

Absolute Winding Number by fi 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.

Day d5 Probe by fi Vol

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

## model term    df1 df2 F.ratio p.value
## Genotype      2  17   7.486  0.0047
## Sex           1  17   0.188  0.6697
## Genotype:Sex   2  17   0.978  0.3961

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   5.015  0.0194
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   2.727  0.0939

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.096  0.7604
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
```

```

## Sex          1  17   1.090  0.3110
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex          1  17   0.786  0.3876

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

## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq Mean Sq F value    Pr(>F)
## fi              1 155.368 155.368 17.8124 0.0005756 ***
## Genotype        2 138.410  69.205   7.9341 0.0036832 **
## Sex             1  35.961  35.961   4.1227 0.0582560 .
## fi:Genotype     2  45.035  22.517   2.5815 0.1049454
## fi:Sex          1   0.164   0.164   0.0188 0.8924384
## Genotype:Sex    2  12.716   6.358   0.7289 0.4969182
## fi:Genotype:Sex 2 105.172  52.586   6.0288 0.0104982 *
## Residuals      17 148.283   8.723
## ---
## 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)
## fi              1 152.355 152.355 10.7125 0.01362 *
## Genotype        2  74.249  37.124   2.6103 0.14224
## fi:Genotype     2 141.555  70.777   4.9765 0.04524 *
## Residuals       7  99.556  14.222
## ---
## 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)
## fi              1  21.158  21.1579   4.3421 0.06379 .
## Genotype        2  47.621  23.8103   4.8865 0.03309 *
## fi:Genotype     2   6.672   3.3358   0.6846 0.52645
## Residuals      10 48.727   4.8727
## ---
## 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  -0.592 1.91 17  -0.310  0.7604
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male  -3.075 2.94 17  -1.044  0.3110

```

```

##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    1.886 2.13 17   0.887  0.3876

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    4.83 3.01 17   1.608  0.2694
## APOE22 - APOE44   -4.55 2.21 17  -2.058  0.1287
## APOE33 - APOE44   -9.38 3.10 17  -3.027  0.0197
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    2.35 1.81 17   1.299  0.4151
## APOE22 - APOE44   -2.07 1.82 17  -1.139  0.5039
## APOE33 - APOE44   -4.42 1.89 17  -2.333  0.0780
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## [1] "slopes"

## $emtrends
## Genotype fi.trend    SE df lower.CL upper.CL
## APOE22      -1897 16721 17   -37176   33382
## APOE33      11232 12406 17   -14942   37407
## APOE44     -22760  7199 17   -37950  -7571
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33  -13130 20821 17  -0.631  0.8055
## APOE22 - APOE44   20863 18205 17   1.146  0.5001
## APOE33 - APOE44   33993 14344 17   2.370  0.0728
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
## Genotype fi.trend    SE df lower.CL upper.CL
## APOE22      12461 14178 17   -17453   42375
## APOE33      45226 21547 17    -234   90685
## APOE44     -36817  9967 17   -57845  -15788
##
## Sex = male:
## Genotype fi.trend    SE df lower.CL upper.CL
## APOE22     -16256 30288 17   -80159   47647
## APOE33     -22761 12304 17   -48720   3197
## APOE44     -8704 10392 17   -30628  13220
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:

```

```
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33  -32765 25793 17  -1.270  0.4303
## APOE22 - APOE44   49278 17331 17   2.843  0.0287
## APOE33 - APOE44   82043 23740 17   3.456  0.0080
##
## Sex = male:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33    6506 32692 17   0.199  0.9784
## APOE22 - APOE44  -7552 32022 17  -0.236  0.9699
## APOE33 - APOE44 -14058 16105 17  -0.873  0.6641
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d5 Probe By fi FA

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

## model term    df1 df2 F.ratio p.value
## Genotype      2  17   4.095  0.0353
## Sex           1  17   0.416  0.5276
## Genotype:Sex   2  17   0.461  0.6381

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype    2  17   3.923  0.0397
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype    2  17   0.868  0.4377

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.152  0.7012
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.064  0.8035
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex        1  17   1.487  0.2393

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

## Analysis of Variance Table
##
## Response: Probe_d5
##          Df Sum Sq Mean Sq F value    Pr(>F)
## fi          1    3.117    3.117   0.2120 0.651043
## Genotype     2 204.346 102.173   6.9491 0.006229 **
## Sex          1  36.344   36.344   2.4718 0.134327
## fi:Genotype   2 119.848   59.924   4.0756 0.035816 *
## fi:Sex        1    3.599    3.599   0.2448 0.627086
## Genotype:Sex   2  13.096    6.548   0.4453 0.647875
```

```

## fi:Genotype:Sex  2  10.806   5.403  0.3675 0.697839
## Residuals       17 249.953  14.703
## ---
## 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)
## fi          1   1.972    1.972   0.0813 0.78385
## Genotype     2 223.020  111.510   4.5948 0.05315 .
## fi:Genotype  2   72.842   36.421   1.5008 0.28682
## Residuals    7  169.880   24.269
## ---
## 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)
## fi          1   8.650   8.6498   1.0802 0.3231
## Genotype     2  32.041  16.0204   2.0007 0.1858
## fi:Genotype  2   3.413   1.7067   0.2131 0.8116
## Residuals   10  80.073   8.0073
##
## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
## contrast      estimate    SE df t.ratio p.value
## female - male      1.02 2.61 17   0.390  0.7012
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male    -0.96 3.80 17  -0.253  0.8035
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male      3.42 2.81 17   1.219  0.2393
##
## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33      3.83 3.10 17   1.233  0.4504
## APOE22 - APOE44    -4.86 2.82 17  -1.721  0.2262
## APOE33 - APOE44    -8.68 3.15 17  -2.757  0.0342
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33      1.85 3.41 17   0.543  0.8513
## APOE22 - APOE44    -2.45 2.59 17  -0.948  0.6184
## APOE33 - APOE44    -4.30 3.52 17  -1.223  0.4560
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

```

```

## $emtrends
## Genotype fi.trend SE df lower.CL upper.CL
## APOE22 -40.3 78.2 17 -205.3 125
## APOE33 -48.2 101.4 17 -262.0 166
## APOE44 144.8 96.4 17 -58.6 348
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast estimate SE df t.ratio p.value
## APOE22 - APOE33 7.87 128 17 0.061 0.9979
## APOE22 - APOE44 -185.09 124 17 -1.491 0.3197
## APOE33 - APOE44 -192.96 140 17 -1.380 0.3731
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
## Genotype fi.trend SE df lower.CL upper.CL
## APOE22 -95.5 84.1 17 -272.9 82.0
## APOE33 -108.3 66.3 17 -248.2 31.6
## APOE44 185.9 119.3 17 -65.8 437.5
##
## Sex = male:
## Genotype fi.trend SE df lower.CL upper.CL
## APOE22 14.9 131.9 17 -263.3 293.1
## APOE33 12.0 191.6 17 -392.2 416.1
## APOE44 103.7 151.4 17 -215.8 423.2
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
## contrast estimate SE df t.ratio p.value
## APOE22 - APOE33 12.8 107 17 0.120 0.9921
## APOE22 - APOE44 -281.3 146 17 -1.928 0.1613
## APOE33 - APOE44 -294.2 136 17 -2.156 0.1082
##
## Sex = male:
## contrast estimate SE df t.ratio p.value
## APOE22 - APOE33 2.9 233 17 0.012 0.9999
## APOE22 - APOE44 -88.8 201 17 -0.442 0.8984
## APOE33 - APOE44 -91.7 244 17 -0.376 0.9255
##
## P value adjustment: tukey method for comparing a family of 3 estimates

```

Day d5 Probe By fi DEG

```

## [1] "fi: Probe d5 AWN DEG"
## [1] "omnibus test"
## model term df1 df2 F.ratio p.value

```

```

## Genotype      2  17   6.072  0.0102
## Sex           1  17   1.141  0.3004
## Genotype:Sex  2  17   0.829  0.4534

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype    2  17   5.157  0.0178
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype    2  17   1.368  0.2812

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex         1  17   0.451  0.5108
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex         1  17   0.096  0.7599
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex         1  17   2.417  0.1385

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

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## fi         1   8.333   8.333   0.5610 0.464102
## Genotype    2 207.999 103.999   7.0013 0.006052 **
## Sex         1  29.277  29.277   1.9709 0.178355
## fi:Genotype  2  49.614  24.807   1.6700 0.217686
## fi:Sex       1  37.329  37.329   2.5130 0.131336
## Genotype:Sex  2  23.258  11.629   0.7829 0.472893
## fi:Genotype:Sex  2  32.777  16.389   1.1033 0.354399
## Residuals   17 252.523  14.854
## ---
## 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)
## fi         1   1.503   1.503   0.0527 0.82502
## Genotype    2 222.582 111.291   3.9007 0.07274 .
## fi:Genotype  2  43.914  21.957   0.7696 0.49875
## Residuals    7 199.715  28.531
## ---
## 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)
## fi           1 17.843 17.8430   3.3789 0.09589 .
## Genotype      2 51.792 25.8960   4.9038 0.03280 *
## fi:Genotype   2  1.734  0.8672   0.1642 0.85080
## Residuals    10 52.808  5.2808
## ---
## 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    1.910 2.84 17   0.672  0.5108
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male   -0.914 2.94 17  -0.311  0.7599
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    4.269 2.75 17   1.555  0.1385
##
## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    3.75 3.20 17   1.172  0.4850
## APOE22 - APOE44   -5.69 2.88 17  -1.975  0.1488
## APOE33 - APOE44   -9.44 3.02 17  -3.121  0.0162
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    0.93 2.55 17   0.365  0.9296
## APOE22 - APOE44   -3.33 2.71 17  -1.228  0.4537
## APOE33 - APOE44   -4.26 2.66 17  -1.601  0.2723
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## [1] "slopes"

## $emtrends
## Genotype fi.trend      SE df lower.CL upper.CL
## APOE22    4.98e-05 0.000188 17 -0.000346 0.000446
## APOE33    4.33e-06 0.000097 17 -0.000200 0.000209
## APOE44   -1.26e-04 0.000108 17 -0.000355 0.000102
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33 4.54e-05 0.000211 17   0.215  0.9748
## APOE22 - APOE44 1.76e-04 0.000217 17   0.813  0.7001
## APOE33 - APOE44 1.31e-04 0.000145 17   0.899  0.6479
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

```



```

## $semtrends
## Sex = female:
##   Genotype fi.trend      SE df  lower.CL upper.CL
##   APOE22    0.000287 0.000295 17 -3.36e-04 0.000909
##   APOE33    0.000173 0.000106 17 -5.16e-05 0.000397
##   APOE44   -0.000144 0.000169 17 -5.01e-04 0.000212
##
## Sex = male:
##   Genotype fi.trend      SE df  lower.CL upper.CL
##   APOE22   -0.000187 0.000232 17 -6.76e-04 0.000302
##   APOE33   -0.000164 0.000162 17 -5.06e-04 0.000178
##   APOE44   -0.000109 0.000135 17 -3.94e-04 0.000177
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##   contrast      estimate      SE df t.ratio p.value
##   APOE22 - APOE33  1.14e-04 0.000314 17   0.363  0.9302
##   APOE22 - APOE44  4.31e-04 0.000340 17   1.267  0.4322
##   APOE33 - APOE44  3.17e-04 0.000200 17   1.587  0.2778
##
## Sex = male:
##   contrast      estimate      SE df t.ratio p.value
##   APOE22 - APOE33 -2.30e-05 0.000283 17  -0.081  0.9964
##   APOE22 - APOE44 -7.84e-05 0.000268 17  -0.292  0.9542
##   APOE33 - APOE44 -5.54e-05 0.000211 17  -0.262  0.9629
##
## P value adjustment: tukey method for comparing a family of 3 estimates

```

Day d5 Probe By fi CLUS

```

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

##   model term  df1 df2 F.ratio p.value
##   Genotype    2  17   6.290  0.0090
##   Sex          1  17   1.568  0.2275
##   Genotype:Sex  2  17   0.947  0.4075

## Sex = female:
##   model term df1 df2 F.ratio p.value
##   Genotype    2  17   5.699  0.0128
##
## Sex = male:
##   model term df1 df2 F.ratio p.value
##   Genotype    2  17   1.297  0.2990

## Genotype = APOE22:
##   model term df1 df2 F.ratio p.value
##   Sex        1  17   0.501  0.4886
##
## Genotype = APOE33:
##   model term df1 df2 F.ratio p.value

```

```

## Sex          1  17   0.047  0.8312
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex          1  17   3.245  0.0894

## model term      df1 df2 F.ratio p.value
## fi              1  17   0.038  0.8472
## Genotype        2  17   3.661  0.0476
## Sex              1  17   2.694  0.1191
## fi:Genotype      2  17   0.257  0.7767
## fi:Sex           1  17   2.118  0.1638
## Genotype:Sex     2  17   0.228  0.7987
## fi:Genotype:Sex  2  17   0.637  0.5412

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

## Analysis of Variance Table
##
## Response: Probe_d5
##              Df  Sum Sq Mean Sq F value  Pr(>F)
## fi              1    0.185    0.185    0.0117 0.91507
## Genotype        2  207.668  103.834    6.5870 0.00762 **
## Sex              1   32.592   32.592    2.0676 0.16862
## fi:Genotype      2   39.408   19.704    1.2500 0.31155
## fi:Sex           1   50.071   50.071    3.1764 0.09258 .
## Genotype:Sex     2   23.133   11.567    0.7338 0.49470
## fi:Genotype:Sex  2   20.075   10.037    0.6368 0.54116
## Residuals       17  267.977   15.763
## ---
## 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)
## fi              1  14.005   14.005    0.4649 0.51727
## Genotype        2  206.587  103.293    3.4286 0.09162 .
## fi:Genotype      2   36.234   18.117    0.6014 0.57410
## Residuals       7  210.888   30.127
## ---
## 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)
## fi              1  13.939  13.9392    2.4416 0.14922
## Genotype        2  51.958  25.9792    4.5506 0.03933 *
## fi:Genotype      2   1.190   0.5949    0.1042 0.90200
## Residuals      10  57.089   5.7089
## ---
## 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    2.721 3.84 17    0.708  0.4886
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male   -0.648 2.99 17   -0.216  0.8312
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    4.922 2.73 17    1.801  0.0894
##
## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    4.082 3.94 17    1.036  0.5653
## APOE22 - APOE44   -5.762 3.61 17   -1.597  0.2738
## APOE33 - APOE44   -9.844 2.97 17   -3.313  0.0109
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    0.713 2.86 17    0.249  0.9665
## APOE22 - APOE44   -3.562 3.04 17   -1.173  0.4847
## APOE33 - APOE44   -4.274 2.76 17   -1.550  0.2935
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends
## Genotype fi.trend      SE df lower.CL upper.CL
## APOE22    0.02577 0.1142 17   -0.215  0.2666
## APOE33   -0.00704 0.0464 17   -0.105  0.0908
## APOE44   -0.04449 0.0465 17   -0.143  0.0536
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33    0.0328 0.1232 17    0.266  0.9618
## APOE22 - APOE44    0.0703 0.1233 17    0.570  0.8377
## APOE33 - APOE44    0.0375 0.0657 17    0.570  0.8376
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
## Genotype fi.trend      SE df lower.CL upper.CL
## APOE22    0.1357 0.1902 17   -0.2657  0.5371
## APOE33    0.0656 0.0417 17   -0.0225  0.1537
## APOE44   -0.0354 0.0578 17   -0.1574  0.0866
##
## Sex = male:

```

```

## Genotype fi.trend      SE df lower.CL upper.CL
## APOE22      -0.0842 0.1262 17  -0.3505  0.1821
## APOE33      -0.0797 0.0829 17  -0.2545  0.0952
## APOE44      -0.0536 0.0728 17  -0.2072  0.1001
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33  0.0701 0.1948 17   0.360  0.9313
## APOE22 - APOE44  0.1711 0.1988 17   0.861  0.6716
## APOE33 - APOE44  0.1010 0.0713 17   1.416  0.3551
##
## Sex = male:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33 -0.0045 0.1510 17  -0.030  0.9995
## APOE22 - APOE44 -0.0306 0.1457 17  -0.210  0.9760
## APOE33 - APOE44 -0.0261 0.1103 17  -0.237  0.9697
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## [1] "slopes"
## $emtrends
## Genotype fi.trend      SE df lower.CL upper.CL
## APOE22      0.02577 0.1142 17  -0.215  0.2666
## APOE33     -0.00704 0.0464 17  -0.105  0.0908
## APOE44     -0.04449 0.0465 17  -0.143  0.0536
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33  0.0328 0.1232 17   0.266  0.9618
## APOE22 - APOE44  0.0703 0.1233 17   0.570  0.8377
## APOE33 - APOE44  0.0375 0.0657 17   0.570  0.8376
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates
## $emtrends
## Sex = female:
## Genotype fi.trend      SE df lower.CL upper.CL
## APOE22      0.1357 0.1902 17  -0.2657  0.5371
## APOE33      0.0656 0.0417 17  -0.0225  0.1537
## APOE44     -0.0354 0.0578 17  -0.1574  0.0866
##
## Sex = male:
## Genotype fi.trend      SE df lower.CL upper.CL
## APOE22     -0.0842 0.1262 17  -0.3505  0.1821
## APOE33     -0.0797 0.0829 17  -0.2545  0.0952
## APOE44     -0.0536 0.0728 17  -0.2072  0.1001
##

```

```

## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##   contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33   0.0701 0.1948 17   0.360  0.9313
## APOE22 - APOE44   0.1711 0.1988 17   0.861  0.6716
## APOE33 - APOE44   0.1010 0.0713 17   1.416  0.3551
##
## Sex = male:
##   contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33  -0.0045 0.1510 17  -0.030  0.9995
## APOE22 - APOE44  -0.0306 0.1457 17  -0.210  0.9760
## APOE33 - APOE44  -0.0261 0.1103 17  -0.237  0.9697
##
## P value adjustment: tukey method for comparing a family of 3 estimates

```

