Package ‘MF’

February 19, 2015

Type Package

Title Mitigated Fraction

Version 4.3.2

Date 2014-01-10

Author David Siev

Maintainer Marie Vendettuoli `<marie.c.vendettuoli@aphis.usda.gov>`

Description Calculate MF (mitigated fraction) with clustering and bootstrap options. See http://goo.gl/pcXYVr for definition of MF.

LazyLoad yes

LazyData yes

Depends R (>= 2.15.0), methods

Collate 'aaa.r' 'classes.r' 'generic_methods.r' 'MF-package.r'
'HLBoot.r' 'MFBoot.r' 'MFClus.r' 'MFClusBoot.r' 'MFmp.r'
'MFr.r' 'MFSubj.r'

NeedsCompilation no

Repository CRAN

Date/Publication 2014-01-13 16:04:51

R topics documented:

`MF-package` *MF Package*

Description

Includes functions related to mitigated fraction.

For internal use only at the USDA Center for Veterinary Biologics.

Details

Package:	MF-package
Type:	Package
Version:	4.3.2
Date:	2014-01-10
License:	MIT
LazyLoad:	yes

Author(s)

David Siev <`David.Siev@aphis.usda.gov`>

Examples

```
#--------------------------------------------
# Checking MF package
#--------------------------------------------
example(MFr)
#--------------------------------------------
# End examples
#--------------------------------------------
invisible()
```

`calflung` *calflung dataset*

Description

something here

Format

a data frame with 50 observations of the following 2 variables, no NAs

group Treatment group. One of con = control or vac = vaccinate

lesion Percent lung lesion, in decimal form

`HLBoot` *Bootstrap CI for MF, HL, and Qdif*

Description

Estimates bootstrap confidence intervals for MF, HL, and Qdif.

Usage

```
HLBoot(formula, data, compare = c("con", "vac"), b = 100,
  B = 100, alpha = 0.05, hpd = TRUE, bca = FALSE,
  return.boot = FALSE, trace.it = FALSE, seed = NULL)
```

Arguments

`formula`	Formula of the form `y ~ x + cluster(w)`, where y is a continuous response, x is a factor with two levels of treatment, and w is a factor indicating the clusters.
`data`	Data frame
`compare`	Text vector stating the factor levels - `compare[1]` is the control or reference group to which `compare[2]` is compared
`b`	Number of bootstrap samples to take with each cycle
`B`	Number of cycles, giving the total number of samples = B * b
`alpha`	Complement of the confidence level
`hpd`	Estimate highest density intervals for MF and HL? Default TRUE.
`bca`	Estimate BCa intervals for MF? Default FALSE.
`return.boot`	Save the bootstrap samples of the statistics? Default FALSE.
`trace.it`	Verbose tracking of the cycles? Default FALSE.
`seed`	initial seed value. Ignored.

Details

Estimates bootstrap confidence intervals for the mitigated fraction (MF), Hodge-Lehmann estimator (HL), and the difference of medians and quartiles (Qdif). The Hodges-Lehmann estimator is the media difference; it assumes that the two distributions have the same shape and differ by a constant shift.

Value

a `mfhlboot-class` data object

Author(s)

David Siev `<david.siev@aphis.usda.gov>`

References

Hodges JL, Lehmann EL, (1963). Estimates of location based on rank tests. *Annals of Mathematical Statistics.* **34:598–611**.

Siev D, (2005). An estimator of intervention effect on disease severity. *Journal of Modern Applied Statistical Methods.* **4:500–508**.

Efron B, Tibshirani RJ. *An Introduction to the Bootstrap.* Chapman and Hall, New York, 1993.

See Also

`mfhlboot-class`

Examples

```
HLBoot(lesion~group,calflung)

#  Bootstrapping . . . . . . . . . . . .
#
#  10000 bootstrap samples
#  95% confidence intervals
#  Comparing vac to con
#
#
#  Mitigated Fraction
#
#                  observed median  lower  upper
#  Equal Tailed        0.44 0.4464 0.1264 0.7056
#  Highest Density     0.44 0.4464 0.1392 0.7120
#
#
#  Hodges-Lehmann
#
#                  observed   median      lower    upper
#  Equal Tailed    -0.07335 -0.07125 -0.1720537 -0.01430
#  Highest Density -0.07335 -0.07125 -0.1563500 -0.00555
```

```
#
#
#  Quartile Differences (quartiles of vac - quartiles of con)
#
#       observed    median      lower     upper
#  Q25 -0.041500 -0.041300 -0.1034000 -0.000905
#  Q50 -0.112525 -0.111175 -0.2811688  0.023200
#  Q75 -0.168000 -0.168000 -0.3858500  0.023975
```

`mf-class` *Class mf*

Description

Parent class for package MF data objects.

Fields

- `nboot:` numeric value specifying number of samples
- `alpha:` numeric value specifying complement of confidence interval
- `seed:` vector of integers specifying seed for pseudo-random number generator used
- `compare:` vector of character strings naming groups compared
- `rng:` character string naming type of random number generator

Author(s)

Marie Vendettuoli <`marie.c.vendettuoli@aphis.usda.gov`>

See Also

Other mf: `mfboot-class`, `mfbootcluster-class`, `mfhlboot-class`

`MFBoot` *Bootstrap MF CI*

Description

Estimates bootstrap confidence intervals for the mitigated fraction.

Usage

```
MFBoot(formula, data, compare = c("con", "vac"), b = 100,
  B = 100, alpha = 0.05, hpd = TRUE, bca = FALSE,
  return.boot = FALSE, trace.it = FALSE)
```

Arguments

`formula`	Formula of the form `y ~ x`, where y is a continuous response and x is a factor with two levels
`data`	Data frame
`compare`	Text vector stating the factor levels - `compare[1]` is the control or reference group to which `compare[2]` is compared
`b`	Number of bootstrap samples to take with each cycle
`B`	Number of cycles, giving the total number of samples = B * b
`alpha`	Complement of the confidence level
`hpd`	Estimate highest density intervals? Default TRUE.
`bca`	Estimate BCa intervals? Default FALSE.
`return.boot`	Save the bootstrap sample of the MF statistic? Default FALSE.
`trace.it`	Verbose tracking of the cycles? Default FALSE.

Details

Resamples the data and produces bootstrap confidence intervals. Equal tailed intervals are estimated by the percentile method. Highest density intervals are estimated by selecting the shortest of all possible intervals. For BCa intervals, see Efron and Tibshirani section 14.3.

Value

a `mfboot-class` data object

Author(s)

David Siev `<david.siev@aphis.usda.gov>`

References

Siev D. (2005). An estimator of intervention effect on disease severity. *Journal of Modern Applied Statistical Methods.* **4:500–508**

Efron B, Tibshirani RJ. *An Introduction to the Bootstrap.* Chapman and Hall, New York, 1993.

See Also

`mfboot-class`

Examples

```
MFBoot(lesion~group, calflung)

# 10000 bootstrap samples
# 95% confidence interval
#
# Comparing vac to con
```

```
#                  observed median  lower  upper
# Equal Tailed         0.44 0.4464 0.1360 0.7056
# Highest Density      0.44 0.4464 0.1456 0.7088
```

`mfboot-class` *Class mfboot*

Description

class for data objects produced by MFBoot, contains class mf with the two additional fields *stat* and *stuff*.

Fields

- `nboot:` numeric value specifying number of samples
- `alpha:` numeric value specifying complement of confidence interval
- `seed:` vector of integers specifying seed for pseudo-random number generator used
- `compare:` vector of character strings naming groups compared
- `rng:` character string naming type of random number generator
- `sample:` what is this?
- `stat:` matrix of estimates

Contains

`mf-class`

Author(s)

Marie Vendettuoli <`marie.c.vendettuoli@aphis.usda.gov`>

See Also

`MFBoot`

Other mf: `mf-class`, `mfbootcluster-class`, `mfhlboot-class`

`mfbootcluster-class` *Class mfbootcluster*

Description

Class mfbootcluster is created from output of function MFClusBoot

Fields

- `nboot:` numeric value specifying number of samples
- `alpha:` numeric value specifying complement of confidence interval
- `seed:` vector of integers specifying seed for pseudo-random number generator used
- `compare:` vector of character strings naming groups compared
- `rng:` character string naming type of random number generator
- `stat:` matrix matrix with columns *observed, median, lower, upper* for estimates
- `what:` character vector naming what was resampled: *clusters*, *units*, *both*
- `excludedClusters:` character vector naming clusters excluded because of missing treatment(s)
- `call:` the call to `MFClusBoot`
- `sample:` what is this?

Contains

`mf-class`

Author(s)

Marie Vendettuoli <`marie.c.vendettuoli@aphis.usda.gov`>

See Also

`MFClusBoot`

Other mf: `mf-class`, `mfboot-class`, `mfhlboot-class`

`MFClus` *Clustered mitigated fraction*

Description

Estimates mitigated fraction from clustered or stratified data.

Usage

```
MFClus(formula, data, compare = c("con", "vac"),
  trace.it = FALSE)
```

Arguments

`formula`	Formula of the form `y ~ x + cluster(w)`, where y is a continuous response, x is a factor with two levels of treatment, and w is a factor indicating the clusters.
`data`	Data frame. See `Note` for handling of input data with more than two levels.
`compare`	Text vector stating the factor levels - `compare[1]` is the control or reference group to which `compare[2]` is compared
`trace.it`	Verbose tracking of the cycles? Default FALSE.

Details

Averages the U statistic over the clusters and computes MF from it. Clusters are excluded if they do not include both treatments.

Value

a `mfcluster-class` data object

Note

If input data contains more than two levels of treatment, rows associated with unused treatment levels will be removed.
Factor levels for treatments not present in the input data will be ignored.
Clusters with missing treatments will be excluded. See `mfbootcluster-class` or use `trace.it` to identify excluded clusters.

Author(s)

David Siev `<david.siev@aphis.usda.gov>`

References

Siev D. (2005). An estimator of intervention effect on disease severity. *Journal of Modern Applied Statistical Methods.* **4:500–508**

See Also

mfcluster-class

Examples

```
## Not run:
MFClus(lesion ~ group + cluster(litter), piglung)

#  Comparing vac to con
#
#  MF = 0.3533835
#
#  By Cluster
#     w  u         r n1 n2         mf
#  U 25 10 0.4000000  5  5 -0.2000000
#  K 12  2 0.2500000  4  2 -0.5000000
#  Z 16 10 0.8333333  3  4  0.6666667
#  D  3  2 1.0000000  1  2  1.0000000
#  N  1  0 0.0000000  1  3 -1.0000000
#  T  8  5 0.8333333  2  3  0.6666667
#  P  4  1 0.5000000  2  1  0.0000000
#  L  3  2 0.6666667  1  3  0.3333333
#  G 15  9 0.7500000  3  4  0.5000000
#  J 15  9 1.0000000  3  3  1.0000000
#  W  6  3 0.7500000  2  2  0.5000000
#  A  9  3 0.3333333  3  3 -0.3333333
#  X 12  6 1.0000000  3  2  1.0000000
#  F 13  7 0.7777778  3  3  0.5555556
#  S 21 11 0.9166667  4  3  0.8333333
#  H 14  8 0.8888889  3  3  0.7777778
#  Y  2  1 1.0000000  1  1  1.0000000
#  E  2  1 1.0000000  1  1  1.0000000
#
#  All
#        w  u         r n1 n2        mf
#  All 181 90 0.6766917 50 52 0.3533835
#
#  Excluded Clusters
#  [1] M, Q, R, B, O, V, I, C

## End(Not run)
```

MFClusBoot *Boostrap MF CI from clustered data*

Description

Estimates bootstrap confidence intervals for the mitigated fraction from clustered or stratified data.

Usage

```
MFClusBoot(formula, data, compare = c("con", "vac"),
  boot.cluster = TRUE, boot.unit = FALSE, b = 100, B =
  100, alpha = 0.05, hpd = TRUE, return.boot = FALSE,
  trace.it = FALSE)
```

Arguments

`formula`	Formula of the form `y ~ x + cluster(w)`, where y is a continuous response, x is a factor with two levels of treatment, and w is a factor indicating the clusters.
`data`	Data frame. See `Note` for handling of input data with more than two levels.
`compare`	Text vector stating the factor levels - `compare[1]` is the control or reference group to which `compare[2]` is compared
`boot.cluster`	Resample the clusters? Default TRUE
`boot.unit`	Resample the units within cluster? Default FALSE
`b`	Number of bootstrap samples to take with each cycle
`B`	Number of cycles, giving the total number of samples = B * b
`alpha`	Complement of the confidence level
`hpd`	Estimate highest density intervals? Default TRUE
`return.boot`	Save the bootstrap sample of the MF statistic? Default FALSE
`trace.it`	Verbose tracking of the cycles? Default FALSE

Details

Resamples the data and produces bootstrap confidence intervals. Equal tailed intervals are estimated by the percentile method. Highest density intervals are estimated by selecting the shortest of all possible intervals.

Value

a `mfbootcluster-class` data object

Note

If input data contains more than two levels of treatment, rows associated with unused treatment levels will be removed.
Factor levels for treatments not present in the input data will be ignored.
Clusters with missing treatments will be excluded. See `mfbootcluster-class` or use `trace.it` to identify excluded clusters.

Author(s)

David Siev `<david.siev@aphis.usda.gov>`

References

Siev D. (2005). An estimator of intervention effect on disease severity. *Journal of Modern Applied Statistical Methods.* **4:500–508**

Efron B, Tibshirani RJ. *An Introduction to the Bootstrap.* Chapman and Hall, New York, 1993.

Examples

```
## Not run:
MFClusBoot(lesion ~ group + cluster(litter), piglung)

#  Bootstrapping clusters. . . . .
#
#  10000 bootstrap samples of clusters
#  Comparing vac to con
#
#   95% confidence interval
#
#                   observed    median      lower     upper
#  Equal Tailed    0.3533835 0.3630573 0.07382550 0.6567271
#  Highest Density 0.3533835 0.3630573 0.07262462 0.6551724
#
#  Excluded Clusters
#  [1] M, Q, R, B, O, V, I, C

MFClusBoot(lesion ~ group + cluster(litter), piglung, boot.unit = T, b = 12, B = 12)

#### 144 resamples to save time
#
#  Bootstrapping clusters. . . . . . . . . . . . . . . .
#  Bootstrapping units. . . . . . . . . . . . . . . . .
#
#  10000 bootstrap samples of clusters and units in treatment in cluster
#  Comparing vac to con
#
#   95% confidence interval
#
#                   observed    median         lower     upper
#  Equal Tailed    0.3533835 0.3714286 -0.0138888889 0.7162213
#  Highest Density 0.3533835 0.3714286 -0.0001472081 0.7297387
#
#  Excluded Clusters
#  [1] M, Q, R, B, O, V, I, C

## End(Not run)
```

`mfcluster-class` *Class mfcluster*

Description

Class mfcluster is created from output of function MFClus

Fields

- `All:` vector with elements:
  - *w* Wilcoxon statistic
  - *u* Mann-Whitney statistic
  - *r* mean ridit
  - *n1* size of group 1
  - *n2* size of group 2
  - *mf* mitigated fraction
- `byCluster:` As for All, by clusters
- `excludedClusters:` character vector naming clusters excluded because of missing treatment
- `call:` the call to `MFClus`
- `compare:` character vector naming groups compared

Author(s)

Marie Vendettuoli <`marie.c.vendettuoli@aphis.usda.gov`>

See Also

`MFClus`

`mfcomponents-class` *Class mfcomponents*

Description

Class mfcomponens is created from output of function MFSubj

Fields

- `mf:` numeric estimator for mitigated fraction
- `x:` numeric vector containing responses of group 1
- `y:` numeric vector containing responses of group 2
- `subj:` matrix where `mf.j` are the subject components
- `compare:` character vector naming groups being compared

Author(s)

Marie Vendettuoli <`marie.c.vendettuoli@aphis.usda.gov`>

See Also

MFSubj

`mfhlboot-class` *Class mfhlboot*

Description

class for data objects produced by HLBoot, contains class mf with addtional fields *MFstat, HLstat, QDIFstat, QXstat, QYstat*

Fields

- `nboot:` numeric value specifying number of samples
- `alpha:` numeric value specifying complement of confidence interval
- `seed:` vector of integers specifying seed for pseudo-random number generator used
- `compare:` vector of character strings naming groups compared
- `rng:` character string naming type of random number generator
- `sample:` what is this?
- `MFstat`matrix with columns *observed, median, lower, upper* for Equal Tailed and Highest Density estimates of mitigated fraction (MF)
- `HLstat`matrix with columns *observed, median, lower, upper* for Equal Tailed and Highest Density estimates of Hodge-Lehmann estimator (HL)
- `QDIFstat`matrix with columns *observed, median, lower, upper* for estimates of Quartile Differences
- `QXstat`matrix with columns *observed, median, lower, upper* for quartiles of treatments
- `QYstat`matrix with columns *observed, median, lower, upper* for quartiles of responses
- `sample:` what is this?

Contains

mf-class

Author(s)

Marie Vendettuoli <`marie.c.vendettuoli@aphis.usda.gov`>

See Also

HLBoot

Other mf: `mf-class`, `mfboot-class`, `mfbootcluster-class`

`MFmp` *Mitigated fraction from matched pairs*

Description

Estimates mitigated fraction from matched pairs.

Usage

```
MFmp(formula=NULL, data=NULL, compare = c("con", "vac"),
  x=NULL, alpha=0.05, df=NULL, tdist=T)
```

Arguments

`formula`	Formula of the form `y ~ x + cluster(w)`, where y is a continuous response, x is a factor with two levels of treatment, and w is a factor indicating the clusters.
`data`	Data frame
`compare`	Text vector stating the factor levels - `compare[1]` is the control or reference group to which `compare[2]` is compared
`x`	Trinomial vector $\{\Sigma I(x < y), \Sigma I(x = y), \Sigma I(x > y)\}$
`alpha`	Complement of the confidence level.
`df`	Degrees of freedom. Default N-2
`tdist`	Use quantiles of t or Gaussian distribution for confidence interval? Default t distribution.

Details

Estimates *MF* from matched pairs by the difference of multinomial fractions $(\Sigma I(x < y) - \Sigma I(x > y))/N$. The trinomial vector is $\{\Sigma I(x < y), \Sigma I(x = y), \Sigma I(x > y)\}$

Value

a `mfmp-class` data object

Author(s)

David Siev `<david.siev@aphis.usda.gov>`

References

Siev D. (2005). An estimator of intervention effect on disease severity. *Journal of Modern Applied Statistical Methods.* **4:500–508**

See Also

`mfmp-class`

Examples

```
MFmp(les ~ tx + cluster(cage), mlesions, compare = c('con', 'vac'))
MFmp(x = c(12, 12, 2))
```

`mfmp-class` *Class mfmp*

Description

Class mfmp is created from output of funtion MFmp

Fields

- `ci:` numeric vector of point and interval estimates
- `x:` numeric vector of length three holding data
- `what:` text string describing interval type
- `alpha:` numeric value specifying complement of confidence interval
- `tdist:` Logical indicating if t distribution(TRUE) or gaussian (FALSE)
- `df:` numeric value indicating degrees freedom

Author(s)

Marie Vendettuoli <`marie.c.vendettuoli@aphis.usda.gov`>

See Also

`MFmp`

`MFr` *Mitigated fraction*

Description

Mitigated fraction comparing treatment to control.

Usage

```
MFr(formula, data, compare = c("con", "vac"))
```

Arguments

`formula`	Formula of the form `y ~ x`, where y is a continuous response and x is a factor with two levels
`data`	Data frame
`compare`	Text vector stating the factor levels – `compare[1]` is the control or reference group to which `compare[2]` is compared

Details

The mitigated fraction is an estimator that quantifies an intervention's effect on reducing the severity of a condition. Since its units are on the probability scale, it is often a good idea to accompany it with an estimator on the original scale of measurement.

Value

The estimated mitigated fraction.

Author(s)

David Siev

References

Siev D, 2005. An estimator of intervention effect on disease severity. *Journal of Modern Applied Statistical Methods.* 4:500-508

Examples

```
MFr(lesion~group,calflung)
# [1] 0.44
```

`MFSubj` *Subject components of mitigated fraction*

Description

Estimates the subject components of the mitigated fraction.

Usage

```
  MFSubj(formula, data, compare = c("con", "vac"))
```

Arguments

`formula`	Formula of the form `y ~ x`, where y is a continuous response and x is a factor with two levels
`data`	Data frame
`compare`	Text vector stating the factor levels - `compare[1]` is the control or reference group to which `compare[2]` is compared

Details

The mitigated fraction is an estimator that quantifies an intervention's effect on reducing the severity of a condition. Since its units are on the probability scale, it is often a good idea to accompany it with an estimator on the original scale of measurement.

The subject components are the individual contributions of the treated subjects to *MF*, which is the average of the subject components.

Value

a `mfcomponents-class` data object

Author(s)

David Siev `<david.siev@aphis.usda.gov>`

References

Siev D. (2005). An estimator of intervention effect on disease severity. *Journal of Modern Applied Statistical Methods.* **4:500–508**

Examples

```
x <- MFSubj(lesion ~ group, calflung)
x

#  MF = 0.44 comparing vac to con
#
#  MF Subject Components
#
#    mf.j freq    min.y   max.y
#    1.00    6 0.000030 0.00970
#    0.84    1 0.012500 0.01250
#    0.76    3 0.016650 0.02030
#    0.68    6 0.023250 0.03190
#    0.04    1 0.132100 0.13210
#   -0.04    3 0.144575 0.16325
#   -0.20    2 0.210000 0.21925
#   -0.36    1 0.292000 0.29200
#   -0.52    1 0.356500 0.35650
#   -0.84    1 0.461500 0.46150


mean(x$subj[,'mf.j'])

# [1] 0.44
```

`mlesions` *mlesions dataset*

Description

something here

Format

a data frame with 52 observations of the following 3 variables, no NAs

cage Cage ID. 1 - 26

tx Treatment. One of 'con' or 'vac'

les Percent lung lesion

`piglung` *piglung dataset*

Description

something here

Format

a data frame with 102 observations of the following 3 variables, no NAs

lesion Percent lung lesion

group Treatment group. One of 'con' or 'vac'

litter Litter ID

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