Package: BayesDIP (via r-universe)

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Type Package

Title Bayesian Decreasingly Informative Priors for Early Termination Phase II Trials

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Description Provide early termination phase II trial designs with a decreasingly informative prior (DIP) or a regular Bayesian prior chosen by the user. The program can determine the minimum planned sample size necessary to achieve the user-specified admissible designs. The program can also perform power and expected sample size calculations for the tests in early termination Phase II trials. See Wang C and Sabo RT (2022) <doi:10.18203/2349-3259.ijct20221110>; Sabo RT (2014) <doi:10.1080/10543406.2014.888441>.

License GPL (>= 2)

URL <`https://github.com/chenw10/BayesDIP`>

Imports stats

Encoding UTF-8

RoxygenNote 7.2.2

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Repository https://chenw10.r-universe.dev

RemoteUrl https://github.com/chenw10/bayesdip

RemoteRef HEAD

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Contents

`OneSampleBernoulli` *One sample Bernoulli model*

Description

For a given planned sample size, the efficacy and futility boundaries, return the power, the type I error, the expected sample size and its standard deviation, the probability of reaching the efficacy and futility boundaries.

Usage

```
OneSampleBernoulli(
  prior,
  N = 100,
  p0,
  p1,
  d = 0,
  ps = 0.95,
  pf = 0.05,
  alternative = c("less", "greater"),
  seed = 202209,
  sim = 5000
)
```

Arguments

`prior`	A list of length 3 containing the distributional information of the prior. The first element is a number specifying the type of prior. Options are 1. DIP ; 2. Beta(a,b), where a = shape, b = scale The second and third elements of the list are the parameters a and b, respectively.
`N`	The planned sample size.
`p0`	The null response rate, which could be taken as the standard or historical rate.
`p1`	The response rate of the new treatment.
`d`	The target improvement (minimal clinically meaningful difference).
`ps`	The efficacy boundary (upper boundary).

`pf`	The futility boundary (lower boundary).
`alternative`	less (lower values imply greater efficacy) or greater (larger values imply greater efficacy).
`seed`	The seed for simulations.
`sim`	The number of simulations.

Value

A list of the arguments with method and computed elements

Examples

```
# with traditional Bayesian prior Beta(1,1)
OneSampleBernoulli(list(2,1,1), N = 100, p0 = 0.3, p1 = 0.5, d = 0.05,
                   ps = 0.98, pf = 0.05, alternative = "greater",
                   seed = 202210, sim = 10)
# with DIP
OneSampleBernoulli(list(1,0,0), N = 100, p0 = 0.3, p1 = 0.5, d = 0.05,
                   ps = 0.98, pf = 0.05, alternative = "greater",
                   seed = 202210, sim = 10)
```

`OneSampleBernoulli.Design`

One sample Bernoulli model - Trial Design

Description

Calculate the minimum planned sample size under an admissible design. The users decide the power and type-I-error, and pick the efficacy and futility boundaries. If there are no admissible design based on controlled type-I-error, then default to output the designs with the lowest type-I-error and at least the user-defined (e.g. 80%) power.

Usage

```
OneSampleBernoulli.Design(
  prior,
  nmin = 10,
  nmax = 100,
  p0,
  p1,
  d = 0,
  ps,
  pf,
  power = 0.8,
  t1error = 0.05,
  alternative = c("less", "greater"),
  seed = 202209,
  sim = 1000
)
```

Arguments

`prior`	A list of length 3 containing the distributional information of the prior. The first element is a number specifying the type of prior. Options are 1. DIP ; 2. Beta(a,b), where a = shape, b = scale The second and third elements of the list are the parameters a and b, respectively.
`nmin`	The start searching sample size
`nmax`	The stop searching sample size
`p0`	The null response rate, which could be taken as the standard or historical rate.
`p1`	The response rate of the new treatment.
`d`	The target improvement (minimal clinically meaningful difference).
`ps`	The efficacy boundary (upper boundary).
`pf`	The futility boundary (lower boundary).
`power`	The power to achieve.
`t1error`	The controlled type-I-error.
`alternative`	less (lower values imply greater efficacy) or greater (larger values imply greater efficacy).
`seed`	The seed for simulations.
`sim`	The number of simulations.

Value

A list of the arguments with method and computed elements.

Examples

```
# with traditional Bayesian prior Beta(1,1)
OneSampleBernoulli.Design(list(2,1,1), nmin = 10, nmax=100, p0 = 0.3, p1 = 0.5, d = 0,
                ps = 0.98, pf = 0.02, power = 0.80, t1error=0.05, alternative = "greater",
                   seed = 202210, sim = 10)
# with DIP
OneSampleBernoulli.Design(list(1,0,0), nmin = 10, nmax=100, p0 = 0.3, p1 = 0.5, d = 0,
                ps = 0.98, pf = 0.02, power = 0.80, t1error=0.05, alternative = "greater",
                   seed = 202210, sim = 10)
```

`OneSampleNormal1` *One sample Normal model with one-parameter unknown, given variance*

Description

For a given planned sample size, the efficacy and futility boundaries, return the power, the type I error, the expected sample size and its standard deviation, the probability of reaching the efficacy and futility boundaries.

Usage

```
OneSampleNormal1(
  prior,
  N = 100,
  mu0,
  mu1,
  var,
  d = 0,
  ps = 0.95,
  pf = 0.05,
  alternative = c("less", "greater"),
  seed = 202209,
  sim = 5000
)
```

Arguments

`prior`	A list of length 2 containing the distributional information of the prior. The first element is a number specifying the type of prior. Options are 1. DIP ; 2. Normal(mu0,var/n0), where mu0 = prior mean, var = the known variance The second elements of the list is the parameter n0.
`N`	The planned sample size.
`mu0`	The null mean value, which could be taken as the standard or current mean.
`mu1`	The mean value of the new treatment.
`var`	The variance
`d`	The target improvement (minimal clinically meaningful difference).
`ps`	The efficacy boundary (upper boundary).
`pf`	The futility boundary (lower boundary).
`alternative`	less (lower values imply greater efficacy) or greater (larger values imply greater efficacy).
`seed`	The seed for simulations.
`sim`	The number of simulations.

Value

A list of the arguments with method and computed elements.

Examples

```
# with traditional Bayesian prior Beta(1,1)
OneSampleNormal1(list(2,6), N = 100, mu0 = 100, mu1 = 95, var=15, d = 0.05,
                 ps = 0.95, pf = 0.05, alternative = "less",
                 seed = 202210, sim = 10)
OneSampleNormal1(list(1,0), N = 100, mu0 = 100, mu1 = 95, var=15, d = 0.05,
                 ps = 0.95, pf = 0.05, alternative = "less",
                 seed = 202210, sim = 10)
```

`OneSampleNormal1.Design` *One sample Normal model with one-parameter unknown, given variance*

Description

#' Calculate the minimum planned sample size under an admissible design. The users decide the power and type-I-error, and pick the efficacy and futility boundaries. If there are no admissible design based on controlled type-I-error, then default to output the designs with the lowest type-I-error and at least the user-defined (e.g. 80%) power.

Usage

```
OneSampleNormal1.Design(
  prior,
  nmin = 10,
  nmax = 100,
  mu0,
  mu1,
  var,
  d = 0,
  ps,
  pf,
  power = 0.8,
  t1error = 0.05,
  alternative = c("less", "greater"),
  seed = 202209,
  sim = 1000
)
```

Arguments

`prior`	A list of length 2 containing the distributional information of the prior. The first element is a number specifying the type of prior. Options are 1. DIP ; 2. Normal(mu0,var/n0), where mu0 = prior mean, var = the known variance The second elements of the list is the parameter n0.
`nmin`	The start searching sample size
`nmax`	The stop searching sample size
`mu0`	The null mean value, which could be taken as the standard or current mean.
`mu1`	The mean value of the new treatment.
`var`	The variance
`d`	The target improvement (minimal clinically meaningful difference).
`ps`	The efficacy boundary (upper boundary).
`pf`	The futility boundary (lower boundary).
`power`	The power to achieve.
`t1error`	The controlled type-I-error.
`alternative`	less (lower values imply greater efficacy) or greater (larger values imply greater efficacy).
`seed`	The seed for simulations.
`sim`	The number of simulations.

Value

A list of the arguments with method and computed elements.

Examples

```
# with traditional Bayesian prior Beta(1,1)
OneSampleNormal1.Design(list(2,6), nmin = 10, nmax = 100, mu0 = 100, mu1 = 95, var=15, d = 0.05,
                 ps = 0.95, pf = 0.05, power = 0.8, t1error = 0.05, alternative = "less",
                  seed = 202210, sim = 10)
# with DIP
OneSampleNormal1.Design(list(1,0), nmin = 10, nmax = 100, mu0 = 100, mu1 = 95, var=15, d = 0.05,
                 ps = 0.95, pf = 0.05, power = 0.8, t1error = 0.05, alternative = "less",
                  seed = 202210, sim = 10)
```

`OneSampleNormal2` *One sample Normal model with two-parameter unknown - both mean and variance unknown*

Description

For a given planned sample size, the efficacy and futility boundaries, return the power, the type I error, the expected sample size and its standard deviation, the probability of reaching the efficacy and futility boundaries.

Usage

```
OneSampleNormal2(
  prior,
  N = 100,
  mu0,
  mu1,
  var0,
  var,
  d = 0,
  ps = 0.95,
  pf = 0.05,
  alternative = c("less", "greater"),
  seed = 202209,
  sim = 5000
)
```

Arguments

`prior`	A list of length 3 containing the distributional information of the prior. The first element is a number specifying the type of prior. Options are 1. DIP ; 2. Normal(mu0,var/k) and var ~ Inverse-Gamma(v/2, v*var0/2) where mu0 = prior mean, k = sample size of prior observations (Normal prior), v = sample size of prior observations (Gamma prior), var0 = prior sample variance The second and third elements of the list are the parameters k and v, respectively.
`N`	The planned sample size.
`mu0`	The null mean value, which could be taken as the standard or current mean.
`mu1`	The mean value of the new treatment.
`var0`	The prior sample variance
`var`	The variance
`d`	The target improvement (minimal clinically meaningful difference).

`ps`	The efficacy boundary (upper boundary).
`pf`	The futility boundary (lower boundary).
`alternative`	less (lower values imply greater efficacy) or greater (larger values imply greater efficacy).
`seed`	The seed for simulations.
`sim`	The number of simulations.

Value

A list of the arguments with method and computed elements.

Examples

```
# with traditional Bayesian prior Beta(1,1)
OneSampleNormal2(list(2,2,1), N = 100, mu0 = 100, mu1 = 95, var0=225, var=225, d = 0,
                        ps = 0.95, pf = 0.05, alternative = "less",
                        seed = 202210, sim = 10)
# with DIP
OneSampleNormal2(list(1,0,0), N = 100, mu0 = 100, mu1 = 95, var0=225, var=225, d = 0,
                        ps = 0.95, pf = 0.05, alternative = "less",
                        seed = 202210, sim = 10)
```

`OneSampleNormal2.Design` *One sample Normal model with two-parameter unknown - both mean and variance unknown*

Description

Calculate the minimum planned sample size under an admissible design. The users decide the power and type-I-error, and pick the efficacy and futility boundaries. If there are no admissible design based on controlled type-I-error, then default to output the designs with the lowest type-I-error and at least the user-defined (e.g. 80%) power.

Usage

```
OneSampleNormal2.Design(
  prior,
  nmin = 10,
  nmax = 100,
  mu0,
  mu1,
  var0,
  var,
  d = 0,
  ps,
  pf,
```

```
    power = 0.8,
    t1error = 0.05,
    alternative = c("less", "greater"),
    seed = 202209,
    sim = 1000
  )
```

Arguments

`prior`	A list of length 3 containing the distributional information of the prior. The first element is a number specifying the type of prior. Options are 1. DIP ; 2. Normal(mu0,var/k) and var ~ Inverse-Gamma(v/2, v*var0/2) where mu0 = prior mean, k = sample size of prior observations (Normal prior), v = sample size of prior observations (Gamma prior), var0 = prior sample variance The second and third elements of the list are the parameters k and v, respectively.
`nmin`	The start searching sample size
`nmax`	The stop searching sample size
`mu0`	The null mean value, which could be taken as the standard or current mean.
`mu1`	The mean value of the new treatment.
`var0`	The prior sample variance
`var`	The variance
`d`	The target improvement (minimal clinically meaningful difference).
`ps`	The efficacy boundary (upper boundary).
`pf`	The futility boundary (lower boundary).
`power`	The power to achieve.
`t1error`	The controlled type-I-error.
`alternative`	less (lower values imply greater efficacy) or greater (larger values imply greater efficacy).
`seed`	The seed for simulations.
`sim`	The number of simulations.

Value

A list of the arguments with method and computed elements.

Examples

```
# with traditional Bayesian prior Beta(1,1)
OneSampleNormal2.Design(list(2,2,1), nmin = 10, nmax = 100, mu0 = 100, mu1 = 95,
                      var0=225, var=225, d = 0, ps = 0.95, pf = 0.05,
                      power = 0.8, t1error = 0.05, alternative = "less",
```

```
                        seed = 202210, sim = 10)
# with DIP
OneSampleNormal2.Design(list(1,0,0), nmin = 10, nmax = 100, mu0 = 100, mu1 = 95,
                        var0=225, var=225, d = 0, ps = 0.95, pf = 0.05,
                        power = 0.8, t1error = 0.05, alternative = "less",
                        seed = 202210, sim = 10)
```

`OneSamplePoisson` *One sample Poisson model*

Description

For a given planned sample size, the efficacy and futility boundaries, return the power, the type I error, the expected sample size and its standard deviation, the probability of reaching the efficacy and futility boundaries.

Usage

```
OneSamplePoisson(
  prior,
  N = 100,
  m0,
  m1,
  d = 0,
  ps = 0.95,
  pf = 0.05,
  alternative = c("less", "greater"),
  seed = 202209,
  sim = 5000
)
```

Arguments

`prior`	A list of length 3 containing the distributional information of the prior. The first element is a number specifying the type of prior. Options are 1. DIP ; 2. Gamma(a,b), where a = shape, b = rate The second and third elements of the list are the parameters a and b, respectively.
`N`	The planned sample size.
`m0`	The null event rate, which could be taken as the standard or current event rate.
`m1`	The event rate of the new treatment.
`d`	The target improvement (minimal clinically meaningful difference).
`ps`	The efficacy boundary (upper boundary).
`pf`	The futility boundary (lower boundary).

`alternative`	less (lower values imply greater efficacy) or greater (larger values imply greater efficacy).
`seed`	The seed for simulations.
`sim`	The number of simulations.

Value

A list of the arguments with method and computed elements

Examples

```
# with traditional Bayesian prior Gamma(0.5,0.001)
OneSamplePoisson(list(2,0.5,0.001), N = 100, m0 = 0.5, m1 = 0.4, d = 0.05,
                 ps = 0.95, pf = 0.05, alternative = "less",
                 seed = 202210, sim = 10)
# with DIP
OneSamplePoisson(list(1,0,0), N = 100, m0 = 0.5, m1 = 0.4, d = 0.05,
                 ps = 0.95, pf = 0.05, alternative = "less",
                 seed = 202210, sim = 10)
```

`OneSamplePoisson.Design`

One sample Poisson model - Trial Design

Description

Calculate the minimum planned sample size under an admissible design. The users decide the power and type-I-error, and pick the efficacy and futility boundaries. If there are no admissible design based on controlled type-I-error, then default to output the designs with the lowest type-I-error and at least the user-defined (e.g. 80%) power.

Usage

```
OneSamplePoisson.Design(
  prior,
  nmin = 10,
  nmax = 100,
  m0,
  m1,
  d = 0,
  ps,
  pf,
  power = 0.8,
  t1error = 0.05,
  alternative = c("less", "greater"),
  seed = 202209,
  sim = 1000
)
```

Arguments

`prior`	A list of length 3 containing the distributional information of the prior. The first element is a number specifying the type of prior. Options are 1. DIP ; 2. Gamma(a,b), where a = shape, b = rate The second and third elements of the list are the parameters a and b, respectively.
`nmin`	The start searching sample size
`nmax`	The stop searching sample size
`m0`	The null event rate, which could be taken as the standard or current event rate.
`m1`	The event rate of the new treatment.
`d`	The target improvement (minimal clinically meaningful difference).
`ps`	The efficacy boundary (upper boundary).
`pf`	The futility boundary (lower boundary).
`power`	The expected power to achieve.
`t1error`	The controlled type-I-error.
`alternative`	less (lower values imply greater efficacy) or greater (larger values imply greater efficacy).
`seed`	The seed for simulations.
`sim`	The number of simulations.

Value

A list of the arguments with method and computed elements

Examples

```
# with traditional Bayesian prior Gamma(0.5,0.001)
OneSamplePoisson.Design(list(2,0.5,0.001), nmin = 10, nmax=100, m0 = 5, m1 = 4, d = 0,
                  ps = 0.95, pf = 0.05, power = 0.80, t1error=0.05, alternative = "less",
                   seed = 202210, sim = 10)
# with DIP
OneSamplePoisson.Design(list(1,0,0), nmin = 10, nmax=100, m0 = 5, m1 = 4, d = 0,
                  ps = 0.95, pf = 0.05, power = 0.80, t1error=0.05, alternative = "less",
                   seed = 202210, sim = 10)
```

`TwoSampleBernoulli` *Two sample Bernoulli model*

Description

For a given planned sample size, the efficacy and futility boundaries, return the power, the type I error, the expected sample size and its standard deviation, the probability of reaching the efficacy and futility boundaries. Equal allocation between two treatment groups.

Usage

```
TwoSampleBernoulli(
  prior,
  N = 200,
  p1,
  p2,
  d = 0,
  ps = 0.95,
  pf = 0.05,
  alternative = c("less", "greater"),
  seed = 202209,
  sim = 5000
)
```

Arguments

`prior`	A list of length 3 containing the distributional information of the prior. The first element is a number specifying the type of prior. Options are 1. DIP ; 2. Beta(a,b), where a = shape, b = scale The second and third elements of the list are the parameters a and b, respectively.
`N`	The total planned sample size for two treatment groups.
`p1`	The response rate of the new treatment.
`p2`	The response rate of the compared treatment.
`d`	The target improvement (minimal clinically meaningful difference).
`ps`	The efficacy boundary (upper boundary).
`pf`	The futility boundary (lower boundary).
`alternative`	less (lower values imply greater efficacy) or greater (larger values imply greater efficacy).
`seed`	The seed for simulations.
`sim`	The number of simulations.

Value

A list of the arguments with method and computed elements

Examples

```
# with traditional Bayesian prior Beta(1,1)
TwoSampleBernoulli(list(2,1,1), N = 200, p1 = 0.5, p2 = 0.3, d = 0,
                   ps = 0.90, pf = 0.05, alternative = "greater",
                   seed = 202210, sim = 5)
# with DIP
TwoSampleBernoulli(list(1,0,0), N = 200, p1 = 0.5, p2 = 0.3, d = 0,
                   ps = 0.90, pf = 0.05, alternative = "greater",
                   seed = 202210, sim = 5)
```

`TwoSampleBernoulli.Design`

Two sample Bernoulli model - Trial Design

Description

Calculate the minimum planned sample size under an admissible design. The users decide the power and type-I-error, and pick the efficacy and futility boundaries. If there are no admissible design based on controlled type-I-error, then default to output the designs with the lowest type-I-error and at least the user-defined (e.g. 80%) power.

Usage

```
TwoSampleBernoulli.Design(
  prior,
  nmin = 10,
  nmax = 200,
  p1,
  p2,
  d = 0,
  ps = 0.95,
  pf = 0.05,
  power = 0.8,
  t1error = 0.05,
  alternative = c("less", "greater"),
  seed = 202209,
  sim = 500
)
```

Arguments

`prior`	A list of length 3 containing the distributional information of the prior. The first element is a number specifying the type of prior. Options are 1. DIP ; 2. Beta(a,b), where a = shape, b = scale The second and third elements of the list are the parameters a and b, respectively.

`nmin`	The start searching total sample size for two treatment groups.
`nmax`	The stop searching total sample size for two treatment groups.
`p1`	The response rate of the new treatment.
`p2`	The response rate of the compared treatment.
`d`	The target improvement (minimal clinically meaningful difference).
`ps`	The efficacy boundary (upper boundary).
`pf`	The futility boundary (lower boundary).
`power`	The power to achieve.
`t1error`	The controlled type-I-error.
`alternative`	less (lower values imply greater efficacy) or greater (larger values imply greater efficacy).
`seed`	The seed for simulations.
`sim`	The number of simulations.

Value

A list of the arguments with method and computed elements

Examples

```
# with traditional Bayesian prior Beta(1,1)
TwoSampleBernoulli.Design(list(2,1,1), nmin = 100, nmax = 120, p1 = 0.5, p2 = 0.3, d = 0,
                ps = 0.90, pf = 0.05, power = 0.8, t1error = 0.05, alternative = "greater",
                    seed = 202210, sim = 10)
# with DIP
TwoSampleBernoulli.Design(list(1,0,0), nmin = 100, nmax = 120, p1 = 0.5, p2 = 0.3, d = 0,
                ps = 0.90, pf = 0.05, power = 0.8, t1error = 0.05, alternative = "greater",
                    seed = 202210, sim = 10)
```

Index