

Package ‘PSpower’

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Type Package

Title Sample Size Calculation for Propensity Score Analysis

Version 0.1.1

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Description Sample size calculations in causal inference with observational data are increasingly desired. This package is a tool to calculate sample size under prespecified power with minimal summary quantities needed.

Depends ggplot2

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Contents

plot.PSpower	2
plot_overlap	2
print.PSpower	3
PSpower	3

Index	5
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plot.PSpower	<i>Plots PSpower object</i>
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Description

Plots PSpower object

Usage

```
## S3 method for class 'PSpower'
plot(x, power = seq(0.6, 0.99, length.out = 100), ...)
```

Arguments

x	PSpower object
power	a range of powers to plot the power curve
...	ignored

Value

an object (class ggplot) containing a figure

Examples

```
obj <- PSpower(tau = 1/sqrt(20), sig.level = 0.05, power = 0.956,
               r = 0.5, phi = 0.99, rho_sq = 0.02)
plot(obj)
```

plot_overlap	<i>Plot density of propensity scores given treatment probability and overlap coefficient</i>
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Description

Plot density of propensity scores given treatment probability and overlap coefficient

Usage

```
plot_overlap(r, phi)
```

Arguments

r	treatment probability
phi	overlap coefficient

Value

a ggplot of the density of propensity scores in two treatment arms

Examples

```
plot_overlap(0.6, 0.9)
```

print.PSpower	<i>Prints PSpower object</i>
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Description

Prints PSpower object

Usage

```
## S3 method for class 'PSpower'
print(x, ...)
```

Arguments

x	PSpower object
...	ignored

Value

no return value; called for side effect to output a string

PSpower	<i>Calculate sample size needed to achieve a prespecified power</i>
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Description

Calculate sample size needed to achieve a prespecified power

Usage

```
PSpower(
  tau,
  sig.level = 0.05,
  power = NULL,
  sample.size = NULL,
  r,
  phi,
  rho_sq,
  test = "two-sided",
  estimand = "ATE"
)
```

Arguments

<code>tau</code>	the anticipated standardized treatment effect
<code>sig.level</code>	the significance level, or the type-I error rate (default 0.05)
<code>power</code>	the desired power to achieve (only specify for sample size calculation)
<code>sample.size</code>	the total sample size (only specify for power calculation)
<code>r</code>	the proportion of treated units
<code>phi</code>	the overlap coefficient (usually between 0.8 and 1); use function <code>plot_overlap(r, phi)</code> for visual aid
<code>rho_sq</code>	the squared correlation between propensity score and outcome; recommend treating as a sensitivity parameter: a grid of values between 0 and the R-squared statistic of predicting the outcomes with covariates.
<code>test</code>	whether one-sided or two-sided test is considered
<code>estimand</code>	the estimand (ATE, ATT, ATC or ATO), or a customized tilting function $h(e(x))$

Value

an object with the calculated sample size

Examples

```
PSPower(tau = 1/sqrt(20), sig.level = 0.05, power = 0.956, r = 0.5, phi = 0.99, rho_sq = 0.02)
```

Index

`plot.PSpower`, [2](#)
`plot_overlap`, [2](#)
`print.PSpower`, [3](#)
`PSpower`, [3](#)