Package ‘mthapower’

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Type Package

Title Sample Size and Power for Association Studies Involving Mitochondrial DNA Haplogroups

Version 0.1.1

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Description Calculate Sample Size and Power for Association Studies Involving Mitochondrial DNA Haplogroups.

License GPL-3

Encoding UTF-8

LazyData true

Suggests ggplot2, car

URL https://github.com/aurora-mareviv/mthapower

BugReports https://github.com/aurora-mareviv/mthapower/issues

RoxygenNote 6.1.1

NeedsCompilation no

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R topics documented:

mthacases ......................................................... 2
mthapower ......................................................... 3

Index 5
Description

Determine the minimum number of cases (Ncmin), required to detect: either a change from p0 (haplogroup frequency in controls) to p1 (haplogroup frequency in cases), or a given OR, with a predefined confidence interval, in a study with Nh haplogroups. Note: I assume that case-control equations are valid for cohorts with a balanced number of cases and controls. This function may not be generalizable for all studies involving mtDNA haplogroups.

Usage

mthacases(p0 = p0, Nh = Nh, OR.cas.ctrl = OR.cas.ctrl, power = power, sig.level = sig.level)

Arguments

- p0: the frequency of the haplogroup in the control population, (that is, the controls among exposed). It depends on haplogroup baseline frequency.
- Nh: number of haplogroup categories. Usually 10 haplogroups plus one category for rare haplogroups: Nh <- 11.
- OR.cas.ctrl: (p1 / (1-p1)) / (p0 / (1-p0)) the OR you want to detect with your data. It can be either a single value, or a sequence: OR.cas.ctrl <- 2; OR.cas.ctrl <- seq(1.25,3 by=0.5).
- power: the power to detect a given OR in my study (usually 80-90).
- sig.level: the alpha error accepted. Can take 3 possible values: 0.05, 0.01 and 0.001 (see [Table 2] of Samuels et al).

Value

Gives the result in a data frame, easy to print in a plot.

Author(s)

Author and maintainer: Aurora Baluja. Email: <mariauror@gmail.com>

References

**mthapower**

**Description**

For a given study size, determine the minimum effect size that can be detected with the desired power and significance level, in a study with Nh haplogroups. Note: I assume that case-control equations are valid for cohorts with a balanced number of cases and controls. This function may not be generalizable for all studies involving mtDNA haplogroups.

**Usage**

```r
mthapower(n.cases = ncases, p0 = p0, Nh = Nh,
        OR.cas.ctrl = OR.cas.ctrl, sig.level = sig.level)
```

**Arguments**

- **n.cases**
  - number of cases or controls from the study. It can be either a single value, or a sequence: n.cases <- 300; n.cases <- seq(50,500 by=10).

- **p0**
  - the frequency of the haplogroup in the control population. It depends on haplogroup baseline frequency.

- **Nh**
  - number of categories for haplogroups. Usually 10 haplogroups plus one category for rare haplogroups: Nh <- 11.

- **OR.cas.ctrl**
  - (p1 / (1-p1)) / (p0 / (1-p0)) the OR you want to detect with your data.

- **sig.level**
  - the alpha error accepted. Can take 3 possible values: 0.05, 0.01 and 0.001 (see [Table 2] of Samuels et al).

**Value**

Calculates power given the number of cases and other parameters. The output is an object of class `data.frame`, ready to plot.

**Author(s)**

Author and maintainer: Aurora Baluja. Email: <mariauror@gmail.com>
References


Examples

# Example 1:
pow <- mthapower(n.cases=203, p0=0.443, Nh=13, OR.cas.ctrl=2.33, sig.level=0.05)

# Example 2:
# Create data frames
pow.H150 <- mthapower(n.cases=seq(50,1000,by=50), p0=0.433, Nh=11, OR.cas.ctrl=1.5, sig.level=0.05)
pow.H175 <- mthapower(n.cases=seq(50,1000,by=50), p0=0.433, Nh=11, OR.cas.ctrl=1.75, sig.level=0.05)
pow.H200 <- mthapower(n.cases=seq(50,1000,by=50), p0=0.433, Nh=11, OR.cas.ctrl=2, sig.level=0.05)
pow.H250 <- mthapower(n.cases=seq(50,1000,by=50), p0=0.433, Nh=11, OR.cas.ctrl=2.5, sig.level=0.05)

# Bind the three data frames:
# Adds column OR to binded data frame:
bindata$OR <- rep(factor(c(1.50,1.75,2,2.5)),
times = c(nrow(pow.H150),
nrow(pow.H175),
nrow(pow.H200),
nrow(pow.H250)))

# Create plot:
# install.packages("car")
library(car)
scatterplot(power~ncases | OR, regLine=FALSE, smooth=FALSE, boxplots=FALSE, by.groups=TRUE, data=bindata)
Index

mthacases, 2
mthapower, 3