Aneurismi

Single allelic variants frequency in patients group compared to healthy people

Reference: Table 1

CYP2A6*2

```
filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - CYP2A6 2.csv"
dat = read.csv(filepath)
ctable <- table(dat)
ctable = ctable + 1 # To avoid p-value = 1
print(ctable)
```

```
##          allelic.variant
## group      AA  AT
##   control 145   7
##   patient 319  14
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.8138
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.3348569 2.7207877
## sample estimates:
## odds ratio
##  0.9092758
```

CYP2A6*B2

```
filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - CYP2A6 B2.csv"
dat = read.csv(filepath)
ctable <- table(dat)
print(ctable)
```

```
##          allelic.variant
## group      AA  AG  GG
##   control  27 121   2
##   patient  44 286   1
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
```

```
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.126
## alternative hypothesis: two.sided
```

CYP2A6*14

```
filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - CYP2A6 14.csv"
dat = read.csv(filepath)
ctable <- table(dat)
print(ctable)
```

```
##           allelic.variant
## group       CC   CT
##   control 146    4
##   patient 320   11
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.7857
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.3638609 5.4910320
## sample estimates:
## odds ratio
##   1.254086
```

Allelic combinations frequency in patients group compared to healthy people

```
filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - allelic-combinations.csv"
dat = read.csv(filepath)
ctable <- table(dat)
print(ctable)
```

```
##           combination
## group      AA-AA-CC AA-AA-CT AA-AG-CC AA-AG-CT AA-GG-CC AT-AA-CC AT-AG-CC
##   control       23        1      117        1        2        3        1
##   patient       42        0      264       11        1        2       11
##           combination
## group      AT-AG-CT
##   control        2
##   patient        0
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
```

```
## data:  ctable
## p-value = 0.01129
## alternative hypothesis: two.sided
```

Clinical features in patients

CYP2A6 2 - singolo vs multiplo

```
filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - CYP2A6 2 - multipli.csv"
dat = read.csv(filepath)
ctable <- table(dat)
print(ctable)
```

```
##                  multipli
## allelic.variant   0   1
##              AA 265  53
##              AT  13   0
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.2364
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.000000 1.703047
## sample estimates:
## odds ratio
##          0
```

CYP2A6 2 - sangunanti vs non sanguinanti

```
filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - CYP2A6 2 - sah.csv"
dat = read.csv(filepath)
ctable <- table(dat)
print(ctable)
```

```
##                sah
## allelic.variant  0   1
##              AA 72 246
##              AT  4   9
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.505
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.1775993 3.0171264
## sample estimates:
```

```
## odds ratio
##  0.6594533
```

CYP2A6 2 - fumo vs non fumo

```
filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - CYP2A6 2 - smoke.csv"
dat = read.csv(filepath)
ctable <- table(dat)
print(ctable)
```

```
##                 fumo
## allelic.variant   0   1
##              AA 235  83
##              AT  12   1
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.1969
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.005458611 1.645295289
## sample estimates:
## odds ratio
##    0.23663
```

CYP2A6 B2 - singolo vs multiplo

```
filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - CYP2A6 B2 - multipli.csv"
dat = read.csv(filepath)
ctable <- table(dat)
print(ctable)
```

```
##               multipli
## allelic.variant   0   1
##              AA  35   9
##              AG 242  44
##              GG   1   0
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.4813
## alternative hypothesis: two.sided
```

CYP2A6 B2 - sangunanti vs non sanguinanti

```
filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - CYP2A6 B2 - sah.csv"
dat = read.csv(filepath)
```

```
ctable <- table(dat)
ctable = ctable + 1
print(ctable)
```

```
##              sah
## allelic.variant   0   1
##              AA  11  35
##              AG  67 221
##              GG   1   2
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.8699
## alternative hypothesis: two.sided
```

CYP2A6 B2 - fumo vs non fumo

```
filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - CYP2A6 B2 - smoke.csv"
dat = read.csv(filepath)
ctable <- table(dat)
print(ctable)
```

```
##              fumo
## allelic.variant   0   1
##              AA  34  10
##              AG 212  74
##              GG   1   0
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.7868
## alternative hypothesis: two.sided
```

CYP2A6 14 - singolo vs multiplo

```
filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - CYP2A6 14 - multipli.csv"
dat = read.csv(filepath)
ctable <- table(dat)
ctable = ctable + 2
print(ctable)
```

```
##              multipli
## allelic.variant   0   1
##              CC 270  54
##              CT  12   3
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.7246
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.218925 4.846200
## sample estimates:
## odds ratio
##   1.249121
```

CYP2A6 14 - sangunanti vs non sanguinanti

```
filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - CYP2A6 14 - sah.csv"
dat = read.csv(filepath)
ctable <- table(dat)
print(ctable)
```

```
##                 sah
## allelic.variant   0    1
##              CC  76 244
##              CT   0   11
```

```
fisher.test(ctable)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.0749
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.7596854       Inf
## sample estimates:
## odds ratio
##        Inf
```

CYP2A6 14 - fumo vs non fumo

```
filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - CYP2A6 14 - smoke.csv"
dat = read.csv(filepath)
ctable <- table(dat)
print(ctable)
```

```
##                 fumo
## allelic.variant   0    1
##              CC 240   80
##              CT   7    4
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
```

```
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.4798
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.3578376 6.9387894
## sample estimates:
## odds ratio
##   1.711172
```

Allelic combinations - multiplo vs non multiplo

```
filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - allelic_combinations - multipli.csv"
dat = read.csv(filepath)
ctable <- table(dat)
ctable = ctable + 2
print(ctable)
```

```
##            multipli
## combination   0   1
##     AA-AA-CC  35  11
##     AA-AG-CC 223  45
##     AA-AG-CT  12   3
##     AA-GG-CC   3   2
##     AT-AA-CC   4   2
##     AT-AG-CC  13   2
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.3926
## alternative hypothesis: two.sided
```

Allelic combinations - sangunanti vs non

```
filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - allelic_combinations - sah.csv"
dat = read.csv(filepath)
ctable <- table(dat)
ctable = ctable + 2
print(ctable)
```

```
##            sah
## combination  0   1
##     AA-AA-CC 11  35
##     AA-AG-CC 65 203
##     AA-AG-CT  2  13
##     AA-GG-CC  2   3
##     AT-AA-CC  3   3
##     AT-AG-CC  5  10
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.4328
## alternative hypothesis: two.sided
```

Allelic combinations - fumo vs non fumo

```
filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - allelic_combinations - smoke.csv"
dat = read.csv(filepath)
ctable <- table(dat)
ctable = ctable + 2
print(ctable)
```

```
##               fumo
## combination    0    1
##     AA-AA-CC  34   12
##     AA-AG-CC 197   71
##     AA-AG-CT   9    6
##     AA-GG-CC   3    2
##     AT-AA-CC   4    2
##     AT-AG-CC  12    3
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.7547
## alternative hypothesis: two.sided
```

Single polymorphisms and combinations correlation with IA rupture and smoking habits

Reference Table 4 ## Smoke + SAH vs No smoke + SAH ## CYP2A6 2

```
filepath = "aneurismi_fumo - sah - smoke - nosmoke - CYP2A6 2.csv"
dat = read.csv(filepath)
ctable <- table(dat)
print(ctable)
```

```
##                 Smoke...SAH
## allelic.variant   0    1
##              AA 165   81
##              AT   8    1
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
```

```
## data:  ctable
## p-value = 0.2789
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.005673704 1.961495500
## sample estimates:
## odds ratio
##  0.2556439
```

Smoke + SAH vs No smoke + SAH

CYP2A6 B2

```
filepath = "aneurismi_fumo - sah - smoke - nosmoke - CYP2A6 B2.csv"
dat = read.csv(filepath)
ctable <- table(dat)
print(ctable)
```

```
##              Smoke...SAH
## allelic.variant   0    1
##            AA  24   10
##            AG 148   72
##            GG   1    0
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.8943
## alternative hypothesis: two.sided
```

Smoke + SAH vs No smoke + SAH

CYP2A6 14

```
filepath = "aneurismi_fumo - sah - smoke - nosmoke - CYP2A6 14.csv"
dat = read.csv(filepath)
ctable <- table(dat)
print(ctable)
```

```
##              Smoke...SAH
## allelic.variant   0    1
##            CC 166   78
##            CT   7    4
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.7494
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
```

```
##  0.253243 4.946661
## sample estimates:
## odds ratio
##   1.215131
```

Smoke + NOSAH vs No smoke + NOSAH

CYP2A6 2

```
filepath = "aneurismi_fumo - no sah - smoke - nosmoke - CYP2A6 2.csv"
dat = read.csv(filepath)
ctable <- table(dat)
ctable = ctable + 1
print(ctable)
```

```
##                 Smoke...NO.SAH
## allelic.variant  0  1
##              AA 71  3
##              AT  5  1
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.2725
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##   0.075263 71.139361
## sample estimates:
## odds ratio
##   4.574082
```

Smoke + NOSAH vs No smoke + NOSAH

CYP2A6 B2

```
filepath = "aneurismi_fumo - no sah - smoke - nosmoke - CYP2A6 B2.csv"
dat = read.csv(filepath)
ctable <- table(dat)
ctable = ctable + 1
print(ctable)
```

```
##                 Smoke...NO.SAH
## allelic.variant  0  1
##              AA 11  1
##              AG 65  3
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.4851
```

```
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##   0.03708556 29.04874789
## sample estimates:
## odds ratio
##  0.5129739
```

Smoke + NOSAH vs No smoke + NOSAH

CYP2A6 14

Fisher's exact test is appropriate only for tables, or parts of tables, with two rows and two columns that contain values (for example, a nested section of a larger table may be valid for this test). Rows and columns with no respondent data are ignored by the test, so a table with two rows and two columns may not be valid if, for example, one of the rows has no data. Conversely, a table with three rows and two columns may be suitable for the test if one of the rows has no data. You can use this test on its own or in addition to the chi-square test. If you request the chi-square test and Fisher's exact test on the same table, a single chi-square column is used to display the results for both tests. If you request Fisher's exact test on a table that does not meet the requirements, it is not carried out. The value returned by Fisher's exact test is the two-tailed p value, which does not distinguish between significantly high and significantly low results.

Serve aggiungere CT 0 nel dataframe

```
filepath = "aneurismi_fumo - no sah - smoke - nosmoke - CYP2A6 14.csv"
dat = read.csv(filepath)
ctable <- table(dat)
print(ctable)
```

```
##                 Smoke...NO.SAH
## allelic.variant  0  1
##              CC 74  2
##              CT  1  0
```

```
fisher.test(ctable, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 1
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##     0.000 1429.848
## sample estimates:
## odds ratio
##          0
```

Smoke + NOSAH vs No smoke + NOSAH

Allelic combinations

```
filepath = "aneurismi_fumo - no sah - smoke - nosmoke - allelic-comb.csv"
dat <- read.csv(filepath, header=TRUE, sep=",", row.names=1)
fisher.test(dat, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
```

```
##
## data:  dat
## p-value = 1
## alternative hypothesis: two.sided
```

Smoke + SAH vs No smoke + SAH

Allelic combinations

```
filepath = "aneurismi_fumo - sah - smoke - nosmoke - allelic-comb.csv"
dat <- read.csv(filepath, header=TRUE, sep=",", row.names=1)
fisher.test(dat, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  dat
## p-value = 0.8598
## alternative hypothesis: two.sided
```

Bleeding and smoking in AA-AG-CC polymorphisms combination group

```
filepath = "bleeding_smoking_in_AA-AG-CC.csv"
dat <- read.csv(filepath, header=TRUE, sep=",", row.names=1)
fisher.test(dat, alternative="two.sided")
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  dat
## p-value = 1.413e-05
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.01103686 0.37781542
## sample estimates:
## odds ratio
## 0.09563267
```