Package

June 16, 2019

Title Calculate Power and Sample Size with Beta Regression.

Version 0.1.0

Description Power calculations are a critical component of any research study to determine theminimum sample size necessary to detect differences between multiple groups. Researchersoften work with data taking the form of proportions that can be modeled with a betadistribution. Here we present anRpackage, BetaPASS, and analogous SAS macro, thatperform power and sample size calculations using a beta distribution with comparativenonparametric output. This package allows flexibility with multiple options for link func-tions to fit the data.

Depends R (>= 3.5.1)

License GPL (>= 2)

Encoding UTF-8

LazyData true

RoxygenNote 6.1.0

Imports betareg,
lmtest,
reshape,
ggplot2,
Rcpp

Suggests knitr,
rmarkdown

VignetteBuilder knitr

R topics documented:

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betapower   *Find Power with Beta distribution*

Description

Find the power for a given sample size when testing the null hypothesis that the means for the control and treatment groups are equal against a two-sided alternative.

Usage

```
betapower(mu0, sd0, mu1.start, mu1.end, mu1.by, ss.start, ss.end, ss.by,
trials = 100, seed = 1, link.type = "logit", equal.precision = TRUE, sd1 = NULL)
```

Arguments

mu0	the mean for the control group
sd0	the standard deviation for the control group
mu1.start	the starting value of mean for the treatment group under the alternative mu1
mu1.end	the ending value of mean for the treatment group under the alternative mu1
mu1.by	the step length of mean for the treatment group under the alternative mu1
ss.start	the starting value of sample size
ss.end	the ending value of sample size
ss.by	the step length of sample size
trials	the number of trials
seed	the seed used in the simulation
link.type	the type of link used in the beta regression. Default value is "logit", or you can use "all" or choose one or more of the following: "logit", "probit", "cloglog", "cauchit", "log", "loglog"
equal.precision	
	equal dispersion parameter assumption in simulation
sd1	the standard deviation for the treatment group. Only applicable when equal.precision = FALSE

Details

betapower function allows you to control the number of trials in the simulation, the sample sizes used, and the alternative means. You can fix the alternative and vary sample size to match a desired power; You can fix the sample size and vary the alternative to see which will match a desired power; You can vary both; Start with a small number of trials (say 100) to determine the rough range of sample sizes or alternatives; Use a larger number of trials (say 1000) to get better estimates.

Value

Return a matrix with 7 to 12 columns:

power.of.GLM: link name

the power using regression method; it will return the power with every links if you use link.type = "all" statement.

```
power.of.Wilcoxon.test
                the power from Wilcoxon Rank sum test.
sample size     sample size.
mu1             the mean for the treatment group under the alternative.
mu0             the mean for the control group.
sd0             the standard deviation for the control group.
trials          the number of trials.
```

Examples

```
betapower(0.56,0.255,.70,.75,.05,30,50, 20,40,610201501)
betapower(0.56,0.255,.60,.75,.05,30,50, 5,100,617201501,"all")
betapower(0.56,0.255,.70,.75,.05,30,50, 20,40,610201501,c("logit","loglog","log"))
```

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plot.betapower	*Plots of Beta power*

Description

Generate several comparison plots of power.

Usage

```
plot.betapower(betapower.matrix,link.type,by)
```

Arguments

link.type   the type of link used in the beta regression. You can choose one or more of the
                  following: "logit", "probit", "cloglog", "cauchit", "log", "loglog", "all"

by   the type of plot. see details.

betapower.matrix
                  a matrix obtained by the function betapower.(the formula was described as the
                  output formula in the function betapower)

Details

plot.betapower() returns different plots depends on by

by = "linktype": plot.betapower() returns graphs that plot power against mu1, where mu1 is the mean for the treatment group under the alternative. The number of plots will vary depending on the number of link types selected with the last plot showing power based on Wilcoxon Rank Sum Test. The first one or several plots show comparisons of power with different sample size, using GLM method with one or several link types. The last plot shows a comparison of the power with different sample size using Wilcoxon Rank Sum Test. Y-axis denotes power and X-axis denotes mu1, the mean for the treatment group under the alternative.

by = "samplesize": plot.betapower() returns a number of plots equal to the number of sample sizes tested. Each plot compares power calculated with different link types and the Wilcoxon Rank Sum Test. Y-axis denotes power and X-axis denotes mu1, the mean for the treatment group under the alternative.

by = "mu1": plot.betapower() returns a number of plots equal to the number of mu1 used in the procedure. Each plot compares power calculated with different link types and the Wilcoxon Rank Sum Test. Y-axis denotes power and X-axis denotes sample size.

Examples

```
BPmat <- betapower(0.56,0.255,.70,.75,.05,30,50, 20,40,610201501,"all")
plot.betapower(BPmat,link.type = "all",by="linktype")
plot.betapower(BPmat,link.type = "all",by="samplesize")
plot.betapower(BPmat,link.type = "all",by="mu1")
BPmat2 <- betapower(0.56,0.255,.61,.76,.05,30,45,5,200,610201511,c("logit","loglog","log"))
plot.betapower(BPmat2,link.type = c("logit","loglog","log"),by="linktype")
plot.betapower(BPmat2,link.type = c("logit","loglog","log"),by="samplesize")
plot.betapower(BPmat2,link.type = c("logit","loglog","log"),by="mu1")
```

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plot.samplesize   *Plots by mu1*

Description

Generate the comparison plots using GLM method and Wilcoxon Rank Sum Test with different mu1.

Usage

```
plot.samplesize(SS.matrix,link.type)
```

Arguments

link.type	the type of link used in the beta regression(or Wilcoxon Rank Sum Test). You can choose one or more of the following: "logit", "probit", "cloglog", "cauchit", "log", "loglog", "wilcoxon", "all"
SS.matrix	the matrix obtained by the function samplesize.(the formula was described as the output formula in the function samplesize)

Details

plot.samplesize() returns a series of plots equal to the number of mu1 used in the procedure. Y-axis denotes minimum sample size and X-axis denotes minimum power.

Examples

```
SSmat <- samplesize(mu0=0.56, sd0=0.255, mu1.start = 0.60, mu1.end = 0.70, mu1.by = 0.05,
power.start = 0.7, power.end = 0.9, power.by = 0.1, link.type = "all")
plot.samplesize(SSmat, "all")
SSmat2 <- samplesize(mu0=0.56, sd0=0.255, mu1.start = 0.60, mu1.end = 0.70, mu1.by = 0.05,
power.start = 0.7, power.end = 0.9, power.by = 0.1, link.type = c("logit","loglog","log"))
plot.samplesize(SSmat2,link.type = c("logit","loglog","log"))
```

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samplesize	*Find minimum sample size with Beta distribution*

Description

Find minimum sample sizes with Beta distribution and given mu0,sd0,mu1 and target powers.

Usage

```
samplesize(mu0, sd0, mu1.start, mu1.end, mu1.by, power.start, power.end, power.by,
sig.level = 0.05, trials = 100, delta = NuLL, seed = 1,
link.type = "logit", equal.precision = TRUE, sd1 = NULL)
```

Arguments

mu0	the mean for the control group
sd0	the standard deviation for the control group
mu1.start	the starting value of mean for the treatment group under the alternative mu1
mu1.end	the ending value of mean for the treatment group under the alternative mu1
mu1.by	the step length of mean for the treatment group under the alternative mu1
power.start	the starting value of target power
power.end	the ending value of target power
power.by	the step length of target power
sig.level	significant level; default value is 0.05
trials	the number of trials; default value is 100
delta	the accuracy of the result; must be integer
seed	the seed used in the simulation
link.type	default link is "logit". Other link options include: "logit", "probit", "cloglog", "log", "loglog", "wilcoxon", or you can use "all" for all types of link
equal.precision	
	equal dispersion parameter assumption in simulation
sd1	the standard deviation for the treatment group. Only applicable when equal.precision = FALSE

Details

The samplesize function allows you to control the number of trials in the simulation, the target power, delta, and the alternative means. You can fix the alternative and vary power to match a desired sample size; Use default values for the number of trials and delta for a quick view; Use a larger number of trials (say 1000) and a smaller delta (say 1) to get better estimates.

Value

Return a matrix including minimum sample size and power, as well as the target power and mu1:

`minimum sample size:  link type:`
minimum sample size for given given mu0, sd0, mu1, target power and type of link.

`minimum power:  link type:`
the minimum power greater than or equal to target power.

`target power:`   the target power.

`mu1:`   mean for the treatment group under the alternative.

`mu0:`   the mean for the control group.

`sd0:`   the standard deviation for the control group.

Examples

```
samplesize(mu0=0.56, sd0=0.255, mu1.start = 0.65, mu1.end = 0.75, mu1.by = 0.05,
power.start = 0.7, power.end = 0.9, power.by = 0.1)
samplesize(mu0=0.56, sd0=0.255, mu1.start = 0.65, mu1.end = 0.75, mu1.by = 0.05,
power.start = 0.7, power.end = 0.9, power.by = 0.1, link.type = c("logit","loglog","log"))
samplesize(mu0=0.56, sd0=0.255, mu1.start = 0.65, mu1.end = 0.75, mu1.by = 0.05,
power.start = 0.7, power.end = 0.9, power.by = 0.1, link.type = "all")
```

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