Absolute Winding Number by Hc Probe Day d5

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Contents

Aim

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

Day d5 Probe by Hc Vol

```
## [1] "Hc: Probe d5 AWN VOL"

## [1] "omnibus test"

##  model term    df1 df2 F.ratio p.value
##  Genotype        2  17   1.360  0.2833
##  Sex             1  17   0.154  0.6993
##  Genotype:Sex    2  17   0.540  0.5926

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   1.167  0.3352
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   0.232  0.7953

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.285  0.6002
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
```

```
## Sex            1  17   0.236  0.6333
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex            1  17   2.616  0.1242

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

## Analysis of Variance Table
##
## Response: Probe_d5
##                   Df   Sum Sq  Mean Sq F value  Pr(>F)
## Hc                 1    9.084    9.084  0.4902 0.49329
## Genotype           2  216.414  108.207  5.8397 0.01173 *
## Sex                1   14.908   14.908  0.8046 0.38226
## Hc:Genotype        2   16.190    8.095  0.4369 0.65311
## Hc:Sex             1   38.755   38.755  2.0915 0.16630
## Genotype:Sex       2   25.643   12.822  0.6919 0.51416
## Hc:Genotype:Sex    2    5.109    2.554  0.1379 0.87219
## Residuals         17  315.005   18.530
## ---
## 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)
## Hc            1  35.942   35.942  1.0077 0.3489
## Genotype      2 172.057   86.028  2.4118 0.1597
## Hc:Genotype   2  10.030    5.015  0.1406 0.8712
## Residuals     7 249.685   35.669

## [1] "males"

## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq  Mean Sq F value  Pr(>F)
## Hc            1 13.040  13.0402  1.9964 0.18804
## Genotype      2 38.705  19.3525  2.9627 0.09762 .
## Hc:Genotype   2  7.112   3.5561  0.5444 0.59644
## Residuals    10 65.320   6.5320
## ---
## 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      3.19 5.98 17   0.534  0.6002
##
## Genotype = APOE33:
##  contrast       estimate   SE df t.ratio p.value
##  female - male     -4.19 8.62 17  -0.486  0.6333
##
## Genotype = APOE44:
```

```
##  contrast        estimate   SE df  t.ratio p.value
##  female - male     5.31 3.28 17   1.618  0.1242

## Sex = female:
##  contrast        estimate   SE df  t.ratio p.value
##  APOE22 - APOE33   7.4778 9.79 17   0.764  0.7297
##  APOE22 - APOE44  -4.2088 5.95 17  -0.708  0.7622
##  APOE33 - APOE44 -11.6866 8.30 17  -1.408  0.3589
##
## Sex = male:
##  contrast        estimate   SE df  t.ratio p.value
##  APOE22 - APOE33   0.0992 3.75 17   0.026  0.9996
##  APOE22 - APOE44  -2.0885 3.34 17  -0.626  0.8083
##  APOE33 - APOE44  -2.1877 4.02 17  -0.544  0.8510
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends
##  Genotype Hc.trend   SE df lower.CL upper.CL
##  APOE22       2940 5941 17    -9595    15475
##  APOE33      -4928 6832 17   -19343     9487
##  APOE44       -265 2335 17    -5191     4661
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##  contrast         estimate   SE df t.ratio p.value
##  APOE22 - APOE33      7868 9054 17   0.869  0.6665
##  APOE22 - APOE44      3205 6384 17   0.502  0.8713
##  APOE33 - APOE44     -4663 7220 17  -0.646  0.7972
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
##  Genotype Hc.trend    SE df lower.CL upper.CL
##  APOE22       7466 10628 17   -14956    29889
##  APOE33      -4159 12325 17   -30163    21845
##  APOE44       1017  2615 17    -4500     6534
##
## Sex = male:
##  Genotype Hc.trend    SE df lower.CL upper.CL
##  APOE22      -1586  5315 17   -12801     9628
##  APOE33      -5698  5900 17   -18146     6751
##  APOE44      -1547  3868 17    -9708     6614
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast         estimate    SE df t.ratio p.value
##  APOE22 - APOE33   11624.7 16274 17   0.714  0.7585
```

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```
## APOE22 - APOE44    6449.3 10945 17   0.589  0.8277
## APOE33 - APOE44   -5175.4 12600 17  -0.411  0.9117
##
## Sex = male:
## contrast         estimate    SE df t.ratio p.value
## APOE22 - APOE33    4111.4  7941 17   0.518  0.8638
## APOE22 - APOE44     -39.2  6574 17  -0.006  1.0000
## APOE33 - APOE44   -4150.6  7055 17  -0.588  0.8281
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d5 Probe By Hc FA

```
## [1] "Hc: Probe d5 AWN FA"

## [1] "omnibus test"

## model term   df1 df2 F.ratio p.value
## Genotype       2  17   4.135  0.0344
## Sex            1  17   0.522  0.4798
## Genotype:Sex   2  17   0.752  0.4865

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype     2  17   3.067  0.0729
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype     2  17   1.083  0.3607

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex          1  17   0.287  0.5993
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex          1  17   0.241  0.6296
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex          1  17   1.596  0.2235

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

## Analysis of Variance Table
##
## Response: Probe_d5
##                Df  Sum Sq Mean Sq F value  Pr(>F)
## Hc              1 118.580 118.580  7.2625 0.01534 *
## Genotype        2 170.837  85.419  5.2315 0.01696 *
## Sex             1  16.903  16.903  1.0353 0.32319
## Hc:Genotype     2   2.652   1.326  0.0812 0.92235
## Hc:Sex          1  24.879  24.879  1.5237 0.23385
## Genotype:Sex    2  28.290  14.145  0.8663 0.43825
## Hc:Genotype:Sex 2   1.396   0.698  0.0427 0.95826
## Residuals      17 277.571  16.328
```

```
## ---
## 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)
## Hc           1 132.222 132.222  4.7761 0.06512 .
## Genotype     2 140.176  70.088  2.5317 0.14883
## Hc:Genotype  2   1.527   0.763  0.0276 0.97291
## Residuals    7 193.789  27.684
## ---
## 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)
## Hc           1  0.126  0.1256  0.0150 0.9050
## Genotype     2 36.850 18.4248  2.1991 0.1616
## Hc:Genotype  2  3.420  1.7099  0.2041 0.8187
## Residuals   10 83.782  8.3782

## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
##  contrast        estimate   SE df t.ratio p.value
##  female - male       1.81 3.38 17   0.535  0.5993
##
## Genotype = APOE33:
##  contrast        estimate   SE df t.ratio p.value
##  female - male      -1.64 3.33 17  -0.491  0.6296
##
## Genotype = APOE44:
##  contrast        estimate   SE df t.ratio p.value
##  female - male       3.93 3.11 17   1.263  0.2235

## Sex = female:
##  contrast         estimate   SE df t.ratio p.value
##  APOE22 - APOE33      5.60 4.01 17   1.398  0.3638
##  APOE22 - APOE44     -3.72 3.82 17  -0.975  0.6019
##  APOE33 - APOE44     -9.32 3.77 17  -2.473  0.0598
##
## Sex = male:
##  contrast         estimate   SE df t.ratio p.value
##  APOE22 - APOE33      2.16 2.54 17   0.848  0.6795
##  APOE22 - APOE44     -1.60 2.55 17  -0.628  0.8068
##  APOE33 - APOE44     -3.76 2.56 17  -1.466  0.3312
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends
```

```
##  Genotype Hc.trend  SE df lower.CL upper.CL
##  APOE22       -124 159 17     -460      211
##  APOE33       -200 262 17     -752      353
##  APOE44        -48 179 17     -425      329
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##  contrast         estimate  SE df t.ratio p.value
##  APOE22 - APOE33     75.2 306 17   0.246  0.9674
##  APOE22 - APOE44    -76.4 239 17  -0.319  0.9456
##  APOE33 - APOE44   -151.6 317 17  -0.478  0.8824
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
##  Genotype Hc.trend  SE df lower.CL upper.CL
##  APOE22     -222.1 243 17     -734      290
##  APOE33     -287.0 189 17     -685      111
##  APOE44     -208.2 195 17     -620      204
##
## Sex = male:
##  Genotype Hc.trend  SE df lower.CL upper.CL
##  APOE22      -26.6 206 17     -460      407
##  APOE33     -112.1 488 17    -1142      918
##  APOE44      112.2 299 17     -519      744
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast         estimate  SE df t.ratio p.value
##  APOE22 - APOE33     64.9 308 17   0.211  0.9758
##  APOE22 - APOE44    -13.9 312 17  -0.045  0.9989
##  APOE33 - APOE44    -78.8 272 17  -0.290  0.9548
##
## Sex = male:
##  contrast         estimate  SE df t.ratio p.value
##  APOE22 - APOE33     85.5 530 17   0.161  0.9857
##  APOE22 - APOE44   -138.8 363 17  -0.382  0.9230
##  APOE33 - APOE44   -224.3 573 17  -0.392  0.9193
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d5 Probe By Hc DEG

```
## [1] "Hc: Probe d5 AWN DEG"

## [1] "omnibus test"

##  model term   df1 df2 F.ratio p.value
##  Genotype       2  17   3.172  0.0675
```

```
## Sex             1  17   0.797  0.3845
## Genotype:Sex    2  17   1.777  0.1991

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype      2  17   5.058  0.0189
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype      2  17   0.175  0.8410

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.709  0.4114
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.830  0.3751
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   3.278  0.0879

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

## Analysis of Variance Table
##
## Response: Probe_d5
##                 Df  Sum Sq Mean Sq F value  Pr(>F)
## Hc               1  15.305  15.305  1.0885 0.31141
## Genotype         2 195.804  97.902  6.9632 0.00618 **
## Sex              1  28.919  28.919  2.0569 0.16966
## Hc:Genotype      2  69.296  34.648  2.4643 0.11487
## Hc:Sex           1  11.482  11.482  0.8166 0.37880
## Genotype:Sex     2  28.221  14.111  1.0036 0.38727
## Hc:Genotype:Sex  2  53.062  26.531  1.8870 0.18193
## Residuals       17 239.020  14.060
## ---
## 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)
## Hc           1   6.659   6.659  0.2597 0.62599
## Genotype     2 208.055 104.027  4.0571 0.06761 .
## Hc:Genotype  2  73.515  36.758  1.4336 0.30073
## Residuals    7 179.485  25.641
## ---
## 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)
## Hc            1 27.464 27.4636  4.6131 0.05728 .
## Genotype      2 24.642 12.3212  2.0696 0.17696
## Hc:Genotype   2 12.537  6.2683  1.0529 0.38462
## Residuals    10 59.534  5.9534
## ---
## 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       5.67 6.73 17   0.842  0.4114
##
## Genotype = APOE33:
##  contrast        estimate   SE df t.ratio p.value
##  female - male      -3.13 3.44 17  -0.911  0.3751
##
## Genotype = APOE44:
##  contrast        estimate   SE df t.ratio p.value
##  female - male       4.58 2.53 17   1.811  0.0879

## Sex = female:
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33    8.8967 6.78 17   1.312  0.4082
##  APOE22 - APOE44   -0.3043 6.63 17  -0.046  0.9988
##  APOE33 - APOE44   -9.2009 2.93 17  -3.143  0.0155
##
## Sex = male:
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33    0.0931 3.34 17   0.028  0.9996
##  APOE22 - APOE44   -1.3916 2.79 17  -0.499  0.8728
##  APOE33 - APOE44   -1.4848 3.11 17  -0.477  0.8828
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends
##  Genotype  Hc.trend      SE df   lower.CL upper.CL
##  APOE22   1.18e-04 1.11e-04 17 -1.16e-04 3.52e-04
##  APOE33   3.89e-07 3.33e-05 17 -6.99e-05 7.07e-05
##  APOE44  -6.15e-05 4.74e-05 17 -1.62e-04 3.86e-05
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##  contrast        estimate       SE df t.ratio p.value
##  APOE22 - APOE33 1.18e-04 0.000116 17   1.018  0.5760
##  APOE22 - APOE44 1.80e-04 0.000120 17   1.491  0.3199
##  APOE33 - APOE44 6.18e-05 0.000058 17   1.067  0.5465
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
```

```
## Sex = female:
##  Genotype  Hc.trend       SE df  lower.CL upper.CL
##  APOE22    1.92e-04 1.86e-04 17 -2.01e-04 5.86e-04
##  APOE33    6.94e-05 4.16e-05 17 -1.84e-05 1.57e-04
##  APOE44   -1.03e-04 7.04e-05 17 -2.51e-04 4.55e-05
##
## Sex = male:
##  Genotype  Hc.trend       SE df  lower.CL upper.CL
##  APOE22    4.37e-05 1.20e-04 17 -2.09e-04 2.96e-04
##  APOE33   -6.87e-05 5.21e-05 17 -1.79e-04 4.13e-05
##  APOE44   -1.99e-05 6.36e-05 17 -1.54e-04 1.14e-04
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast       estimate       SE df t.ratio p.value
##  APOE22 - APOE33 1.23e-04 1.91e-04 17   0.644  0.7979
##  APOE22 - APOE44 2.95e-04 1.99e-04 17   1.483  0.3233
##  APOE33 - APOE44 1.72e-04 8.18e-05 17   2.109  0.1177
##
## Sex = male:
##  contrast       estimate       SE df t.ratio p.value
##  APOE22 - APOE33  1.12e-04 1.30e-04 17   0.861  0.6712
##  APOE22 - APOE44  6.36e-05 1.35e-04 17   0.470  0.8863
##  APOE33 - APOE44 -4.87e-05 8.22e-05 17  -0.593  0.8258
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d5 Probe By Hc CLUS

```
## [1] "Hc: Probe d5 AWN CLUSTERING"

## [1] "omnibus test"

##  model term    df1 df2 F.ratio p.value
##  Genotype        2  17   4.503  0.0270
##  Sex             1  17   0.484  0.4959
##  Genotype:Sex    2  17   1.712  0.2102

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   5.715  0.0126
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   0.452  0.6440

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.185  0.6721
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.553  0.4674
```

```
## 
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   4.357  0.0522

##  model term      df1 df2 F.ratio p.value
##  Hc               1  17   0.000  0.9877
##  Genotype         2  17   2.864  0.0847
##  Sex              1  17   0.718  0.4087
##  Hc:Genotype      2  17   0.413  0.6679
##  Hc:Sex           1  17   0.726  0.4060
##  Genotype:Sex     2  17   0.362  0.7013
##  Hc:Genotype:Sex  2  17   0.863  0.4394

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

## Analysis of Variance Table
## 
## Response: Probe_d5
##                 Df  Sum Sq Mean Sq F value   Pr(>F)
## Hc               1   3.709   3.709  0.2363 0.633066
## Genotype         2 204.560 102.280  6.5168 0.007928 **
## Sex              1  31.755  31.755  2.0233 0.172995
## Hc:Genotype      2  47.908  23.954  1.5262 0.245692
## Hc:Sex           1  22.984  22.984  1.4645 0.242780
## Genotype:Sex     2  36.281  18.141  1.1558 0.338336
## Hc:Genotype:Sex  2  27.100  13.550  0.8633 0.439444
## Residuals       17 266.811  15.695
## ---
## 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)
## Hc           1  10.542  10.542  0.3571 0.56897
## Genotype     2 202.377 101.189  3.4272 0.09168 .
## Hc:Genotype  2  48.117  24.058  0.8148 0.48069
## Residuals    7 206.678  29.525
## ---
## 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)
## Hc           1 30.756 30.7559  5.1146 0.04724 *
## Genotype     2 28.919 14.4597  2.4046 0.14039
## Hc:Genotype  2  4.368  2.1842  0.3632 0.70423
## Residuals   10 60.133  6.0133
## ---
## 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      3.31 7.69 17   0.431  0.6721
##
## Genotype = APOE33:
##  contrast       estimate   SE df t.ratio p.value
##  female - male     -2.53 3.41 17  -0.743  0.4674
##
## Genotype = APOE44:
##  contrast       estimate   SE df t.ratio p.value
##  female - male      5.34 2.56 17   2.087  0.0522

## Sex = female:
##  contrast         estimate   SE df t.ratio p.value
##  APOE22 - APOE33    6.114 7.80 17   0.784  0.7175
##  APOE22 - APOE44   -4.200 7.60 17  -0.553  0.8465
##  APOE33 - APOE44  -10.314 3.05 17  -3.379  0.0095
##
## Sex = male:
##  contrast         estimate   SE df t.ratio p.value
##  APOE22 - APOE33    0.269 3.15 17   0.085  0.9960
##  APOE22 - APOE44   -2.171 2.81 17  -0.772  0.7245
##  APOE33 - APOE44   -2.440 2.97 17  -0.820  0.6959
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends
##  Genotype Hc.trend     SE df lower.CL upper.CL
##  APOE22    0.03248 0.0842 17  -0.1452   0.2102
##  APOE33   -0.00383 0.0248 17  -0.0562   0.0486
##  APOE44   -0.03009 0.0270 17  -0.0871   0.0269
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##  contrast         estimate     SE df t.ratio p.value
##  APOE22 - APOE33    0.0363 0.0878 17   0.413  0.9106
##  APOE22 - APOE44    0.0626 0.0885 17   0.707  0.7625
##  APOE33 - APOE44    0.0263 0.0367 17   0.716  0.7576
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
##  Genotype Hc.trend     SE df lower.CL upper.CL
##  APOE22     0.0694 0.1479 17  -0.2425   0.3814
##  APOE33     0.0407 0.0258 17  -0.0137   0.0952
##  APOE44    -0.0333 0.0348 17  -0.1067   0.0400
##
## Sex = male:
##  Genotype Hc.trend     SE df lower.CL upper.CL
##  APOE22    -0.0045 0.0807 17  -0.1748   0.1658
```

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```
##   APOE33     -0.0484 0.0424 17  -0.1379     0.0411
##   APOE44     -0.0268 0.0414 17  -0.1141     0.0604
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast           estimate      SE df t.ratio p.value
##  APOE22 - APOE33   0.0287 0.1501 17   0.191  0.9801
##  APOE22 - APOE44   0.1028 0.1519 17   0.677  0.7800
##  APOE33 - APOE44   0.0741 0.0433 17   1.712  0.2296
##
## Sex = male:
##  contrast           estimate      SE df t.ratio p.value
##  APOE22 - APOE33   0.0439 0.0912 17   0.481  0.8810
##  APOE22 - APOE44   0.0223 0.0907 17   0.246  0.9672
##  APOE33 - APOE44  -0.0216 0.0593 17  -0.364  0.9299
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends
##  Genotype Hc.trend      SE df lower.CL upper.CL
##  APOE22     0.03248 0.0842 17  -0.1452   0.2102
##  APOE33    -0.00383 0.0248 17  -0.0562   0.0486
##  APOE44    -0.03009 0.0270 17  -0.0871   0.0269
##
## Results are averaged over the levels of: Sex
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##  APOE22 - APOE33   0.0363 0.0878 17   0.413  0.9106
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##  APOE33 - APOE44   0.0263 0.0367 17   0.716  0.7576
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
##  Genotype Hc.trend      SE df lower.CL upper.CL
##  APOE22     0.0694 0.1479 17  -0.2425   0.3814
##  APOE33     0.0407 0.0258 17  -0.0137   0.0952
##  APOE44    -0.0333 0.0348 17  -0.1067   0.0400
##
## Sex = male:
##  Genotype Hc.trend      SE df lower.CL upper.CL
##  APOE22    -0.0045 0.0807 17  -0.1748   0.1658
##  APOE33    -0.0484 0.0424 17  -0.1379   0.0411
##  APOE44    -0.0268 0.0414 17  -0.1141   0.0604
##
## Confidence level used: 0.95
##
```

```
## $contrasts
## Sex = female:
##  contrast         estimate     SE df t.ratio p.value
##  APOE22 - APOE33    0.0287 0.1501 17   0.191  0.9801
##  APOE22 - APOE44    0.1028 0.1519 17   0.677  0.7800
##  APOE33 - APOE44    0.0741 0.0433 17   1.712  0.2296
##
## Sex = male:
##  contrast         estimate     SE df t.ratio p.value
##  APOE22 - APOE33    0.0439 0.0912 17   0.481  0.8810
##  APOE22 - APOE44    0.0223 0.0907 17   0.246  0.9672
##  APOE33 - APOE44   -0.0216 0.0593 17  -0.364  0.9299
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```