Package ‘bacistool’

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Title Bayesian Classification and Information Sharing (BaCIS) Tool for the Design of Multi-Group Phase II Clinical Trials
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Description Provides the design of multi-group phase II clinical trials with binary outcomes using the hierarchical Bayesian classification and information sharing (BaCIS) model. Subgroups are classified into two clusters on the basis of their outcomes mimicking the hypothesis testing framework. Subsequently, information sharing takes place within subgroups in the same cluster, rather than across all subgroups. This method can be applied to the design and analysis of multi-group clinical trials with binary outcomes.
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**bacisCheckDIC**

Compute the DIC value for the classification model.

**Description**

In this function, the classification model is applied using the input parameter values and the DIC value is calculated.

**Usage**

```r
caxisCheckDIC(numGroup, tau1, tau2, phi1, phi2,
               MCNum, nDat, xDat, seed)
```

**Arguments**

- `numGroup`: Number of subgroups in the trial.
- `tau1`: The precision parameter of subgroups clustering for the classification model.
- `tau2`: The precision prior for the latent variable for the classification.
- `phi1`: Center for the low response rate cluster.
- `phi2`: Center for the high response rate cluster.
- `MCNum`: The number of MCMC sampling iterations.
- `nDat`: The vector of total sample sizes of all subgroups.
- `xDat`: The vector of the response numbers of all subgroups.
- `seed`: Random seed value. If its value is NA, a time dependent random seed is generated and applied.

**Value**

The classification model is applied using the input parameter values and the DIC value is returned.

**Author(s)**

Nan Chen and J. Jack Lee / Department of Biostatistics UT MD Anderson Cancer Center
Examples

```r
# An example to compute the DIC value.
library(bacistool)
result<-bacisCheckDIC(numGroup=5,
    tau1=NA,
    tau2=.001,
    phi1=0.1, phi2=0.3,
    MCNum=5000,
    nDat=c(25,25,25,25,25),
    xDat=c(3,4,3,8,7),
    seed=100
)
```

bacisClassification  
*Conduct classification for subgroups.*

Description

The classification model is conducted based on the BaCIS method and the subgroups are classified into two clusters: high response rate cluster and low response rate cluster.

Usage

```r
bacisClassification(numGroup, tau1, tau2, phi1, phi2,
    clusterCutoff, MCNum, nDat, xDat, seed)
```

Arguments

- `numGroup` Number of subgroups in the trial.
- `tau1` The precision parameter of subgroups clustering for the classification model.
- `tau2` The precision prior for the latent variable for the classification.
- `phi1` Center for the low response rate cluster.
- `phi2` Center for the high response rate cluster.
- `clusterCutoff` The cutoff value of the cluster classification. If its value is NA, adaptive classification is applied.
- `MCNum` The number of MCMC sampling iterations.
- `nDat` The vector of total sample sizes of all subgroups.
- `xDat` The vector of the response numbers of all subgroups.
- `seed` Random seed value. If its value is NA, a time dependent random seed is generated and applied.
Value

The classification model is applied using the input parameter values and subgroup outcomes. The classification results are returned. The return list includes highResponseGroup and lowResponseGroup index values.

Author(s)

Nan Chen and J. Jack Lee / Department of Biostatistics UT MD Anderson Cancer Center

Examples

```r
## An example to conduct subgroup classification.
library(bacistool)
result<-bacisClassification(numGroup=5,
                           tau1=NA,
                           tau2=.001,
                           phi1=0.1, phi2=0.3,
                           clusterCutoff = NA,
                           MCNum=5000,
                           nDat=c(25,25,25,25,25),
                           xDat=c(3,4,3,8,7),seed=100)
```

Description

The bacisOneTrial function takes data and parameter values as input. It conducts a trial computation based on the BaCIS model. It calls the JAGS for the Bayesian MCMC sampling for the subgroup classification and hierarchical model information borrowing. It illustrates plots of the classification results and the posterior response distributions of subgroups, and returns the inference results.

Usage

```r
bacisOneTrial(numGroup, tau1, tau2, phi1, phi2, tau4, alpha, beta,
               clusterCutoff, finalCutoff, MCNum, nDat, xDat, cols,
               clusterCols, ylim, seed)
```
Arguments

numGroup  Number of subgroups in the trial.
tau1  The precision parameter of subgroups clustering for the classification model.
tau2  The precision prior for the latent variable for the classification.
phi1  Center for the low response rate cluster.
phi2  Center for the high response rate cluster.
tau4  The precision prior for the center of the cluster in the information borrowing model.
alpha  Hyperprior parameters alpha to control the magnitude of information borrowing model.
beta  Hyperprior parameters beta to control the magnitude of the information borrowing model.
clusterCutoff  The cutoff value of the cluster classification. If its value is NA, adaptive classification is applied.
finalCutoff  The posterior cutoff value of the final inference for each subgroup.
MCNum  The number of MCMC sampling iterations.
ndat  The vector of total sample sizes of all subgroups.
xdat  The vector of the response numbers of all subgroups.
cols  The color vector of all subgroups in the illustration.
clusterCols  The color vector of all clusters in the illustration.
ylim  The maximum Y-axis value in the illustration.
seed  Random seed value. If its value is NA, a time dependent random seed is generated and applied.

Value

The trial simulation illustrates the plot of posterior distribution of classification, posterior response rates of all subgroups, and the posterior response distributions of two clusters.

It also return a matrix including the following information of all subgroups:

\[
\text{Prob}(p_i > \phi_1)
\]
\[
\text{Prob}(p_i > \phi_2)
\]
\[
\theta > 0
\]
\[
\text{Classified to high response cluster}
\]
\[
\text{The treatment is effective}
\]
\[
\text{Posterior Resp.}
\]
bacisPlotClassification

Plot the posterior density of $\theta$ in the classification model.

Description

The classification model is conducted based on the BaCIS method and the posterior density of $\theta$ is plotted.
bacisPlotClassification

Usage

bacisPlotClassification(numGroup, tau1, tau2, phi1, phi2,
  clusterCutoff, MCNum, nDat, xDat, cols, seed)

Arguments

numGroup  Number of subgroups in the trial.
tau1      The precision parameter of subgroups clustering for the classification model.
tau2      The precision prior for the latent variable for the classification.
phi1      Center for the low response rate cluster.
phi2      Center for the high response rate cluster.
clusterCutoff The cutoff value of the cluster classification. If its value is NA, adaptive classification is applied.
MCNum     The number of MCMC sampling iterations.
nDat      The vector of total sample sizes of all subgroups.
xDat      The vector of the response numbers of all subgroups.
cols      The color vector of all subgroups in the illustration.
seed      Random seed value. If its value is NA, a time dependent random seed is generated and applied.

Value

The classification model is conducted using the input parameter values and subgroup outcomes. The posterior density of $\theta$ is plotted.

Author(s)

Nan Chen and J. Jack Lee / Department of Biostatistics UT MD Anderson Cancer Center

Examples

## Compute the posterior distribution of $\theta$.
library(bacisTool)
bacisPlotClassification(numGroup=5,
  tau1=NA,
  tau2=.001,
  phi1=0.1, phi2=0.3,
  clusterCutoff=NA,
  MCNum=5000,
  nDat=c(25,25,25,25,25),
  xDat=c(3,4,3,8,7),
  cols = c("brown", "red", "orange", "blue", "green")
)
bacisSubgroupPosterior

**Description**

In this function, a trial computation is conducted based on the BaCIS model. It calls the JAGS for the Bayesian MCMC sampling for the subgroup classification and hierarchical model information borrowing. The response rate posterior distributions of subgroups are returned from this function.

**Usage**

```
bacisSubgroupPosterior(numGroup, tau1, tau2, phi1, phi2, tau4, alpha, beta, clusterCutoff, MCNum, nDat, xDat, seed)
```

**Arguments**

- **numGroup**: Number of subgroups in the trial.
- **tau1**: The precision parameter of subgroups clustering for the classification model.
- **tau2**: The precision prior for the latent variable for the classification.
- **phi1**: Center for the low response rate cluster.
- **phi2**: Center for the high response rate cluster.
- **tau4**: The precision prior for the center of the cluster in the information borrowing model.
- **alpha**: Hyperprior parameters alpha to control the magnitude of information borrowing model.
- **beta**: Hyperprior parameters beta to control the magnitude of the information borrowing model.
- **clusterCutoff**: The cutoff value of the cluster classification. If its value is NA, adaptive classification is applied.
- **MCNum**: The number of MCMC sampling iterations.
- **nDat**: The vector of total sample sizes of all subgroups.
- **xDat**: The vector of the response numbers of all subgroups.
- **seed**: Random seed value. If its value is NA, a time dependent random seed is generated and applied.

**Value**

The MCMC sampling data of the response rate posterior distributions of all subgroups is returned as an matrix format. Each column of the return matrix corresponds to the response rate distribution of one subgroup.
Author(s)

Nan Chen and J. Jack Lee / Department of Biostatistics UT MD Anderson Cancer Center

Examples

```r
## Compute the response rate posterior distributioni
## of each subgroup using the BaCIS method
## Not run:
library(bacistool)
result<-bacisSubgroupPosterior(numGroup=5,
    tau1=NA,
    tau2=.001,
    phi1=0.1, phi2=0.3,
    tau4=0.1,
    alpha=50,
    beta=20,
    clusterCutoff=NA,
    MCNum=5000,
    nDat=c(25,25,25,25,25),
    xDat=c(3,4,3,8,7))
```

## End(Not run)

---

**bacisThetaPosterior**  
*Compute the posterior distribution of $\theta$ in the classification model.*

Description

The classification model is conducted based on the BaCIS method and the posterior distribution of $\theta$ is returned for further analyses.

Usage

```r
bacisThetaPosterior(numGroup, tau1, tau2, phi1, phi2,
                     MCNum, nDat, xDat, seed)
```

Arguments

- **numGroup**: Number of subgroups in the trial.
- **tau1**: The precision parameter of subgroups clustering for the classification model.
- **tau2**: The precision prior for the latent variable for the classification.
- **phi1**: Center for the low response rate cluster.
phi2  Center for the high response rate cluster.
MCNum  The number of MCMC sampling iterations.
ndat  The vector of total sample sizes of all subgroups.
xdat  The vector of the response numbers of all subgroups.
seed  Random seed value. If its value is NA, a time dependent random seed is generated and applied.

Value

The classification model is conducted using the input parameter values and subgroup outcomes. The posterior distribution of \( \theta \) is returned. The returned value is an matrix in which each column corresponds the data of one subgroup.

Author(s)

Nan Chen and J. Jack Lee / Department of Biostatistics UT MD Anderson Cancer Center

Examples

```r
## Conduct subgroup classification and
## compute the posterior distribution of \( \theta \).

library(bacistoolI
result <- bacisThetaPosterior(numGroup=5,
                           tau1=NA,
                           tau2=.001,
                           phi1=0.1, phi2=0.3,
                           MCNum=5000,
                           ndat=c(25,25,25,25,25),
                           xDat=c(3,4,3,8,7)
)
```
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