

# Package ‘MedSurvey’

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**Title** Mediation Analysis for Complex Surveys

**Version** 1.1.0

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## Description

It is a computer tool to conduct mediation analysis for complex surveys using multi-stage sampling. Specifically, the mediation analysis method using balanced repeated replications was proposed by Mai, Ha, and Soulakova (2019) <DOI:10.1080/10705511.2018.1559065>. The development of 'MedSurvey' was sponsored by American Lebanese Syrian Associated Charities (ALSAC). However, the contents of MedSurvey do not necessarily represent the policy of the ALSAC.

**Depends** R (>= 2.50), stats, Matrix, survey, lavaan, parallel

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**URL** <https://CRAN.R-project.org/package=MedSurvey>

<https://github.com/YujiaoMai/MedSurvey>

<https://sjbiostat.shinyapps.io/MedSurvey/>

**RoxxygenNote** 6.1.1

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chisq.BRR

*Adjust the model fit statistics***Description**

This function is used to adjust model fit statistics for complex surveys with balanced repeated replications (Oberski, 2014; Satorra & Muthen, 1995). It saves time to only obtain the model fit statistics during the model selection stage.

**Usage**

```
chisq.BRR(model, lavaan.fit, data, mwgtname, repwgtnames,
  fayfactor = 0.5, estimator = c("ML"), test = c("satorra.bentler"))
```

**Arguments**

model	The model being fitted. It is written in lavaan model syntax (Rossee, 2012).
lavaan.fit	The model fit results using 'ML' estimator with sample main weights, but without adjusting the fit statistics or standard errors for complex surveys. Note that it is a lavaan object.
data	The raw data including the variables of interest and the survey weights. It should be a dataset or dataframe.
mwgtname	The variable name indicating the sample main weight in the dataset. See balanced repeated replications method (Wolter, 2007) for more information about the main weight.
repwgtnames	The variable names indicating the set of replicate weights in the dataset. See balanced repeated replications method (Wolter, 2007) for more information about the replicate weight.
fayfactor	The fayfactor used in the standard error calculation by fay's method (Fay & Train, 1995; Judkins, 1990) for balanced repeated replications. Fayfactor is a value between 0 and 1. The default is 0.5.
estimator	The method used to estimate the model. 'ML' is the default option and the only available option for current version. It is not required.
test	The method used to generate adjusted standard errors. 'satorra.bentler' is the default option and the only available option for current version. It is not required.

**Value**

The model fit results as a lavaan object (Rossee, 2012) with the adjusted model fit statistics.

**References**

- Fay, R. E., & Train, G. F. (1995). Aspects of survey and model-based postcensal estimation of income and poverty characteristics for states and counties. In Proceedings of the Section on Government Statistics, American Statistical Association, Alexandria, VA (pp. 154-159).
- Judkins, D. R. (1990). Fay's method for variance estimation. *Journal of Official Statistics*, 6(3), 223-239.
- Oberski, D. (2014). lavaan. survey: An R package for complex survey analysis of structural equation models. *Journal of Statistical Software*, 57(1), 1-27. DOI:10.18637/jss.v057.i01

Rosseel, Y. (2012). Lavaan: An R package for structural equation modeling and more. Version 0.5–12 (BETA). Journal of statistical software, 48(2), 1-36. DOI:10.18637/jss.v048.i02

Satorra, A., & Muthen, B. (1995). Complex sample data in structural equation modeling. Sociological methodology, 25(1), 267-316.

Wolter, K. (2007). Introduction to variance estimation. New York, NY: Springer.

## Examples

```
R <- 160
wgtnames <- paste("repwgt", seq(0,R,by=1), sep="")
mwgtname=wgtnames[1]
repwgtnames=wgtnames[2:(R+1)]
fayfactor=0.5

model3 <- ' # outcome
            numcg ~ u0*1 + c*workban + b1*sp_adltban + b2*sp_kidsban
            # mediator
            sp_adltban ~ u1*1 + a1*workban
            sp_kidsban ~ u2*1 + a2*workban
            # indirect effect (a*b)
            a1b1 := a1*b1
            a2b2 := a2*b2
            # total effect
            total := c + (a1*b1) + (a2*b2)
            '

fit <- lavaan::sem(model=model3, data=MedData, estimator='ML', test='standard')
chisq.BRR(model3,fit,MedData,mwgtname, repwgtnames)
#
# MedSurvey 1.1.0 Adjusted Model Fit Statistics using BRR
#
# chisq   df   pvalue    CFI      RMSEA      SRMR        AIC        BIC
#
# 305.25   1   0.00000    0.40561  0.27852   0.07416   88699.43   88768.45
```

---

med.fit.BRR

*Estimate the mediation effects and standard errors adjusting for complex surveys with BRR*

---

## Description

This function is used to estimate the mediation effects adjusted for complex surveys with balanced repeated replications (BRR) (Mai, Ha, Soualakova, 2019).

## Usage

```
med.fit.BRR(model = NULL, data = NULL, mwgtname = NULL,
            repwgtnames = NULL, fayfactor = 0.5, estimator = c("ML"),
            test = c("satorra.bentler"), parallel = c("no", "parallel", "snow"),
            ncore = Sys.getenv("NUMBER_OF_PROCESSORS"), cl = NULL, ...)
```

## Arguments

model	The model being fitted. It is written in lavaan model syntax (Rosseel, 2012).
data	The raw data including the variables of interest and the survey weights. It should be a dataset or dataframe.
mwgtname	The variable name indicating the sample main weight in the dataset. See balanced repeated replications method (Wolter, 2007) for more information about the main weight.
repwgtnames	The variable names indicating the set of replicate weights in the dataset. See balanced repeated replications method (Wolter, 2007) for more information about the replicate weight.
fayfactor	The fayfactor used in the standard error calculation by fay's method (Fay & Train, 1995; Judkins, 1990) for balanced repeated replications. Fayfactor is a value between 0 and 1. The default is 0.5.
estimator	The method used to estimate the model. 'ML' is the default option and the only available option for current version. It is not required.
test	The method used to generate adjusted standard errors. 'satorra.bentler' is the default option and the only available option for current version. It is not required.
parallel	Parallel computing ("no" or "parallel" or "snow"). It is "no" by default, which means it will not use parallel computing. The option "parallel" is to use multiple cores in a computer for parallel computing. It is used with the number of cores (ncore). The option "snow" is to use clusters for parallel computing. It is used with the number of clusters (cl).
ncore	Number of processors used for parallel computing. By default, ncore = Sys.getenv('NUMBER_OF_PROCESSORS').
cl	Number of clusters. It is NULL by default. When it is NULL, the program will detect the number of clusters automatically.
...	Extra arguments. For example, ordered=c('z1','z2') is an argument to tell 'z1' and 'z2' are ordinal variables. It is not required.

## Value

The model fit results as a lavaan object with the adjusted estimates, standard errors, and model fit statistics. It is a lavaan object (Rosseel, 2012).

## References

- Fay, R. E., & Train, G. F. (1995). Aspects of survey and model-based postcensal estimation of income and poverty characteristics for states and counties. In Proceedings of the Section on Government Statistics, American Statistical Association, Alexandria, VA (pp. 154-159).
- Judkins, D. R. (1990). Fay's method for variance estimation. *Journal of Official Statistics*, 6(3), 223-239.
- Mai, Y., Ha, T., & Soulakova, J. N. (2019). Multimediation Method With Balanced Repeated Replications For Analysis Of Complex Surveys. *Structural Equation Modeling: A Multidisciplinary Journal*. DOI:10.1080/10705511.2018.1559065
- Rosseel, Y. (2012). Lavaan: An R package for structural equation modeling and more. Version 0.5–12 (BETA). *Journal of statistical software*, 48(2), 1-36. DOI:10.18637/jss.v048.i02
- Wolter, K. (2007). Introduction to variance estimation. New York, NY: Springer.

## Examples

```

R <- 160
wgtname <- paste("repwgt", seq(0,R,by=1), sep="")
mwgtname=wgtname[1]
repwgtname=wgtname[2:(R+1)]

model2 <- ' # outcome
            numcg ~ u0*1 + c*workban + b1*sp_adltban + b2*sp_kidsban
            # mediator
            sp_adltban ~ u1*1 + a1*workban
            sp_kidsban ~ u2*1 + a2*workban
            #covariance of residuals
            sp_adltban ~~ sp_kidsban
            # indirect effect (a*b)
            a1b1 := a1*b1
            a2b2 := a2*b2
            # total effect
            total := c + (a1*b1) + (a2*b2)
            '

fit.BRR <- med.fit.BRR(model=model2, data=MedData, mwgtname=mwgtname,
                       repwgtname=repwgtname, fayfactor=0.5, parallel='parallel', ncore=2)
lavaan::summary(fit.BRR)
#
# lavaan 0.6-3 ended normally after 41 iterations
#
# Optimization method                    NLMINB
# Number of free parameters                12
#
# Number of observations                    3922
#
# Estimator                                ML      Robust
# Model Fit Test Statistic                  0.000    0.000
# Degrees of freedom                        0        0
# Minimum Function Value                    0.000000000000000
# Scaling correction factor                  NA
# for the Satorra-Bentler correction
#
# Parameter Estimates:
#
# Information                                Expected
# Information saturated (h1) model          Structured
# Standard Errors                          BRR
#
# Regressions:
#           Estimate Std.Err z-value P(>|z|)
# numcg ~
#   workban   (c)   -0.101   0.039  -2.572   0.010
#   sp_adltbn (b1)  -0.253   0.048  -5.270   0.000
#   sp_kidsbn (b2)  -0.361   0.051  -7.006   0.000
# sp_adltban ~
#   workban   (a1)    0.069   0.018   3.753   0.000
# sp_kidsban ~
#   workban   (a2)    0.020   0.016   1.250   0.211
#

```

```

# Covariances:
#               Estimate Std.Err z-value P(>|z|)
# .sp_adltban ~~
#   .sp_kidsban      2.784   0.195  14.300   0.000
#
# Intercepts:
#               Estimate Std.Err z-value P(>|z|)
# .numcg      (u0)    18.485   0.566  32.668   0.000
# .sp_adltbn  (u1)     4.221   0.167  25.281   0.000
# .sp_kidsbn  (u2)     7.926   0.143  55.272   0.000
#
# Variances:
#               Estimate Std.Err z-value P(>|z|)
# .numcg        54.283   1.716  31.628   0.000
# .sp_adltban    11.011   0.239  46.140   0.000
# .sp_kidsban     9.402   0.209  44.998   0.000
#
# Defined Parameters:
#               Estimate Std.Err z-value P(>|z|)
# a1b1          -0.017   0.006  -2.905   0.004
# a2b2          -0.007   0.006  -1.234   0.217
# total         -0.125   0.040  -3.169   0.002

```

---

med.p.adjust

*To adjust the p values for multimediation tests*


---

## Description

This function is used to adjust the p values when there are multiple mediators (Mai et al., 2019).

## Usage

```
med.p.adjust(fit = NULL, med.eff = NULL, p.adj.method = c("holm",
  "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr"))
```

## Arguments

fit	The model fit results of a model with multiple mediators. Note that it is a lavaan object.
med.eff	A vector of labels. The labels should be of the mediation effects in the estimated model.
p.adj.method	The method used to adjust for multiplicity ('holm' or 'hochberg' or 'hommel' or 'bonferroni' or 'BH' or 'BY' or 'fdr'). Conservative method includes the Bonferroni correction ('bonferroni') in which the p-values are multiplied by the number of comparisons. Less conservative corrections are also included by Holm (1979) ('holm'), Hochberg (1988) ('hochberg'), Hommel (1988) ('hommel'), Benjamini & Hochberg (1995) ('BH' or its alias 'fdr'), and Benjamini & Yekutieli (2001) ('BY'), respectively. It is 'holm' by default. It is not required.

## Value

The adjusted p values along with the effect labels and original p values. It is a list.

## References

- Benjamini, Y., & Hochberg, Y. (1995). Controlling the false discovery rate: a practical and powerful approach to multiple testing. *Journal of the Royal Statistical Society Series B*, 57, 289–300. DOI:10.2307/2346101
- Benjamini, Y., & Yekutieli, D. (2001). The control of the false discovery rate in multiple testing under dependency. *Annals of Statistics*, 29, 1165–1188. DOI:10.1214/aos/1013699998
- Holm, S. (1979). A simple sequentially rejective multiple test procedure. *Scandinavian Journal of Statistics*, 6, 65–70.
- Hommel, G. (1988). A stagewise rejective multiple test procedure based on a modified Bonferroni test. *Biometrika*, 75, 383–386. DOI:10.1093/biomet/75.2.383
- Hochberg, Y. (1988). A sharper Bonferroni procedure for multiple tests of significance. *Biometrika*, 75, 800–803. DOI:10.1093/biomet/75.4.800
- Rosseel, Y. (2012). *Lavaan: An R package for structural equation modeling and more*. Version 0.5–12 (BETA). *Journal of statistical software*, 48(2), 1–36. DOI:10.18637/jss.v048.i02
- Shaffer, J. P. (1995). Multiple hypothesis testing. *Annual Review of Psychology*, 46, 561–576.
- Sarkar, S. (1998). Some probability inequalities for ordered MTP2 random variables: a proof of Simes conjecture. *Annals of Statistics*, 26, 494–504. DOI:10.1214/aos/1028144846

## Examples

```
R <- 160
wgtnames <- paste("repwgt", seq(0,R,by=1), sep="")
mwgtname=wgtnames[1]
repwgtnames=wgtnames[2:(R+1)]
fayfactor=0.5

model2 <- ' # outcome
            numcg ~ u0*1 + c*workban + b1*sp_adltban + b2*sp_kidsban
            # mediator
            sp_adltban ~ u1*1 + a1*workban
            sp_kidsban ~ u2*1 + a2*workban
            #covariance of residuals
            sp_adltban ~~ sp_kidsban
            # indirect effect (a*b)
            a1b1 := a1*b1
            a2b2 := a2*b2
            # total effect
            total := c + (a1*b1) + (a2*b2)
            '

fit.BRR2 <- med.fit.BRR(model=model2, data=MedData, mwgtname=mwgtname,
                        repwgtnames=repwgtnames, fayfactor, parallel='parallel', ncore=4)
temp <- med.p.adjust(fit=fit.BRR2, med.eff=c('a1b1' , 'a2b2'))
#
# Adjustment for multi mediation tests:
#
#      Effect          p Value      adj.p Value
#      a1b1      0.003667674      0.007335347
#      a2b2      0.217228711      0.217228711
#
# NOTE:  p Value adjustment method is holm
#
```

```
#####
# To catch the unformatted results:
temp
#
# $med.eff
# [1] "a1b1" "a2b2"
#
# $org.p.value
# [1] 0.003667674 0.217228711
#
# $adj.p.value
# [1] 0.007335347 0.217228711
```

---

med.summary	<i>To print the summary results of the mediation analysis</i>
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---

**Description**

This function is used to print the summary results of the mediation analysis with adjustment for multiplicity.

**Usage**

```
med.summary(fit = NULL, med.eff = NULL, p.adj.method = c("holm",
  "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr"))
```

**Arguments**

fit	The model fit results of a mediation model. Note that it is a lavaan object.
med.eff	A vector of labels. The labels should be of the mediation effects in the estimated model.
p.adj.method	The method used to adjust for multiplicity ('holm' or 'hochberg' or 'hommel' or 'bonferroni' or 'BH' or 'BY' or 'fdr'). Conservative method includes the Bonferroni correction ('bonferroni') in which the p-values are multiplied by the number of comparisons. Less conservative corrections are also included by Holm (1979) ('holm'), Hochberg (1988) ('hochberg'), Hommel (1988) ('hommel'), Benjamini & Hochberg (1995) ('BH' or its alias 'fdr'), and Benjamini & Yekutieli (2001) ('BY'), respectively. It is 'holm' by default. It is not required.

**Value**

A list including the effect labels, estimates, standard errors, p values, and adjusted p values if there are more than one mediation effects.

**References**

Benjamini, Y., & Hochberg, Y. (1995). Controlling the false discovery rate: a practical and powerful approach to multiple testing. *Journal of the Royal Statistical Society Series B*, 57, 289–300. DOI:10.2307/2346101

Benjamini, Y., & Yekutieli, D. (2001). The control of the false discovery rate in multiple testing under dependency. *Annals of Statistics*, 29, 1165–1188. DOI:10.1214/aos/1013699998



- Holm, S. (1979). A simple sequentially rejective multiple test procedure. *Scandinavian Journal of Statistics*, 6, 65–70.
- Hommel, G. (1988). A stagewise rejective multiple test procedure based on a modified Bonferroni test. *Biometrika*, 75, 383–386. DOI:10.1093/biomet/75.2.383
- Hochberg, Y. (1988). A sharper Bonferroni procedure for multiple tests of significance. *Biometrika*, 75, 800–803. DOI:10.1093/biomet/75.4.800
- Mai, Y., Ha, T., & Soulakova, J. N. (2019). Multimediation Method With Balanced Repeated Replications For Analysis Of Complex Surveys. *Structural Equation Modeling: A Multidisciplinary Journal*. DOI:10.1080/10705511.2018.1559065
- Rosseel, Y. (2012). Lavaan: An R package for structural equation modeling and more. Version 0.5–12 (BETA). *Journal of statistical software*, 48(2), 1–36. DOI:10.18637/jss.v048.i02
- Shaffer, J. P. (1995). Multiple hypothesis testing. *Annual Review of Psychology*, 46, 561–576.
- Sarkar, S. (1998). Some probability inequalities for ordered MTP2 random variables: a proof of Simes conjecture. *Annals of Statistics*, 26, 494–504. DOI:10.1214/aos/1028144846

## Examples

```
R <- 160
wgtnames <- paste("repwgt", seq(0,R,by=1), sep="")
mwgtname=wgtnames[1]
repwgtnames=wgtnames[2:(R+1)]
fayfactor=0.5

model2 <- ' # outcome
            numcg ~ u0*1 + c*workban + b1*sp_adltban + b2*sp_kidsban
# mediator
            sp_adltban ~ u1*1 + a1*workban
            sp_kidsban ~ u2*1 + a2*workban
#covariance of residuals
            sp_adltban ~~ sp_kidsban
# indirect effect (a*b)
            a1b1 := a1*b1
            a2b2 := a2*b2
# total effect
            total := c + (a1*b1) + (a2*b2)
            '

fit.BRR2 <- med.fit.BRR(model=model2, data=MedData, mwgtname=mwgtname,
                        repwgtnames=repwgtnames, fayfactor, parallel='parallel')
temp <- med.summary(fit=fit.BRR2, med.eff=c('a1b1' , 'a2b2'))
#
# MedSurvey 1.1.0
#
# Multimediation with Complex Survey Data:
#
#   Effect           Est.           BRR SE.           p Value           adj.p Value
#
#   a1b1    -0.017475544      0.006014820      0.003667674      0.007335347
#   a2b2    -0.007244189      0.005870823      0.217228711      0.217228711
#
# NOTE:
#   p Value adjustment method is holm
#   Standard errors type is BRR SE.
```

```

#
#
#####
# To catch the unformatted results:
temp
#
# $med.label
# [1] "a1b1" "a2b2"
#
# $med.est
# [1] -0.017475544 -0.007244189
#
# $med.se
# [1] 0.006014820 0.005870823
#
# $org.p.value
# [1] 0.003667674 0.217228711
#
# $adj.p.value
# [1] 0.007335347 0.217228711
#
# $se.type
# [1] "BRR SE."
#
# $p.adj.method
# [1] "holm"
#

```

---

MedData

---

CPS-TUS data 2014-2015

---

## Description

Data from 2014-15 CPS Tobacco Use Supplement (TUS; U.S. Department of Commerce and U.S. Census Bureau 2016), employed adult daily smokers (Non-Hispanic White males only). Missing data are removed from the dataset. Due to the CRAN limitation of the size (5MB) of an R package, only half of the observations remained in this internal dataset for the purpose of illustration.

## Usage

```
MedData
```

## Format

A data frame with 3922 rows and 167 variables:

PRTAGE Age

PESEX Gender, 0=Male, 1=Female

repwgt0 Sample main weights

repwgt1 BRR replicate weights

repwgt2 BRR replicate weights

repwgt3 BRR replicate weights  
repwgt4 BRR replicate weights  
repwgt5 BRR replicate weights  
repwgt6 BRR replicate weights  
repwgt7 BRR replicate weights  
repwgt8 BRR replicate weights  
repwgt9 BRR replicate weights  
repwgt10 BRR replicate weights  
repwgt11 BRR replicate weights  
repwgt12 BRR replicate weights  
repwgt13 BRR replicate weights  
repwgt14 BRR replicate weights  
repwgt15 BRR replicate weights  
repwgt16 BRR replicate weights  
repwgt17 BRR replicate weights  
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repwgt156 BRR replicate weights  
repwgt157 BRR replicate weights  
repwgt158 BRR replicate weights  
repwgt159 BRR replicate weights  
repwgt160 BRR replicate weights  
sp\_adltban Supporting toward smoking ban in adults-exclusive areas (e.g., casinos, bars)  
sp\_kidsban Supporting toward smoking ban in kids-related areas (e.g., children playground)  
workban Score of smoking restriction score at workplace  
numcg Number of cigarretes smoked per day

**Source**

[http://thedataweb.rm.census.gov/ftp/cps\\_ftp.html#cpssupps](http://thedataweb.rm.census.gov/ftp/cps_ftp.html#cpssupps)

**References**

U.S. Department of Commerce, & U.S. Census Bureau. (2016). National Cancer Institute and Food and Drug Administration co-sponsored Tobacco Use Supplement to the Current Population Survey. 2014-15.

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