

# Package: mthapower (via r-universe)

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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>.

**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

**Repository** <https://aurora-mareviv.r-universe.dev>

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

**RemoteRef** HEAD

**RemoteSha** 5d740d2d83be0602a9b95e244a0580d1e09aa193

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 mthacases

*Sample size calculations - mtDNA haplogroups*


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### 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 &lt;- 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 &lt;- 2</code> ; <code>OR.cas.ctrl &lt;- 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](https://github.com/aurora-mareviv/mthapower).
3. Shiny app: [aurora.shinyapps.io/mtDNA\\_power\\_calc](https://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)

```

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mthapower

*Power calculations - mtDNA haplogroups*


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**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 &lt;- 300</code> ; <code>n.cases &lt;- 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 &lt;- 11</code> .
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

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](https://github.com/aurora-mareviv/mthapower).
3. Shiny app: [aurora.shinyapps.io/mtDNA\\_power\\_calc](https://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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