

## 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
```

```
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
```

```
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
```

```
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
```

```
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

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
```

```
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
```

```
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
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
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
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

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

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
```

```
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
```

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

```
##              smoke_sah
## allelic.variant  0    1
##              AA   3  82
##              AT   1   2
```

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

```
##
## Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.1317
```

```

## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
## 0.003177969 5.743285269
## sample estimates:
## odds ratio
## 0.07965272

filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - CYP2A6 B2 - smoke_sah.csv"
dat = read.csv(filepath)
ctable <- table(dat)
ctable = ctable + 1
print(ctable)

##              smoke_sah
## allelic.variant 0  1
##              AA  1 11
##              AG  3 73

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

##
## Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.4498
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
## 0.03866126 30.18746483
## sample estimates:
## odds ratio
## 2.186659

filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - CYP2A6 14 - smoke_sah.csv"
dat = read.csv(filepath)
ctable <- table(dat)
ctable = ctable + 1
print(ctable)

##              smoke_sah
## allelic.variant 0  1
##              CC  3 79
##              CT  1  5

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

##
## Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.2499
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
## 0.01265357 11.94137830
## sample estimates:
## odds ratio
## 0.196653

```



```

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

```

```

##              smoke_sah
## allelic.variant  0    1
##              AA   70 165
##              AT    4    8

```

```

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

```

```

##
## Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.7555
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.2187697 3.9804140
## sample estimates:
## odds ratio
##  0.8490807

```

```

filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - CYP2A6 B2 - nosmoke_sah.csv"
dat = read.csv(filepath)
ctable <- table(dat)
ctable = ctable + 2
print(ctable)

```

```

##              smoke_sah
## allelic.variant  0    1
##              AA   12  26
##              AG   66 150
##              GG    2    3

```

```

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

```

```

##
## Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.8955
## alternative hypothesis: two.sided

```

```

filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - CYP2A6 14 - nosmoke_sah.csv"
dat = read.csv(filepath)
ctable <- table(dat)
ctable = ctable + 1
print(ctable)

```

```

##              smoke_sah
## allelic.variant  0    1
##              CC   75 167
##              CT    1    8

```

```

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

##
## Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.2843
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##    0.4658156 161.4087004
## sample estimates:
## odds ratio
##    3.579108

filepath = "/home/frpnz/Projects/aneurismi/aneurismi_fumo - allelic_combinations - smoke_sah.csv"
dat = read.csv(filepath)
ctable <- table(dat)
ctable = ctable + 1
print(ctable)

##           fumo
## combination  0  1
##   AA-AA-CC   1 11
##   AA-AG-CC   3 68
##   AA-AG-CT   1  5
##   AT-AG-CC   1  2

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

##
## Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.08428
## alternative hypothesis: two.sided

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

##           fumo
## combination   0   1
##   AA-AA-CC    9  23
##   AA-AG-CC   61 134
##   AA-AG-CT    0   7
##   AA-GG-CC    0   1
##   AT-AA-CC    1   1
##   AT-AG-CC    3   7

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

##
## Fisher's Exact Test for Count Data
##
## data:  ctable
## p-value = 0.5

```

```
## alternative hypothesis: two.sided
```