Package: BCHM (via r-universe)

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Title Clinical Trial Calculation Based on BCHM Design

Version 1.00

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Description Users can estimate the treatment effect for multiple subgroups basket trials based on the Bayesian Cluster Hierarchical Model (BCHM). In this model, a Bayesian non-parametric method is applied to dynamically calculate the number of clusters by conducting the multiple cluster classification based on subgroup outcomes. Hierarchical model is used to compute the posterior probability of treatment effect with the borrowing strength determined by the Bayesian non-parametric clustering and the similarities between subgroups. To use this package, 'JAGS' software and 'rjags' package are required, and users need to pre-install them.

Depends R (>= 3.5), rjags

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Suggests testthat

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Contents

BCHM 2
BCHMplot_cluster 4
BCHMplot_post_dist 6
BCHMplot_post_value 7

Index **10**

BCHM *Perform the analysis based on the BCHM design.*

Description

The BCHM computation is based on the Bayesian Cluster Hierarchical Model (BCHM) to perform the non-parametric Bayesian clustering and posterior probability calculation with the Bayesian hierarchical model for binary response data in several subgroups. Due to the potential heterogeneity among subgroups, the exchangeability assumption across all subgroups may not hold. A Bayesian non-parametric method is applied to calculate the number of clusters by conducting the multiple cluster classification based on subgroup outcomes. Due to the MCMC sampling, the clustering result is dynamic. A cluster matrix (Similarity Matrix) is constructed to depict the strength of association between any two subgroups to be classified into the same cluster. The Bayesian hierarchical model is used to compute the posterior probability of treatment effect with the borrowing strength determined by the similarity matrix values calculated from the Bayesian non-parametric clustering.

Usage

```
BCHM(
  nDat,
  xDat,
  mu = 0.2,
  sigma02 = 10,
  sigmaD2 = 0.001,
  alpha = 1e-60,
  d0 = 0.05,
  alpha1 = 50,
  beta1 = 10,
  tau2 = 0.1,
  phi1 = 0.1,
  deltaT = 0.05,
  thetaT = 0.6,
  burnIn = 10000,
  MCIter = 20000,
  MCNum = 20000,
  seed = 1000
)
```

Arguments

nDat	Number of patients in each subgroup.
xDat	Number of responses in each subgroup.
mu	Hyperprior mean for the cluster.
sigma02	Hyperprior variance for the cluster.
sigmaD2	Variance of subgroup response rate.
alpha	Alpha value of the Dirichlet Process determining number of clusters.
d0	Minimum value for the similarity matrix.
alpha1	Prior for borrowing strength gamma(alpha1, beta1) in the hierarchical model.
beta1	Prior for borrowing strength gamma(alpha1, beta1) in the hierarchical model.
tau2	Hyperprior precision parameter of subgroup means in the hierarchical model
phi1	The response rate of the standard treatment.
deltaT	The expected improvement in the response rate over the standard treatment.
thetaT	Threshold value for the inference claiming efficacy.
burnIn	Number of burn_in in MCMC.
MCIter	Number of MCMC iterations.
MCNum	Number of MCMC iterations in the hierarchical model.
seed	Random seed.

Value

The return is a list including three elements: `Samples`, `SMatrix`, and `Result`.

The return list element `Samples` is the sampled posterior response rates of all subgroups.

The return list element `SMatrix` is the similarity matrix of all subgroups.

The return list element `Result` is the calculation results of all subgroups. It has seven columns: the number of responses of each subgroups, the number of patients in each subgroups, the observe response rates of each subgroups, the cluster index of each subgroups, the posterior mean response rates of each subgroups, the probability of Pr(P>Phi1+deltaT) of each subgroups, and the final decision (0: Not rejected the null, 1 Rejected the null). Note: Because a MCMC computation is applied in the clustering calculation, there are many possible clustering configurations. The cluster index in column 4 is the most possible clustering configuration.

See Also

`BCHMplot_cluster` Plot the clustering results of subgroups.

`BCHMplot_post_value` Plot the posterior response of subgroups.

`BCHMplot_post_dist` Plot the posterior distributions of subgroups.

Examples

```
nDat = c(25, 25, 25, 25) # total number of patients
xDat = c(2, 3, 8, 6)  # number of responses
alpha <- 1e-20
d0 <- 0.0
alpha1 = 50
beta1 = 10
tau2 <- 0.1
phi1 <- 0.1
deltaT <- 0.2
thetaT <- 0.60

res <- BCHM(nDat = nDat,
            xDat = xDat,
            alpha = alpha,
            d0 = d0,
            alpha1 = alpha1,
            beta1 = beta1,
            tau2 = tau2,
            phi1 = phi1,
            deltaT = deltaT,
            thetaT = thetaT,
            burnIn = 100,
            MCIter = 200,
            MCNum = 1000,
            seed = 1000
)
print(res$SMatrix)
print(res$Result)
col <- res$Result[,4]

BCHMplot_cluster(res, col, pch=16)
BCHMplot_post_value(res, col, HPD = 0.8)
BCHMplot_post_dist(res, col, lty=1:length(nDat), lwd =3, xlim=c(0, 0.8))
```

`BCHMplot_cluster` *Plot the clustering results of subgroups.*

Description

plot the observed response rate versus subgroup ID with clusters coded by the color of dots.

Usage

```
BCHMplot_cluster(
  res,
  col = res$Result[, 4],
  pch = 16,
```

```
  xlim = c(0, dim(res$Result)[1] + 2),
  ylim = c(0, 1),
  cex = 2,
  ...
)
```

Arguments

res	BCHM calculation results.
col	Color vector
pch	pch vector
xlim	X-axis range
ylim	Y-axis range
cex	size of points
...	other options

Value

None

See Also

BCHM Perform the analysis based on the BCHM design.

BCHMplot_post_value Plot the posterior response of subgroups.

BCHMplot_post_dist Plot the posterior distributions of subgroups.

Examples

```
nDat = c(25, 25, 25, 25) # total number of patients
xDat = c(2, 3, 8, 6)  # number of responses
alpha <- 1e-20
d0 <- 0.0
alpha1 = 50
beta1 = 10
tau2 <- 0.1
phi1 <- 0.1
deltaT <- 0.2
thetaT <- 0.60

res <- BCHM(nDat = nDat,
            xDat = xDat,
            alpha = alpha,
            d0 = d0,
            alpha1 = alpha1,
            beta1 = beta1,
            tau2 = tau2,
            phi1 = phi1,
            deltaT = deltaT,
            thetaT = thetaT,
```

```
            burnIn = 100,
            MCIter = 200,
            MCNum = 1000,
            seed = 1000
)
print(res$SMatrix)
print(res$Result)
col <- res$Result[,4]

BCHMplot_cluster(res, col, pch=16)
```

`BCHMplot_post_dist` *Plot the posterior distributions of subgroups.*

Description

plot the posterior distribution by subgroup ID

Usage

```
BCHMplot_post_dist(
  res,
  col = res$Result[, 4],
  lty = 1:dim(res$Result)[1],
  lwd = 2,
  xlim = c(0, 1),
  ylim = c(0, 20),
  ...
)
```

Arguments

`res`	BCHM calculation results.
`col`	Color vector
`lty`	line types
`lwd`	line width
`xlim`	X-axis range
`ylim`	Y-axis range
`...`	other options

Value

None

See Also

BCHM Perform the analysis based on the BCHM design.

BCHMplot_cluster Plot the clustering results of subgroups.

BCHMplot_post_value Plot the posterior response of subgroups.

Examples

```
nDat = c(25, 25, 25, 25) # total number of patients
xDat = c(2, 3, 8, 6)  # number of responses
alpha <- 1e-20
d0 <- 0.0
alpha1 = 50
beta1 = 10
tau2 <- 0.1
phi1 <- 0.1
deltaT <- 0.2
thetaT <- 0.60

res <- BCHM(nDat = nDat,
            xDat = xDat,
            alpha = alpha,
            d0 = d0,
            alpha1 = alpha1,
            beta1 = beta1,
            tau2 = tau2,
            phi1 = phi1,
            deltaT = deltaT,
            thetaT = thetaT,
            burnIn = 100,
            MCIter = 200,
            MCNum = 1000,
            seed = 1000
)
print(res$SMatrix)
print(res$Result)
col <- res$Result[,4]

BCHMplot_post_dist(res, col, lty=1:length(nDat), lwd =3, xlim=c(0, 0.8))
```

BCHMplot_post_value *Plot the posterior response of subgroups.*

Description

plot the posterior response rate with its highest probability density (HPD) interval by subgroup ID

Usage

```
BCHMplot_post_value(
  res,
  col = res$Result[, 4],
  pch = c(19, 4),
  cex = 2,
  HPD = 0.95,
  xlim = c(0, dim(res$Result)[1] + 2),
  ylim = c(0, 1),
  ObsMean = FALSE,
  ...
)
```

Arguments

res	BCHM calculation results.
col	Color vector
pch	pch vector pch[1] Posterior mean pch[2] Observed mean
cex	size of points
HPD	Highest Posterior Density level for drawing (NA: No HPD drawing)
xlim	X-axis range
ylim	Y-axis range
ObsMean	Draw the observed mean of subgroups if this parameter is TRUE
...	other options

Value

None

See Also

BCHM Perform the analysis based on the BCHM design.

BCHMplot_cluster Plot the clustering results of subgroups.

BCHMplot_post_dist Plot the posterior distributions of subgroups.

Examples

```
nDat = c(25, 25, 25, 25) # total number of patients
xDat = c(2, 3, 8, 6)  # number of responses
alpha <- 1e-20
d0 <- 0.0
alpha1 = 50
beta1 = 10
tau2 <- 0.1
phi1 <- 0.1
deltaT <- 0.2
```

```
thetaT <- 0.60

res <- BCHM(nDat = nDat,
            xDat = xDat,
            alpha = alpha,
            d0 = d0,
            alpha1 = alpha1,
            beta1 = beta1,
            tau2 = tau2,
            phi1 = phi1,
            deltaT = deltaT,
            thetaT = thetaT,
            burnIn = 100,
            MCIter = 200,
            MCNum = 1000,
            seed = 1000
)
print(res$SMatrix)
print(res$Result)
col <- res$Result[,4]

BCHMplot_post_value(res, col, HPD = 0.8)
```

Index

BCHM, 2, *5*, *7*, *8*
BCHMplot_cluster, *3*, 4, *7*, *8*
BCHMplot_post_dist, *3*, *5*, 6, *8*
BCHMplot_post_value, *3*, *5*, 7, *7*