

# Absolute Winding Number by cbw Probe Day d8

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## Aim

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

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## Day d8 Probe by cbw Vol

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

## model term    df1 df2 F.ratio p.value
## Genotype      2  17   9.830  0.0015
## Sex           1  17   0.636  0.4360
## Genotype:Sex   2  17   0.218  0.8067

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   6.986  0.0061
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   3.685  0.0468

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17   2.264  0.1507
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
```

```

## Sex          1  17   0.012  0.9123
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex          1  17   0.670  0.4243
## [1] "anova: males and females"
## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## cbw           1   1.345    1.345   0.3542   0.55960
## Genotype      2 203.830 101.915 26.8375 5.496e-06 ***
## Sex           1   5.404    5.404   1.4231   0.24928
## cbw:Genotype  2   1.448    0.724   0.1906   0.82818
## cbw:Sex       1   1.185    1.185   0.3121   0.58365
## Genotype:Sex  2   1.425    0.712   0.1876   0.83066
## cbw:Genotype:Sex 2 20.604 10.302  2.7128   0.09495 .
## Residuals    17 64.557    3.797
## ---
## 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)
## cbw           1   5.071    5.071   1.1641 0.316385
## Genotype      2 83.686  41.843   9.6058 0.009843 **
## cbw:Genotype  2 18.108    9.054   2.0785 0.195620
## Residuals     7 30.492    4.356
## ---
## 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)
## cbw           1 16.147   16.147   4.7402 0.054504 .
## Genotype      2 83.870  41.935 12.3102 0.002011 **
## cbw:Genotype  2   3.953    1.977   0.5802 0.577558
## Residuals    10 34.065    3.407
## ---
## 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    1.845 1.23 17    1.505  0.1507
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male   -0.345 3.09 17   -0.112  0.9123

```

```

##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    1.549 1.89 17   0.819  0.4243

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    4.75 2.63 17   1.805  0.1979
## APOE22 - APOE44   -3.60 1.31 17  -2.755  0.0343
## APOE33 - APOE44   -8.36 2.65 17  -3.153  0.0152
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    2.56 2.02 17   1.268  0.4313
## APOE22 - APOE44   -3.90 1.84 17  -2.122  0.1149
## APOE33 - APOE44   -6.46 2.47 17  -2.621  0.0448
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## [1] "slopes"

## $emtrends
## Genotype cbw.trend    SE df lower.CL upper.CL
## APOE22      -2611.6 2787 17   -8491    3268
## APOE33       -26.7 3205 17   -6790    6736
## APOE44      1239.6 1986 17   -2950    5429
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33   -2585 4247 17  -0.609  0.8174
## APOE22 - APOE44   -3851 3422 17  -1.125  0.5120
## APOE33 - APOE44   -1266 3771 17  -0.336  0.9399
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
## Genotype cbw.trend    SE df lower.CL upper.CL
## APOE22      -7484 4634 17   -17260    2293
## APOE33       3265 2653 17   -2331    8862
## APOE44       3688 2814 17   -2250    9625
##
## Sex = male:
## Genotype cbw.trend    SE df lower.CL upper.CL
## APOE22       2261 3097 17   -4275    8796
## APOE33      -3319 5836 17  -15632    8995
## APOE44      -1208 2802 17   -7120    4703
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:

```

```
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33   -10749 5339 17  -2.013  0.1393
## APOE22 - APOE44   -11171 5421 17  -2.061  0.1282
## APOE33 - APOE44    -422 3867 17  -0.109  0.9935
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33     5579 6607 17   0.844  0.6813
## APOE22 - APOE44     3469 4177 17   0.831  0.6897
## APOE33 - APOE44    -2110 6474 17  -0.326  0.9433
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

## Day d8 Probe By cbw FA

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

## model term    df1 df2 F.ratio p.value
## Genotype      2  17  13.661  0.0003
## Sex           1  17   2.708  0.1182
## Genotype:Sex   2  17   0.163  0.8508

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   7.435  0.0048
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   6.444  0.0083

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17   1.905  0.1854
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.137  0.7158
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex        1  17   1.830  0.1939

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

## Analysis of Variance Table
##
## Response: Probe_d8
##          Df Sum Sq Mean Sq F value    Pr(>F)
## cbw        1   1.783    1.783   0.4537    0.5096
## Genotype    2 200.779  100.389 25.5505 7.534e-06 ***
## Sex         1  10.010   10.010   2.5477    0.1289
## cbw:Genotype 2   1.807    0.904   0.2300    0.7970
## cbw:Sex      1   9.444    9.444   2.4036    0.1395
## Genotype:Sex 2   2.481    1.241   0.3157    0.7334
```

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## cbw:Genotype:Sex  2    6.700    3.350  0.8526    0.4437
## Residuals        17  66.794    3.929
## ---
## 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)
## cbw         1   0.750    0.750   0.1262  0.73286
## Genotype     2  93.133   46.567   7.8362  0.01635 *
## cbw:Genotype  2   1.876    0.938   0.1579  0.85692
## Residuals    7  41.598    5.943
## ---
## 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)
## cbw         1   2.506    2.506   0.9947  0.342114
## Genotype     2 101.105   50.552  20.0633  0.000316 ***
## cbw:Genotype  2   9.228    4.614   1.8313  0.210059
## Residuals   10  25.196    2.520
## ---
## 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    2.206 1.60 17    1.380  0.1854
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male    0.757 2.04 17    0.370  0.7158
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    1.881 1.39 17    1.353  0.1939

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    3.65 2.05 17    1.783  0.2048
## APOE22 - APOE44   -3.15 1.68 17   -1.876  0.1761
## APOE33 - APOE44   -6.80 1.80 17   -3.783  0.0040
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    2.20 1.59 17    1.381  0.3723
## APOE22 - APOE44   -3.47 1.29 17   -2.691  0.0390
## APOE33 - APOE44   -5.68 1.70 17   -3.345  0.0102
##

```

```
## P value adjustment: tukey method for comparing a family of 3 estimates
## [1] "slopes"
## $emtrends
##      Genotype cbw.trend      SE df lower.CL upper.CL
##      APOE22      -70.9  86.1 17      -253      111
##      APOE33       19.9 123.1 17      -240      280
##      APOE44       77.8  96.0 17      -125      280
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##      contrast      estimate      SE df t.ratio p.value
##      APOE22 - APOE33      -90.8 150 17   -0.604  0.8198
##      APOE22 - APOE44     -148.6 129 17   -1.153  0.4963
##      APOE33 - APOE44      -57.9 156 17   -0.371  0.9274
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates
## $emtrends
## Sex = female:
##      Genotype cbw.trend      SE df lower.CL upper.CL
##      APOE22      -94.6 105.7 17   -317.7    128.4
##      APOE33      -42.2  40.3 17   -127.2     42.8
##      APOE44     -111.2 115.7 17   -355.4    133.0
##
## Sex = male:
##      Genotype cbw.trend      SE df lower.CL upper.CL
##      APOE22      -47.1 135.9 17   -333.8    239.7
##      APOE33       82.0 242.9 17   -430.6    594.5
##      APOE44      266.7 153.2 17    -56.5    590.0
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##      contrast      estimate      SE df t.ratio p.value
##      APOE22 - APOE33     -52.5 113 17   -0.464  0.8890
##      APOE22 - APOE44       16.5 157 17    0.106  0.9939
##      APOE33 - APOE44       69.0 123 17    0.563  0.8412
##
## Sex = male:
##      contrast      estimate      SE df t.ratio p.value
##      APOE22 - APOE33    -129.1 278 17   -0.464  0.8890
##      APOE22 - APOE44   -313.8 205 17   -1.532  0.3014
##      APOE33 - APOE44   -184.8 287 17   -0.643  0.7986
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

## Day d8 Probe By cbw DEG

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

```

## [1] "omnibus test"

## model term    df1 df2 F.ratio p.value
## Genotype      2  17  19.917 <.0001
## Sex           1  17   0.074  0.7883
## Genotype:Sex   2  17   0.566  0.5783

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype    2  17   8.935  0.0022
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype    2  17  11.404  0.0007

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.407  0.5318
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.835  0.3737
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.339  0.5678

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

## Analysis of Variance Table
##
## Response: Probe_d8
##          Df Sum Sq Mean Sq F value    Pr(>F)
## cbw        1   8.910    8.910   2.1739  0.15865
## Genotype    2 186.737   93.369  22.7797 1.55e-05 ***
## Sex         1  14.660   14.660   3.5768  0.07576 .
## cbw:Genotype 2   2.427    1.214   0.2961  0.74749
## cbw:Sex      1   2.865    2.865   0.6989  0.41475
## Genotype:Sex 2    0.168    0.084   0.0205  0.97968
## cbw:Genotype:Sex 2 14.351    7.175   1.7506  0.20356
## Residuals   17  69.679    4.099
## ---
## 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)
## cbw        1 15.989   15.989   3.2298 0.11536
## Genotype    2  71.676   35.838   7.2394 0.01976 *
## cbw:Genotype 2  15.039    7.519   1.5189 0.28320
## Residuals    7  34.653    4.950
## ---
## 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)
## cbw         1  1.009    1.009   0.2882  0.603127
## Genotype     2 99.098   49.549  14.1463  0.001215 **
## cbw:Genotype  2   2.902    1.451   0.4143  0.671622
## Residuals    10 35.026    3.503
## ---
## 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   -1.38 2.16 17  -0.638  0.5318
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male    1.40 1.53 17   0.914  0.3737
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    0.79 1.36 17   0.583  0.5678
##
## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33  -0.717 2.31 17  -0.311  0.9482
## APOE22 - APOE44  -6.439 2.20 17  -2.932  0.0240
## APOE33 - APOE44  -5.722 1.53 17  -3.734  0.0045
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33   2.064 1.31 17   1.579  0.2811
## APOE22 - APOE44  -4.270 1.30 17  -3.288  0.0115
## APOE33 - APOE44  -6.334 1.36 17  -4.665  0.0006
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends
## Genotype cbw.trend      SE df  lower.CL upper.CL
## APOE22    -1.84e-05 5.06e-05 17 -1.25e-04 8.82e-05
## APOE33     9.69e-06 3.08e-05 17 -5.53e-05 7.47e-05
## APOE44     1.42e-05 2.06e-05 17 -2.93e-05 5.78e-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 -2.81e-05 5.92e-05 17  -0.475  0.8839
## APOE22 - APOE44 -3.27e-05 5.46e-05 17  -0.599  0.8228
## APOE33 - APOE44 -4.56e-06 3.71e-05 17  -0.123  0.9917
##

```



```

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

## $emtrends
## Sex = female:
##      Genotype cbw.trend      SE df  lower.CL upper.CL
##      APOE22    -8.98e-05 6.37e-05 17 -2.24e-04 4.46e-05
##      APOE33     1.29e-05 3.53e-05 17 -6.16e-05 8.75e-05
##      APOE44     4.36e-05 2.89e-05 17 -1.74e-05 1.05e-04
##
## Sex = male:
##      Genotype cbw.trend      SE df  lower.CL upper.CL
##      APOE22     5.29e-05 7.86e-05 17 -1.13e-04 2.19e-04
##      APOE33     6.44e-06 5.05e-05 17 -1.00e-04 1.13e-04
##      APOE44    -1.51e-05 2.95e-05 17 -7.73e-05 4.72e-05
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##      contrast      estimate      SE df t.ratio p.value
##      APOE22 - APOE33 -1.03e-04 7.28e-05 17  -1.411  0.3578
##      APOE22 - APOE44 -1.33e-04 6.99e-05 17  -1.907  0.1670
##      APOE33 - APOE44 -3.06e-05 4.57e-05 17  -0.671  0.7833
##
## Sex = male:
##      contrast      estimate      SE df t.ratio p.value
##      APOE22 - APOE33 4.65e-05 9.34e-05 17   0.498  0.8734
##      APOE22 - APOE44 6.80e-05 8.39e-05 17   0.810  0.7020
##      APOE33 - APOE44 2.15e-05 5.85e-05 17   0.368  0.9284
##
## P value adjustment: tukey method for comparing a family of 3 estimates

```

## Day d8 Probe By cbw CLUS

```

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

##      model term    df1 df2 F.ratio p.value
##      Genotype      2   17  21.927 <.0001
##      Sex            1   17   0.111  0.7426
##      Genotype:Sex    2   17   0.870  0.4366

## Sex = female:
##      model term df1 df2 F.ratio p.value
##      Genotype    2   17  11.458  0.0007
##
## Sex = male:
##      model term df1 df2 F.ratio p.value
##      Genotype    2   17  10.921  0.0009

## Genotype = APOE22:
##      model term df1 df2 F.ratio p.value
##      Sex        1   17   0.671  0.4240
##

```

```

## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex          1  17   1.049  0.3202
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex          1  17   0.469  0.5028

## model term          df1 df2 F.ratio p.value
## cbw                  1  17   0.004  0.9490
## Genotype              2  17  23.206 <.0001
## Sex                  1  17   0.000  0.9860
## cbw:Genotype          2  17   0.948  0.4070
## cbw:Sex               1  17   0.414  0.5287
## Genotype:Sex          2  17   1.448  0.2626
## cbw:Genotype:Sex      2  17   1.927  0.1761

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

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## cbw            1  21.974   21.974   6.0616  0.02480 *
## Genotype        2 175.285   87.643  24.1767 1.069e-05 ***
## Sex            1  16.213   16.213   4.4723  0.04952 *
## cbw:Genotype    2   8.722    4.361   1.2030  0.32461
## cbw:Sex         1   1.269    1.269   0.3499  0.56193
## Genotype:Sex    2   0.739    0.369   0.1019  0.90365
## cbw:Genotype:Sex 2  13.970    6.985   1.9269  0.17610
## Residuals      17  61.626    3.625
## ---
## 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)
## cbw            1  18.725   18.725   5.3107  0.054629 .
## Genotype        2  71.072   35.536  10.0783  0.008695 **
## cbw:Genotype    2  22.877   11.439   3.2440  0.100697
## Residuals       7  24.682    3.526
## ---
## 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)
## cbw            1  12.512   12.512   3.3867  0.095551 .
## Genotype        2  87.661   43.831  11.8639  0.002291 **
## cbw:Genotype    2   0.918    0.459   0.1242  0.884502
## Residuals      10  36.944    3.694

```

```

## ---
## 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   -1.492 1.82 17  -0.819  0.4240
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male    1.459 1.42 17   1.024  0.3202
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    0.927 1.35 17   0.685  0.5028

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33  -0.838 1.92 17  -0.436  0.9012
## APOE22 - APOE44  -6.616 1.81 17  -3.652  0.0053
## APOE33 - APOE44  -5.778 1.42 17  -4.075  0.0022
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33   2.112 1.28 17   1.647  0.2539
## APOE22 - APOE44  -4.197 1.37 17  -3.073  0.0179
## APOE33 - APOE44  -6.310 1.36 17  -4.636  0.0007
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends
## Genotype cbw.trend      SE df lower.CL upper.CL
## APOE22      -0.0257 0.0263 17  -0.0813  0.0299
## APOE33       0.0148 0.0198 17  -0.0270  0.0566
## APOE44       0.0132 0.0139 17  -0.0160  0.0424
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33 -0.04053 0.0330 17  -1.229  0.4527
## APOE22 - APOE44 -0.03893 0.0298 17  -1.308  0.4100
## APOE33 - APOE44  0.00159 0.0242 17   0.066  0.9976
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
## Genotype cbw.trend      SE df lower.CL upper.CL
## APOE22      -0.06803 0.0348 17 -0.14154  0.00549
## APOE33       0.01803 0.0157 17 -0.01501  0.05107
## APOE44       0.02933 0.0182 17 -0.00917  0.06782

```

```

##
## Sex = male:
## Genotype cbw.trend      SE df lower.CL upper.CL
## APOE22      0.01660 0.0395 17 -0.06676  0.09997
## APOE33      0.01160 0.0364 17 -0.06523  0.08843
## APOE44     -0.00289 0.0208 17 -0.04687  0.04110
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33 -0.08606 0.0382 17 -2.253  0.0906
## APOE22 - APOE44 -0.09736 0.0393 17 -2.475  0.0596
## APOE33 - APOE44 -0.01130 0.0240 17 -0.470  0.8862
##
## Sex = male:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33  0.00501 0.0537 17  0.093  0.9952
## APOE22 - APOE44  0.01949 0.0447 17  0.436  0.9010
## APOE33 - APOE44  0.01448 0.0420 17  0.345  0.9367
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## [1] "slopes"
## $emtrends
## Genotype cbw.trend      SE df lower.CL upper.CL
## APOE22     -0.0257 0.0263 17 -0.0813  0.0299
## APOE33      0.0148 0.0198 17 -0.0270  0.0566
## APOE44      0.0132 0.0139 17 -0.0160  0.0424
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33 -0.04053 0.0330 17 -1.229  0.4527
## APOE22 - APOE44 -0.03893 0.0298 17 -1.308  0.4100
## APOE33 - APOE44  0.00159 0.0242 17  0.066  0.9976
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates
## $emtrends
## Sex = female:
## Genotype cbw.trend      SE df lower.CL upper.CL
## APOE22     -0.06803 0.0348 17 -0.14154  0.00549
## APOE33      0.01803 0.0157 17 -0.01501  0.05107
## APOE44      0.02933 0.0182 17 -0.00917  0.06782
##
## Sex = male:
## Genotype cbw.trend      SE df lower.CL upper.CL
## APOE22      0.01660 0.0395 17 -0.06676  0.09997
## APOE33      0.01160 0.0364 17 -0.06523  0.08843

```

```

## APOE44      -0.00289 0.0208 17 -0.04687  0.04110
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33 -0.08606 0.0382 17  -2.253  0.0906
## APOE22 - APOE44 -0.09736 0.0393 17  -2.475  0.0596
## APOE33 - APOE44 -0.01130 0.0240 17  -0.470  0.8862
##
## Sex = male:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33  0.00501 0.0537 17   0.093  0.9952
## APOE22 - APOE44  0.01949 0.0447 17   0.436  0.9010
## APOE33 - APOE44  0.01448 0.0420 17   0.345  0.9367
##
## P value adjustment: tukey method for comparing a family of 3 estimates

```

