Absolute Winding Number by fi Probe Day d8

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Contents

Aim

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

Day d8 Probe by fi Vol

```
## [1] "fi: Probe d8 AWN VOL"

## [1] "omnibus test"

##  model term    df1 df2 F.ratio p.value
##  Genotype       2  17  29.615  <.0001
##  Sex            1  17   1.216  0.2855
##  Genotype:Sex   2  17   0.987  0.3929

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17  15.627  0.0001
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17  15.718  0.0001

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.481  0.4971
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
```

```
## Sex           1  17    0.082  0.7779
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex           1  17    3.616  0.0743

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

## Analysis of Variance Table
##
## Response: Probe_d8
##                  Df   Sum Sq Mean Sq F value    Pr(>F)
## fi               1    0.144   0.144  0.0488   0.82781
## Genotype         2  204.378 102.189 34.5435 1.028e-06 ***
## Sex              1   13.071  13.071  4.4184   0.05076 .
## fi:Genotype      2    8.179   4.089  1.3823   0.27782
## fi:Sex           1    1.210   1.210  0.4092   0.53092
## Genotype:Sex     2    4.169   2.085  0.7046   0.50816
## fi:Genotype:Sex  2   18.356   9.178  3.1024   0.07102 .
## Residuals       17   50.291   2.958
## ---
## 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)
## fi           1  5.914   5.914  1.2498 0.300482
## Genotype     2 93.859  46.930  9.9176 0.009065 **
## fi:Genotype  2  4.460   2.230  0.4712 0.642686
## Residuals    7 33.124   4.732
## ---
## 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)
## fi           1  5.648   5.648  3.2901   0.09977 .
## Genotype     2 94.872  47.436 27.6318 8.446e-05 ***
## fi:Genotype  2 20.349  10.175  5.9268   0.02006 *
## Residuals   10 17.167   1.717
## ---
## 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    0.772 1.11 17   0.694  0.4971
##
## Genotype = APOE33:
##  contrast      estimate   SE df t.ratio p.value
##  female - male   -0.491 1.71 17  -0.287  0.7779
```

```
##
## Genotype = APOE44:
##  contrast       estimate   SE df t.ratio p.value
##  female - male     2.355 1.24 17   1.902  0.0743

## Sex = female:
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33       3.29 1.75 17   1.879  0.1751
##  APOE22 - APOE44      -5.62 1.29 17  -4.370  0.0012
##  APOE33 - APOE44      -8.91 1.80 17  -4.937  0.0003
##
## Sex = male:
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33       2.03 1.05 17   1.921  0.1631
##  APOE22 - APOE44      -4.04 1.06 17  -3.819  0.0037
##  APOE33 - APOE44      -6.06 1.10 17  -5.497  0.0001
##
## 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      5977 9738 17   -14568    26523
##  APOE33      5385 7225 17    -9858    20628
##  APOE44      9325 4193 17      480    18171
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##  contrast          estimate    SE df t.ratio p.value
##  APOE22 - APOE33        593 12126 17   0.049  0.9987
##  APOE22 - APOE44      -3348 10602 17  -0.316  0.9467
##  APOE33 - APOE44      -3941  8353 17  -0.472  0.8854
##
## 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     11552  8257 17    -5869    28973
##  APOE33     23170 12548 17    -3304    49645
##  APOE44      6466  5804 17    -5780    18713
##
## Sex = male:
##  Genotype fi.trend    SE df lower.CL upper.CL
##  APOE22       403 17639 17   -36812    37618
##  APOE33    -12401  7165 17   -27518     2716
##  APOE44     12184  6052 17     -584    24952
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
```

```
## contrast         estimate     SE df t.ratio p.value
## APOE22 - APOE33    -11618 15021 17  -0.773  0.7238
## APOE22 - APOE44      5086 10093 17   0.504  0.8704
## APOE33 - APOE44     16704 13826 17   1.208  0.4646
##
## Sex = male:
## contrast         estimate     SE df t.ratio p.value
## APOE22 - APOE33     12804 19039 17   0.673  0.7823
## APOE22 - APOE44    -11781 18648 17  -0.632  0.8049
## APOE33 - APOE44    -24585  9379 17  -2.621  0.0448
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d8 Probe By fi FA

```
## [1] "fi: Probe d8 AWN FA"

## [1] "omnibus test"

## model term    df1 df2 F.ratio p.value
## Genotype        2  17  23.536  <.0001
## Sex             1  17   6.393  0.0216
## Genotype:Sex    2  17   0.250  0.7815

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype     2  17  14.310  0.0002
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype     2  17  10.430  0.0011

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex          1  17   5.015  0.0388
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex          1  17   0.474  0.5002
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex          1  17   3.414  0.0821

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

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df  Sum Sq Mean Sq F value    Pr(>F)
## fi            1   1.720   1.720  0.5752   0.45857
## Genotype      2 212.070 106.035 35.4629 8.587e-07 ***
## Sex           1  21.455  21.455  7.1756   0.01586 *
## fi:Genotype   2   0.101   0.050  0.0169   0.98328
## fi:Sex        1   4.024   4.024  1.3459   0.26203
## Genotype:Sex  2   3.169   1.584  0.5299   0.59808
```

```
## fi:Genotype:Sex  2   6.429   3.214  1.0750    0.36339
## Residuals      17  50.830   2.990
## ---
## 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)
## fi            1   8.895   8.895   3.441 0.105987
## Genotype      2 108.675  54.338  21.020 0.001099 **
## fi:Genotype   2   1.691   0.845   0.327 0.731544
## Residuals     7  18.096   2.585
## ---
## 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)
## fi            1   0.098   0.098  0.0300 0.8659567
## Genotype      2 100.042  50.021 15.2807 0.0009108 ***
## fi:Genotype   2   5.161   2.580  0.7882 0.4809680
## Residuals    10  32.735   3.273
## ---
## 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       2.63 1.18 17   2.239  0.0388
##
## Genotype = APOE33:
##  contrast        estimate   SE df t.ratio p.value
##  female - male       1.18 1.71 17   0.689  0.5002
##
## Genotype = APOE44:
##  contrast        estimate   SE df t.ratio p.value
##  female - male       2.34 1.27 17   1.848  0.0821

## Sex = female:
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33       3.59 1.40 17   2.567  0.0498
##  APOE22 - APOE44      -3.94 1.27 17  -3.096  0.0171
##  APOE33 - APOE44      -7.53 1.42 17  -5.302  0.0002
##
## Sex = male:
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33       2.14 1.54 17   1.393  0.3664
##  APOE22 - APOE44      -4.24 1.17 17  -3.628  0.0056
##  APOE33 - APOE44      -6.37 1.59 17  -4.019  0.0024
##
```

```
## 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      -22.6 35.3 17      -97     51.8
##  APOE33      -53.9 45.7 17     -150     42.5
##  APOE44      -60.0 43.5 17     -152     31.7
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##  contrast         estimate   SE df t.ratio p.value
##  APOE22 - APOE33     31.28 57.7 17   0.542  0.8519
##  APOE22 - APOE44     37.37 56.0 17   0.668  0.7851
##  APOE33 - APOE44      6.08 63.1 17   0.096  0.9949
##
## 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      -94.9 37.9 17   -174.9   -14.84
##  APOE33      -60.3 29.9 17   -123.4     2.83
##  APOE44      -60.1 53.8 17   -173.5    53.42
##
## Sex = male:
##  Genotype fi.trend   SE df lower.CL upper.CL
##  APOE22       49.6 59.5 17    -75.8   175.09
##  APOE33      -47.5 86.4 17   -229.8   134.74
##  APOE44      -59.9 68.3 17   -204.0    84.20
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast         estimate   SE df t.ratio p.value
##  APOE22 - APOE33   -34.584 48.3 17  -0.716  0.7575
##  APOE22 - APOE44   -34.789 65.8 17  -0.529  0.8585
##  APOE33 - APOE44    -0.205 61.5 17  -0.003  1.0000
##
## Sex = male:
##  contrast         estimate    SE df t.ratio p.value
##  APOE22 - APOE33    97.151 104.9 17   0.926  0.6315
##  APOE22 - APOE44   109.520  90.6 17   1.209  0.4638
##  APOE33 - APOE44    12.370 110.1 17   0.112  0.9931
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d8 Probe By fi DEG

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

```
## [1] "omnibus test"

##  model term    df1 df2 F.ratio p.value
##  Genotype       2  17  28.193  <.0001
##  Sex            1  17   8.078  0.0113
##  Genotype:Sex   2  17   1.086  0.3599

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17  16.302  0.0001
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17  12.041  0.0006

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   6.069  0.0247
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.181  0.6758
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   4.388  0.0515

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

## Analysis of Variance Table
##
## Response: Probe_d8
##                  Df  Sum Sq Mean Sq F value  Pr(>F)
## fi                1   8.131   8.131  2.9606 0.10346
## Genotype          2 196.463  98.231 35.7660 8.1e-07 ***
## Sex               1  16.863  16.863  6.1400 0.02401 *
## fi:Genotype       2   0.685   0.343  0.1248 0.88350
## fi:Sex            1  17.204  17.204  6.2638 0.02282 *
## Genotype:Sex      2   3.296   1.648  0.6001 0.55998
## fi:Genotype:Sex   2  10.464   5.232  1.9050 0.17927
## Residuals        17  46.691   2.747
## ---
## 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)
## fi            1   7.062   7.062  2.5663 0.153194
## Genotype      2 105.709  52.855 19.2082 0.001437 **
## fi:Genotype   2   5.324   2.662  0.9675 0.425611
## Residuals     7  19.262   2.752
## ---
## 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)
## fi          1  5.447   5.447  1.9858 0.1891140
## Genotype    2 94.686  47.343 17.2602 0.0005717 ***
## fi:Genotype 2 10.474   5.237  1.9094 0.1984551
## Residuals  10 27.429   2.743
## ---
## 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     3.011 1.22 17   2.464  0.0247
##
## Genotype = APOE33:
##  contrast       estimate   SE df t.ratio p.value
##  female - male     0.539 1.27 17   0.425  0.6758
##
## Genotype = APOE44:
##  contrast       estimate   SE df t.ratio p.value
##  female - male     2.474 1.18 17   2.095  0.0515

## Sex = female:
##  contrast        estimate   SE df t.ratio p.value
##  APOE22 - APOE33     3.68 1.38 17   2.670  0.0407
##  APOE22 - APOE44    -3.69 1.24 17  -2.983  0.0216
##  APOE33 - APOE44    -7.37 1.30 17  -5.666  0.0001
##
## Sex = male:
##  contrast        estimate   SE df t.ratio p.value
##  APOE22 - APOE33     1.20 1.10 17   1.098  0.5281
##  APOE22 - APOE44    -4.23 1.16 17  -3.631  0.0056
##  APOE33 - APOE44    -5.43 1.14 17  -4.753  0.0005
##
## 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   9.02e-05 8.07e-05 17 -8.00e-05 2.60e-04
##  APOE33   1.18e-05 4.17e-05 17 -7.61e-05 9.98e-05
##  APOE44   9.10e-05 4.65e-05 17 -7.18e-06 1.89e-04
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##  contrast         estimate       SE df t.ratio p.value
##  APOE22 - APOE33  7.84e-05 9.08e-05 17   0.863  0.6701
##  APOE22 - APOE44 -8.24e-07 9.31e-05 17  -0.009  1.0000
##  APOE33 - APOE44 -7.92e-05 6.25e-05 17  -1.267  0.4318
##
```

```
## 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    2.87e-04 1.27e-04 17   1.90e-05 5.54e-04
##  APOE33    9.98e-05 4.57e-05 17   3.34e-06 1.96e-04
##  APOE44    1.10e-04 7.26e-05 17  -4.32e-05 2.63e-04
##
## Sex = male:
##  Genotype  fi.trend       SE df  lower.CL upper.CL
##  APOE22   -1.06e-04 9.97e-05 17  -3.17e-04 1.04e-04
##  APOE33   -7.61e-05 6.98e-05 17  -2.23e-04 7.11e-05
##  APOE44    7.20e-05 5.82e-05 17  -5.08e-05 1.95e-04
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast         estimate       SE df t.ratio p.value
##  APOE22 - APOE33  1.87e-04 1.35e-04 17   1.386  0.3699
##  APOE22 - APOE44  1.77e-04 1.46e-04 17   1.208  0.4646
##  APOE33 - APOE44 -1.03e-05 8.58e-05 17  -0.120  0.9921
##
## Sex = male:
##  contrast         estimate       SE df t.ratio p.value
##  APOE22 - APOE33 -3.02e-05 1.22e-04 17  -0.248  0.9667
##  APOE22 - APOE44 -1.78e-04 1.15e-04 17  -1.545  0.2959
##  APOE33 - APOE44 -1.48e-04 9.09e-05 17  -1.630  0.2605
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d8 Probe By fi CLUS

```
## [1] "fi: Probe d8 AWN CLUSTERING"

## [1] "omnibus test"

##  model term    df1 df2 F.ratio p.value
##  Genotype        2  17  21.723  <.0001
##  Sex             1  17   5.873  0.0268
##  Genotype:Sex    2  17   0.824  0.4555

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17  12.018  0.0006
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   9.970  0.0014

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   4.149  0.0575
##
```

```
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.278  0.6046
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   2.283  0.1491

##  model term      df1 df2 F.ratio p.value
##  fi               1  17   1.945  0.1811
##  Genotype         2  17  22.788  <.0001
##  Sex              1  17   7.421  0.0144
##  fi:Genotype      2  17   0.948  0.4069
##  fi:Sex           1  17   4.506  0.0488
##  Genotype:Sex     2  17   0.877  0.4341
##  fi:Genotype:Sex  2  17   1.287  0.3017

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

## Analysis of Variance Table
##
## Response: Probe_d8
##                 Df  Sum Sq Mean Sq F value    Pr(>F)
## fi               1  19.263  19.263  5.7847   0.02784 *
## Genotype         2 187.755  93.878 28.1920 3.992e-06 ***
## Sex              1  15.144  15.144  4.5479   0.04784 *
## fi:Genotype      2   0.991   0.495  0.1488   0.86288
## fi:Sex           1  10.187  10.187  3.0592   0.09831 .
## Genotype:Sex     2   1.278   0.639  0.1919   0.82717
## fi:Genotype:Sex  2   8.571   4.285  1.2869   0.30169
## Residuals       17  56.609   3.330
## ---
## 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)
## fi           1 16.059  16.059  4.3404 0.075708 .
## Genotype     2 90.953  45.476 12.2915 0.005126 **
## fi:Genotype  2  4.446   2.223  0.6009 0.574333
## Residuals    7 25.899   3.700
## ---
## 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)
## fi           1  6.039   6.039  1.9664 0.1911001
## Genotype     2 94.179  47.089 15.3335 0.0008991 ***
## fi:Genotype  2  7.108   3.554  1.1573 0.3531108
## Residuals   10 30.710   3.071
```

```
## ---
## 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     3.599 1.77 17   2.037  0.0575
##
## Genotype = APOE33:
##  contrast        estimate   SE df t.ratio p.value
##  female - male     0.726 1.38 17   0.528  0.6046
##
## Genotype = APOE44:
##  contrast        estimate   SE df t.ratio p.value
##  female - male     1.897 1.26 17   1.511  0.1491

## Sex = female:
##  contrast         estimate   SE df t.ratio p.value
##  APOE22 - APOE33      4.10 1.81 17   2.262  0.0891
##  APOE22 - APOE44     -2.60 1.66 17  -1.565  0.2871
##  APOE33 - APOE44     -6.69 1.37 17  -4.901  0.0004
##
## Sex = male:
##  contrast         estimate   SE df t.ratio p.value
##  APOE22 - APOE33      1.23 1.32 17   0.931  0.6289
##  APOE22 - APOE44     -4.30 1.40 17  -3.078  0.0178
##  APOE33 - APOE44     -5.52 1.27 17  -4.358  0.0012
##
## 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    0.05185 0.0525 17  -0.0588   0.1625
##  APOE33   -0.00202 0.0213 17  -0.0470   0.0430
##  APOE44    0.03460 0.0214 17  -0.0105   0.0797
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##  contrast         estimate     SE df t.ratio p.value
##  APOE22 - APOE33    0.0539 0.0566 17   0.951  0.6164
##  APOE22 - APOE44    0.0172 0.0567 17   0.304  0.9503
##  APOE33 - APOE44   -0.0366 0.0302 17  -1.213  0.4618
##
## 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    0.1384 0.0874 17  -0.0461   0.3229
##  APOE33    0.0350 0.0192 17  -0.0055   0.0755
##  APOE44    0.0395 0.0266 17  -0.0166   0.0956
```

```
##
## Sex = male:
##  Genotype fi.trend     SE df lower.CL upper.CL
##  APOE22    -0.0347 0.0580 17  -0.1571   0.0877
##  APOE33    -0.0390 0.0381 17  -0.1194   0.0413
##  APOE44     0.0297 0.0335 17  -0.0409   0.1003
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast        estimate     SE df t.ratio p.value
##  APOE22 - APOE33  0.10344 0.0895 17   1.156  0.4946
##  APOE22 - APOE44  0.09892 0.0914 17   1.082  0.5374
##  APOE33 - APOE44 -0.00452 0.0328 17  -0.138  0.9896
##
## Sex = male:
##  contrast        estimate     SE df t.ratio p.value
##  APOE22 - APOE33  0.00430 0.0694 17   0.062  0.9979
##  APOE22 - APOE44 -0.06443 0.0670 17  -0.962  0.6099
##  APOE33 - APOE44 -0.06873 0.0507 17  -1.355  0.3854
##
## 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    0.05185 0.0525 17  -0.0588   0.1625
##  APOE33   -0.00202 0.0213 17  -0.0470   0.0430
##  APOE44    0.03460 0.0214 17  -0.0105   0.0797
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
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##  APOE33 - APOE44  -0.0366 0.0302 17  -1.213  0.4618
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
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##  Genotype fi.trend     SE df lower.CL upper.CL
##  APOE22    0.1384 0.0874 17  -0.0461   0.3229
##  APOE33    0.0350 0.0192 17  -0.0055   0.0755
##  APOE44    0.0395 0.0266 17  -0.0166   0.0956
##
## Sex = male:
##  Genotype fi.trend     SE df lower.CL upper.CL
##  APOE22   -0.0347 0.0580 17  -0.1571   0.0877
##  APOE33   -0.0390 0.0381 17  -0.1194   0.0413
```

```
##  APOE44     0.0297 0.0335 17  -0.0409   0.1003
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast         estimate      SE df t.ratio p.value
##  APOE22 - APOE33  0.10344 0.0895 17   1.156  0.4946
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##  APOE33 - APOE44 -0.00452 0.0328 17  -0.138  0.9896
##
## Sex = male:
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##  APOE33 - APOE44 -0.06873 0.0507 17  -1.355  0.3854
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```