds::mice.1chain( dat, predictorMatrix=predM, burnin=10, iter=20, Nimp=4,
                             alpha.se=alpha.se, method=impMethod, allow.na=TRUE, alpha=alpha,
                             scale.values=scale.values )
summary(imp2)

#-----
#### Imputation Model 3: Imputation including group level variables

# use group indicator for plausible value estimation
predM[ "scale1", "group" ] <- -2
# V7 and B1 should be aggregated at the group level
predM[ "scale1", c("V7","B1") ] <- 2
predM[ "scale2", "group" ] <- -2
predM[ "scale2", c("V7","A1") ] <- 2

# perform single imputation (m=1)
imp <- mice::mice( dat, predictorMatrix=predM, m=1, maxit=10,
                  method=impMethod, allow.na=TRUE, alpha=alpha,
                  scale.values=scale.values )
dat10 <- mice::complete(imp)

# multilevel model
library(lme4)
mod <- lme4::lmer( scale1 ~ ( 1 | group), data=dat11 )
summary(mod)

mod <- lme4::lmer( scale1 ~ ( 1 | group), data=dat10)
summary(mod)

#####
# EXAMPLE 2: Plausible value imputation with chained equations
#####

# - simulate a latent variable theta and dichotomous item responses
# - two covariates X in which the second covariate has measurement error

library(sirt)
library(TAM)
library(lavaan)

set.seed(7756)
N <- 2000 # number of persons
I <- 10 # number of items

# simulate covariates
X <- MASS::mvrnorm( N, mu=c(0,0), Sigma=matrix( c(1,.5,.5,1),2,2 ) )
colnames(X) <- paste0("X",1:2)

```

```

# second covariate with measurement error with variance var.err
var.err <- .3
X.err <- X
X.err[,2] <- X[,2] + stats::rnorm(N, sd=sqrt(var.err) )
# simulate theta
theta <- .5*X[,1] + .4*X[,2] + stats::rnorm( N, sd=.5 )
# simulate item responses
itemdiff <- seq( -2, 2, length=I) # item difficulties
dat <- sirt::sim.raschtype( theta, b=itemdiff )

#*****
#*** Model 0: Regression model with true variables
mod0 <- stats::lm( theta ~ X )
summary(mod0)

#*****
# plausible value imputation for abilities and error-prone
# covariates using the mice package

# creating the likelihood for plausible value for abilities
mod11 <- TAM::tam.mml( dat )
likePV <- IRT.likelihood(mod11)
# creating the likelihood for error-prone covariate X2
# The known measurement error variance is 0.3.
lavmodel <- "
  X2true=~ 1*X2
  X2 ~~ 0.3*X2
  "
mod12 <- lavaan::cfa( lavmodel, data=as.data.frame(X.err) )
summary(mod12)
likeX2 <- IRTLikelihood.cfa( data=X.err, cfaobj=mod12)
str(likeX2)

#-- create data input for mice package
data <- data.frame( "PVA"=NA, "X1"=X[,1], "X2"=NA )
vars <- colnames(data)
V <- length(vars)
predictorMatrix <- 1 - diag(V)
rownames(predictorMatrix) <- colnames(predictorMatrix) <- vars
method <- rep("norm", V )
names(method) <- vars
method[c("PVA","X2")] <- "plausible.values"

#-- create argument lists for plausible value imputation
# likelihood and theta grid of plausible value derived from IRT model
like <- list( "PVA"=likePV, "X2"=likeX2 )
theta <- list( "PVA"=attr(likePV,"theta"),
              "X2"=attr(likeX2, "theta") )

#-- initial imputations
data.init <- data
data.init$PVA <- mod11$person$EAP
data.init$X2 <- X.err[, "X2"]

```

```

#-- imputation using the mice and miceadds package
imp1 <- mice::mice( as.matrix(data), predictorMatrix=predictorMatrix, m=4,
                  maxit=6, method=method, allow.na=TRUE,
                  theta=theta, like=like, data.init=data.init )
summary(imp1)

# compute linear regression
mod4a <- with( imp1, stats::lm( PVA ~ X1 + X2 ) )
summary( mice::pool(mod4a) )

#####
# EXAMPLE 3: Plausible value imputation with known error variance
#####

#--- simulate data
set.seed(987)
N <- 1000      # number of persons
var_err <- .4  # error variance
dat <- data.frame( x1=stats::rnorm(N), x2=stats::rnorm(N) )
dat$theta <- .3 * dat$x1 - .5*dat$x2 + stats::rnorm(N)
dat$y <- dat$theta + stats::rnorm( N, sd=sqrt(var_err) )

#-- linear regression for measurement-error-free data
mod0a <- stats::lm( theta ~ x1 + x2, data=dat )
summary(mod0a)
#-- linear regression for data with measurement error
mod0b <- stats::lm( y ~ x1 + x2, data=dat )
summary(mod0b)

#-- process data for imputation

dat1 <- dat
dat1$theta <- NA
scale.values <- list( "theta"=list( "M"=dat$y, "SE"=rep(sqrt(var_err),N) ))
dat1$y <- NULL

cn <- colnames(dat1)
V <- length(cn)
method <- rep("", length(cn) )
names(method) <- cn
method["theta"] <- "plausible.values"

#-- imputation in mice
imp <- mice::mice( dat1, maxit=1, m=5, allow.na=TRUE, method=method,
                  scale.values=scale.values )
summary(imp)

#-- inspect first dataset
summary( mice::complete(imp, action=1) )

#-- linear regression based on imputed datasets
mod1 <- with(imp, stats::lm( theta ~ x1 + x2 ) )
summary( mice::pool(mod1) )

```

```
## End(Not run)
```

```
mice.impute.pls
```

```
Imputation using Partial Least Squares for Dimension Reduction
```

Description

This function imputes a variable with missing values using PLS regression (Mevik & Wehrens, 2007) for a dimension reduction of the predictor space.

Usage

```
mice.impute.pls(y, ry, x, type, pls.facs=NULL,
  pls.impMethod="pmm", pls.impMethodArgs=NULL, pls.print.progress=TRUE,
  imputationWeights=rep(1, length(y)), pcamaxcols=1E+09,
  min.int.cor=0, min.all.cor=0, N.largest=0, pls.title=NULL, print.dims=TRUE,
  pls.maxcols=5000, envir_pos=NULL, extract_data=TRUE, ...)

mice.impute.2l.pls2(y, ry, x, type, pls.facs=NULL, pls.impMethod="pmm",
  pls.print.progress=TRUE, imputationWeights=rep(1, length(y)), pcamaxcols=1E+09,
  tricube.pmm.scale=NULL, min.int.cor=0, min.all.cor=0, N.largest=0,
  pls.title=NULL, print.dims=TRUE, pls.maxcols=5000, envir_pos=parent.frame(), ...)
```

Arguments

y	Incomplete data vector of length n
ry	Vector of missing data pattern (FALSE – missing, TRUE – observed)
x	Matrix (n x p) of complete covariates.
type	type=1 – variable is used as a predictor, type=4 – create interactions with the specified variable with all other predictors, type=5 – create a quadratic term of the specified variable type=6 – if some interactions are specified, ignore the variables with entry 6 when creating interactions type=-2 – specification of a cluster variable. The cluster mean of the outcome y (when eliminating the subject under study) is included as a further predictor in the imputation.
pls.facs	Number of factors used in PLS regression. This argument can also be specified as a list defining different numbers of factors for all variables to be imputed.
pls.impMethod	Imputation method used for in PLS estimation. Any imputation method can be used except if <code>imputationWeights</code> is provided. Then, only <code>norm</code> and <code>pmm</code> are available. The method <code>xpls.facs</code> creates only PLS factors of the regression model.
pls.impMethodArgs	Arguments for imputation method <code>pls.impMethod</code> .

pls.print.progress	Print progress during PLS regression.
imputationWeights	Vector of sample weights to be used in imputation models.
pcamaxcols	Amount of variance explained by principal components (must be a number between 0 and 1)
min.int.cor	Minimum absolute correlation for an interaction of two predictors to be included in the PLS regression model
min.all.cor	Minimum absolute correlation for inclusion in the PLS regression model.
N.largest	Number of variable to be included which do have the largest absolute correlations.
pls.title	Title for progress print in console output.
print.dims	An optional logical indicating whether dimensions of inputs should be printed.
pls.maxcols	Maximum number of interactions to be created.
envir_pos	Position of the environment from which the data should be extracted.
extract_data	Logical indicating whether input data should be extracted from parent environment within <code>mice::mice</code> routine
...	Further arguments to be passed.
tricube.pmm.scale	Scale factor for tricube PMM imputation.

Value

A vector of length `nmis=sum(!ry)` with imputations if `pls.impMethod != "xplsfac"`. In case of `pls.impMethod=="xplsfac"` a matrix with PLS factors is computed.

Note

The `mice.impute.2l.pls2` function is just included for reasons of backward compatibility to former **miceadds** versions.

References

Mevik, B. H., & Wehrens, R. (2007). The **pls** package: Principal component and partial least squares regression in R. *Journal of Statistical Software*, 18, 1-24.

Examples

```
## Not run:
#####
# EXAMPLE 1: PLS imputation method for internet data
#####

data(data.internet)
dat <- data.internet

# specify predictor matrix
```

```

predictorMatrix <- matrix( 1, ncol(dat), ncol(dat) )
rownames(predictorMatrix) <- colnames(predictorMatrix) <- colnames(dat)
diag( predictorMatrix) <- 0

# use PLS imputation method for all variables
impMethod <- rep( "pls", ncol(dat) )
names(impMethod) <- colnames(dat)

# define predictors for interactions (entries with type 4 in predictorMatrix)
predictorMatrix[c("IN1","IN15","IN16"),c("IN1","IN3","IN10","IN13")] <- 4
# define predictors which should appear as linear and quadratic terms (type 5)
predictorMatrix[c("IN1","IN8","IN9","IN10","IN11"),c("IN1","IN2","IN7","IN5")] <- 5

# use 9 PLS factors for all variables
pls.facs <- as.list( rep( 9, length(impMethod) ) )
names(pls.facs) <- names(impMethod)
pls.facs$IN1 <- 15 # use 15 PLS factors for variable IN1

# choose norm or pmm imputation method
pls.impMethod <- as.list( rep("norm", length(impMethod) ) )
names(pls.impMethod) <- names(impMethod)
pls.impMethod[ c("IN1","IN6")] <- "pmm5"

# some arguments for imputation method
pls.impMethodArgs <- list( "IN1"=list( "donors"=10 ),
                          "IN2"=list( "ridge2"=1E-4 ) )

# Model 1: Three parallel chains
imp1 <- mice::mice(data=dat, method=impMethod,
  m=3, maxit=5, predictorMatrix=predictorMatrix,
  pls.facs=pls.facs, # number of PLS factors
  pls.impMethod=pls.impMethod, # Imputation Method in PLS imputation
  pls.impMethodArgs=pls.impMethodArgs, # arguments for imputation method
  pls.print.progress=TRUE, ls.meth="ridge" )
summary(imp1)

# Model 2: One long chain
imp2 <- miceadds::mice.1chain(data=dat, method=impMethod,
  burnin=10, iter=21, Nimp=3, predictorMatrix=predictorMatrix,
  pls.facs=pls.facs, pls.impMethod=pls.impMethod,
  pls.impMethodArgs=pls.impMethodArgs, ls.meth="ridge" )
summary(imp2)

## End(Not run)

```

Description

This function imputes values by predictive mean matching like the `mice::mice.impute.pmm` method in the **mice** package.

Usage

```
mice.impute.pmm3(y, ry, x, donors=3, noise=10^5, ridge=10^(-5), ...)
mice.impute.pmm4(y, ry, x, donors=3, noise=10^5, ridge=10^(-5), ...)
mice.impute.pmm5(y, ry, x, donors=3, noise=10^5, ridge=10^(-5), ...)
mice.impute.pmm6(y, ry, x, donors=3, noise=10^5, ridge=10^(-5), ...)
```

Arguments

<code>y</code>	Incomplete data vector of length n
<code>ry</code>	Vector of missing data pattern (FALSE – missing, TRUE – observed)
<code>x</code>	Matrix ($n \times p$) of complete covariates.
<code>donors</code>	Number of donors used for imputation
<code>noise</code>	Numerical value to break ties
<code>ridge</code>	Ridge parameter in the diagonal of $X'X$
<code>...</code>	Further arguments to be passed

Details

The imputation method `pmm3` imitates `mice::mice.impute.pmm` imputation method in **mice**.

The imputation method `pmm4` ignores ties in predicted y values. With many predictors, this does not probably implies any substantial problem.

The imputation method `pmm5` suffers from the same problem. Contrary to the other PMM methods, it searches D donors (specified by `donors`) smaller than the predicted value and D donors larger than the predicted value and randomly samples a value from this set of $2 \cdot D$ donors.

The imputation method `pmm6` is just the **Rcpp** implementation of `pmm5`.

Value

A vector of length `nmis=sum(!ry)` with imputed values.

See Also

See `data.largescale` and `data.smallscale` for speed comparisons of different functions for predictive mean matching.

Examples

```
## Not run:
#####
# SIMULATED EXAMPLE 1: Two variables x and y with missing y
#####
set.seed(1413)
```

```

rho <- .6 # correlation between x and y
N <- 6800 # number of cases
x <- stats::rnorm(N)
My <- .35 # mean of y
y.com <- y <- My + rho * x + stats::rnorm(N, sd=sqrt( 1 - rho^2 ) )

# create missingness on y depending on rho.MAR parameter
rho.mar <- .4 # correlation response tendency z and x
missrate <- .25 # missing response rate
# simulate response tendency z and missings on y
z <- rho.mar * x + stats::rnorm(N, sd=sqrt( 1 - rho.mar^2 ) )
y[ z < stats::qnorm( missrate ) ] <- NA
dat <- data.frame(x, y )

# mice imputation
impmethod <- rep("pmm", 2 )
names(impmethod) <- colnames(dat)

# pmm (in mice)
imp1 <- mice::mice( as.matrix(dat), m=1, maxit=1, imputationMethod=impmethod)
# pmm3 (in miceadds)
imp3 <- mice::mice( as.matrix(dat), m=1, maxit=1,
  imputationMethod=gsub("pmm","pmm3",impmethod) )
# pmm4 (in miceadds)
imp4 <- mice::mice( as.matrix(dat), m=1, maxit=1,
  imputationMethod=gsub("pmm","pmm4",impmethod) )
# pmm5 (in miceadds)
imp5 <- mice::mice( as.matrix(dat), m=1, maxit=1,
  imputationMethod=gsub("pmm","pmm5",impmethod) )
# pmm6 (in miceadds)
imp6 <- mice::mice( as.matrix(dat), m=1, maxit=1,
  imputationMethod=gsub("pmm","pmm6",impmethod) )

dat.imp1 <- mice::complete( imp1, 1 )
dat.imp3 <- mice::complete( imp3, 1 )
dat.imp4 <- mice::complete( imp4, 1 )
dat.imp5 <- mice::complete( imp5, 1 )
dat.imp6 <- mice::complete( imp6, 1 )

dfr <- NULL
# means
dfr <- rbind( dfr, c( mean( y.com ), mean( y, na.rm=TRUE ), mean( dat.imp1$y),
  mean( dat.imp3$y), mean( dat.imp4$y), mean( dat.imp5$y), mean( dat.imp6$y) ) )
# SD
dfr <- rbind( dfr, c( stats::sd( y.com ), stats::sd( y, na.rm=TRUE ),
  stats::sd( dat.imp1$y), stats::sd( dat.imp3$y), stats::sd( dat.imp4$y),
  stats::sd( dat.imp5$y), stats::sd( dat.imp6$y) ) )
# correlations
dfr <- rbind( dfr, c( stats::cor( x,y.com ),
  stats::cor( x[ ! is.na(y) ], y[ ! is.na(y) ] ),
  stats::cor( dat.imp1$x, dat.imp1$y), stats::cor( dat.imp3$x, dat.imp3$y),
  stats::cor( dat.imp4$x, dat.imp4$y), stats::cor( dat.imp5$x, dat.imp5$y),

```



```

stats::cor( dat.imp6$x, dat.imp6$y)
) )
rownames(dfr) <- c("M_y", "SD_y", "cor_xy" )
colnames(dfr) <- c("compl", "ld", "pmm", "pmm3", "pmm4", "pmm5", "pmm6")
##      compl   ld   pmm  pmm3  pmm4  pmm5  pmm6
## M_y    0.3306 0.4282 0.3314 0.3228 0.3223 0.3264 0.3310
## SD_y   0.9910 0.9801 0.9873 0.9887 0.9891 0.9882 0.9877
## cor_xy 0.6057 0.5950 0.6072 0.6021 0.6100 0.6057 0.6069

## End(Not run)

```

```
mice.impute.tricube.pmm
```

Imputation by Tricube Predictive Mean Matching

Description

This function performs tricube predictive mean matching (see `{Hmisc::aregImpute}`) in which donors are weighted according to distances of predicted values.

Usage

```
mice.impute.tricube.pmm(y, ry, x, tricube.pmm.scale=0.2, tricube.boot=FALSE, ...)
```

```
mice.impute.tricube.pmm2(y, ry, x, tricube.pmm.scale=0.2, tricube.boot=FALSE, ...)
```

Arguments

<code>y</code>	Incomplete data vector of length <code>n</code>
<code>ry</code>	Vector of missing data pattern (FALSE – missing, TRUE – observed)
<code>x</code>	Matrix (<code>n x p</code>) of complete covariates.
<code>tricube.pmm.scale</code>	A scaling factor for traicube matching. The default is 0.2.
<code>tricube.boot</code>	A logical indicating whether tricube matching should be performed using a bootstrap sample
<code>...</code>	Further arguments to be passed

Value

A vector of length `nmis=sum(!ry)` with imputed values.

Note

The imputation method `tricube.pmm2` is usually somewhat faster than `tricube.pmm`.

See Also

`{Hmisc::aregImpute}`

Examples

```
## Not run:
#####
# EXAMPLE 1: Tricube predictive mean matching for nhanes data
#####

library(mice)
data(nhanes, package="mice")
set.seed(9090)

#### Model 1: Use default of tricube predictive mean matching
varnames <- colnames(nhanes)
VV <- length(varnames)
method <- rep("tricube.pmm2", VV )
names(method) <- varnames
# imputation with mice
imp.mi1 <- mice::mice( nhanes, m=5, maxit=4, method=method )

#### Model 2: use item-specific imputation methods
iM2 <- method
iM2["bmi"] <- "pmm6"
# use tricube.pmm2 for hyp and chl
# select different scale parameters for these variables
tricube.pmm.scale1 <- list( "hyp"=.15, "chl"=.30 )
imp.mi2 <- miceadds::mice.1chain( nhanes, burnin=5, iter=20, Nimp=4,
  method=iM2, tricube.pmm.scale=tricube.pmm.scale1 )

## End(Not run)
```

mice.impute.weighted.pmm

Imputation by Weighted Predictive Mean Matching or Weighted Normal Linear Regression

Description

Imputation by predictive mean matching or normal linear regression using sampling weights.

Usage

```
mice.impute.weighted.pmm(y, ry, x, imputationWeights=NULL,
  pls.facs=NULL, interactions=NULL, quadratics=NULL, ...)

mice.impute.weighted.norm(y, ry, x, ridge=1e-05, pls.facs=NULL,
  imputationWeights=NULL, interactions=NULL, quadratics=NULL, ...)
```

Arguments

y	Incomplete data vector of length n
ry	Vector of missing data pattern (FALSE – missing, TRUE – observed)
x	Matrix (n x p) of complete covariates.
imputationWeights	Optional vector of sampling weights
pls.facs	Number of factors in PLS regression (if used). The default is NULL which means that no PLS regression is used for dimension reduction.
interactions	Optional vector of variables for which interactions should be created
quadratics	Optional vector of variables which should also be included as quadratic effects.
...	Further arguments to be passed
ridge	Ridge parameter in the diagonal of $X'X$

Value

A vector of length $\text{nmis}=\text{sum}(!\text{ry})$ with imputed values.

Examples

```
## Not run:
#####
# EXAMPLE 1: Imputation using sample weights
#####

data( data.ma01)
set.seed(977)

# select subsample
dat <- as.matrix(data.ma01)
dat <- dat[ 1:1000, ]

# empty imputation
imp0 <- mice::mice( dat, maxit=0)

# redefine imputation methods
meth <- imp0$method
meth[ meth=="pmm" ] <- "weighted.pmm"
meth[ c("paredu", "books", "migrant" ) ] <- "weighted.norm"
# redefine predictor matrix
pm <- imp0$predictorMatrix
pm[, 1:3 ] <- 0
# do imputation
imp <- mice::mice( dat, predictorMatrix=pm, method=meth,
                  imputationWeights=dat[, "studwgt"], m=3, maxit=5)

## End(Not run)
```

mice.nmi

Nested Multiple Imputation

Description

Performs nested multiple imputation (Rubin, 2003) for the functions `mice::mice` and `mice.1chain`. The function `mice.nmi` generates an object of class `mids.nmi`.

Usage

```
mice.nmi(datlist, type="mice", ...)

## S3 method for class 'mids.nmi'
summary(object, ...)

## S3 method for class 'mids.nmi'
print(x, ...)
```

Arguments

<code>datlist</code>	List of datasets for which nested multiple imputation should be applied
<code>type</code>	Imputation model: <code>type="mice"</code> for <code>mice::mice</code> or <code>type="mice.1chain"</code> for <code>mice.1chain</code> .
<code>...</code>	Arguments to be passed to <code>mice::mice</code> or <code>mice.1chain</code> .
<code>object</code>	Object of class <code>mids.nmi</code> .
<code>x</code>	Object of class <code>mids.nmi</code> .

Value

Object of class `mids.nmi` with entries

<code>imp</code>	List of nested multiply imputed datasets whose entries are of class <code>mids</code> or <code>mids.1chain</code> .
<code>Nimp</code>	Number of between and within imputations.

References

Rubin, D. B. (2003). Nested multiple imputation of NMES via partially incompatible MCMC. *Statistica Neerlandica*, 57(1), 3-18.

See Also

For imputation models see `mice::mice` and `mice.1chain`.

Functions for analyses of nested multiply imputed datasets: `complete.mids.nmi`, `with.mids.nmi`, `pool.mids.nmi`

Examples

```
## Not run:
#####
# EXAMPLE 1: Nested multiple imputation for TIMSS data
#####

library(BIFIEsurvey)
data(data.timss2, package="BIFIEsurvey" )
datlist <- data.timss2
  # list of 5 datasets containing 5 plausible values

##* define imputation method and predictor matrix
data <- datlist[[1]]
V <- ncol(data)
# variables
vars <- colnames(data)
# variables not used for imputation
vars_unused <- miceadds::scan.vec("IDSTUD TOTWGT JKZONE JKREP" )

#- define imputation method
impMethod <- rep("norm", V )
names(impMethod) <- vars
impMethod[ vars_unused ] <- ""

#- define predictor matrix
predM <- matrix( 1, V, V )
colnames(predM) <- rownames(predM) <- vars
diag(predM) <- 0
predM[, vars_unused ] <- 0

#####
# (1) nested multiple imputation using mice
imp1 <- miceadds::mice.nmi( datlist, method=impMethod, predictorMatrix=predM,
  m=4, maxit=3 )
summary(imp1)

#####
# (2) nested multiple imputation using mice.1chain
imp2 <- miceadds::mice.nmi( datlist, method=impMethod, predictorMatrix=predM,
  Nimp=4, burnin=10, iter=22, type="mice.1chain")
summary(imp2)

## End(Not run)
```

Description

These functions have been removed or replaced in the **miceadds** package.

Usage

```
fast.groupmean(...)
fast.groupsum(...)
mice.impute.2l.eap(...)
mice.impute.2l.plausible.values(...)
mice.impute.2l.pls(...)
mice.impute.2lonly.norm2(...)
mice.impute.2lonly.pmm2(...)
```

Arguments

... Arguments to be passed.

Details

The `fast.groupmean` function has been replaced by [GroupMean](#).

The `fast.groupsum` function has been replaced by [GroupSum](#).

The `mice.impute.2l.eap` function has been replaced by [mice.impute.eap](#).

The `mice.impute.2l.plausible.values` function has been replaced by [mice.impute.plausible.values](#).

The `mice.impute.2l.pls2` function has been replaced by [mice.impute.pls](#).

The `mice.impute.2lonly.norm2` and `mice.impute.2lonly.pmm2` functions can be safely replaced by the `mice::mice.impute.2lonly.norm` and `mice::mice.impute.2lonly.pmm` functions in the **mice** package.

miceadds-utilities *Utility Functions in **miceadds***

Description

Utility functions in **miceadds**.

Usage

```
## searches for objects in parent environments
ma_exists_get( x, pos, n_index=1:8)
ma_exists( x, pos, n_index=1:8)
```

Arguments

x	Object name (character)
pos	Environment
n_index	Levels in parent.frame in which object is searched

Details

The function `ma_exists_get` is used in `miceadds:::mice_imputation_get_states`.

mice_impute_2l_lmer *Imputation of a Continuous or a Binary Variable From a Two-Level Regression Model using **lme4** or **blme***

Description

The function `mice.impute.2l.continuous` imputes values of continuous variables with a linear mixed effects model using `lme4::lmer` or `blme::blmer`. The `lme4::lmer` or `blme::blmer` function is also used for predictive mean matching where the match is based on predicted values which contain the fixed and (sampled) random effects. Binary variables can be imputed from a two-level logistic regression model fitted with the `lme4::glmer` or `blme::bglmer` function. See Snijders and Bosker (2012) and Zinn (2013) for details.

Usage

```
mice.impute.2l.continuous(y, ry, x, type, intercept=TRUE,
  groupcenter.slope=FALSE, draw.fixed=TRUE, random.effects.shrinkage=1E-6,
  glmer.warnings=TRUE, blme_use=FALSE, blme_args=NULL, ... )
```

```
mice.impute.2l.pmm(y, ry, x, type, intercept=TRUE,
  groupcenter.slope=FALSE, draw.fixed=TRUE, random.effects.shrinkage=1E-6,
  glmer.warnings=TRUE, donors=5, match_sampled_pars=TRUE,
  blme_use=FALSE, blme_args=NULL, ... )
```

```
mice.impute.2l.binary(y, ry, x, type, intercept=TRUE,
  groupcenter.slope=FALSE, draw.fixed=TRUE, random.effects.shrinkage=1E-6,
  glmer.warnings=TRUE, blme_use=FALSE, blme_args=NULL, ... )
```

Arguments

<code>y</code>	Incomplete data vector of length <code>n</code>
<code>ry</code>	Vector of missing data pattern (FALSE – missing, TRUE – observed)
<code>x</code>	Matrix (<code>n x p</code>) of complete predictors.
<code>type</code>	Type of predictor variable. The cluster identifier has type -2, fixed effects predictors without a random slope type 1 and predictors with fixed effects and random effects have type 2. If the cluster mean should be included for a covariate, 3 should be chosen. The specification 4 includes the cluster mean, the fixed effect and the random effect.
<code>intercept</code>	Optional logical indicating whether the intercept should be included.
<code>groupcenter.slope</code>	Optional logical indicating whether covariates should be centered around group means
<code>draw.fixed</code>	Optional logical indicating whether fixed effects parameter should be randomly drawn

<code>random.effects.shrinkage</code>	Shrinkage parameter for stabilizing the covariance matrix of random effects
<code>glmer.warnings</code>	Optional logical indicating whether warnings from <code>glmer</code> should be displayed
<code>blme_use</code>	Logical indicating whether the blme package should be used.
<code>blme_args</code>	(Prior) Arguments for blme , see <code>blme::blmer</code> and <code>blme::bmerDist-class</code> .
<code>donors</code>	Number of donors used for predictive mean matching
<code>match_sampled_pars</code>	Logical indicating whether values of nearest neighbors should also be sampled in pmm imputation.
<code>...</code>	Further arguments to be passed

Value

A vector of length `nmiss=sum(!ry)` with imputed values.

References

- Snijders, T. A. B., & Bosker, R. J. (2012). *Multilevel analysis: An introduction to basic and advanced multilevel modeling*. Thousand Oaks, CA: Sage.
- Zinn, S. (2013). *An imputation model for multilevel binary data*. NEPS Working Paper No 31.

See Also

See `mice.impute.ml.lmer` for imputation for datasets with more than two levels (e.g., three-level datasets or cross-classified datasets).

Variables at a higher level (e.g. at level 2) can be imputed using `2lonly` functions, for example the `mice::mice.impute.2lonly.norm` function in the **mice** package or the general `mice.impute.2lonly.function` function in the **miceadds** package which using an already defined imputation method at level 1. If a level-2 variable for 3-level data should be imputed, then `mice.impute.ml.lmer` can also be used to impute this variable with a two-level imputation model in which level 1 corresponds to the original level-2 units and level 2 corresponds to the original level-3 units.

See `mice::mice.impute.2l.norm` and `mice::mice.impute.2l.pan` for imputation functions in the **mice** package under fully conditional specification for normally distributed variables. The function `mice::mice.impute.2l.norm` allows for residual variances which are allowed to vary across groups while `mice::mice.impute.2l.pan` assumes homogeneous residual variances.

The **micemd** package provides further imputation methods for the **mice** package for imputing multilevel data with fully conditional specification. The function `micemd::mice.impute.2l.jomo` has similar functionality like `mice::mice.impute.2l.pan` and imputes normally distributed two-level data with a Bayesian MCMC approach, but relies on the **jomo** package instead of the **pan** package. The functions `mice::mice.impute.2l.lmer` and `micemd::mice.impute.2l.glm.norm` have similar functionality like `mice.impute.2l.continuous` and imputes normally distributed two-level data. The function `{micemd::mice.impute.2l.glm.bin}` has similar functionality like `mice.impute.2l.binary` and imputes binary two-level data.

The **hmi** package imputes single-level and multilevel data and is also based on fully conditional specification. The package relies on the MCMC estimation implemented in the **MCMCglmm** package. The imputation procedure can be run with the `hmi::hmi` function.

See the **pan** (`pan::pan`) and the **jomo** (`jomo::jomo`) package for joint multilevel imputation. See `mitml::panImpute` and `mitml::jomoImpute` for wrapper functions to these packages in the **mitml** package.

Imputation by chained equations can also be conducted in blocks of multivariate conditional distributions since **mice** 3.0.0 (see the `blocks` argument in `mice::mice`). The `mitml::panImpute` and `mitml::jomoImpute` functions can be used with `mice::mice` by specifying imputation methods "panImpute" (see `mice::mice.impute.panImpute`) and "jomoImpute" (see `mice::mice.impute.jomoImpute`).

Examples

```
## Not run:
#####
# EXAMPLE 1: Imputation of a binary variable
#####

#--- simulate missing values
set.seed(976)
G <- 30      # number of groups
n <- 8       # number of persons per group
iccx <- .2   # intra-class correlation X
iccy <- .3   # latent intra-class correlation binary outcome
bx <- .4     # regression coefficient
threshy <- stats::qnorm(.70) # threshold for y
x <- rep( rnorm( G, sd=sqrt( iccx ) ), each=n ) +
      rnorm(G*n, sd=sqrt( 1 - iccx ) )
y <- bx * x + rep( rnorm( G, sd=sqrt( iccy ) ), each=n ) +
      rnorm(G*n, sd=sqrt( 1 - iccy ) )
y <- 1 * ( y > threshy )
dat <- data.frame( group=100+rep(1:G, each=n), x=x, y=y )

#* create some missings
dat1 <- dat
dat1[ seq( 1, G*n, 3 ), "y" ] <- NA
dat1[ dat1$group==2, "y" ] <- NA

#--- prepare imputation in mice
vars <- colnames(dat1)
V <- length(vars)
#* predictor matrix
predmat <- matrix( 0, nrow=V, ncol=V)
rownames(predmat) <- colnames(predmat) <- vars
predmat["y", ] <- c(-2,2,0)
#* imputation methods
impmeth <- rep("",V)
names(impmeth) <- vars
impmeth["y"] <- "2l.binary"

#** imputation with logistic regression ('2l.binary')
imp1 <- mice::mice( data=as.matrix(dat1), method=impmeth,
                   predictorMatrix=predmat, maxit=1, m=5 )

#** imputation with predictive mean matching ('2l.pmm')
```

```

impmeth["y"] <- "2l.pmm"
imp2 <- mice::mice( data=as.matrix(dat1), method=impmeth,
                  predictorMatrix=predmat, maxit=1, m=5 )

##** imputation with logistic regression using blme package
blme_args <- list( "cov.prior"="invwishart")
imp3 <- mice::mice( data=as.matrix(dat1), method=impmeth,
                  predictorMatrix=predmat, maxit=1, m=5,
                  blme_use=TRUE, blme_args=blme_args )

## End(Not run)

```

mice_inits

Arguments for mice::mice Function

Description

Defines initial arguments of imputation method and predictor matrix for `mice::mice` function.

Usage

```
mice_inits(dat, ignore=NULL)
```

Arguments

<code>dat</code>	Dataset
<code>ignore</code>	Vector of variables which should be ignored in imputation

Value

List with entries

<code>method</code>	Imputation method
<code>predictorMatrix</code>	Predictor matrix

See Also

See [mice::make.predictorMatrix](#) and [mice::make.method](#) for generating an initial predictor matrix and a vector of imputation methods.

Examples

```

#####
# EXAMPLE 1: Inits for mice imputation
#####

data(data.ma04, package="miceadds")
dat <- data.ma04

```

```
res <- miceadds::mice_inits(dat, ignore=c("group"))
str(res)
```

micombine.chisquare *Combination of Chi Square Statistics of Multiply Imputed Datasets*

Description

This function does inference for the χ^2 statistic based on multiply imputed datasets (see e.g. Enders, 2010, p. 239 ff.; Allison, 2002). This function is also denoted as the D_2 statistic.

Usage

```
micombine.chisquare(dk, df, display=TRUE, version=1)
```

Arguments

dk	Vector of chi square statistics
df	Degrees of freedom of χ^2 statistic
display	An optional logical indicating whether results should be printed at the R console.
version	Integer indicating which calculation formula should be used. The default <code>version=1</code> refers to the correct formula as in Enders (2010), while <code>version=0</code> uses an incorrect formula as printed in Allison (2001). The incorrect calculation <code>version=0</code> was included in miceadds versions smaller than version 2.0. See also http://statisticalhorizons.com/wp-content/uploads/2012/01/combchi.sas .

Value

A vector with following entries

D	Combined D_2 statistic which is approximately F -distributed with (df, df2) degrees of freedom
p	The p value corresponding to D
df	Numerator degrees of freedom
df2	Denominator degrees of freedom

References

Allison, P. D. (2002). *Missing data*. Newbury Park, CA: Sage.
 Enders, C. K. (2010). *Applied missing data analysis*. Guilford Press.

See Also

See also `mice::pool.compare` for a Wald test to compare two fitted models in the **mice** package.

Examples

```
#####
# EXAMPLE 1: Chi square values of analyses from 7 multiply imputed datasets
#####

# Vector of 7 chi square statistics
dk <- c(24.957, 18.051, 18.812, 17.362, 21.234, 18.615, 19.84)
dk.comb <- miceadds::micombine.chisquare(dk=dk, df=4 )
## Combination of Chi Square Statistics for Multiply Imputed Data
## Using 7 Imputed Data Sets
## F(4, 482.06)=4.438    p=0.00157
```

micombine.cor

Inference for Correlations and Covariances for Multiply Imputed Datasets

Description

Statistical inference for correlations and covariances for multiply imputed datasets

Usage

```
micombine.cor(mi.res, variables=NULL, conf.level=0.95,
              method="pearson", nested=FALSE, partial=NULL )

micombine.cov(mi.res, variables=NULL, conf.level=0.95,
              nested=FALSE )
```

Arguments

<code>mi.res</code>	Object of class <code>mids</code> or <code>mids.lchain</code>
<code>variables</code>	Indices of variables for selection
<code>conf.level</code>	Confidence level
<code>method</code>	Method for calculating correlations. Must be one of "pearson" or "spearman". The default is the calculation of the Pearson correlation.
<code>nested</code>	Logical indicating whether the input dataset stems from a nested multiple imputation.
<code>partial</code>	Formula object for computing partial correlations. The terms which should be residualized are written in the formula object <code>partial</code> .

Value

A data frame containing the coefficients (`r`, `cov`) and its corresponding standard error (`rse`, `cov_se`), fraction of missing information (`fmi`) and a *t* value (`t`).

The corresponding coefficients can also be obtained as matrices by requesting `attr(result, "r_matrix")`.

See Also

See `stats::cor.test` for testing correlation coefficients.

Examples

```
## Not run:
#####
# EXAMPLE 1: nhanes data | combination of correlation coefficients
#####

library(mice)
data(nhanes, package="mice")
set.seed(9090)

# nhanes data in one chain
imp.mi <- miceadds::mice.lchain( nhanes, burnin=5, iter=20, Nimp=4,
                               method=rep("norm", 4) )
# correlation coefficients of variables 4, 2 and 3 (indexed in nhanes data)
res <- miceadds::micombine.cor(mi.res=imp.mi, variables=c(4,2,3) )
##      variable1 variable2      r    rse fisher_r fisher_rse   fmi      t      p
## 1      chl      bmi  0.2458 0.2236   0.2510    0.2540 0.3246  0.9879 0.3232
## 2      chl      hyp  0.2286 0.2152   0.2327    0.2413 0.2377  0.9643 0.3349
## 3      bmi      hyp -0.0084 0.2198  -0.0084    0.2351 0.1904 -0.0358 0.9714
##      lower95 upper95
## 1 -0.2421  0.6345
## 2 -0.2358  0.6080
## 3 -0.4376  0.4239

# extract matrix with correlations and its standard errors
attr(res, "r_matrix")
attr(res, "rse_matrix")

# inference for covariance
res2 <- miceadds::micombine.cov(mi.res=imp.mi, variables=c(4,2,3) )

# inference can also be conducted for non-imputed data
res3 <- miceadds::micombine.cov(mi.res=nhanes, variables=c(4,2,3) )

#####
# EXAMPLE 2: nhanes data | comparing different correlation coefficients
#####

library(psych)
library(mitools)

# imputing data
imp1 <- mice::mice( nhanes, method=rep("norm", 4) )
summary(imp1)

**** Pearson correlation
res1 <- miceadds::micombine.cor(mi.res=imp1, variables=c(4,2) )
```

```

**** Spearman rank correlation
res2 <- miceadds::micombine.cor(mi.res=imp1, variables=c(4,2), method="spearman")

**** Kendalls tau
# test of computation of tau for first imputed dataset
dat1 <- mice::complete(imp1, action=1)
tau1 <- psych::corr.test(x=dat1[,c(4,2)], method="kendall")
tau1$r[1,2] # estimate
tau1$se # standard error

# results of Kendalls tau for all imputed datasets
res3 <- with( data=imp1,
              expr=psych::corr.test( x=cbind( chl, bmi ), method="kendall" ) )
# extract estimates
betas <- lapply( res3$analyses, FUN=function(l1){ l1$r[1,2] } )
# extract variances
vars <- lapply( res3$analyses, FUN=function(l1){ (l1$se[1,2])^2 } )
# Rubin inference
tau_comb <- mitools::MIcombine( results=betas, variances=vars )
summary(tau_comb)

#####
# EXAMPLE 3: Inference for correlations for nested multiply imputed datasets
#####

library(BIFIEsurvey)
data(data.timss4, package="BIFIEsurvey" )
datlist <- data.timss4

# object of class nested.datlist
datlist <- miceadds::nested.datlist_create(datlist)
# inference for correlations
res2 <- miceadds::micombine.cor(mi.res=datlist, variables=c("lang", "migrant", "ASMMAT"))

## End(Not run)

```

micombine.F

Combination of F Statistics for Multiply Imputed Datasets Using a Chi Square Approximation

Description

Several F statistics from multiply imputed datasets are combined using an approximation based on χ^2 statistics (see [micombine.chisquare](#)).

Usage

```
micombine.F(Fvalues, df1, display=TRUE, version=1)
```

Arguments

Fvalues	Vector containing F values.
df1	Degrees of freedom of the numerator. Degrees of freedom of the numerator are approximated by ∞ (large number of degrees of freedom).
display	A logical indicating whether results should be displayed at the console
version	Integer indicating which calculation formula should be used. The default version=1 refers to the correct formula as in Enders (2010), while version=0 uses an incorrect formula as printed in Allison (2001). The incorrect calculation version=0 was included in miceadds versions smaller than version 2.0. See also http://statisticalhorizons.com/wp-content/uploads/2012/01/combchi.sas .

Value

The same output as in [micombine.chisquare](#)

References

- Allison, P. D. (2002). *Missing data*. Newbury Park, CA: Sage.
- Enders, C. K. (2010). *Applied missing data analysis*. Guilford Press.
- Grund, S., Luedtke, O., & Robitzsch, A. (2016). Pooling ANOVA results from multiply imputed datasets: A simulation study. *Methodology*, 12, 75-88.

See Also

[micombine.chisquare](#)

Examples

```
#####
# EXAMPLE 1: F statistics for 5 imputed datasets
#####

Fvalues <- c( 6.76, 4.54, 4.23, 5.45, 4.78 )
micombine.F(Fvalues, df1=4 )
## Combination of Chi Square Statistics for Multiply Imputed Data
## Using 5 Imputed Data Sets
## F(4, 52.94)=3.946    p=0.00709
```

mids2datlist

Converting a mids, mids.1chain or mids.nmi Object in a Dataset List

Description

Converts a mids, mids.1chain or mids.nmi object in a dataset list.

Usage

```
mids2datlist(midsobj, X=NULL)
```

Arguments

```
midsobj      Object of class mids, mids.1chain or mids.nmi
X            Optional data frame of variables to be included in imputed datasets.
```

Value

List of multiply imputed datasets of classes `datlist` or `nested.datlist`.

Examples

```
## Not run:
#####
# EXAMPLE 1: Imputing nhanes data and convert result into a dataset list
#####

data(nhanes,package="mice")

#**** imputation using mice
imp1 <- mice::mice( nhanes, m=3, maxit=5 )
# convert mids object into list
datlist1 <- miceadds::mids2datlist( imp1 )

#**** imputation using mice.1chain
imp2 <- miceadds::mice.1chain( nhanes, burnin=4, iter=20, Nimp=5 )
# convert mids.1chain object into list
datlist2 <- miceadds::mids2datlist( imp2 )

#####
# EXAMPLE 2: Nested multiple imputation and datalist conversion
#####

library(BIFIEsurvey)
data(data.timss2, package="BIFIEsurvey" )
datlist <- data.timss2
  # list of 5 datasets containing 5 plausible values

# remove first four variables
M <- length(datlist)
for (ll in 1:M){
  datlist[[ll]] <- datlist[[ll]][, -c(1:4) ]
}

#*****
# (1) nested multiple imputation using mice
imp1 <- miceadds::mice.nmi( datlist, m=4, maxit=3 )
summary(imp1)
```



```

#####
# (2) nested multiple imputation using mice.1chain
imp2 <- miceadds::mice.nmi( datlist, Nimp=4, burnin=10, iter=22, type="mice.1chain")
summary(imp2)

#####
# conversion into a datalist
datlist.i1 <- miceadds::mids2datlist( imp1 )
datlist.i2 <- miceadds::mids2datlist( imp2 )

#####
# EXAMPLE 3: mids object conversion and inclusion of further variables
#####

data(data.ma05)
dat <- data.ma05

# imputation
resp <- dat[, - c(1:2) ]
imp <- mice::mice( resp, imputationMethod="norm", maxit=2, m=3 )

# convert mids object into datalist
datlist0 <- miceadds::mids2datlist( imp )
# convert mids object into datalist and include some id variables
datlist1 <- miceadds::mids2datlist( imp, X=dat[,c(1,2) ] )

## End(Not run)

```

mids2mlwin

Export mids object to MLwiN

Description

Converts a mids object into a format recognized by the multilevel software MLwiN.

Usage

```
mids2mlwin(imp, file.prefix, path=getwd(), sep=" ", dec=".", silent=FALSE,
           X=NULL)
```

Arguments

imp	The imp argument is an object of class mids, typically produced by the mice() function.
file.prefix	A character string describing the prefix of the output data files.
path	A character string containing the path of the output file. By default, files are written to the current R working directory.
sep	The separator between the data fields.

dec	The decimal separator for numerical data.
silent	A logical flag stating whether the names of the files should be printed.
X	Optional data frame of variables to be included in imputed datasets.

Value

The return value is NULL.

Author(s)

Thorsten Henke

Examples

```
## Not run:  
# imputation nhanes data  
data(nhanes)  
imp <- mice::mice(nhanes)  
# write files to MLwiN  
mids2mlwin(imp, file.prefix="nhanes" )  
  
## End(Not run)
```

mi_dstat

Cohen's d Effect Size for Missingness Indicators

Description

Computes Cohen's d effect size indicating whether missingness on a variable is related to other variables (covariates).

Usage

```
mi_dstat(dat)
```

Arguments

dat Data frame

Value

A matrix. Missingness indicators refer to rows and covariates to columns.

Examples

```
#####
# EXAMPLE 1: d effect size for missingness indicators data.ma01
#####

data(data.ma01)
dat <- data.ma01

# compute d effect sizes
md <- miceadds::mi_dstat(dat)
round( md, 3 )
```

ml_mcmc

*MCMC Estimation for Mixed Effects Model***Description**

Fits a mixed effects model via MCMC. The outcome can be normally distributed or ordinal (Goldstein, 2011; Goldstein, Carpenter, Kenward & Levin, 2009).

Usage

```
ml_mcmc( formula, data, iter=3000, burnin=500, print_iter=100, outcome="normal",
         nu0=NULL, s0=1, inits_lme4=TRUE, thresh_fac=5.8)

## S3 method for class 'ml_mcmc'
summary(object, digits=4, file=NULL, ...)

## S3 method for class 'ml_mcmc'
plot(x, ask=TRUE, ...)

## S3 method for class 'ml_mcmc'
coef(object, ...)

## S3 method for class 'ml_mcmc'
vcov(object, ...)

ml_mcmc_fit(y, X, Z_list, beta, Psi_list, sigma2, alpha, u_list, idcluster_list,
            onlyintercept_list, ncluster_list, sigma2_nu0, sigma2_sigma2_0, psi_nu0_list,
            psi_S0_list, est_sigma2, est_probit, parameter_index, est_parameter, npar, iter,
            save_iter, verbose=TRUE, print_iter=500, parnames0=NULL, K=9999, est_thresh=FALSE,
            thresh_fac=5.8, parm_summary=TRUE )

## exported Rcpp functions
miceadds_rcpp_ml_mcmc_sample_beta(xtx_inv, X, Z_list, y, u_list, idcluster_list, sigma2,
                                  onlyintercept_list, NR)
miceadds_rcpp_ml_mcmc_sample_u(X, beta, Z_list, y, ztz_list, idcluster_list,
```

```

ncluster_list, sigma2, Psi_list, onlyintercept_list, NR, u0_list)
miceadds_rcpp_ml_mcmc_sample_psi(u_list, nu0_list, S0_list, NR)
miceadds_rcpp_ml_mcmc_sample_sigma2(y, X, beta, Z_list, u_list, idcluster_list,
  onlyintercept_list, nu0, sigma2_0, NR)
miceadds_rcpp_ml_mcmc_sample_latent_probit(X, beta, Z_list, u_list, idcluster_list, NR,
  y_int, alpha, minval, maxval)
miceadds_rcpp_ml_mcmc_sample_thresholds(X, beta, Z_list, u_list, idcluster_list, NR, K,
  alpha, sd_proposal, y_int)
miceadds_rcpp_ml_mcmc_predict_fixed_random(X, beta, Z_list, u_list, idcluster_list, NR)
miceadds_rcpp_ml_mcmc_predict_random_list(Z_list, u_list, idcluster_list, NR, N)
miceadds_rcpp_ml_mcmc_predict_random(Z, u, idcluster)
miceadds_rcpp_ml_mcmc_predict_fixed(X, beta)
miceadds_rcpp_ml_mcmc_subtract_fixed(y, X, beta)
miceadds_rcpp_ml_mcmc_subtract_random(y, Z, u, idcluster, onlyintercept)
miceadds_rcpp_ml_mcmc_compute_ztz(Z, idcluster, ncluster)
miceadds_rcpp_ml_mcmc_compute_xtx(X)
miceadds_rcpp_ml_mcmc_probit_category_prob(y_int, alpha, mu1, use_log)
miceadds_rcpp_pnorm(x, mu, sigma)
miceadds_rcpp_qnorm(x, mu, sigma)
miceadds_rcpp_rtnorm(mu, sigma, lower, upper)

```

Arguments

formula	An R formula in lme4 -like specification
data	Data frame
iter	Number of iterations
burnin	Number of burnin iterations
print_iter	Integer indicating that every print_iterth iteration progress should be displayed
outcome	Outcome distribution: "normal" or "probit"
nu0	Prior sample size
s0	Prior guess for variance
inits_lme4	Logical indicating whether initial values should be obtained from fitting the model in the lme4 package
thresh_fac	Factor for proposal variance for estimating thresholds which is determined as $\text{thresh_fac}/N$ (5.8/ N as default).
object	Object of class ml_mcmc
digits	Number of digits after decimal used for printing
file	Optional file name
...	Further arguments to be passed
x	Object of class ml_mcmc
ask	Logical indicating whether display of the next plot should be requested via clicking
y	Outcome vector

X	Design matrix fixed effects
Z_list	Design matrices random effects
beta	Initial vector fixed coefficients
Psi_list	Initial covariance matrices random effects
sigma2	Initial residual covariance matrix
alpha	Vector of thresholds
u_list	List with initial values for random effects
idcluster_list	List with cluster identifiers for random effects
onlyintercept_list	List of logicals indicating whether only random intercepts are used for a corresponding random effect
ncluster_list	List containing number of clusters for each random effect
sigma2_nu0	Prior sample size residual variance
sigma2_sigma2_0	Prior guess residual variance
psi_nu0_list	List of prior sample sizes for covariance matrices of random effects
psi_S0_list	List of prior guesses for covariance matrices of random effects
est_sigma2	Logical indicating whether residual variance should be estimated
est_probit	Logical indicating whether probit model for ordinal outcomes should be estimated
parameter_index	List containing integers for saving parameters
est_parameter	List of logicals indicating which parameter type should be estimated
npar	Number of parameters
save_iter	Vector indicating which iterations should be used
verbose	Logical indicating whether progress should be displayed
parnames0	Optional vector of parameter names
K	Number of categories
est_thresh	Logical indicating whether thresholds should be estimated
parm_summary	Logical indicating whether a parameter summary table should be computed
xtx_inv	Matrix
NR	Integer
ztz_list	List containing design matrices for random effects
u0_list	List containing random effects
nu0_list	List with prior sample sizes
S0_list	List with prior guesses
sigma2_0	Numeric
y_int	Integer vector
minval	Numeric

maxval	Numeric
sd_proposal	Numeric vector
N	Integer
Z	Matrix
u	Matrix containing random effects
idcluster	Integer vector
onlyintercept	Logical
ncluster	Integer
mu1	Vector
use_log	Logical
mu	Vector
sigma	Numeric
lower	Vector
upper	Vector

Details

Fits a linear mixed effects model $y = X\beta + Zu + e$ with MCMC sampling. In case of ordinal data, the ordinal variable y is replaced by an underlying latent normally distributed variable y^* and the residual variance is fixed to 1.

Value

List with following entries (selection)

sampld_values	Sampled values
par_summary	Parameter summary

References

- Goldstein, H. (2011). *Multilevel statistical models*. New York: Wiley.
- Goldstein, H., Carpenter, J., Kenward, M., & Levin, K. (2009). Multilevel models with multivariate mixed response types. *Statistical Modelling*, 9(3), 173-197.

See Also

See also the **MCMCglmm** package for MCMC estimation and the **lme4** package for maximum likelihood estimation.

Examples

```

## Not run:
#####
# EXAMPLE 1: Multilevel model continuous data
#####

library(lme4)

###* simulate data
set.seed(9097)

# number of clusters and units within clusters
K <- 150
n <- 15
iccx <- .2
idcluster <- rep( 1:K, each=n )
w <- stats::rnorm( K )
x <- rep( stats::rnorm( K, sd=sqrt(iccx) ), each=n) +
      stats::rnorm( n*K, sd=sqrt( 1 - iccx ) )
X <- data.frame(int=1, "x"=x, xaggr=miceadds::gm(x, idcluster),
               w=rep( w, each=n ) )
X <- as.matrix(X)
Sigma <- diag( c(2, .5 ) )
u <- MASS::mvrnorm( K, mu=c(0,0), Sigma=Sigma )
beta <- c( 0, .3, .7, 1 )
Z <- X[, c("int", "x") ]
ypred <- as.matrix(X) %*% beta + rowSums( Z * u[ idcluster, ] )
y <- ypred[,1] + stats::rnorm( n*K, sd=1 )
data <- as.data.frame(X)
data$idcluster <- idcluster
data$y <- y

###* estimate mixed effects model with miceadds::ml_mcmc() function
formula <- y ~ x + miceadds::gm(x, idcluster) + w + ( 1 + x | idcluster)
mod1 <- miceadds::ml_mcmc( formula, data)
plot(mod1)
summary(mod1)

###* compare results with lme4 package
mod2 <- lme4::lmer(formula, data=data)
summary(mod2)

#####
# EXAMPLE 2: Multilevel model for ordinal outcome
#####

###* simulate data
set.seed(456)
# number of clusters and units within cluster
K <- 500
n <- 10
iccx <- .2

```

```

idcluster <- rep( 1:K, each=n )
w <- rnorm( K )
x <- rep( stats::rnorm( K, sd=sqrt(iccx)), each=n) +
      stats::rnorm( n*K, sd=sqrt( 1 - iccx ))
X <- data.frame("int"=1, "x"=x, "xaggr"=miceadds::gm(x, idcluster),
              w=rep( w, each=n ) )
X <- as.matrix(X)
u <- matrix( stats::rnorm(K, sd=sqrt(.5) ), ncol=1)
beta <- c( 0, .3, .7, 1 )
Z <- X[, c("int") ]
ypred <- as.matrix(X) %%% beta + Z * u[ idcluster, ]
y <- ypred[,1] + stats::rnorm( n*K, sd=1 )
data <- as.data.frame(X)
data$idcluster <- idcluster
alpha <- c(-Inf, -.4, 0, 1.7, Inf)
data$y <- cut( y, breaks=alpha, labels=FALSE ) - 1

### estimate model
formula <- y ~ miceadds::cwc(x, idcluster) + miceadds::gm(x,idcluster) + w + ( 1 | idcluster)
mod <- miceadds::ml_mcmc( formula, data, iter=2000, burnin=500, outcome="probit",
                        inits_lme4=FALSE)

summary(mod)
plot(mod)

## End(Not run)

```

NestedImputationList *Functions for Analysis of Nested Multiply Imputed Datasets*

Description

The function `NestedImputationList` takes a list of lists of datasets and converts this into an object of class `NestedImputationList`.

Statistical models can be estimated with the function `with.NestedImputationList`.

The `mitools::MIcombine` method can be used for objects of class `NestedImputationResultList` which are the output of `with.NestedImputationList`.

Usage

```

NestedImputationList( datasets )

## S3 method for class 'NestedImputationList'
print(x, ...)

## S3 method for class 'NestedImputationResultList'
MIcombine(results, ...)

```


Arguments

datasets	List of lists of datasets which are created by nested multiple imputation.
x	Object of class NestedImputationResultsList
results	Object of class NestedImputationResultsList
...	Further arguments to be passed.

Value

Function `NestedImputationList`: Object of class `NestedImputationList`.

Function `MIcombine.NestedImputationList`: Object of class `mipo.nmi`.

See Also

[with.NestedImputationList](#), [within.NestedImputationList](#), [pool.mids.nmi](#), [MIcombine](#)

Examples

```
## Not run:
#####
# EXAMPLE 1: Nested multiple imputation and conversion into an object of class
#           NestedImputationList
#####

library(BIFIEsurvey)
data(data.timss2, package="BIFIEsurvey" )
datlist <- data.timss2

# remove first four variables
M <- length(datlist)
for (ll in 1:M){
  datlist[[ll]] <- datlist[[ll]][, -c(1:4) ]
}

# nested multiple imputation using mice
imp1 <- miceadds::mice.nmi( datlist, m=3, maxit=2 )
summary(imp1)

# create object of class NestedImputationList
datlist1 <- miceadds::mids2datlist( imp1 )
datlist1 <- miceadds::NestedImputationList( datlist1 )

# estimate linear model using with
res1 <- with( datlist1, stats::lm( ASMMAT ~ female + migrant ) )
# pool results
mres1 <- mitools::MIcombine( res1 )
summary(mres1)
coef(mres1)
vcov(mres1)

## End(Not run)
```

nestedList2List *Converting a Nested List into a List (and Vice Versa)*

Description

Converts a nested list into a list (and vice versa).

Usage

```
nestedList2List(nestedList)
```

```
List2nestedList(List, N_between, N_within=NULL, loop_within=TRUE)
```

Arguments

nestedList	A nested list
List	A list
N_between	Number of between list elements
N_within	Number of within list elements
loop_within	Optional logical indicating whether looping should start from within list

Value

A list or a nested list

Examples

```
#####
# EXAMPLE 1: List conversions using a small example
#####

# define a nestedList
nestedList <- as.list(1:3)
nestedList[[1]] <- as.list( 2:4 )
nestedList[[2]] <- as.list( 34 )
nestedList[[3]] <- as.list( 4:9 )

# convert a nested list into a list
v2 <- miceadds::nestedList2List( nestedList)

## reconvert list v2 into a nested list, looping within first
v3 <- miceadds::List2nestedList(v2, N_between=5)
# looping between first
v4 <- miceadds::List2nestedList(v2, N_between=5, loop_within=FALSE)
```

NMIwaldtest

Wald Test for Nested Multiply Imputed Datasets

Description

Performs a Wald test for nested multiply imputed datasets (NMIwaldtest) and ordinary multiply imputed datasets (MIwaldtest), see Reiter and Raghanathan (2007). The correspondent statistic is also called the D_1 statistic.

The function `create.designMatrices.waldtest` is a helper function for the creation of design matrices.

Usage

```
NMIwaldtest(qhat, u, Cdes=NULL, rdes=NULL, testnull=NULL)
```

```
MIwaldtest(qhat, u, Cdes=NULL, rdes=NULL, testnull=NULL)
```

```
## S3 method for class 'NMIwaldtest'
summary(object,digits=4,...)
```

```
## S3 method for class 'MIwaldtest'
summary(object,digits=4,...)
```

```
create.designMatrices.waldtest( pars, k )
```

Arguments

qhat	List or array of estimated parameters
u	List or array of estimated covariance matrices of parameters
Cdes	Design matrix C for parameter test (see Details)
rdes	Constant vector r (see Details)
testnull	Vector containing names of parameters which should be tested for a parameter value of zero.
object	Object of class NMIwaldtest
digits	Number of digits after decimal for print
...	Further arguments to be passed
pars	Vector of parameter names
k	Number of linear hypotheses which should be tested

Details

The Wald test is performed for a linear hypothesis $C\theta = r$ for a parameter vector θ .

Value

List with following entries

stat	Data frame with test statistic
qhat	Transformed parameter according to linear hypothesis
u	Covariance matrix of transformed parameters

Note

The function `create.designMatrices.waldtest` is a helper function for the creation of design matrices.

References

Reiter, J. P. and Raghunathan, T. E. (2007). The multiple adaptations of multiple imputation. *Journal of the American Statistical Association*, 102, 1462-1471.

See Also

[NMIcombine](#)

Examples

```
## Not run:
#####
# EXAMPLE 1: Nested multiple imputation and Wald test | TIMSS data
#####

library(BIFIEsurvey)
data(data.timss2, package="BIFIEsurvey" )
datlist <- data.timss2
# remove first four variables
M <- length(datlist)
for (ll in 1:M){
  datlist[[ll]] <- datlist[[ll]][, -c(1:4) ]
}

#####
# (1) nested multiple imputation using mice
imp1 <- miceadds::mice.nmi( datlist, m=3, maxit=2 )
summary(imp1)

####* Model 1: Linear regression with interaction effects
res1 <- with( imp1, stats::lm( likesc ~ female*migrant + female*books ) )
pres1 <- miceadds::pool.mids.nmi( res1 )
summary(pres1)

# test whether both interaction effects equals zero
pars <- dimnames(pres1$qhat)[[3]]
des <- miceadds::create.designMatrices.waldtest( pars=pars, k=2)
Cdes <- des$Cdes
```

```

rdes <- des$rdes
Cdes[1, "female:migrant"] <- 1
Cdes[2, "female:books"] <- 1
wres1 <- miceadds::NMIwaldtest( qhat=pres1$qhat, u=pres1$u, Cdes=Cdes, rdes=rdes )
summary(wres1)

# a simpler specification is the use of "testnull"
testnull <- c("female:migrant", "female:books")
wres1b <- miceadds::NMIwaldtest( qhat=qhat, u=u, testnull=testnull )
summary(wres1b)

#*** Model 2: Multivariate linear regression
res2 <- with( imp1, stats::lm( cbind( ASMMAT, ASSSCI ) ~
                             0 + I(1*(female==1)) + I(1*(female==0)) ) )
pres2 <- miceadds::pool.mids.nmi( res2 )
summary(pres2)

# test whether both gender differences equals -10 points
pars <- dimnames(pres2$qhat)[[3]]
## > pars
## [1] "ASMMAT:I(1 * (female==1))" "ASMMAT:I(1 * (female==0))"
## [3] "ASSSCI:I(1 * (female==1))" "ASSSCI:I(1 * (female==0))"

des <- miceadds::create.designMatrices.waldtest( pars=pars, k=2)
Cdes <- des$Cdes
rdes <- c(-10,-10)
Cdes[1, "ASMMAT:I(1*(female==1))"] <- 1
Cdes[1, "ASMMAT:I(1*(female==0))"] <- -1
Cdes[2, "ASSSCI:I(1*(female==1))"] <- 1
Cdes[2, "ASSSCI:I(1*(female==0))"] <- -1

wres2 <- miceadds::NMIwaldtest( qhat=pres2$qhat, u=pres2$u, Cdes=Cdes, rdes=rdes )
summary(wres2)

# test only first hypothesis
wres2b <- miceadds::NMIwaldtest( qhat=pres2$qhat, u=pres2$u, Cdes=Cdes[1,,drop=FALSE],
                               rdes=rdes[1] )
summary(wres2b)

#####
# EXAMPLE 2: Multiple imputation and Wald test | TIMSS data
#####

library(BIFIEsurvey)
data(data.timss2, package="BIFIEsurvey" )
dat <- data.timss2[[1]]
dat <- dat[, - c(1:4) ]

# perform multiple imputation
imp <- mice::mice( dat, m=6, maxit=3 )

# define analysis model
res1 <- with( imp, lm( likesc ~ female*migrant + female*books ) )

```

```

pres1 <- mice::pool( res1 )
summary(pres1)

# Wald test for zero interaction effects
qhat <- pres1$qhat
u <- pres1$u
pars <- dimnames(pres1$qhat)[[2]]
des <- miceadds::create.designMatrices.waldtest( pars=pars, k=2)
Cdes <- des$Cdes
rdes <- des$rdes
Cdes[1, "female:migrant"] <- 1
Cdes[2, "female:books"] <- 1

# apply MIwaldtest function
wres1 <- miceadds::MIwaldtest( qhat, u, Cdes, rdes )
summary(wres1)

# use again "testnull"
testnull <- c("female:migrant", "female:books")
wres1b <- miceadds::MIwaldtest( qhat=qhat, u=u, testnull=testnull )
summary(wres1b)

#***** linear regression with cluster robust standard errors

# convert object of class mids into a list object
datlist_imp <- miceadds::mids2datlist( imp )
# define cluster
idschool <- as.numeric( substring( data.timss2[[1]]$IDSTUD, 1, 5 ) )
# linear regression
res2 <- lapply( datlist_imp, FUN=function(data){
  miceadds::lm.cluster( data=data, formula=likesc ~ female*migrant + female*books,
    cluster=idschool ) } )
# extract parameters and covariance matrix
qhat <- lapply( res2, FUN=function(rr){ coef(rr) } )
u <- lapply( res2, FUN=function(rr){ vcov(rr) } )
# perform Wald test
wres2 <- miceadds::MIwaldtest( qhat, u, Cdes, rdes )
summary(wres2)

## End(Not run)

```

output.format1

R Utilities: Formatting R Output on the R Console

Description

This function does some formatting of output.

Usage

```
output.format1(stringtype, label, rep.N=1,stringlength=70)
```

Arguments

stringtype	Type of string for display, e.g. "*", "-", ...
label	Some comment which should be displayed at the console
rep.N	Number of lines which shall be left blank
stringlength	Length of vector with label

Value

Generates a string output at the R console

Examples

```
output.format1(stringtype="*", label="HELLO WORLD", stringlength=20)
##  *'*'*'*'*'*'*'*'*'*'*'*'*'*'*'*'*'*'*'*'*'*'*'*'*
##  HELLO WORLD
```

pca.covridge

Principal Component Analysis with Ridge Regularization

Description

Performs a principal component analysis for a dataset while a ridge parameter is added on the diagonal of the covariance matrix.

Usage

```
pca.covridge(x, ridge=1E-10 )
```

Arguments

x	A numeric matrix
ridge	Ridge regularization parameter for the covariance matrix

Value

A list with following entries:

loadings	Matrix of factor loadings
scores	Matrix of principal component scores
sdev	Vector of standard deviations of factors (square root of eigenvalues)

See Also

Principal component analysis in **stats**: [stats::princomp](#)

For calculating first eigenvalues of a symmetric matrix see also [sirt::eigenvalues.sirt](#) in the **sirt** package.

Examples

```
## Not run:
#####
# EXAMPLE 1: PCA on imputed internet data
#####

library(mice)
data(data.internet)
dat <- as.matrix( data.internet)

# single imputation in mice
imp <- mice::mice( dat, m=1, maxit=10 )

# apply PCA
pca.imp <- miceadds::pca.covridge( complete(imp) )
## > pca.imp$sdev
##   Comp.1   Comp.2   Comp.3   Comp.4   Comp.5   Comp.6   Comp.7
## 3.0370905 2.3950176 2.2106816 2.0661971 1.8252900 1.7009921 1.6379599

# compare results with princomp
pca2.imp <- stats::princomp( complete(imp) )
## > pca2.imp
## Call:
## stats::princomp(x=complete(imp))
##
## Standard deviations:
##   Comp.1   Comp.2   Comp.3   Comp.4   Comp.5   Comp.6   Comp.7
## 3.0316816 2.3907523 2.2067445 2.0625173 1.8220392 1.6979627 1.6350428

## End(Not run)
```

pool.mids.nmi

Pooling for Nested Multiple Imputation

Description

Statistical inference for scalar parameters for nested multiply imputed datasets (Rubin, 2003; Harel & Schafer, 2002, 2003; Reiter & Raghanathan, 2007; Harel, 2007).

The `NMIcombine` (`pool_nmi` as a synonym) and `NMIextract` functions are extensions of `mitools::MIcombine` and `mitools::MIextract`.

Usage

```
pool.mids.nmi(object, method="largesample")
```

```
NMIcombine( qhat, u=NULL, se=NULL, NMI=TRUE, comp_cov=TRUE, is_list=TRUE,
            method=1)
```

```
pool_nmi( qhat, u=NULL, se=NULL, NMI=TRUE, comp_cov=TRUE, is_list=TRUE,
```



```

        method=1)

NMIextract(results, expr, fun)

## S3 method for class 'mipo.nmi'
summary(object, digits=4, ...)

## S3 method for class 'mipo.nmi'
coef(object, ...)

## S3 method for class 'mipo.nmi'
vcov(object, ...)

```

Arguments

object	Object of class <code>mids.nmi</code> . For <code>summary</code> it must be an object of class <code>mipo.nmi</code> .
method	For <code>pool.mids.nmi</code> : Method for calculating degrees of freedom. Until now, only the method "largesample" is available. For <code>NMIcombine</code> and <code>pool_nmi</code> : Computation method of fraction of missing information. <code>method=1</code> is due to Harel and Schafer (2003) or Shen (2007). <code>method=2</code> is due to Harel and Schafer (2002) and is coherent to the calculation for multiply imputed datasets, while the former method is not.
qhat	List of lists of parameter estimates. In case of an ordinary imputation it can only be a list.
u	Optional list of lists of covariance matrices of parameter estimates
se	Optional vector of standard errors. This argument overwrites <code>u</code> if it is provided.
NMI	Optional logical indicating whether the <code>NMIcombine</code> function should be applied for results of nested multiply imputed datasets. It is set to <code>FALSE</code> if only a list results of multiply imputed datasets is available.
comp_cov	Optional logical indicating whether covariances between parameter estimates should be estimated.
is_list	Optional logical indicating whether <code>qhat</code> and <code>u</code> are provided as lists as an input. If <code>is_list=FALSE</code> , appropriate arrays can be used as input.
results	A list of objects
expr	An expression
fun	A function of one argument
digits	Number of digits after decimal for printing results in <code>summary</code> .
...	Further arguments to be passed.

Value

Object of class `mipo.nmi` with following entries

qhat	Estimated parameters in all imputed datasets
u	Estimated covariance matrices of parameters in all imputed datasets

qbar	Estimated parameter
ubar	Average estimated variance within imputations
Tm	Total variance of parameters
df	Degrees of freedom
lambda	Total fraction of missing information
lambda_Between	Fraction of missing information of between imputed datasets (first stage imputation)
lambda_Within	Fraction of missing information of within imputed datasets (second stage imputation)

References

- Harel, O., & Schafer, J. (2002). *Two stage multiple imputation*. Joint Statistical Meetings - Biometrics Section.
- Harel, O., & Schafer, J. (2003). *Multiple imputation in two stages*. In Proceedings of Federal Committee on Statistical Methodology 2003 Conference.
- Harel, O. (2007). Inferences on missing information under multiple imputation and two-stage multiple imputation. *Statistical Methodology*, 4(1), 75-89.
- Reiter, J. P., & Raghunathan, T. E. (2007). The multiple adaptations of multiple imputation. *Journal of the American Statistical Association*, 102(480), 1462-1471.
- Rubin, D. B. (2003). Nested multiple imputation of NMES via partially incompatible MCMC. *Statistica Neerlandica*, 57(1), 3-18.

See Also

[mice::pool](#), [mitools::MIcombine](#), [mitools::MIextract](#)
[mice.nmi](#), [MIcombine.NestedImputationResultList](#)

Examples

```
## Not run:
#####
# EXAMPLE 1: Nested multiple imputation and statistical inference
#####

library(BIFIEsurvey)
data(data.timss2, package="BIFIEsurvey" )
datlist <- data.timss2
# remove first four variables
M <- length(datlist)
for (ll in 1:M){
  datlist[[ll]] <- datlist[[ll]][, -c(1:4) ]
}

#####
# (1) nested multiple imputation using mice
imp1 <- miceadds::mice.nmi( datlist, m=3, maxit=2 )
```

```

summary(imp1)

#####
# (2) first linear regression: ASMMAT ~ migrant + female
res1 <- with( imp1, stats::lm( ASMMAT ~ migrant + female ) ) # fit
pres1 <- miceadds::pool.mids.nmi( res1 ) # pooling
summary(pres1) # summary
coef(pres1)
vcov(pres1)

#####
# (3) second linear regression: likesc ~ migrant + books
res2 <- with( imp1, stats::lm( likesc ~ migrant + books ) )
pres2 <- miceadds::pool.mids.nmi( res2 )
summary(pres2)

#####
# (4) some descriptive statistics using the mids.nmi object
res3 <- with( imp1, c( "M_lsc"=mean(likesc), "SD_lsc"=stats::sd(likesc) ) )
pres3 <- miceadds::NMIcombine( qhat=res3$analyses )
summary(pres3)

#####
# (5) apply linear regression based on imputation list

# convert mids object to datlist
datlist2 <- miceadds::mids2datlist( imp1 )
str(datlist2, max.level=1)

# double application of lapply to the list of list of nested imputed datasets
res4 <- lapply( datlist2, FUN=function(dl){
  lapply( dl, FUN=function(data){
    stats::lm( ASMMAT ~ migrant + books, data=data )
  } )
} )

# extract coefficients
qhat <- lapply( res4, FUN=function(bb){
  lapply( bb, FUN=function(ww){
    coef(ww)
  } )
} )

# shorter function
NMIextract( results=res4, fun=coef )

# extract covariance matrices
u <- lapply( res4, FUN=function(bb){
  lapply( bb, FUN=function(ww){
    vcov(ww)
  } )
} )

# shorter function
NMIextract( results=res4, fun=vcov )

```

```

# apply statistical inference using the NMICombine function
pres4 <- miceadds::NMICombine( qhat=qhat, u=u )
summary(pres4)

#--- statistical inference if only standard errors are available
# extract standard errors
se <- lapply( res4, FUN=function(bb){
  lapply( bb, FUN=function(ww){
    # ww <- res4[[1]][[1]]
    sww <- summary(ww)
    sww$coef[, "Std. Error"]
  } )
} )
se
# apply NMICombine function
pres4b <- miceadds::NMICombine( qhat=qhat, se=se )
# compare results
summary(pres4b)
summary(pres4)

#####
# EXAMPLE 2: Some comparisons for a multiply imputed dataset
#####

library(mitools)
data(data.ma02)

# save dataset as imputation list
imp <- mitools::imputationList( data.ma02 )
print(imp)
# save dataset as an mids object
imp1 <- miceadds::datlist2mids( imp )

# apply linear model based on imputationList
mod <- with( imp, stats::lm( read ~ hisei + female ) )
# same linear model based on mids object
mod1 <- with( imp1, stats::lm( read ~ hisei + female ) )

# extract coefficients
cmod <- mitools::MIextract( mod, fun=coef)
# extract standard errors
semod <- lapply( mod, FUN=function(mm){
  smm <- summary(mm)
  smm$coef[, "Std. Error"]
} )
# extract covariance matrix
vmod <- mitools::MIextract( mod, fun=vcov)

*** pooling with NMICombine with se (1a) and vcov (1b) as input
pmod1a <- miceadds::NMICombine( qhat=cmod, se=semod, NMI=FALSE )
pmod1b <- miceadds::NMICombine( qhat=cmod, u=vmod, NMI=FALSE )
# use method 2 which should conform to MI inference of mice::pool

```

```

pmod1c <- miceadds::NMCombine( qhat=cmod, u=vmod, NMI=FALSE, method=2)

#### pooling with mitools::MIcombine function
pmod2 <- mitools::MIcombine( results=cmod, variances=vmod )
#### pooling with mice::pool function
pmod3a <- mice::pool( mod1 )
pmod3b <- mice::pool( mod1, method="Rubin")

#--- compare results
summary(pmod1a) # method=1 (the default)
summary(pmod1b) # method=1 (the default)
summary(pmod1c) # method=2
summary(pmod2)
summary(pmod3a)
summary(pmod3b)

## End(Not run)

```

pool_mi

Statistical Inference for Multiply Imputed Datasets

Description

Statistical inference for multiply imputed datasets. See [mitools::MIcombine](#) or [mice::pool](#) for functions of the same functionality.

Usage

```

pool_mi(qhat, u=NULL, se=NULL, dfcom=1e+07, method="smallsample")

## S3 method for class 'pool_mi'
summary(object, alpha=0.05, ...)

## S3 method for class 'pool_mi'
coef(object, ...)

## S3 method for class 'pool_mi'
vcov(object, ...)

```

Arguments

qhat	List of parameter vectors
u	List of covariance matrices
se	List of vector of standard errors. Either u or se must be provided.
dfcom	Degrees of freedom of statistical analysis
method	The default is the small sample inference ("smallsample"). Any other input provides large sample inference.

object	Object of class pool_mi
alpha	Confidence level
...	Further arguments to be passed

Value

Object of with similar output as produced by the `mice::pool` function.

See Also

`mitools::MIcombine`, `mice::pool`, `mitml::testEstimates`

For statistical inference for nested multiply imputed datasets see `NMIcombine`.

Examples

```
## Not run:
#####
# EXAMPLE 1: Statistical inference for models based on imputationList
#####

library(mitools)
library(mice)
library(Zelig)
library(mitml)
library(lavaan)
library(semTools)
data(data.ma02)

# save dataset as imputation list
imp <- mitools::imputationList( data.ma02 )
# mids object
imp0 <- miceadds::datlist2mids( imp )
# datlist object
imp1 <- miceadds::datlist_create(data.ma02)

#--- apply linear model based on imputationList
mod <- with( imp, stats::lm( read ~ hisei + female ) )
#--- apply linear model for mids object
mod0 <- with( imp0, stats::lm( read ~ hisei + female ) )
# extract coefficients
cm0d <- mitools::MIextract( mod, fun=coef)
# extract standard errors
sem0d <- lapply( mod, FUN=function(mm){
  smm <- summary(mm)
  smm$coef[, "Std. Error"]
} )
# extract covariance matrix
vm0d <- mitools::MIextract( mod, fun=vcov)

#*** pooling based on covariance matrices
res1 <- miceadds::pool_mi( qhat=cm0d, u=vm0d )
```

```

summary(res1)
coef(res1)
vcov(res1)

#### pooling based on standard errors
res2 <- miceadds::pool_mi( qhat=cmod, se=semod )

#### pooling with MIcombine
res3 <- mitools::MIcombine( results=cmod, variances=vmod )

#### pooling with pool function in mice
res4 <- mice::pool( mod0 )

#### analysis in Zelig
# convert datalist into object of class amelia
mi02 <- list( "imputations"=data.ma02)
class(mi02) <- "amelia"
res5 <- Zelig::zelig( read ~ hisei + female, model="ls", data=mi02 )

#### analysis in lavaan
lavamodel <- "
  read ~ hisei + female
  read ~~ a*read
  read ~ 1
  # residual standard deviation
  sde :=sqrt(a)
  "
# analysis for first imputed dataset
mod6a <- lavaan::sem( lavamodel, data=imp1[[1]] )
summary(mod6a)
# analysis based on all datasets using with
mod6b <- lapply( imp1, FUN=function(data){
  res <- lavaan::sem( lavamodel, data=data )
  return(res)
} )
# extract parameters and covariance matrices
qhat0 <- lapply( mod6b, FUN=function(l1){ coef(l1) } )
u0 <- lapply( mod6b, FUN=function(l1){ vcov(l1) } )
res6b <- mitools::MIcombine( results=qhat0, variances=u0 )

# extract informations for all parameters
qhat <- lapply( mod6b, FUN=function(l1){
  h1 <- lavaan::parameterEstimates(l1)
  parnames <- paste0( h1$lhs, h1$op, h1$rhs )
  v1 <- h1$est
  names(v1) <- parnames
  return(v1)
} )
se <- lapply( mod6b, FUN=function(l1){
  h1 <- lavaan::parameterEstimates(l1)
  parnames <- paste0( h1$lhs, h1$op, h1$rhs )
  v1 <- h1$se
  names(v1) <- parnames

```

```

        return(v1)
    } )
res6c <- miceadds::pool_mi( qhat=qhat, se=se )

# function runMI in semTools package
res6d <- semTools::runMI(model=lavmodel, data=imp1, m=length(imp1) )
# semTools version 0.4-9 provided an error message
# perform inference with mitml package
se2 <- lapply( se, FUN=function(ss){ ss^2 } ) # input variances
res6e <- mitml::testEstimates(qhat=qhat, uhat=se2)

### complete model estimation and inference in mitml

# convert into object of class mitml.list
ml02 <- mitml::as.mitml.list( data.ma02)
# estimate regression
mod7 <- with( ml02, stats::lm( read ~ hisei + female ) )
# inference
res7 <- mitml::testEstimates( mod7 )

### model comparison
summary(res1)
summary(res2)
summary(res3)
summary(res4)
summary(res5)
summary(res6b)
summary(res6c)
print(res6e)
print(res7)

## End(Not run)

```

Reval

R Utilities: Evaluates a String as an Expression in R

Description

This function evaluates a string as an R expression.

Usage

```
Reval(Rstring, print.string=TRUE, n.eval.parent=1)
```

```
# Reval( print(Rstring) )
Revalpr(Rstring, print.string=TRUE)
```

```
# Reval( print(str(Rstring)) )
Revalprstr(Rstring, print.string=TRUE)
```



```
# Reval( print(round(Rstring, digits)) )
Revalpr_round( Rstring, digits=5, print.string=TRUE)

# Reval( print(max(abs(Rstring_x - Rstring_y)) ) )
Revalpr_maxabs( Rstring_x, Rstring_y, print.string=TRUE, na.rm=FALSE)
```

Arguments

Rstring	String which shall be evaluated in R
print.string	Should the string printed on the console?
n.eval.parent	Index of parent environment in which the R command should be evaluated.
digits	Number of digits after decimal.
Rstring_x	String corresponding to an R object
Rstring_y	String corresponding to an R object
na.rm	Logical indicating whether missing values should be removed from calculation

Details

The string is evaluated in the parent environment. See [base::eval](#) for the definition of environments in R.

Examples

```
# This function is simply a shortage function
# See the definition of this function:
Reval <- function( Rstring, print.string=TRUE){
  if (print.string){ cat( paste( Rstring ), "\n" ) }
  eval.parent( parse( text=paste( Rstring ) ), n=1 )
}

Reval( "a <- 2^3" )
## a <- 2^3
a
## [1] 8
```

Rfunction_include_argument_values

Utility Functions for Writing R Functions

Description

Utility functions for writing R functions.

Usage

```
## include argument values in a function input
Rfunction_include_argument_values(string, maxlen=70)

## assign objects to entries in a list
Rfunction_output_list_result_function(string, mid=" <- res$")

## delete declaration of Rcpp and RcppArmadillo object classes
Rcppfunction_remove_classes(string, maxlen=70, remove=TRUE)
```

Arguments

string	String
maxlen	Maximal string length for output
mid	Middle term in the output
remove	Logical indicating whether object classes should be removed

Value

String

Examples

```
#####
# EXAMPLE 1: Toy examples
#####

####* extend missing arguments

string <- "
  mice.impute.2l.pls2(y, ry, x, type, pls.facs=pls.facs )
"

cat( miceadds::Rfunction_include_argument_values(string) )
##   mice.impute.2l.pls2( y=y, ry=ry, x=x, type=type, pls.facs=pls.facs )

####* assignment to objects as entries in a list

string <- "
  list( vname=vname, p, type=type, data=data, levels_id )
"

cat( miceadds::Rfunction_output_list_result_function( string ) )
##
## vname <- res$vname
## p <- res$p
## type <- res$type
## data <- res$data
## levels_id <- res$levels_id

string <- "
```

```

arma::colvec miceadds_rcpp_rtnorm2( arma::colvec mu,
                                   double sigma0, arma::colvec lower, arma::colvec upper,
                                   double minval, double maxval)
"

cat( miceadds::Rcppfunction_remove_classes(string, maxlen=70) )
cat( miceadds::Rcppfunction_remove_classes(string, maxlen=70, remove=FALSE) )

```

Rhat.mice

Rhat Convergence Statistic of a mice Imputation

Description

Computes the Rhat statistic for a `mids` object.

Usage

```
Rhat.mice(mice.object)
```

Arguments

`mice.object` Object of class `mids`

Value

Data frame containing the Rhat statistic for mean and variances for all variables of the Markov chains used for imputation

References

Gelman, A., & Hill, J. (2007). *Data analysis using regression and multilevel/hierarchical models*. Cambridge University Press.

Examples

```

## Not run:
#####
# EXAMPLE 1: Rhat statistic for nhanes data
#####

library(mice)
data(nhanes, package="mice")
set.seed(9090)

# nhanes 3 parallel chains
imp1 <- mice::mice( nhanes, m=3, maxit=10, method=rep("norm", 4 ))
miceadds::Rhat.mice( imp1 )
##      variable MissProp Rhat.M.imp Rhat.Var.imp
## 1      bmi      36 1.0181998    1.155807
## 2      hyp      32 1.0717677    1.061174

```

```
## 3      chl      40 0.9717109    1.318721
## End(Not run)
```

```
round2      R Utilities: Rounding DIN 1333 (Kaufmaennisches Runden)
```

Description

This is a rounding function which rounds up for all numbers according to the rule of 'kaufmaennisches Runden' (DIN 1333).

Usage

```
round2(vec, digits=0)
```

Arguments

```
vec          Numeric vector
digits       Number of digits after decimal for rounding
```

Value

Vector with rounded values

Examples

```
#####
# EXAMPLE 1:
#####

vec <- c( 1.5, 2.5, 3.5, 1.51, 1.49)
vec
round(vec)
round2(vec)
## > vec
## [1] 1.50 2.50 3.50 1.51 1.49
## > round(vec)
## [1] 2 2 4 2 1
## > miceadds::round2(vec)
## [1] 2 3 4 2 1

#####
# EXAMPLE 2:
#####

vec <- - c( 1.5, 2.5, 3.5, 1.51, 1.49)
vec
round(vec)
```

```

round2(vec)
## > vec
## [1] -1.50 -2.50 -3.50 -1.51 -1.49
## > round(vec)
## [1] -2 -2 -4 -2 -1
## > miceadds::round2(vec)
## [1] -2 -3 -4 -2 -1

#####
# EXAMPLE 3:
#####

vec <- c(8.4999999, 8.5, 8.501, 7.4999999, 7.5, 7.501 )
round(vec)
round2( vec )
round2( vec, digits=1)
round2( -vec )
## > round(vec)
## [1] 8 8 9 7 8 8
## > miceadds::round2( vec )
## [1] 8 9 9 7 8 8
## > miceadds::round2( vec, digits=1)
## [1] 8.5 8.5 8.5 7.5 7.5 7.5
## > miceadds::round2( -vec )
## [1] -8 -9 -9 -7 -8 -8

```

Rsessinfo

R Utilities: R Session Information

Description

Informs about current R session.

Usage

```
Rsessinfo()
```

Value

A string containing reduced information about R session info

Examples

```

Rsessinfo()
## > miceadds::Rsessinfo()
## [1] "R version 2.15.2 (2012-10-26) x86_64, mingw32 | nodename=SD70 | login=robitzsch"

```

save.data

*R Utilities: Saving/Writing Data Files using miceadds***Description**

This function is a wrapper function for saving or writing data frames or matrices.

Usage

```
save.data( data, filename, type="Rdata", path=getwd(), row.names=FALSE, na=NULL,
           suffix=NULL, suffix_space="__", index=FALSE, systime=FALSE, ...)
```

Arguments

data	Data frame or matrix to be saved
filename	Name of data file
type	The type of file in which the data frame or matrix should be loaded. This can be Rdata (for R binary format, using <code>base::save</code> , csv (using <code>utils::write.csv2</code>), csv (using <code>utils::write.csv</code>), table (using <code>utils::write.table</code>) or sav (using <code>sjlabelled::write_spss</code>). type can also be a vector if the data frame should be saved in multiple formats.
path	Directory from which the dataset should be loaded
row.names	Optional logical indicating whether row names should be included in saved csv or csv2 files.
na	Missing value handling. The default is "" for type="csv" and type="csv2" and is "." for type="table".
suffix	Optional suffix in file name.
suffix_space	Optional place holder if a suffix is used.
index	Optional logical indicating whether an index should be included in the first column using the function <code>index.dataframe</code> .
systime	If index=TRUE, this optional logical indicates whether a time stamp should be included in the second column.
...	Further arguments to be passed to <code>save</code> , <code>write.csv2</code> , <code>write.csv</code> , <code>write.table</code> or <code>sjlabelled::write_spss</code> .

See Also

See `load.Rdata` and `load.data` for saving/writing R data frames.

Examples

```

## Not run:
#####
# EXAMPLE 1: Save dataset data.ma01
#####

#*** use data.ma01 as an example for writing data files using save.data
data(data.ma01)
dat <- data.ma01

# set a working directory
pf2 <- "P:/ARb/temp_miceadds"

# save data in Rdata format
miceadds::save.data( dat, filename="ma01data", type="Rdata", path=pf2)

# save data in table format without row and column names
miceadds::save.data( dat, filename="ma01data", type="table", path=pf2,
  row.names=FALSE, na=".", col.names=FALSE)

# save data in csv2 format, including time stamp in file name
# and row index and time stamp in saved data
miceadds::save.data( dat, filename="ma01data", type="csv2", path=pf2,
  row.names=FALSE, na="", suffix=systime()[5],
  index=TRUE, systime=TRUE )

# save data in sav format
miceadds::save.data( dat, filename="ma02data", type="sav", path=pf2 )

# save data file in different formats
types <- c("Rdata", "csv2", "sav")
sapply( types, FUN=function(type){
  miceadds::save.data( dat, filename="ma02data", type=type, path=pf2,
    suffix=miceadds::systime()[3], row.names=TRUE )
} )

# save data frame in multiple file formats (sav, table and csv2)
miceadds::save.data( dat, filename="ma03data", type=c("sav","table","csv2"), path=pf2,
  suffix=miceadds::systime()[7] )

## End(Not run)

```

save.Rdata

*R Utilities: Save a Data Frame in Rdata Format***Description**

This function saves a data frame in a Rdata format.

Usage

```
save.Rdata(dat, name, path=NULL, part.numb=1000)
```

Arguments

dat	Data frame
name	Name of the R object to be saved
path	Directory for saving the object
part.numb	Number of rows of the data frame which should also be saved in csv format. The default is saving 1000 rows.

Examples

```
## Not run:
dfr <- matrix( 2*1:12-3, 4,3 )
save.Rdata( dfr, "dataframe_test" )
## End(Not run)
```

scale_datlist	<i>Adding a Standardized Variable to a List of Multiply Imputed Datasets or a Single Datasets</i>
---------------	---

Description

Adds a standardized variable to a list of multiply imputed datasets or a single dataset. This function extends `base::scale` for a data frame to a list of multiply imputed datasets.

Usage

```
scale_datlist(datlist, orig_var, trafo_var, weights=NULL, M=0, SD=1,
  digits=NULL)
```

Arguments

datlist	A data frame, a list of multiply imputed datasets of one of the classes <code>datlist</code> or <code>imputationList</code> or a list of nested multiply imputed datasets of one of the classes <code>nested_datlist</code> or <code>NestedImputationList</code> .
orig_var	Vector with names of the variables to be transformed
trafo_var	Vector with names of the standardized variables
weights	Optional vector of sample weights. Alternatively, the weights can also be a string indicating the variable used from <code>datlist</code> .
M	Mean of the transformed variable
SD	Standard deviation of the transformed variable
digits	Number of digits used for rounding the standardized variable

Value

A vector or a matrix

See Also

[base::scale](#), [ma.scale2](#)

Examples

```
## Not run:
#####
# EXAMPLE 1: Standardized variables in list of multiply imputed datasets
#####

data(data.ma02)
datlist <- data.ma02

#--- object of class 'datlist'
datlist <- miceadds::datlist_create( datlist )

# mean and SD of variable hisei
miceadds::ma.wtd.meanNA(data=datlist, weights=datlist[[1]]$studwgt, vars="hisei" )
mean( unlist( lapply( datlist, FUN=function(data){
  stats::weighted.mean( data$hisei, data$studwgt ) } ) ) )
miceadds::ma.wtd.sdNA(data=datlist, weights=datlist[[1]]$studwgt, vars="hisei" )
mean( unlist( lapply( datlist, FUN=function(data){
  sqrt( Hmisc::wtd.var( data$hisei, data$studwgt ) ) } ) ) )

# standardize variable hisei to M=100 and SD=15
datlist1a <- miceadds::scale_datlist( datlist=datlist, orig_var="hisei",
  trafo_var="hisei100", weights=datlist[[1]]$studwgt, M=100, SD=15 )

# check mean and SD
miceadds::ma.wtd.meanNA(data=datlist1a, weights=datlist[[1]]$studwgt, vars="hisei100")
miceadds::ma.wtd.sdNA(data=datlist1a, weights=datlist[[1]]$studwgt, vars="hisei100")

#--- do standardization for unweighted sample with books <=3
# -> define a weighting variable at first
datlist0 <- mitools::imputationList( datlist )
datlist2a <- miceadds::within.imputationList( datlist0, {
  # define weighting variable
  wgt_books <- 1 * ( books <=3 )
} )

# standardize variable hisei to M=100 and SD=15 with respect to weighting variable
datlist2b <- miceadds::scale_datlist( datlist=datlist2a, orig_var="hisei", trafo_var="hisei100",
  weights="wgt_books", M=100, SD=15 )

# check mean and SD (groupwise)
miceadds::ma.wtd.meanNA(data=datlist1a, weights=datlist[[1]]$studwgt, vars="hisei100")
miceadds::ma.wtd.sdNA(data=datlist1a, weights=datlist[[1]]$studwgt, vars="hisei100")
```

```

#--- transformation for a single dataset
dat0 <- datlist[[1]]
dat0a <- miceadds::scale_datlist( datlist=dat0, orig_var="hisei", trafo_var="hisei100",
                                weights=dat0$studwgt, M=100, SD=15 )
stats::weighted.mean( dat0a[, "hisei"], w=dat0a$studwgt )
stats::weighted.mean( dat0a[, "hisei100"], w=dat0a$studwgt )
sqrt( Hmisc::wtd.var( dat0a[, "hisei100"], weights=dat0a$studwgt ) )

#--- Standardizations for objects of class imputationList
datlist2 <- mitools::imputationList(datlist) # object class conversion
datlist2a <- miceadds::scale_datlist( datlist=datlist2, orig_var="hisei",
                                     trafo_var="hisei100", weights=datlist[[1]]$studwgt, M=100, SD=15 )

#####
# EXAMPLE 2: Standardized variables in list of nested multiply imputed datasets
#####

# nested multiply imputed dataset in BIFIEsurvey package
data(data.timss4, package="BIFIEsurvey")
datlist <- data.timss4
wgt <- datlist[[1]][[1]]$TOTWGT

# class nested.datlist
imp1 <- miceadds::nested.datlist_create( datlist )
# class NestedImputationList
imp2 <- miceadds::NestedImputationList( datlist )

# standardize variable scsci
imp1a <- miceadds::scale_datlist( datlist=imp1, orig_var="scsci", trafo_var="zscsci", weights=wgt)
# check descriptives
miceadds::ma.wtd.meanNA( imp1a, weights=wgt, vars=c("scsci", "zscsci" ) )
miceadds::ma.wtd.sdNA( imp1a, weights=wgt, vars=c("scsci", "zscsci" ) )

#####
# EXAMPLE 3: Standardization of variables for imputed data in mice package
#####

data(nhanes, package="mice")
set.seed(76)

#--- impute nhanes data
imp <- mice::mice(nhanes)
#--- convert into datlist
datlist <- miceadds::mids2datlist(imp)
#--- scale datlist (all variables)
vars <- colnames(nhanes)
sdatlist <- miceadds::scale_datlist(datlist, orig_var=vars, trafo_var=paste0("z",vars) )
#--- revert to mids object
imp2 <- miceadds::datlist2mids(sdatlist)
#*** compare descriptive statistics of objects
round( miceadds::mean0( mice::complete(imp, action=1) ), 2 )
round( miceadds::mean0( mice::complete(imp2, action=1) ), 2 )

```

```
## End(Not run)
```

```
scan.vec
```

```
R Utilities: Scan a Character Vector
```

Description

The function `scan.vec` function splits a string into a character vector. The function `scan0` is the `base::scan` function using the default `what="character"`.

Usage

```
scan.vec(vec)
scan.vector(vec)

scan0(file="", ...)
```

Arguments

<code>vec</code>	A string which should be split according to blanks
<code>file</code>	File to be scanned. See <code>base::scan</code> .
<code>...</code>	Further arguments to be passed. See <code>base::scan</code> .

See Also

[base::scan](#)

Examples

```
#####
# EXAMPLE 1: Example scan.vec | reading a string
#####

vars <- miceadds::scan.vector( "female urbgrad groesse Nausg grpgroesse privat ")
vars
## [1] "female"      "urbgrad"      "groesse"      "Nausg"        "grpgroesse"
## [6] "privat"

## the next lines are only commented out to fulfill CRAN checks
## vars2 <- miceadds::scan0()
##   female urbgrad groesse Nausg grpgroesse privat
```

 source.all

 R Utilities: Source all R or **Rcpp** Files within a Directory

Description

The function `source.all` sources all R files within a specified directory and is based on `base::source`.

The function `source.Rcpp.all` sources all **Rcpp** files within a specified directory and is based on `Rcpp::sourceCpp`.

The function `rcpp_create_header_file` creates a cpp header file for a **Rcpp** file.

Usage

```
source.all( path, grepstring="\\.R", print.source=TRUE, file_sep="__" )
```

```
source.Rcpp.all( path, file_names=NULL, ext="\\.cpp", excl="RcppExports",
  remove_temp_file=FALSE )
```

```
rcpp_create_header_file(file_name, pack=NULL, path=getwd() )
```

Arguments

<code>path</code>	Path where the files are located
<code>grepstring</code>	Which strings should be looked for? <code>grepstring</code> can also be a vector.
<code>print.source</code>	An optional logical whether the source process printed on the console?
<code>file_sep</code>	String at which file name should be split for looking for most recent files
<code>file_names</code>	Optional vector of (parts of) file names
<code>ext</code>	File extension for Rcpp files
<code>excl</code>	String indicating which files should be omitted from sourcing
<code>remove_temp_file</code>	Logical indicating whether temporary Rcpp files should be removed.
<code>file_name</code>	File name
<code>pack</code>	Optional string for package

Details

For loading header files, the line `// [include_header_file]` has to be included before loading the header file using a line of the form `#include "my_function.h"`.

Examples

```
## Not run:
# define path
path <- "c:/myfiles/"
# source all files containing the string 'Rex'
source.all( path, "Rex" )
## End(Not run)
```

Description

Applies descriptive statistics to a vector or a data frame. The function `stats0` is a general function. This function is used for extending the basic descriptive statistics functions from the **base** and **stats** package. The function `prop_miss` computes the proportion of missing data for each variable.

Usage

```
stats0(x, FUN, na.rm=TRUE,...)

max0(x, na.rm=TRUE)
mean0(x, na.rm=TRUE)
min0(x, na.rm=TRUE)
quantile0(x, probs=seq(0, 1, 0.25), na.rm=TRUE)
sd0(x, na.rm=TRUE)
var0(x, na.rm=TRUE)

prop_miss(x)
```

Arguments

<code>x</code>	Vector or a data frame
<code>FUN</code>	Function which is applied to <code>x</code>
<code>na.rm</code>	Logical indicating whether missing data should be removed
<code>probs</code>	Probabilities
<code>...</code>	Further arguments to be passed

Value

A vector or a matrix

See Also

[base::max](#), [base::mean](#), [base::min](#), [stats::quantile](#), [stats::sd](#), [stats::var](#)

Examples

```
#####
# EXAMPLE 1: Descriptive statistics toy datasets
#####

#-- simulate vector y and data frame dat
set.seed(765)
N <- 25 # number of observations
```

```

y <- stats::rnorm(N)
V <- 4 # number of variables
dat <- matrix( stats::rnorm( N*V ), ncol=V )
colnames(dat) <- paste0("V",1:V)

#-- standard deviation
apply( dat, 2, stats::sd )
sd0( dat )
#-- mean
apply( dat, 2, base::mean )
mean0( dat )
#-- quantile
apply( dat, 2, stats::quantile )
quantile0( dat )
#-- minimum and maximum
min0(dat)
max0(dat)

**** apply functions to missing data
dat1 <- dat
dat1[ cbind( c(2,5),2 ) ] <- NA

#-- proportion of missing data
prop_miss( dat1 )
#-- MAD statistic
stats0( dat, FUN=stats::mad )
#-- SD
sd0(y)

```

str_C.expand.grid *R Utilities: String Paste Combined with expand.grid*

Description

String paste combined with expand.grid

Usage

```
str_C.expand.grid(xlist, indices=NULL)
```

Arguments

xlist	A list of character vectors
indices	Optional vector of indices to be permuted in xlist

Value

A character vector

Examples

```
#####
# EXAMPLE 1: Some toy examples
#####

x1 <- list( c("a","b" ), c("t", "r","v") )
str_C.expand.grid( x1 )
## [1] "at" "bt" "ar" "br" "av" "bv"

x1 <- list( c("a","b" ), paste0("_", 1:4 ), c("t", "r","v") )
str_C.expand.grid( x1, indices=c(2,1,3) )
## [1] "_1at" "_1bt" "_2at" "_2bt" "_3at" "_3bt" "_4at" "_4bt" "_1ar" "_1br"
## [11] "_2ar" "_2br" "_3ar" "_3br" "_4ar" "_4br" "_1av" "_1bv" "_2av" "_2bv"
## [21] "_3av" "_3bv" "_4av" "_4bv"

## Not run:
#####
## The function 'str_C.expand.grid' is currently defined as
function( xlist, indices=NULL )
{
  xeg <- expand.grid( xlist)
  if ( ! is.null(indices) ){ xeg <- xeg[, indices ]}
  apply( xeg, 1, FUN=function(vv){ paste0( vv, collapse="" ) } )
}
#####

## End(Not run)
```

subset_datlist

Subsetting Multiply Imputed Datasets and Nested Multiply Imputed Datasets

Description

Returns a subsets of multiply imputed datasets or nested multiply imputed datasets. These function allows choosing parts of the imputed datasets using the `index` argument for multiply imputed datasets and `index_between` and `index_within` for nested multiply imputed datasets as well as the application of the `base::subset` S3 method for selecting cases and variables in datasets.

Usage

```
subset_datlist(datlist, subset=TRUE, select=NULL, expr_subset=NULL,
              index=NULL, toclass="datlist")

## S3 method for class 'datlist'
subset(x, subset, select=NULL, expr_subset=NULL,
      index=NULL, ...)

## S3 method for class 'imputationList'
subset(x, subset, select=NULL, expr_subset=NULL,
```

```

        index=NULL, ...)
## S3 method for class 'mids'
subset(x, subset, select=NULL, expr_subset=NULL,
       index=NULL, ...)
## S3 method for class 'mids.1chain'
subset(x, subset, select=NULL, expr_subset=NULL,
       index=NULL, ...)

subset_nested.datlist( datlist, subset=TRUE, select=NULL, expr_subset=NULL,
                      index_between=NULL, index_within=NULL, toclass="nested.datlist",
                      simplify=FALSE )

## S3 method for class 'nested.datlist'
subset(x, subset, select=NULL, expr_subset=NULL,
       index_between=NULL, index_within=NULL, simplify=FALSE, ...)
## S3 method for class 'NestedImputationList'
subset(x, subset, select=NULL, expr_subset=NULL,
       index_between=NULL, index_within=NULL, simplify=FALSE, ...)

```

Arguments

datlist	For subset_datlist it is a list of datasets or an object of class datlist, imputationList, mids or mids.1chain. For subset_nested.datlist it is a list of datasets or an object of class nested.datlist or NestedImputationList.
subset	Logical expression indicating elements or rows to keep, see base::subset . subset can also be a numeric vector containing row indices.
select	Expression indicating columns to select from a data frame
expr_subset	Expression indicating a selection criterion for selection rows.
index	Vector of indices indicating which of the multiply imputed datasets should be selected.
toclass	The object class in which the datasets should be saved.
index_between	Index for between nest datasets
index_within	Index for within nest datasets
simplify	Optional logical indicating whether a nested multiply imputed dataset should be simplified to a multiplied imputed dataset.
x	Object containing multiply imputed or nested multiply imputed datasets
...	Further arguments to be passed.

Value

For multiply imputed datasets: Object of class datlist, imputationList or mids
 For nested multiply imputed datasets: Object of class nested.datlist or NestedImputationList.

Note

If subsetting is applied to objects of class `mids` (or `mids.1chain`), then informations about the imputation procedure are lost.

See Also

[base::subset](#)

Examples

```
#####
# EXAMPLE 1: Subsetting and selection of multiply imputed datasets
#####

data(data.ma02)

# define original list of datasets
datlist1a <- data.ma02
# object of class datlist
datlist1b <- miceadds::datlist_create(datlist1a)
datlist1b
# object of class imputationList
datlist1c <- mitools::imputationList(datlist1a)
datlist1c
# object of class mids
datlist1d <- miceadds::datlist2mids(datlist1a)
datlist1d

# select some imputed datasets
datlist2a <- miceadds::subset_datlist( datlist1a, index=c(5,3,7) )
datlist2a
# convert to class imputationList
datlist2b <- miceadds::subset_datlist( datlist1a, index=c(5,3,7),
                                     toclass="imputationList")
datlist2b
# convert to class mids
datlist2c <- miceadds::subset_datlist( datlist1a, index=1:3, toclass="mids")
datlist2c

## Not run:
# select some variables
datlist3a <- miceadds::subset_datlist( datlist1a, select=c("idstud", "books") )
datlist3a
# Because datlist1b is a datlist it is equivalent to
datlist3b <- subset( datlist1b, select=c("idstud", "books") )
datlist3b
# operating on imputationList class
datlist3c <- miceadds::subset_datlist( datlist1c, select=c("idstud", "books") )
datlist3c
# operating on mids class
datlist3d <- miceadds::subset_datlist( datlist1d, select=c("idstud", "books") )
datlist3d
```

```

# selection of rows and columns in multiply imputed datasets
datlist4a <- miceadds::subset_datlist( datlist1a, index=1:5,
                                     subset=datlist1a[[1]]$idschool < 1067,
                                     select=c("idstud", "idschool","hisei") )
datlist4a
# convert to class mids
datlist4b <- miceadds::subset_datlist( datlist1a, index=1:5,
                                     subset=datlist1a[[1]]$idschool < 1067,
                                     select=c("idstud", "idschool","hisei"), toclass="mids" )
datlist4b
# The same functionality, but now applying to object of class mids datlist1d
datlist4c <- subset( datlist1d, index=1:5, subset=datlist1a[[1]]$idschool < 1067,
                   select=c("idstud", "idschool","hisei") )
datlist4c

# expression for selecting rows specific in each data frame
# which can result in differently sized datasets (because the variable
# migrant is imputed)
datlist5a <- miceadds::subset_datlist( datlist1a, expr_subset=migrant==1 )
datlist5a

# select the first 100 cases
datlist6a <- miceadds::subset_datlist( datlist1a, select=c("idstud", "books"),
                                     subset=1:100 )
datlist6a

#####
# EXAMPLE 2: Subsetting and selection of nested multiply imputed datasets
#####

library(BIFIEsurvey)
data(data.timss4, package="BIFIEsurvey")
dat <- data.timss4

# create object of class 'nested.datlist'
datlist1a <- miceadds::nested.datlist_create( dat )
# create object of class 'NestedImputationList'
datlist1b <- miceadds::NestedImputationList(dat)
# create object of class 'mids.nmi'
datlist1c <- miceadds::datlist2mids(dat)

# select some between datasets
datlist2a <- subset_nested.datlist( datlist1a, index_between=c(1,3,4) )
datlist2a
# shorter version
datlist2b <- subset( datlist1a, index_between=c(1,3,4) )
datlist2b
# conversion of a NestedImputationList
datlist2c <- subset( datlist1b, index_between=c(1,3,4))
datlist2c
# select rows and columns
sel_cases <- datlist1a[[1]][[1]]$JKZONE <=42
datlist3a <- subset( datlist1a, subset=sel_cases,

```

```

                                select=c("IDSTUD","books", "ASMMAT") )
datlist3a
# remove within nest
datlist4a <- subset( datlist1a, index_within=1 )
datlist4a
# remove within nest and simplify structure
datlist4b <- subset( datlist1a, index_within=1, simplify=TRUE)
datlist4b
datlist4c <- subset( datlist1b, index_within=1, simplify=TRUE)
datlist4c
# remove between nest
datlist5a <- subset( datlist1a, index_between=1, simplify=TRUE)
datlist5a
datlist5b <- subset( datlist1b, index_between=1, simplify=TRUE)
datlist5b

## End(Not run)

```

sumpreserving.rounding

Sum Preserving Rounding

Description

This function implements sum preserving rounding. If the supplied data is a matrix, then the sum of all row entries is preserved.

Usage

```
sumpreserving.rounding(data, digits=0, preserve=TRUE)
```

Arguments

data	Vector or data frame
digits	Number of digits to be round
preserve	Should the sum be preserved?

Examples

```

#####
# EXAMPLE 1:
#####

# define example data
data <- c( 1455, 1261, 1067, 970, 582, 97 )
data <- 100 * data / sum(data)

( x1 <- round( data ) )
sum(x1)

```

```

(x2 <- miceadds::sumpreserving.rounding( data ) )
sum(x2)

## > ( x1 <- round( data ) )
## [1] 27 23 20 18 11 2
## > sum(x1)
## [1] 101
## > (x2 <- miceadds::sumpreserving.rounding( data ) )
## [1] 27 23 20 18 10 2
## > sum(x2)
## [1] 100

#####
# EXAMPLE 2:
#####

# matrix input
data <- rbind( data, data )
( x1 <- round( data ) )
rowSums(x1)
(x2 <- miceadds::sumpreserving.rounding( data ) )
rowSums(x2)

#####
# EXAMPLE 3:
#####

x2 <- c( 1.4, 1.4, 1.2 )
round(x2)
sumpreserving.rounding(x2)
## > round(x2)
## [1] 1 1 1
## > miceadds::sumpreserving.rounding(x2)
## [1] 1 2 1

```

systemtime

R Utilities: Various Strings Representing System Time

Description

This function generates system time strings in several formats.

Usage

```
systemtime()
```

Value

A vector with entries of system time (see Examples).

Examples

```
#####
# EXAMPLE 1: Output of systime
#####

systime()
##
## > miceadds::systime()
## [1] "2016-02-29 10:25:44"
## [2] "2016-02-29"
## [3] "20160229"
## [4] "2016-02-29_1025"
## [5] "2016-02-29_1000"
## [6] "20160229_102544"
## [7] "20160229102544"
## [8] "IPNERZW-C014_20160229102544"
```

tw.imputation	<i>Two-Way Imputation</i>
---------------	---------------------------

Description

Two-way imputation using the simple method of Sijtsma and van der Ark (2003) and the MCMC based imputation of van Ginkel, van der Ark, Sijtsma and Vermunt (2007).

Usage

```
tw.imputation(data, integer=FALSE)

tw.mcmc.imputation(data, iter=100, integer=FALSE)
```

Arguments

data	Matrix of item responses corresponding to a scale
integer	A logical indicating whether imputed values should be integers. The default is FALSE.
iter	Number of iterations

Details

For persons p and items i , the two-way imputation is conducted by posing a linear model of tau-equivalent measurements:

$$X_{pi} = \theta_p + b_i + \varepsilon_{ij}$$

If the score X_{pi} is missing then it is imputed by

$$\hat{X}_{pi} = \tilde{X}_p + b_i$$

where \tilde{X}_p is the person mean of person p of the remaining items with observed responses.

The two-way imputation can also be seen as a scaling procedure to obtain a scale score which takes different item means into account.

Value

A matrix with original and imputed values

References

Sijtsma, K., & Van der Ark, L. A. (2003). Investigation and treatment of missing item scores in test and questionnaire data. *Multivariate Behavioral Research*, 38, 505-528.

Van Ginkel, J. R., Van der Ark, A., Sijtsma, K., & Vermunt, J. K. (2007). Two-way imputation: A Bayesian method for estimating missing scores in tests and questionnaires, and an accurate approximation. *Computational Statistics & Data Analysis*, 51, 4013-4027.

See Also

The two-way imputation method is also implemented in the `TestDataImputation::Twoway` function of the **TestDataImputation** package.

Examples

```
#####
# EXAMPLE 1: Two-way imputation data.internet
#####

data(data.internet)
data <- data.internet

###
# Model 1: Two-way imputation method of Sijtsma and van der Ark (2003)
set.seed(765)
dat.imp <- miceadds::tw.imputation( data )
dat.imp[ 278:281,]
##      IN9      IN10      IN11      IN12
## 278  5 4.829006 5.000000 4.941611
## 279  5 4.000000 4.78979 4.000000
## 280  7 4.000000 7.000000 7.000000
## 281  4 3.000000 5.000000 5.000000

## Not run:
###
# Model 2: Two-way imputation method using MCMC
dat.imp <- miceadds::tw.mcmc.imputation( data, iter=3)
dat.imp[ 278:281,]
##      IN9      IN10      IN11      IN12
## 278  5 6.089222 5.000000 3.017244
## 279  5 4.000000 5.063547 4.000000
## 280  7 4.000000 7.000000 7.000000
## 281  4 3.000000 5.000000 5.000000

## End(Not run)
```

VariableNames2String *Stringing Variable Names with Line Breaks*

Description

Stringing variable names with line breaks.

Usage

```
VariableNames2String(vars, breaks=80, sep=" ")
```

Arguments

vars	Vector with variable names
breaks	Numeric value for line break of variable string
sep	Separator

Value

String with line breaks

Examples

```
#####  
# EXAMPLE 1: Toy example  
#####  
  
data(data.ma01)  
# extract variable names  
vars <- colnames(data.ma01)  
# convert into a long string with line breaks at column 25  
vars2 <- miceadds::VariableNames2String( vars, breaks=25)  
vars  
## [1] "idstud" "idschool" "studwgt" "math" "read" "migrant"  
## [7] "books" "hisei" "paredu" "female" "urban"  
vars2  
## idstud idschool studwgt  
## math read migrant books  
## hisei paredu female  
## urban
```

 visitSequence.determine

Automatic Determination of a Visit Sequence in mice

Description

This function automatically determines a visit sequence for a specified model in `mice::mice` when passive variables are defined as imputation methods. Note that redundant visits could be computed and a user should check the plausibility of the result.

Usage

```
visitSequence.determine(impMethod, vis, data, maxit=10)
```

Arguments

<code>impMethod</code>	Vector with imputation methods
<code>vis</code>	Initial vector of visit sequence
<code>data</code>	Data frame to be used for multiple imputations
<code>maxit</code>	Maximum number of iteration for computation of the updated visit sequence

Value

Updated vector of the visit sequence

See Also

Used in the `mice::mice` function as an argument. The function `mice::make.visitSequence` creates a visit sequence.

Examples

```
#####
# EXAMPLE 1: Visit sequence for a small imputation model
#####

data( data.smallscale )
# select a small number of variables
dat <- data.smallscale[, paste0("v",1:4) ]
V <- ncol(dat)

# define initial vector of imputation methods
impMethod <- rep("norm", V)
names(impMethod) <- colnames(dat)
# define variable names and imputation method for passive variables in a data frame
dfr.impMeth <- data.frame( "variable"=NA,
                          "impMethod"=NA )
dfr.impMeth[1,] <- c("v1_v1", "~ I(v1^2)" )
```



```

dfr.impMeth[2,] <- c("v2_v4", "~ I(v2*v4)" )
dfr.impMeth[3,] <- c("v4log", "~ I( log(abs(v4)))" )
dfr.impMeth[4,] <- c("v12", "~ I( v1 + v2 + 3*v1_v1 - v2_v4 )" )
# add variables to dataset and imputation methods
VV <- nrow(dfr.impMeth)
for (vv in 1:VV){
  impMethod[ dfr.impMeth[vv,1] ] <- dfr.impMeth[vv,2]
  dat[, dfr.impMeth[vv,1] ] <- NA
}

# run empty imputation model to obtain initial vector of visit sequence
imp0 <- mice::mice( dat, m=1, method=impMethod, maxit=0 )
imp0$vis

# update visit sequence
vis1 <- miceadds::visitSequence.determine( impMethod=impMethod, vis=imp0$vis, data=dat)

# imputation with updated visit sequence
imp <- mice::mice( dat, m=1, method=impMethod, visitSequence=vis1, maxit=2)

```

with.miceadds

Evaluates an Expression for (Nested) Multiply Imputed Datasets

Description

Evaluates an expression for (nested) multiply imputed datasets. These functions extend the following functions: [mice::with.mids](#), [base::with](#), [base::within.data.frame](#), [mitools::with.imputationList](#).

The withPool functions try to pool estimates (by simple averaging) obtained by with or a list of results of imputed datasets.

Usage

```

## S3 method for class 'mids.1chain'
with(data, expr, ...)
## S3 method for class 'datlist'
with(data, expr, fun, ...)

## S3 method for class 'mids.nmi'
with(data, expr, ...)
## S3 method for class 'nested.datlist'
with(data, expr, fun, ...)
## S3 method for class 'NestedImputationList'
with(data, expr, fun, ...)

## S3 method for class 'datlist'
within(data, expr, ...)
## S3 method for class 'imputationList'
within(data, expr, ...)

```

```
## S3 method for class 'nested.datlist'
within(data, expr, ...)
## S3 method for class 'NestedImputationList'
within(data, expr, ...)

withPool_MI(x, ...)

withPool_NMI(x, ...)

## S3 method for class 'mira.nmi'
summary(object, ...)
```

Arguments

data	Object of class <code>mids.1chain</code> , <code>mids.nmi</code> , <code>imputationList</code> or <code>NestedImputationList</code>
expr	Expression with a formula object.
fun	A function taking a data frame argument
...	Additional parameters to be passed to <code>expr</code> .
object	Object of class <code>mira.nmi</code> .
x	List with vectors or matrices as results of an analysis for (nested) multiply imputed datasets.

Value

`with.mids.1chain`: List of class `mira`.

`with.mids.nmi`: List of class `mira.nmi`.

`with.datlist`: List of class `imputationResultList`.

`with.NestedImputationList` or `with.nested.datlist`: List of class `NestedImputationResultList`.

`within.imputationList`: List of class `imputationList`.

`within.NestedImputationList`: List of class `NestedImputationList`.

`withPool_MI` or `withPool_NMI`: Vector or matrix with pooled estimates

Author(s)

Slightly modified code of `mice::with.mids`, `mice::summary.mira`, `base::within.data.frame`

See Also

See the corresponding functionality in **base**, **mice**, **mitools** and **mitml** packages:
[mice::with.mids](#), [mitools::with.imputationList](#), [mitml::with.mitml.list](#), [base::with](#)
[base::within.data.frame](#), [mitml::within.mitml.list](#),
[mice::summary.mira](#),
Imputation functions in **miceadds**: [mice.1chain](#), [mice.nmi](#)

Examples

```
#####
# EXAMPLE 1: One chain nhanes data | application of 'with' and 'within'
#####

library(mice)
data(nhanes, package="mice")
set.seed(9090)

# nhanes data in one chain
imp <- miceadds::mice.1chain( nhanes, burnin=5, iter=40, Nimp=4 )
# apply linear regression
res <- with( imp, expr=stats::lm( hyp ~ age + bmi ) )
summary(res)
# pool results
summary( mice::pool(res))

# calculate some descriptive statistics
res2 <- with( imp, expr=c("M1"=mean(hyp), "SD_age"=stats::sd(age) ) )
# pool estimates
withPool_MI(res2)

# with method for datlist
imp1 <- miceadds::datlist_create(imp)
res2b <- with( imp1, fun=function(data){
  dfr <- data.frame("M"=colMeans(data),
                    "Q5"=apply( data, 2, stats::quantile, .05 ),
                    "Q95"=apply( data, 2, stats::quantile, .95 ) )
  return(dfr)
} )
withPool_MI(res2b)

# convert mids object into an object of class imputationList
datlist <- miceadds::mids2datlist( imp )
datlist <- mitools::imputationList(datlist)

## Not run:
# define formulas for modification of the data frames in imputationList object
datlist2 <- within( datlist, {
  age.D3 <- 1*(age==3)
  hyp_chl <- hyp * chl
} )
# look at modified dataset
head( datlist2$imputations[[1]] )

# convert into a datlist
datlist2b <- miceadds::datlist_create( datlist2 )

# apply linear model using expression
mod1a <- with( datlist2, expr=stats::lm( hyp ~ age.D3 ) )
# do the same but now with a function argument
mod1b <- with( datlist2, fun=function(data){
```

```

        stats::lm( data$hyp ~ data$age.D3 )
      } )
# apply the same model for object datlist2b
mod2a <- with( datlist2b, expr=lm( hyp ~ age.D3 ) )
mod2b <- with( datlist2b, fun=function(data){
  stats::lm( data$hyp ~ data$age.D3 )
} )

mitools::MIcombine(mod1a)
mitools::MIcombine(mod1b)
mitools::MIcombine(mod2a)
mitools::MIcombine(mod2b)

#####
# EXAMPLE 2: Nested multiple imputation and application of with/within methods
#####

library(BIFIEsurvey)
data(data.timss2, package="BIFIEsurvey" )
datlist <- data.timss2

# remove first four variables
M <- length(datlist)
for (ll in 1:M){
  datlist[[ll]] <- datlist[[ll]][, -c(1:4) ]
}

# nested multiple imputation using mice
imp1 <- miceadds::mice.nmi( datlist, m=4, maxit=3 )
summary(imp1)
# apply linear model and use summary method for all analyses of imputed datasets
res1 <- with( imp1, stats::lm( ASMMAT ~ migrant + female ) )
summary(res1)

# convert mids.nmi object into an object of class NestedImputationList
datlist1 <- miceadds::mids2datlist( imp1 )
datlist1 <- miceadds::NestedImputationList( datlist1 )
# convert into nested.datlist object
datlist1b <- miceadds::nested.datlist_create(datlist1)

# use with function
res1b <- with( datlist1, stats::glm( ASMMAT ~ migrant + female ) )
# apply for nested.datlist
res1c <- with( datlist1b, stats::glm( ASMMAT ~ migrant + female ) )

# use within function for data transformations
datlist2 <- within( datlist1, {
  highsc <- 1*(ASSSCI > 600)
  books_dum <- 1*(books>=3)
  rm(scsci) # remove variable scsci
} )

# include random number in each dataset

```

```

N <- attr( datlist1b, "nobs")
datlist3 <- within( datlist1b, {
  rn <- stats::runif( N, 0, .5 )
} )

#-- some applications of withPool_NMI
# mean and SD
res3a <- with( imp1, c( "m1"=mean(ASMMAT), "sd1"=stats::sd(ASMMAT) ) )
withPool_NMI(res3a)
# quantiles
vars <- c("ASMMAT", "lang", "scsci")
res3b <- with( datlist1b, fun=function(data){
  dat <- data[,vars]
  res0 <- sapply( vars, FUN=function(vv){
    stats::quantile( dat[,vv], probs=c(.25, .50, .75) )
  } )
  t(res0)
} )
withPool_NMI(res3b)

## End(Not run)

```

write.datlist

Write a List of Multiply Imputed Datasets

Description

Writes a list of multiply imputed datasets.

Usage

```

write.datlist(datlist, name, include.varnames=TRUE, type="csv2",
  separate=TRUE, Mplus=FALSE, round=NULL, Rdata=TRUE,
  subdir=TRUE, ...)

```

Arguments

datlist	List of imputed datasets. Can also be an object of class <code>mids</code> , <code>mids.1chain</code> or <code>imputationList</code>
name	Name of files to be saved
include.varnames	Logical indicating whether variables should be saved
type	File type of datasets to be saved, see save.data .
separate	Logical indicating whether imputed datasets should be written in separate files.
Mplus	Logical indicating whether files should be written for usage in Mplus software
round	Number of digits to round after decimal. The default is no rounding.
Rdata	Logical indicating whether <code>datlist</code> should also be saved in R binary format.
subdir	Logical indicating whether results should be written into a subdirectory.
...	Further arguments to be passed to save.data .

See Also

See also [mice::mids2mplus](#), [mice::mids2spss](#) and [write.mice.imputation](#) for writing objects of class `mids`.

See also [Amelia::write.amelia](#) for writing imputed datasets in **Amelia**.

Examples

```
## Not run:
#####
# EXAMPLE 1: Write data list imputed in mice
#####

data(data.ma01)
dat <- as.matrix(data.ma01)

# start with empty imputation
imp0 <- mice::mice( dat, maxit=0)

# modify predictor matrix
predM <- imp0$predictorMatrix
predM[, c("idschool", "idstud" ) ] <- 0
# modify imputation method
impMeth <- imp0$method
impMeth[ impMeth=="pmm" ] <- "norm"

# do imputations in mice
imp <- mice::mice( dat, predictorMatrix=predM, method=impMeth, m=3, maxit=4 )

# write imputed data in format "csv2" and round after 4 digits
write.datlist( datlist=imp, name="mice_imp_csv2", round=4 )
# write imputed data in R binary format
write.datlist( datlist=imp, name="mice_imp_Rdata", type="Rdata")
# write data for Mplus usage
write.datlist( datlist=imp, name="mice_imp_Mplus", Mplus=TRUE, round=5)

## End(Not run)
```

write.fwf2

Reading and Writing Files in Fixed Width Format

Description

Reads and writes files in fixed width format. The functions are written for being more efficient than [utils::read.fwf](#).

Usage

```
write.fwf2(dat, format.full, format.round, file)
```

```
read.fwf2( file, format.full, variables=NULL)
```

Arguments

dat	Data frame (or matrix). Variables can be numeric or strings. However, string length of string variables are not allowed to be larger than what is specified in format.full.
format.full	Vector with fixed width variable lengths
format.round	Vector with digits after decimals
file	File name
variables	Optional vector with variable names

See Also

[utils::read.fwf](#)

Examples

```
## Not run:
#####
# EXAMPLE 1: Write and read a file in fixed width format
#####

# set working directory
path <- "P:/ARb/temp"
setwd(path)

# define a data frame
set.seed(9876)
dat <- data.frame( "x"=seq( 1, 21, len=5), "y"=stats::runif( 5 ),
                  "z"=stats::rnorm( 5 ) )

# save data frame in fixed width format
format.full <- c(6, 6, 8 )
format.round <- c( 0, 2, 3 )
write.fwf2( dat, format.full=format.full, format.round=format.round,
            file="testdata" )

# read the data
dat1 <- miceadds::read.fwf2( file="testdata.dat", format.full=c(6,6,8),
                            variables=c("x","y","z") )
# check differences between data frames
dat - dat1

#####
# EXAMPLE 2: Write datasets containing some string variables in fwf format
#####

n <- 5
dat <- data.frame( "x"=stats::runif(n, 0, 9 ), "y"=LETTERS[1:n] )
write.fwf2(dat, format.full=c(4,2), format.round=c(2,0), file="testdata")

## End(Not run)
```

write.mice.imputation *Export Multiply Imputed Datasets from a mids Object*

Description

Exports multiply imputed datasets and information about the imputation. Objects of class `mids` (generated by `mice::mice`) and `mids.lchain` (generated by `mice.lchain`) are supported.

Usage

```
write.mice.imputation(mi.res, name, include.varnames=TRUE,
  long=TRUE, mids2spss=TRUE, spss.dec=",", dattype=NULL)
```

Arguments

<code>mi.res</code>	Object of class <code>mids</code> or <code>mids.lchain</code>
<code>name</code>	Name of created subdirectory and datasets
<code>include.varnames</code>	An optional logical indicating whether variable names should be included in the imputed dataset. The default is <code>TRUE</code> .
<code>long</code>	An optional logical indicating whether the dataset should also be saved in a long format?
<code>mids2spss</code>	An optional logical indicating whether a syntax for reading imputed datasets in SPSS should be included
<code>spss.dec</code>	SPSS decimal separator (can be <code>,</code> , <code>.</code> or <code>."</code>)
<code>dattype</code>	Format of the saved dataset: <code>csv</code> or <code>csv2</code>

Value

Several files are saved using `impxxx` (the name) as the prefix:

<code>impxxx.Rdata</code>	Saved object of class <code>mids</code>
<code>impxxx__DATALIST.Rdata</code>	Saved object of a list containing multiply imputed datasets
<code>impxxx__IMP_LIST</code>	File with list of multiply imputed datasets
<code>impxxx__IMP_SUMMARY</code>	Summary file of the imputation
<code>impxxx__IMPDATA_nn</code>	Imputed datasets <code>nn</code>
<code>impxxx__IMPMETHOD</code>	File containing imputation methods
<code>impxxx__LEGENDE</code>	File with variable names of the dataset


```

impxxx__LONG      Imputed datasets in long format
impxxx__PREDICTORMATRIX
                  File containing the predictor matrix
impxxx__SPSS.sps
                  SPSS syntax for reading the corresponding txt file into SPSS format.

```

See Also

See also [mice::mids2mplus](#) and [mice::mids2spss](#)

Examples

```

## Not run:
#####
# EXAMPLE 1: Imputation of nhanes data and write imputed datasets on disk
#####

data(nhanes,package="mice")

#####
# Model 1: Imputation using mice
imp1 <- mice::mice( nhanes, m=3, maxit=5 )
# write results
write.mice.imputation(mi.res=imp1, name="mice_imp1" )

#####
# Model 2: Imputation using mice.1chain
imp2 <- miceadds::mice.1chain( nhanes, burnin=10, iter=20, Nimp=4 )
# write results
write.mice.imputation(mi.res=imp2, name="mice_imp2" )

## End(Not run)

```

write.pspp

Writing a Data Frame into SPSS Format Using PSPP Software

Description

Writes a data frame into SPSS format using the *PSPP* software. To use this function, download and install PSPP at first: <http://www.gnu.org/software/pspp/pspp.html>.

Usage

```

write.pspp(data, datafile, pspp.path, decmax=6,
           as.factors=TRUE, use.bat=FALSE)

```

Arguments

data	Data frame
datafile	Name of the output file (without file ending)
pspp.path	Path where the PSPP executable is located, e.g. "C:/Program Files (x86)/PSPP/bin/"
decmax	Maximum number of digits after decimal
as.factors	A logical indicating whether all factors and string entries should be treated as factors in the output file.
use.bat	A logical indicating whether PSPP executed via a batch file in the DOS mode (TRUE) or directly invoked via the system command from within R (FALSE).

Value

A dataset in *sav* format (SPSS format).

Author(s)

The code was adapted from <https://stat.ethz.ch/pipermail/r-help/2006-January/085941.html>

See Also

See also `foreign::write.foreign`.

For writing sav files see also `haven::write_sav` and `sjlabelled::write_spss`.

For convenient viewing *sav* files we recommend the freeware program *ViewSav*, see <http://www.asselberghs.dds.nl/stuff.htm>.

Examples

```
## Not run:
#####
# EXAMPLE 1: Write a data frame into SPSS format
#####

#****
# (1) define data frame
data <- data.frame( "pid"=1000+1:5, "height"=round(rnorm( 5 ),4),
                  "y"=10*c(1,1,1,2,2), "r2"=round( rnorm(5),2),
                  "land"=as.factor( c( rep("A",1), rep("B", 4 ) ) ) )

#****
# (2) define variable labels
v1 <- rep( "", ncol(data) )
names(v1) <- colnames(data)
attr( data, "variable.labels" ) <- v1
attr(data,"variable.labels")["pid"] <- "Person ID"
attr(data,"variable.labels")["height"] <- "Height of a person"
attr(data,"variable.labels")["y"] <- "Gender"

#****
```

```
# (3) define some value labels
v1 <- c(10,20)
names(v1) <- c("male", "female" )
attr( data$y, "value.labels" ) <- v1

#####
# (4a) run PSPP to produce a sav file
write.pspp( data, datafile="example_data1",
            pspp.path="C:/Program Files (x86)/PSPP/bin/" )

#####
# (4b) produce strings instead of factors
write.pspp( data, datafile="example_data2",
            pspp.path="C:/Program Files (x86)/PSPP/bin/", as.factors=FALSE )

#####
# write sav file using haven package
library(haven)
haven::write_sav( data, "example_data1a.sav" )

#####
# write sav file using sjlabelled package
library(sjlabelled)
data <- sjlabelled::set_label( data, attr(data, "variable.labels") )
sjlabelled::write_spss( data, "example_data1b.sav" )

## End(Not run)
```

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