Package: bacistool (via r-universe)

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Type Package

Title Bayesian Classification and Information Sharing (BaCIS) Tool for the Design of Multi-Group Phase II Clinical Trials

Version 1.0.0

Author Nan Chen and J. Jack Lee

Maintainer J. Jack Lee <jjlee@mdanderson.org>

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. Reference: Nan Chen and J. Jack Lee (2019) <doi:10.1002/bimj.201700275>.

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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

```
bacisCheckDIC(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

```
## 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 subgroupos are classified into two clusters: high respone rate cluster and low response rate cluster.

Usage

```
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 vlaues.

Author(s)

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

Examples

```
## 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)
```

`bacisOneTrial` *Running one trial computation based on the BaCIS model.*

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 classficaiton results and the posterior response distributions of subgroups, and returns the inference results.

Usage

```
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 classificaiton, 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:

Prob(p_i>phi_1)	Posterior probability of response probability being greater than phi_1.
Prob(p_i>phi_2)	Posterior probability of response probability being greater than phi_2.
theta>0	Posterior probability of latent variable being greater than 0.
Classified to high response cluster	0: Classified into the lower response cluster, 1: classified into the high response cluster.
The treatment is effective	0: The subgroup is not effective, 1: the subgroup is effective.
Posterior Resp.	Posterior response rates of subgroups.
Observed Resp.	Observe response rates of subgroups.
Number of response	Number of responses of subgroups.
Total sample size	Total sample sizes of subgroups.
Effective sample size	Effective sample sizes of subgroups.

Author(s)

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

Examples

```
## Not run:
## An example for running a simulation trial using the BaCIS method
library(bacistool)
bacisOneTrial(
  numGroup=5,
  tau1=NA,
  tau2=.001,
  phi1=0.1, phi2=0.3,
  tau4=0.1,
  alpha=50,
  beta=2,
  clusterCutoff = NA,
  finalCutoff = 0.92,
  MCNum=50000,
  nDat=c(25,25,25,25,25),
  xDat=c(2,3,7,6,10),
  cols=c("brown","red","orange","blue","green"),
  clusterCols=c(6,4),
  yLim=22,
  seed=100
)

## End(Not run)
```

---

bacisPlotClassification

Plot the posterior density of θ in the classification model.

Description

The classification model is conducted based on the BaCIS method and the posterior density of θ is plotted.

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 θ is plotted.

Author(s)

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

Examples

```
## Compute the posterior distribution of \eqn{\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` *Compute the posterior distribution of response rates of subgroups using the BaCIS method.*

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

```
## 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 θ in the classification model.*

Description

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

Usage

```
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 θ 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

```
## Conduct subgroup classification and
## compute the posterior distribution of \eqn{\theta}.

library(bacistool)
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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