Absolute Winding Number by Hc 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 Hc Vol

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

## [1] "omnibus test"

##  model term    df1 df2 F.ratio p.value
##  Genotype       2  17   8.293  0.0031
##  Sex            1  17   0.018  0.8942
##  Genotype:Sex   2  17   2.484  0.1131

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype    2  17   4.752  0.0229
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype    2  17   5.373  0.0155

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex         1  17   3.509  0.0784
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
```

```
## Sex            1  17   1.962  0.1792
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex            1  17   0.517  0.4820

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

## Analysis of Variance Table
##
## Response: Probe_d8
##                  Df  Sum Sq Mean Sq F value    Pr(>F)
## Hc               1   8.886   8.886  2.4504    0.1359
## Genotype         2 204.234 102.117 28.1617 4.02e-06 ***
## Sex              1   1.412   1.412  0.3893    0.5409
## Hc:Genotype      2   2.642   1.321  0.3644    0.6999
## Hc:Sex           1   0.075   0.075  0.0207    0.8872
## Genotype:Sex     2   8.164   4.082  1.1258    0.3474
## Hc:Genotype:Sex  2  12.741   6.370  1.7568    0.2025
## Residuals       17  61.644   3.626
## ---
## 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)
## Hc           1  0.627   0.627  0.1524 0.707860
## Genotype     2 87.960  43.980 10.6830 0.007465 **
## Hc:Genotype  2 19.951   9.976  2.4231 0.158600
## Residuals    7 28.818   4.117
## ---
## 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)
## Hc           1   0.152   0.152  0.0462 0.8340898
## Genotype     2 101.612  50.806 15.4775 0.0008679 ***
## Hc:Genotype  2   3.446   1.723  0.5249 0.6070557
## Residuals   10  32.826   3.283
## ---
## 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      4.95 2.64 17   1.873  0.0784
##
## Genotype = APOE33:
##  contrast       estimate   SE df t.ratio p.value
##  female - male     -5.34 3.81 17  -1.401  0.1792
```

```
##
## Genotype = APOE44:
##  contrast        estimate   SE df t.ratio p.value
##  female - male       1.04 1.45 17   0.719  0.4820

## Sex = female:
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33     10.939 4.33 17   2.525  0.0541
##  APOE22 - APOE44     -0.369 2.63 17  -0.140  0.9892
##  APOE33 - APOE44    -11.308 3.67 17  -3.080  0.0177
##
## Sex = male:
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33      0.646 1.66 17   0.389  0.9202
##  APOE22 - APOE44     -4.277 1.48 17  -2.896  0.0258
##  APOE33 - APOE44     -4.923 1.78 17  -2.766  0.0336
##
## 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       3589 2628 17    -1956     9134
##  APOE33      -5990 3022 17   -12367      387
##  APOE44       -719 1033 17    -2898     1460
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33      9579 4005 17   2.392  0.0699
##  APOE22 - APOE44      4308 2824 17   1.526  0.3043
##  APOE33 - APOE44     -5271 3194 17  -1.650  0.2526
##
## 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       7598 4701 17    -2321    17517
##  APOE33      -8896 5452 17   -20399     2608
##  APOE44      -1321 1157 17    -3762     1119
##
## Sex = male:
##  Genotype Hc.trend   SE df lower.CL upper.CL
##  APOE22       -419 2351 17    -5380     4542
##  APOE33      -3084 2610 17    -8591     2422
##  APOE44       -116 1711 17    -3727     3494
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
```

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```
##  contrast        estimate   SE df t.ratio p.value
##  APOE22 - APOE33    16493 7199 17   2.291  0.0844
##  APOE22 - APOE44     8919 4842 17   1.842  0.1861
##  APOE33 - APOE44    -7574 5574 17  -1.359  0.3836
##
## Sex = male:
##  contrast        estimate   SE df t.ratio p.value
##  APOE22 - APOE33     2665 3513 17   0.759  0.7326
##  APOE22 - APOE44     -303 2908 17  -0.104  0.9940
##  APOE33 - APOE44    -2968 3121 17  -0.951  0.6165
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d8 Probe By Hc FA

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

## [1] "omnibus test"

##  model term    df1 df2 F.ratio p.value
##  Genotype        2  17  19.581  <.0001
##  Sex             1  17   3.569  0.0761
##  Genotype:Sex    2  17   1.529  0.2450

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   8.229  0.0032
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17  15.142  0.0002

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   6.035  0.0251
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.036  0.8508
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.329  0.5736

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

## Analysis of Variance Table
##
## Response: Probe_d8
##               Df  Sum Sq Mean Sq F value     Pr(>F)
## Hc             1  31.852  31.852 10.1539   0.005402 **
## Genotype       2 175.243  87.622 27.9323 4.241e-06 ***
## Sex            1   9.619   9.619  3.0664   0.097948 .
## Hc:Genotype    2   4.401   2.200  0.7015   0.509661
## Hc:Sex         1  13.229  13.229  4.2172   0.055729 .
## Genotype:Sex   2   9.826   4.913  1.5661   0.237536
```

```
## Hc:Genotype:Sex  2    2.300    1.150   0.3666   0.698405
## Residuals         17  53.328    3.137
## ---
## 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)
## Hc           1 41.228  41.228 12.1421 0.010203 *
## Genotype     2 68.153  34.076 10.0359 0.008791 **
## Hc:Genotype  2  4.208   2.104  0.6197 0.565226
## Residuals    7 23.768   3.395
## ---
## 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)
## Hc           1   2.125   2.125  0.7190 0.4163150
## Genotype     2 100.943  50.472 17.0746 0.0005962 ***
## Hc:Genotype  2   5.408   2.704  0.9147 0.4316884
## Residuals   10  29.560   2.956
## ---
## 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     3.636 1.48 17   2.457  0.0251
##
## Genotype = APOE33:
##  contrast       estimate   SE df t.ratio p.value
##  female - male     0.279 1.46 17   0.191  0.8508
##
## Genotype = APOE44:
##  contrast       estimate   SE df t.ratio p.value
##  female - male     0.782 1.36 17   0.574  0.5736

## Sex = female:
##  contrast        estimate   SE df t.ratio p.value
##  APOE22 - APOE33     5.06 1.76 17   2.885  0.0264
##  APOE22 - APOE44    -1.44 1.67 17  -0.860  0.6721
##  APOE33 - APOE44    -6.50 1.65 17  -3.936  0.0029
##
## Sex = male:
##  contrast        estimate   SE df t.ratio p.value
##  APOE22 - APOE33     1.71 1.12 17   1.531  0.3017
##  APOE22 - APOE44    -4.29 1.12 17  -3.840  0.0036
##  APOE33 - APOE44    -6.00 1.12 17  -5.341  0.0002
##
```

```
## 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     -107.3  69.7 17     -254     39.8
##  APOE33     -107.3 114.7 17     -349    134.7
##  APOE44       59.8  78.3 17     -105    225.0
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##  contrast          estimate  SE df t.ratio p.value
##  APOE22 - APOE33     0.0184 134 17   0.000  1.0000
##  APOE22 - APOE44  -167.0614 105 17  -1.593  0.2754
##  APOE33 - APOE44  -167.0798 139 17  -1.203  0.4676
##
## 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     -244.5 106.4 17   -469.0    -20.0
##  APOE33     -141.2  82.8 17   -315.8     33.4
##  APOE44      -86.6  85.6 17   -267.3     94.1
##
## Sex = male:
##  Genotype Hc.trend    SE df lower.CL upper.CL
##  APOE22       29.9  90.1 17   -160.2    220.0
##  APOE33      -73.4 214.0 17   -524.9    378.1
##  APOE44      206.1 131.2 17    -70.6    482.8
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast         estimate  SE df t.ratio p.value
##  APOE22 - APOE33    -103.3 135 17  -0.766  0.7282
##  APOE22 - APOE44    -157.9 137 17  -1.156  0.4942
##  APOE33 - APOE44     -54.6 119 17  -0.459  0.8912
##
## Sex = male:
##  contrast         estimate  SE df t.ratio p.value
##  APOE22 - APOE33     103.3 232 17   0.445  0.8973
##  APOE22 - APOE44    -176.2 159 17  -1.107  0.5226
##  APOE33 - APOE44    -279.5 251 17  -1.114  0.5190
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d8 Probe By Hc DEG

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

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

##  model term    df1 df2 F.ratio p.value
##  Genotype       2  17  20.165  <.0001
##  Sex            1  17   4.869  0.0414
##  Genotype:Sex   2  17   2.289  0.1317

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17  16.343  0.0001
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   7.222  0.0054

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   4.547  0.0479
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.117  0.7363
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   3.045  0.0991

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

## Analysis of Variance Table
##
## Response: Probe_d8
##                   Df  Sum Sq Mean Sq F value     Pr(>F)
## Hc                 1   0.860   0.860  0.3014    0.59016
## Genotype           2 197.921  98.961 34.6762 1.001e-06 ***
## Sex                1  20.731  20.731  7.2642    0.01533 *
## Hc:Genotype        2   6.600   3.300  1.1564    0.33817
## Hc:Sex             1   8.134   8.134  2.8500    0.10963
## Genotype:Sex       2  14.595   7.297  2.5570    0.10694
## Hc:Genotype:Sex    2   2.442   1.221  0.4278    0.65877
## Residuals         17  48.515   2.854
## ---
## 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)
## Hc           1 11.530  11.530  4.0446 0.084226 .
## Genotype     2 98.444  49.222 17.2669 0.001965 **
## Hc:Genotype  2  7.428   3.714  1.3029 0.330347
## Residuals    7 19.955   2.851
## ---
## 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)
## Hc            1  6.538   6.538  2.2893 0.1612140
## Genotype      2 93.957  46.979 16.4486 0.0006884 ***
## Hc:Genotype   2  8.979   4.490  1.5720 0.2549045
## Residuals    10 28.561   2.856
## ---
## 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    6.468   3.03 17   2.132  0.0479
##
## Genotype = APOE33:
##  contrast        estimate   SE df  t.ratio p.value
##  female - male   -0.531   1.55 17  -0.342  0.7363
##
## Genotype = APOE44:
##  contrast        estimate   SE df  t.ratio p.value
##  female - male    1.989   1.14 17   1.745  0.0991

## Sex = female:
##  contrast         estimate   SE df t.ratio p.value
##  APOE22 - APOE33    8.37   3.06 17   2.738  0.0355
##  APOE22 - APOE44    1.02   2.99 17   0.342  0.9377
##  APOE33 - APOE44   -7.35   1.32 17  -5.569  0.0001
##
## Sex = male:
##  contrast         estimate   SE df t.ratio p.value
##  APOE22 - APOE33    1.37   1.50 17   0.910  0.6416
##  APOE22 - APOE44   -3.46   1.26 17  -2.750  0.0347
##  APOE33 - APOE44   -4.83   1.40 17  -3.443  0.0083
##
## 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   1.19e-04 4.99e-05 17  1.42e-05 2.25e-04
##  APOE33   4.03e-06 1.50e-05 17 -2.77e-05 3.57e-05
##  APOE44   2.96e-05 2.14e-05 17 -1.55e-05 7.47e-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  1.15e-04 5.21e-05 17   2.216  0.0970
##  APOE22 - APOE44  8.99e-05 5.43e-05 17   1.656  0.2502
##  APOE33 - APOE44 -2.56e-05 2.61e-05 17  -0.979  0.5996
##
```

```
## 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    1.79e-04 8.40e-05 17   2.21e-06 3.57e-04
##  APOE33    4.06e-05 1.87e-05 17   1.01e-06 8.01e-05
##  APOE44    4.72e-05 3.17e-05 17  -1.97e-05 1.14e-04
##
## Sex = male:
##  Genotype  Hc.trend       SE df  lower.CL upper.CL
##  APOE22    5.96e-05 5.39e-05 17  -5.41e-05 1.73e-04
##  APOE33   -3.25e-05 2.35e-05 17  -8.20e-05 1.70e-05
##  APOE44    1.20e-05 2.86e-05 17  -4.85e-05 7.24e-05
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast         estimate       SE df t.ratio p.value
##  APOE22 - APOE33  1.39e-04 8.60e-05 17   1.613  0.2672
##  APOE22 - APOE44  1.32e-04 8.98e-05 17   1.472  0.3284
##  APOE33 - APOE44 -6.66e-06 3.68e-05 17  -0.181  0.9821
##
## Sex = male:
##  contrast         estimate       SE df t.ratio p.value
##  APOE22 - APOE33  9.21e-05 5.88e-05 17   1.567  0.2864
##  APOE22 - APOE44  4.77e-05 6.10e-05 17   0.781  0.7196
##  APOE33 - APOE44 -4.45e-05 3.70e-05 17  -1.201  0.4687
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d8 Probe By Hc CLUS

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

## [1] "omnibus test"

##  model term    df1 df2 F.ratio p.value
##  Genotype        2  17  17.032  0.0001
##  Sex             1  17   1.185  0.2915
##  Genotype:Sex    2  17   0.507  0.6113

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17  10.659  0.0010
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   7.843  0.0039

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.769  0.3928
##
```

```
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.007  0.9325
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   1.487  0.2393

##  model term      df1 df2 F.ratio p.value
##  Hc                1  17   0.739  0.4018
##  Genotype          2  17  19.383  <.0001
##  Sex               1  17   1.448  0.2453
##  Hc:Genotype       2  17   0.371  0.6953
##  Hc:Sex            1  17   1.218  0.2851
##  Genotype:Sex      2  17   0.118  0.8898
##  Hc:Genotype:Sex   2  17   0.252  0.7800

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

## Analysis of Variance Table
##
## Response: Probe_d8
##                 Df  Sum Sq Mean Sq F value    Pr(>F)
## Hc               1   0.956   0.956  0.2460   0.62624
## Genotype         2 200.220 100.110 25.7680 7.137e-06 ***
## Sex              1  17.562  17.562  4.5204   0.04844 *
## Hc:Genotype      2   0.418   0.209  0.0538   0.94779
## Hc:Sex           1   8.179   8.179  2.1052   0.16500
## Genotype:Sex     2   4.459   2.230  0.5739   0.57388
## Hc:Genotype:Sex  2   1.959   0.979  0.2521   0.78002
## Residuals       17  66.046   3.885
## ---
## 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)
## Hc           1 13.038  13.038  2.8339 0.136169
## Genotype     2 91.795  45.898  9.9764 0.008928 **
## Hc:Genotype  2  0.319   0.160  0.0347 0.966038
## Residuals    7 32.204   4.601
## ---
## 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)
## Hc           1  2.891   2.891  0.8544 0.377084
## Genotype     2 97.815  48.907 14.4520 0.001122 **
## Hc:Genotype  2  3.488   1.744  0.5154 0.612307
## Residuals   10 33.841   3.384
```

```
## ---
## 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      3.355 3.83 17   0.877  0.3928
##
## Genotype = APOE33:
##  contrast        estimate    SE df t.ratio p.value
##  female - male     -0.146 1.70 17  -0.086  0.9325
##
## Genotype = APOE44:
##  contrast        estimate    SE df t.ratio p.value
##  female - male      1.552 1.27 17   1.220  0.2393

## Sex = female:
##  contrast          estimate    SE df t.ratio p.value
##  APOE22 - APOE33       4.63 3.88 17   1.194  0.4724
##  APOE22 - APOE44      -2.38 3.78 17  -0.629  0.8064
##  APOE33 - APOE44      -7.01 1.52 17  -4.617  0.0007
##
## Sex = male:
##  contrast          estimate    SE df t.ratio p.value
##  APOE22 - APOE33       1.13 1.57 17   0.722  0.7542
##  APOE22 - APOE44      -4.18 1.40 17  -2.989  0.0213
##  APOE33 - APOE44      -5.31 1.48 17  -3.590  0.0061
##
## 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   0.02378 0.0419 17  -0.0646   0.1122
##  APOE33   0.00074 0.0124 17  -0.0253   0.0268
##  APOE44   0.01479 0.0134 17  -0.0136   0.0431
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##  contrast         estimate     SE df t.ratio p.value
##  APOE22 - APOE33   0.02304 0.0437 17   0.527  0.8592
##  APOE22 - APOE44   0.00898 0.0440 17   0.204  0.9773
##  APOE33 - APOE44  -0.01405 0.0183 17  -0.770  0.7260
##
## 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   0.04373 0.0736 17 -0.11149   0.1989
##  APOE33   0.02241 0.0128 17 -0.00467   0.0495
##  APOE44   0.02362 0.0173 17 -0.01286   0.0601
```

```
##
## Sex = male:
##  Genotype Hc.trend     SE df lower.CL upper.CL
##  APOE22    0.00383 0.0402 17 -0.08091   0.0886
##  APOE33   -0.02093 0.0211 17 -0.06546   0.0236
##  APOE44    0.00596 0.0206 17 -0.03745   0.0494
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast         estimate     SE df t.ratio p.value
##  APOE22 - APOE33   0.02132 0.0747 17   0.285  0.9562
##  APOE22 - APOE44   0.02011 0.0756 17   0.266  0.9618
##  APOE33 - APOE44  -0.00121 0.0215 17  -0.056  0.9982
##
## Sex = male:
##  contrast         estimate     SE df t.ratio p.value
##  APOE22 - APOE33   0.02475 0.0454 17   0.546  0.8501
##  APOE22 - APOE44  -0.00214 0.0451 17  -0.047  0.9988
##  APOE33 - APOE44  -0.02689 0.0295 17  -0.912  0.6402
##
## 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    0.02378 0.0419 17  -0.0646   0.1122
##  APOE33    0.00074 0.0124 17  -0.0253   0.0268
##  APOE44    0.01479 0.0134 17  -0.0136   0.0431
##
## Results are averaged over the levels of: Sex
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##  APOE22 - APOE33   0.02304 0.0437 17   0.527  0.8592
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##
## 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    0.04373 0.0736 17 -0.11149   0.1989
##  APOE33    0.02241 0.0128 17 -0.00467   0.0495
##  APOE44    0.02362 0.0173 17 -0.01286   0.0601
##
## Sex = male:
##  Genotype Hc.trend     SE df lower.CL upper.CL
##  APOE22    0.00383 0.0402 17 -0.08091   0.0886
##  APOE33   -0.02093 0.0211 17 -0.06546   0.0236
```

```
## APOE44    0.00596 0.0206 17 -0.03745    0.0494
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast          estimate      SE df t.ratio p.value
##  APOE22 - APOE33  0.02132 0.0747 17   0.285  0.9562
##  APOE22 - APOE44  0.02011 0.0756 17   0.266  0.9618
##  APOE33 - APOE44 -0.00121 0.0215 17  -0.056  0.9982
##
## Sex = male:
##  contrast          estimate      SE df t.ratio p.value
##  APOE22 - APOE33  0.02475 0.0454 17   0.546  0.8501
##  APOE22 - APOE44 -0.00214 0.0451 17  -0.047  0.9988
##  APOE33 - APOE44 -0.02689 0.0295 17  -0.912  0.6402
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Winding Number ~ Volume:Hc; males and females

Winding Number: Probe Day d8

Winding Number ~ FA: Hc, males and females

Winding Number: Probe Day d8

Winding Number ~ DEG: Hc, males and females

Winding Number: Probe Day d8

Winding Number ~ CLUS: Hc, males and females

Clustering Coefficient