Package: midas2 (via r-universe)

September 10, 2024

Type Package

Title An Information Borrowing Drug-Combination Bayesian Platform Design(MIDAS-2)

Version 0.1.0

Author Su Liwen

Maintainer Su Liwen <cpusullivan@163.com>

Description An Information borrowing drug-combination Bayesian platform design with subgroup exploration and hierarchical constrain.

License GPL-3

Encoding UTF-8

LazyData true

Imports MCMCpack,coda,R2jags

RoxygenNote 7.1.2

Repository https://sullivan0147.r-universe.dev

RemoteUrl https://github.com/sullivan0147/midas2

RemoteRef HEAD

RemoteSha aae8d4c55cf5b798ee80672c3d3fc843fed34871

Contents

`hc_platform` *An Information Borrowing Drug-Combination Bayesian Platform Design(MIDAS-2)*

Description

An Information borrowing drug-combination Bayesian platform design with subgroup exploration and hierarchical constrain.

Usage

```
hc_platform(seed, p, p_tox)
```

Arguments

`seed`	set a random seed to maintain the repeatability of the simulation results.
`p`	a matrix indicating the efficacy. Row number represents the number of candidate drugs.
`p_tox`	a vector indicating the toxicity.

Value

term.tox the indicator of whether early stopping for toxicity

term.fut the indicator of whether early stopping for futility

term.eff the indicator of whether early stopping for efficacy

final.eff a vector of final decision, either efficacy or inefficacy

post.subg subgroup analysis for treatments

post.sign signature analysis for treatments

post.spike posterior estimation for spike parameters

best selection of best treatment for each subgroup

Examples

```
p0 <- c(    0.1,    0.1,    0.1,   0.1)
p1 <- c(    0.1,    0.1,    0.1,   0.1)
p2 <- c(    0.1,    0.1,    0.1,   0.1)
p3 <- c(    0.1,    0.1,    0.1,   0.1)
p4 <- c(    0.1,    0.1,    0.1,   0.1)
p5 <- c(    0.1,    0.1,    0.1,   0.1)
p6 <- c(    0.1,    0.1,    0.1,   0.1)
p7 <- c(    0.1,    0.1,    0.1,   0.1)
p <- rbind(p0, p1, p2, p3, p4, p5, p6, p7)
p_tox <- c(0.1,0.1,0.1,0.1,0.1,0.1,0.1,0.1)
```

```
# consider 7 candidate drugs with 4 subgroups
result <- hc_platform(seed=12,p,p_tox)
result
```

Index