# Absolute Winding Number by cbw 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.

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## Day d5 Probe by cbw Vol

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

## [1] "omnibus test"

##  model term    df1 df2 F.ratio p.value
##  Genotype       2  17    6.725  0.0071
##  Sex            1  17    0.028  0.8687
##  Genotype:Sex   2  17    0.246  0.7847

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17    5.840  0.0117
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17    2.038  0.1609

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17    0.019  0.8929
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
```

```
## Sex          1  17    0.294   0.5946
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17    0.209   0.6532

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

## Analysis of Variance Table
##
## Response: Probe_d5
##                  Df  Sum Sq Mean Sq F value   Pr(>F)
## cbw               1   8.048   8.048  0.5104 0.484654
## Genotype          2 254.126 127.063  8.0588 0.003454 **
## Sex               1   3.352   3.352  0.2126 0.650593
## cbw:Genotype      2  46.134  23.067  1.4630 0.259263
## cbw:Sex           1   3.402   3.402  0.2158 0.648185
## Genotype:Sex      2  17.256   8.628  0.5472 0.588413
## cbw:Genotype:Sex  2  40.753  20.377  1.2924 0.300275
## Residuals        17 268.038  15.767
## ---
## 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)
## cbw            1   4.120   4.120  0.1331 0.72603
## Genotype       2 212.207 106.103  3.4272 0.09168 .
## cbw:Genotype   2  34.671  17.336  0.5599 0.59486
## Residuals      7 216.716  30.959
## ---
## 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)
## cbw            1  0.812  0.8120  0.1582 0.69916
## Genotype       2 45.552 22.7762  4.4379 0.04173 *
## cbw:Genotype   2 26.491 13.2454  2.5809 0.12481
## Residuals     10 51.322  5.1322
## ---
## 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    0.341 2.50 17   0.137  0.8929
##
## Genotype = APOE33:
##  contrast      estimate   SE df t.ratio p.value
##  female - male   -3.411 6.29 17  -0.542  0.5946
```

```
##
## Genotype = APOE44:
##  contrast        estimate   SE df t.ratio p.value
##  female - male     1.763 3.85 17   0.457  0.6532
##
## Sex = female:
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33      8.17 5.37 17   1.522  0.3057
##  APOE22 - APOE44     -6.96 2.66 17  -2.614  0.0454
##  APOE33 - APOE44    -15.13 5.40 17  -2.803  0.0312
##
## Sex = male:
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33      4.42 4.12 17   1.073  0.5430
##  APOE22 - APOE44     -5.54 3.74 17  -1.481  0.3246
##  APOE33 - APOE44     -9.96 5.02 17  -1.983  0.1468
##
## 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       -3486 5679 17   -15467     8494
##  APOE33        -404 6531 17   -14184    13376
##  APOE44        4778 4046 17    -3758    13314
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33     -3082 8655 17  -0.356  0.9327
##  APOE22 - APOE44     -8264 6972 17  -1.185  0.4775
##  APOE33 - APOE44     -5182 7683 17  -0.674  0.7812
##
## 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       -7998  9442 17   -27918    11922
##  APOE33        7894  5405 17    -3509    19297
##  APOE44        2081  5734 17   -10018    14179
##
## Sex = male:
##  Genotype cbw.trend    SE df lower.CL upper.CL
##  APOE22        1026  6312 17   -12291    14342
##  APOE33       -8702 11892 17   -33792    16389
##  APOE44        7475  5709 17    -4570    19520
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
```

```
## contrast           estimate     SE df t.ratio p.value
## APOE22 - APOE33     -15892 10879 17  -1.461  0.3337
## APOE22 - APOE44     -10079 11047 17  -0.912  0.6401
## APOE33 - APOE44       5813  7880 17   0.738  0.7449
##
## Sex = male:
## contrast           estimate     SE df t.ratio p.value
## APOE22 - APOE33       9727 13463 17   0.722  0.7537
## APOE22 - APOE44      -6450  8511 17  -0.758  0.7331
## APOE33 - APOE44     -16177 13192 17  -1.226  0.4544
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

## Day d5 Probe By cbw FA

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

## [1] "omnibus test"

##  model term    df1 df2 F.ratio p.value
##  Genotype        2  17   4.927  0.0205
##  Sex             1  17   0.351  0.5613
##  Genotype:Sex    2  17   0.780  0.4740

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   4.544  0.0263
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   0.957  0.4039

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.045  0.8347
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.130  0.7232
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   2.372  0.1420

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

## Analysis of Variance Table
##
## Response: Probe_d5
##               Df  Sum Sq Mean Sq F value    Pr(>F)
## cbw            1  34.136  34.136  1.9558  0.179939
## Genotype       2 226.481 113.240  6.4880  0.008058 **
## Sex            1  17.528  17.528  1.0043  0.330330
## cbw:Genotype   2  25.792  12.896  0.7389  0.492385
## cbw:Sex        1   4.559   4.559  0.2612  0.615873
## Genotype:Sex   2  33.581  16.790  0.9620  0.401983
```

```
## cbw:Genotype:Sex  2    2.319   1.159   0.0664 0.935975
## Residuals        17 296.713  17.454
## ---
## 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)
## cbw           1  16.283  16.283  0.5253 0.49209
## Genotype      2 231.688 115.844  3.7373 0.07866 .
## cbw:Genotype  2   2.764   1.382  0.0446 0.95667
## Residuals     7 216.980  30.997
## ---
## 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)
## cbw           1  5.703  5.7026  0.7152 0.4175
## Genotype      2 34.617 17.3087  2.1708 0.1648
## cbw:Genotype  2  4.124  2.0618  0.2586 0.7771
## Residuals    10 79.733  7.9733

## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
##  contrast       estimate   SE df t.ratio p.value
##  female - male     0.714 3.37 17   0.212  0.8347
##
## Genotype = APOE33:
##  contrast       estimate   SE df t.ratio p.value
##  female - male    -1.552 4.31 17  -0.360  0.7232
##
## Genotype = APOE44:
##  contrast       estimate   SE df t.ratio p.value
##  female - male     4.514 2.93 17   1.540  0.1420

## Sex = female:
##  contrast        estimate   SE df t.ratio p.value
##  APOE22 - APOE33     4.91 4.31 17   1.139  0.5043
##  APOE22 - APOE44    -6.04 3.54 17  -1.706  0.2318
##  APOE33 - APOE44   -10.95 3.79 17  -2.890  0.0261
##
## Sex = male:
##  contrast        estimate   SE df t.ratio p.value
##  APOE22 - APOE33     2.65 3.36 17   0.788  0.7152
##  APOE22 - APOE44    -2.24 2.72 17  -0.822  0.6948
##  APOE33 - APOE44    -4.88 3.58 17  -1.366  0.3802
##
## 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      -86.42 181 17     -469      296
##  APOE33        3.01 260 17     -545      551
##  APOE44     -192.19 202 17     -619      235
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##  contrast          estimate  SE df t.ratio p.value
##  APOE22 - APOE33      -89.4 317 17  -0.282  0.9571
##  APOE22 - APOE44      105.8 272 17   0.389  0.9203
##  APOE33 - APOE44      195.2 329 17   0.593  0.8256
##
## 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       -91.1 222.8 17     -561    379.1
##  APOE33      -113.1  84.9 17     -292     66.1
##  APOE44      -209.6 244.0 17     -724    305.1
##
## Sex = male:
##  Genotype cbw.trend    SE df lower.CL upper.CL
##  APOE22       -81.7 286.5 17     -686    522.7
##  APOE33       119.1 512.0 17     -961   1199.4
##  APOE44      -174.8 322.9 17     -856    506.5
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast          estimate  SE df t.ratio p.value
##  APOE22 - APOE33       22.0 238 17   0.092  0.9953
##  APOE22 - APOE44      118.5 330 17   0.359  0.9318
##  APOE33 - APOE44       96.5 258 17   0.374  0.9263
##
## Sex = male:
##  contrast          estimate  SE df t.ratio p.value
##  APOE22 - APOE33     -200.9 587 17  -0.342  0.9377
##  APOE22 - APOE44       93.0 432 17   0.216  0.9748
##  APOE33 - APOE44      293.9 605 17   0.485  0.8791
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

## Day d5 Probe By cbw DEG

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

## [1] "omnibus test"

##  model term   df1 df2 F.ratio p.value
```

```
## Genotype        2  17   5.246   0.0168
## Sex             1  17   0.367   0.5524
## Genotype:Sex    2  17   1.488   0.2537

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   5.200  0.0173
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   0.804  0.4637

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.203  0.6577
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.000  0.9989
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   4.212  0.0559

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

## Analysis of Variance Table
##
## Response: Probe_d5
##                  Df Sum Sq Mean Sq F value Pr(>F)
## cbw               1   7.22   7.215  0.3820 0.5447
## Genotype          2 199.67  99.834  5.2857 0.0164 *
## Sex               1  33.92  33.919  1.7958 0.1979
## cbw:Genotype      2  13.26   6.629  0.3510 0.7090
## cbw:Sex           1   5.92   5.916  0.3132 0.5830
## Genotype:Sex      2  42.93  21.466  1.1365 0.3441
## cbw:Genotype:Sex  2  17.11   8.555  0.4529 0.6432
## Residuals        17 321.09  18.888
## ---
## 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)
## cbw           1  27.299  27.299  0.8079 0.3986
## Genotype      2 176.837  88.419  2.6169 0.1417
## cbw:Genotype  2  27.062  13.531  0.4005 0.6844
## Residuals     7 236.516  33.788

## [1] "males"

## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq Mean Sq F value Pr(>F)
```

```
## cbw           1  0.346  0.3460   0.0409 0.8438
## Genotype      2 37.501 18.7504   2.2170 0.1596
## cbw:Genotype  2  1.755  0.8777   0.1038 0.9024
## Residuals    10 84.575  8.4575

## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
##  contrast        estimate   SE df t.ratio p.value
##  female - male -2.09256 4.64 17  -0.451  0.6577
##
## Genotype = APOE33:
##  contrast        estimate   SE df t.ratio p.value
##  female - male -0.00471 3.29 17  -0.001  0.9989
##
## Genotype = APOE44:
##  contrast        estimate   SE df t.ratio p.value
##  female - male  5.97096 2.91 17   2.052  0.0559

## Sex = female:
##  contrast         estimate   SE df t.ratio p.value
##  APOE22 - APOE33   -0.144 4.95 17  -0.029  0.9995
##  APOE22 - APOE44   -9.816 4.71 17  -2.082  0.1234
##  APOE33 - APOE44   -9.672 3.29 17  -2.940  0.0236
##
## Sex = male:
##  contrast         estimate   SE df t.ratio p.value
##  APOE22 - APOE33    1.944 2.81 17   0.693  0.7708
##  APOE22 - APOE44   -1.752 2.79 17  -0.629  0.8066
##  APOE33 - APOE44   -3.696 2.91 17  -1.268  0.4315
##
## 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   -2.16e-05 1.09e-04 17 -0.000251 2.07e-04
##  APOE33    2.04e-05 6.62e-05 17 -0.000119 1.60e-04
##  APOE44   -1.84e-05 4.43e-05 17 -0.000112 7.51e-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 -4.20e-05 1.27e-04 17  -0.331  0.9418
##  APOE22 - APOE44 -3.20e-06 1.17e-04 17  -0.027  0.9996
##  APOE33 - APOE44  3.88e-05 7.96e-05 17   0.487  0.8782
##
## 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   -6.76e-05 1.37e-04 17 -3.56e-04 0.000221
```

```
## APOE33     7.53e-05 7.59e-05 17 -8.48e-05 0.000235
## APOE44    -2.85e-05 6.20e-05 17 -1.59e-04 0.000102
##
## Sex = male:
##  Genotype cbw.trend      SE df  lower.CL upper.CL
##  APOE22     2.44e-05 1.69e-04 17 -3.31e-04 0.000380
##  APOE33    -3.45e-05 1.08e-04 17 -2.63e-04 0.000194
##  APOE44    -8.31e-06 6.33e-05 17 -1.42e-04 0.000125
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast          estimate       SE df t.ratio p.value
##  APOE22 - APOE33 -1.43e-04 0.000156 17  -0.914  0.6388
##  APOE22 - APOE44 -3.91e-05 0.000150 17  -0.261  0.9633
##  APOE33 - APOE44  1.04e-04 0.000098 17   1.059  0.5511
##
## Sex = male:
##  contrast          estimate       SE df t.ratio p.value
##  APOE22 - APOE33  5.89e-05 0.000200 17   0.294  0.9536
##  APOE22 - APOE44  3.27e-05 0.000180 17   0.182  0.9820
##  APOE33 - APOE44 -2.62e-05 0.000126 17  -0.209  0.9763
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

## Day d5 Probe By cbw CLUS

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

## [1] "omnibus test"

##  model term    df1 df2 F.ratio p.value
##  Genotype       2  17   6.355  0.0087
##  Sex            1  17   0.488  0.4945
##  Genotype:Sex   2  17   1.579  0.2350

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   6.580  0.0076
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   1.048  0.3723

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.323  0.5770
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.019  0.8919
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
```

```
## Sex            1  17   4.005  0.0616

## model term       df1 df2 F.ratio p.value
## cbw               1  17   0.348  0.5632
## Genotype          2  17   5.038  0.0191
## Sex               1  17   0.275  0.6068
## cbw:Genotype      2  17   0.466  0.6353
## cbw:Sex           1  17   0.009  0.9252
## Genotype:Sex      2  17   1.086  0.3600
## cbw:Genotype:Sex  2  17   0.389  0.6834

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

## Analysis of Variance Table
##
## Response: Probe_d5
##                  Df  Sum Sq Mean Sq F value  Pr(>F)
## cbw               1   5.732   5.732  0.3398 0.56761
## Genotype          2 203.343 101.671  6.0274 0.01051 *
## Sex               1  31.074  31.074  1.8422 0.19245
## cbw:Genotype      2  51.780  25.890  1.5348 0.24391
## cbw:Sex           1   6.703   6.703  0.3974 0.53684
## Genotype:Sex      2  42.583  21.292  1.2622 0.30824
## cbw:Genotype:Sex  2  13.133   6.567  0.3893 0.68343
## Residuals        17 286.761  16.868
## ---
## 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)
## cbw           1  21.32  21.320  0.7353 0.4196
## Genotype      2 182.79  91.393  3.1518 0.1057
## cbw:Genotype  2  60.63  30.315  1.0455 0.4006
## Residuals     7 202.98  28.997

## [1] "males"

## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq Mean Sq F value Pr(>F)
## cbw           1  0.122  0.1216  0.0145 0.9065
## Genotype      2 40.010 20.0048  2.3877 0.1420
## cbw:Genotype  2  0.262  0.1309  0.0156 0.9845
## Residuals    10 83.784  8.3784

## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
##  contrast       estimate   SE df t.ratio p.value
##  female - male   -2.233 3.93 17  -0.569  0.5770
##
## Genotype = APOE33:
##  contrast       estimate   SE df t.ratio p.value
```

```
##  female - male     0.424 3.07 17    0.138  0.8919
##
## Genotype = APOE44:
##  contrast        estimate   SE df t.ratio p.value
##  female - male    5.844 2.92 17    2.001  0.0616

## Sex = female:
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33     -0.77 4.15 17   -0.186  0.9812
##  APOE22 - APOE44    -10.44 3.91 17   -2.672  0.0405
##  APOE33 - APOE44     -9.67 3.06 17   -3.162  0.0149
##
## Sex = male:
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33      1.89 2.77 17    0.682  0.7768
##  APOE22 - APOE44     -2.36 2.95 17   -0.802  0.7070
##  APOE33 - APOE44     -4.25 2.94 17   -1.448  0.3399
##
## 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     -0.0330 0.0568 17  -0.1529   0.0869
##  APOE33      0.0177 0.0428 17  -0.0725   0.1079
##  APOE44     -0.0302 0.0299 17  -0.0932   0.0329
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##  contrast         estimate     SE df t.ratio p.value
##  APOE22 - APOE33 -0.05068 0.0711 17  -0.713  0.7594
##  APOE22 - APOE44 -0.00282 0.0642 17  -0.044  0.9989
##  APOE33 - APOE44  0.04787 0.0522 17   0.918  0.6368
##
## 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    -0.05772 0.0752 17  -0.2163   0.1009
##  APOE33     0.04650 0.0338 17  -0.0248   0.1178
##  APOE44    -0.04161 0.0394 17  -0.1246   0.0414
##
## Sex = male:
##  Genotype cbw.trend     SE df lower.CL upper.CL
##  APOE22    -0.00827 0.0852 17  -0.1881   0.1716
##  APOE33    -0.01112 0.0786 17  -0.1768   0.1546
##  APOE44    -0.01875 0.0450 17  -0.1136   0.0761
##
## Confidence level used: 0.95
##
## $contrasts
```

```
## Sex = female:
##  contrast        estimate     SE df t.ratio p.value
##  APOE22 - APOE33 -0.10422 0.0824 17  -1.265  0.4333
##  APOE22 - APOE44 -0.01611 0.0848 17  -0.190  0.9803
##  APOE33 - APOE44  0.08811 0.0519 17   1.699  0.2343
##
## Sex = male:
##  contrast        estimate     SE df t.ratio p.value
##  APOE22 - APOE33  0.00285 0.1159 17   0.025  0.9997
##  APOE22 - APOE44  0.01048 0.0964 17   0.109  0.9935
##  APOE33 - APOE44  0.00763 0.0905 17   0.084  0.9961
##
## 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     -0.0330 0.0568 17  -0.1529   0.0869
##  APOE33      0.0177 0.0428 17  -0.0725   0.1079
##  APOE44     -0.0302 0.0299 17  -0.0932   0.0329
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##  contrast        estimate     SE df t.ratio p.value
##  APOE22 - APOE33 -0.05068 0.0711 17  -0.713  0.7594
##  APOE22 - APOE44 -0.00282 0.0642 17  -0.044  0.9989
##  APOE33 - APOE44  0.04787 0.0522 17   0.918  0.6368
##
## 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    -0.05772 0.0752 17  -0.2163   0.1009
##  APOE33     0.04650 0.0338 17  -0.0248   0.1178
##  APOE44    -0.04161 0.0394 17  -0.1246   0.0414
##
## Sex = male:
##  Genotype cbw.trend     SE df lower.CL upper.CL
##  APOE22    -0.00827 0.0852 17  -0.1881   0.1716
##  APOE33    -0.01112 0.0786 17  -0.1768   0.1546
##  APOE44    -0.01875 0.0450 17  -0.1136   0.0761
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast        estimate     SE df t.ratio p.value
##  APOE22 - APOE33 -0.10422 0.0824 17  -1.265  0.4333
##  APOE22 - APOE44 -0.01611 0.0848 17  -0.190  0.9803
##  APOE33 - APOE44  0.08811 0.0519 17   1.699  0.2343
```

```
## 
## Sex = male:
##  contrast          estimate      SE df t.ratio p.value
##  APOE22 - APOE33   0.00285  0.1159 17   0.025  0.9997
##  APOE22 - APOE44   0.01048  0.0964 17   0.109  0.9935
##  APOE33 - APOE44   0.00763  0.0905 17   0.084  0.9961
## 
## P value adjustment: tukey method for comparing a family of 3 estimates
```