

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

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Suggests testthat, assertthat

NeedsCompilation no

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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)
```

calculateBasicStatistics

calculateBasicStatistics

Description

This function calculates the following statistics 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. ShortExperimentNames=c("E1","E2","E3","E4") FullExperimentNames=c("EUBAS","R1UCLM","R2UCI Groups=c("A","B","C","D") Type=c(rep("4G",4)) StudyID="S2" Control="SC" ReshapedData= ExtractExperimentData(KitchenhamEtAl.CorrelationsAmongParticipants.Scanniello14TOSEM,ExperimentNames=FullExperi idvar="ParticipantID",timevar="Period",ConvertToWide=TRUE) NewTable= ConstructLevel1ExperimentRData(ReshapedD calculateBasicStatistics(NewTable\$r) # N Mean Median Variance SE LowerBound UpperBound #
 1 32 0.06175 0.1688 0.2482 0.08808 -0.1109 0.2344

Author(s)

Barbara Kitchenham and Lech Madeyski

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 identifier 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

```

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 <code>ExtractLevel1ExperimentRData</code> .
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.

Usage

```
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

Author(s)

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
```

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

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 M_c , the mean value of the treatment group M_t , the standard deviation of the control group SD_c , standard deviation of the the treatment group SD_t , the number of observations (participants) in the control group N_c , and the number of observations (participants) in the treatment group N_t). 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 Hedges'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 sequence 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 identifier 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> <lg1> <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 the 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.Scanniello14T0SEM
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 identifier 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.

Usage

```
ExtractMAStatistics(mareults, Nc, Nt, Transform = TRUE, type = "d", sig = 4)
```

Arguments

<code>mareults</code>	is the output from the <code>rma</code> function.
<code>Nc</code>	is the number of participants in the control condition group.
<code>Nt</code>	is the number of participants in the treatment condition group.
<code>Transform</code>	is a boolean value indicating whether the outcome values need to be transformed back to standardized mean difference ("d" i.e. Hg) or point biserial correlations ("r"). It is defaulted to TRUE. If this parameter is set to FALSE, no transformation will be applied.
<code>type</code>	this indicates the type of transformation required - it defaults to "d" which requests transformation from Z_r to Hg, using "r" requests transformation from Z_r to r.
<code>sig</code>	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.

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 is the p-value of the heterogeneity statistic

Author(s)

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
```

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: $\text{var.dIG.Fromt} = \text{var.t} * (1 - r) * ((N1 + N2) / (2 * N1 * N2))$ # dRM.Fromt.ipe - dRM calculated from t: $\text{dRM.Fromt} = t * \sqrt{((N1 + N2) / (2 * N1 * N2))}$
 # var.dRM.Fromt.ipe - var.dRM calculated from t: $\text{var.dRM.Fromt} = \text{var.t} * ((N1 + N2) / (2 * N1 * N2))$
 # var.dRM.Fromt2.ipe - var.dRM calculated from t or rather dRM.Fromt: $\text{var.dRM.Fromt2} = (df / (df - 2)) * ((N1 + N2) / (2 * N1 * N2) + \text{dRM.Fromt}^2) - \text{dRM.Fromt}^2 / c^2$ # 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<-getEffectSizesABBAlgnoringPeriodEffect(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 `getSimulationData()` 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 theoreticalvar - variance of t theoreticalvardIG - variance of the effect size dIG based on the parameters built into crossover model data simulated by the getSimulationData function theoreticalvardRM - variance of the effect size dRM based on the parameters built into crossover model data simulated by the getSimulationData 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)
```

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.Gravino15JVL

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.Ricca14T0SEM

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 Methodology, 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 Methodology, 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.Scanniello17T0SEM

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.Torchiano17JVL

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 (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.

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 Maki from the TIEKE organisation see Barbara Kitchenham and Kari Kansala, 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

Completeness1 Assessment by judge of question 1: Is the reason for the project clear? Can take values: Yes/No/Partly

Completeness2 Assessment by judge of question 2: Is the specific aim/purpose of the study clear? Can take values: Yes/No/Partly

Completeness3 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

Completeness4 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

Completeness5 Assessment by judge of question 5: Is there a description of how the evaluation process was organised? Can take values: Yes/No/Partly

Completeness6 Assessment by judge of question 6: Are the results of the evaluation clearly described? Can take values: Yes/No/Partly

Completeness7 Assessment by judge of question 7: Are any limitations of the study reported?: Yes/No/Partly

Completeness8 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.

Completeness1NumValue A numerical value for completeness question 1 where 0=No, Partly=0.5, yes =1

Completeness2NumValue A numerical value for completeness question 2 where 0=No, Partly=0.5, yes =1, NA means not applicable

Completeness3NumValue A numerical value for completeness question 3 where 0=No, Partly=0.5, yes =1, NA means not applicable or not answered

Completeness4NumValue A numerical value for completeness question 4 where 0=No, Partly=0.5, yes =1, NA means not applicable

Completeness5NumValue A numerical value for completeness question 5 where 0=No, Partly=0.5, yes =1, NA means not applicable

Completeness6NumValue A numerical value for completeness question 6 where 0=No, Partly=0.5, yes =1, NA means not applicable

Completeness7NumValue A numerical value for completeness question 7 where 0=No, Partly=0.5, yes =1, NA means not applicable

Completeness8NumValue 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 English: 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

Completeness1NumValue The numeric answer to completeness question 1

Completeness2NumValue The numeric answer to completeness question 2

Completeness3NumValue The numeric answer to completeness question 3

Completeness4NumValue The numeric answer to completeness question 4

Completeness5NumValue The numeric answer to completeness question 5

Completeness6NumValue The numeric answer to completeness question 6

Completeness7NumValue The numeric answer to completeness question 7

Completeness8NumValue The numeric answer to completeness question 8

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

NumberOfAnsweredCompletenessQuestions 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

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

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

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. $\text{Diff} = \text{M_PBR} - \text{M_C}$
- Inc** The percentage increase in defect rate detection, i.e. $\text{Inc} = 100 * [(\text{M_PBR} - \text{M_C}) / \text{M_C}]$
- 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 $\text{V_C} = \text{SD_C}^2$
- 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 $\text{SS} = \text{V_C} * (\text{n} - 1)$. For between subjects studies $\text{SS} = \text{V_C} * (\text{n_C} - 1)$
- 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)

sshUriOfRepository 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

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 Z_r and $\text{var}(Z_r)$ 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 , z_r , vi - variance of z_r , r and p value

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)
```

`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-analysis 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 datasets 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")
```

transformHgtoR	<i>transformHgtoR</i>
----------------	-----------------------

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 Hedges 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	<i>transformHgtoZr</i>
-----------------	------------------------

Description

The functions transforms a vector of Hedges g values to their normal approximation of point bi-serial 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	<i>transformRtoHg</i>
----------------	-----------------------

Description

This function covers 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

<code>r</code>	A vector of point bi-serial correlation values.
<code>Nc</code>	A vector of the number of observations in the control condition for the related experiments.
<code>Nt</code>	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
```

<code>transformRtoZr</code>	<i>transformRtoZr</i>
-----------------------------	-----------------------

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

<code>r</code>	A vector of <i>r</i> -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	<i>transformZrtoHg</i>
-----------------	------------------------

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
```


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
```

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