Package ‘smartDesign’

August 12, 2021

Type Package
Title Sequential Multiple Assignment Randomized Trial Design
Version 0.72
Date 2021-8-10
Description SMART trial design, as described by He, J., McClish, D., Sabo, R. (2021) <doi:10.1080/19466315.2021.1883472>, includes multiple stages of randomization, where participants are randomized to an initial treatment in the first stage and then subsequently re-randomized between treatments in the following stage.
License GPL (>= 3)
Depends R (>= 3.6.0), methods, graphics, stats
Imports knitr
NeedsCompilation no
RoxygenNote 7.1.0
VignetteBuilder knitr
URL https://cran.r-project.org/package=smartDesign
Suggests testthat
Author Jason Sinnwell [aut, cre] (<https://orcid.org/0000-0003-1964-5522>), Jun(Jessie) He [aut] (<https://orcid.org/0000-0003-1831-1168>), Abraham Eyman Casey [aut]
Maintainer Jason Sinnwell <sinnwell.jason@mayo.edu>
Repository CRAN
Date/Publication 2021-08-12 09:20:02 UTC

R topics documented:

  powerDTR ................................................................. 2
  powerSST ................................................................. 3
  smartDTR ................................................................. 4
  smartSST ................................................................. 5

Index 7
powerDTR  

*Power Dynamic Treatment Regimen (DTR) Trial design clinical trial calculations*

**Description**

Power Calculations Comparing two Dynamic Treatment Regimen (DTR) Trial design clinical trial calculations

**Usage**

```r
powerDTR(dtr1, dtr2, pG_A1 = 0.8, pG_A2 = 0.8, alpha=0.05)
```

**Arguments**

- `dtr1`: an object of smartDTR class, created by function of the same name
- `dtr2`: an object of smartDTR class, created by function of the same name
- `pG_A1`: probability of response to therapy given assignment to A1
- `pG_A2`: probability of response to therapy given assignment to A2
- `alpha`: accepted type-I error rate for power calculations

**Details**

more details on power DTR

**Value**

An object of the powerDTR S3 class, with the following elements:

- `powerdat`: data.frame with sens, spec, mu, sigsq and sample size, power

**Author(s)**

Jun (Jessie) He, Aberaham Eyman-Casey, Jason P. Sinnwell, Mayo Clinic

**Examples**

```r
mumat13 <- cbind(G1=c(30,35), G0=c(20,28))
varmat13 <- cbind(G1=c(100,100),G0=c(100,100))
dtr13 <- smartDTR(mu_Barm=mumat13, sigsq_Barm=varmat13, Barm=c(1,3), nsubject=252, pG_A1=0.8)
mumat24 <- cbind(G1=c(25,32), G0=c(18,23))
varmat24 <- cbind(G1=c(100,100),G0=c(100,100))
dtr24 <- smartDTR(mu_Barm=mumat24, sigsq_Barm=varmat24, Barm=c(2,4), nsubject=252, pG_A1=0.8, pG_A2=0.8)
```
powerSST

Power for Single Sequential Treatment (SST) Trial design clinical trial calculations

Description

Power Calculations Comparing two Single Sequential Treatment Treatment (SST) Trial design clinical trial calculations

Usage

```r
powerSST(sst1, sst2, pG_A1 = 0.8, pG_A2 = 0.8, alpha=0.05)
```

Arguments

- `sst1`: an object of smartSST class, created by function of the same name
- `sst2`: an object of smartSST class, created by function of the same name
- `pG_A1`: probability of response to therapy given assignment to A1
- `pG_A2`: probability of response to therapy given assignment to A2
- `alpha`: accepted type-I error rate for power calculations

Details

more details to come

Value

An object of the powerSST S3 class, with the following elements:

- `powerdat`: data.frame with sens, spec, mu, sigsq and sample size, power

Author(s)

Jun (Jessie) He, Aberaham Eyman-Casey, Jason P. Sinnwell, Mayo Clinic

Examples

```r
sst1 <- smartSST(mu_Barm=c(G1=30, G0=20), sigsq_Barm=c(G1=16,G0=16), Barm=1, sens=seq(.6, 1, by=.1), spec=seq(.6, 1, by=.1), nsubject=252)

sst2 <- smartSST(mu_Barm=c(G1=20, G0=30), sigsq_Barm=c(G1=16,G0=16), Barm=2, sens=seq(.6, 1, by=.1), spec=seq(.6, 1, by=.1), nsubject=252)
```
psst12 <- powerSST(sst1, sst2)
print(psst12) ## plot(psst12)

smartDTR <- Dynamic Treatment Regimen (DTR) Trial design clinical trial calculations

Description
Dynamic Treatment Regimen (DTR) Trial design clinical trial calculations

Usage
smartDTR(mu_Barm=cbind(G1=c(30,25), G0=c(20,20)),
sigma_Barm=cbind(G1=c(100,100), G0=c(100,100)),
nsubject=500, Barm=c(1,3), type="continuous",
sens=seq(0.5,1, by=0.1), spec=seq(0.5, 1, by=0.1),
pG_A1 = 0.8, pG_A2 = 0.8, pran_A1 = 0.5,
pran_Barm = c(0.5, 0.5))

Arguments
mu_Barm matrix of two named vectors of the means for the two B arms (columns) for the smart DTR trial, with rows as 'G1' and 'G0'
sigma_Barm matrix of two named vectors of the variances (sigma-squared) for the two B levels (columns) for the smart DTR trial, with rows as 'G1' and 'G0'
nsubject total sample size for the trial
Barm for the second phase of the trial, the 'B' levels for which the DTR means/variances apply
type trial response variable type; only continuous is implemented currently
sens range of sensitivity for smart SST calculations; (0,1]
spec range of specificity for smart SST calculations; (0,1]
pG_A1 probability of response to therapy given assignment to A1
pG_A2 probability of response to therapy given assignment to A2
pran_A1 probability of random assignment to A1
pran_Barm probability of assignment to Barms

Details
see details in the reference
**smartSST**

**Value**

An object of the smartDTR S3 class, with the following elements:

- **dtrdat**: data.frame with sens, spec, mu, sigsq and sample size (n)
- **sst1**: smartSST object from the first Barm
- **sst2**: smartSST object from the second Barm
- **true_mumix**: true mu mixture
- **true_sigmix**: true sigma mixture
- **mu_Barm, sigsq_Barm, Barm**: input B-arm, mu, and sigsq for DTR

**Author(s)**

Jun (Jessie) He, Aberaham Eyman-Casey, Jason P. Sinnwell, Mayo Clinic

**References**


**Examples**

```r
mumat13 <- cbind(G1=c(30,35), G0=c(20,28))
varmat13 <- cbind(G1=c(100,100),G0=c(100,100))

dtr13 <- smartDTR(mu_Barm=mumat13, sigsq_Barm=varmat13, Barm=c(1,3), nsubject=252, pG_A1=0.8)

print(dtr13)
```

---

**smartSST**

*Single Sequential Trial design clinical trial calculations*

**Description**

Single Sequential Trial design clinical trial calculations

**Usage**

```r
smartSST(mu_Barm=c(G1=30, G0=20), sigsq_Barm=c(G1=100, G0=100), nsubject=500, Barm=1, type="continuous", sens=seq(0.5,1, by=0.1), spec=seq(0.5, 1, by=0.1), pG_A1 = 0.8, pG_A2=0.8, pran_A1 = 0.5, pran_Barm = 0.5)
```
smartSST

Arguments

mu_Barm named vector of the means for the Barm for the smart SST trial, with names 'G1' and 'G0'
sigsq_Barm named vector of the variances (sigma-squared) for the Barm for the smart SST trial, with names 'G1' and 'G0'
nssubject total sample size for the trial
Barm for the second phase of the trial, the 'B' level for which the means/variances apply
type trial response variable type; only continuous is implemented currently
sens range of sensitivity for smart SST calculations; (0,1]
spec range of specificity for smart SST calculations; (0,1]
pG_A1 probability of response to therapy given assignment to A1
pG_A2 probability of response to therapy given assignment to A2
pran_A1 probability of random assignment to A1
pran_Barm probability of assignment to Barm

Details

more details on smart SST

Value

An object of the smartSST S3 class, with the following elements:
sstdat: data.frame with sens, spec, mu, sigsq and sample size (n)
mu_Barm: The value of mu_Barm passed to the function
sigsq_Barm: The value of sigsq_Barm passed to the function

Author(s)

Jun (Jessie) He, Aberaham Eyman-Casey, Jason P. Sinnwell, Mayo Clinic

References


Examples

sst1 <- smartSST(mu_Barm=c(G1=30, G0=20), sigsq_Barm=c(G1=16,G0=16),
Barm=1, sens=seq(.6, 1, by=.1), spec=seq(.6, 1, by=.1),
nssubject=252)
print(sst1$sstdat, digits=2)
Index

plot.powerDTR (powerDTR), 2
plot.powerSST (powerSST), 3
plot.smartDTR (smartDTR), 4
plot.smartSST (smartSST), 5
powerDTR, 2
powerSST, 3
print.powerDTR (powerDTR), 2
print.powerSST (powerSST), 3
print.smartDTR (smartDTR), 4
print.smartSST (smartSST), 5

smartDTR, 4
smartSST, 5