

Absolute Winding Number by ic 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 ic Vol

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

## model term    df1 df2 F.ratio p.value
## Genotype      2  17  4.316  0.0305
## Sex           1  17  2.306  0.1473
## Genotype:Sex   2  17  1.481  0.2553

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype   2  17  6.029  0.0105
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype   2  17  0.980  0.3955

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17  0.051  0.8239
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
```

```

## Sex          1 17 0.392 0.5394
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex          1 17 4.070 0.0597

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

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## ic          1 30.663 30.663 2.2702 0.150242
## Genotype     2 203.811 101.905 7.5447 0.004516 **
## Sex          1 24.361 24.361 1.8036 0.196934
## ic:Genotype  2 101.179 50.589 3.7455 0.044902 *
## ic:Sex       1 4.155 4.155 0.3076 0.586361
## Genotype:Sex  2 28.919 14.460 1.0705 0.364837
## ic:Genotype:Sex 2 18.406 9.203 0.6813 0.519227
## Residuals    17 229.616 13.507
## ---
## 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)
## ic          1 53.502 53.502 2.4281 0.16314
## Genotype     2 193.352 96.676 4.3874 0.05821 .
## ic:Genotype  2 66.615 33.308 1.5116 0.28466
## Residuals    7 154.245 22.035
## ---
## 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)
## ic          1 2.233 2.2329 0.2963 0.5982
## Genotype     2 39.417 19.7086 2.6149 0.1220
## ic:Genotype  2 7.156 3.5780 0.4747 0.6354
## Residuals    10 75.371 7.5371

## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
## contrast      estimate SE df t.ratio p.value
## female - male -0.514 2.27 17 -0.226 0.8239
##
## Genotype = APOE33:
## contrast      estimate SE df t.ratio p.value
## female - male 1.807 2.88 17 0.626 0.5394
##
## Genotype = APOE44:

```

```

## contrast      estimate    SE df t.ratio p.value
## female - male    5.783 2.87 17    2.017  0.0597

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    0.584 2.71 17    0.215  0.9748
## APOE22 - APOE44   -7.174 2.37 17   -3.026  0.0198
## APOE33 - APOE44   -7.758 2.72 17   -2.856  0.0280
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    2.905 2.48 17    1.173  0.4846
## APOE22 - APOE44   -0.878 2.79 17   -0.315  0.9470
## APOE33 - APOE44   -3.782 3.03 17   -1.250  0.4414
##
## 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      -9880 11806 17   -34788    15028
## APOE33      22265 16049 17   -11597    56126
## APOE44     -2520 26809 17   -59081    54042
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33   -32145 19924 17   -1.613  0.2672
## APOE22 - APOE44   -7360 29293 17   -0.251  0.9659
## APOE33 - APOE44    24784 31246 17    0.793  0.7121
##
## 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     -20943 18905 17   -60829    18943
## APOE33      27226 23028 17   -21359    75812
## APOE44     -32022 13677 17   -60879   -3166
##
## Sex = male:
## Genotype ic.trend    SE df lower.CL upper.CL
## APOE22      1183 14146 17   -28662    31029
## APOE33      17303 22362 17   -29876    64482
## APOE44      26983 51843 17   -82397   136363
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33   -48169 29794 17   -1.617  0.2658

```

```
## APOE22 - APOE44      11079 23334 17    0.475  0.8840
## APOE33 - APOE44      59249 26784 17    2.212  0.0977
##
## Sex = male:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33   -16120 26460 17   -0.609  0.8171
## APOE22 - APOE44   -25800 53739 17   -0.480  0.8816
## APOE33 - APOE44    -9680 56460 17   -0.171  0.9839
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d5 Probe By ic FA

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

## model term    df1 df2 F.ratio p.value
## Genotype      2  17   1.330  0.2905
## Sex           1  17   0.532  0.4758
## Genotype:Sex   2  17   1.327  0.2914

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   2.082  0.1554
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   0.500  0.6150

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.092  0.7655
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.192  0.6667
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex        1  17   2.419  0.1383

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

## Analysis of Variance Table
##
## Response: Probe_d5
##          Df Sum Sq Mean Sq F value Pr(>F)
## ic        1 127.532  127.532   7.7675 0.01265 *
## Genotype   2  167.734   83.867   5.1080 0.01831 *
## Sex        1    0.116    0.116   0.0070 0.93409
## ic:Genotype 2    8.177    4.088   0.2490 0.78237
## ic:Sex      1    7.892    7.892   0.4807 0.49748
## Genotype:Sex 2   26.809   13.404   0.8164 0.45861
## ic:Genotype:Sex 2   23.731   11.866   0.7227 0.49977
## Residuals 17  279.117   16.419
```

```

## ---
## 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)
## ic           1 102.203 102.203   3.1999 0.1168
## Genotype      2 140.325  70.163   2.1967 0.1818
## ic:Genotype   2   1.608   0.804   0.0252 0.9752
## Residuals     7 223.578  31.940

## [1] "males"

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## ic           1  0.083   0.0833  0.0150 0.90494
## Genotype      2 37.555 18.7775   3.3809 0.07558 .
## ic:Genotype   2 30.999 15.4996   2.7907 0.10888
## Residuals    10 55.540   5.5540

## ---
## 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    -1.03 3.39 17  -0.303  0.7655
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male    -1.81 4.12 17  -0.438  0.6667
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male      8.36 5.37 17   1.555  0.1383

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33   4.194 3.58 17   1.170  0.4861
## APOE22 - APOE44  -5.523 4.20 17  -1.313  0.4072
## APOE33 - APOE44  -9.717 4.77 17  -2.037  0.1337
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33   3.416 3.95 17   0.864  0.6695
## APOE22 - APOE44   3.861 4.76 17   0.811  0.7017
## APOE33 - APOE44   0.445 4.81 17   0.093  0.9953
##
## 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 -102.3 129 17 -375 170
## APOE33 -68.5 303 17 -709 572
## APOE44 293.2 280 17 -297 883
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast estimate SE df t.ratio p.value
## APOE22 - APOE33 -33.8 330 17 -0.102 0.9942
## APOE22 - APOE44 -395.5 308 17 -1.284 0.4229
## APOE33 - APOE44 -361.8 413 17 -0.877 0.6618
##
## 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 -110.25 204 17 -541 320.1
## APOE33 -144.05 105 17 -366 77.5
## APOE44 -85.06 163 17 -429 259.2
##
## Sex = male:
## Genotype ic.trend SE df lower.CL upper.CL
## APOE22 -94.34 159 17 -429 240.8
## APOE33 6.97 598 17 -1254 1268.2
## APOE44 671.51 535 17 -457 1800.0
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
## contrast estimate SE df t.ratio p.value
## APOE22 - APOE33 33.8 229 17 0.147 0.9881
## APOE22 - APOE44 -25.2 261 17 -0.096 0.9949
## APOE33 - APOE44 -59.0 194 17 -0.304 0.9505
##
## Sex = male:
## contrast estimate SE df t.ratio p.value
## APOE22 - APOE33 -101.3 619 17 -0.164 0.9853
## APOE22 - APOE44 -765.9 558 17 -1.373 0.3767
## APOE33 - APOE44 -664.5 802 17 -0.828 0.6910
##
## P value adjustment: tukey method for comparing a family of 3 estimates

```

Day d5 Probe By ic DEG

```

## [1] "ic: Probe d5 AWN DEG"
## [1] "omnibus test"
## model term df1 df2 F.ratio p.value
## Genotype 2 17 6.370 0.0086

```

```

## Sex          1  17   0.000  0.9883
## Genotype:Sex  2  17   1.012  0.3843

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype    2  17   5.260  0.0167
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype    2  17   1.601  0.2306

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex          1  17   0.055  0.8168
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex          1  17   0.865  0.3655
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex          1  17   1.316  0.2672

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

## Analysis of Variance Table
##
## Response: Probe_d5
##           Df  Sum Sq Mean Sq F value    Pr(>F)
## ic           1    2.882    2.882   0.1835 0.673738
## Genotype      2  224.497  112.249   7.1481 0.005586 **
## Sex           1   18.572   18.572   1.1827 0.291988
## ic:Genotype   2    1.091    0.546   0.0348 0.965914
## ic:Sex        1    7.267    7.267   0.4628 0.505499
## Genotype:Sex  2   59.797   29.899   1.9040 0.179418
## ic:Genotype:Sex 2   60.047   30.023   1.9119 0.178257
## Residuals    17  266.955   15.703
## ---
## 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)
## ic           1  14.213   14.213   0.4962 0.50392
## Genotype      2  204.431  102.215   3.5687 0.08542 .
## ic:Genotype   2   48.574   24.287   0.8479 0.46800
## Residuals     7  200.497   28.642
## ---
## 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)
## ic           1  1.648  1.6479  0.2480 0.6293
## Genotype      2 36.951 18.4757  2.7801 0.1096
## ic:Genotype   2 19.120  9.5599  1.4385 0.2824
## Residuals    10 66.458  6.6458

## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
## contrast      estimate    SE df t.ratio p.value
## female - male    0.633 2.69 17   0.235  0.8168
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male   -3.954 4.25 17  -0.930  0.3655
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    3.408 2.97 17   1.147  0.2672

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    6.12 4.27 17   1.431  0.3479
## APOE22 - APOE44   -6.34 2.68 17  -2.363  0.0737
## APOE33 - APOE44  -12.45 4.33 17  -2.877  0.0268
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    1.53 2.66 17   0.575  0.8350
## APOE22 - APOE44   -3.56 2.98 17  -1.196  0.4714
## APOE33 - APOE44   -5.09 2.86 17  -1.780  0.2061
##
## 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      9.71e-05 0.000464 17 -0.000883 0.001077
## APOE33      4.41e-05 0.000348 17 -0.000690 0.000778
## APOE44     -1.02e-04 0.000327 17 -0.000792 0.000588
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33 0.000053 0.000580 17   0.091  0.9954
## APOE22 - APOE44 0.000199 0.000568 17   0.351  0.9347
## APOE33 - APOE44 0.000146 0.000477 17   0.306  0.9497
##
## 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    0.000450 0.000691 17 -0.001007 0.001908
## APOE33    0.000369 0.000249 17 -0.000157 0.000894
## APOE44   -0.000607 0.000510 17 -0.001682 0.000468
##
## Sex = male:
## Genotype  ic.trend      SE df  lower.CL upper.CL
## APOE22    -0.000256 0.000620 17 -0.001565 0.001053
## APOE33    -0.000280 0.000649 17 -0.001650 0.001089
## APOE44     0.000402 0.000410 17 -0.000462 0.001267
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33 8.18e-05 0.000735 17  0.111  0.9932
## APOE22 - APOE44 1.06e-03 0.000859 17  1.231  0.4517
## APOE33 - APOE44 9.75e-04 0.000567 17  1.719  0.2270
##
## Sex = male:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33 2.41e-05 0.000898 17  0.027  0.9996
## APOE22 - APOE44 -6.59e-04 0.000743 17 -0.886  0.6562
## APOE33 - APOE44 -6.83e-04 0.000768 17 -0.889  0.6541
##
## P value adjustment: tukey method for comparing a family of 3 estimates

```

Day d5 Probe By ic CLUS

```

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

## model term  df1 df2 F.ratio p.value
## Genotype    2  17  6.823  0.0067
## Sex          1  17  0.303  0.5894
## Genotype:Sex  2  17  1.308  0.2963

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype    2  17  6.339  0.0088
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype    2  17  1.341  0.2879

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17  0.178  0.6780
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex        1  17  0.588  0.4538
##
## Genotype = APOE44:

```

```
## model term df1 df2 F.ratio p.value
## Sex          1  17   2.761  0.1149

## model term      df1 df2 F.ratio p.value
## ic              1  17   0.080  0.7805
## Genotype        2  17   0.991  0.3915
## Sex             1  17   0.219  0.6455
## ic:Genotype      2  17   0.268  0.7680
## ic:Sex           1  17   0.102  0.7530
## Genotype:Sex     2  17   0.517  0.6051
## ic:Genotype:Sex  2  17   1.750  0.2036

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

## Analysis of Variance Table
##
## Response: Probe_d5
##          Df Sum Sq Mean Sq F value Pr(>F)
## ic          1  0.003   0.003   0.0002 0.989219
## Genotype    2 227.190 113.595   7.2229 0.005364 **
## Sex         1  18.729  18.729   1.1909 0.290376
## ic:Genotype  2   2.461   1.231   0.0782 0.925068
## ic:Sex       1   1.155   1.155   0.0734 0.789698
## Genotype:Sex  2  69.156  34.578   2.1987 0.141502
## ic:Genotype:Sex  2  55.056  27.528   1.7504 0.203600
## Residuals   17 267.359  15.727
## ---
## 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)
## ic          1   2.568   2.568   0.0945 0.76751
## Genotype    2 215.165 107.583   3.9578 0.07081 .
## ic:Genotype  2  59.706  29.853   1.0983 0.38474
## Residuals   7 190.275  27.182
## ---
## 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)
## ic          1   3.791   3.7912  0.4918 0.4991
## Genotype    2  33.278 16.6389   2.1585 0.1662
## ic:Genotype  2  10.024   5.0120   0.6502 0.5427
## Residuals   10  77.084   7.7084

## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
## contrast      estimate    SE df t.ratio p.value
## female - male      1.33 3.15 17   0.422  0.6780
```

```

##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male   -2.91 3.79 17  -0.767  0.4538
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    4.71 2.83 17   1.662  0.1149
##
## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    5.69 3.94 17   1.444  0.3419
## APOE22 - APOE44   -6.57 2.74 17  -2.399  0.0690
## APOE33 - APOE44  -12.25 3.79 17  -3.237  0.0127
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    1.45 2.96 17   0.488  0.8778
## APOE22 - APOE44   -3.19 3.23 17  -0.988  0.5942
## APOE33 - APOE44   -4.64 2.84 17  -1.631  0.2601
##
## 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      0.1027 0.205 17   -0.330    0.535
## APOE33      0.0300 0.101 17   -0.184    0.244
## APOE44     -0.0587 0.127 17   -0.326    0.209
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    0.0727 0.229 17   0.318  0.9459
## APOE22 - APOE44    0.1614 0.241 17   0.669  0.7841
## APOE33 - APOE44    0.0886 0.162 17   0.546  0.8499
##
## 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      0.2809 0.3355 17  -0.4269    0.989
## APOE33      0.1163 0.0796 17  -0.0516    0.284
## APOE44     -0.2395 0.1768 17  -0.6124    0.133
##
## Sex = male:
## Genotype ic.trend    SE df lower.CL upper.CL
## APOE22     -0.0755 0.2359 17  -0.5732    0.422
## APOE33     -0.0563 0.1865 17  -0.4497    0.337
## APOE44      0.1222 0.1820 17  -0.2619    0.506
##

```

```

## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33  0.1647 0.345 17   0.478  0.8827
## APOE22 - APOE44  0.5204 0.379 17   1.372  0.3768
## APOE33 - APOE44  0.3557 0.194 17   1.835  0.1882
##
## Sex = male:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33 -0.0192 0.301 17  -0.064  0.9978
## APOE22 - APOE44 -0.1976 0.298 17  -0.663  0.7875
## APOE33 - APOE44 -0.1785 0.261 17  -0.685  0.7753
##
## 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      0.1027 0.205 17   -0.330    0.535
## APOE33      0.0300 0.101 17   -0.184    0.244
## APOE44     -0.0587 0.127 17   -0.326    0.209
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33  0.0727 0.229 17   0.318  0.9459
## APOE22 - APOE44  0.1614 0.241 17   0.669  0.7841
## APOE33 - APOE44  0.0886 0.162 17   0.546  0.8499
##
## 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      0.2809 0.3355 17  -0.4269    0.989
## APOE33      0.1163 0.0796 17  -0.0516    0.284
## APOE44     -0.2395 0.1768 17  -0.6124    0.133
##
## Sex = male:
## Genotype ic.trend      SE df lower.CL upper.CL
## APOE22     -0.0755 0.2359 17  -0.5732    0.422
## APOE33     -0.0563 0.1865 17  -0.4497    0.337
## APOE44      0.1222 0.1820 17  -0.2619    0.506
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
## contrast      estimate      SE df t.ratio p.value

```

```
## APOE22 - APOE33 0.1647 0.345 17 0.478 0.8827
## APOE22 - APOE44 0.5204 0.379 17 1.372 0.3768
## APOE33 - APOE44 0.3557 0.194 17 1.835 0.1882
##
```

```
## Sex = male:
```

```
## contrast estimate SE df t.ratio p.value
## APOE22 - APOE33 -0.0192 0.301 17 -0.064 0.9978
## APOE22 - APOE44 -0.1976 0.298 17 -0.663 0.7875
## APOE33 - APOE44 -0.1785 0.261 17 -0.685 0.7753
##
```

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

