

# Absolute Winding Number by fx Probe Day d5

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## Aim

We examine whether APOE2, APOE3, and APOE4 carriers use a hippocampal or caudate based spatial navigation strategy.

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## Day d5 Probe by fx Vol

```
## [1] "fx: Probe d5 AWN VOL"
## [1] "omnibus test"

## model term    df1 df2 F.ratio p.value
## Genotype      2  17   5.866  0.0116
## Sex           1  17   0.189  0.6693
## Genotype:Sex   2  17   0.474  0.6307

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   7.221  0.0054
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   1.762  0.2017

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.760  0.3954
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
```

```

## Sex          1  17   0.142  0.7113
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex          1  17   0.239  0.6312

## [1] "anova: males and females"

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## fx          1  32.069  32.069   2.3724 0.141903
## Genotype     2 174.847  87.424   6.4675 0.008153 **
## Sex          1  33.922  33.922   2.5095 0.131589
## fx:Genotype   2  26.781  13.390   0.9906 0.391802
## fx:Sex        1  37.212  37.212   2.7529 0.115413
## Genotype:Sex   2  53.773  26.887   1.9890 0.167422
## fx:Genotype:Sex 2  52.708  26.354   1.9496 0.172862
## Residuals    17 229.797  13.517
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "females"

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## fx          1  14.268  14.268   0.6053 0.46205
## Genotype     2 192.582  96.291   4.0849 0.06674 .
## fx:Genotype   2  95.858  47.929   2.0333 0.20128
## Residuals     7 165.007  23.572
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "males"

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## fx          1   7.877   7.8769   1.2158 0.2960
## Genotype     2  29.100  14.5499   2.2457 0.1565
## fx:Genotype   2  22.410  11.2050   1.7294 0.2264
## Residuals    10  64.790   6.4790

## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
## contrast      estimate    SE df t.ratio p.value
## female - male    -3.36  3.86 17  -0.872  0.3954
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male    -1.10  2.93 17  -0.376  0.7113
##
## Genotype = APOE44:

```

```

## contrast      estimate    SE df t.ratio p.value
## female - male      1.81 3.71 17   0.489  0.6312

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33      1.44 3.12 17   0.461  0.8901
## APOE22 - APOE44     -8.09 2.69 17  -3.009  0.0205
## APOE33 - APOE44     -9.53 2.90 17  -3.287  0.0115
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33      3.70 3.70 17   1.000  0.5869
## APOE22 - APOE44     -2.92 4.63 17  -0.630  0.8057
## APOE33 - APOE44     -6.62 3.73 17  -1.773  0.2082
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## [1] "slopes"

## $emtrends
## Genotype fx.trend      SE df lower.CL upper.CL
## APOE22      -113043 97906 17  -319607   93521
## APOE33       28869 72820 17  -124768   182507
## APOE44       22333 89005 17  -165450   210117
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33  -141912 122018 17  -1.163  0.4902
## APOE22 - APOE44  -135377 132316 17  -1.023  0.5728
## APOE33 - APOE44    6536 114998 17   0.057  0.9982
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates
##
## $emtrends
## Sex = female:
## Genotype fx.trend      SE df lower.CL upper.CL
## APOE22      -123352 112767 17  -361270   114567
## APOE33       105184  64041 17   -29932   240299
## APOE44      -128391  69526 17  -275078   18297
##
## Sex = male:
## Genotype fx.trend      SE df lower.CL upper.CL
## APOE22      -102734 160081 17  -440476   235007
## APOE33      -47445 130805 17  -323420   228530
## APOE44       173058 163870 17  -172678   518793
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33  -228535 129683 17  -1.762  0.2119

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```
## APOE22 - APOE44      5039 132478 17    0.038  0.9992
## APOE33 - APOE44     233574  94526 17    2.471  0.0600
##
## Sex = male:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33   -55289 206727 17   -0.267  0.9614
## APOE22 - APOE44  -275792 229084 17   -1.204  0.4670
## APOE33 - APOE44  -220503 209674 17   -1.052  0.5557
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

## Day d5 Probe By fx FA

```
## [1] "fx: Probe d5 AWN FA"
## [1] "omnibus test"

## model term    df1 df2 F.ratio p.value
## Genotype      2  17   6.890  0.0064
## Sex           1  17   0.322  0.5780
## Genotype:Sex   2  17   1.127  0.3471

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   5.374  0.0155
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   1.782  0.1983

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.009  0.9267
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.260  0.6165
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex        1  17   2.708  0.1182

## [1] "anova: males and females"

## Analysis of Variance Table
##
## Response: Probe_d5
##          Df Sum Sq Mean Sq F value    Pr(>F)
## fx          1  65.299   65.299   4.0030 0.061652 .
## Genotype    2 213.991  106.995   6.5590 0.007741 **
## Sex          1   5.674    5.674   0.3478 0.563113
## fx:Genotype  2   4.441    2.221   0.1361 0.873666
## fx:Sex       1   3.028    3.028   0.1856 0.671989
## Genotype:Sex 2  54.696   27.348   1.6765 0.216511
## fx:Genotype:Sex 2  16.665    8.333   0.5108 0.608931
## Residuals   17 277.315   16.313
```

```

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "females"

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## fx          1  34.899   34.899   1.1098 0.3271
## Genotype     2 191.510   95.755   3.0450 0.1118
## fx:Genotype   2  21.181   10.591   0.3368 0.7250
## Residuals    7 220.124   31.446

## [1] "males"

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## fx          1   3.515    3.5153   0.6147 0.45121
## Genotype     2 47.553   23.7766   4.1574 0.04853 *
## fx:Genotype   2 15.917    7.9587   1.3916 0.29296
## Residuals   10 57.191    5.7191

## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
## contrast      estimate    SE df t.ratio p.value
## female - male    0.327 3.51 17   0.093  0.9267
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male  -1.943 3.81 17  -0.510  0.6165
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    5.023 3.05 17   1.645  0.1182

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    5.48 4.15 17   1.320  0.4037
## APOE22 - APOE44  -6.97 3.54 17  -1.966  0.1511
## APOE33 - APOE44  -12.45 3.92 17  -3.178  0.0144
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    3.21 3.09 17   1.039  0.5635
## APOE22 - APOE44  -2.27 3.01 17  -0.756  0.7340
## APOE33 - APOE44  -5.48 2.91 17  -1.885  0.1734
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends

```

```

## Genotype fx.trend SE df lower.CL upper.CL
## APOE22 -51.1 89.2 17 -239 137
## APOE33 -188.2 238.8 17 -692 316
## APOE44 -84.5 88.2 17 -270 101
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast estimate SE df t.ratio p.value
## APOE22 - APOE33 137.1 255 17 0.538 0.8540
## APOE22 - APOE44 33.4 125 17 0.267 0.9617
## APOE33 - APOE44 -103.7 255 17 -0.407 0.9131
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates
##
## $emtrends
## Sex = female:
## Genotype fx.trend SE df lower.CL upper.CL
## APOE22 -74.7 156.3 17 -405 255.1
## APOE33 -102.2 65.9 17 -241 36.8
## APOE44 16.3 81.2 17 -155 187.6
##
## Sex = male:
## Genotype fx.trend SE df lower.CL upper.CL
## APOE22 -27.4 85.7 17 -208 153.5
## APOE33 -274.1 473.1 17 -1272 724.0
## APOE44 -185.3 156.5 17 -516 144.9
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
## contrast estimate SE df t.ratio p.value
## APOE22 - APOE33 27.4 170 17 0.162 0.9857
## APOE22 - APOE44 -91.1 176 17 -0.517 0.8642
## APOE33 - APOE44 -118.5 105 17 -1.133 0.5075
##
## Sex = male:
## contrast estimate SE df t.ratio p.value
## APOE22 - APOE33 246.7 481 17 0.513 0.8660
## APOE22 - APOE44 157.9 178 17 0.885 0.6568
## APOE33 - APOE44 -88.8 498 17 -0.178 0.9827
##
## P value adjustment: tukey method for comparing a family of 3 estimates

```

## Day d5 Probe By fx DEG

```

## [1] "fx: Probe d5 AWN DEG"
## [1] "omnibus test"
## model term df1 df2 F.ratio p.value
## Genotype 2 17 8.488 0.0028

```

```

## Sex          1  17   2.317  0.1464
## Genotype:Sex  2  17   2.621  0.1018

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype    2  17   8.950  0.0022
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype    2  17   1.099  0.3556

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex          1  17   0.034  0.8566
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex          1  17   0.026  0.8745
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex          1  17   9.169  0.0076

## [1] "anova: males and females"

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df  Sum Sq Mean Sq F value    Pr(>F)
## fx           1   13.567    13.567    1.0230  0.325978
## Genotype      2  200.304   100.152    7.5521  0.004498 **
## Sex           1   31.988    31.988    2.4121  0.138817
## fx:Genotype   2   57.832    28.916    2.1805  0.143565
## fx:Sex        1    6.971     6.971    0.5257  0.478286
## Genotype:Sex  2   67.454    33.727    2.5432  0.108079
## fx:Genotype:Sex 2   37.544    18.772    1.4155  0.270005
## Residuals    17  225.446    13.262
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "females"

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df  Sum Sq Mean Sq F value    Pr(>F)
## fx           1   10.203    10.203    0.4812  0.5103
## Genotype      2  194.044    97.022    4.5755  0.0536 .
## fx:Genotype   2  115.035    57.517    2.7125  0.1342
## Residuals     7  148.433    21.205
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "males"

## Analysis of Variance Table
##
## Response: Probe_d5

```

```

##              Df Sum Sq Mean Sq F value Pr(>F)
## fx              1  1.836   1.8360   0.2384 0.6359
## Genotype        2 40.040  20.0201   2.5996 0.1233
## fx:Genotype     2   5.288   2.6439   0.3433 0.7175
## Residuals      10 77.013   7.7013

## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
## contrast      estimate    SE df t.ratio p.value
## female - male    0.570 3.11 17    0.183  0.8566
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male   -0.451 2.81 17   -0.160  0.8745
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    7.222 2.38 17    3.028  0.0076

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    3.18 3.35 17    0.950  0.6174
## APOE22 - APOE44   -8.06 3.09 17   -2.610  0.0458
## APOE33 - APOE44  -11.25 2.79 17   -4.036  0.0023
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    2.16 2.52 17    0.859  0.6726
## APOE22 - APOE44   -1.41 2.41 17   -0.585  0.8297
## APOE33 - APOE44   -3.57 2.42 17   -1.479  0.3251
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends
## Genotype fx.trend      SE df lower.CL upper.CL
## APOE22    0.000405 0.000724 17 -0.00112 0.001933
## APOE33    0.000064 0.000625 17 -0.00125 0.001382
## APOE44   -0.000236 0.000378 17 -0.00103 0.000562
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33 0.000341 0.000956 17    0.357  0.9325
## APOE22 - APOE44 0.000641 0.000817 17    0.785  0.7172
## APOE33 - APOE44 0.000300 0.000730 17    0.411  0.9117
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
## Genotype fx.trend      SE df lower.CL upper.CL

```



```

## APOE22    0.000435 0.000841 17 -0.001339 2.21e-03
## APOE33    0.000508 0.000297 17 -0.000118 1.13e-03
## APOE44   -0.000953 0.000407 17 -0.001810 -9.51e-05
##
## Sex = male:
## Genotype  fx.trend      SE df  lower.CL  upper.CL
## APOE22    0.000375 0.001179 17 -0.002111 2.86e-03
## APOE33   -0.000380 0.001213 17 -0.002940 2.18e-03
## APOE44    0.000481 0.000638 17 -0.000864 1.83e-03
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33 -7.32e-05 0.000892 17 -0.082 0.9963
## APOE22 - APOE44 1.39e-03 0.000934 17 1.486 0.3222
## APOE33 - APOE44 1.46e-03 0.000503 17 2.903 0.0255
##
## Sex = male:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33 7.55e-04 0.001692 17 0.447 0.8965
## APOE22 - APOE44 -1.06e-04 0.001340 17 -0.079 0.9966
## APOE33 - APOE44 -8.61e-04 0.001371 17 -0.628 0.8067
##
## P value adjustment: tukey method for comparing a family of 3 estimates

```

## Day d5 Probe By fx CLUS

```

## [1] "fx: Probe d5 AWN CLUSTERING"
## [1] "omnibus test"

## model term  df1 df2 F.ratio p.value
## Genotype    2  17  6.732 0.0070
## Sex          1  17  1.391 0.2545
## Genotype:Sex  2  17  2.327 0.1279

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype    2  17  7.624 0.0043
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype    2  17  0.763 0.4818

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17  0.000 0.9947
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex        1  17  0.042 0.8397
##
## Genotype = APOE44:

```

```
## model term df1 df2 F.ratio p.value
## Sex          1  17   7.872  0.0122

## model term      df1 df2 F.ratio p.value
## fx              1  17   0.061  0.8076
## Genotype        2  17   3.951  0.0390
## Sex             1  17   0.228  0.6389
## fx:Genotype     2  17   0.131  0.8784
## fx:Sex          1  17   0.052  0.8215
## Genotype:Sex    2  17   0.077  0.9265
## fx:Genotype:Sex 2  17   1.531  0.2447

## [1] "anova: males and females"

## Analysis of Variance Table
##
## Response: Probe_d5
##          Df Sum Sq Mean Sq F value Pr(>F)
## fx          1  15.796   15.796   1.0688 0.315697
## Genotype     2 198.991   99.496   6.7320 0.007025 **
## Sex          1  32.715   32.715   2.2135 0.155120
## fx:Genotype  2  38.368   19.184   1.2980 0.298800
## fx:Sex       1   0.932    0.932   0.0630 0.804776
## Genotype:Sex 2  57.797   28.898   1.9553 0.172067
## fx:Genotype:Sex 2  45.259   22.630   1.5312 0.244666
## Residuals    17 251.250   14.779
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "females"

## Analysis of Variance Table
##
## Response: Probe_d5
##          Df Sum Sq Mean Sq F value Pr(>F)
## fx          1  16.164   16.164   0.6403 0.44992
## Genotype     2 189.449   94.724   3.7521 0.07809 .
## fx:Genotype  2  85.380   42.690   1.6910 0.25169
## Residuals    7 176.721   25.246
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "males"

## Analysis of Variance Table
##
## Response: Probe_d5
##          Df Sum Sq Mean Sq F value Pr(>F)
## fx          1   0.586    0.5859  0.0786 0.7849
## Genotype     2  39.345  19.6723  2.6396 0.1201
## fx:Genotype  2   9.718   4.8589  0.6520 0.5418
## Residuals   10  74.529   7.4529

## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
## contrast      estimate    SE df t.ratio p.value
## female - male    0.026 3.87 17   0.007  0.9947
```

```

##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male   -0.619 3.01 17  -0.205  0.8397
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    7.103 2.53 17   2.806  0.0122

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    2.861 3.68 17   0.777  0.7216
## APOE22 - APOE44   -8.073 3.41 17  -2.365  0.0735
## APOE33 - APOE44  -10.934 2.94 17  -3.721  0.0046
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    2.216 3.24 17   0.684  0.7761
## APOE22 - APOE44   -0.995 3.12 17  -0.319  0.9456
## APOE33 - APOE44   -3.212 2.62 17  -1.226  0.4546
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## [1] "slopes"

## $emtrends
## Genotype fx.trend    SE df lower.CL upper.CL
## APOE22      0.1098 0.292 17   -0.507    0.726
## APOE33      0.0174 0.152 17   -0.303    0.338
## APOE44     -0.0404 0.121 17   -0.297    0.216
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    0.0924 0.329 17   0.280  0.9577
## APOE22 - APOE44    0.1503 0.316 17   0.475  0.8840
## APOE33 - APOE44    0.0579 0.195 17   0.297  0.9525
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
## Genotype fx.trend    SE df lower.CL upper.CL
## APOE22      0.0852 0.2807 17  -0.5070    0.6774
## APOE33      0.1593 0.0981 17  -0.0476    0.3663
## APOE44     -0.2381 0.1340 17  -0.5207    0.0446
##
## Sex = male:
## Genotype fx.trend    SE df lower.CL upper.CL
## APOE22      0.1345 0.5126 17  -0.9470    1.2159
## APOE33     -0.1244 0.2878 17  -0.7317    0.4828
## APOE44      0.1572 0.2026 17  -0.2701    0.5846
##

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## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33 -0.0741 0.297 17  -0.249  0.9664
## APOE22 - APOE44  0.3233 0.311 17   1.039  0.5631
## APOE33 - APOE44  0.3974 0.166 17   2.393  0.0697
##
## Sex = male:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33  0.2589 0.588 17   0.440  0.8992
## APOE22 - APOE44 -0.0228 0.551 17  -0.041  0.9991
## APOE33 - APOE44 -0.2816 0.352 17  -0.800  0.7079
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## [1] "slopes"
## $emtrends
## Genotype fx.trend      SE df lower.CL upper.CL
## APOE22      0.1098 0.292 17  -0.507    0.726
## APOE33      0.0174 0.152 17  -0.303    0.338
## APOE44     -0.0404 0.121 17  -0.297    0.216
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33  0.0924 0.329 17   0.280  0.9577
## APOE22 - APOE44  0.1503 0.316 17   0.475  0.8840
## APOE33 - APOE44  0.0579 0.195 17   0.297  0.9525
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates
## $emtrends
## Sex = female:
## Genotype fx.trend      SE df lower.CL upper.CL
## APOE22      0.0852 0.2807 17  -0.5070    0.6774
## APOE33      0.1593 0.0981 17  -0.0476    0.3663
## APOE44     -0.2381 0.1340 17  -0.5207    0.0446
##
## Sex = male:
## Genotype fx.trend      SE df lower.CL upper.CL
## APOE22      0.1345 0.5126 17  -0.9470    1.2159
## APOE33     -0.1244 0.2878 17  -0.7317    0.4828
## APOE44      0.1572 0.2026 17  -0.2701    0.5846
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
## contrast      estimate      SE df t.ratio p.value

```

```
## P value adjustment: tukey method for comparing a family of 3 estimates
```

