Package: FBCRM (via r-universe)

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Type Package

Title Phase I Optimal Dose Assignment using the FBCRM and MFBCRM Methods

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Description Performs dose assignment and trial simulation for the FBCRM (Fully Bayesian Continual Reassessment Method) and MFBCRM (Mixture Fully Bayesian Continual Reassessment Method) phase I clinical trial designs. These trial designs extend the Continual Reassessment Method (CRM) and Bayesian Model Averaging Continual Reassessment Method (BMA-CRM) by allowing the prior toxicity skeleton itself to be random, with posterior distributions obtained from Markov Chain Monte Carlo. On average, the FBCRM and MFBCRM methods outperformed the CRM and BMA-CRM methods in terms of selecting an optimal dose level across thousands of randomly generated simulation scenarios. Details on the methods and results of this simulation study are available on request, and the manuscript is currently under review.

License GPL-2

Encoding UTF-8

Imports Rcpp (>= 0.12.18)

LinkingTo Rcpp, RcppArmadillo

RoxygenNote 7.1.1

NeedsCompilation yes

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`FBCRMSimTrial` *Provides simulation results using FBCRM*

Description

Provides simulation results using FBCRM

Usage

```
FBCRMSimTrial(max_samp, Cohort, ptrue, mu, p_rho, sigma, mtd, p_u, B, M)
```

Arguments

`max_samp`	Total number of patients recruited/will be recruited in the trial.
`Cohort`	Number of patients within each cohort.
`ptrue`	True toxicity probability vector.
`mu`	Prior expected toxicity probability at each dose.
`p_rho`	Prior probability that two dose-toxicity probabilities will not cluster together.
`sigma`	Prior standard deviation for the parameter alpha.
`mtd`	Maximum Tolerated dose toxicity probability (pre defined).
`p_u`	Cut-off toxicity probability for first dose.
`B`	Number of Iterations to run for MCMC.
`M`	Number of simulations to run.

Value

A list containing (1) Design parameters and prior hyperparameters used for simulating the trials and (2) a summary of the trial simulation results including the percent of times each dose was selected and the average number of toxicities seen in the trial.

Examples

```
max_samp=15
Cohort=3
ptrue=c(0.01,0.05,0.15,0.3,0.45,0.5,0.6,0.8)
mu=seq(0.1,0.8,0.1)
p_rho=0.9
sigma = 2
mtd = 0.3
p_u=0.9
B=200 ##Number of iterations, Change to 2k
M=10 ##Number of simulations, Change to larger
Z=FBCRMSimTrial(max_samp,Cohort,ptrue,mu,p_rho,sigma,mtd,p_u,B,M)
Z
```

GetFBCRM *Provides the optimal dose level closest to the mtd where the next cohort of patients should be allotted based on the data.*

Description

Provides the optimal dose level closest to the mtd where the next cohort of patients should be allotted based on the data.

Usage

```
GetFBCRM(X, Y, Cohort, mu, p_rho, sigma, mtd, B, p_u)
```

Arguments

X	Vector of patients allotted to each dose level.
Y	Vector of toxicity events in each dose.
Cohort	Number of patients within each cohort.
mu	Prior expected toxicity probability at each dose.
p_rho	Prior probability that two dose-toxicity probabilities will not cluster together.
sigma	Prior standard deviation for the parameter alpha.
mtd	Maximum Tolerated dose toxicity probability (pre defined).
B	Number of Iterations to run for MCMC.
p_u	Cut-off toxicity probability for first dose.

Value

A list containing (1) Design parameters and prior hyperparameters used for running the trials and (2) a posterior summary of the resuls, including the next dose to assign patients to.

Examples

```
X=c(3, 6, 3, 3, 3, 9, 15, 6)
Y=c(1, 0, 1, 0, 0, 2,  4, 5)
Cohort=3
mu=seq(0.1,0.8,0.1)
p_rho=0.9
sigma = 2
mtd = 0.3
B=2000 ##Number of iterations
p_u=0.9
Z=GetFBCRM(X, Y, Cohort, mu, p_rho, sigma, mtd, B, p_u)
Z
```

`GetMFBCRM` *Provides the optimal dose level closest to the mtd where the next cohort of patients should be allotted based on the data*

Description

Provides the optimal dose level closest to the mtd where the next cohort of patients should be allotted based on the data

Usage

```
GetMFBCRM(X, Y, Cohort, mu_mat, p_rho, sigma, mtd, B, p_u)
```

Arguments

`X`	Vector of patients allotted to each dose level .
`Y`	Vector of toxicity events in each dose.
`Cohort`	Number of patients within each cohort.
`mu_mat`	Prior expected toxicity probability matrix at each dose.
`p_rho`	Prior probability that two dose-toxicity probabilities will not cluster together.
`sigma`	Prior standard deviation for the parameter alpha.
`mtd`	Maximum Tolerated dose toxicity probability (pre defined).
`B`	Number of Iterations to run for MCMC.
`p_u`	Cut-off toxicity probability for first dose

Value

A list containing (1) Design parameters and prior hyperparameters used for running the trials and (2) a posterior summary of the resuls, including the next dose to assign patients to.

Examples

```
X=c(3, 6, 3, 3, 3, 9, 15, 6)
Y=c(1, 0, 1, 0, 0, 2,  4, 5)
Cohort=3
##Skeletons for 8 doses
mu1=c(0.02,0.06,0.08,0.12,0.2,0.3,0.4,0.5)
mu2=c(0.01,0.05,0.09,0.14,0.18,0.22,0.26,0.30)
mu3=c(0.10,0.20,0.30,0.40,0.50,0.60,0.70,0.80)
mu4=c(0.20,0.30,0.40,0.50,0.60,0.65,0.70,0.75)
mu_mat=matrix(c(mu1,mu2,mu3,mu4),nrow = 4,byrow = TRUE)
p_rho=0.9
sigma = 2
mtd = 0.3
B=2000 ##Number of iterations
p_u=0.9
Z=GetMFBCRM(X, Y, Cohort, mu_mat, p_rho, sigma, mtd, B, p_u)
Z
```

`MFBCRMSimTrial` *Provides simulation results using MFBCRM*

Description

Provides simulation results using MFBCRM

Usage

```
MFBCRMSimTrial(max_samp, Cohort, ptrue, mu_mat, p_rho, sigma, mtd, p_u, B, M)
```

Arguments

`max_samp`	Total number of patients recruited/will be recruited in the trial.
`Cohort`	Number of patients within each cohort.
`ptrue`	True toxicity probability vector.
`mu_mat`	Prior expected toxicity probability matrix at each dose.
`p_rho`	Prior probability that two dose-toxicity probabilities will not cluster together.
`sigma`	Prior standard deviation for the parameter alpha.
`mtd`	Maximum Tolerated dose toxicity probability (pre defined).
`p_u`	Cut-off toxicity probability for first dose.
`B`	Number of Iterations to run for MCMC.
`M`	Number of simulations to run.

Value

A list containing (1) Design parameters and prior hyperparameters used for simulating the trials and (2) a summary of the trial simulation results including the percent of times each dose was selected and the average number of toxicities seen in the trial.

Examples

```
max_samp=15   ##Change to larger size
Cohort=3
ptrue=c(0.01,0.05,0.15,0.3,0.45,0.5,0.6,0.8)
##Skeletons for 8 doses
mu1=c(0.02,0.06,0.08,0.12,0.2,0.3,0.4,0.5)
mu2=c(0.01,0.05,0.09,0.14,0.18,0.22,0.26,0.30)
mu3=c(0.10,0.20,0.30,0.40,0.50,0.60,0.70,0.80)
mu4=c(0.20,0.30,0.40,0.50,0.60,0.65,0.70,0.75)
mu_mat=matrix(c(mu1,mu2,mu3,mu4),nrow = 4,byrow = TRUE)
p_rho=0.9
sigma = 2
mtd = 0.3
p_u=0.9
B=200 ##Number of iterations, change to 2k
M=10 ##Number of simulations, change to larger
Z=MFBCRMSimTrial(max_samp,Cohort,ptrue,mu_mat,p_rho,sigma,mtd,p_u,B,M)
Z
```

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