aneurismi

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

```
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
```

```
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
```