

Absolute Winding Number by ic Probe Day d8

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10/28/2021

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Aim

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

Day d8 Probe by ic Vol

```
## [1] "ic: Probe d8 AWN VOL"
## [1] "omnibus test"

## model term    df1 df2 F.ratio p.value
## Genotype      2  17  16.656  0.0001
## Sex            1  17   3.326  0.0858
## Genotype:Sex   2  17   0.201  0.8201

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype   2  17  11.682  0.0006
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   6.470  0.0081

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.497  0.4902
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
```

```

## Sex          1  17   1.128  0.3031
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex          1  17   1.786  0.1990

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

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## ic           1   0.058    0.058   0.0147  0.90491
## Genotype      2 195.431   97.715  24.6351 9.498e-06 ***
## Sex           1  14.303   14.303   3.6060  0.07468 .
## ic:Genotype   2   8.285    4.143   1.0444  0.37342
## ic:Sex         1   6.553    6.553   1.6521  0.21591
## Genotype:Sex   2   1.950    0.975   0.2458  0.78478
## ic:Genotype:Sex 2   5.787    2.893   0.7294  0.49668
## Residuals     17  67.431    3.967
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "females"

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## ic           1   0.257    0.257   0.0567  0.81864
## Genotype      2  84.428   42.214   9.3246 0.01062 *
## ic:Genotype   2  20.982   10.491   2.3173 0.16893
## Residuals      7  31.690    4.527
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "males"

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## ic           1   2.232    2.232   0.6246  0.447684
## Genotype      2  99.633   49.816  13.9384 0.001283 **
## ic:Genotype   2   0.430    0.215   0.0602  0.941901
## Residuals     10  35.740    3.574
## ---
## 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    0.869 1.23 17   0.705  0.4902
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male    1.660 1.56 17   1.062  0.3031

```

```

##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    2.076 1.55 17    1.336 0.1990

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    1.29 1.47 17    0.876 0.6622
## APOE22 - APOE44   -5.01 1.28 17   -3.898 0.0031
## APOE33 - APOE44   -6.30 1.47 17   -4.277 0.0014
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    2.08 1.34 17    1.549 0.2942
## APOE22 - APOE44   -3.80 1.51 17   -2.516 0.0550
## APOE33 - APOE44   -5.88 1.64 17   -3.585 0.0061
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## [1] "slopes"

## $emtrends
## Genotype ic.trend    SE df lower.CL upper.CL
## APOE22      -7949  6398 17   -21447    5549
## APOE33       4199  8697 17   -14151   22548
## APOE44      11021 14528 17   -19631   41672
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33  -12148 10797 17   -1.125 0.5122
## APOE22 - APOE44  -18970 15874 17   -1.195 0.4720
## APOE33 - APOE44   -6822 16932 17   -0.403 0.9149
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates
##
## $emtrends
## Sex = female:
## Genotype ic.trend    SE df lower.CL upper.CL
## APOE22     -19839 10245 17   -41454    1776
## APOE33      4828 12479 17   -21501   31157
## APOE44      8739  7412 17    -6899   24376
##
## Sex = male:
## Genotype ic.trend    SE df lower.CL upper.CL
## APOE22      3941  7666 17   -12233   20114
## APOE33      3569 12118 17   -21998   29136
## APOE44     13303 28095 17   -45972   72577
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:

```

```
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33   -24667 16146 17  -1.528  0.3033
## APOE22 - APOE44   -28578 12645 17  -2.260  0.0894
## APOE33 - APOE44    -3910 14514 17  -0.269  0.9609
##
## Sex = male:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33      372 14339 17   0.026  0.9996
## APOE22 - APOE44   -9362 29122 17  -0.321  0.9448
## APOE33 - APOE44   -9734 30597 17  -0.318  0.9459
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d8 Probe By ic FA

```
## [1] "ic: Probe d8 AWN FA"
## [1] "omnibus test"

## model term    df1 df2 F.ratio p.value
## Genotype      2  17   7.791  0.0040
## Sex           1  17   0.000  0.9892
## Genotype:Sex   2  17   0.377  0.6916

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   2.716  0.0947
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   5.416  0.0151

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.307  0.5867
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.156  0.6975
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.401  0.5348

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

## Analysis of Variance Table
##
## Response: Probe_d8
##          Df Sum Sq Mean Sq F value    Pr(>F)
## ic        1  53.343   53.343 12.6130  0.002454 **
## Genotype   2 169.108   84.554 19.9929 3.426e-05 ***
## Sex        1   0.226    0.226  0.0534  0.819975
## ic:Genotype 2   0.785    0.393  0.0928  0.911806
## ic:Sex      1   0.248    0.248  0.0587  0.811448
## Genotype:Sex 2   1.525    0.762  0.1803  0.836616
```

```

## ic:Genotype:Sex  2   2.666   1.333  0.3152  0.733838
## Residuals       17  71.897   4.229
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "females"

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## ic           1  29.576   29.576   5.2301 0.05606 .
## Genotype      2  67.090   33.545   5.9320 0.03113 *
## ic:Genotype   2   1.106    0.553   0.0978 0.90808
## Residuals     7  39.585    5.655
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "males"

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## ic           1   1.844    1.844   0.5706 0.4674520
## Genotype      2 100.901   50.450  15.6136 0.0008396 ***
## ic:Genotype   2   2.980    1.490   0.4611 0.6433621
## Residuals    10  32.312    3.231
## ---
## 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    0.954 1.72 17   0.554  0.5867
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male    0.827 2.09 17   0.395  0.6975
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male   -1.728 2.73 17  -0.634  0.5348

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    3.04 1.82 17   1.671  0.2446
## APOE22 - APOE44   -2.43 2.13 17  -1.139  0.5040
## APOE33 - APOE44   -5.47 2.42 17  -2.260  0.0895
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    2.91 2.01 17   1.451  0.3381
## APOE22 - APOE44   -5.11 2.42 17  -2.115  0.1165
## APOE33 - APOE44   -8.03 2.44 17  -3.290  0.0114
##

```

```

## P value adjustment: tukey method for comparing a family of 3 estimates
## [1] "slopes"
## $emtrends
##   Genotype ic.trend    SE df lower.CL upper.CL
##   APOE22      -82.4  65.6 17    -221      56
##   APOE33       19.0 154.0 17    -306     344
##   APOE44     -161.6 141.9 17    -461     138
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##   contrast      estimate    SE df t.ratio p.value
##   APOE22 - APOE33   -101.5 167 17   -0.606  0.8188
##   APOE22 - APOE44    79.1 156 17    0.506  0.8694
##   APOE33 - APOE44   180.6 209 17    0.862  0.6705
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates
## $emtrends
## Sex = female:
##   Genotype ic.trend    SE df lower.CL upper.CL
##   APOE22     -110.0 103.5 17    -328    108.4
##   APOE33     -53.6  53.3 17    -166     58.8
##   APOE44     -80.9  82.8 17    -256     93.8
##
## Sex = male:
##   Genotype ic.trend    SE df lower.CL upper.CL
##   APOE22     -54.8  80.6 17    -225    115.3
##   APOE33      91.6 303.4 17    -548    731.8
##   APOE44    -242.2 271.5 17    -815    330.5
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##   contrast      estimate    SE df t.ratio p.value
##   APOE22 - APOE33   -56.5 116.4 17   -0.485  0.8793
##   APOE22 - APOE44   -29.2 132.6 17   -0.220  0.9737
##   APOE33 - APOE44    27.3  98.5 17    0.277  0.9587
##
## Sex = male:
##   contrast      estimate    SE df t.ratio p.value
##   APOE22 - APOE33  -146.5 313.9 17   -0.467  0.8877
##   APOE22 - APOE44   187.4 283.2 17    0.662  0.7883
##   APOE33 - APOE44   333.9 407.1 17    0.820  0.6960
##
## P value adjustment: tukey method for comparing a family of 3 estimates

```

Day d8 Probe By ic DEG

```
## [1] "ic: Probe d8 AWN DEG"
```

```

## [1] "omnibus test"

## model term    df1 df2 F.ratio p.value
## Genotype      2  17  19.871 <.0001
## Sex           1  17   1.405  0.2522
## Genotype:Sex   2  17   0.619  0.5501

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype   2  17  10.665  0.0010
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   9.871  0.0014

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17   2.550  0.1287
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.071  0.7930
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex        1  17   1.606  0.2221

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

## Analysis of Variance Table
##
## Response: Probe_d8
##          Df Sum Sq Mean Sq F value    Pr(>F)
## ic         1   6.196    6.196   1.5907    0.2243
## Genotype    2 201.981  100.990  25.9300 6.856e-06 ***
## Sex         1   6.128    6.128   1.5734    0.2267
## ic:Genotype  2   0.842    0.421   0.1081    0.8982
## ic:Sex       1  10.694   10.694   2.7457    0.1159
## Genotype:Sex  2   5.028    2.514   0.6454    0.5368
## ic:Genotype:Sex  2   2.720    1.360   0.3491    0.7102
## Residuals   17  66.211    3.895
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "females"

## Analysis of Variance Table
##
## Response: Probe_d8
##          Df Sum Sq Mean Sq F value    Pr(>F)
## ic         1   4.435    4.435   0.9388 0.364862
## Genotype    2  96.272   48.136  10.1890 0.008452 **
## ic:Genotype  2   3.579    1.790   0.3788 0.697888
## Residuals    7  33.070    4.724
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "males"

```

```

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## ic           1 24.347   24.347   7.3468 0.021915 *
## Genotype      2 77.201   38.601  11.6476 0.002444 **
## ic:Genotype   2  3.347    1.673   0.5049 0.618135
## Residuals    10 33.140    3.314
## ---
## 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    2.139 1.34 17   1.597  0.1287
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male   -0.565 2.12 17  -0.267  0.7930
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    1.875 1.48 17   1.267  0.2221

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    3.93 2.13 17   1.847  0.1847
## APOE22 - APOE44   -4.68 1.34 17  -3.506  0.0072
## APOE33 - APOE44   -8.61 2.16 17  -3.995  0.0026
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    1.23 1.32 17   0.928  0.6305
## APOE22 - APOE44   -4.95 1.48 17  -3.334  0.0104
## APOE33 - APOE44   -6.17 1.42 17  -4.334  0.0012
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends
## Genotype ic.trend      SE df lower.CL upper.CL
## APOE22    8.18e-05 0.000231 17 -0.000406 0.000570
## APOE33   -1.44e-05 0.000173 17 -0.000380 0.000351
## APOE44    1.79e-04 0.000163 17 -0.000165 0.000522
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33  9.63e-05 0.000289 17   0.333  0.9408
## APOE22 - APOE44 -9.67e-05 0.000283 17  -0.342  0.9378
## APOE33 - APOE44 -1.93e-04 0.000238 17  -0.812  0.7010
##

```



```

## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
##      Genotype  ic.trend      SE df  lower.CL upper.CL
##      APOE22    4.58e-04 0.000344 17 -0.000268 0.001184
##      APOE33    1.57e-04 0.000124 17 -0.000105 0.000418
##      APOE44    3.28e-04 0.000254 17 -0.000207 0.000864
##
## Sex = male:
##      Genotype  ic.trend      SE df  lower.CL upper.CL
##      APOE22   -2.94e-04 0.000309 17 -0.000946 0.000358
##      APOE33   -1.85e-04 0.000323 17 -0.000868 0.000497
##      APOE44    2.85e-05 0.000204 17 -0.000402 0.000459
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##      contrast      estimate      SE df t.ratio p.value
##      APOE22 - APOE33  0.000301 0.000366 17   0.823  0.6942
##      APOE22 - APOE44  0.000129 0.000428 17   0.302  0.9511
##      APOE33 - APOE44 -0.000172 0.000283 17  -0.609  0.8173
##
## Sex = male:
##      contrast      estimate      SE df t.ratio p.value
##      APOE22 - APOE33 -0.000109 0.000447 17  -0.243  0.9681
##      APOE22 - APOE44 -0.000322 0.000370 17  -0.871  0.6653
##      APOE33 - APOE44 -0.000214 0.000382 17  -0.560  0.8430
##
## P value adjustment: tukey method for comparing a family of 3 estimates

```

Day d8 Probe By ic CLUS

```

## [1] "ic: Probe d8 AWN CLUSTERING"
## [1] "omnibus test"

##      model term   df1 df2 F.ratio p.value
##      Genotype      2  17  20.457 <.0001
##      Sex            1  17   2.101  0.1654
##      Genotype:Sex    2  17   0.684  0.5177

## Sex = female:
##      model term df1 df2 F.ratio p.value
##      Genotype      2  17   9.925  0.0014
##
## Sex = male:
##      model term df1 df2 F.ratio p.value
##      Genotype      2  17  10.911  0.0009

## Genotype = APOE22:
##      model term df1 df2 F.ratio p.value
##      Sex          1  17   3.185  0.0922
##

```

```

## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex          1  17   0.001  0.9789
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex          1  17   0.925  0.3496

## model term      df1 df2 F.ratio p.value
## ic              1  17   2.590  0.1259
## Genotype        2  17   7.383  0.0049
## Sex             1  17   5.177  0.0361
## ic:Genotype     2  17   0.564  0.5790
## ic:Sex          1  17   4.328  0.0529
## Genotype:Sex    2  17   1.169  0.3344
## ic:Genotype:Sex 2  17   0.835  0.4507

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

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## ic          1   0.116    0.116   0.0315    0.8613
## Genotype    2 213.103  106.551  28.8961 3.397e-06 ***
## Sex         1   4.865    4.865   1.3195    0.2666
## ic:Genotype 2   2.406    1.203   0.3263    0.7260
## ic:Sex      1   7.447    7.447   2.0197    0.1734
## Genotype:Sex 2   3.014    1.507   0.4086    0.6709
## ic:Genotype:Sex 2   6.161    3.081   0.8354    0.4507
## Residuals   17  62.686    3.687
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "females"

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## ic          1   0.238    0.238   0.0628  0.809392
## Genotype    2 100.888   50.444  13.3263  0.004105 **
## ic:Genotype 2   9.734    4.867   1.2857  0.334522
## Residuals   7  26.497    3.785
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "males"

## Analysis of Variance Table
##
## Response: Probe_d8
##           Df Sum Sq Mean Sq F value    Pr(>F)
## ic          1 10.999   10.999   3.0394  0.111870
## Genotype    2  89.197   44.598  12.3240  0.002003 **
## ic:Genotype 2   1.652    0.826   0.2282  0.799992
## Residuals  10  36.188    3.619

```

```

## ---
## 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   2.7202 1.52 17   1.785  0.0922
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male  -0.0494 1.84 17  -0.027  0.9789
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male   1.3194 1.37 17   0.962  0.3496

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    4.06 1.91 17   2.131  0.1132
## APOE22 - APOE44   -3.61 1.33 17  -2.724  0.0365
## APOE33 - APOE44   -7.68 1.83 17  -4.188  0.0017
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    1.29 1.44 17   0.901  0.6467
## APOE22 - APOE44   -5.01 1.56 17  -3.205  0.0136
## APOE33 - APOE44   -6.31 1.38 17  -4.580  0.0007
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends
## Genotype ic.trend      SE df lower.CL upper.CL
## APOE22      0.1083 0.0993 17  -0.1012   0.318
## APOE33      0.0144 0.0491 17  -0.0892   0.118
## APOE44      0.0812 0.0614 17  -0.0484   0.211
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33   0.0939 0.1108 17   0.848  0.6792
## APOE22 - APOE44   0.0271 0.1168 17   0.232  0.9707
## APOE33 - APOE44  -0.0668 0.0786 17  -0.850  0.6782
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
## Genotype ic.trend      SE df lower.CL upper.CL
## APOE22      0.2846 0.1624 17  -0.0582   0.627
## APOE33      0.0480 0.0385 17  -0.0333   0.129
## APOE44      0.1348 0.0856 17  -0.0458   0.315

```

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##
## Sex = male:
##   Genotype ic.trend      SE df lower.CL upper.CL
##   APOE22      -0.0680 0.1142 17  -0.3090   0.173
##   APOE33      -0.0192 0.0903 17  -0.2097   0.171
##   APOE44       0.0275 0.0881 17  -0.1584   0.213
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##   contrast      estimate      SE df t.ratio p.value
##   APOE22 - APOE33   0.2366 0.1670 17   1.417  0.3545
##   APOE22 - APOE44   0.1498 0.1836 17   0.816  0.6986
##   APOE33 - APOE44  -0.0868 0.0939 17  -0.925  0.6323
##
## Sex = male:
##   contrast      estimate      SE df t.ratio p.value
##   APOE22 - APOE33  -0.0488 0.1456 17  -0.335  0.9403
##   APOE22 - APOE44  -0.0955 0.1443 17  -0.662  0.7881
##   APOE33 - APOE44  -0.0468 0.1262 17  -0.371  0.9274
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## P value adjustment: tukey method for comparing a family of 3 estimates
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##   APOE44      0.1348 0.0856 17  -0.0458   0.315
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```

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```

