Package 'reproducer'

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Title Reproduce Statistical Analyses and Meta-Analyses

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Description Includes data analysis functions (e.g., to calculate effect sizes and 95% Confidence Intervals (CI) on Standardised Effect Sizes (d) for AB/BA cross-over repeated-measures experimental designs), data presentation functions (e.g., density curve overlaid on histogram), and the data sets analyzed in different research papers in software engineering (e.g., related to software defect prediction or multi-site experiment concerning the extent to which structured abstracts were clearer and more complete than conventional abstracts) to streamline reproducible research in software engineering.

Depends R (>= 3.5.0)

License GPL (>= 2)

LazyData true

URL <https://madeyski.e-informatyka.pl/reproducible-research/>

Imports openxlsx (>= 2.4.0), ggplot2 (>= 2.0.0), gridExtra(>= 0.9.1), xtable(>= 1.7-4), metafor(>= 1.9-2), lme4(>= 1.1-10), MASS(>= 7.3-45), stats(>= 3.5.2), reshape(>= 0.8.8), GetoptLong(>= 0.1.7), dplyr(>= 0.8.0.1), httr(>= 1.4.0), jsonlite(>= 1.6), tidyr(>= 0.8.3), readr(>= 1.3.1), stringr(>= 1.4.0), tibble(>= 2.1.1)

RoxygenNote 7.1.1

Suggests testthat, assertthat

NeedsCompilation no

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R **topics documented:**

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aggregateIndividualDocumentStatistics

aggregateIndividualDocumentStatistics

Description

This function assumes an ABBA crossover experiment has reported means and variances for each technique in each time period. We calculate the weighted mean and pooled within group variance for the observations arising from the two different sets of materials for a specific technique.

Usage

```
aggregateIndividualDocumentStatistics(D1.M, D1.SD, D1.N, D2.M, D2.SD, D2.N)
```

Arguments

D1.M	is a vector of mean values from a set of experiments in a family reporting observations from participants using a specific document in the first time period with either the control or the treatment technique.
D1.SD	is a vector of results from the set of experiment in a family reporting the standard deviations of observations from participants using the same document in the first time period with the same technique.
D1.N	is a vector of the numbers of participants in each experiment in a family, using the same document for participants using either the same technique.
D2.M	is a vector of mean values of observations from participants using the alternative document in the second time period, but using the same technique.
D2.SD	is a vector of the standard deviations of observations from participants using the alternative document in the second time period with the same technique.
D2.N	is a vector of the numbers of participants using the same document in the second time period for participants using the same technique.

Value

data frame incl. the overall weighted mean and pooled standard deviation

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
aggregateIndividualDocumentStatistics(10, 2, 20, 15, 2, 20)
#     M SD
#1 12.5  2
```

---

boxplotAndDensityCurveOnHistogram

boxplotAndDensityCurveOnHistogram

Description

Boxplot and density curve overlaid on histogram

Usage

```
boxplotAndDensityCurveOnHistogram(df, colName, limLow, limHigh)
```

Arguments

df	Data frame with data to be displayed
colName	Name of the selected column in a given data frame
limLow	the limit on the lower side of the displayed range
limHigh	the limit on the higher side of the displayed range

Value

A figure being a density curve overlaid on histogram

Author(s)

Lech Madeyski

Examples

```
library(ggplot2)
library(grid)
library(gridExtra)
boxplotAndDensityCurveOnHistogram(Madeyski15EISEJ.PropProjects, "STUD", 0, 100)
boxplotAndDensityCurveOnHistogram(Madeyski15SQJ.NDC, "simple", 0, 100)
```

---

boxplotHV   *boxplotHV*

Description

Box plot

Usage

```
boxplotHV(df, colName, limLow, limHigh, isHorizontal)
```

Arguments

df	Data frame with data to be displayed
colName	Name of the selected column in a given data frame
limLow	the limit on the lower side of the displayed range
limHigh	the limit on the higher side of the displayed range
isHorizontal	Boolean value to control whether the box plot should be horizontal or not (i.e., vertical)

Value

A box plot

Author(s)

Lech Madeyski

Examples

```
boxplotHV(Madeyski15EISEJ.PropProjects, "STUD", 0, 100, TRUE)
boxplotHV(Madeyski15EISEJ.PropProjects, "STUD", 0, 100, FALSE)
boxplotHV(Madeyski15SQJ.NDC, "simple", 0, 100, FALSE)
boxplotHV(Madeyski15SQJ.NDC, "simple", 0, 100, TRUE)
```

Calc4GroupNPStats   *Calc4GroupNPStats*

Description

This function does a non-parametric analysis of a randomized blocks experiment assuming 2 blocks and 2 treatment conditions.

Usage

```
Calc4GroupNPStats(x1, x2, x3, x4, sigfig = -1, alpha = 0.05)
```

Arguments

x1	is the data associated with treatment A in one block 1
x2	is the data associated with treatment B in block 1
x3	is the data associated with treatment A in block 2
x4	is the data associated with treatment B in block 2
sigfig	is the number of significant digits in the data. If >0 the datav will be appropriately truncated
alpha	is the significance level for all statistical tests

Value

The function returns the point biserial version of Kendall's tau and its variance, Cliff's d and its variance, the probability of superiority, phat, and its variance, for the 4 group experiment experiment.

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
set.seed(123)
x=list()
x[[1]]=stats::rnorm(10,0,1)
x[[2]]=stats::rnorm(10,0.8,1)
x[[3]]=stats::rnorm(10,0.5,1)
x[[4]]=stats::rnorm(10,1.3,1)
Calc4GroupNPStats(x[[1]],x[[2]],x[[3]],x[[4]],sigfig=-1,alpha=0.05)
# A tibble: 1 x 17
#     N phat phat.var phat.df phat.test phat.pvalue phat.sig    d  vard d.sig   cor   sqse
# <int> <dbl>   <dbl>   <dbl>    <dbl>       <dbl> <lgl>    <dbl> <dbl> <lgl> <dbl>  <dbl>
#   1   40 0.17  0.00497   31.0    -4.68   0.0000532 TRUE    -0.660 0.0206 TRUE -0.347 0.0132
# . . . with 5 more variables: ctvar <dbl>, n1 <int>, n2 <int>, sigCVt <lgl>, sigCVn <lgl>
```

---

calculateBasicStatistics

calculateBasicStatistics

Description

This function calculates the following statistcs for a set of data: length, mean, median, variance, standard error of the mean, and confidence interval bounds. The input data must be a vector of 2 or more numerical values.

Usage

```
calculateBasicStatistics(x, alpha = 0.05)
```

Arguments

x	The data to be summarized
alpha	The probability level to be used when constructing the confidence interval bounds.

Value

A dataframe comprising the length, mean, variance, standard error and confidence limit bounds of the input data x.

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
ShortExperimentNames=c("E1","E2","E3","E4")
FullExperimentNames=c("EUBAS","R1UCLM","R2UCLM","R3UCLM")
Metrics=c("Comprehension","Modification")
Groups=c("A","B","C","D")
Type=c(rep("4G",4))
StudyID="S2"
Control="SC"
ReshapedData=ExtractExperimentData(KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14TOSEM
,ExperimentNames=FullExperimentNames, idvar="ParticipantID",timevar="Period",ConvertToWide=TRUE)
NewTable= ConstructLevel1ExperimentRData(ReshapedData,StudyID,ShortExperimentNames,Groups,
Metrics,Type,Control)
calculateBasicStatistics(NewTable$r)
 #    N    Mean Median Variance      SE LowerBound UpperBound
 # 1 32 0.06175 0.1688   0.2482 0.08808    -0.1109     0.2344
```

---

calculateGroupSummaryStatistics

calculateGroupSummaryStatistics

Description

This function calculates the following statistics data within groups: length, mean, median, variance, standard error of the mean, and confidence interval bounds.

Usage

```
calculateGroupSummaryStatistics(x, Group)
```

Arguments

x	The data to be summarized. This must be a vector of 2 or more numerical values
Group	The categorical data data defining the groups. This must vector of the same length as x containing factors specifying the data groups

Value

A dataframe comprising the number, mean, variance, standard error and confidence limit bounds of the data in each category

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
ShortExperimentNames=c("E1","E2","E3","E4")
FullExperimentNames=c("EUBAS","R1UCLM","R2UCLM","R3UCLM")
Metrics=c("Comprehension","Modification")
Groups=c("A","B","C","D")
Type=c(rep("4G",4))
StudyID="S2"
Control="SC"
ReshapedData= ExtractExperimentData(
  KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14TOSEM,
  ExperimentNames=FullExperimentNames, idvar="ParticipantID",timevar="Period",
  ConvertToWide=TRUE
)
NewTable= ConstructLevel1ExperimentRData(ReshapedData, StudyID,
  ShortExperimentNames, Groups, Metrics, Type, Control
)
SeqGroupLev=NULL
N.NT=length(NewTable$r)
for (i in 1:N.NT) {
if (NewTable$n[i]<=8) SeqGroupLev[i]=as.character(NewTable$n[i])
if (NewTable$n[i]>8) SeqGroupLev[i]=as.character(9)
 }
 calculateGroupSummaryStatistics(NewTable$r,Group=SeqGroupLev)
#     N    Mean  Median Variance StDev      SE
# 1   4 -0.0833 -0.1699   0.2314 0.4810 0.2405
# 2  12  0.3658  0.4477   0.2109 0.4592 0.1326
# 3  16 -0.1300 -0.2214   0.1933 0.4397 0.1099
```

---

calculateHg	*calculateHg*

Description

This function calculates Hedges g and Hedges g adjusted given the basic experimental statistics - the mean values for participants, number of observations (participants), and standard deviation in both the control group and the treatment group. . Hence, the function assumes the data is held as summary statistics including the control group mean, standard deviation and sample size and equivalent values for treatment group

Usage

```
calculateHg(Mc, Mt, Nc, Nt, SDc, SDt)
```

Arguments

Mc	is a vector containing the mean value of the control group for each experiment.
Mt	is a vector containing the mean value of the treatment group for each experiment.
Nc	is a vector containing the the number of observations (participants) in the control group for each experiment.
Nt	is a vector of the number of observations (participants) in the treatment group for each experiment.
SDc	is a vector of the standard deviations of the control group for each experiment.
SDt	is a vector of the standard deviations of the the treatment group for each experiment.

Value

data frame composed of Hedges' g and Hedges' g adjusted effect sizes

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
calculateHg(10, 15, 20, 20, 2, 2)
#    Hg    HgAdjusted
# 1  2.5   2.450276
```

```
CalculateLevel2ExperimentRData
```
CalculateLevel2ExperimentRData

Description

This function analyses data on r values obtained in the format obtained from the ConstructLevel1ExperimentRData function and finds the r-value for each metric for each experiment.

Usage

```
CalculateLevel2ExperimentRData(
  Level1Data,
  Groups,
  StudyID,
  ExperimentNames,
  Metrics,
  Type
)
```

Arguments

Level1Data	a tibble in the format produced by the ConstructLevel1ExperimentRData function which has r-values for each sequence group in a crossover experiment
Groups	This is a list that defines the sequence group labels used in the dataset.
StudyID	This holds an identifer used to identify the origin of the experimental data in the output from this function.
ExperimentNames	
	This a list of identifiers used to define each experiment in the output from this function.
Metrics	This is a list of of character strings identifying each outcome metric reported in each of the experiments in the set of replicated experiments.
Type	this is a list of character strings specifying for each experiment whether the experiment is a two sequence group "2G" or four sequence group "4G" experiment. return RExp.Table This is a table containing the pooled data variance and the pooled difference variance for the experiment and the value r for the experiment for eachm metric

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
ShortExperimentNames=c("E1","E2","E3","E4")
FullExperimentNames=c("EUBAS","R1UCLM","R2UCLM","R3UCLM")
Metrics=c("Comprehension","Modification")
Groups=c("A","B","C","D")
Type=c(rep("4G",4))
StudyID="S2"
Control="SC"
# Obtain experimental data from each file and put in wide format
ReshapedData = ExtractExperimentData(
  KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14TOSEM,
 ExperimentNames=FullExperimentNames, idvar="ParticipantID",timevar="Period",ConvertToWide=TRUE)
Lev1Data= ConstructLevel1ExperimentRData(ReshapedData, StudyID, ShortExperimentNames, Groups,
  Metrics, Type, Control)
CalculateLevel2ExperimentRData(Lev1Data,Groups=Groups,StudyID=StudyID,
  ExperimentNames=ShortExperimentNames,Metrics=Metrics,Type=Type)
# A tibble: 8 x 10
#  StudyID ExpID     N Metric      PooledVar1 PooledVar2 VarProp PooledVar PooledDiffVar   r.Exp
#  <chr>   <chr> <int> <chr>            <dbl>      <dbl>   <dbl>     <dbl>         <dbl>   <dbl>
# 1 S2      S2E1     24 Comprehension   0.0148     0.0212   0.412    0.0180        0.0248  0.311
# 3 S2      S2E2     22 Comprehension   0.0487     0.0224   0.684    0.0356        0.0534  0.250
# 4 S2      S2E2     22 Modification    0.0445     0.0266   0.626    0.0356        0.0628  0.117
# 5 S2      S2E3     22 Comprehension   0.0353     0.0402   0.467    0.0377        0.105  -0.391
# 6 S2      S2E3     22 Modification    0.0433     0.0414   0.511    0.0424        0.0997 -0.176
# 7 S2      S2E4     18 Comprehension   0.0439     0.0237   0.649    0.0338        0.0355  0.475
# 8 S2      S2E4     18 Modification    0.0322     0.0592   0.353    0.0457        0.0894  0.0222
```

---

calculatePhat *calculatePhat*

Description

This function extract the probability of superiority (i.e., Phat) and its confidence interval based on Brunner and Munzel (2000) heteroscedastic analog of WMW test. It is based on Wilcox'x bmp function with some amendments. It does not include a plotit facility. It uses the smallest non-zero variance to idetify confidence intervals and statistical significance for values of Phat=0 and Phat=1. It ensure that confidence intervals do not take on invalid values such as values <0 or >1.

Usage

```
calculatePhat(x, y, alpha = 0.05, sigfig = -1)
```

Arguments

x	is a vector of values from group 1
y	is a vector of values from group 2
alpha	is the Type 1 error level for statistical tests
sigfig	If sigfig>0 the data in x and y is truncated to the specified number of significant digits.

Value

list including the value of the t-test for PHat, the estimate of PHat and Cliff's d, and the confidence intervals for PHat.

Author(s)

Rand Wilcox amendments by Barbara Kitchenham and Lech Madeyski

Examples

```
x=c(1.2, 3.0, 2.2, 4.0, 2.5, 3.0)
y=c(3,4.2,4,6,7,5.9)
calculatePhat(x,y)
# $test.stat
# [1] 6.381249
# $phat
# [1] 0.9305556
# $dhat
# [1] 0.8611111
# $sig.level
# [1] 0.0001191725
# $s.e.
# [1] 0.06747199
# $ci.p
```

```
# [1] 0.7783001 1.0000000
# $df
# [1] 9.148489
# Another example:
z=c(1,2,3,4)
y=c(5,6,7,8)
calculatePhat(z,y)
# $test.stat
# [1] 10.6066
# $phat
# [1] 1
# $dhat
# [1] 1
# $sig.level
# [1] 4.135921e-05
# $s.e.
# [1] 0.04419417
# $ci.p
# [1] 0.8918608 1.0000000
# $df
# [1] 6
```

CalculateRLevel1   *CalculateRLevel1*

Description

This function calculates the r value for a 2-group (2G) or 4-Group (4G) Crossover experiment for each sequence group and each outcome metric. The function returns both the exact r value and the r value based on pooled variances for each sequence group and outcome metric

Usage

```
CalculateRLevel1(
  Dataset,
  StudyID,
  Groups = c("A", "B", "C", "D"),
  ExperimentName,
  Metrics,
  Type,
  Control
)
```

Arguments

Dataset   This holds the data for each participant in a 2-group or 4-group crossover experiment in the "wide" format. I.e., there is only one entry per participant. The data set should have been generated from a long version of the data based on a variable labelled "Period" which is used to define which participant data was collected in the first period of the experiment - see function ExtractLevel1ExperimentRData.

StudyID	This holds an identifier used to identify the origin of the experimental data in the output from this function.
Groups	This is a list that defined the sequence group identifiers used in the dataset.
ExperimentName	This an identifiers used to define the specific experiment in the output from this function.
Metrics	This is a list of metrics, e.g., ("Correctness","Time","Efficiency").
Type	this is a character string specifying whether the experiment is a two sequence group of four sequence group experiment.
Control	this is a character string that defines the control treatment in the experiment.

Details

script to obtain correlation coefficients

Value

table this is a tibble holding information identifying for each metric and sequence group the first time period and second time period variance, the pooled variance, the variance of the difference values and the exact r and pooled r. # importFrom stats # importFrom var # importFrom tibble

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
ExperimentNames=c("EUBAS","R1UCLM","R2UCLM","R3UCLM")
ShortExperimentNames=c("E1","E2","E3","E4")
Metrics=c("Comprehension","Modification")
Type=c("4G", "4G", "4G", "4G")
Groups=c("A","B","C","D")
StudyID="S2"
Control="SC"
# Obtain experimental data from a file and put in wide format
dataset2= KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14TOSEM
ReshapedData=ExtractExperimentData(dataset2, ExperimentNames=ExperimentNames,
  idvar="ParticipantID",timevar="Period",ConvertToWide=TRUE)
# Calculate the correlations for each sequence group and each metric.
 CalculateRLevel1(Dataset=ReshapedData[[1]], StudyID, Groups=c("A","B","C","D"),
   ExperimentName=ShortExperimentNames[1],Metrics,Type=Type[1],Control)
# A tibble: 8 x 15
# # A tibble: 8 x 15
# Study Exp   Group Metric Id        n ControlFirst    var1    var2
# <chr> <chr> <chr> <chr>  <chr> <int> <lgl>          <dbl>   <dbl>
#   1 S2    E1    A     Compr... S2E1A     6 FALSE         0.0183  0.0163
# 2 S2    E1    B     Compr... S2E1B     6 TRUE          0.0201  0.0326
# 3 S2    E1    C     Compr... S2E1C     6 FALSE         0.00370 0.0155
# 4 S2    E1    D     Compr... S2E1D     6 TRUE          0.0173  0.0201
# 5 S2    E1    A     Modif... S2E1A     6 FALSE         0.0527  0.0383
# 6 S2    E1    B     Modif... S2E1B     6 TRUE          0.0185  0.0482
```

```
# 7 S2    E1    C     Modif... S2E1C     6 FALSE      0.00655 0.0244
# 8 S2    E1    D     Modif... S2E1D     6 TRUE       0.0222  0.0266
# # ... with 6 more variables: varp <dbl>, ControlVarProp <dbl>,
# #   VarProp <dbl>, vardiff <dbl>, r <dbl>, r.p <dbl>
```

---

calculateSmallSampleSizeAdjustment

calculateSmallSampleSizeAdjustment

Description

Function calculates the Hedges small sample size adjustment for standardized mean effect sizes. It calculates the exact value unless the caller sets the parameter exact to FALSE, or the degrees of freedom is too large.

Function calculates the small sample size adjustment for standardized mean effect sizes

Usage

```
calculateSmallSampleSizeAdjustment(df, exact = TRUE)
```

```
calculateSmallSampleSizeAdjustment(df, exact = TRUE)
```

Arguments

df	A vector of degrees of freedom
exact	Default value=TRUE, if exact==TRUE the function returns the exact value of the adjustment(s) which is suitable for small values of df, if exact==FALSE the function returns the approximate version of the adjustment(s). See Hedges and Olkin 'Statistical methods for Meta-Analysis' Academic Press 1985.

Value

small sample size adjustment value

small sample size adjustment value

Author(s)

Barbara Kitchenham and Lech Madeyski

Barbara Kitchenham and Lech Madeyski

Examples

```
df <- 2
c <- calculateSmallSampleSizeAdjustment(df)

df=c(5,10,17)
adjexact=calculateSmallSampleSizeAdjustment(df)
# adjexact=0.8407487 0.9227456 0.9551115
# Hedges and Olkin values 0.8408, 0.9228,0.9551
adjapprox=calculateSmallSampleSizeAdjustment(df,FALSE)
# adjapprox=0.8421053 0.9230769 0.9552239
df <- 2
a <- calculateSmallSampleSizeAdjustment(df)
# > a
# [1] 0.5641896

df=c(5,10,17)
adjexact=calculateSmallSampleSizeAdjustment(df)
# > adjexact
# [1] 0.8407487 0.9227456 0.9551115
# Hedges and Olkin values 0.8408, 0.9228,0.9551
adjapprox=calculateSmallSampleSizeAdjustment(df,FALSE)
# > adjapprox
# [1] 0.8421053 0.9230769 0.9552239
# Another example:
df=c(10,25,50)
calculateSmallSampleSizeAdjustment(df,exact=TRUE)
# [1] 0.9227456 0.9696456 0.9849119
calculateSmallSampleSizeAdjustment(df,exact=FALSE)
# [1] 0.9230769 0.9696970 0.9849246
```

CalculateTheoreticalEffectSizes

CalculateTheoreticalEffectSizes

Description

This function constructs the theoretical effect sizes and distribution statistics four (normal, lognormal, Laplace & gamma) given specific parameter values for the distributions

Usage

```
CalculateTheoreticalEffectSizes(mean, std, type = "n")
```

Arguments

mean	The theoretical central location parameter for the distribution specified by the type parameter.
std	The theoretical spread parameter for the distribution specified by the type parameter.

type String identifying the distribution, "n" for normal, "ln" for lognormal, "lap" for Laplace, "g" for Gamm

Value

dataframe containing the expected standardized effect size, mean, variance, skewness and kurtosis statistics for samples from the specifie distribution

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
CalculateTheoreticalEffectSizes(mean=0, std=1, type="l")
# A tibble: 1 x 5
#   RawMean RawVariance RawEffectSize RawSkewness RawKurtosis
#     <dbl>       <dbl>         <dbl>       <dbl>       <dbl>
# 1    1.65        4.67         0.763        6.18        88.5
CalculateTheoreticalEffectSizes(mean=0, std=1, type="n")
#A tibble: 1 x 5
#  RawMean RawVariance RawEffectSize RawSkewness RawKurtosis
#    <dbl>       <dbl>         <dbl>       <dbl>       <dbl>
#1       0           1             0           0           3
```

Ciolkowski09ESEM.MetaAnalysis.PBRvsCBRorAR

Ciolkowski09ESEM.MetaAnalysis.PBRvsCBRorAR data form a set of primary studies on reading methods for software inspections. They were reported and analysed by M. Ciolkowski ("What do we know about perspective-based reading? an approach for quantitative aggregation in software engineering", in Proceedings of the 3rd International Symposium on Empirical Software Engineering and Measurement, ESEM'09, pp. 133-144, IEEE Computer Society, 2009), corrected and re-analysed by Madeyski and Kitchenham ("How variations in experimental designs impact the construction of comparable effect sizes for meta-analysis" (to be submitted)).

Description

If you use this data set please cite: Lech Madeyski and Barbara Kitchenham, "How variations in experimental designs impact the construction of comparable effect sizes for meta-analysis", 2015.

Usage

```
Ciolkowski09ESEM.MetaAnalysis.PBRvsCBRorAR
```

Format

A data frame with 21 rows and 7 variables:

Study Name of empirical study

Ref. Reference to the paper reporting primary study or experimental run where data were originally reported

Control Control treatment: Check-Based Reading (CBR) or Ad-hoc Reading (AR)

Within-subjects Yes - if the primary study used the within-subjects experimental design, No - if the primary study did not use the within-subjects experimental design

Cross-over Yes - if the primary study used the cross-over experimental design, No - if the primary study did not use the cross-over experimental design

d_ByCiolkowski d effect size calculated by Ciolkowski

d_ByOriginalAuthors d effect size as reported by the original authors

Source

<https://madeyski.e-informatyka.pl/reproducible-research/>

Examples

```
Ciolkowski09ESEM.MetaAnalysis.PBRvsCBRorAR
```

Cliffd	*Cliffd*

Description

This function implements finds Cliff's d and its confidence intervals. The null hypothesis is that for two independent group, P(X<Y)=P(X>Y). The function reports a 1-alpha confidence interval for P(X>Y)-P(X<Y). The algorithm computes a confidence interval for Cliff's d using the method in Cliff, 1996, p. 140, eq 5.12. The function is based on code produce by Rand Wilcox but has been amended. The plotting function has been removed and the dependency on Wilcox's binomci function has been removed. Construction of confidence intervals if values in one group are all larger than values in the other group has been amended to use the smallest non-zero variance method. Upper and lower confidence interval bounds cannot assume invalid values, i.e. values <-1 or >1.

Usage

```
Cliffd(x, y, alpha = 0.05, sigfig = -1)
```

Arguments

x	is a vector of values from group 1
y	is a vector of values from group 2
alpha	is the Type 1 error level for statistical tests
sigfig	is the number of significant digit. If sigfig>0 the data in x and y is truncated to the specified value.

Value

list including the value of Cliffs d its consistent variance and confidence intervals and the equivalent probability of superiority value and its confidence intervals. x=c(1.2,3,2.2,4,2.5,3) y=c(3,4.2,4,6,7,5.9) # Cliffd(x,y) # $n1 # [1] 6 # $n2 # [1] 6 # $cl # [1] -0.9772519 # $cu # [1] -0.3476461 # $d # [1] -0.8611111 # $sqse.d # [1] 0.02017931 # $phat # [1] 0.06944444 # $summary.dvals # P(X<Y) P(X=Y) P(X>Y) # [1,] 0.8888889 0.08333333 0.02777778 # $p.cl # [1] 0.01137405 # $p.cu # [1] 0.326177 # z=c(1,2,3,4) y=c(5,6,7,8) Cliffd(z,y) # $n1 # [1] 4 # $n2 # [1] 4 # $cl # [1] -1 # $cu # [1] -0.4368172 # $d # [1] -1 # $sqse.d # [1] 0.009765625 # $phat # [1] 0 # $summary.dvals # P(X<Y) P(X=Y) P(X>Y) # [1,] 1 0 0 # $p.cl # [1] 0 # $p.cu # [1] 0.2815914

Author(s)

Rand Wilcox, amendments Barbara Kitchenham and Lech Madeyski

---

constructEffectSizes   *constructEffectSizes*

Description

The function constructs various different d-style effect sizes for a set of different experiments given basic statistics from each experiment (the mean value of the control group Mc, the mean value of the treatment group Mt, the standard deviation of the control group SDc, standard deviation of the the treatment group SDt, the number of observations (participants) in the control group Nc, and the number of observations (participants) in the treatment group Nt). The input variables can be vectors or individual numbers but all input vectors must be of the same length. The function returns Glass's Delta, Cohen's D, point bi-serial r (based on Hedges'g unadjusted), Hedges'g and Hegdes' g adjusted for small sample size.

Usage

```
constructEffectSizes(Mc, Mt, SDc, SDt, Nc, Nt)
```

Arguments

Mc	is a vector containing the mean value of the control group for each experiment.
Mt	is a vector containing the mean value of the treatment group for each experiment.
SDc	is a vector of the standard deviations of the control group for each experiment.
SDt	is a vector of the standard deviations of the the treatment group for each experiment.
Nc	is a vector containing the the number of observations (participants) in the control group for each experiment.
Nt	is a vector of the number of observations (participants) in the treatment group for each experiment.

Value

data frame composed of five effect sizes (Glass delta, Cohen's d, Hedges' g, r, Hedges' g adjusted)

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
constructEffectSizes(10, 15, 0.3, 0.2, 15, 15)

Mt = c(0.633, 0.673, 0.423, 0.727, 0.631)
Mc = c(0.612, 0.526, 0.356, 0.618, 0.534)
SDt = c(0.198, 0.115, 0.172, 0.088, 0.122)
SDc = c(0.159, 0.089, 0.111, 0.166, 0.119)
Nt = c(12, 12, 14, 10, 8)
Nc= c(12, 12, 14, 10, 8)
EffectSizes=constructEffectSizes(Mc, Mt, SDc,SDt,Nt,Nc)
EffectSizes
# GlassDelta    Cohend   Hedgesg           r HedgesgAdjusted
# 1  0.1320755 0.1221516 0.1169513 0.05837591       0.1129107
# 2  1.6516854 1.4931812 1.4296121 0.58151846       1.3802200
# 3  0.6036036 0.4803405 0.4628677 0.22547423       0.4493641
# 4  0.6566265 0.8648343 0.8204538 0.37953300       0.7857047
# 5  0.8151261 0.8604924 0.8049169 0.37335594       0.7608781
```

ConstructLevel1ExperimentRData

ConstructLevel1ExperimentRData

Description

This function returns the r value for a 2-group (2G) or 4-Group (4G) Crossover experiment for a group of 1 or more experiments for each sequence group and each outcome metric. For sets of 2 or more experiments, the experiments are assumed to be replicates and to report the same sets of Metrics and have the same Control treatment and use the same squence Group identifiers, but are not necessarily the same Type. We return both the exact r value and the r value based on pooled variances for each sequence group and outcome metric.

Usage

```
ConstructLevel1ExperimentRData(
  Data,
  StudyID,
  ExperimentNames,
  Groups,
  Metrics,
  Type,
```

```
    Control
)
```

Arguments

Data
: This is a list parameter each entry in the list holds the data for each participant in a 2-group or 4-group crossover experiment in the "wide" format. I.e., there is only one entry per participant. The data should have been generated from a long version of the data based on a variable labelled "Period" which is used to define which participant data was collected in the first period of the experiment - see function ExtractLevel1ExperimentRData.

StudyID
: This holds an identifer used to identify the origin of the experimental data in the output from this function.

ExperimentNames
: This a list of identifiers used to define each experiment in the output from this function.

Groups
: This is a list that defined the sequence group identifiers used in the dataset.

Metrics
: This is a list of of character strings identifying each outcome metric reported in each of the experiments in the set of replicated experiments.

Type
: this is a list of character strings specifying for each experiment whether the experiment is a 2-group or 4-group experiment

Control
: this is a character string that defines the control treatment in the experiment.

Value

R.Data.Table this is a tibble holding information identifying for each metric and sequence group the first time period and second time period variance, the pooled variance, the variance of the difference values and the exact r and pooled r.

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
#
ShortExperimentNames=c("E1","E2","E3","E4")
FullExperimentNames=c("EUBAS","R1UCLM","R2UCLM","R3UCLM")
Metrics=c("Comprehension","Modification")
Groups=Groups=c("A","B","C","D")
Type=c(rep("4G",4))
StudyID="S2"
Control="SC"
# Obtain experimental data from each file and put in wide format
dataset2= KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14TOSEM
ReshapedData=ExtractExperimentData(dataset2, ExperimentNames=FullExperimentNames,
  idvar="ParticipantID",timevar="Period",ConvertToWide=TRUE)
# Calculate the correlations for each sequence group and each metric in each experiment
ConstructLevel1ExperimentRData(Data=ReshapedData, StudyID=StudyID,
```

```
    ExperimentNames=ShortExperimentNames, Groups=Groups, Metrics=Metrics, Type=Type,
    Control=Control
)
# # A tibble: 32 x 15
# Study Exp   Group Metric Id          n ControlFirst  var1    var2    varp
# <chr> <chr> <chr> <chr>  <chr>   <int> <lgl>         <dbl>   <dbl>   <dbl>
#  1 S2   E1    A     Compr... S2E1A     6 FALSE         0.0183  0.0163  0.0173
# 2 S2    E1    B     Compr... S2E1B     6 TRUE          0.0201  0.0326  0.0263
# 3 S2    E1    C     Compr... S2E1C     6 FALSE         0.00370 0.0155  0.00962
# 4 S2    E1    D     Compr... S2E1D     6 TRUE          0.0173  0.0201  0.0187
# 5 S2    E1    A     Modif... S2E1A     6 FALSE         0.0527  0.0383  0.0455
# 6 S2    E1    B     Modif... S2E1B     6 TRUE          0.0185  0.0482  0.0333
# 7 S2    E1    C     Modif... S2E1C     6 FALSE         0.00655 0.0244  0.0155
# 8 S2    E1    D     Modif... S2E1D     6 TRUE          0.0222  0.0266  0.0244
# 9 S2    E2    A     Compr... S2E2A     6 FALSE         0.0194  0.0425  0.0309
# 10 S2   E2    B     Compr... S2E2B     6 TRUE          0.0198  0.0192  0.0195
# # ... with 22 more rows, and 5 more variables: ControlVarProp <dbl>,
# #   VarProp <dbl>, vardiff <dbl>, r <dbl>, r.p <dbl>
```

---

densityCurveOnHistogram

densityCurveOnHistogram

Description

Density curve overlaid on histogram

Usage

```
densityCurveOnHistogram(df, colName, limLow, limHigh)
```

Arguments

df	Data frame with data to be displayed
colName	Name of the selected column in a given data frame
limLow	the limit on the lower side of the displayed range
limHigh	the limit on the higher side of the displayed range

Value

A figure being a density curve overlaid on histogram

Author(s)

Lech Madeyski

Examples

```
densityCurveOnHistogram(Madeyski15EISEJ.PropProjects, "STUD", 0, 100)
# densityCurveOnHistogram(data.frame(x<-rnorm(50, mean=50, sd=5)), "x", 0, 100)
```

---

effectSizeCI   *effectSizeCI*

Description

95 The procedure is based on finding the upper and lower 0.025 bounds for the related t-variable. The t-variable needs to be adjusted for bias by multiplying by c The upper and lower bounds on the t-variable are then used to calculate to upper and lower bounds on the repeated measures effect size (d_RM) by multiplying the upper and lower bound of the t-variable by sqrt((n1+n2)/(2*(n1*n2))). Upper and lower bounds on the equivalent independent groups effect size (d_IG) are found by multiplying the upper and lower bounds on d_RM by sqrt(1-r).

Usage

```
effectSizeCI(
  expDesign,
  t,
  n1,
  n2,
  r = 0,
  epsilon = 1e-10,
  maxsteps = 1000,
  stepsize = 3
)
```

Arguments

expDesign	Experimental design: 1) crossover repeated measures ("CrossOverRM"), 2) before-after repeated measures (expDesign=="BeforeAfterRM"), 3) independent groups ("IG)
t	t-statistics (t must be less than or equal to 37.62, the limit from the R function documentation)
n1	The number of observations in sequence group 1 (expDesign=="CrossOverRM"), the number of observations in group 1 (expDesign=="IG"), or the total number of observations (expDesign=="BeforeAfterRM")
n2	The number of observations in sequence group 2 (expDesign=="CrossOverRM") or the number of observations in group 2 (expDesign=="IG")
r	The correlation between outcomes for individual subject (the within subject correlation)
epsilon	The precision of the iterative procedure
maxsteps	The maximum number of steps of the iterative procedure (the procedure terminates at maxsteps or earlier if CI with enough precision have been calculated)
stepsize	The size of steps (influences the convergence of the calculations, i.e., the number of steps required to obtain the final result of precision defined by the epsilon)

Value

A list of Confidence Intervals for: t-statistic (t_LB and t_UB), repeated-measures effect size d_RM (d_RM_LB, d_RM_UB), independent groups effect size (d_IG_LB, d_IG_UB)

Author(s)

Lech Madeyski and Barbara Kitchenham

Examples

```
effectSizeCI(expDesign="CrossOverRM", t=14.4, n1=15, n2=15, r=0.6401)
effectSizeCI(expDesign = "BeforeAfterRM", t=14.16536, n1=15, n2=0, r=0.6146771)
effectSizeCI(expDesign = "IG", t=-6.344175, n1=15, n2=15)
effectSizeCI(expDesign="CrossOverRM", t=0.5581, n1=6, n2=6, r=0.36135)
effectSizeCI(expDesign = "CrossOverRM", r=0.855,t=4.33, n1=7, n2=6)
```

ExtractExperimentData *ExtractExperimentData*

Description

This function reads datasets from a defined directory in the reproducer package that hold the results of a family crossover experiments in the long format. It converts the data to the wide format if required.

Usage

```
ExtractExperimentData(
  DataSet,
  ExperimentNames,
  idvar = "ParticipantID",
  timevar = "Period",
  ConvertToWide = TRUE
)
```

Arguments

DataSet   This is a tibble holding the data for each crossover experiment in a family (a family can include only one experiment).

ExperimentNames
                 This is a list with the full names of each experiment.

idvar   This is the name of the column that contains the data for specific participants. It is only assumed to be unique within an experiment (default idvar="ParticipantID").

timevar   This is the name of the table column that defines which data was collected in a specific time period. This function assumes that there are only two time periods (default timevar="Period").

ConvertToWide   This determine whether the function converts the data to the wide format (default ConvertToWide=TRUE).

Value

A list with an entry for the data for each experiment. If ConvertToWide is TRUE, it returns the data in the wide format otherwise it returns the data as it was read. Within each list item the data is returned as a tibble #importFrom stats # importFrom tibble # importFrom base

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
ExperimentNames=c("EUBAS","R1UCLM","R2UCLM","R3UCLM")
Metrics=c("Comprehension","Modification")
Groups=c("A","B","C","D")
Type=c(rep("4G",4))
StudyID="S2"
Control="SC"
# Obtain experimental data from each file and put in wide format
dataset2= KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14TOSEM
ReshapedData = ExtractExperimentData(dataset2, ExperimentNames=ExperimentNames,
  idvar="ParticipantID",timevar="Period",ConvertToWide=TRUE)
ReshapedData[[1]]

# A tibble: 24 x 15
# ParticipantID ExperimentID.1 SequenceGroup.1 System.1 Treatment.1 Comprehension.1
# <fct>         <fct>          <fct>           <fct>    <fct>              <dbl>
#   1 1            EUBAS           A              S1       AM               0.77
# 2 5            EUBAS           A              S1       AM               0.61
# 3 9            EUBAS           A              S1       AM               0.61
# 4 13           EUBAS           A              S1       AM               0.52
# 5 17           EUBAS           A              S1       AM               0.43
# 6 21           EUBAS           A              S1       AM               0.77
# 7 2            EUBAS           B              S1       SC               0.92
# 8 6            EUBAS           B              S1       SC               0.63
# 9 10           EUBAS           B              S1       SC               0.51
# 10 14           EUBAS           B              S1       SC               0.64
# ... with 14 more rows, and 9 more variables: Modification.1 <dbl>, CrossOverID.1 <fct>,
#   ExperimentID.2 <fct>, SequenceGroup.2 <fct>, System.2 <fct>, Treatment.2 <fct>,
#   Comprehension.2 <dbl>, Modification.2 <dbl>, CrossOverID.2 <fct>
```

ExtractGroupSizeData   *ExtractGroupSizeData*

Description

This function constructs a table identifying the number of participants in each sequence group for a set of experiments each of which used a crossover design.

Usage

```
ExtractGroupSizeData(
  ExpDataWide,
  StudyID,
  ShortExperimentNames,
  Type,
  Groups = c("A", "B", "C", "D")
)
```

Arguments

ExpDataWide	this is a list of tibbles each comprising data from one experiment in its wide format
StudyID	an identifer for the group of related experiments (i.e., a family).
ShortExperimentNames	
	a list of character strings identifying each experiment.
Type	A list identifying the type of crossover "2G" or "4G" for each experiment in the family
Groups	a list of the terms used to specify sequence groups in the experiments.

Value

A tibble containing the number of participants in each sequence group in each experiment.

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
ExperimentNames=c("EUBAS","R1UCLM","R2UCLM","R3UCLM")
ShortExperimentNames=c("E1","E2","E3","E4")
Metrics=c("Comprehension","Modification")
Type=c("4G", "4G", "4G", "4G")
Groups=c("A","B","C","D")
StudyID="S2"
Control="SC"
# Obtain experimental data from a file and put in wide format
dataset2= KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14TOSEM
ReshapedData=ExtractExperimentData(dataset2, ExperimentNames=ExperimentNames,
  idvar="ParticipantID", timevar="Period", ConvertToWide=TRUE
  )
ExtractGroupSizeData(ReshapedData, StudyID, ShortExperimentNames, Type, Groups=Groups)
# A tibble: 16 x 4
#  Study Exp   Group     n
#  <chr> <chr> <chr> <int>
#1 S2    Exp1  A         6
#2 S2    Exp1  B         6
#3 S2    Exp1  C         6
```

```
#4  S2    Exp1  D       6
#5  S2    Exp2  A       6
#6  S2    Exp2  B       6
#7  S2    Exp2  C       5
#8  S2    Exp2  D       5
#9  S2    Exp3  A       5
#10 S2     Exp3  B        5
#11 S2     Exp3  C       6
#12 S2     Exp3  D       6
#13 S2    Exp4  A       5
#14 S2    Exp4  B       5
#15 S2    Exp4  C       4
#16 S2    Exp4  D       4
```

ExtractMAStatistics   *ExtractMAStatistics*

Description

This function extracts summary statistics from meta-analysis results obtained from the rma function of the metafor R package. If required the function transform back to standardized mean difference (effect size type "d" i.e. Hg) or point biserial correlations (effect size type "r"). Warning: the 'ExtractMAStatistics' function works with 'metafor' version 2.0-0, but changes to metafor's method of providing access to its individual results may introduce errors into the function.

This function extracts summary statistics from meta-analysis results obtained from the rma function of the metafor R package. If required the function transform back to standardized mean difference (effect size type "d" i.e. Hg) or point biserial correlations (effect size type "r"). Warning: the 'ExtractMAStatistics' function works with 'metafor' version 2.0-0, but changes to metafor's method of providing access to its individual results may introduce errors into the function.

Usage

```
ExtractMAStatistics(
  maresults,
  Nc,
  Nt,
  Transform = TRUE,
  type = "d",
  sig = 4,
  returnse = FALSE
)

ExtractMAStatistics(
  maresults,
  Nc,
  Nt,
  Transform = TRUE,
  type = "d",
```

```
    sig = 4,
    returnse = FALSE
)
```

Arguments

maresults   is the output from the rma function.

Nc   is the number of participants in the control condition group.

Nt   is the number of participants in the treatment condition group.

Transform   is a boolean value indicating whether the outcome values need to be transformed
                back to standardized mean difference ("d" i.e. Hg or d) or point biserial corre-
                lations ("r"). It is defaulted to TRUE. If this parameter is set to FALSE, no
                transformation will be applied.

type   this indicates the type of transformation required - it defaults to "d" which re-
                quests transformation from Zr to Hg, using "r" requests transformation from Zr
                to r.

sig   indicates the number of significant digits requested in the output, the default is
                4; it rounds the values of mean, pvalue, upper and lower bound to the specified
                number of significant digits.

returnse   default to FALSE, if set to TRUE returns the standard error of the effect size

Value

data frame incl. summary statistics from meta-analysis results: overall mean value for the effect
sizes, the p-value of the mean, the upper and lower confidence interval bounds (UB and LB), QE
which is the heterogeneity test statistic and QEp which the the p-value of the heterogeneity statistic

data frame incl. summary statistics from meta-analysis results: overall mean value for the effect
sizes, the p-value of the mean, the upper and lower confidence interval bounds (UB and LB), QE
which is the heterogeneity test statistic and QEp which the the p-value of the heterogeneity statistic

Author(s)

Barbara Kitchenham and Lech Madeyski

Barbara Kitchenham and Lech Madeyski

Examples

```
ExpData=reproducer::KitchenhamMadeyskiBrereton.ExpData
#Extract the experiment basic statics
S1data=subset(ExpData,ExpData=="S1")
#Use the descriptive data to construct effect size
S1EffectSizes = reproducer::PrepareForMetaAnalysisGtoR(
S1data$Mc,S1data$Mt,S1data$SDc,S1data$SDt,S1data$Nc,S1data$Nt)
# Do a random effect meta-analysis of the transformed r_pbs effect size
S1MA = metafor::rma(S1EffectSizes$zr, S1EffectSizes$vi)
# Extract summary statistics from meta-analysis results and transform back to Hg scale
S1MAStats=reproducer::ExtractMAStatistics(S1MA, sum(S1data$Nc),sum(S1data$Nt), TRUE, "d", 4)
#    mean   pvalue   UB    LB QE  QEp
```

```
#1 0.6658 0.002069 1.122 0.2384  4 0.41
ExpData=reproducer::KitchenhamMadeyskiBrereton.ExpData
#Extract the experiment basic statics
S1data=subset(ExpData,ExpData=="S1")
#Use the descriptive data to construct effect size
S1EffectSizes = reproducer::PrepareForMetaAnalysisGtoR(
  S1data$Mc,S1data$Mt,S1data$SDc,S1data$SDt,S1data$Nc,S1data$Nt)
# Do a random effect meta-analysis of the transformed r_pbs effect size
S1MA = metafor::rma(S1EffectSizes$zr, S1EffectSizes$vi)
# Extract summary statistics from meta-analysis results and transform back to Hg scale
ExtractMAStatistics(S1MA, sum(S1data$Nc),sum(S1data$Nt), TRUE, "d", 4)
#   A tibble: 1 x 6
#      mean  pvalue    UB    LB    QE   QEp
#     <dbl>   <dbl> <dbl> <dbl> <dbl> <dbl>
#   1 0.666 0.00207  1.12 0.238     4  0.41
```

ExtractSummaryStatisticsRandomizedExp

ExtractSummaryStatisticsRandomizedExp

Description

This function extracts data obtained from the lme4 package lmer function. It assumes a simple randomized experiment with each element having one or more repeated measures. It outputs the mean together with its standard error and confidence interval bounds.

Usage

```
ExtractSummaryStatisticsRandomizedExp(lmeRA, N, alpha = 0.05)
```

Arguments

lmeRA	The output from the lmer function
N	The total number of observations
alpha	the probability level to be used when constructing the confidence interval bounds.

Value

REA.Summary A dataframe holding the number of observations N, the overall mean value as its standard error reported as by the lmer function, and its confidence interval bounds.

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
ShortExperimentNames=c("E1","E2","E3","E4")
FullExperimentNames=c("EUBAS","R1UCLM","R2UCLM","R3UCLM")
Metrics=c("Comprehension","Modification")
Groups=c("A","B","C","D")
Type=c(rep("4G",4))
StudyID="S2"
Control="SC"
ReshapedData= ExtractExperimentData(
  KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14TOSEM,
  ExperimentNames=FullExperimentNames, idvar="ParticipantID", timevar="Period",
  ConvertToWide=TRUE
)
NewTable= ConstructLevel1ExperimentRData(ReshapedData, StudyID, ShortExperimentNames, Groups,
  Metrics,Type,Control
  )
resRe=lme4::lmer(r~(1|Id),data=NewTable)
summary(resRe)
# Linear mixed model fit by REML ['lmerMod']
# Formula: r ~ (1 | Id)
# REML criterion at convergence: 47.8
# Scaled residuals:
#    Min     1Q  Median     3Q     Max
# -1.4382 -0.9691  0.2190  0.8649  1.4761
#
# Random effects:
#  Groups    Name         Variance Std.Dev.
#   Id      (Intercept) 0.03978  0.1994
#    Residual              0.20974  0.4580
#  Number of obs: 32, groups:  Id, 16
#
#  Fixed effects:
#             Estimate Std. Error t value
#  (Intercept)  0.06175    0.09508   0.649
#  N=length(NewTable$r)
 ExtractSummaryStatisticsRandomizedExp(lmeRA=resRe,N=32,alpha=0.05)
#     N   Mean      SE LowerBound UpperBound
#   1 32 0.06175 0.09508    -0.1319     0.2554
```

---

fmt   *fmt*

Description

Formatting function to set decimal precision in labels

Usage

```
fmt()
```

Author(s)

Lech Madeyski

---

getEffectSizesABBA   *getEffectSizesABBA*

Description

Function to calculate both effect sizes (dIG, dRM), i.e., independent groups and repeated measures standardized effect sizes and variances, for AB/BA crossover design studies. Function is used in a paper "Effect Sizes and their Variance for AB/BA Crossover Design Studies" by Lech Madeyski and Barbara Kitchenham.

Usage

```
getEffectSizesABBA(simulationData)
```

Arguments

simulationData - data set in a form required to calculate effect sizes in AB/BA crossover experimental designs

Value

data frame incl. calculated effect sizes and variances: # dIG - independent groups standardized effect size # var.dIG - variance of independent groups standardized effect size # dRM - repeated measures (within-subjects) standardized effect size # var.dRM - variance of repeated measures (within-subjects) standardized effect size # dIG.Fromt - independent groups standardized effect size calculated from t: dIG.Fromt=t*sqrt(1-r)*sqrt((N1+N2)/(2*N1*N2)) # var.dIG.Fromt - variance of independent groups standardized effect size calculated from t: var.dIG.Fromt=var.t*(1-r)*((N1+N2)/(2*N1*N2)) # dRM.Fromt - dRM calculated from t: dRM.Fromt=t*sqrt((N1+N2)/(2*N1*N2)) # var.dRM.Fromt - var.dRM calculated from t: var.dRM.Fromt = var.t*((N1+N2)/(2*N1*N2)) # var.dRM.Fromt2 - var.dRM calculated from t or rather dRM.Fromt: var.dRM.Fromt2=(df/(df-2))*((N1+N2)/(2*N1*N2)+dRM.Fromt^2/c^2 # var.dRM.Approx - var.dRM calculated on a basis of Johnson and Welch (1940) report an approximate formulate for the variance of a t variable: var.dRM.Approx=((N1+N2)/(2*N1*N2)) + (dRM^2)/(2*(N1+N2-2)) #see paper and Equation 49 # var.dIG.Approx - var.dIG calculated on a basis of Johnson and Welch (1940) report an approximate formulate for the variance of a t variable: var.dIG.Approx=(((N1+N2)*(1-r))/(2*N1*N2)) + (dIG^2)/(2*(N1+N2-2)) #see paper and Equation 50 # unstandardizedES - estimated unstandardized technique effect size # periodES - estimated period effect # var.sig - sum of within-subjects variance and between-subjects variance # var.within - within-subjects variance # var.between - between-subjects variance # t - t-value # var.t - variance of t-variable # gRM - Hedges and Olkin (1985) unbiased estimator of the repeated measures effect size gRM=dRM*c # var.gRM - variance of gRM calculated as follows: var.gRM=(df/(df-2))*(((N1+N2)/(2*N1*N2))*c^2+gRM^2)- gRM^2/c^2 #Equation 56 # var.gRM2 - variance of gRM calculated as follows: var.gRM2=var.dRM*c^2 # gIG - Hedges and Olkin (1985) unbiased estimator of the independent groups effect size gIG=dIG*c # var.gIG - variance of gIG calculated as follows: var.gIG=(df/(df-2))*(((N1+N2)/(2*N1*N2))*c^2+gIG^2)- gIG^2/c^2 #Equation 57 #

var.gIG2 - variance of gRM calculated as follows: var.gIG2=var.dIG*c^2 # r - the correlation between the values observed for the same subject

Author(s)

Lech Madeyski and Barbara Kitchenham

Examples

```
simulationData<-getSimulationData(25, 18.75, 50, 10, 5, 500) #generate simulated data set
es<-getEffectSizesABBA(simulationData) #return effect sizes and variances
#OR
simulationData<-getSimulationData(25, 18.75,50,10,5,15)
es<-getEffectSizesABBA(simulationData) #return effect sizes and variances
```

---

getEffectSizesABBAIgnoringPeriodEffect

getEffectSizesABBAIgnoringPeriodEffect

Description

Function to calculate both effect sizes (dIG.ipe, dRM.ipe), i.e., independent groups and repeated measures standardized effect sizes and variances, for AB/BA crossover design studies ignoring period effect (thus wrong). Function was removed in the revision of the paper "Effect Sizes and their Variance for AB/BA Crossover Design Studies" by Lech Madeyski and Barbara Kitchenham.

Usage

```
getEffectSizesABBAIgnoringPeriodEffect(simulationData)
```

Arguments

simulationData   - data set in a form required to calculate effect sizes in AB/BA crossover experimental designs

Value

data frame incl. calculated effect sizes and variances: # dIG.ipe - independent groups standardized effect size # var.dIG.ipe - variance of independent groups standardized effect size # dRM.ipe - repeated measures (within-subjects) standardized effect size # var.dRM.ipe - variance of repeated measures (within-subjects) standardized effect size # dIG.Fromt.ipe - independent groups standardized effect size calculated from t: dIG.Fromt=t*sqrt(1-r)*sqrt((N1+N2)/(2*N1*N2)) # var.dIG.Fromt.ipe - variance of independent groups standardized effect size calculated from t: var.dIG.Fromt=var.t*(1-r)*((N1+N2)/(2*N1*N2)) # dRM.Fromt.ipe - dRM calculated from t: dRM.Fromt=t*sqrt((N1+N2)/(2*N1*N2)) # var.dRM.Fromt.ipe - var.dRM calculated from t: var.dRM.Fromt = var.t*((N1+N2)/(2*N1*N2)) # var.dRM.Fromt2.ipe - var.dRM calculated from t or rather dRM.Fromt: var.dRM.Fromt2=(df/(df-2))*((N1+N2)/(2*N1*N2)+dRM.Fromt^2)- dRM.Fromt^2/c^2 # unstandardizedES.ipe - estimated unstandardized technique effect size # var.sig.ipe - sum of within-subjects variance and between-subjects variance # var.within.ipe - within-subjects variance # var.between.ipe - between-subjects variance # t.ipe - t-value # var.t.ipe - variance of t-variable

Author(s)

Lech Madeyski and Barbara Kitchenham

Examples

```
simulationData<-getSimulationData(25, 18.75, 50, 10, 5, 500) #generate simulated data set
es.ipe<-getEffectSizesABBAIgnoringPeriodEffect(simulationData) #return effect sizes and variances
```

---

getSimulationData   *getSimulationData*

Description

Function to generate the simulated data set used in a paper "Effect Sizes and their Variance for AB/BA Crossover Design Studies" by Lech Madeyski and Barbara Kitchenham

Usage

```
getSimulationData(
  var,
  covar,
  meanA1,
  treatmentDiff,
  periodEffect,
  numOfSamples
)
```

Arguments

var	Variance among subjects is a sum of the between subjects variance and the within subjects variance
covar	Covariance equal to the between subjects variance
meanA1	Mean for treatment sequence A1
treatmentDiff	technique effect which is the difference between the effect of technique A and technique B
periodEffect	Period effect which is the difference between period 1 and period 2
numOfSamples	Number of samples ("rows" of data) required for each technique and period

Details

——- Functions related to a paper "Effect sizes and their variance for AB/BA crossover design studies" by Lech Madeyski and Barbara Kitchenham ——— ————————————-

Value

Data frame: 'data.frame': 4*numOfSamples obs. of 5 variables: $ pid : int 1 2 3 4 5 6 7 8 9 10 ... $ technique: Factor w/ 2 levels "T1","T2": ... $ period : Factor w/ 2 levels "P1","P2": ... $ sequence : Factor w/ 2 levels "S1","S2": ... $ result : num ...

Author(s)

Lech Madeyski and Barbara Kitchenham

Examples

```
data<-getSimulationData(25, 18.75, 50, 10, 5, 500) # generate the simulated data set from the paper
data<-getSimulationData(25, 18.75, 50, 10, 5, 15)
```

---

getTheoreticalEffectSizeVariancesABBA
getTheoreticalEffectSizeVariancesABBA

Description

Function provides the theoretical value of the t-statistic, variance of t, and variance of the effect sizes based on the parameters built into crossover model data simulated by the getSimilationData() function. Function is used in a paper "Effect Sizes and their Variance for AB/BA Crossover Design Studies" by Lech Madeyski and Barbara Kitchenham.

Usage

```
getTheoreticalEffectSizeVariancesABBA(
  theoreticalvarW,
  theoreticalTechniqueEffect,
  theoreticalrho,
  N1,
  N2
)
```

Arguments

theoreticalvarW
- The within subject variance used to construct the simulation, i.e., the built-in Variance - the built-in Covariance

theoreticalTechniqueEffect
- The technique effect built into the crossover model data

theoreticalrho - The between subject correlation built into the crossover model simulation data

N1 - The number of subjects in sequence group 1 in the crossover model simulation

N2 - The number of subjects in sequence group 2 in the crossover model simulation

Value

data frame incl. calculated: theoreticalt - the theoretical value of the t-statistic theoreticalvart - variance of t theoreticalvardIG - variance of the effect size dIG based on the parameters built into crossover model data simulated by the getSimilationData function theoreticalvardRM - variance of the effect size dRM based on the parameters built into crossover model data simulated by the getSimilationData function

Author(s)

Lech Madeyski and Barbara Kitchenham

Examples

```
# Generates data used in Table 15 of the paper
theoreticalEffectSizeVariances <- getTheoreticalEffectSizeVariancesABBA(6.25,-10,0.75,15,15)
```

Kendalltaupb *Kendalltaupb*

Description

Computes point bi-serial version of Kendall's tau plus a 1-alpha confidence interval using the method recommended by Long and Cliff (1997). The algorithm is based on Wilcox's code but was extended to return the consistent variance and the confidence intervals based on the t-distribution. Also added a Diagnostic parameter to output internal calculations.

Usage

```
Kendalltaupb(x, y = NULL, alpha = 0.05)
```

Arguments

x	either a matrix with two columns containg two correlated variables or a vector of variables
y	if y=NULL, assume x is a matrix with two columns, otherwise y is a vector of variables with x[i] and x[i] being from the same experimental unit
alpha	= 0.05, the Type 1 error level used for statistical tests

Value

list containing the estimate of Kendall's tau, it hypothesis testing variance, and the t-test value obtained from it, the significance of the t-test, the consistent variance of tau and its confidence intervals based on both the normal dstribution and the t-test (recommended by Long and Cliff)

Author(s)

Rand Wilcox, Barbara Kitchenham and Lech Madeyski

Examples

```
x=c(1.2,3,1.8,2,2,0.5,0.5,1,3,1)
y=c(1,1,1,1,1,0,0,0,0,0)
Kendalltaupb(x,y,alpha=.05)
# $cor
# [1] 0.3555556
# $ci
# [1] -0.04198026  0.55555556
# $cit
# [1] -0.1240567  0.5555556
# $test
# [1] 1.431084
# $sqse
# [1] 0.0617284
# $consistentvar
# [1] 0.04113925
# $siglevel
# [1] 0.1524063
```

KitchenhamEtAl.CorrelationsAmongParticipants.Abrahao13TSE

> *KitchenhamEtAl.CorrelationsAmongParticipants.Abrahao13TSE data illustrate correlations between results from individual participants in a family of five cross-over experiments conducted by Abrahao et al: [1] S. Abrahao, C. Gravino, E. Insfran Pelozo, G. Scanniello, and G. Tortora, "Assessing the effectiveness of sequence diagrams in the comprehension of functional requirements: Results from a family of five experiments," IEEE Transactions on Software Engineering, vol. 39, no. 3, pp. 327–342, March 2013 The five experiments assess whether the comprehensibility of function requirements improve when software models include UML sequence diagrams. If you use this data set please cite: [1] S. Abrahao, C. Gravino, E. Insfran Pelozo, G. Scanniello, and G. Tortora, "Assessing the effectiveness of sequence diagrams in the comprehension of functional requirements: Results from a family of five experiments," IEEE Transactions on Software Engineering, vol. 39, no. 3, pp. 327–342, March 2013 [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).*

Description

KitchenhamEtAl.CorrelationsAmongParticipants.Abrahao13TSE data illustrate correlations between results from individual participants in a family of five cross-over experiments conducted by Abrahao et al: [1] S. Abrahao, C. Gravino, E. Insfran Pelozo, G. Scanniello, and G. Tortora, "Assessing the effectiveness of sequence diagrams in the comprehension of functional requirements: Results from a family of five experiments," IEEE Transactions on Software Engineering, vol. 39, no. 3,

pp. 327–342, March 2013 The five experiments assess whether the comprehensibility of function requirements improve when software models include UML sequence diagrams. If you use this data set please cite: [1] S. Abrahao, C. Gravino, E. Insfran Pelozo, G. Scanniello, and G. Tortora, "Assessing the effectiveness of sequence diagrams in the comprehension of functional requirements: Results from a family of five experiments," IEEE Transactions on Software Engineering, vol. 39, no. 3, pp. 327–342, March 2013 [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Usage

```
KitchenhamEtAl.CorrelationsAmongParticipants.Abrahao13TSE
```

Format

A data frame with 224 rows and 8 variables:

ExperimentID <fct>|ExperimentID: A unique identifier for each of the five experiments in the data set.

ParticipantID <fct>|Participant ID: An identifier for each participant, unique for a specific experiment.

SequenceGroup <fct>|Experimental Sequence Group: A (DM-NODM,ECP-EPlat or MShop-Theatre), B (NODM-DM,ECP-EPlat or MShop-Theatre), C(DM-NODM,EPlat-ECP or Theatre-MShop), D(NODM-DM,EPlat-ECP or Theatre-MShop)

System <fct>|Software systems used in the experiment: ECP an e-commerce platform from which CDs and books can be bought, EPlat a system for the management of courses, lectures and students of a university, M-Shop a system for managing sales at a music shop, Theatre a system for managing bookings for a theatre.

Period <fct>|Time period of the cross-over experiment: 1 or 2

Treatment <fct>|Experimental Treatment: A Dynamic Model (DM) vs No Dynamic Model (NODM)

Comprehension <dbl>|Dependent variable: The comprehension level the software engineer achieved based on the F-measure

CrossOverID <fct>|CrossOver category: For 4 group crossover designs, the crossover category specifies the matching pairs of sequence groups, CO1 and CO2. For a 2 group crossover, the category is set to CO1 only

Ability <fct>|Ability: An assessment of the ability of participants: Low, High, NA (not available)

Examples

```
KitchenhamEtAl.CorrelationsAmongParticipants.Abrahao13TSE
```

KitchenhamEtAl.CorrelationsAmongParticipants.Gravino15JVLC

> *KitchenhamEtAl.CorrelationsAmongParticipants.Gravino15JVLC data illustrate correlations between results from individual participants in a family of 2 cross-over experiments conducted by Gravino et al.: [1] C. Gravino, G. Scanniello, and G. Tortora, "Source-code comprehension tasks supported by UML design models: Results from a controlled experiment and a differentiated replication," Journal of Visual Languages and Computing, vol. 28, pp. 23–38, 2015. The experiments assess whether the comprehension of object oriented source-code increases used with UML class and sequence diagrams produced in the software design phase. If you use this data set please cite: [1] C. Gravino, G. Scanniello, and G. Tortora, "Source-code comprehension tasks supported by UML design models: Results from a controlled experiment and a differentiated replication," Journal of Visual Languages and Computing, vol. 28, pp. 23–38, 2015. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).*

Description

KitchenhamEtAl.CorrelationsAmongParticipants.Gravino15JVLC data illustrate correlations between results from individual participants in a family of 2 cross-over experiments conducted by Gravino et al.: [1] C. Gravino, G. Scanniello, and G. Tortora, "Source-code comprehension tasks supported by UML design models: Results from a controlled experiment and a differentiated replication," Journal of Visual Languages and Computing, vol. 28, pp. 23–38, 2015. The experiments assess whether the comprehension of object oriented source-code increases used with UML class and sequence diagrams produced in the software design phase. If you use this data set please cite: [1] C. Gravino, G. Scanniello, and G. Tortora, "Source-code comprehension tasks supported by UML design models: Results from a controlled experiment and a differentiated replication," Journal of Visual Languages and Computing, vol. 28, pp. 23–38, 2015. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Usage

KitchenhamEtAl.CorrelationsAmongParticipants.Gravino15JVLC

Format

A data frame with 64 rows and 9 variables:

ExperimentID <fct>|ExperimentID: A unique identifier for each of the three experiments in the data set.

ParticipantID <fct>|Participant ID: An identifier for each participant, unique for a specific experiment.

SequenceGroup <fct>|Experimental Sequence Group: A , B , C, D

System <fct>|Software systems used in the experiment: Music shop, a system for handling the sales of a music shop. Theater ticket, a system for managing theatre reservations.

Period <fct>|Time period of the cross-over experiment: 1 or 2

Treatment <fct>|Experimental Treatment: Mo, design models were available, NOMo design models were not available

Comprehension <dbl>|Dependent variable: The level of comprehension achieved by the software engineer.

Time <dbl>|Dependent variable: The time [min] taken to complete the comprehension task.

CrossOverID <fct>|CrossOver category: For 4 group crossover designs, the crossover category specifies the matching pairs of sequence groups, CO1 and CO2. For 2 group crossover, the category is set to CO1 only

Examples

```
KitchenhamEtAl.CorrelationsAmongParticipants.Gravino15JVLC
```

KitchenhamEtAl.CorrelationsAmongParticipants.Madeyski10

KitchenhamEtAl.CorrelationsAmongParticipants.Madeyski10 data illustrate correlations between results from individual participants in cross-over experiment P2007 (Smell\&Library) conducted by Madeyski, see: [1] Lech Madeyski, Test-Driven Development: An Empirical Evaluation of Agile Practice. (Heidelberg, London, New York): Springer, 2010. Foreword by Prof. Claes Wohlin. If you use this data set please cite: [1] Lech Madeyski, Test-Driven Development: An Empirical Evaluation of Agile Practice. (Heidelberg, London, New York): Springer, 2010. Foreword by Prof. Claes Wohlin. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Description

KitchenhamEtAl.CorrelationsAmongParticipants.Madeyski10 data illustrate correlations between results from individual participants in cross-over experiment P2007 (Smell\&Library) conducted by Madeyski, see: [1] Lech Madeyski, Test-Driven Development: An Empirical Evaluation of Agile Practice. (Heidelberg, London, New York): Springer, 2010. Foreword by Prof. Claes Wohlin. If you use this data set please cite: [1] Lech Madeyski, Test-Driven Development: An Empirical Evaluation of Agile Practice. (Heidelberg, London, New York): Springer, 2010. Foreword by Prof. Claes Wohlin. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Usage

```
KitchenhamEtAl.CorrelationsAmongParticipants.Madeyski10
```

Format

'KitchenhamEtAl.CorrelationsAmongParticipants.Madeyski10': a data frame with 45 rows and 10 variables:

ExperimentID <fct>| ExperimentID: This experiment is the only cross-over experiment in the family of TDD and Pair-Programming experiments conducted by Madeyski, so all values in this column are set to "P2007".

ParticipantID <fct> | Participant ID: An identifier for each participant, unique for a specific experiment.

SequenceGroup <fct> | Experimental Sequence Group: A (TLSP-TFSP), B (TFSP-TLSP)

System <fct> | Software system to develop: Smell (a tool for identifying bad code smells in Java source code through the use of a set of software metrics) or Library (a library application)

Period <fct> | Time period of the cross-over experiment: 1 or 2

Treatment <fct> | Experimental Treatment: Test-First Solo Programming (TFSP) vs Test-Last Solo Programming (TLSP)

PATP <dbl> | Dependent variable: Percentage of Acceptance Tests Passed

NATPPH <dbl> | Dependent variable: Number of Acceptance Tests Passed Per Hour

CBO <dbl> | Dependent variable: Mean value of Coupling Between Objects (CBO), see CK set of metrics

WMC <dbl> | Dependent variable: Mean value of Weighted Number of Methods in Class (WMC), see CK set of metrics

RFC <dbl> | Dependent variable: Mean value of Response For a Class (RFC), see CK set of metrics

CrossOverID <fct> | Cross-Over Code. This experiment is a simple two-group cross-over experiment with one cross-over code, so all values in this column are set to "CO1". However, four-group experiments require a code to identify the linked sequence groups (although that can be deduced from the system used in the first time period). A crossover code is also essential for non-parametric analysis.

Source

<https://madeyski.e-informatyka.pl/reproducible-research/>

Examples

```
KitchenhamEtAl.CorrelationsAmongParticipants.Madeyski10
```

KitchenhamEtAl.CorrelationsAmongParticipants.Reggio15SSM

> *KitchenhamEtAl.CorrelationsAmongParticipants.Reggio15SSM data illustrate correlations between results from individual participants in a family of two cross-over experiments conducted by Reggio et al: [1] G. Reggio, F. Ricca, G. Scanniello, F. D. Cerbo, and G. Dodero,"On the comprehension of workflows modeled with a precise style: results from a family of controlled experiments". Software and Systems Modeling, vol. 14, pp. 1481–1504, 2015. The experiments assess whether the level of formality/precision in workflow model influences comprehension. If you use this data set please cite: [1] G. Reggio, F. Ricca, G. Scanniello, F. D. Cerbo, and G. Dodero, "On the comprehension of workflows modeled with a precise style: results from a family of controlled experiments". Software and Systems Modeling, vol. 14, pp. 1481–1504, 2015. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The Importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).*

Description

KitchenhamEtAl.CorrelationsAmongParticipants.Reggio15SSM data illustrate correlations between results from individual participants in a family of two cross-over experiments conducted by Reggio et al: [1] G. Reggio, F. Ricca, G. Scanniello, F. D. Cerbo, and G. Dodero,"On the comprehension of workflows modeled with a precise style: results from a family of controlled experiments". Software and Systems Modeling, vol. 14, pp. 1481–1504, 2015. The experiments assess whether the level of formality/precision in workflow model influences comprehension. If you use this data set please cite: [1] G. Reggio, F. Ricca, G. Scanniello, F. D. Cerbo, and G. Dodero, "On the comprehension of workflows modeled with a precise style: results from a family of controlled experiments". Software and Systems Modeling, vol. 14, pp. 1481–1504, 2015. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The Importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Usage

KitchenhamEtAl.CorrelationsAmongParticipants.Reggio15SSM

Format

A data frame with 78 rows and 9 variables:

ExperimentID <fct>|ExperimentID: A unique identifier for each of the three experiments in the data set.

ParticipantID <fct>|Participant ID: An identifier for each participant, unique for a specific experiment.

SequenceGroup <fct>|Experimental Sequence Group: A , B , C, D

System <fct>|Software systems used in the experiment: PO, a system to process orders for an online shop. DM, a system to manage an online document review process.

Period <fct>|Time period of the cross-over experiment: 1 or 2

Treatment <fct>|Experimental Treatment:

Comprehension <dbl>|Dependent variable: The comprehension level obtained by each participant.

Time <dbl>|Dependent variable: The time [min] taken by each participant to complete the comprehension task.

CrossOverID <fct>|CrossOver category: For 4 group crossover designs, the crossover category specifies the matching pairs of sequence groups, CO1 and CO2. For a 2 group crossover, the category is set to CO1 only

Examples

```
KitchenhamEtAl.CorrelationsAmongParticipants.Reggio15SSM
```

KitchenhamEtAl.CorrelationsAmongParticipants.Ricca10TSE

> *KitchenhamEtAl.CorrelationsAmongParticipants.Ricca10TSE data illustrate correlations between results from individual participants in a family of four cross-over experiments conducted by Ricca et al.: [1] F. Ricca, M. D. Penta, M. Torchiano, P. Tonella, and M. Ceccato "How developers' experience and ability influence web application comprehension tasks supported by uml stereotypes: A series of four experiments", IEEE Transactions on Software Engineering, vol. 36, no. 1, pp. 96-118, 2010. Although we present the full data set, only the first two experiments were used in the correlation study, because many of the observations in the final two studies were unpaired. The experiments assess whether participants performance comprehension tasks better when using source code complemented by standard UML diagrams (UML) or by diagrams stereotyped using the Conallen notation (Conallen). If you use this data set please cite: [1] F. Ricca, M. D. Penta, M. Torchiano, P. Tonella, and M. Ceccato "How developers' experience and ability influence web application comprehension tasks supported by uml stereotypes: A series of four experiments", IEEE Transactions on Software Engineering, vol. 36, no. 1, pp. 96—118, 2010. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The Importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).*

Description

KitchenhamEtAl.CorrelationsAmongParticipants.Ricca10TSE data illustrate correlations between results from individual participants in a family of four cross-over experiments conducted by Ricca et al.: [1] F. Ricca, M. D. Penta, M. Torchiano, P. Tonella, and M. Ceccato "How developers' experience and ability influence web application comprehension tasks supported by uml stereotypes: A series of four experiments", IEEE Transactions on Software Engineering, vol. 36, no. 1, pp. 96-118, 2010. Although we present the full data set, only the first two experiments were used in the correlation study, because many of the observations in the final two studies were unpaired. The experiments assess whether participants performance comprehension tasks better when using source code complemented by standard UML diagrams (UML) or by diagrams stereotyped using the Conallen notation (Conallen). If you use this data set please cite: [1] F. Ricca, M. D. Penta, M. Torchiano, P. Tonella, and M. Ceccato "How developers' experience and ability influence web application comprehension tasks supported by uml stereotypes: A series of four experiments", IEEE Transactions on Software Engineering, vol. 36, no. 1, pp. 96—118, 2010. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The Importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Usage

```
KitchenhamEtAl.CorrelationsAmongParticipants.Ricca10TSE
```

Format

A data frame with 176 rows and 10 variables:

ExperimentID <fct>|ExperimentID: A unique identifier for each of the four experiments in the data set.

ParticipantID <fct>|Participant ID: An identifier for each participant, unique for a specific experiment.

SequenceGroup <fct>|Experimental Sequence Group: A , B , C, D

System <fct>|Software systems used in the experiment: Two Java-based Web applications, Claros and WfMS

Period <fct>|Time period of the cross-over experiment: 1 or 2

Treatment <fct>|Experimental Treatment: UML or Conallon

FMeasure <dbl>|Dependent variable: The comprehension level achieved by the participant.

Time <dbl>|Dependent variable: The time [min] to complete the experimental task

CrossOverID <fct>|CrossOver category: For 4 group crossover designs, the crossover category specifies the matching pairs of sequence groups, CO1 and CO2. For 2 group crossover, the category is set to CO1 only

Ability <fct>| h: High l: Low, NA: Not available

Experience <fct>| G: Master students, U: undergraduates, P: researchers

Examples

```
KitchenhamEtAl.CorrelationsAmongParticipants.Ricca10TSE
```

KitchenhamEtAl.CorrelationsAmongParticipants.Ricca14TOSEM

KitchenhamEtAl.CorrelationsAmongParticipants.Ricca14TOSEM data illustrate correlations between results from individual participants in a family of three of four cross-over experiments conducted by Ricca et al: [1] F. Ricca, G. Scanniello, M. Torchiano, G. Reggio, and E. Astesiano, "Assessing the effect of screen mockups on the comprehension of functional requirements," ACM Transactions on Software Engineering and Methodology, vol. 24, no. 1, pp. 1:1–1:38, Oct. 2014. The goal of the study was to assess whether stakeholders benefit from the presence of screen mock-ups in the comprehension of functional requirements represented with use cases. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Description

KitchenhamEtAl.CorrelationsAmongParticipants.Ricca14TOSEM data illustrate correlations between results from individual participants in a family of three of four cross-over experiments conducted by Ricca et al: [1] F. Ricca, G. Scanniello, M. Torchiano, G. Reggio, and E. Astesiano, "Assessing the effect of screen mockups on the comprehension of functional requirements," ACM Transactions on Software Engineering and Methodology, vol. 24, no. 1, pp. 1:1–1:38, Oct. 2014. The goal of the study was to assess whether stakeholders benefit from the presence of screen mock-ups in the comprehension of functional requirements represented with use cases. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Usage

KitchenhamEtAl.CorrelationsAmongParticipants.Ricca14TOSEM

Format

A data frame with 176 rows and 10 variables:

ExperimentID <fct>|ExperimentID: A unique identifier for each of the three experiments in the data set.

ParticipantID <fct>|Participant ID: An identifier for each participant, unique for a specific experiment.

SequenceGroup <fct>|Experimental Sequence Group: A , B , C, D

System <fct>|Software systems used in the experiment: AMICO, a system for management of condominiums. EasyCoin, a system for cataloguing collections of coins.

Period <fct>|Time period of the cross-over experiment: 1 or 2

Treatment <fct>|Experimental Treatment: Screen mockup available (S) vs Text only (T)

Time <dbl>|Dependent variable: The time [min] taken to perform the software engineering task.

Comprehension <dbl>|Dependent variable: The comprehension level the software engineers.

Efficiency <dbl>|Dependent variable: The ratio of comprehension to time.

CrossOverID <fct>|CrossOver category: For 4 group crossover designs, the crossover category specifies the matching pairs of sequence groups, CO1 and CO2. For a 2 group crossover, the category is set to CO1 only.

Examples

```
KitchenhamEtAl.CorrelationsAmongParticipants.Ricca14TOSEM
```

KitchenhamEtAl.CorrelationsAmongParticipants.Romano18ESEM

KitchenhamEtAl.CorrelationsAmongParticipants.Romano18ESEM data illustrate correlations between results from individual participants in a cross-over experiment conducted by Romano et al.: [1] S. Romano, G. Scanniello, D. Fucci, N. Juristo, and B. Turhan, "The effect of noise on software engineers' performance", in Proceedings of the 12th ACM/IEEE International Symposium on Empirical Software Engineering and Measurement, ser. ESEM'18, 2018. The experiments assess whether noise has an impact on the performance of software engineers. If you use this data set please cite: [1] S. Romano, G. Scanniello, D. Fucci, N. Juristo, and B. Turhan, "The effect of noise on software engineers' performance", in Proceedings of the 12th ACM/IEEE International Symposium on Empirical Software Engineering and Measurement, ser. ESEM'18, 2018. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The Importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020). The experiment had two parts but Kitchenham et al. only use the data from the first part of the experiment.

Description

KitchenhamEtAl.CorrelationsAmongParticipants.Romano18ESEM data illustrate correlations between results from individual participants in a cross-over experiment conducted by Romano et al.: [1] S. Romano, G. Scanniello, D. Fucci, N. Juristo, and B. Turhan, "The effect of noise on software engineers' performance", in Proceedings of the 12th ACM/IEEE International Symposium on Empirical Software Engineering and Measurement, ser. ESEM'18, 2018. The experiments assess whether noise has an impact on the performance of software engineers. If you use this data set please cite: [1] S. Romano, G. Scanniello, D. Fucci, N. Juristo, and B. Turhan, "The effect of noise on software engineers' performance", in Proceedings of the 12th ACM/IEEE International Symposium on Empirical Software Engineering and Measurement, ser. ESEM'18, 2018. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The Importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020). The experiment had two parts but Kitchenham et al. only use the data from the first part of the experiment.

Usage

```
KitchenhamEtAl.CorrelationsAmongParticipants.Romano18ESEM
```

Format

A data frame with 194 and 10 variables:

ExperimentID <fct>|ExperimentID: A unique identifier for each part of the experiment. Exp.1 identifies data from the first part of the experiment, Exp.2 identifies data from the second part of the experiment.

ParticipantID <fct>|Participant ID: An identifier for each participant, unique for both parts of the experiment.

SequenceGroup <fct>|Experimental Sequence Group: A , B

System <fct>|Software systems used in the experiment: For the first part of the experiment, M-Shop (a system for managing a music shop) and Theater (a system for managing theatre reservations). For the second part of the experiment: AveCalc (a system that manages as electronic register and LaTazza (a system for a drinks vending machine)

Period <fct>|Time period of the cross-over experiment: 1 or 2

Treatment <fct>|Experimental Treatment: NOISE, participants were asked to perform a comprehension task in a noisy environment. NORMAL, participants were asked to perform a comprehension task under normal working conditions.

Fc <dbl>|Dependent variable: the balanced F-measure which represents the trade-off between precision and recall, measured in the first part of the experiment.

Avg <dbl>|Dependent variable: The average number of fully correct answers, measured in the first part of the experiment.

Ff <dbl>|Dependent variable: Effectiveness of fault correction. Measured in the second part of the experiment.

CrossOverID <fct>|CrossOver category: For 4 group crossovers, the crossover category specifies the matching pairs of sequence groups, CO1 and CO2. For 2 group crossover, the category is set to CO1 only.

Examples

```
KitchenhamEtAl.CorrelationsAmongParticipants.Romano18ESEM
```

KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14EASE

KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14EASE data illustrate correlations between results from individual participants in a family of two cross-over experiments conducted by Scanniello et al: [1] G. Scanniello, M. Staron, H. Burden, and R. Heldal, "On the effect of using SysML requirement diagrams to comprehend requirements: results from two controlled experiments," in Proceedings of the 18th International Conference on Evaluation and Assessment in Software Engineering, EASE. ACM, 2014. The two experiments investigate whether requirements specified as SysML requirement diagrams improve the comprehensibility of requirements. If you use this data set please cite: [1] G. Scanniello, M. Staron, H. Burden, and R. Heldal, "On the effect of using SysML requirement diagrams to comprehend requirements: results from two controlled experiments", in Proceedings of the 18th International Conference on Evaluation and Assessment in Software Engineering, EASE. ACM, 2014. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Description

KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14EASE data illustrate correlations between results from individual participants in a family of two cross-over experiments conducted by Scanniello et al: [1] G. Scanniello, M. Staron, H. Burden, and R. Heldal, "On the effect of using SysML requirement diagrams to comprehend requirements: results from two controlled experiments," in Proceedings of the 18th International Conference on Evaluation and Assessment in Software Engineering, EASE. ACM, 2014. The two experiments investigate whether requirements specified as SysML requirement diagrams improve the comprehensibility of requirements. If you use this data set please cite: [1] G. Scanniello, M. Staron, H. Burden, and R. Heldal, "On the effect of using SysML requirement diagrams to comprehend requirements: results from two controlled experiments", in Proceedings of the 18th International Conference on Evaluation and Assessment in Software Engineering, EASE. ACM, 2014. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Usage

KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14EASE

Format

A data frame with 174 rows and 9 variables:

ExperimentID <fct>|ExperimentID: A unique identifier for each experiment in the data set.

ParticipantID <fct>|Participant ID: An identifier for each participant, unique for a specific experiment.

SequenceGroup <fct>|Experimental Sequence Group: A (RD-NORD,Automobile-ESS), B (NORD-RD,ESS-Automobile), C(NORD-RD,Automobile-ESS), D(RD-NORD,ESS-Automobile).

System <fct>|Software systems used in the experiment: Automobile: A system for controlling car behavior with use cases about entering the car, anti-lock breaking or operating the climate control of a car. ESS (Enhanced Security System) a system designed to detect potential home intruders.

Period <fct>|Time period of the cross-over experiment: 1 or 2

Treatment <fct>|Experimental Treatment: RD availability of a SysML requirements diagram vs No requirements diagram (NORD)

Time <dbl>|Dependent variable: The time [min] required for the comprehension task.

Comprehension <dbl>|Dependent variable: The comprehension level the software engineer achieved.

CrossOverID <fct>|CrossOver category: For 4 group crossover designs, the crossover category specifies the matching pairs of sequence groups, CO1 and CO2. For 2 group crossover, the category is set to CO1 only

Examples

```
KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14EASE
```

KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14JVLC

KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14JVLC data illustrate correlations between results from individual participants in a cross-over experiment conducted by Scanniello and Erra: [1] G. Scanniello and U. Erra, "Distributed modeling of use case diagrams with a method based on think-pair-square: Results from two controlled experiments", Journal of Visual Languages and Computing, vol. 25, no. 4, pp. 494–517, 2014. The experiment investigated whether a new method based on think-pair-square and its implementation in a integrated communication/modeling environment (TPS approach) is as effective as traditional face-to-face (F2F approach) for requirements elicitation. The experiment was performed in two stages using different software systems. If you use this data set please cite: [1] G. Scanniello and U. Erra, "Distributed modeling of use case diagrams with a method based on think-pair-square: Results from two controlled experiments," Journal of Visual Languages and Computing, vol. 25, no. 4, pp. 494–517, 2014. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The Importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Description

KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14JVLC data illustrate correlations between results from individual participants in a cross-over experiment conducted by Scanniello and Erra: [1] G. Scanniello and U. Erra, "Distributed modeling of use case diagrams with a method based on think-pair-square: Results from two controlled experiments", Journal of Visual Languages and Computing, vol. 25, no. 4, pp. 494–517, 2014. The experiment investigated whether a new method based on think-pair-square and its implementation in a integrated communication/modeling environment (TPS approach) is as effective as traditional face-to-face (F2F approach) for requirements elicitation. The experiment was performed in two stages using different software systems. If you use this data set please cite: [1] G. Scanniello and U. Erra, "Distributed modeling of use case diagrams with a method based on think-pair-square: Results from two controlled experiments," Journal of Visual Languages and Computing, vol. 25, no. 4, pp. 494–517, 2014. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The Importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Usage

```
KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14JVLC
```

Format

A data frame with 36 rows and 12 variables:

ExperimentID <fct>|ExperimentID: A unique identifier for each experiment in the data set.

ParticipantID <fct>|Participant ID: An identifier for each team of four participants, unique for the specific experiment.

SequenceGroup <fct>|Experimental Sequence Group: A , B

System <fct>|Software systems used in the experiment: Library (a software system to manage books and users of a library) and FilmCollection (a software system for the selling and the rental of films in a shop) in ExperimentStage1 and Rent (a car rental software to manage cars, customers, and reservations) and ECP (an E-Commerce Platform to order CDs and books via the Internet from an on line catalogue), in ExperimentStage2.

Treatment <fct>|Experimental Treatment: TPS vs F2F.

Period <fct>|Time period of the cross-over experiment: 1 or 2 within each stage of the experiment

Time <dbl>|Dependent variable: The total time [min] to accomplish the requirement engineering task.

Quality <dbl>|Dependent variable: The quality of the requirements engineering task.

CrossOverID <fct>|Crossover category: For a single 2 group crossover experiment, the value is set to CO1 for each experiment stage.

ExperimentPeriod <fct>|ExperimentPeriod: The time period across both stages of the experiment.

ExperimentStage <fct>|ExperimentStage: 1 first stage, 2 second stage.

Examples

```
KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14JVLC
```

KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14TOSEM

KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14TOSEM data illustrate correlations between results from individual participants in a family of four cross-over experiments conducted by Scanniello et al: [1] G. Scanniello, C. Gravino, M. Genero, J.A. Cruz-Lemus, and G. Tortora, "On the Impact of UML Analysis Models on Source-Code Comprehensibility and Modifiability", ACM Transactions on Software Engineering and Methodlogy, vol. 23, no. 2, pp. 13:1-13:26, 2014 The family of experiments investigated whether the availability of analysis models in addition to the source code made the code easier to understand and modify. If you use this data set please cite: [1] G. G. Scanniello, C. Gravino, M. Genero, J.A. Cruz-Lemus, and G. Tortora, "On the Impact of UML Analysis Models on Source-Code Comprehensibility and Modifiability", ACM Transactions on Software Engineering and Methodology, vol. 23, no. 2, pp. 13:1-13:26, 2014 [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Description

KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14TOSEM data illustrate correlations between results from individual participants in a family of four cross-over experiments conducted by Scanniello et al: [1] G. Scanniello, C. Gravino, M. Genero, J.A. Cruz-Lemus, and G. Tortora, "On the Impact of UML Analysis Models on Source-Code Comprehensibility and Modifiability", ACM Transactions on Software Engineering and Methodlogy, vol. 23, no. 2, pp. 13:1-13:26, 2014 The family of experiments investigated whether the availability of analysis models in addition to the source code made the code easier to understand and modify. If you use this data set please cite: [1] G. G. Scanniello, C. Gravino, M. Genero, J.A. Cruz-Lemus, and G. Tortora, "On the Impact of UML Analysis Models on Source-Code Comprehensibility and Modifiability", ACM Transactions on Software Engineering and Methodology, vol. 23, no. 2, pp. 13:1-13:26, 2014 [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Usage

KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14TOSEM

Format

'KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14TOSEM': a data frame with 172 rows and 9 variables:

ExperimentID <fct> | ExperimentID: A unique identifier for each experiment in the data set.

ParticipantID <fct> | Participant ID: An identifier for each participant, unique for a specific experiment.

Treatment <fct> | Experimental Treatment: AM an Analysis Model with source code (AM) vs Source Code only (SC)

SequenceGroup <fct> | Experimental Sequence Group: A (AM-SC,S1-S2), B (SC-AM,S1-S2), C(AM-SC,S2-S1), D(SC-AM,S2-S1)

System <fct> | Software systems used in the experiment: S1 A system to sell and manage CDs/DVDs in a music shop, S2 A system to book and by theater tickets.

Comprehension <dbl> | Dependent variable: The comprehension level the software engineer achieved based on the F-measure

Modification <dbl> | Dependent variable: The modifiability level the software engineer achieved based on the F-measure

Period <fct> | Time period of the cross-over experiment: 1 or 2

CrossOverID <fct> | CrossOver category: For 4 group the crossover category specifies the matching pairs of sequence groups, CO1 and CO2. For 2 group crossover, the category is set to CO1 only

Examples

```
KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14TOSEM
```

KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello15EMSE

> *KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello15EMSE data illustrate correlations between results from individual participants in cross-over experiment usb2 conducted by Scanniello et al: [1] G. Scanniello, A. Marcus, and D. Pascale, "Link analysis algorithms for static concept location: an empirical assessment", Empirical Software Engineering, vol. 20, no. 6, pp. 1666–1720, 2015. The goal of the experiment is to assess whether a new technique (implemented as an Eclipse plug-in) for static concept location (proposed by the authors) supports users in identifying the places in the code where changes are to be made.*

Description

If you use this data set please cite: [1] G. Scanniello, A. Marcus, and D. Pascale, "Link analysis algorithms for static concept location: an empirical assessment", Empirical Software Engineering, vol. 20, no. 6, pp. 1666–1720, 2015. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Usage

```
KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello15EMSE
```

Format

'KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello15EMSE': a data frame with 48 rows and 10 variables:

ExperimentID <fct>|ExperimentID: A unique identifier for each experiment in the data set.

ParticipantID <fct>|Participant ID: An identifier for each participant, unique for a specific experiment.

SequenceGroup <fct>|Experimental Sequence Group: A (CL-NOCL,Jedit-Atunes), B (NOCL-CL,Atunes-Jedit), C(NOCL-CL,Jedit-Atunes), D(CL-NOCL,Atunes-Jedit)

System <fct>|Software systems used in the experiment: Jedit and Atunes

Treatment <fct>|Experimental Treatment: Use of Concept Location plug-in (CL) vs no Concept Location plug-in (NOCL)

Period <fct>|Time period of the cross-over experiment: 1 or 2

Correctness <int>|Dependent variable: 0, 1, 2, 3, 4. The participants are asked to indicate a single change method for each of 4 bug reports. A change method is correctly identified if that method is in the change set of the bug report.

Time <dbl>|Dependent variable: The total time [min] to accomplish concept location tasks, i.e.,to identify (four) bugs given their reports

Efficiency <dbl>|Dependent variable: The participants' efficiency in the execution of concept location tasks. It is computed dividing correctness by time.

CrossOverID <fct>|Crossover category: For 4 group crossover designs, the crossover category specifies the matching pairs of sequence groups, CO1 and CO2.

Examples

```
KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello15EMSE
```

KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello17TOSEM

KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello17TOSEM data illustrate correlations between results from individual participants in a family of four cross-over experiments conducted by Scanniello et al.: [1] G. Scanniello, M. Risi, P. Tramontana, and S. Romano, "Fixing faults in C and Java source code: Abbreviated vs. full-word identifier names", ACM Transactions on Software Engineering Methodology, vol. 26, no. 2, 2017. The experiments assess whether whether the use of abbreviated identifier names (ABBR), impacts the effectiveness of fault fixing in C and Java source code in comparison with full-word identifier names (FULL). If you use this data set please cite: [1] G. Scanniello, M. Risi, P. Tramontana, and S. Romano, "Fixing faults in C and Java source code: Abbreviated vs. full-word identifier names", ACM Transactions on Software Engineering Methodology, vol. 26, no. 2, 2017. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "On the Importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Description

KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello17TOSEM data illustrate correlations between results from individual participants in a family of four cross-over experiments conducted by Scanniello et al.: [1] G. Scanniello, M. Risi, P. Tramontana, and S. Romano, "Fixing faults in C and Java source code: Abbreviated vs. full-word identifier names", ACM Transactions on Software Engineering Methodology, vol. 26, no. 2, 2017. The experiments assess whether whether the use of abbreviated identifier names (ABBR), impacts the effectiveness of fault fixing in C and Java source code in comparison with full-word identifier names (FULL). If you use this data set please cite: [1] G. Scanniello, M. Risi, P. Tramontana, and S. Romano, "Fixing faults in C and Java source code: Abbreviated vs. full-word identifier names", ACM Transactions on Software Engineering Methodology, vol. 26, no. 2, 2017. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "On the Importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Usage

KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello17TOSEM

Format

A data frame with 200 rows and 17 variables:

ExperimentID <fct>|ExperimentID: A unique identifier for each of the experiments in the data set.

ParticipantID <fct>|Participant ID: An identifier for each participant, unique for a specific experiment.

SequenceGroup <fct>|Experimental Sequence Group: A , B , C, D

System <fct>|Software systems used in the experiments: The Unibas experiment used Agenda (a system for tracking personal contacts) and Gas-Station (a system for managing a petrol station). The UniNa experiment used Financial (a system which is a command line option price calculator) and Hotel-Reservation. The POLINA and PROF experiments used AveCalc (a system that manages as electronic register and LaTazza (a system for a drinks vending machine).

Period <fct>|Time period of the cross-over experiment: 1 or 2

Treatment <fct>|Experimental Treatment:ABBR, abbreviated names. FULL, full names

Time <dbl>|Dependent variable: The time each participant spent performing the SE task.

FMeasure <dbl>|Dependent variable: The effectiveness of the participants taking into account correctness and completeness of the fault fixing tasks

Efficiency <dbl>|Dependent variable: The ratio of effectiveness to time.

CrossOverID <fct>|CrossOver category: For 4 group crossover designs, the crossover category specifies the matching pairs of sequence groups, CO1 and CO2. For 2 group crossover, the category is set to CO1 only.

Language <fct>|Java or C. The language was the same for all participants in a specific experiment. POLINA and PROF used Java, UNIBAS and UNINA used C.

Ident <dbl>|Dependent variable: The number of faults identified.

Fixed <dbl>|Dependent variable: The number of faults identified.

WrongIdent <dbl>|Dependent variable: The number of faults incorrectly identified

WronglyFixed <dbl>|Dependent variable: The number of faults incorrectly fixed.

precision <dbl>|Dependent variable: The ratio of number of faults correctly fixed to the number of faults correctly identified.

recall <dbl>|Dependent variable: The ratio of number of faults correctly fixed to the total number of fault.

Examples

```
KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello17TOSEM
```

KitchenhamEtAl.CorrelationsAmongParticipants.Torchiano17JVLC

> *KitchenhamEtAl.CorrelationsAmongParticipants.Torchiano17JVLC data illustrate correlations between results from individual participants in a family of three cross-over experiments conducted by Torchiano et al: [1] M. Torchiano, G. Scanniello, F. Ricca, G. Reggio, and M. Leotta, "Do UML object diagrams affect design comprehensibility? Results from a family of four controlled experiments." Journal of Visual Languages and Computing, vol. 41, pp. 10–21, 2017. Although the paper reports four experiment, we only have data from three of those experiments. The experiments assess whether the comprehensibility of UML specifications improve when the software documents include UML object diagrams as well as the standard UML class diagrams. If you use this data set please cite: [1] M. Torchiano, G. Scanniello, F. Ricca, G. Reggio, and M. Leotta, "Do UML object diagrams affect design comprehensibility? Results from a family of four controlled experiments." Journal of Visual Languages and Computing, vol. 41, pp. 10–21, 2017. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).*

Description

KitchenhamEtAl.CorrelationsAmongParticipants.Torchiano17JVLC data illustrate correlations between results from individual participants in a family of three cross-over experiments conducted by Torchiano et al: [1] M. Torchiano, G. Scanniello, F. Ricca, G. Reggio, and M. Leotta, "Do UML object diagrams affect design comprehensibility? Results from a family of four controlled experiments." Journal of Visual Languages and Computing, vol. 41, pp. 10–21, 2017. Although the paper reports four experiment, we only have data from three of those experiments. The experiments assess whether the comprehensibility of UML specifications improve when the software documents include UML object diagrams as well as the standard UML class diagrams. If you use this data set please cite: [1] M. Torchiano, G. Scanniello, F. Ricca, G. Reggio, and M. Leotta, "Do UML object diagrams affect design comprehensibility? Results from a family of four controlled experiments." Journal of Visual Languages and Computing, vol. 41, pp. 10–21, 2017. [2] Barbara Kitchenham, Lech Madeyski, Giuseppe Scanniello and Carmine Gravino, "The importance of the Correlation between Results from Individual Participants in Crossover Experiments" (to be submitted as of 2020).

Usage

KitchenhamEtAl.CorrelationsAmongParticipants.Torchiano17JVLC

Format

A data frame with 214 rows and 8 variables:

ExperimentID <fct>|ExperimentID: A unique identifier for each of the three experiments in the data set.

ParticipantID <fct>|Participant ID: An identifier for each participant, unique for a specific experiment.

SequenceGroup <fct>|Experimental Sequence Group: A , B , C, D

System <fct>|Software systems used in the experiment: File System manager (FS) for folders, files, links. Roads system (R) handles maps made up of cities connected by means of roads. Train (T) a system to manage timetables, trains, and paths. Catalogue system (C). It collects category of items (e.g., cars) and items (e.g., car models) based on a set of features (e.g., number of doors). In PoliTo2, only FS and T were administered to the participants, while in UniBas1 and UniGe1 all the four experimental objects were used.

Period <fct>|Time period of the cross-over experiment: 1 or 2

Treatment <fct>|Experimental Treatment: Object Diagram (OD) vs No Object Diagram (NoOD)

Comprehension <dbl>|Dependent variable: The comprehension level the software engineers. For PoliTo2 Comprehension was based on answering a set of 4 questions, for UniBas and UniGe comprehension was measured using the F metric.

CrossOverID <fct>|CrossOver category: For 4 group crossover designs, the crossover category specifies the matching pairs of sequence groups, CO1 and CO2. For 2 group crossover, the category is set to CO1 only

Examples

```
KitchenhamEtAl.CorrelationsAmongParticipants.Torchiano17JVLC
```

KitchenhamMadeyski.SimulatedCrossoverDataSets

KitchenhamMadeyski.SimulatedCrossoverDataSets data

Description

If you use this data set please cite this R package and the following paper: Lech Madeyski and Barbara Kitchenham, "Effect Sizes and their Variance for AB/BA Crossover Design Studies", Empirical Software Engineering, vol. 24, no.4, p. 1982-2017, 2018. DOI: 10.1007/s10664-017-9574-5

Usage

```
KitchenhamMadeyski.SimulatedCrossoverDataSets
```

Format

A data frame with variables:

actualSampleSize Sample size

SSFull Sample Size

CFull Correlation

ESFull Effect Size

Accuracy Accuracy

PropSig ...

WrongTSig ...

Details

This is simulated normally distributed data from 30 subjects, with technique A being 10 units more effective than technique B, and there is a period effect equaling 5 units. Subject 1 to 15 used technique B first while subjects 16 to 30 used technique A first.

Source

https://madeyski.e-informatyka.pl/reproducible-research/

Examples

```
KitchenhamMadeyski.SimulatedCrossoverDataSets
```

KitchenhamMadeyskiBrereton.ABBAMetaAnalysisReportedResults

KitchenhamMadeyskiBrereton.ABBAMetaAnalysisReportedResults data

---

Description

This data is used in the paper: Barbara Kitchenham, Lech Madeyski and Pearl Brereton. Meta-analysis for Families of Experiments: A Systematic Review and Reproducibility Assessment, Empirical Software Engineering (2019) doi:10.1007/s10664-019-09747-0. This data set reports the meta-analysis results reported by the authors of the primary studies included in the systematic review that reported results on a per document basis which for S7 and S11 was equivalent to reporting the results for each time period.

Usage

```
KitchenhamMadeyskiBrereton.ABBAMetaAnalysisReportedResults
```

Format

A text file with variables:

Study This field includes the study identifier of each of the the 3 primary studies which reported results per document.

Type This identifies the type of effect size used by the study authors. d or g refer to d_IG and g_IG, P is the aggregated p values, if the repeated measures (RM) estimate was obtained it is appropriately specified.

Source Always set to Rep. This identifies that the data was as reported by the primary study authors.

mean The overall mean effect size reported by the study authors

pvalue The one-sided p-value associated with the overall mean reported by the study authors. NA means the authors did not report this statistic.

UB The upper bound of the confidence interval of the overall mean as reported by the primary study authors. NA means the authors did not report this statistic.

LB The lower bound of the confidence interval of the overall mean as reported by the primary study authors. NA means the authors did not report this statistic.

QE The heterogeneity statistic associated with the meta-analysis as reported by the study authors. NA means the authors did not report this statistic.

Qep The p-value of the heterogeneity statistic associated with the meta-analysis as reported by the study authors. NA means the authors did not report this statistic.

Source

https://madeyski.e-informatyka.pl/reproducible-research/

Examples

```
KitchenhamMadeyskiBrereton.ABBAMetaAnalysisReportedResults
```

KitchenhamMadeyskiBrereton.ABBAReportedEffectSizes

KitchenhamMadeyskiBrereton.ABBAReportedEffectSizes data

Description

This data is used in the paper: Barbara Kitchenham, Lech Madeyski and Pearl Brereton. Meta-analysis for Families of Experiments: A Systematic Review and Reproducibility Assessment, Empirical Software Engineering (2019) doi:10.1007/s10664-019-09747-0. This file holds the individual effect sizes for the first time period (or equivalently the first document), as reported by the 3 primary studies in the systematic review that reported results for each document/time period separately.

Usage

```
KitchenhamMadeyskiBrereton.ABBAReportedEffectSizes
```

Format

A text file with variables:

Study This field includes the study identifier of each of the 3 primary studies which were included in the systematic review. The studies are S3, S7 and S11.

Type This identifies the type of effect size used by the study authors. d or g refer to dIG and gIG.

Source Always set to Rep. This identifies that the data was as reported by the primary study authors.

Design Mixed means different experiments in a particular family used different methods (onlyS3 used mixed methods and 4 experiments used the 4 goup crossover and one used an independent groups design). ABBACO is the standard 2-group crossover design.

Exp1 This is the reported standardised effect size for the first time period and the first experiment in the family.

Exp2 This is the reported standardised effect size for the first time period and second experiment in the family.

Exp3 This is the reported standardised effect size for the first time period and the third experiment in the family.

Exp4 This is the reported standardised effect size for the first time period and the fourth experiment in the family. NA means there was no fourth experiment in the family.

Exp5 This is the reported standardised effect size for the first time period and the fifth experiment in the family. NA means there was no fifth experiment in the family.

Source

https://madeyski.e-informatyka.pl/reproducible-research/

Examples

```
KitchenhamMadeyskiBrereton.ABBAReportedEffectSizes
```

KitchenhamMadeyskiBrereton.DocData

KitchenhamMadeyskiBrereton.DocData data

Description

This data is used in the paper: Barbara Kitchenham, Lech Madeyski and Pearl Brereton. Meta-analysis for Families of Experiments: A Systematic Review and Reproducibility Assessment, Empirical Software Engineering (2019) doi:10.1007/s10664-019-09747-0. This file holds the descriptive data for each document and each experiment for studies 3, 7 and 11 which include the mean, standard deviation and sample size for the control and treatment techniques. These studies performed ABBA crossover experiments and reported data for each document separately. Note Study 3 also undertook an independent groups study but data from that experiment is held in the ExpData file.

Usage

```
KitchenhamMadeyskiBrereton.DocData
```

Format

A text file with variables:

Study This field includes the study identifier of each of the 3 primary studies which reported their basic statistics on a time period & document basis.

Exp This identifies the experiment to which the descriptive data belongs.

Doc This identifies whether the data arose from the document used in the first or second time period. The value "Doc1" identifies the data as coming from the first document or first time period. The value "Doc2" identifies the data as coming from the second time period or document. Note for Study 3 we used the analysis of a specific document that was used in all 4 ABBA experiments. For studies 7 and 11, the authors identified which we used in r=each time period and Doc1 refers to data from the first time period.

Mc The mean value of the observations obtained using the control technique for the identified document.

SDc The standard deviation of the observations obtained using the control technique for the identified document.

Nc The number of participants using the control technique in the first time period for the identified document.

Mt The mean value of the observations obtained using the treatment technique for the identified document.

SDt The standard deviation of the observations obtained using the treatment technique for the identified document.

Nt The number of participants using the treatment technique in the first time period for the identified document.

Source

https://madeyski.e-informatyka.pl/reproducible-research/

Examples

```
KitchenhamMadeyskiBrereton.DocData
```

KitchenhamMadeyskiBrereton.ExpData
KitchenhamMadeyskiBrereton.ExpData data

Description

This data is used in the paper: Barbara Kitchenham, Lech Madeyski and Pearl Brereton. Meta-analysis for Families of Experiments: A Systematic Review and Reproducibility Assessment, Empirical Software Engineering (2019) doi:10.1007/s10664-019-09747-0. This file holds the descriptive data for each experiment which include the mean, standard deviation and sample size for the control and treatment techniques. Note in the case of studies 3, 7 and 11, which reported descriptive data for each time period (or equivalently each document) separately, the values for of the descriptive data were obtained by analysing the data reported in the DocData file.

Usage

KitchenhamMadeyskiBrereton.ExpData

Format

A text file with variables:

Study This field includes the study identifier of each of the 13 primary studies which were included in the systematic review.

Exp This identifies the experiment to which the descriptive data belongs.

Source Always set to Rep. This identifies that the data was as reported by the primary study authors.

Mc The mean value of the observations obtained using the control technique.

SDc The standard deviation of the observations obtained using the control technique.

Nc The number of participants using the control technique in the first time period.

Mt The mean value of the observations obtained using the treatment technique.

SDt The standard deviation of the observations obtained using the treatment technique.

Nt The number of participants using the treatment technique in the first time period.

r The correlation between repeated measures. NA if not reported. Note only study 13 reported this correlation.

Source

https://madeyski.e-informatyka.pl/reproducible-research/

Examples

KitchenhamMadeyskiBrereton.ExpData

KitchenhamMadeyskiBrereton.MetaAnalysisReportedResults

KitchenhamMadeyskiBrereton.MetaAnalysisReportedResults data

Description

This data is used in the paper: Barbara Kitchenham, Lech Madeyski and Pearl Brereton. Meta-analysis for Families of Experiments: A Systematic Review and Reproducibility Assessment (to be submitted). This data set reports the meta-analysis results reported by the authors of the 13 primary studies included in the systematic review.

Usage

KitchenhamMadeyskiBrereton.MetaAnalysisReportedResults

Format

A text file file with variables:

Study This field includes the study identifier of each of the 13 primary studies which were included in the systematic review.

Type This identifies the type of effect size used by the study authors. d or g refer to d_IG and g_IG, P is the aggregated p values, if the repeated measures estimate was obtained it is appropriately specified, r refers to the point bi-serial correlation.

Source Always set to Rep. This identifies that the data was as reported by the primary study authors.

mean The overall mean effect size reported by the study authors

pvalue The one-sided p-value associated with the overall mean reported by the study authors. NA means the authors did not report this statistic.

UB The upper bound of the confidence interval of the overall mean as reported by the primary study authors. NA means the authors did not report this statistic.

LB The lower bound of the confidence interval of the overall mean as reported by the primary study authors. NA means the authors did not report this statistic.

QE The heterogeneity statistic associated with the meta-analysis as reported by the study authors. NA means the authors did not report this statistic.

Qep The p-value of the heterogeneity statistic associated with the meta-analysis as reported by the study authors. NA means the authors did not report this statistic.

Source

https://madeyski.e-informatyka.pl/reproducible-research/

Examples

KitchenhamMadeyskiBrereton.MetaAnalysisReportedResults

KitchenhamMadeyskiBrereton.ReportedEffectSizes
KitchenhamMadeyskiBrereton.ReportedEffectSizes data

Description

This data is used in the paper: Barbara Kitchenham, Lech Madeyski and Pearl Brereton. Meta-analysis for Families of Experiments: A Systematic Review and Reproducibility Assessment, Empirical Software Engineering (2019) doi:10.1007/s10664-019-09747-0. This file holds the individual effect sizes for each experiment, as reported by 13 primary studies in the systematic review.

Usage

KitchenhamMadeyskiBrereton.ReportedEffectSizes

Format

A text file with variables:

Study This field includes the study identifier of each of the 13 primary studies which were included in the systematic review.

Type This identifies the type of effect size used by the study authors. d or g refer to dIG and gIG, p is the p-value used for aggregation, if the repeated measures estimate was obtained it is appropriately specified as gRM, r refers to the point bi-serial correlation.

Source Always set to Rep. This identifies that the data was as reported by the primary study authors.

Design The refers to the design method used by the study author. 4GroupCO is a 4-group crossover design. Mixed means different experiments in a particular family used different methods (only S3 used mixed methods and 4 experiments used the 4 group crossover and one used an independent groups design). ABBACO is the standard 2-group crossover design. IndGroups is the independent groups design also called between groups design or a randomised design. PrePost is pretest and posttest design with a post test control.

Exp1 This is the reported standardised effect size for the first experiment in the family.

Exp2 This is the reported standardised effect size for the second experiment in the family.

Exp3 This is the reported standardised effect size for the third experiment in the family.

Exp4 This is the reported standardised effect size for the fourth experiment in the family. NA means there was no fourth experiment in the family.

Exp5 This is the reported standardised effect size for the fifth experiment in the family. NA means there was no fifth experiment in the family.

Source

https://madeyski.e-informatyka.pl/reproducible-research/

Examples

```
KitchenhamMadeyskiBrereton.ReportedEffectSizes
```

```
KitchenhamMadeyskiBudgen16.COCOMO
```
KitchenhamMadeyskiBudgen16.COCOMO data

Description

If you use this data set please cite this R package and the following paper when accepted: Barbara Kitchenham, Lech Madeyski, David Budgen, Jacky Keung, Pearl Brereton, Stuart Charters, Shirley Gibbs, and Amnart Pohthong, "Robust Statistical Methods for Empirical Software Engineering", Empirical Software Engineering, vol. 22, no.2, p. 579-630, 2017. DOI: 10.1007/s10664-016-9437-5 (https://dx.doi.org/10.1007/s10664-016-9437-5), URL: https://madeyski.e-informatyka.pl/download/KitchenhamMadeyski

Usage

```
KitchenhamMadeyskiBudgen16.COCOMO
```

Format

A data frame with variables:

Project Project ID

Type A categorical variable describing the type of the project

Year The year the project was completed

Lang A categorical variable describing the development language used

Rely Ordinal value defining the required software reliability

Data Ordinal value defining the data complexity / Data base size

Cplx Ordinal value defining the complexity of the software / Process complexity

Aaf ??

Time Ordinal value defining the stringency of timing constraints / Time constraint for cpu

Stor Ordinal value defining the stringency of the data storage requirements / Main memory constraint

Virt Virtual Machine volatility

Turn Turnaround time

Type2 A categorical variable defining the hardware type: mini, max=mainframe, midi

Acap Ordinal value defining the analyst capability

Aexp Ordinal value defining the analyst experience / application experience

Pcap Ordinal value defining the programming capability of the team / Programmers capability

Vexp Ordinal value defining the virtual machine experience of the team

Lexp Ordinal value defining the programming language experience of the team

Cont ??

Modp / Modern programming practices

Tool Ordinal value defining the extent of tool use / Use of software tools

ToolCat Recoding of Tool to labelled ordinal scale

Sced Ordinal value defining the stringency of the schedule requirements / Schedule constraint

Rvol Ordinal value defining the requirements volatility of the project

Select Categorical value calculated by BAK for an analysis example

Rvolcat Recoding of Rvol to a labelled ordinal scale

Modecat Mode of the projects: O=Organic, E=Embedded, SD-Semi-Detached

Mode1 Dummy variable calculated by BAK: 1 if the project is Organic, 0 otherwise

Mode2 Dummy variable calculated by BAK: 1 if the project is Semi-detached, 0 otherwise

Mode3 Dummy variable calculated by BAK: 1 if the project is Embedded, 0 otherwise

KDSI Product Size Thousand of Source Instructions

AKDSI Adjusted Product Size for Project in Thousand Source Instructions - differs from KDSI for enhancement projects

Effort Project Effort in Man months

Duration Duration in months

Productivity Productivity of project calculated by BAK as AKDSI/Effort, so the the larger the value the better the productivity

Details

Data set collected at TRW by Barry Boehm see: B.W. Boehm. 1981. Software Engineering Economics. Prentice-Hall.

Explanations by Barbara Kitchenham / https://terapromise.csc.ncsu.edu:8443/!/#repo/view/head/effort/cocomo/cocomo1/nas

COCOMO.txt: pro type year Lang Rely Data CPLX aaf time store virt turn type2 acap aexp pcap vexp lexp cont modp TOOL TOOLcat SCED RVOL Select rvolcat Modecat Mode1 Mode2 Mode3 KDSI AKDSI Effort Dur Productivity

Source

<https://madeyski.e-informatyka.pl/reproducible-research/>

Examples

```
KitchenhamMadeyskiBudgen16.COCOMO
```

KitchenhamMadeyskiBudgen16.DiffInDiffData
                    KitchenhamMadeyskiBudgen16.DiffInDiffData data

---

Description

If you use this data set please cite this R package and the following paper when accepted: Barbara Kitchenham, Lech Madeyski, David Budgen, Jacky Keung, Pearl Brereton, Stuart Charters, Shirley Gibbs, and Amnart Pohthong, "Robust Statistical Methods for Empirical Software Engineering", Empirical Software Engineering, vol. 22, no.2, p. 579-630, 2017. DOI: 10.1007/s10664-016-9437-5 (https://dx.doi.org/10.1007/s10664-016-9437-5), URL: https://madeyski.e-informatyka.pl/download/KitchenhamMadeyski

Usage

KitchenhamMadeyskiBudgen16.DiffInDiffData

Format

A data frame with variables:

Abstract The abstract identifier

Site A numeric identifier of the site

Treatment A three character alphanumeric identifying the journal and time period of the abstract

Journal The journal in which the abstract was published: IST or JSS

Timeperiod The time period in which the abstract: 1 or 2

J1 The identifier for the judge who made the next 2 assessments

J1Completeness The average completeness made by judge J1 based on the 8 completeness questions

J1Clarity The clarity assessment made by judge J1

J2 The identifier for the judge who made the next 2 assessments

J2Completeness The average completeness made by judge J2 based on the 8 completeness questions

J2Clarity The clarity assessment made by judge J2

J3 The identifier for the judge who made the next 2 assessments

J3Completeness The average completeness made by judge J3 based on the 8 completeness questions

J3Clarity The clarity assessment made by judge J3

J4 The identifier for the judge who made the next 2 assessments

J4Completeness The average completeness made by judge J4 based on the 8 completeness questions

J4Clarity The clarity assessment made by judge J4

MeanCompleteness The mean of J1Completeness, J2Completeness, J3Completeness, J4Completeness

MedianCompleteness The median of J1Completeness, J2Completeness, J3Completeness, J4Completeness

MedianClarity The median clarity of J1Clarity, J2Clarity, J3Clarity, J4Clarity

MeanClarity The mean clarity of J1Clarity, J2Clarity, J3Clarity, J4Clarity

VarCompleteness The variance of J1Completeness, J2Completeness, J3Completeness, J4Completeness

VarClarity The variance clarity of J1Clarity, J2Clarity, J3Clarity, J4Clarity

Details

Data set was derived from the data reported in the SubjectData data set (subjectdata.txt). It contains the summary completeness and clarity data from 4 judges who assessed the same abstract. Only the initial 5 sites are included.

dinddata.txt

Source

<https://madeyski.e-informatyka.pl/reproducible-research/>

Examples

```
KitchenhamMadeyskiBudgen16.DiffInDiffData
```

```
KitchenhamMadeyskiBudgen16.FINNISH
```
                    KitchenhamMadeyskiBudgen16.FINNISH data

Description

If you use this data set please cite this R package and the following paper when accepted: Barbara Kitchenham, Lech Madeyski, David Budgen, Jacky Keung, Pearl Brereton, Stuart Charters, Shirley Gibbs, and Amnart Pohthong, "Robust Statistical Methods for Empirical Software Engineering", Empirical Software Engineering, vol. 22, no.2, p. 579-630, 2017. DOI: 10.1007/s10664-016-9437-5 (https://dx.doi.org/10.1007/s10664-016-9437-5), URL: https://madeyski.e-informatyka.pl/download/KitchenhamMadeyski

Usage

```
KitchenhamMadeyskiBudgen16.FINNISH
```

Format

A data frame with variables:

Project Project ID

DevEffort Development Effort measured in hours

UserEffort Effort provided by the customer/user organisation measured in hours

Duration Project duration measured in months

HWType A categorical variable defining the hardware type

AppType A categorical variable defining the application type

FP Function Points measured using the TIEKE organisation method

Co A categorical variable defining the company

Details

Data set collected from 9 Finish companies by Mr Hanna M\"aki from the TIEKE organisation see Barbara Kitchenham and Kari K\"ans\"al\"a, Inter-item correlations among function points, Proceedings ICSE 15, 1983, pp 477-480

Source

<https://madeyski.e-informatyka.pl/reproducible-research/>

Examples

```
KitchenhamMadeyskiBudgen16.FINNISH
```

KitchenhamMadeyskiBudgen16.PolishData

KitchenhamMadeyskiBudgen16.PolishData data

Description

If you use this data set please cite this R package and the following paper when accepted: Barbara Kitchenham, Lech Madeyski, David Budgen, Jacky Keung, Pearl Brereton, Stuart Charters, Shirley Gibbs, and Amnart Pohthong, "Robust Statistical Methods for Empirical Software Engineering", Empirical Software Engineering, vol. 22, no.2, p. 579-630, 2017. DOI: 10.1007/s10664-016-9437-5 (https://dx.doi.org/10.1007/s10664-016-9437-5), URL: https://madeyski.e-informatyka.pl/download/KitchenhamMadeyski

Usage

```
KitchenhamMadeyskiBudgen16.PolishData
```

Format

A data frame with variables:

Abstract The abstract identifier

Site Numeric identifier for the site

Treatment The first three characters of the Abstract field which identifies the journal and time period of the abstract

Journal An acronym for the journal from which the abstract was obtained: IST or JSS

Timeperiod The Time period in which the abstract was found: 1 or 2

J1 The identifier for the judge who made the next 2 assessments

J1Completeness The average completeness made by judge J1 based on the 8 completeness questions

J1Clarity The clarity assessment made by judge J1

J2 The identifier for the judge who made the next 2 assessments

J2Completeness The average completeness made by judge J2 based on the 8 completeness questions

J2Clarity The clarity assessment made by judge J2

J3 The identifier for the judge who made the next 2 assessments

J3Completeness The average completeness made by judge J3 based on the 8 completeness questions

J3Clarity The clarity assessment made by judge J3

J4 The identifier for the judge who made the next 2 assessments

J4Completeness The average completeness made by judge J4 based on the 8 completeness questions

J4Clarity The clarity assessment made by judge J4

MedianCompleteness The median of J1Completeness, J2Completeness, J3Completeness, J4Completeness

MedianClarity The median of J1Clarity, J2Clarity, J3Clarity, J4Clarity

Details

Data set derived from PolishSubjects data set collected at Wroclaw University. It summarizes the completeness and clarity data collected from 4 judges about the same abstract.

PolishData.txt

Source

<https://madeyski.e-informatyka.pl/reproducible-research/>

Examples

```
KitchenhamMadeyskiBudgen16.PolishData
```

KitchenhamMadeyskiBudgen16.PolishSubjects
KitchenhamMadeyskiBudgen16.PolishSubjects data

Description

If you use this data set please cite this R package and the following paper when accepted: Barbara Kitchenham, Lech Madeyski, David Budgen, Jacky Keung, Pearl Brereton, Stuart Charters, Shirley Gibbs, and Amnart Pohthong, "Robust Statistical Methods for Empirical Software Engineering", Empirical Software Engineering, vol. 22, no.2, p. 579-630, 2017. DOI: 10.1007/s10664-016-9437-5 (https://dx.doi.org/10.1007/s10664-016-9437-5), URL: https://madeyski.e-informatyka.pl/download/KitchenhamMadeyski

Usage

```
KitchenhamMadeyskiBudgen16.PolishSubjects
```

Format

A data frame with variables:

Judge The identifier for each subject

Abstract The identifier for each abstract - the code starts with a three alphanumeric string that defines the source of the abstract

OrderViewed Each judge assessed 4 abstracts in sequence, this data item identifies the order in which the subject viewed the specified abstract

Completness1 Assessment by judge of question 1:Is the reason for the project clear? Can take values: Yes/No/Partly

Completness2 Assessment by judge of question 2: Is the specific aim/purpose of the study clear? Can take values: Yes/No/Partly

Completness3 Assessment by judge of question 3: If the aim is to describe a new or enhanced software technology (e.g. method, tool, procedure or process) is the method used to develop this technology defined? Can take values: Yes/No/Partly/NA

Completness4 Assessment by judge of question 4: Is the form (e.g. experiment, general empirical study, data mining, case study, survey, simulation etc.) that was used to evaluate the technology made clear? Can take values: Yes/No/Partly

Completness5 Assessment by judge of question 5: Is there a description of how the evaluation process was organised? Can take values: Yes/No/Partly

Completness6 Assessment by judge of question 6: Are the results of the evaluation clearly described? Can take values: Yes/No/Partly

Completness7 Assessment by judge of question 7: Are any limitations of the study reported?: Yes/No/Partly

Completness8 Assessment by judge of question 8: Are any ideas for future research presented?: Yes/No/Partly

Clarity Assessment by judge of question regarding the overall understandability of the abstract: Please give an assessment of the clarity of this abstract by circling a number on the scale of 1-10 below, where a value of 1 represents Very Obscure and 10 represents Extremely Clearly Written.

Completness1NumValue A numerical value for completeness question 1 where 0=No, Partly=0.5, yes =1

Completness2NumValue A numerical value for completeness question 2 where 0=No, Partly=0.5, yes =1, NA means not applicable

Completness3NumValue A numerical value for completeness question 3 where 0=No, Partly=0.5, yes =1, NA means not applicable or not answered

Completness4NumValue A numerical value for completeness question 4 where 0=No, Partly=0.5, yes =1, NA means not applicable

Completness5NumValue A numerical value for completeness question 5 where 0=No, Partly=0.5, yes =1, NA means not applicable

Completness6NumValue A numerical value for completeness question 6 where 0=No, Partly=0.5, yes =1, NA means not applicable

Completness7NumValue A numerical value for completeness question 7 where 0=No, Partly=0.5, yes =1, NA means not applicable

Completness8NumValue A numerical value for completeness question 8 where 0=No, Partly=0.5, yes =1, NA means not applicable

Sum The sum of the numerical completeness questions excluding those labelled NA

TotalQuestions The count of the number of question related to completeness excluding questions considered not applicable

Completeness Sum/TotalQuestions

Details

Data set collected at Wroclaw University of Technology (POLAND) by Lech Madeyski includes separate entries for each abstract assessed by a judge, that is 4 entries for each judge. Data collected from 16 subjects recruited from Wroclaw University of Technology who were each asked to assess 4 abstracts.

Note Only completeness question 2 was expected to be context dependent and have a NA (not applicable) answer, if other completeness answers were left blank, BAK coded the answer as NA

polishsubjects.txt

Source

<https://madeyski.e-informatyka.pl/reproducible-research/>

Examples

```
KitchenhamMadeyskiBudgen16.PolishSubjects
```

KitchenhamMadeyskiBudgen16.SubjectData
KitchenhamMadeyskiBudgen16.SubjectData

Description

If you use this data set please cite this R package and the following paper when accepted: Barbara Kitchenham, Lech Madeyski, David Budgen, Jacky Keung, Pearl Brereton, Stuart Charters, Shirley Gibbs, and Amnart Pohthong, "Robust Statistical Methods for Empirical Software Engineering", Empirical Software Engineering, vol. 22, no. 2, pp. 579–630, 2017. DOI: 10.1007/s10664-016-9437-5 (https://dx.doi.org/10.1007/s10664-016-9437-5), URL: https://madeyski.e-informatyka.pl/download/KitchenhamMa

Usage

```
KitchenhamMadeyskiBudgen16.SubjectData
```

Format

A data frame with variables:

Judge Alphanumeric identifier for each judge

Institution Numerical value identifying each site from which data was collected

JudgeID Numerical value identifying each judge

Age Age of the judge in years

Eng1st Whether the judge's first language was Enlish: Yes/No

YearsStudy The number of years have student been studying computing at University: 1, 2, 3, 4

AbstractsRead Number of abstracts the judge had read prior to the study" 0, 1 to 10, 10+

AbstractsWritten Whether the judge had ever written an abstract for a scientific report/article

AbstractID Alphanumeric identifier for an abstract. The first character identifies the journal, I=IST, J=JSS, the third digit identifies the time period as 1 or 2, the remaining digits identify the abstract number within the set of abstracts found for the specified journal and time period

Treat The initial 3 characters of AbstractID

TreatID A numeric identifier for the journal and time period, 1=IB1, 2=IB2, 3=JB1, 4=JB2

Order The order in which the judge should have viewed the specified abstract

Completness1NumValue The numeric answer to completeness question 1

Completness2NumValue The numeric answer to completeness question 2

Completness3NumValue The numeric answer to completeness question 3

Completness4NumValue The numeric answer to completeness question 4

Completness5NumValue The numeric answer to completeness question 5

Completness6NumValue The numeric answer to completeness question 6

Completness7NumValue The numeric answer to completeness question 7

Completness8NumValue The numeric answer to completeness question 8

Clarity The response to the clarity question or NA if not answered

NumberOfAnsweredCompletnessQuestions The number of completeness questions excluding those with NA

TotalScore Sum of the numeric values of the 8 completeness questions

MeanScore Sum of the completeness questions 1 to 8 divided by TotalScore

Site The name of the site which provided the data. HongKong refers to the Polytechnic University, HongKong.2 refers to the City University

Details

Data set collected from 16 judges assessing 4 abstracts at 6 sites: Lincoln University NZ=1, Hong Kong Polytechnic University=2, PSu Thailand=3, Durham=4, Keele=5, Hong Kong City University=6

subjectdata.txt: Judge Institution JudgeID age eng1st years.study abs.read Absid Treat TreatID Order Com.1 Com.2 Com.3 Com.4 Com.5 Com.6 Com.7 Com.8 Clarity num.questions total.score av.score Site

Source

<https://madeyski.e-informatyka.pl/reproducible-research/>

Examples

```
KitchenhamMadeyskiBudgen16.SubjectData
```

LaplaceDist	*LaplaceDist*

Description

Returns a sample of N observations from a Laplace distribution with specified mean and spread.

Usage

```
LaplaceDist(N, mean, spread, max = 0.5, min = -0.5)
```

Arguments

N	is the required sample size
mean	is the required mean
spread	is the spread of the function
max	upper limits of the distribution, must be finite
min	lower limit of the distribution, must be finite

Value

N values from a Laplace distribution

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
set.seed(123)
LaplaceDist(10,0,1)
# [1] -0.55311564 0.85946218 -0.20094937 1.45258293 2.12808209 -2.39565480 0.05785263...
```

Madeyski15EISEJ.OpenProjects

Madeyski15EISEJ.OpenProjects data

Description

If you use this data set please cite: Marian Jureczko and Lech Madeyski, "Cross-project defect prediction with respect to code ownership model: An empirical study", e-Informatica Software Engineering Journal, vol. 9, no. 1, pp. 21-35, 2015. DOI: 10.5277/e-Inf150102 (https://dx.doi.org/10.5277/e-Inf150102) URL: https://madeyski.e-informatyka.pl/download/JureczkoMadeyski15.pdf)

Usage

Madeyski15EISEJ.OpenProjects

Format

A data frame with variables:

PROP The percentage of classes of proprietary (i.e., industrial) projects that must be tested in order to find 80% of defects in case of software defect prediction models built on open source projects.

NOTOPEN The percentage of classes of projects which are not open source projects that must be tested in order to find 80% of defects in case of software defect prediction models built on open source projects.

STUD The percentage of classes of student (i.e., academic) projects that must be tested in order to find 80% of defects in case of software defect prediction models built on open source projects.

OPEN The percentage of classes of open source projects that must be tested in order to find 80% of defects in case of software defect prediction models built on open source projects.

Details

This paper presents an analysis of 84 versions of industrial, open-source and academic projects. We have empirically evaluated whether those project types constitute separate classes of projects with regard to defect prediction. The predictions obtained from the models trained on the data from the open source projects were compared with the predictions from the other models (built on proprietary, i.e. industrial, student, open source, and not open source projects).

Source

<https://madeyski.e-informatyka.pl/reproducible-research/>

Examples

Madeyski15EISEJ.OpenProjects

Madeyski15EISEJ.PropProjects

Madeyski15EISEJ.PropProjects data

Description

If you use this data set please cite: Marian Jureczko and Lech Madeyski, "Cross-project defect prediction with respect to code ownership model: An empirical study", e-Informatica Software Engineering Journal, vol. 9, no. 1, pp. 21-35, 2015. DOI: 10.5277/e-Inf150102 (https://dx.doi.org/10.5277/e-Inf150102) URL: https://madeyski.e-informatyka.pl/download/JureczkoMadeyski15.pdf)

Usage

Madeyski15EISEJ.PropProjects

Format

A data frame with variables:

NOTPROP The percentage of classes of non-proprietary (i.e., non-industrial) projects that must be tested in order to find 80% of defects in case of software defect prediction models built on proprietary (i.e., industrial) projects.

OPEN The percentage of classes of open source projects that must be tested in order to find 80% of defects in case of software defect prediction models built on proprietary (i.e., industrial) projects.

STUD The percentage of classes of student (i.e., academic) projects that must be tested in order to find 80% of defects in case of software defect prediction models built on proprietary (i.e., industrial) projects.

PROP The percentage of classes of proprietary (i.e., industrial) projects that must be tested in order to find 80% of defects in case of software defect prediction models built on proprietary (i.e., industrial) projects.

Source

https://madeyski.e-informatyka.pl/reproducible-research/

Examples

Madeyski15EISEJ.PropProjects

Madeyski15EISEJ.StudProjects
                         Madeyski15EISEJ.StudProjects data

Description

If you use this data set please cite: Marian Jureczko and Lech Madeyski, "Cross-project defect prediction with respect to code ownership model: An empirical study", e-Informatica Software Engineering Journal, vol. 9, no. 1, pp. 21-35, 2015. DOI: 10.5277/e-Inf150102 (https://dx.doi.org/10.5277/e-Inf150102) URL: https://madeyski.e-informatyka.pl/download/JureczkoMadeyski15.pdf)

Usage

Madeyski15EISEJ.StudProjects

Format

A data frame with variables:

PROP The percentage of classes of proprietary (i.e., industrial) projects that must be tested in order to find 80% of defects in case of software defect prediction models built on student (i.e., academic) projects.

NOTSTUD The percentage of classes of projects which are not student projects that must be tested in order to find 80% of defects in case of software defect prediction models built on student (i.e., academic) projects.

STUD The percentage of classes of student (i.e., academic) projects that must be tested in order to find 80% of defects in case of software defect prediction models built on student (i.e., academic) projects.

OPEN The percentage of classes of open source projects that must be tested in order to find 80% of defects in case of software defect prediction models built on student (i.e., academic) projects.

Source

<https://madeyski.e-informatyka.pl/reproducible-research/>

Examples

Madeyski15EISEJ.StudProjects

Madeyski15SQJ.NDC   *Madeyski15SQJ.NDC data*

Description

If you use this data set please cite: Lech Madeyski and Marian Jureczko, "Which Process Metrics Can Significantly Improve Defect Prediction Models? An Empirical Study," Software Quality Journal, vol. 23, no. 3, pp.393-422, 2015. DOI: 10.1007/s11219-014-9241-7

Usage

Madeyski15SQJ.NDC

Format

A data frame with variables:

Project In case of open source projects this field includes the name of the project as well as its version. In case of industrial projects this field includes the string "proprietary" (we were not allowed to disclose the names of the analyzed industrial software projects developed by Capgemini Polska).

simple The percentage of classes that must be tested in order to find 80% of defects in case of simple defect prediction models, i.e., using only software product metrics as predictors.

advanced The percentage of classes that must be tested in order to find 80% of defects in case of advanced defect prediction models, using not only software product metrics but also the NDC (Number of distinct committers) process metric.

Details

"This paper presents an empirical evaluation in which several process metrics were investigated in order to identify the ones which significantly improve the defect prediction models based on product metrics. Data from a wide range of software projects (both, industrial and open source) were collected. The predictions of the models that use only product metrics (simple models) were compared with the predictions of the models which used product metrics, as well as one of the process metrics under scrutiny (advanced models). To decide whether the improvements were significant or not, statistical tests were performed and effect sizes were calculated. The advanced defect prediction models trained on a data set containing product metrics and additionally Number of Distinct Committers (NDC) were significantly better than the simple models without NDC, while the effect size was medium and the probability of superiority (PS) of the advanced models over simple ones was high ($p=.016$, $r=-.29$, PS=.76), which is a substantial finding useful in defect prediction. A similar result with slightly smaller PS was achieved by the advanced models trained on a data set containing product metrics and additionally all of the investigated process metrics ($p=.038$, $r=-.29$, PS=.68). The advanced models trained on a data set containing product metrics and additionally Number of Modified Lines (NML) were significantly better than the simple models without NML, but the effect size was small ($p=.038$, $r=.06$). Hence, it is reasonable to recommend the NDC process metric in building the defect prediction models." [https://dx.doi.org/10.1007/s11219-014-9241-7]

Source

Examples

```
Madeyski15SQJ.NDC
```

MadeyskiKitchenham.EUBASdata

MadeyskiKitchenham.EUBASdata data

Description

If you use this data set please cite this R package and the paper where we analyze the data set: Lech Madeyski and Barbara Kitchenham, "Effect Sizes and their Variance for AB/BA Crossover Design Studies", Empirical Software Engineering, vol. 24, no.4, p. 1982-2017, 2018. DOI: 10.1007/s10664-017-9574-5

Usage

```
MadeyskiKitchenham.EUBASdata
```

Format

A data frame with variables:

ID Project ID

TimePeriod Period of time (run): R1, R2

SequenceGroup Sequence group: G1, G2, G3, G4

System Software system identifier indicates the system (i.e., S1 or S2) used as the experimental object: S1. A software system to sell and manage CDs/DVDs in a music shop, S2. A software system to book and buy theater tickets

Technique The independent variable. It is a nominal variable that can assume the following two values: AM (analysis models plus source code) and SC (source code alone)

Comp_Level This denotes the comprehension level of the source code achieved by a software engineer

Modi_Level This denotes the capability of a maintainer to modify source code

Details

Data set comes from an experiment conducted in Italy at the University of Basilicata (with 24 first-year students from the Master's Program in Computer Science) to answer the question "Do the software models produced in the requirements analysis process aid in the comprehensibility and modifiability of source code?", see G. Scanniello, C. Gravino, M. Genero, J. A. Cruz-Lemus, and G. Tortora, "On the Impact of UML Analysis Models on Source-code Comprehensibility and Modifiability," ACM Transactions on Software Engineering and Methodology, vol. 23, pp. 13:1-13:26, Apr. 2014. However, the inconsistent subject data for subject 2 was removed, see the aforementioned paper by Madeyski and Kitchenham.

Source

https://madeyski.e-informatyka.pl/reproducible-research/

Examples

```
MadeyskiKitchenham.EUBASdata
```

MadeyskiKitchenham.MetaAnalysis.PBRvsCBRorAR

> *MadeyskiKitchenham.MetaAnalysis.PBRvsCBRorAR data form a set of primary studies on reading methods for software inspections. They were analysed by Lech Madeyski and Barbara Kitchenham, "How variations in experimental designs impact the construction of comparable effect sizes for meta-analysis", 2015.*

Description

If you use this data set please cite: Lech Madeyski and Barbara Kitchenham, "How variations in experimental designs impact the construction of comparable effect sizes for meta-analysis", 2015.

Usage

```
MadeyskiKitchenham.MetaAnalysis.PBRvsCBRorAR
```

Format

A data frame with 17 rows and 26 variables:

Study Name of empirical study

Ref. Reference to the paper reporting primary study or experimental run where data were originally reported

Teams The number of teams including both, PBR and Control teams

DesignDesc Experimental design description: Before-after, Between-groups, Cross-over

ExpDesign Experimental design: between-groups (BG), within-subjects cross-over (WSCO), within-subjects before-after (WSBA)

M_PBR The average proportion of defects found by teams using PBR

M_C The average proportion of defects found by teams using Control treatment: Check-Based Reading (CBR) or Ad-Hoc Reading (AR)

Diff The difference between M_PBR and M_C, i.e. Diff = M_PBR - M_C

Inc The percentage increase in defect rate detection, i.e. Inc=100*[(M_PBR-M_C)/M_C]

SD_C_ByAuthors The standard deviation of the control group values reported by the original Authors, i.e., obtained from the papers/raw data

SD_C The standard deviation of the control group values equals SD_C_ByAuthors for studies for which the data was available OR the weighted average of SD_C_ByAuthors (i.e., 0.169) for studies where SD_C_ByAuthors is missing.

V_C The variance of the Control group observations, i.e., the variance obtained from the teams using the Control method V_C=SD_C^2

V_D The variance of the unstandardized mean difference D (between the mean value for the treatment group and the mean value for the Control group)

SD_C_Alt This is the equivalent of SD_C (the standard deviation of the control group) based on a different variance for the student studies or the practitioner studies depending on the subject type of the study with the missing value.

V_Alt The variance of the mean difference in the meta-analysis based on SD_C_Alt

SS_C The sum of squares of the Control group values. For within subjects studies SS=V_C*(n-1). For between subjects studies SS=V_C*(n_C-1)

n_PBR The number of PBR teams

n_C The number of Control (CBR or AR) teams

ControlType Type of Control treatment: CRB or AR

ParticipantsType Type of participants: Engineers or Students

TeamType Type of team: Nominal or Real

TwoPersonTeamVsLargerTeam Reflects size of the teams: 2-PersonTeam or LargerTeam

ArtefactType The type of artefact: Requirements or Other

AssociatedWithBasili Whether study is associated with Basili (the forerunner): Yes or No

ControlType_Basili Combined ControlType and AssociatedWithBasili: AH_AssociatedWithBasili, CBR_AssociatedWithBasili, CBR_NotAssociatedWithBasili

Source

https://madeyski.e-informatyka.pl/reproducible-research/

Examples

```
MadeyskiKitchenham.MetaAnalysis.PBRvsCBRorAR
```

MadeyskiLewowski.IndustryRelevantGitHubJavaProjects20190324

MadeyskiLewowski.IndustryRelevantGitHubJavaProjects20190324
data

Description

This data is used in the paper: Tomasz Lewowski and Lech Madeyski, "Creating Evolving Project Data Sets in Software Engineering", vol. 851 of Studies in Computational Intelligence, pp. 1–14. Cham: Springer, 2020. DOI: 10.1007/978-3-030-26574-8_1

Usage

MadeyskiLewowski.IndustryRelevantGitHubJavaProjects20190324

Format

A text file with variables:

rowID unique id assigned to projects before filtering (source: API)

id GitHub repository ID (source: API)

repository owner the organization or user owning the repository (source: API)

project name name of the project (source: API)

manual link to best found project documentation - wiki, webpage, documentation directory or readme. Projects with limited documentation were marked with (limited) and ones that had documentation in Chinese - (Chinese) (source: manual)

installation the recommended installation medium(s) for the project. Some mediums may be missing for projects with multiple recommendations. (source: manual)

support channel(s) that can be used to get support and/or report bugs. Some channels may be missing for projects with multiple ones. Abbreviations used (source: manual): GH GitHub Issues SO Stack Overflow GG Google Groups ML Mailing list FB Facebook MM Mattermost LI LinkedIn ? not found

is not sample/playground/docs/... 1 if the project is an actual application or library, 0 if it is a set of samples, only documentation or some experimental area (source: manual)

is industrial whether the project can be treated as industrial quality one. Values and their meanings: 1 the repository can be classified as industrial grade; 0,5 the repository can sometimes be classified as industrial grade, but it is either a minor project or its documentation or support may be lacking the depth; 0 the repository cannot be classified as industrial-grade; -1 the repository is no longer actively maintained as of the date of data acquisition; -2 the repository is no longer in Java as of the date of data acquisition. (source: manual)

createdAt the date at which the repository was created (source: API)

updatedAt the date of last repository update - including changes in projects, watchers, issues etc. (source: API)

pushedAt the date of last push to the repository - NOT the date of last pushed commit (source: API)

diskUsage total number of bytes on disk that are needed to store the repository (source: API)

forkCount number of existing repository forks (independent copies managed by other entities) (source: API)

isArchived true if the repository is archived (no longer maintained), false otherwise (source: API)

isFork true if the repository is a fork (not the main repository), false otherwise (source: API)

isMirror true if the repository is a mirror, false otherwise (source: API)

sshUrlOfRepository URL that can be used to immediately clone the repository (source: API)

licenseInfo.name name of license under which the project is distributed. Names are the same as in https://choosealicense.com/appendix/ (source: API)

commitSHA unique Git identifier of commit that was top of the main branch at the time of data acquisition (source: API)

defaultBranchRef.target.history.totalCount number of commits on the default branch in the repository (usually master) at the time of data acquisition (source: API)

stargazers.totalCount number of stargazers for the repository at the time of data acquisition (source: API)

watchers.totalCount number of watchers for the repository at the time of data acquisition (source: API)

languages.totalSize total size of all source code files (source: API)

Java.byte.count total size of Java files (source: API)

Language main programming language used in the repository, i.e. one that the most code is written in (source: API)

searchQuery query used during search that obtained this project (source: API)

Source

https://madeyski.e-informatyka.pl/reproducible-research/

Examples

```
MadeyskiLewowski.IndustryRelevantGitHubJavaProjects20190324
```

```
MadeyskiLewowski.IndustryRelevantGitHubJavaProjects20191022
```
*MadeyskiLewowski.IndustryRelevantGitHubJavaProjects20191022
data*

Description

This data is used in the paper: Tomasz Lewowski and Lech Madeyski, "How do software engineering data sets evolve? A reproduction study", 2020 (submitted). Generated by: token <- "..." MadeyskiLewowski.IndustryRelevantGitHubJavaProjects20191022<-searchForIndustryRelevantGitHubProjects(token, "2019-03-01", "2018-08-01") usethis::use_data(MadeyskiLewowski.IndustryRelevantGitHubJavaProjects20191022)

Usage

MadeyskiLewowski.IndustryRelevantGitHubJavaProjects20191022

Format

A text file with variables:

rowID unique id assigned to projects before filtering (source: API)

id GitHub repository ID (source: API)

repository owner the organization or user owning the repository (source: API)

project name name of the project (source: API)

manual link to best found project documentation - wiki, webpage, documentation directory or readme. Projects with limited documentation were marked with (limited) and ones that had documentation in Chinese - (Chinese) (source: manual)

installation the recommended installation medium(s) for the project. Some mediums may be missing for projects with multiple recommendations. (source: manual)

support channel(s) that can be used to get support and/or report bugs. Some channels may be missing for projects with multiple ones. Abbreviations used (source: manual): GH GitHub Issues SO Stack Overflow GG Google Groups ML Mailing list FB Facebook MM Mattermost LI LinkedIn ? not found

is not sample/playground/docs/... 1 if the project is an actual application or library, 0 if it is a set of samples, only documentation or some experimental area (source: manual)

is industrial whether the project can be treated as industrial quality one. Values and their meanings: 1 the repository can be classified as industrial grade; 0,5 the repository can sometimes be classified as industrial grade, but it is either a minor project or its documentation or support may be lacking the depth; 0 the repository cannot be classified as industrial-grade; -1 the repository is no longer actively maintained as of the date of data acquisition; -2 the repository is no longer in Java as of the date of data acquisition. (source: manual)

createdAt the date at which the repository was created (source: API)

updatedAt the date of last repository update - including changes in projects, watchers, issues etc. (source: API)

pushedAt the date of last push to the repository - NOT the date of last pushed commit (source: API)

diskUsage total number of bytes on disk that are needed to store the repository (source: API)

forkCount number of existing repository forks (independent copies managed by other entities) (source: API)

isArchived true if the repository is archived (no longer maintained), false otherwise (source: API)

isFork true if the repository is a fork (not the main repository), false otherwise (source: API)

isMirror true if the repository is a mirror, false otherwise (source: API)

sshUrlOfRepository URL that can be used to immediately clone the repository (source: API)

licenseInfo.name name of license under which the project is distributed. Names are the same as in https://choosealicense.com/appendix/ (source: API)

commitSHA unique Git identifier of commit that was top of the main branch at the time of data acquisition (source: API)

defaultBranchRef.target.history.totalCount number of commits on the default branch in the repository (usually master) at the time of data acquisition (source: API)

stargazers.totalCount number of stargazers for the repository at the time of data acquisition (source: API)

watchers.totalCount number of watchers for the repository at the time of data acquisition (source: API)

languages.totalSize total size of all source code files (source: API)

Java.byte.count total size of Java files (source: API)

Language main programming language used in the repository, i.e. one that the most code is written in (source: API)

searchQuery query used during search that obtained this project (source: API)

Source

https://madeyski.e-informatyka.pl/reproducible-research/

Examples

```
MadeyskiLewowski.IndustryRelevantGitHubJavaProjects20191022
```

MetaAnalysisSimulations

MetaAnalysisSimulations

Description

This function simulates data from many families of experiments. The number of families simulated is defined by the Replications parameter. The parameter Exp determines the number of experiments in each family. The function simulates data from one of four distributions and uses the data to construct two of groups of equal size (GroupSize). The experimental design of individual experiments in each family is determined by the FourGroup parameter. If FourGroup=FALSE, the basic experimental design is a balanced two group randomized experiment, otherwise the experimental design is a balanced four group experiment corresponding to a randomized blocks experiment. The function calls either NP2GroupMetaAnalysisSimulation or NP4GroupMetaAnalysisSimulation to generate and analyse data for each individual family. The function either returns the meta-analysed data from each experiment or provides summary statistics.

Usage

```
MetaAnalysisSimulations(
  mean = 0,
  sd = 1,
  diff = 0.5,
  GroupSize = 10,
  type = "n",
  Replications = 50,
  Exp = 5,
  seed = 456,
  alpha = 0.05,
  FourGroup = FALSE,
  StdAdj = 0,
  BlockEffect = 0,
  BlockStdAdj = 0,
  StdExp = 0,
  MAMethod = "PM",
  returnES = F
)
```

Arguments

mean	the value used for the mean of control group in the simulated data. It can be any real number including zero.
sd	the value used for the spread of the control group and the spread of the treatment group in the simulated data. The value must be a real value greater than 0.
diff	mean+diff is the value used for the mean of the treatment group. It can be zero.
GroupSize	is the size of each of the groups comprising one experiment. GroupSize should be an integer of 4 or more
type	specifies the distribution being simulated. The permited values are "n" for the normal distribution, "l" for the lognormal distribution, "g" for the gamma distribution and "lap" for the Laplace distribution. The parameter defaults to "n".
Replications	The number of times the set of experiments is simulated. It defaults to 500.
Exp	the number of experiments being simulated. Exp should be an integer of 2 or more. It defaults to 5.
seed	specifies the seed to be used to initiate the simulation, so the simulation is repeatable. It defaults to 456.
alpha	This is the Type 1 probability level used in significnace tests. It defaults to 0.05.
FourGroup	is a Boolean variable that determines whether the experiment is a two group experiments or a 4-Group randomised block experiment. It defaults to FALSE which means a two group experiment is the default condition.
StdAdj	specifies the adjustment made to the treatment variance if it is required to simulate variance heterogeneity due to the treatment. It defaults to 0.
BlockEffect	specified a fixed block effect that can be applied to randomized blocks designs.

BlockStdAdj	specifies the adjustment made to the variance of one block if it is required to simulate heterogeneity due to blocks in a randomized blocks experiment. The variance adjusment is made to the same block that any Block affect is applied to. It defaults to 0.
StdExp	specifies the adjustment made to the variance of each experiment if it is required to simulate variance heterogeneity due to individual experiments in a family. It defaults to 0.
MAMethod	specifies the model to be used when experimental effect sizes ar aggregated using the R metafor package.
returnES	if TRUE the function outputs the summary statistics otherwise it outputs the meta-analysis results for each family. The parameter defaults to FALSE

Value

The parameter either returns the meta-analysis values obtained from each family or the average values of the meta-analysis over all replications.

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
MetaAnalysisSimulations(mean=0,sd=1,diff=0.5,GroupSize=10,type="n",Replications=25,Exp=5,
seed=456,alpha=0.05,FourGroup=FALSE,StdAdj=0,BlockEffect=0,BlockStdAdj=0,StdExp=0,MAMethod="PM")
# A tibble: 1 x 26
# Averagektau Averagektauctvar AveragetauSigCVt AverageCliffd AverageCliffdvar AverageCliffdsig
# <dbl>           <dbl>              <dbl>           <dbl>           <dbl>            <dbl>
# 1     0.164          0.00375            0.72          0.311          0.0134           0.72
#. . . with 20 more variables: Averagephat <dbl>, Averagephatvar <dbl>, Averagephatsig <dbl>,
# MAAverage <dbl>, MAVariance <dbl>, MASignificant <dbl>, HetSignificant <dbl>, PMAAverage <dbl>,
# PMASignificant <dbl>, PMAHetSignificant <dbl>, Mean.phat <dbl>, phat.sig <dbl>, Mean.d <dbl>,
# d.sig <dbl>, Mean.g.exact <dbl>, g.exact.sig <dbl>, Mean.g.approx <dbl>, g.approx.sig <dbl>,
#  Mean.Cohend <dbl>, Cohend.sig <dbl>
MetaAnalysisSimulations(mean=0,sd=1,diff=0.734,GroupSize=100,type="l",Replications=25,Exp=5,
seed=456,alpha=0.05,FourGroup=FALSE,StdAdj=0,BlockEffect=0,BlockStdAdj=0,StdExp=0,MAMethod="PM")
#  A tibble: 1 x 26
# Averagektau Averagektauctvar AveragetauSigCVt AverageCliffd AverageCliffdvar AverageCliffdsig
# <dbl>           <dbl>              <dbl>           <dbl>           <dbl>            <dbl>
# 0.200         0.000276              1            0.399          0.00109             1
#. . . with 20 more variables: Averagephat <dbl>, Averagephatvar <dbl>, Averagephatsig <dbl>,
#  MAAverage <dbl>, MAVariance <dbl>, MASignificant <dbl>, HetSignificant <dbl>, PMAAverage <dbl>,
#  PMASignificant <dbl>, PMAHetSignificant <dbl>, Mean.phat <dbl>, phat.sig <dbl>, Mean.d <dbl>,
#  d.sig <dbl>, Mean.g.exact <dbl>, g.exact.sig <dbl>, Mean.g.approx <dbl>, g.approx.sig <dbl>,
#   Mean.Cohend <dbl>, Cohend.sig <dbl>
# MetaAnalysisSimulations(mean=0,sd=1,diff=0.5,GroupSize=10,type="n",Replications=10,Exp=5,
# seed=456,alpha=0.05,FourGroup=TRUE,StdAdj=0,BlockEffect=0.5,BlockStdAdj=0,StdExp=0,
# MAMethod="PM",returnES=TRUE)
# A tibble: 10 x 31
# Family NumExp GroupSize AveKtau AveKtauctvar tauSigCVt AveCliffd AveCliffdvar AveCliffdsig
# <int> <dbl>     <dbl>    <dbl>       <dbl> <lgl>         <dbl>        <dbl> <lgl>
```

```
# 1     1     5     10   0.133    0.00206 TRUE         0.252     0.00742 TRUE
# 2     2     5     10   0.161    0.00190 TRUE         0.306     0.00681 TRUE
# 3     3     5     10   0.135    0.00206 TRUE         0.256     0.00744 TRUE
# 4     4     5     10   0.16     0.00191 TRUE         0.304     0.00686 TRUE
# 5     5     5     10   0.133    0.00178 TRUE         0.252     0.00636 TRUE
# 6     6     5     10   0.192    0.00178 TRUE         0.364     0.00634 TRUE
# 7     7     5     10   0.189    0.00185 TRUE         0.36      0.00661 TRUE
# 8     8     5     10   0.126    0.00199 TRUE         0.24      0.00715 TRUE
# 9     9     5     10   0.132    0.00200 TRUE         0.25      0.00719 TRUE
# 10   10     5     10   0.18     0.00181 TRUE         0.342     0.00646 TRUE
# # . . . with 22 more variables: Avephat <dbl>, Avephatvar <dbl>, Avephatsig <lgl>, MAMean <dbl>,
# #   MAvar <dbl>, MASig <lgl>, QE <dbl>, QEp <dbl>, HetSig <lgl>, P.mean <dbl>, P.rsig <lgl>,
# #   P.hetsig <lgl>, Mean.phat <dbl>, phat.sig <lgl>, Mean.d <dbl>, d.sig <lgl>,
# #   Mean.g.exact <dbl>, g.exact.sig <lgl>, Mean.g.approx <dbl>, g.approx.sig <lgl>,
# #   Cohend.mean <dbl>, Cohend.sig <lgl>
```

NP2GroupMetaAnalysisSimulation

NP2GroupMetaAnalysisSimulation

Description

This function simulates data from a family of experiments. The parameter Exp deteremines the number of experiments in the family. The function simulates data from one of four distributions and uses the data to construct two of groups of equal size (GroupSize). The distribution for one of the groups corresponds to the control and is based on the given mean and spread, the distribution for the other group corresponds to the treatment group and is based on the mean+diff and the spread plus any variance adjusemtn (determined by the parametrt StdAdj). The data from each experiment is analysed separately to estimate three non-parametric effect sizes: the point bi-serial version of Kendall's tau, Cliff's d and the probability of superiority referred to as phat and their variances. Parametric effect sizes Cohen's d (also known as the standarized means difference, SMD) and the small sample size adjusted standardized mean difference g are also calculated to gether with their variances. The effect sizes are then meta-analysed using two main methods: the simple avarge of the effect size and the variance weighted average. The function uses the metafor package for formal meta-analysis, and the specific method of formal meta-analysis used is determined by the MAAMethod. All tests of signficance are done at the 0.05 level. If the parameter returnES is TRUE, the function returns it returns the effect sizes for each experiment in the family, otherwise it returns the meta-analysis results.

Usage

```
NP2GroupMetaAnalysisSimulation(
  mean,
  sd,
  diff,
  GroupSize,
  Exp = 5,
  type = "n",
```

```
    StdAdj = 0,
    alpha = 0.05,
    seed = 123,
    StdExp = 0,
    MAMethod,
    returnES = FALSE
)
```

Arguments

mean	the value used for the mean of control group in the simulated data. It can be any real number including zero.
sd	the value used for the spread of the control group and the spread of the treatment group in the simulated data. The value must be a real value greater than 0.
diff	mean+diff is the value used for the mean of the treatment group. It can be zero.
GroupSize	is the size of each of the 2 groups comprising one experiment. GroupSize should be an integer of 4 or more
Exp	is the number of experiments being simulated. Exp should be an integer of 2 or more. It defaults to 5.
type	specifies the distribution being simulated. The permited values are "n" for the normal distribution, "l" for the lognormal distribution, "g" for the gamma distribution and "lap" for the Laplace distribution. The parameter defaults to "n".
StdAdj	specifies a level used to adjust the treatment variance. It allows heterogeneity to be modelled. It defaults to zero meaning no variance heterogeneity is introduced.
alpha	the Type 1 error rate level use for statistical tests itb defaults to 0.05.
seed	specifies the seed to be used to initiate the simulation, so the simulation is repeatable. It defauls to 123.
StdExp	specifies the adjustment made to the variance of each experiment, if it is required to simulate variance heterogeneity due to individual experiments in a family. It defaults to 0.
MAMethod	the meta-analysis method needed for the call to the metafor package rma algorithm
returnES	Determines the format of the output. It defaults to FALSE which causes the function to output the meta-anaysis results for the family of experiments. If set to TRUE it returns the effect sizes for each experiment.

Value

Depending on the value of the returnES parameter, the function either returnd the effect sizes for each experiment or the aggregated resutls for the family

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
NP2GroupMetaAnalysisSimulation(mean=0,sd=1,diff=0.5,GroupSize=100,Exp=5,type="n",StdAdj=0,
alpha=0.05,seed=123,StdExp=1,MAMethod="PM",returnES=FALSE)
# A tibble: 1 x 30
# NumExp GroupSize AveKtau AveKtauctvar tauSigCVt AveCliffd AveCliffdvar AveCliffdsig Avephat
#  Avephatvar Avephatsig
#  <dbl>     <dbl>   <dbl>       <dbl> <lgl>        <dbl>       <dbl> <lgl>          <dbl>
#  <dbl> <lgl>
# 1     5       100   0.126    0.000315 TRUE        0.250     0.00125 TRUE           0.625
# 0.000310 TRUE
# . . . with 19 more variables: MAMean <dbl>, MAvar <dbl>, MASig <lgl>, QE <dbl>, QEp <dbl>,
# HetSig <lgl>, P.mean <dbl>,
NP2GroupMetaAnalysisSimulation(mean=0,sd=1,diff=0.5,GroupSize=10,Exp=5,type="n",StdAdj=0,
alpha=0.05,seed=123,StdExp=1,MAMethod="PM",returnES=TRUE)
# A tibble: 5 x 17
# MeanExp VarExp StdESExp   df   tval  tpval   tciL   tciU Cliffd Cliffdvar PHat PHatvar
# PHatdf       g gvar.exact
#   <dbl>  <dbl>    <dbl> <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>     <dbl> <dbl>  <dbl>
# <dbl>   <dbl> <lgl>
#1  0.226   1.03    0.223  17.9 -0.498  0.624  -1.18  0.728   0.1     0.0808 0.55 0.0197
# 17.8  0.213  NA
#2  1.00    0.622   1.27   15.4 -2.84   0.0122 -1.75 -0.251   0.64    0.0400 0.82 0.00947
# 15.0  1.21   NA
#3  0.432   0.848   0.469  18.0 -1.05   0.308  -1.30  0.434   0.36    0.0725 0.68 0.0177
# 15.5  0.449  NA
#4  0.434   0.967   0.441  13.7 -0.986  0.341  -1.38  0.512   0.22    0.0759 0.61 0.0184
# 14.6  0.416  NA
#5 -0.0342  0.782  -0.0387 14.9  0.0865 0.932  -0.809 0.878  -0.2     0.0817 0.4  0.02
# 17.3 -0.0367 NA
# . . . with 2 more variables: gvar.approx <dbl>, ...17 <dbl>
NP2GroupMetaAnalysisSimulation(mean=0,sd=1,diff=0.724,GroupSize=10,Exp=5,type="l",StdAdj=0,
alpha=0.05,seed=123,StdExp=1,MAMethod="PM",returnES=FALSE)
# A tibble: 1 x 30
# NumExp GroupSize AveKtau AveKtauctvar tauSigCVt AveCliffd AveCliffdvar AveCliffdsig Avephat
# Avephatvar Avephatsig
#  <dbl>     <dbl>   <dbl>       <dbl> <lgl>        <dbl>       <dbl> <lgl>          <dbl>
# <dbl> <lgl>
# 1     5        10   0.181     0.00360 TRUE        0.344      0.0129 TRUE           0.672
# 0.00312 TRUE
# . . . with 19 more variables: MAMean <dbl>, MAvar <dbl>, MASig <lgl>, QE <dbl>, QEp <dbl>,
# HetSig <lgl>, P.mean <dbl>,
# P.rsig <lgl>, P.hetsig <lgl>, Mean.phat <dbl>, phat.sig <lgl>, Mean.d <dbl>, d.sig <lgl>,
# Mean.g.exact <dbl>,
#  g.exact.sig <lgl>, Mean.g.approx <dbl>, g.approx.sig <lgl>, Cohend.mean <dbl>,
# Cohend.sig <lgl>
```

NP4GroupMetaAnalysisSimulation

NP4GroupMetaAnalysisSimulation

Description

This function simulates data from a family of experiments, where the number of experiments in a family is defined by ther parameter Exp. It simulates data from one of four distributions and uses the data to construct four of groups of equal size (GroupSize). Two groups are assigned as control groups and their distribution is based on the parameter mean and the parameter spread, however, the mean and spread for the control group in Block 2 can be adjusted using the parameters BlockEffect and BlockStdAdj respectively. The other two groups are treatment groups and their distribution is based on the mean+diff and the spread parameter, but the distributions can be adjusted using the StdAdj, BlockEffect and BlockStdAdj parameters. The data from each experiment is analysed separately to estimate the non-parametric statistics P-hat, Cliff's d and Kendall's tau and their variances. The statistics are then meta-analysed using the method specified by the MAMethod parameter. We output the average non-parametric effect statistics across the Exp experimet as if from a single large experiment and also the results of meta-analysising each non-parametric effect size. We use the standard parametric effect sizes and their meta-analysis as baselines. All tests of significance are done at the 0.05 level.

Usage

```
NP4GroupMetaAnalysisSimulation(
  mean,
  sd,
  diff,
  GroupSize,
  Exp = 5,
  type = "n",
  alpha = 0.05,
  seed = 123,
  StdAdj = 0,
  BlockEffect = 0,
  BlockStdAdj = 0,
  StdExp = 0,
  MAMethod,
  returnES = FALSE
)
```

Arguments

mean	The default value used for the group means in the simulated data. It can be any real number including zero.
sd	The default value used for the spread of the control group and the spread of the treatment group in the simulated data. The value must be a real value greater than 0.
diff	mean+diff is the value used for the mean of the treatment group. It can be zero.
GroupSize	is the size of each of the 4 groups comprising one experiment. GroupSize should be an integer of 4 or more
Exp	is the number of experiments being simulated. Exp should be an integer of 2 or more. It defaults to 5.

type	specifies the distribution being simulated. The permitted values are "n" for the normal distribution, "l" for the lognormal distribution, "g" for the gamma distribution and "lap" for the Laplace dsitribution. The parameter defaults to "n".
alpha	The Type 1 value used in all significance tests. It defaults to 0.05.
seed	specifies the seed to be used to initiate the simulation, so the simulation is repeatable. It defaults to 123.
StdAdj	The value used to introduce heterogeneity into the treatment groups variance if required.
BlockEffect	is the effect of having two different blocks
BlockStdAdj	is the variance associated with the Block. If BlockStdAdj is zero it means we are treat the block effect as a fixed effect. If BlockStdAdj>0, we treat the block effect as a random effect and increase the variance of Block 2 data.
StdExp	The value used to introduce heterogeneity into experiments in a family required.
MAMethod	defines the method used for meta-analysis
returnES	default to FALSE

Value

If returnES is true, the function returns the summary meta-analysis summary statistics otherwise the function returns the effect sizes for each experiment

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
NP4GroupMetaAnalysisSimulation(mean=0,sd=1,diff=0.5,GroupSize=10,Exp=5,type="n",alpha=0.05,
seed=123,StdAdj=0,BlockEffect=0.5,BlockStdAdj=0,StdExp=0,MAMethod="PM")
# A tibble: 1 x 30
# NumExp GroupSize AveKtau AveKtauctvar tauSigCVt AveCliffd AveCliffdvar AveCliffdsig Avephat
# Avephatvar Avephatsig
#  <dbl>   <dbl>   <dbl>      <dbl> <lgl>      <dbl>       <dbl> <lgl>         <dbl>
# <dbl> <lgl>
# 1    5      10  0.182    0.00188 TRUE       0.346     0.00673 TRUE          0.673
# 0.00163 TRUE
# . . . with 19 more variables: MAMean <dbl>, MAvar <dbl>, MASig <lgl>, QE <dbl>, QEp <dbl>,
# HetSig <lgl>, P.mean <dbl>,
NP4GroupMetaAnalysisSimulation(mean=0,sd=1,diff=0.724,GroupSize=10,Exp=5,type="l",alpha=0.05,
seed=123,StdAdj=0,BlockEffect=0.5,BlockStdAdj=0,StdExp=0,MAMethod="PM")
# A tibble: 1 x 30
# NumExp GroupSize AveKtau AveKtauctvar tauSigCVt AveCliffd AveCliffdvar AveCliffdsig Avephat
# Avephatvar Avephatsig
#  <dbl>   <dbl>   <dbl>      <dbl> <lgl>      <dbl>       <dbl> <lgl>         <dbl>
#  <dbl> <lgl>
# 1    5      10  0.244    0.00167 TRUE       0.464     0.00593 TRUE          0.732
# 0.00144 TRUE
# . . . with 19 more variables: MAMean <dbl>, MAvar <dbl>, MASig <lgl>, QE <dbl>, QEp <dbl>,
# HetSig <lgl>, P.mean <dbl>,
```

```
NP4GroupMetaAnalysisSimulation(mean=0,sd=1,diff=0.5,GroupSize=10,Exp=5,type="n",alpha=0.05,
seed=123,StdAdj=0,BlockEffect=0.5,BlockStdAdj=0,StdExp=0,MAMethod="PM",returnES=TRUE)
# A tibble: 5 x 16
#  MeanExp VarExp StdESExp   df  tval   tpval   tciL  tciU Cliffd Cliffdvar  PHat PHatvar
# PHatdf     g gvar.approx
#   <dbl> <dbl>   <dbl> <dbl> <dbl>   <dbl>  <dbl> <dbl>  <dbl>    <dbl> <dbl>   <dbl>
# <dbl> <dbl>     <dbl>
#1   0.940  0.783    1.06   31.3 3.36  0.00206  0.370  1.51   0.58     0.0243  0.29  0.00587
# 30.2 1.04       0.112
#2   0.372  0.943   0.383   35.0 1.21  0.234   -0.251  0.996  0.21     0.0380  0.105 0.00927
# 31.3 0.375      0.0977
#3   0.598  0.619   0.761   28.6 2.40  0.0229   0.0892 1.11   0.37     0.0336  0.185 0.00813
# 30.8 0.740      0.104
#4   0.873  1.13    0.821   28.1 2.60  0.0148   0.184  1.56   0.440    0.0333  0.220 0.00813
# 23.8 0.799      0.106
#5   0.243  1.03    0.240   31.5 0.758 0.454   -0.410  0.896  0.13     0.0390  0.065 0.00946
# 32.8 0.234      0.0961
# ... with 1 more variable: Cohendvar <dbl>
```

---

percentageInaccuracyOfLargeSampleVarianceApproximation

percentageInaccuracyOfLargeSampleVarianceApproximation

Description

Plot the extent of inaccuracy using the large sample approximate effect size variance on 4 related graphs corresponding to the four different correlation values. Plot visualizes the relationship between sample size and effect size and the percentage inaccuracy of the large sample variance approximation. Function is used in a paper "Effect Sizes and their Variance for AB/BA Crossover Design Studies" by Lech Madeyski and Barbara Kitchenham.

Usage

```
percentageInaccuracyOfLargeSampleVarianceApproximation(data)
```

Arguments

data   - data behind the plot returned by getSimulatedCrossoverDataSets() or stored in
                         reproducer::KitchenhamMadeyski.SimulatedCrossoverDataSets

Value

plot described in description

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
data <- KitchenhamMadeyski.SimulatedCrossoverDataSets
myPlot <- percentageInaccuracyOfLargeSampleVarianceApproximation(data)
```

---

plotOutcomesForIndividualsInEachSequenceGroup
plotOutcomesForIndividualsInEachSequenceGroup

Description

Function to plot a figure on the outcomes for individuals in each sequence group used in a paper "Effect Sizes and their Variance for AB/BA Crossover Design Studies" by Lech Madeyski and Barbara Kitchenham

Usage

```
plotOutcomesForIndividualsInEachSequenceGroup(
  var,
  covar,
  meanA1,
  treatmentDiff,
  periodEffect,
  numOfSamples
)
```

Arguments

var	Variance among subjects is a sum of the between subjects variance and the within subjects variance
covar	Covariance equal to the between subjects variance
meanA1	Mean for treatment sequence A1
treatmentDiff	technique effect which is the difference between the effect of technique A and technique B
periodEffect	Period effect which is the difference between period 1 and period 2
numOfSamples	Number of samples ("rows" of data) required for each technique and period

Value

plot

Author(s)

Lech Madeyski and Barbara Kitchenham

Examples

```
myPlot<-plotOutcomesForIndividualsInEachSequenceGroup(25, 18.75, 50, 10, 5, 15)
```

PrepareForMetaAnalysisGtoR

PrepareForMetaAnalysisGtoR

Description

This function calculates the standardized effect sizes and their confidence intervals, the equivalence point biserial effect size and the Zr and var(Zr) needed for input into the metafor rma function (meta analysis). In this function the point bi-serial effect size is based on the adjusted Hedges g value. The function uses the Hedges g to r transformation to prepare for meta-analysing the data where the mean values, the standard deviations, and the number of observations are available.

Usage

```
PrepareForMetaAnalysisGtoR(Mc, Mt, SDc, SDt, Nc, Nt)
```

Arguments

Mc	is a vector containing the mean value of the control group for each experiment.
Mt	is a vector containing the mean value of the treatment group for each experiment.
SDc	is a vector of the standard deviations of the control group for each experiment.
SDt	is a vector of the standard deviations of the the treatment group for each experiment.
Nc	is a vector containing the the number of observations (participants) in the control group for each experiment.
Nt	is a vector of the number of observations (participants) in the treatment group for each experiment.

Value

data frame incl. calculated effect sizes (Hedges' g, Hedges' g adjusted), upper and lower confidence bounds on Hedges' g, zr, vi - variance of zr, r and pvalue

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
PrepareForMetaAnalysisGtoR(c(10,10), c(12,14), c(4,4), c(4,4), c(20,20), c(40,40))
#HGvalues.Hg HGvalues.HgAdjusted Hgupper   Hglower      zr        vi       r       pvalue
#    0.5         0.4935018 1.082017 -0.06156572 0.2305901 0.01754386 0.2265882 0.0816981743
#    1.0         0.9870036 1.634701  0.40620071 0.4499419 0.01754386 0.4218513 0.0006813222
```

printXTable   *printXTable*

Description

print data table using xtable R package

Usage

```
printXTable(
  data,
  selectedColumns,
  tableType = "latex",
  alignCells,
  digits,
  caption,
  label,
  fontSize,
  captionPlacement = "bottom",
  alignHeader
)
```

Arguments

data	Data structure including columns to be printed.
selectedColumns	
	Columns selected to be printed.
tableType	Type of table to produce. Possible values are "latex" or "html". Default value is "latex".
alignCells	Defines how to align data cells.
digits	Defines the number of decimal points in each column.
caption	Caption of the table.
label	Label of the table.
fontSize	Size of the font used to produce a table.
captionPlacement	
	The caption will be have placed at the bottom of the table if captionPlacement is "bottom" and at the top of the table if it equals "top". Default value is "bottom".
alignHeader	Defines how to align column headers of a table.

Value

A table generated on the fly on a basis of passed data (data, selectedColumns etc.).

Author(s)

Lech Madeyski

Examples

```
d <- reproducer::MadeyskiKitchenham.MetaAnalysis.PBRvsCBRorAR
reproducer::printXTable(d, '"Study"', "latex", '"cc"', 0, "C", "L", "tiny", "top", "l")
```

---

proportionOfSignificantTValuesUsingCorrectAnalysis
proportionOfSignificantTValuesUsingCorrectAnalysis

Description

Plots visualize the relationship between sample size, effect size and the proportion of significant t-values using the correct analysis. Function is used in a paper "Effect Sizes and their Variance for AB/BA Crossover Design Studies" by Lech Madeyski and Barbara Kitchenham.

Usage

```
proportionOfSignificantTValuesUsingCorrectAnalysis(data)
```

Arguments

data   - data behind the plot returned by getSimulatedCrossoverDataSets() or stored in
                        reproducer::KitchenhamMadeyski.SimulatedCrossoverDataSets

Value

plot described in description

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
data <- KitchenhamMadeyski.SimulatedCrossoverDataSets
myPlot <- proportionOfSignificantTValuesUsingCorrectAnalysis(data)
```

proportionOfSignificantTValuesUsingIncorrectAnalysis
proportionOfSignificantTValuesUsingIncorrectAnalysis

Description

Plots visualize the relationship between sample size, effect size and the proportion of significant t-values using the incorrect analysis. Function is used in a paper "Effect Sizes and their Variance for AB/BA Crossover Design Studies" by Lech Madeyski and Barbara Kitchenham.

Usage

```
proportionOfSignificantTValuesUsingIncorrectAnalysis(data)
```

Arguments

data   - data behind the plot returned by getSimulatedCrossoverDataSets() or stored in
                  reproducer::KitchenhamMadeyski.SimulatedCrossoverDataSets

Value

plot described in description

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
data  <- KitchenhamMadeyski.SimulatedCrossoverDataSets
myPlot <- proportionOfSignificantTValuesUsingIncorrectAnalysis(data)
```

RandomExperimentSimulations
RandomExperimentSimulations

Description

This function performs multiple simulations of two-group balanced experiments for one of four distributions and a specific group size. It identifies the average value of phat, Cliff' d and Kendall's point biserial tau and their variances. It either returns the effect sizes for each non-parametric effect size or it reports the number of times the each non-parametric effect size is assessed to be significantly different from zero. We also present the values for the t-test as a comparison. For log-normal data the results of analysing the transformed data are also reported.

Usage

```
RandomExperimentSimulations(
  mean,
  sd,
  diff,
  N,
  reps,
  type = "n",
  seed = 123,
  StdAdj = 0,
  returnData = FALSE
)
```

Arguments

mean	The default mean used for both groups (one treatment group and one control group). It can be changed for the treatment group using the parameter diff
sd	This is the default spread for both groups. It must be a real value greater than 0. It can be adjusted for the treatment group using the parameter StdAdj
diff	This is added to the treatment group mean. It can be a real value and can take the value zero.
N	this is the number of observations in each group. It must be an integer greater than 3.
reps	this identifies the number of times each experiment simulation is replicated.
type	this specifies the underlying distribution used to generate the data. It takes the values "n" for a normal distribution, "l" for lognormal distribution,"g" for a gamma distribution, "lap" for a Laplace distribution.
seed	This specifies the initial seed for the set of replications (default 123).
StdAdj	this specifes the extent of variance instability introduced by the treatment and it must be non-negative but can be 0.
returnData	If TRUE, the function returns the individual effect sizes and their variances, otherwise it returns summary statistics (default FALSE).

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
#RandomExperimentSimulations(mean=0,sd=1,diff=0.5,N=20, reps=500,type="n",seed=123,StdAdj=0)
#reps=500 may take a bit too for CRAN so let us use reps=50
RandomExperimentSimulations(mean=0,sd=1,diff=0.5,N=20, reps=50,type="n",seed=123,StdAdj=0)
# A tibble: 1 x 17
#   phat phatvar sigphat emp.phat.var    d  dvar  sigd emp.d.var  ktau ktauvar emp.tau.var
# kpowerCVt tpower    ES
# <dbl>  <dbl>  <dbl>       <dbl> <dbl> <dbl> <dbl>    <dbl> <dbl>  <dbl>      <dbl>
# <dbl>  <dbl> <dbl>
```

```
#1 0.639 0.00793   0.33     0.00790 0.278 0.0324 0.306   0.0316 0.143 0.00854    0.00832
# 0.328  0.338 0.500
# . . . with 3 more variables: Variance <dbl>, StdES <dbl>, MedDiff <dbl>
#RandomExperimentSimulations(mean=0,sd=1,diff=0.5,N=20, reps=500,type="l",seed=123,StdAdj=0)
#reps=500 may take a bit too for CRAN so let us use reps=50
RandomExperimentSimulations(mean=0,sd=1,diff=0.5,N=20, reps=50,type="l",seed=123,StdAdj=0)
# A tibble: 1 x 20
#   phat phatvar sigphat emp.phat.var   d   dvar  sigd emp.d.var  ktau ktauvar emp.tau.var
# kpowerCVt tpower    ES
# <dbl>  <dbl>   <dbl>        <dbl> <dbl> <dbl> <dbl>     <dbl> <dbl>  <dbl>       <dbl>
# <dbl>  <dbl> <dbl>
#1 0.639 0.00793   0.33     0.00790 0.278 0.0324 0.306   0.0316 0.143 0.00854    0.00832
# 0.328  0.218  1.05
# . . . with 6 more variables: Variance <dbl>, StdES <dbl>, MedDiff <dbl>, ESLog <dbl>,
# StdESLog <dbl>, VarLog <dbl>
RandomExperimentSimulations(mean=0,sd=1,diff=0.5,N=20, reps=10,type="n",seed=123,StdAdj=0,
returnData=TRUE)
#  A tibble: 10 x 3
#    Cliffd  PHat   StdES
#     <dbl> <dbl>   <dbl>
# 1  0.175 0.588   0.340
# 2  0.19  0.595   0.283
# 3 -0.125 0.438  -0.305
# 4  0.195 0.597   0.345
# 5  0.15  0.575   0.200
# 6  0.3   0.65    0.430
# 7  0.455 0.728   0.762
# 8  0.015 0.507   0.0622
# 9  0.16  0.58    0.340
# 10 0.2   0.6     0.336
```

RandomizedBlockDesignEffectSizes

RandomizedBlockDesignEffectSizes

Description

This function finds the theoretical effect sizes for a four-group randomized block experiments assuming one of four different underlying distributions specified by the type parameter. The design assumes two blocks each comprising a control and treatment group. If required a fixed Blocking effect is added to the mean for Block 2.

Usage

```
RandomizedBlockDesignEffectSizes(
  m1,
  std1,
  m2,
  std2,
```

```
    m3,
    std3,
    m4,
    std4,
    BE = 0,
    type = "n"
)
```

Arguments

`m1`	The theoretical mean for the control group in Block 1
`std1`	The theoretical variance for the control group in Block 1
`m2`	The theoretical mean for the treatment group in Block 1
`std2`	The theoretical variance for the treatment group in Block 1
`m3`	The theoretical mean for the control group in Block 2
`std3`	The theoretical variance for the control group in Block 2
`m4`	The theoretical mean for the treatment group in Block 2
`std4`	The theoretical variance for the treatment group in Block 2
`BE`	A fixed block effect to be added to the Block 2 mean values.
`type`	String identifying the distribution, "n" for normal, "ln" for lognormal, "lap" for Laplace, "g" for Gamma

Value

dataframe holing the expected unstandardized mean difference effect size, the pooled within group variance, the standardized effect size and the point bi-serial correlation.

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
RandomizedBlockDesignEffectSizes(m1=0,std1=1,m2=1,std2=1,m3=0,std3=1,m4=1,std4=1,BE=1,type="n")
#  A tibble: 1 x 4
#      ES   Var StdES  rPBS
#   <dbl> <dbl> <dbl> <dbl>
# 1     1     1     1 0.447
RandomizedBlockDesignEffectSizes(m1=0,std1=1,m2=1,std2=1,m3=0,std3=1,m4=1,std4=1,BE=1,type="l")
#  A tibble: 1 x 4
#      ES   Var StdES  rPBS
#   <dbl> <dbl> <dbl> <dbl>
# 1  5.27  82.2 0.581 0.279
RandomizedBlockDesignEffectSizes(m1=0,std1=1,m2=0.266,std2=1,m3=0,std3=1,m4=0.266,std4=1,BE=0,
 type = "l")
#  A tibble: 1 x 4
#      ES    Var StdES   rPBS
#   <dbl>  <dbl> <dbl>  <dbl>
# 1 0.502   6.31 0.200 0.0995
```

RandomizedBlocksAnalysis

RandomizedBlocksAnalysis

Description

The function performs a heteroscedastic test of a two treatment by J blocks randomized blocks effect size. The data are assumed to be stored in x in list mode, a matrix or a data frame. If in list mode, length(x) is assumed to correspond to the total number of groups. All groups are assumed to be independent. Missing values are automatically removed.

Usage

```
RandomizedBlocksAnalysis(x, con = c(-0.5, 0.5, -0.5, 0.5), alpha = 0.05)
```

Arguments

x   the structure holding the data. In list format, for a 2 treatment by J block randomized blocks experiments, there are 2J list elements each one specifying the outcome for a specific block and a specific treatment.

con   is a 2J list containing the contrast coefficients that are used to calculate the mean effet size.

alpha   default to 0.05 is the Type 1 error level used for the test of significance

Value

The t-test and its associated metrics (i.e., critical value stansard error and degrees of freedom) and the estimate of the contrast with its upper and lower confidence interval bounds and p-value.

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
set.seed(123)
x=list()
x[[1]]=stats::rnorm(10,0,1)
x[[2]]=stats::rnorm(10,0.8,1)
x[[3]]=stats::rnorm(10,0.5,1)
x[[4]]=stats::rnorm(10,1.3,1)
vec=c(-1,1,-1,1)/2
RandomizedBlocksAnalysis(x,con=vec,alpha=0.05)
# $n
# [1] 10 10 10 10
# $test
#      test    crit       se       df
# [1,] 4.432644 2.038622 0.2798104 31.33793
```

```
# $psihat
#      psihat  ci.lower ci.upper      p.value
# [1,] 1.2403 0.6698721 1.810728 0.0001062952
# dat=c(x[[1]],x[[2]],x[[3]],x[[4]])
# matx=matrix(dat,nrow=10,ncol=4)
# RandomizedBlocksAnalysis(matx,con=c(-1,1,-1,1)/2,alpha=0.05)
#$n
#[1] 10 10 10 10
#$test
#         test     crit       se       df
#[1,] 4.432644 2.038622 0.2798104 31.33793
#$psihat
#      psihat  ci.lower ci.upper      p.value
#[1,] 1.2403 0.6698721 1.810728 0.0001062952
```

RandomizedBlocksExperimentSimulations

RandomizedBlocksExperimentSimulations

Description

This function performs multiple simulations of 4 group balanced randomised Block experiments with two control groups and two treatment groups where one control group and one treatment group are assigned to block 1 and the other control group and treatment group are assigned to block 2. The simulations are based on one of four distributions and a specific group size. The function identifies the average value of the non-paramtric effect sizes P-hat, Cliff' d and Kendall's point biserial tau and their variances and whether ot not the statistics were significant at the 0.05 level. We also present the values of the t-test as a comparison.

Usage

```
RandomizedBlocksExperimentSimulations(
  mean,
  sd,
  diff,
  N,
  reps,
  type = "n",
  alpha = 0.05,
  Blockmean = 0,
  BlockStdAdj = 0,
  StdAdj = 0,
  seed = 123,
  returnData = FALSE
)
```

Arguments

mean	The default mean for all 4 groups. The default for the two treatment groups can be altered using the parameter diff and the block mean for block 2 can be altered using the parameter Blockmean.
sd	The default spread for all 4 groups. It must be a real value greater than 0. If can be altered for treatment groups using the parameter StdAdj and for Block 2 groups using BlockStdAdj
diff	The is is added to the parameter mean, to define the mean of the other treatment group. It can be a real value ad can take the value zero.
N	this is the number of observations in each group. It must be an interger greater than 3.
reps	this identifies the number of tiume the simulation is replicated.
type	this specifies the underlying distribution used to generate the data. it takes the values "n" for a normal distribution, "l" for lognormal distribution,"g" for a gamma distribution, "lap" for a Laplace distribution.
alpha	is the Type 1 error level used for constructing confidence intervals
Blockmean	is the effect of having two different blocks
BlockStdAdj	is the variance associated with the Block mean. If Blockvar is zero it means we are treat the block effect as a fixed effect. If BlockStdAdj>0, we treat the block effect as a random effect.
StdAdj	The value used to introduce heterogeneity into the treatment groups variance if required.
seed	this specifies the seed value for the simulations and allows the experiment to be repeated.
returnData	= FALSE if TRUE the function returns the generated data otherwise it returns summary statistics.

Value

depending on the parameter returnData it returns the generated nonparametric and parametric values or the summary statistics examples RandomizedBlocksExperimentSimulations(mean=0,sd=1,diff=0.5,N=10, reps=500,type="n",alpha=0.05,Blockmean=0.5, BlockStdAdj=0,StdAdj=0,seed=123) # A tibble: 1 x 18 # phat varphat sigphat emp.phat.var d vard sigd emp.d.var ktau kconsistentvar emp.tau.var kpowerCVt StdES # <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> # 1 0.640 0.00832 0.326 0.00773 0.279 0.0343 0.282 0.0309 0.147 0.00956 0.00856 0.168 0.513 # ... with 5 more variables: ES <dbl>, Var <dbl>, emp.StdESvar <dbl>, MedDiff <dbl>, tpower <dbl> RandomizedBlocksExperimentSimulations(mean=0,sd=1,diff=0.5,N=10, reps=10,type="n",alpha=0.05,Block BlockStdAdj=0,StdAdj=0,seed=123,returnData=T) # A tibble: 10 x 3 # Cliffd PHat StdES # <dbl> <dbl> <dbl> # 1 0.58 0.79 1.06 # 3 0.37 0.685 0.761 # 4 0.440 0.72 0.821 # 5 0.13 0.565 0.240 # 6 0.16 0.58 0.222 # 7 0.38 0.69 0.580 # 8 0.48 0.74 0.882 # 9 0.11 0.555 0.181 #10 -0.03 0.485 0.124

Author(s)

Barbara Kitchenham and Lech Madeyski

RandomizedDesignEffectSizes

RandomizedDesignEffectSizes

Description

This function creates the theoretical effect sizes for random samples from one of four different distributions for specified parameter values for the diftribution specified by the type parameter. It assumes there are two samples, one corresponding to a control group and the other to the treatment group. It returns the theoretical effect sizes for a fully randomized experiment.

Usage

```
RandomizedDesignEffectSizes(m1, std1, m2, std2, type = "n")
```

Arguments

m1	The theoretical mean for the control group
std1	The theoretical variance for the control group
m2	The theoretical mean for the treatment group
std2	The theoretical variance for the treatment group
type	String identifying the distribution, "n" for normal, "ln" for lognormal, "lap" for Laplace, "g" for Gamma

Value

dataframe containing the expected values of the unstandardized mean difference effect size, the pooled witjin group variance, the standardized mean difference effect size and the point bi-serial correlation.

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
RandomizedDesignEffectSizes(m1=0, std1=1, m2=1, std2=3, type = "n")
# A tibble: 1 x 4
#      ES   Var StdES  rPBS
#   <dbl> <dbl> <dbl> <dbl>
# 1     1     5 0.447 0.218
RandomizedDesignEffectSizes(m1=0, std1=1, m2=1, std2=3, type = "l")
# A tibble: 1 x 4
#      ES        Var StdES    rPBS
# <dbl>       <dbl> <dbl>   <dbl>
#1  243. 242552663. 0.0156 0.00780
 RandomizedDesignEffectSizes(m1=0, std1=1, m2=0.266, std2=1, type = "l")
```

```
# A tibble: 1 x 4
#    ES   Var StdES   rPBS
# <dbl> <dbl> <dbl>  <dbl>
#1 0.502  6.31 0.200 0.0995
```

readExcelSheet   *readExcelSheet*

Description

Function reads data from an Excel file from a specified sheet

Usage

```
readExcelSheet(path, sheet, colNames)
```

Arguments

path	Path to an Excel file, e.g. /User/lma/datasets/MyDataSet.xls
sheet	Name of a sheet within an Excel file we want to read
colNames	If TRUE, first row of data will be used as column names.

Author(s)

Lech Madeyski

Examples

```
myPath=system.file("extdata", "DataSet.xlsx", package = "reproducer")
Madeyski15SQJ.NDC<-readExcelSheet(path=myPath, sheet="Madeyski15SQJ.NDC", colNames=TRUE)
```

reproduceForestPlotRandomEffects
                    reproduceForestPlotRandomEffects()

Description

Function reproduces Forest Plot of a Random-Effects Meta-analysis of Mean Differences.

Usage

```
reproduceForestPlotRandomEffects()
```

Author(s)

Lech Madeyski

Examples

```
reproduceForestPlotRandomEffects()
```

---

reproduceMixedEffectsAnalysisWithEstimatedVarianceAndExperimentalDesignModerator

reproduceMixedEffectsAnalysisWithEstimatedVarianceAndExperimentalDesignModerator()

Description

Function reproduces Mixed-Effects Analysis using Subject Specific Estimated Variance with Experimental Design as a Moderator.

Usage

```
reproduceMixedEffectsAnalysisWithEstimatedVarianceAndExperimentalDesignModerator(

)
```

Author(s)

Lech Madeyski

Examples

```
reproduceMixedEffectsAnalysisWithEstimatedVarianceAndExperimentalDesignModerator()
```

---

reproduceMixedEffectsAnalysisWithExperimentalDesignModerator

reproduceMixedEffectsAnalysisWithExperimentalDesignModerator()

Description

Function reproduces Mixed-Effects Analysis with Experimental Design as a Moderator.

Usage

```
reproduceMixedEffectsAnalysisWithExperimentalDesignModerator()
```

Author(s)

Lech Madeyski

Examples

```
reproduceMixedEffectsAnalysisWithExperimentalDesignModerator()
```

reproduceMixedEffectsForestPlotWithExperimentalDesignModerator
reproduceMixedEffectsForestPlotWithExperimentalDesignModerator()

Description

Function reproduces Forest Plot of a Mixed Effects Meta-analysis of Mean Differences with Experimental Design as a Moderator Variable.

Usage

```
reproduceMixedEffectsForestPlotWithExperimentalDesignModerator()
```

Author(s)

Lech Madeyski

Examples

```
reproduceMixedEffectsForestPlotWithExperimentalDesignModerator()
```

reproduceSimulationResultsBasedOn500Reps1000Obs
reproduceSimulationResultsBasedOn500Reps1000Obs

Description

Function to calculate simulation results based on 500 repetitions of 1000 observation samples. Function is used in a paper "Effect Sizes and their Variance for AB/BA Crossover Design Studies" by Lech Madeyski and Barbara Kitchenham.

Usage

```
reproduceSimulationResultsBasedOn500Reps1000Obs()
```

Value

data frame including the following simulation results: # treatmentEffect.Ave - Average Technique Effect # dRM.Ave - Average dRM # dRM.Var - Variance of dRM # dRM.Var.Ave - Average of var(dRM) # dRM.Var.ModerateSampleSizeApprox - # dIG.Ave - Average dIG # dIG.Var - Variance of dIG # dIG.Var.Ave - Average of var(dIG) # dIG.Var.ModerateSampleSizeApprox -

Author(s)

Lech Madeyski and Barbara Kitchenham

Examples

```
# return simulation results based on 500 repetitions of 1000 observation samples
simulationResultsTable500x1000<-reproduceSimulationResultsBasedOn500Reps1000Obs()
```

---

reproduceTablesOfPaperMetaAnalysisForFamiliesOfExperiments

reproduceTablesOfPaperMetaAnalysisForFamiliesOfExperiments

Description

This function reproduces five of the output tables used in the systematic review paper "Meta-analysis for Families of Experiments: A Systematic Review and Reproducibility Assessment". It extracts the reported values for effect sizes, meta-analysis and descriptive statistics in the primary studies. It uses the descriptive statistics to re-calculate effect sizes and then performs a meta-analyses using the constructed effect sizes and compares the calculated values with the reported values.

Usage

```
reproduceTablesOfPaperMetaAnalysisForFamiliesOfExperiments()
```

Value

list incl. the data presented in five of the tables presented in the paper.

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
rrData = reproduceTablesOfPaperMetaAnalysisForFamiliesOfExperiments()
# Reproduce Table "Overall Mean Values of Effect Sizes Reported and Calculated":
xtable::xtable(rrData$MAStats)
# Reproduce Table "Calculated and Reported Effect Sizes":
xtable::xtable(rrData$ESdata)
# Report values for 3 papers that reported per document
rrData$MAStatsTP1=data.frame(rrData$MAStatsTP1,row.names=NULL)
rrData$ESTP1res=data.frame(rrData$ESTP1res,row.names=NULL)
xtable::xtable(rrData$MAStatsTP1)
xtable::xtable(rrData$ESTP1res)
# Report extra results for Study 8
# Reproduce Table "Calculating r_PB Effect Size from Probabilities"
xtable::xtable(rrData$GH2015extra)
```

reproduceTableWithEffectSizesBasedOnMeanDifferences
reproduceTableWithEffectSizesBasedOnMeanDifferences()

Description

Function reproduces Table, which shows the effect sizes based on mean differences.

Usage

```
reproduceTableWithEffectSizesBasedOnMeanDifferences()
```

Author(s)

Lech Madeyski

Examples

```
reproduceTableWithEffectSizesBasedOnMeanDifferences()
```

reproduceTableWithPossibleModeratingFactors
reproduceTableWithPossibleModeratingFactors()

Description

Function reproduces Table with possible moderating factors.

Usage

```
reproduceTableWithPossibleModeratingFactors()
```

Author(s)

Lech Madeyski

Examples

```
reproduceTableWithPossibleModeratingFactors()
```

---

reproduceTableWithSourceDataByCiolkowski

reproduceTableWithSourceDataByCiolkowski

Description

Function reproduces Table, which shows the effect sizes reported by Ciolkowski identifying the type of design used in each study.

Usage

```
reproduceTableWithSourceDataByCiolkowski()
```

Author(s)

Lech Madeyski

Examples

```
reproduceTableWithSourceDataByCiolkowski()
```

---

rSimulations   *rSimulations*

Description

This function simulates many datasest from the same bivariate distribution to investigate the distribution of correlations for specific sample sizes.

Usage

```
rSimulations(
  mean,
  var,
  diff,
  r,
  N,
  reps,
  VarAdj = 0,
  seed = 123,
  returntSignificant = F,
  returndata = F,
  plothist = F
)
```

Arguments

mean	The mean used for one of bivariate distributions - assumed to be the control condition in an experiment.
var	The variance used for both treatment groups. It must be a real value greater than 0.
diff	This value is added to the parameter mean to specify the mean for the other bivariate distribution - assumed to be the treatment condition in an experiment.
r	This specifies the correlation coefficient to be used for the bivariate normal distribution it must be a value in the range [-1,1].
N	The number of observations in each simulated bivariate normal data set.
reps	The number of bivariate data sets that will be simulated.
VarAdj	This value will be added to the variance of the treatment condition.
seed	This specifies the seed value for the simulations and allows the experiment to be repeated.
returntSignificant	
	If set to true the percentage of times the t-test delivered a value significant at the 0.05 level is reported (default returntSignificant=F).
returndata	If set to FALSE, the function returns the summary information across all the replications (default returndata=F). If set to TRUE the function outputs the r and variance ratio, and variance accuracy values generated in each replication.
plothist	If set to T, the function outputs a histogram of the r-values, the varprop values and the accuracy values (default plothist=F).

Value

output If returndata=F, the output returns summary information about the average of r and the variance properties across the replicated data sets. If returndata=T, the function returns the r-values obtained for each of the simulated data sets to gather with the variance ratio, the variance accuracy measure and a dummy variable indicating whether a test of significance between the mean values was significant (which is indicated by the dummy variable being set to 1) or not (which is indicated by the dummy variable being set to 0)

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
# output=rSimulations(mean=0,var=1,diff=0,r=0.25,N=4,reps=10000)
# reduced reps to pass CRAN time limits
output=rSimulations(mean=0,var=1,diff=0,r=0.25,N=4,reps=1000)
output=signif(output,4)
output
#  r.Mean r.Median  Var.r PercentNegative Mean.VarProp Variance.VarProp ...
# 1 0.2132   0.3128 0.3126           34.21       0.5036          0.06046 ...
#output=rSimulations(mean=0,var=1,diff=0.8,r=0.25,N=60,reps=10000,returntSignificant=TRUE)
```

```
# reduced reps to pass CRAN time limits
output=rSimulations(mean=0,var=1,diff=0.8,r=0.25,N=60,reps=1000,returntSignificant=TRUE)
output=signif(output,4)
output
#   r.Mean r.Median   Var.r PercentNegative Mean.VarProp Variance.VarProp ...
# 1 0.2492   0.2534 0.01529            2.62       0.5009         0.003897 ...
output=rSimulations(mean=0,var=1,diff=0,r=0.25,N=30,reps=10,returndata=TRUE)
output
#      rvalues   VarProp VarAccuracy VarDiffAccuracy tSig
#1  0.3981111 0.4276398   0.8630528       0.6974386    0
#2  0.2104742 0.4994285   0.7812448       0.8224174    0
#3  0.4252424 0.4933579   1.1568545       0.8866058    0
#4  0.3502651 0.6004373   0.8710482       0.7628923    0
#5  0.3845145 0.6029086   0.9618363       0.7998859    0
#6  0.1397217 0.4201069   1.1817022       1.3582855    0
#7  0.2311455 0.3894894   0.8322239       0.8594886    0
#8  0.3725047 0.5985897   1.1742117       0.9938662    0
#9  0.4881618 0.2712268   0.7585261       0.5723671    0
#10 0.1568071 0.3936400   0.9869924       1.1143561    0
```

---

searchForIndustryRelevantGitHubProjects

searchForIndustryRelevantGitHubProjects

Description

Function searches for industry relevant software projects available from GitHub. The function was used to deliver data set of software projects in an NCBiR project. More details are described in a report: Lech Madeyski, "Training data preparation method," tech. rep., code quest (research project NCBiR POIR.01.01.01-00-0792/16), 2019, as well as a paper: Tomasz Lewowski and Lech Madeyski, "Creating evolving project data sets in software engineering", 2019. If you use this function or the returned data set than please cite: Tomasz Lewowski and Lech Madeyski, "Creating evolving project data sets in software engineering", 2019

Usage

```
searchForIndustryRelevantGitHubProjects(
  myToken,
  earliestPushDate,
  latestCreationDate
)
```

Arguments

myToken   A private token used to access GitHub

earliestPushDate

                Only repositories which were pushed after this date will be included in the re-
                sults (i.e., repositories for which the latest push was before this date will not be
                included in the results)

latestCreationDate

> Only repositories which were created before this date will be included in the
> results (i.e., repositories created after this date will not be included in the results)

Value

selected GitHub projects

Author(s)

Lech Madeyski and Tomasz Lewowski

Examples

```
#to run this function you need to use your own token as a parameter of the function
#use your own token as the first parameter of the function
#searchForIndustryRelevantGitHubProjects("...", "2019-03-01", "2018-08-01")
```

---

simulateRandomizedBlockDesignEffectSizes
simulateRandomizedBlockDesignEffectSizes

Description

This simulates one of four distributions, and finds the values of ktau and Cliffs d and their variances.
It simulates a randomised blocks experiment with two treatment groups and two control groups
each of which being divided into two blocks. By default it assumes equal group sizes but group
spread (standard deviation can be changed, see Stadj). It returns values of both parametric and
non=parametric effect sizes and their variance for simulated experiments. It returns the number of
times each effect size was signficiant. For the logarithmic distribution it calcates effect sizes based
on the log transformed data as well as the raw data.

Usage

```
simulateRandomizedBlockDesignEffectSizes(
  mean,
  sd,
  diff,
  N,
  type = "n",
  alpha = 0.05,
  Blockmean = 0,
  BlockStdAdj = 0,
  StdAdj = 0
)
```

Arguments

mean	The default value for all groups which can be changed for the two treatment groups using the parameter diff and for the two block 2 groups using the parameter Blockmean
sd	The default spread used for all four groups unless adjusted by the StdAdj. It must be a real value greater than 0.
diff	This is added to the parameter mean to obtain the required mean for treatment groups. It can be a real value and can take the value zero.
N	this is the number of observations in each group. It must be an integer greater than 3.
type	this specifies the underlying distribution used to generate the data. it takes the values "n" for a normal distribution, "l" for lognormal distribution,"g" for a gamma distribution, "lap" for a Laplace distribution.
alpha	is the significance level for statistical tests
Blockmean	if >0 an adjusment made to both group means in Block 2
BlockStdAdj	if >0, an adjustment that can be made to the sd of each group in block 2
StdAdj	this specifies the extent of variance instability introduced by the treatment and if >0 will be used to amend the sd parameter for both treatment groups.

Value

data frame incl. the non-parametric and parametric effect sizes and whether the effect sizes are significant at the 0.05 level.

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
set.seed(123)
simulateRandomizedBlockDesignEffectSizes(mean=0,sd=1,diff=.5,N=10,type="n",alpha=0.05,
Blockmean=0.5,BlockStdAdj=0,StdAdj=0)
# A tibble: 1 x 23
#     N phat phat.var phat.df phat.test phat.pvalue phat.sig    d  vard d.sig  cor  sqse
# ctvar    n1    n2
# <int> <dbl>   <dbl>   <dbl>    <dbl>      <dbl> <lgl>    <dbl> <dbl> <lgl> <dbl> <dbl>
# <dbl> <int> <int>
#1   40 0.79  0.00587   30.2     3.79   0.000681 TRUE     0.58 0.0243 TRUE 0.305 0.0132
# 0.00695   20    20
## . . . with 8 more variables: sigCVt <lgl>, sigCVn <lgl>, ttest.sig <lgl>, ES <dbl>,
# Variance <dbl>, StdES <dbl>,
#   BlockEffect <dbl>, MedianDiff <dbl>
set.seed(123)
simulateRandomizedBlockDesignEffectSizes(mean=0,sd=1,diff=.5,N=10,type="l",alpha=0.05,
Blockmean=0.5,BlockStdAdj=0,StdAdj=0)
# A tibble: 1 x 27
#     N phat phat.var phat.df phat.test phat.pvalue phat.sig    d  vard d.sig  cor  sqse
```

```
# ctvar    n1     n2
# <int> <dbl>   <dbl>   <dbl>    <dbl>   <dbl> <lgl>   <dbl> <dbl> <lgl> <dbl> <dbl>
# <dbl> <int> <int>
#1    40 0.79 0.00587   30.2    3.79  0.000681 TRUE    0.58 0.0243 TRUE 0.305 0.0132
# 0.00695   20    20
# ... with 12 more variables: sigCVt <lgl>, sigCVn <lgl>, ttest.sig <lgl>, ES <dbl>,
# Variance <dbl>, StdES <dbl>,
#  BlockEffect <dbl>, MedianDiff <dbl>, Log.sig <lgl>, ES.Trans <dbl>, StdES.Trans <dbl>,
# VarTrans <dbl>
```

---

simulateRandomizedDesignEffectSizes

simulateRandomizedDesignEffectSizes

Description

This simulates one of four distributions, and finds the values of ktau, phat and Cliffs d and their variances. It assumes equal group sizes. It returns values of the effect sizes and their variance for a simulated randomized experiment with two treatments. It returns whether to not each non-parametric effect size was significant. It also returns the parametric (unstandardized and unstandardized) Effect Size and the whether the t-test was signficiant.

Usage

```
simulateRandomizedDesignEffectSizes(mean, sd, diff, N, type = "n", StdAdj = 0)
```

Arguments

mean	The mean used for one of the treatment groups
sd	The spread used for both treatment groups. It mus be a real value greater than 0.
diff	This is added to the parameter mean, to define the mean of the other treatment group. It can be a real value avd can take the value zero.
N	this is the number of observations in each group. It must be an integer greater than 3.
type	this specifies the underlying distribution used to generate the data. it takes the values "n" for a normal distribution, "l" for lognormal distribution,"g" for a gamma distribution, "lap" for a Laplace distribution.
StdAdj	this specifes the extent of variance instability introduced by the treatment.

Value

data frame incl. the non-parametric and parametric effect sizes and whether the effect sizes are significant at the 0.05 level.

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
set.seed(123)
simulateRandomizedDesignEffectSizes(mean=0,sd=1,diff=0.8,N=10,type="n",StdAdj=0)
# A tibble: 1 x 15
# phat varphat dfphat sigphat   d  vard sigd   cor varcor sigCVt ttestp   ES Variance StdES
# MedDiff
# <dbl>  <dbl>  <dbl> <lgl>  <dbl> <dbl> <lgl> <dbl> <dbl> <lgl>  <dbl> <dbl>  <dbl> <dbl>
# <dbl>
#1  0.75 0.0152  17.5 FALSE    0.5 0.0624 FALSE 0.263 0.0175 FALSE  0.0507 0.934  0.994 0.937
# 1.26
set.seed(123)
simulateRandomizedDesignEffectSizes(mean=0,sd=1,diff=0.8,N=10,type="l",StdAdj=0)
# A tibble: 1 x 19
#   phat varphat dfphat sigphat    d  vard sigd   cor varcor sigCVt ttestp   ES Variance
# StdES MedDiff transttest
# <dbl>  <dbl>  <dbl> <lgl>  <dbl> <dbl> <lgl> <dbl> <dbl> <lgl>  <dbl> <dbl>  <dbl>
# <dbl>  <dbl>     <dbl>
#1  0.75 0.0152  17.5 FALSE    0.5 0.0624 FALSE 0.263 0.0175 FALSE  0.0958 2.41    9.01
# 0.802   2.32     0.0507
# ... with 3 more variables: EStrans <dbl>, StdEStrans <dbl>, VarTrans <dbl>
```

---

transformHgtoR   *transformHgtoR*

Description

The functions transforms a vector of Hedges g values to their equivalent point bi-serial values.

Usage

```
transformHgtoR(g, Nc, Nt)
```

Arguments

g	A vector of Hegdes g values.
Nc	A vector of numbers identifying the number of control condition participants in each group
Nt	A vector of numbers identifying the number of treatment condition participants in each group

Value

value of point biserial r

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
transformHgtoR(0.4, 20, 20)
# [1] 0.1961161
```

---

transformHgtoZr *transformHgtoZr*

Description

The functions transforms a vector of Hedges g values to their normal approximation of point biserial values.

Usage

```
transformHgtoZr(g, Nc, Nt)
```

Arguments

g	value of Hedges' g
Nc	the number of observations (participants) in the first (control) group
Nt	the number of observations (participants) in the second (treatment) group

Value

value of normal approximation of point biserial r

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
transformHgtoZr(0.5, 20, 20)
# [1] 0.2474665
```

---

transformRtoHg   *transformRtoHg*

Description

This function coverts a vector of point bi-serial r values with associated sample size information back to the mean difference effect size Hedges g.

Usage

```
transformRtoHg(r, Nc, Nt)
```

Arguments

r	A vector of point bi-serial correlation values.
Nc	A vector of the number of observations in the control condition for the related experiments.
Nt	A vector of the number of observations in the treatment condition for the related experiments.

Value

value of Hedges' g

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
transformRtoHg(c(0.4,0.2), c(20,20), c(20,20))
# [1] 0.8728716 0.4082483
```

---

transformRtoZr   *transformRtoZr*

Description

The function transforms a vector of point biserial r values to their normal approximation. It also works for the correlation r.

Usage

```
transformRtoZr(r)
```

Arguments

r   A vector of r-values

Value

value of normal approximation of point biserial r

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
reproducer::transformRtoZr(0.4)
# [1] 0.4236489
Zr=reproducer::transformRtoZr(c(0.4,0.2))
Zr
# [1] 0.4236489 0.2027326
```

---

transformZrtoHg   *transformZrtoHg*

Description

Transforms Zr to Hedge's g.

Usage

```
transformZrtoHg(Zr, Nc, Nt)
```

Arguments

Zr	the normal variate
Nc	the number of observations (participants) in the first (control) group
Nt	the number of observations (participants) in the second (treatment) group

Value

value of Hedges' g

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
transformZrtoHg(0.5, 20, 20)
#[1] 1.042191
```

---

transformZrtoHgapprox   *transformZrtoHgapprox*

Description

This function provides an approximate transformation from Zr to Hedges g when the number of observations in the treatment and control group are unknown. It is also used to allow the forest plots to display Hedge's g when they are based on r. It is necessary because the transformation function in the forest plot function does not allow any parameters other than effect size used. The function assumes that Nc=Nt and gives the same results as transformZrtoHg when Nc=Nt.

Usage

```
transformZrtoHgapprox(Zr)
```

Arguments

Zr   A vector of normalised point bi-serial values

Value

approx. value of Hedges' g

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
transformZrtoHgapprox(c(0.4,0.2))
# [1] 0.8215047 0.4026720
```

---

transformZrtoR   *transformZrtoR*

Description

The function transforms a vector of standardized normal variates to their equivalent r-values.

Usage

```
transformZrtoR(zr)
```

Arguments

zr   A vector of standard normal variates.

Value

value of point biserial r

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
transformZrtoR(0.4236489)
# [1] 0.4
transformZrtoR(c(0.4236489, 0.2027326))
# [1] 0.4 0.2
```

---

varStandardizedEffectSize

varStandardizedEffectSize

Description

Function calculates the exact variance of a standardized effect size based on the relationship between t and the standardized effect size, see Morris and DeShon, Combining Effect Size Estimates in Meta-Analysis With Repeated Measures and Independent-Groups Designs, Psychological Methods, 7 (1), pp 105-125.

Usage

```
varStandardizedEffectSize(d, A, f, returnVarg = TRUE)
```

Arguments

d	An unadjusted standardized effect size
A	The squared constant linking t and d i.e. t*sqrt(A)=d
f	The degrees of freedom of the t value
returnVarg	if set to TRUE return the variance of the small sample size adjusted standardized effect size (g), otherwise returns var(d) where d is the input parameter

Value

if returnVarg if set to TRUE, return var(g) otherwise var(d)

Author(s)

Barbara Kitchenham and Lech Madeyski

Examples

```
d=0.5
varStandardizedEffectSize(d,sqrt(1/30),29,returnVarg=FALSE)
# [1] 0.2007699
varStandardizedEffectSize(d,sqrt(1/30),29,returnVarg=TRUE)
# [1] 0.1904167
```

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