Package ‘BCHM’

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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.

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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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>nDat</td>
<td>Number of patients in each subgroup.</td>
</tr>
<tr>
<td>xDat</td>
<td>Number of responses in each subgroup.</td>
</tr>
<tr>
<td>mu</td>
<td>Hyperprior mean for the cluster.</td>
</tr>
<tr>
<td>sigma02</td>
<td>Hyperprior variance for the cluster.</td>
</tr>
<tr>
<td>sigmaD2</td>
<td>Variance of subgroup response rate.</td>
</tr>
</tbody>
</table>
### Value

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

- **Samples**: The sampled posterior response rates of all subgroups.
- **SMatrix**: The similarity matrix of all subgroups.
- **Result**: The calculation results of all subgroups. It has seven columns: the number of responses of each subgroup, the number of patients in each subgroup, the observed response rates of each subgroup, the cluster index of each subgroup, the posterior mean response rates of each subgroup, the probability of Pr(P>\(\Phi_1+\delta T\)) of each subgroup, 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

```r
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
```
```r
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))
```

---

### Description

Plot the clustering results of subgroups.

### Usage

```r
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


BCHMplot_cluster

- 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

```r
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

```r
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

\[
n\text{Dat} = c(25, 25, 25, 25) \quad \# \text{total number of patients}
\]
\[
x\text{Dat} = c(2, 3, 8, 6) \quad \# \text{number of responses}
\]
\[
alpha \leftarrow 1e-20
\]
\[
d0 \leftarrow 0.0
\]
\[
alpha1 = 50
\]
\[
beta1 = 10
\]
\[
tau2 \leftarrow 0.1
\]
\[
phi1 \leftarrow 0.1
\]
\[
deltaT \leftarrow 0.2
\]
\[
thetaT \leftarrow 0.60
\]

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,
BCHMplot_post_value

```r
xlim = c(0, dim(res$Result)[1] + 2),
ylim = c(0, 1),
ObsMean = FALSE,
```

Arguments

- `res`: BCHM calculation results.
- `col`: Color vector
- `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

```r
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

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