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. Based on formulae by Samuels et al. AJHG, 2006. 78(4):713-720. <DOI:10.1086/502682>.

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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Contents

`mthacases` *Sample size calculations - mtDNA haplogroups*

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)

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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 `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

```
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)

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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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