Package: mmcm (via r-universe)

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Type Package

Title Modified Maximum Contrast Method

Version 1.2-8

Imports mvtnorm

Description An implementation of modified maximum contrast methods (Sato et al. (2009) <doi:10.1038/tpj.2008.17>; Nagashima et al. (2011) <doi:10.2202/1544-6115.1560>) and the maximum contrast method (Yoshimura et al. (1997) <doi:10.1177/009286159703100213>): Functions mmcm.mvt() and mcm.mvt() give P-value by using randomized quasi-Monte Carlo method with pmvt() function of package 'mvtnorm', and mmcm.resamp() gives P-value by using a permutation method.

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Contents

mmcm-package *The modified maximum contrast method package*

Description

This package provides an implementation of modified maximum contrast methods and the maximum contrast method. This version supports functions mmcm.mvt, mcm.mvt that gives P-value by using randomized quasi-Monte Carlo method from pmvt function of package mvtnorm, and mmcm.resamp that gives P-value by using the permutation method. In a one-way problem testing pattern of several factor level means, the maximum contrast statistics (Yoshimura, I., 1997) may be used. But under unequal sample size situations, denominator of the maximum contrast statistics is overestimated. Thus we propose a modified maximum contrast statistics for the unequal sample size situation. Denominetor of the modified maximum contrast statistics is not influenced under the unequal sample size situation.

References

Nagashima, K., Sato, Y., Hamada, C. (2011). A modified maximum contrast method for unequal sample sizes in pharmacogenomic studies *Stat Appl Genet Mol Biol.* **10**(1): Article 41. http://dx.doi.org/10.2202/1544-6115.1560

Sato, Y., Laird, N.M., Nagashima, K., et al. (2009). A new statistical screening approach for finding pharmacokinetics-related genes in genome-wide studies. *Pharmacogenomics J.* **9**(2): 137–146. http://www.ncbi.nlm.nih.gov/pubmed/19104505

Yoshimura, I., Wakana, A., Hamada, C. (1997). A performance comparison of maximum contrast methods to detect dose dependency. *Drug Information J.* **31**: 423–432.

See Also

mcm.mvt, mmcm.mvt, mmcm.resamp

mcm.mvt *The maximum contrast method by using the randomized quasi-Monte Carlo method*

Description

This function gives P-value for the maximum contrast statistics by using randomized quasi-Monte Carlo method from pmvt function of package mvtnorm.

Usage

```
mcm.mvt(
  x,
  g,
  contrast,
  alternative = c("two.sided", "less", "greater"),
  algorithm = GenzBretz()
)
```

Arguments

x	a numeric vector of data values
g	a integer vector giving the group for the corresponding elements of x
contrast	a numeric contrast coefficient matrix for the maximum contrast statistics
alternative	a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
algorithm	an object of class GenzBretz defining the hyper parameters of this algorithm

Details

mcm.mvt performs the maximum contrast method that is detecting a true response pattern.

$Y_{ij}(i = 1, 2, \ldots; j = 1, 2, \ldots, n_i)$ is an observed response for j-th individual in i-th group.

$\boldsymbol{C}$ is coefficient matrix for the maximum contrast statistics ($i \times k$ matrix, i: No. of groups, k: No. of pattern).

$$\boldsymbol{C} = (\boldsymbol{c}_1, \boldsymbol{c}_2, \ldots, \boldsymbol{c}_k)^{\mathrm{T}}$$

$\boldsymbol{c}_k$ is coefficient vector of kth pattern.

$$\boldsymbol{c}_k = (c_{k1}, c_{k2}, \ldots, c_{ki})^{\mathrm{T}} \qquad (\textstyle\sum_i c_{ki} = 0)$$

$T_{\max}$ is the maximum contrast statistic.

$$\bar{Y}_i = \frac{\sum_{j=1}^{n_i} Y_{ij}}{n_i}, \bar{\boldsymbol{Y}} = (\bar{Y}_1, \bar{Y}_2, \ldots, \bar{Y}_i, \ldots, \bar{Y}_a)^{\mathrm{T}},$$

$$\boldsymbol{D} = diag(n_1, n_2, \ldots, n_i, \ldots, n_a), V = \frac{1}{\gamma} \sum_{j=1}^{n_i} \sum_{i=1}^{a} (Y_{ij} - \bar{Y}_i)^2,$$

$$\gamma = \sum_{i=1}^{a} (n_i - 1), T_k = \frac{\boldsymbol{c}_k^t \bar{\boldsymbol{Y}}}{\sqrt{V \boldsymbol{c}_k^t \boldsymbol{D} \boldsymbol{c}_k}},$$

$$T_{\max} = \max(T_1, T_2, \ldots, T_k).$$

Consider testing the overall null hypothesis $H_0 : \mu_1 = \mu_2 = \ldots = \mu_i$, versus alternative hypotheses H_1 for response petterns ($H_1 : \mu_1 < \mu_2 < \ldots < \mu_i,\ \mu_1 = \mu_2 < \ldots < \mu_i,\ \mu_1 < \mu_2 < \ldots = \mu_i$). The P-value for the probability distribution of $T_{\max}$ under the overall null hypothesis is

$$P\text{-value} = \Pr(T_{\max} > t_{\max} \mid H_0)$$

$t_{\max}$ is observed value of statistics. This function gives distribution of $T_{\max}$ by using randomized quasi-Monte Carlo method from package mvtnorm.

Value

`statistic`	the value of the test statistic with a name describing it.
`p.value`	the p-value for the test.
`alternative`	a character string describing the alternative hypothesis.
`method`	the type of test applied.
`contrast`	a character string giving the names of the data.
`contrast.index`	a suffix of coefficient vector of the kth pattern that gives maximum contrast statistics (row number of the coefficient matrix).
`error`	estimated absolute error and,
`msg`	status messages.

References

Yoshimura, I., Wakana, A., Hamada, C. (1997). A performance comparison of maximum contrast methods to detect dose dependency. *Drug Information J.* **31**: 423–432.

See Also

pmvt, GenzBretz, mmcm.mvt

Examples

```
## Example 1 ##
#  true response pattern: dominant model c=(1, 1, -2)
set.seed(136885)
x <- c(
  rnorm(130, mean =  1 / 6, sd = 1),
  rnorm( 90, mean =  1 / 6, sd = 1),
  rnorm( 10, mean = -2 / 6, sd = 1)
)
g <- rep(1:3, c(130, 90, 10))
boxplot(
  x ~ g,
  width = c(length(g[g==1]), length(g[g==2]), length(g[g==3])),
  main = "Dominant model (sample data)",
  xlab = "Genotype",
  ylab = "PK parameter"
)

# coefficient matrix
# c_1: additive, c_2: recessive, c_3: dominant
contrast <- rbind(
  c(-1, 0, 1), c(-2, 1, 1), c(-1, -1, 2)
)
y <- mcm.mvt(x, g, contrast)
y

## Example 2 ##
#  for dataframe
```

```
#  true response pattern:
#    pos = 1 dominant  model c=( 1,  1, -2)
#          2 additive  model c=(-1,  0,  1)
#          3 recessive model c=( 2, -1, -1)
set.seed(3872435)
x <- c(
  rnorm(130, mean =  1 / 6, sd = 1),
  rnorm( 90, mean =  1 / 6, sd = 1),
  rnorm( 10, mean = -2 / 6, sd = 1),
  rnorm(130, mean = -1 / 4, sd = 1),
  rnorm( 90, mean =  0 / 4, sd = 1),
  rnorm( 10, mean =  1 / 4, sd = 1),
  rnorm(130, mean =  2 / 6, sd = 1),
  rnorm( 90, mean = -1 / 6, sd = 1),
  rnorm( 10, mean = -1 / 6, sd = 1)
)
g   <- rep(rep(1:3, c(130, 90, 10)), 3)
pos <- rep(c("rsXXXX", "rsYYYY", "rsZZZZ"), each=230)
xx  <- data.frame(pos = pos, x = x, g = g)

# coefficient matrix
# c_1: additive, c_2: recessive, c_3: dominant
contrast <- rbind(
  c(-1, 0, 1), c(-2, 1, 1), c(-1, -1, 2)
)
y <- by(xx, xx$pos, function(x) mmcm.mvt(x$x, x$g,
  contrast))
y <- do.call(rbind, y)[,c(3,7,9)]
# miss-detection!
y
```

`mmcm.mvt` *The modified maximum contrast method by using randomized quasi-Monte Carlo method*

Description

This function gives P-value for the modified maximum contrast statistics by using randomized quasi-Monte Carlo method from `pmvt` function of package `mvtnorm`.

Usage

```
mmcm.mvt(
  x,
  g,
  contrast,
  alternative = c("two.sided", "less", "greater"),
  algorithm = GenzBretz()
)
```

Arguments

x	a numeric vector of data values
g	a integer vector giving the group for the corresponding elements of x
contrast	a numeric contrast coefficient matrix for modified maximum contrast statistics
alternative	a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
algorithm	an object of class GenzBretz defining the hyper parameters of this algorithm.

Details

mmcm.mvt performs the modified maximum contrast method that is detecting a true response pattern under the unequal sample size situation.

$Y_{ij}(i = 1, 2, \ldots; j = 1, 2, \ldots, n_i)$ is an observed response for j-th individual in i-th group.

$\boldsymbol{C}$ is coefficient matrix for modified maximum contrast statistics ($i \times k$ matrix, i: No. of groups, k: No. of pattern).

$$\boldsymbol{C} = (\boldsymbol{c}_1, \boldsymbol{c}_2, \ldots, \boldsymbol{c}_k)^{\mathrm{T}}$$

$\boldsymbol{c}_k$ is coefficient vector of kth pattern.

$$\boldsymbol{c}_k = (c_{k1}, c_{k2}, \ldots, c_{ki})^{\mathrm{T}} \qquad (\textstyle\sum_i c_{ki} = 0)$$

$S_{\max}$ is the modified maximum contrast statistic.

$$\bar{Y}_i = \frac{\sum_{j=1}^{n_i} Y_{ij}}{n_i}, \bar{\boldsymbol{Y}} = (\bar{Y}_1, \bar{Y}_2, \ldots, \bar{Y}_i, \ldots, \bar{Y}_a)^{\mathrm{T}},$$

$$V = \frac{1}{\gamma} \sum_{j=1}^{n_i} \sum_{i=1}^{a} (Y_{ij} - \bar{Y}_i)^2, \gamma = \sum_{i=1}^{a} (n_i - 1),$$

$$S_k = \frac{\boldsymbol{c}_k^t \bar{\boldsymbol{Y}}}{\sqrt{V \boldsymbol{c}_k^t \boldsymbol{c}_k}},$$

$$S_{\max} = \max(S_1, S_2, \ldots, S_k).$$

Consider testing the overall null hypothesis $H_0 : \mu_1 = \mu_2 = \ldots = \mu_i$, versus alternative hypotheses H_1 for response petterns ($H_1 : \mu_1 < \mu_2 < \ldots < \mu_i,\ \mu_1 = \mu_2 < \ldots < \mu_i,\ \mu_1 < \mu_2 < \ldots = \mu_i$). The P-value for the probability distribution of $S_{\max}$ under the overall null hypothesis is

$$P\text{-value} = \Pr(S_{\max} > s_{\max} \mid H_0)$$

$s_{\max}$ is observed value of statistics. This function gives distribution of $S_{\max}$ by using randomized quasi-Monte Carlo method from package mvtnorm.

Value

`statistic`	the value of the test statistic with a name describing it.
`p.value`	the p-value for the test.
`alternative`	a character string describing the alternative hypothesis.
`method`	the type of test applied.
`contrast`	a character string giving the names of the data.
`contrast.index`	a suffix of coefficient vector of the kth pattern that gives modified maximum contrast statistics (row number of the coefficient matrix).
`error`	estimated absolute error and,
`msg`	status messages.

References

Nagashima, K., Sato, Y., Hamada, C. (2011). A modified maximum contrast method for unequal sample sizes in pharmacogenomic studies *Stat Appl Genet Mol Biol.* **10**(1): Article 41. http://dx.doi.org/10.2202/1544-6115.1560

Sato, Y., Laird, N.M., Nagashima, K., et al. (2009). A new statistical screening approach for finding pharmacokinetics-related genes in genome-wide studies. *Pharmacogenomics J.* **9**(2): 137–146. http://www.ncbi.nlm.nih.gov/pubmed/19104505

See Also

pmvt, GenzBretz, mmcm.resamp

Examples

```
## Example 1 ##
#  true response pattern: dominant model c=(1, 1, -2)
set.seed(136885)
x <- c(
  rnorm(130, mean =  1 / 6, sd = 1),
  rnorm( 90, mean =  1 / 6, sd = 1),
  rnorm( 10, mean = -2 / 6, sd = 1)
)
g <- rep(1:3, c(130, 90, 10))
boxplot(
  x ~ g,
  width = c(length(g[g==1]), length(g[g==2]), length(g[g==3])),
  main  = "Dominant model (sample data)",
  xlab  = "Genotype", ylab="PK parameter"
)

# coefficient matrix
# c_1: additive, c_2: recessive, c_3: dominant
contrast <- rbind(
  c(-1, 0, 1), c(-2, 1, 1), c(-1, -1, 2)
)
y <- mmcm.mvt(x, g, contrast)
```

```
y

## Example 2 ##
#  for dataframe
#  true response pattern:
#    pos = 1 dominant  model c=( 1,  1, -2)
#          2 additive  model c=(-1,  0,  1)
#          3 recessive model c=( 2, -1, -1)
set.seed(3872435)
x <- c(
  rnorm(130, mean =  1 / 6, sd = 1),
  rnorm( 90, mean =  1 / 6, sd = 1),
  rnorm( 10, mean = -2 / 6, sd = 1),
  rnorm(130, mean = -1 / 4, sd = 1),
  rnorm( 90, mean =  0 / 4, sd = 1),
  rnorm( 10, mean =  1 / 4, sd = 1),
  rnorm(130, mean =  2 / 6, sd = 1),
  rnorm( 90, mean = -1 / 6, sd = 1),
  rnorm( 10, mean = -1 / 6, sd = 1)
)
g   <- rep(rep(1:3, c(130, 90, 10)), 3)
pos <- rep(c("rsXXXX", "rsYYYY", "rsZZZZ"), each=230)
xx  <- data.frame(pos = pos, x = x, g = g)

# coefficient matrix
# c_1: additive, c_2: recessive, c_3: dominant
contrast <- rbind(
  c(-1, 0, 1), c(-2, 1, 1), c(-1, -1, 2)
)
y <- by(xx, xx$pos, function(x) mmcm.mvt(x$x, x$g,
  contrast))
y <- do.call(rbind, y)[,c(3,7,9)]
y
```

`mmcm.resamp` *The permuted modified maximum contrast method*

Description

This function gives P-value for the permuted modified maximum contrast method.

Usage

```
mmcm.resamp(
  x,
  g,
  contrast,
  alternative = c("two.sided", "less", "greater"),
  nsample = 20000,
  abseps = 0.001,
```

```
  seed = NULL,
  nthread = 2
)
```

Arguments

x	a numeric vector of data values
g	a integer vector giving the group for the corresponding elements of x
contrast	a numeric contrast coefficient matrix for permuted modified maximum contrast statistics
alternative	a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
nsample	specifies the number of resamples (default: 20000)
abseps	specifies the absolute error tolerance (default: 0.001)
seed	a single value, interpreted as an integer; see set.seed() function. (default: NULL)
nthread	sthe number of threads used in parallel computing, or FALSE that means single threading (default: 2)

Details

mmcm.resamp performs the permuted modified maximum contrast method that is detecting a true response pattern under the unequal sample size situation.

$Y_{ij}(i = 1, 2, \ldots; j = 1, 2, \ldots, n_i)$ is an observed response for j-th individual in i-th group.

$\boldsymbol{C}$ is coefficient matrix for permuted modified maximum contrast statistics ($i \times k$ matrix, i: No. of groups, k: No. of pattern).

$$\boldsymbol{C} = (\boldsymbol{c}_1, \boldsymbol{c}_2, \ldots, \boldsymbol{c}_k)^{\mathrm{T}}$$

$\boldsymbol{c}_k$ is coefficient vector of k-th pattern.

$$\boldsymbol{c}_k = (c_{k1}, c_{k2}, \ldots, c_{ki})^{\mathrm{T}} \qquad (\textstyle\sum_i c_{ki} = 0)$$

$M_{\max}$ is a permuted modified maximum contrast statistic.

$$\bar{Y}_i = \frac{\sum_{j=1}^{n_i} Y_{ij}}{n_i}, \bar{\boldsymbol{Y}} = (\bar{Y}_1, \bar{Y}_2, \ldots, \bar{Y}_i, \ldots, \bar{Y}_a)^{\mathrm{T}}, M_k = \frac{\boldsymbol{c}_k^t \bar{\boldsymbol{Y}}}{\sqrt{\boldsymbol{c}_k^t \boldsymbol{c}_k}},$$

$$M_{\max} = \max(M_1, M_2, \ldots, M_k).$$

Consider testing the overall null hypothesis $H_0 : \mu_1 = \mu_2 = \ldots = \mu_i$, versus alternative hypotheses H_1 for response petterns ($H_1 : \mu_1 < \mu_2 < \ldots < \mu_i, \mu_1 = \mu_2 < \ldots < \mu_i, \mu_1 < \mu_2 < \ldots = \mu_i$). The P-value for the probability distribution of $M_{\max}$ under the overall null hypothesis is

$$P\text{-value} = \Pr(M_{\max} > m_{\max} \mid H_0)$$

$m_{\max}$ is observed value of statistics. This function gives distribution of $M_{\max}$ by using the permutation method, follow algorithm:

1. Initialize counting variable: $COUNT = 0$. Input parameters: $NRESAMPMIN$ (minimum resampling count, we set 1000), $NRESAMPMAX$ (maximum resampling count), and ϵ (absolute error tolerance).

2. Calculate $m_{\max}$ that is the observed value of the test statistic.

3. Let $y_{ij}^{(r)}$ donate data, which are sampled without replacement, and independently, form observed value y_{ij}. Where, (r) is suffix of the resampling number $(r = 1, 2, \ldots)$.

4. Calculate $m_{\max}^{(r)}$ from $y_{ij}^{(r)}$. If $m_{\max}^{(r)} > m_{\max}$, then increment the counting variable: $COUNT = COUNT+1$. Calculate approximate P-value $\hat{p}^{(r)} = COUNT/r$, and the simulation standard error $SE(\hat{p}^{(r)}) = \sqrt{\hat{p}^{(r)}(1 - \hat{p}^{(r)})/r}$.

5. Repeat 3–4, while $r > 1000$ and $3.5SE(\hat{p}^{(r)}) < \epsilon$ (corresponding to 99% confidence level), or $NRESAMPMAX$ times. Output the approximate P-value $\hat{p}^{(r)}$.

Value

`statistic`	the value of the test statistic with a name describing it.
`p.value`	the p-value for the test.
`alternative`	a character string describing the alternative hypothesis.
`method`	the type of test applied.
`contrast`	a character string giving the names of the data.
`contrast.index`	a suffix of coefficient vector of the kth pattern that gives permuted modified maximum contrast statistics (row number of the coefficient matrix).
`error`	estimated absolute error and,
`msg`	status messages.

References

Nagashima, K., Sato, Y., Hamada, C. (2011). A modified maximum contrast method for unequal sample sizes in pharmacogenomic studies *Stat Appl Genet Mol Biol.* **10**(1): Article 41. http://dx.doi.org/10.2202/1544-6115.1560

Sato, Y., Laird, N.M., Nagashima, K., et al. (2009). A new statistical screening approach for finding pharmacokinetics-related genes in genome-wide studies. *Pharmacogenomics J.* **9**(2): 137–146. http://www.ncbi.nlm.nih.gov/pubmed/19104505

See Also

`mmcm.mvt`

Examples

```
## Example 1 ##
#  true response pattern: dominant model c=(1, 1, -2)
set.seed(136885)
x <- c(
  rnorm(130, mean =  1 / 6, sd = 1),
  rnorm( 90, mean =  1 / 6, sd = 1),
  rnorm( 10, mean = -2 / 6, sd = 1)
```

```
)
g <- rep(1:3, c(130, 90, 10))
boxplot(
  x ~ g,
  width = c(length(g[g==1]), length(g[g==2]), length(g[g==3])),
  main  = "Dominant model (sample data)",
  xlab  = "Genotype", ylab="PK parameter"
)

# coefficient matrix
# c_1: additive, c_2: recessive, c_3: dominant
contrast <- rbind(
  c(-1, 0, 1), c(-2, 1, 1), c(-1, -1, 2)
)
y <- mmcm.resamp(x, g, contrast, nsample = 20000,
                 abseps = 0.01, seed = 5784324)
y

## Example 2 ##
#  for dataframe
#  true response pattern:
#    pos = 1 dominant  model c=( 1,  1, -2)
#          2 additive  model c=(-1,  0,  1)
#          3 recessive model c=( 2, -1, -1)
set.seed(3872435)
x <- c(
  rnorm(130, mean =  1 / 6, sd = 1),
  rnorm( 90, mean =  1 / 6, sd = 1),
  rnorm( 10, mean = -2 / 6, sd = 1),
  rnorm(130, mean = -1 / 4, sd = 1),
  rnorm( 90, mean =  0 / 4, sd = 1),
  rnorm( 10, mean =  1 / 4, sd = 1),
  rnorm(130, mean =  2 / 6, sd = 1),
  rnorm( 90, mean = -1 / 6, sd = 1),
  rnorm( 10, mean = -1 / 6, sd = 1)
)
g   <- rep(rep(1:3, c(130, 90, 10)), 3)
pos <- rep(c("rsXXXX", "rsYYYY", "rsZZZZ"), each = 230)
xx  <- data.frame(pos = pos, x = x, g = g)

# coefficient matrix
# c_1: additive, c_2: recessive, c_3: dominant
contrast <- rbind(
  c(-1, 0, 1), c(-2, 1, 1), c(-1, -1, 2)
)

y <- by(xx, xx$pos, function(x) mmcm.resamp(x$x, x$g,
  contrast, abseps = 0.02, nsample = 10000))
y <- do.call(rbind, y)[,c(3,7,9)]
y
```

print.mmcm *Print function for mmcm object*

Description

This function print result of function mcm.mvt, mmcm.mvt and mmcm.resamp

Usage

```
## S3 method for class 'mmcm'
print(x, digits = getOption("digits"), ...)
```

Arguments

x	Object of class mmcm, which is result of function mcm.mvt, mmcm.mvt and mmcm.resamp.
digits	a non-null value for digits specifies the minimum number of significant digits to be printed in values. The default, NULL, uses getOption(digits). (For the interpretation for complex numbers see signif.) Non-integer values will be rounded down, and only values greater than or equal to 1 and no greater than 22 are accepted.
...	Further arguments passed to or from other methods.

Details

The case where printed "More than 2 contrast coefficient vectors were selected", some contrast may be unsuitable.

See Also

print.default, mmcm.mvt, mmcm.resamp, mcm.mvt

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