

Package ‘mthapower’

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Type Package

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

Version 0.1.1

Maintainer Aurora Baluja <mariauror@gmail.com>

Description Calculate Sample Size and Power for Association Studies Involving Mitochondrial DNA Haplogroups. Based on formulae by Samuels et al. AJHG, 2006. 78(4):713-720. <[DOI:10.1086/502682](https://doi.org/10.1086/502682)>.

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Encoding UTF-8

LazyData true

Suggests ggplot2, car

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

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

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NeedsCompilation no

Author Aurora Baluja [aut, cre] (<<https://orcid.org/0000-0002-5204-0771>>)

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mthacases

Sample size calculations - mtDNA haplogroups

Description

Determine the minimum number of cases (N_{\min}), required to detect: either a change from p_0 (haplogroup frequency in controls) to p_1 (haplogroup frequency in cases), or a given OR, with a predefined confidence interval, in a study with N_h 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

<code>p0</code>	the frequency of the haplogroup in the control population, (that is, the controls among exposed). It depends on haplogroup baseline frequency.
<code>Nh</code>	number of haplogroup categories. Usually 10 haplogroups plus one category for rare haplogroups: <code>Nh <- 11</code> .
<code>OR.cas.ctrl</code>	$(p_1 / (1-p_1)) / (p_0 / (1-p_0))$ the OR you want to detect with your data. It can be either a single value, or a sequence: <code>OR.cas.ctrl <- 2</code> ; <code>OR.cas.ctrl <- seq(1.25, 3 by=0.5)</code> .
<code>power</code>	the power to detect a given OR in my study (usually 80-90).
<code>sig.level</code>	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

1. DC Samuels, AD Carothers, R Horton, PF Chinnery. The Power to Detect Disease Associations with Mitochondrial DNA Haplogroups. *AJHG*, 2006. 78(4):713-720. DOI:10.1086/502682.
2. Source code: github.com/aurora-mareviv/mthapower.
3. Shiny app: aurora.shinyapps.io/mtDNA_power_calc.

Examples

```

mydata <- mthacases(p0=0.445, Nh=11,
                  OR.cas.ctrl=c(2), power=80,
                  sig.level=0.05) # Baudouin study
mydata <- mthacases(p0=0.445, Nh=11,
                  OR.cas.ctrl=c(1.25,1.5,1.75,2,2.25,2.5,2.75,3),
                  power=80, sig.level=0.05)
mydata <- mydata[c(2,6)]
mydata
plot(mydata)

```

mthapower

Power calculations - mtDNA haplogroups

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 N_h 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

```

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: <code>n.cases <- 300</code> ; <code>n.cases <- seq(50, 500 by=10)</code> .
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: <code>Nh <- 11</code> .
OR.cas.ctrl	$(p_1 / (1-p_1)) / (p_0 / (1-p_0))$ 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

1. DC Samuels, AD Carothers, R Horton, PF Chinnery. The Power to Detect Disease Associations with Mitochondrial DNA Haplogroups. *AJHG*, 2006. 78(4):713-720. DOI:10.1086/502682.
2. Source code: github.com/aurora-mareviv/mthapower.
3. Shiny app: aurora.shinyapps.io/mtDNA_power_calc.

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:
bindata <- rbind(pow.H150,pow.H175,pow.H200,pow.H250)
# 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)
```

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