

Package ‘BetaPASS’

May 6, 2026

Title Calculate Power and Sample Size with Beta Regression

Version 1.1-2

Date 2023-10-15

Description Power calculations are a critical component of any research study to determine the minimum sample size necessary to detect differences between multiple groups. Researchers often work with data taking the form of proportions that can be modeled with a beta distribution. Here we present an R package, 'BetaPASS', that perform power and sample size calculations for data following a beta distribution with comparative nonparametric output. This package allows flexibility with multiple options for link functions to fit the data and graphing functionality for visual comparisons.

Depends R (>= 3.6)

License GPL (>= 2)

Encoding UTF-8

RoxygenNote 6.1.1

Imports betareg, ggplot2, pbapply, stats

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Author Jinpu Li [aut, cre],
Ryan Knigge [aut],
Emily Leary [aut]

Maintainer Jinpu Li <lijinp@health.missouri.edu>

Repository CRAN

Date/Publication 2023-10-18 21:00:08 UTC

Contents

betapower	2
samplesize	3
Index	6

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 = NULL, mu1.by = NULL,
ss.start, ss.end = NULL, ss.by = NULL, sig.level = 0.05,
trials = 100, seed = 1, link.type="logit",
equal.precision=TRUE, sd1 = NULL)
```

Arguments

mu0	mean for the control group
sd0	standard deviation for the control group
mu1.start	starting value of mean for the treatment group under the alternative mu1
mu1.end	ending value of mean for the treatment group under the alternative mu1
mu1.by	step length of mean for the treatment group under the alternative mu1
ss.start	starting value of sample size
ss.end	ending value of sample size
ss.by	step length of sample size
sig.level	significant level of test; default value is 0.05
trials	number of trials
seed	seed used in the simulation
link.type	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	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.

The plot function will return different plots depends on "by" statement. 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 = "linktype": return 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": return 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": return 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.

Value

Return a betapower object including basic settings (mean and standard deviation for the control group, significant level, number of trials and link types), and a matrix of estimated power with given sample size and mu1.

beta regression(link name)	estimated power using beta regression method; it will return the power with every links if you use link.type = "all" statement.
Wilcoxon	estimated power from Wilcoxon Rank sum test.
sample size	sample size.
mu1	mean for the treatment group under the alternative.

Examples

```
BPmat <- betapower(mu0 = 0.56, sd0 = 0.255, mu1.start = .70, mu1.end = .75, mu1.by = .05,
ss.start = 30, ss.end = 50, ss.by = 20, trials = 100)
## show the results
BPmat
## add plot
plot(BPmat, link.type = "logit", by = "mu1")
```

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

Arguments

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

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 for a quick view; Use a larger number of trials (say 1000) and a smaller delta (say 1) to get better estimates.

The `plot` function will return a series of plots equal to the number of `mu1` used in the procedure. Type of link used in the beta regression. You can choose one or more of the following: "logit", "probit", "cloglog", "cauchit", "log", "loglog", "all". Y-axis denotes minimum sample size and X-axis denotes minimum power.

Value

Return a `samplesize` object including basic settings (mean and standard deviation for the control group, significant level, number of trials and link types), and a matrix of estimated power with given `mu1` and target power.

minimum sample size: link type:
 minimum sample size for given given μ_0 , sd_0 , μ_1 , target power and type of link.
minimum power: link type:
 the minimum power greater than or equal to target power.
target power: target power.
 μ_1 : mean for the treatment group under alternative.

Examples

```
SSmat <- samplesize(mu0=0.56, sd0=0.255, mu1.start = 0.75,  
power.start = 0.8, power.end = 0.9, power.by = 0.1,  
trials = 25, link.type = c("log", "wilcoxon"))  
## show the results  
SSmat  
## add plot  
plot(SSmat, link.type = c("log", "wilcoxon"))
```

Index

betapower, 2

samplesize, 3