Absolute Winding Number by CPu Probe Day d5

alexandra badea

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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 CPu Vol

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

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

```
##  model term    df1 df2 F.ratio p.value
##  Genotype       2  17   0.781  0.4738
##  Sex            1  17   1.739  0.2047
##  Genotype:Sex   2  17   0.886  0.4305
```

```
## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   0.967  0.4003
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   0.276  0.7618
```

```
## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.001  0.9810
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
```

```
## Sex           1  17    0.992  0.3332
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex           1  17    1.070  0.3154

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

## Analysis of Variance Table
##
## Response: Probe_d5
##                   Df  Sum Sq Mean Sq F value   Pr(>F)
## CPu                1 179.863 179.863  9.8636 0.005962 **
## Genotype           2  50.289  25.145  1.3789 0.278632
## Sex                1  25.410  25.410  1.3935 0.254072
## CPu:Genotype       2  22.167  11.084  0.6078 0.555955
## CPu:Sex            1  18.073  18.073  0.9911 0.333430
## Genotype:Sex       2  10.835   5.417  0.2971 0.746756
## CPu:Genotype:Sex   2  24.476  12.238  0.6711 0.524166
## Residuals         17 309.995  18.235
## ---
## 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)
## CPu           1 185.959 185.959  5.5415 0.05079 .
## Genotype      2  31.561  15.781  0.4703 0.64324
## CPu:Genotype  2  15.290   7.645  0.2278 0.80195
## Residuals     7 234.904  33.558
## ---
## 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)
## CPu           1 13.711 13.7110  1.8259 0.2064
## Genotype      2 23.318 11.6591  1.5527 0.2587
## CPu:Genotype  2 12.056  6.0282  0.8028 0.4750
## Residuals    10 75.091  7.5091

## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
##  contrast       estimate    SE df t.ratio p.value
##  female - male   0.0628  2.60 17   0.024  0.9810
##
## Genotype = APOE33:
##  contrast       estimate    SE df t.ratio p.value
##  female - male  15.3724 15.43 17   0.996  0.3332
##
## Genotype = APOE44:
```

```
## contrast        estimate    SE df t.ratio p.value
## female - male    7.1085    6.87 17   1.034  0.3154

## Sex = female:
## contrast        estimate    SE df t.ratio p.value
## APOE22 - APOE33 -12.884 15.21 17  -0.847  0.6798
## APOE22 - APOE44  -7.541  6.66 17  -1.133  0.5078
## APOE33 - APOE44   5.343 16.38 17   0.326  0.9432
##
## Sex = male:
## contrast        estimate    SE df t.ratio p.value
## APOE22 - APOE33   2.426  3.69 17   0.657  0.7911
## APOE22 - APOE44  -0.495  3.11 17  -0.159  0.9862
## APOE33 - APOE44  -2.921  4.14 17  -0.706  0.7635
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends
## Genotype CPu.trend   SE df lower.CL upper.CL
## APOE22        1257 2231 17    -3450     5965
## APOE33        8400 9343 17   -11312    28111
## APOE44        1811 4070 17    -6777    10399
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast        estimate    SE df t.ratio p.value
## APOE22 - APOE33   -7142 9606 17  -0.744  0.7415
## APOE22 - APOE44    -554 4642 17  -0.119  0.9922
## APOE33 - APOE44    6589 10191 17   0.647  0.7968
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
## Genotype CPu.trend    SE df lower.CL upper.CL
## APOE22      3060.0  3750 17    -4852    10972
## APOE33     17429.7 18216 17   -21003    55863
## APOE44       -60.2  6582 17   -13948    13827
##
## Sex = male:
## Genotype CPu.trend    SE df lower.CL upper.CL
## APOE22      -545.3  2419 17    -5648     4558
## APOE33      -630.3  4162 17    -9412     8152
## APOE44      3682.1  4790 17    -6424    13788
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
## contrast        estimate    SE df t.ratio p.value
## APOE22 - APOE33 -14369.8 18598 17  -0.773  0.7243
```

```
## APOE22 - APOE44   3120.1  7576 17   0.412  0.9112
## APOE33 - APOE44  17489.9 19369 17   0.903  0.6458
##
## Sex = male:
## contrast        estimate    SE df t.ratio p.value
## APOE22 - APOE33     85.1  4814 17   0.018  0.9998
## APOE22 - APOE44  -4227.4  5366 17  -0.788  0.7153
## APOE33 - APOE44  -4312.4  6346 17  -0.680  0.7783
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d5 Probe By CPu FA

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

## [1] "omnibus test"

##  model term    df1 df2 F.ratio p.value
##  Genotype        2  17   2.670  0.0981
##  Sex             1  17   0.123  0.7299
##  Genotype:Sex    2  17   0.481  0.6262

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   2.056  0.1585
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   0.671  0.5242

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.014  0.9080
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.178  0.6782
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.938  0.3464

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

## Analysis of Variance Table
##
## Response: Probe_d5
##                 Df  Sum Sq Mean Sq F value   Pr(>F)
## CPu              1  66.397  66.397  4.5143 0.048576 *
## Genotype         2 194.672  97.336  6.6179 0.007488 **
## Sex              1  15.194  15.194  1.0331 0.323686
## CPu:Genotype     2   5.367   2.683  0.1824 0.834845
## CPu:Sex          1  65.748  65.748  4.4702 0.049568 *
## Genotype:Sex     2  19.363   9.681  0.6582 0.530471
## CPu:Genotype:Sex 2  24.331  12.166  0.8271 0.454148
## Residuals       17 250.037  14.708
```

```
## ---
## 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)
## CPu           1 170.16 170.164  6.5323 0.03778 *
## Genotype      2 105.71  52.857  2.0291 0.20181
## CPu:Genotype  2   9.49   4.745  0.1822 0.83730
## Residuals     7 182.35  26.049
## ---
## 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)
## CPu           1  9.628  9.6278  1.4223 0.2605
## Genotype      2 29.739 14.8694  2.1967 0.1619
## CPu:Genotype  2 17.120  8.5600  1.2646 0.3239
## Residuals    10 67.690  6.7690

## [1] "pairwise-sidak adjustments"

## Genotype = APOE22:
##  contrast       estimate   SE df t.ratio p.value
##  female - male     0.327 2.79 17   0.117  0.9080
##
## Genotype = APOE33:
##  contrast       estimate   SE df t.ratio p.value
##  female - male    -1.423 3.37 17  -0.422  0.6782
##
## Genotype = APOE44:
##  contrast       estimate   SE df t.ratio p.value
##  female - male     2.972 3.07 17   0.968  0.3464

## Sex = female:
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33       3.98 3.38 17   1.178  0.4817
##  APOE22 - APOE44      -3.47 3.21 17  -1.081  0.5380
##  APOE33 - APOE44      -7.46 3.68 17  -2.028  0.1358
##
## Sex = male:
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33       2.23 2.78 17   0.805  0.7053
##  APOE22 - APOE44      -0.83 2.62 17  -0.317  0.9464
##  APOE33 - APOE44      -3.06 2.69 17  -1.136  0.5057
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends
```

```
## Genotype CPu.trend  SE df lower.CL upper.CL
## APOE22      -104.4 128 17    -374      165
## APOE33      -169.2 199 17    -589      250
## APOE44       -66.1 145 17    -372      240
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast        estimate  SE df t.ratio p.value
## APOE22 - APOE33     64.8 236 17   0.274  0.9595
## APOE22 - APOE44    -38.3 193 17  -0.198  0.9786
## APOE33 - APOE44   -103.1 246 17  -0.419  0.9082
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
##  Genotype CPu.trend  SE df lower.CL upper.CL
##  APOE22      -158.1 206 17    -593      277
##  APOE33      -388.9 312 17   -1047      269
##  APOE44      -362.5 197 17    -778       53
##
## Sex = male:
##  Genotype CPu.trend  SE df lower.CL upper.CL
##  APOE22       -50.8 150 17    -368      267
##  APOE33        50.5 247 17    -470      571
##  APOE44       230.3 213 17    -219      679
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast        estimate  SE df t.ratio p.value
##  APOE22 - APOE33    230.8 374 17   0.618  0.8125
##  APOE22 - APOE44    204.4 285 17   0.717  0.7568
##  APOE33 - APOE44    -26.4 369 17  -0.072  0.9972
##
## Sex = male:
##  contrast        estimate  SE df t.ratio p.value
##  APOE22 - APOE33   -101.3 289 17  -0.350  0.9348
##  APOE22 - APOE44   -281.0 261 17  -1.079  0.5397
##  APOE33 - APOE44   -179.8 326 17  -0.552  0.8469
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d5 Probe By CPu DEG

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

## [1] "omnibus test"

## model term   df1 df2 F.ratio p.value
## Genotype       2  17   4.429  0.0283
```

```
## Sex             1  17   1.333  0.2642
## Genotype:Sex    2  17   2.262  0.1346

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   6.741  0.0070
##
## 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   0.215  0.6486
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.353  0.5602
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   6.583  0.0201

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

## Analysis of Variance Table
##
## Response: Probe_d5
##                  Df  Sum Sq Mean Sq F value  Pr(>F)
## CPu               1   3.626   3.626  0.2414 0.62951
## Genotype          2 204.575 102.287  6.8090 0.00673 **
## Sex               1  33.483  33.483  2.2289 0.15378
## CPu:Genotype      2  45.179  22.590  1.5037 0.25043
## CPu:Sex           1  14.601  14.601  0.9720 0.33801
## Genotype:Sex      2  69.502  34.751  2.3133 0.12925
## CPu:Genotype:Sex  2  14.763   7.382  0.4914 0.62021
## Residuals        17 255.380  15.022
## ---
## 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)
## CPu           1  10.088  10.088  0.3688 0.56281
## Genotype      2 202.344 101.172  3.6993 0.08012 .
## CPu:Genotype  2  63.839  31.919  1.1671 0.36524
## Residuals     7 191.445  27.349
## ---
## 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)
## CPu           1 44.465  44.465  6.9547 0.02485 *
## Genotype      2 10.784   5.392  0.8434 0.45871
## CPu:Genotype  2  4.993   2.497  0.3905 0.68660
## Residuals    10 63.935   6.394
## ---
## 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      1.24 2.68 17   0.464  0.6486
##
## Genotype = APOE33:
##  contrast       estimate   SE df t.ratio p.value
##  female - male     -2.04 3.43 17  -0.594  0.5602
##
## Genotype = APOE44:
##  contrast       estimate   SE df t.ratio p.value
##  female - male      6.65 2.59 17   2.566  0.0201

## Sex = female:
##  contrast         estimate   SE df t.ratio p.value
##  APOE22 - APOE33     4.087 3.25 17   1.257  0.4373
##  APOE22 - APOE44    -6.380 2.77 17  -2.307  0.0820
##  APOE33 - APOE44   -10.467 2.99 17  -3.501  0.0073
##
## Sex = male:
##  contrast         estimate   SE df t.ratio p.value
##  APOE22 - APOE33     0.807 2.89 17   0.279  0.9581
##  APOE22 - APOE44    -0.976 2.49 17  -0.391  0.9195
##  APOE33 - APOE44    -1.783 3.09 17  -0.577  0.8341
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends
##  Genotype CPu.trend       SE df  lower.CL upper.CL
##  APOE22    4.82e-05 8.19e-05 17 -0.000125 2.21e-04
##  APOE33    1.29e-05 8.31e-05 17 -0.000162 1.88e-04
##  APOE44   -9.86e-05 6.94e-05 17 -0.000245 4.78e-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 3.53e-05 0.000117 17   0.303  0.9509
##  APOE22 - APOE44 1.47e-04 0.000107 17   1.367  0.3795
##  APOE33 - APOE44 1.11e-04 0.000108 17   1.030  0.5688
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
```

```
## Sex = female:
##  Genotype CPu.trend      SE df  lower.CL upper.CL
##  APOE22    1.22e-04 1.15e-04 17 -1.22e-04 3.65e-04
##  APOE33    1.32e-04 8.28e-05 17 -4.29e-05 3.07e-04
##  APOE44   -8.53e-05 7.89e-05 17 -2.52e-04 8.12e-05
##
## Sex = male:
##  Genotype CPu.trend      SE df  lower.CL upper.CL
##  APOE22   -2.51e-05 1.16e-04 17 -2.71e-04 2.21e-04
##  APOE33   -1.06e-04 1.44e-04 17 -4.10e-04 1.98e-04
##  APOE44   -1.12e-04 1.14e-04 17 -3.53e-04 1.29e-04
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast        estimate      SE df t.ratio p.value
##  APOE22 - APOE33 -1.04e-05 0.000142 17  -0.073  0.9971
##  APOE22 - APOE44  2.07e-04 0.000140 17   1.480  0.3248
##  APOE33 - APOE44  2.17e-04 0.000114 17   1.898  0.1696
##
## Sex = male:
##  contrast        estimate      SE df t.ratio p.value
##  APOE22 - APOE33  8.10e-05 0.000185 17   0.437  0.9005
##  APOE22 - APOE44  8.68e-05 0.000163 17   0.532  0.8568
##  APOE33 - APOE44  5.75e-06 0.000184 17   0.031  0.9995
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d5 Probe By CPu CLUS

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

## [1] "omnibus test"

##  model term    df1 df2 F.ratio p.value
##  Genotype       2  17   5.173  0.0176
##  Sex            1  17   1.289  0.2720
##  Genotype:Sex   2  17   2.206  0.1406

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   6.542  0.0078
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  17   0.443  0.6491

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.416  0.5276
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
##  Sex          1  17   0.524  0.4790
```

```
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex         1  17   6.227  0.0232

##  model term      df1 df2 F.ratio p.value
##  CPu               1  17   0.406  0.5325
##  Genotype          2  17   3.179  0.0672
##  Sex               1  17   3.624  0.0740
##  CPu:Genotype      2  17   0.428  0.6587
##  CPu:Sex           1  17   2.998  0.1015
##  Genotype:Sex      2  17   0.152  0.8606
##  CPu:Genotype:Sex  2  17   1.058  0.3688

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

## Analysis of Variance Table
##
## Response: Probe_d5
##                   Df  Sum Sq Mean Sq F value    Pr(>F)
## CPu                1   0.106   0.106  0.0072 0.933285
## Genotype           2 207.537 103.769  7.0337 0.005946 **
## Sex                1  33.119  33.119  2.2449 0.152397
## CPu:Genotype       2  31.859  15.929  1.0797 0.361876
## CPu:Sex            1  34.668  34.668  2.3499 0.143693
## Genotype:Sex       2  51.791  25.896  1.7553 0.202773
## CPu:Genotype:Sex   2  31.225  15.613  1.0583 0.368844
## Residuals         17 250.803  14.753
## ---
## 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)
## CPu           1  27.903  27.903  0.9491 0.36239
## Genotype      2 193.762  96.881  3.2955 0.09805 .
## CPu:Genotype  2  40.262  20.131  0.6848 0.53504
## Residuals     7 205.787  29.398
## ---
## 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)
## CPu           1 47.027  47.027 10.4468 0.008988 **
## Genotype      2 23.455  11.728  2.6052 0.122825
## CPu:Genotype  2  8.678   4.339  0.9639 0.414181
## Residuals    10 45.016   4.502
## ---
## 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      2.34 3.62 17   0.645  0.5276
##
## Genotype = APOE33:
##  contrast       estimate   SE df t.ratio p.value
##  female - male     -2.32 3.21 17  -0.724  0.4790
##
## Genotype = APOE44:
##  contrast       estimate   SE df t.ratio p.value
##  female - male      6.16 2.47 17   2.495  0.0232

## Sex = female:
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33    4.7371 4.00 17   1.184  0.4785
##  APOE22 - APOE44   -5.8321 3.68 17  -1.586  0.2782
##  APOE33 - APOE44  -10.5692 2.96 17  -3.570  0.0063
##
## Sex = male:
##  contrast          estimate   SE df t.ratio p.value
##  APOE22 - APOE33    0.0748 2.73 17   0.027  0.9996
##  APOE22 - APOE44   -2.0114 2.39 17  -0.841  0.6831
##  APOE33 - APOE44   -2.0862 2.76 17  -0.755  0.7349
##
## P value adjustment: tukey method for comparing a family of 3 estimates

## [1] "slopes"

## $emtrends
##  Genotype CPu.trend     SE df lower.CL upper.CL
##  APOE22      0.0223 0.0627 17   -0.110   0.1547
##  APOE33     -0.0349 0.0514 17   -0.143   0.0735
##  APOE44     -0.0438 0.0356 17   -0.119   0.0313
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##  contrast          estimate      SE df t.ratio p.value
##  APOE22 - APOE33    0.05724 0.0811 17   0.706  0.7634
##  APOE22 - APOE44    0.06616 0.0721 17   0.917  0.6371
##  APOE33 - APOE44    0.00892 0.0625 17   0.143  0.9889
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
##  Genotype CPu.trend     SE df lower.CL upper.CL
##  APOE22      0.0841 0.1070 17  -0.1415   0.3098
##  APOE33      0.0541 0.0332 17  -0.0159   0.1241
##  APOE44     -0.0413 0.0511 17  -0.1491   0.0665
##
## Sex = male:
##  Genotype CPu.trend     SE df lower.CL upper.CL
##  APOE22     -0.0395 0.0656 17  -0.1778   0.0988
```

```
##  APOE33      -0.1239 0.0973 17  -0.3293   0.0814
##  APOE44      -0.0464 0.0496 17  -0.1510   0.0582
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##  contrast          estimate      SE df t.ratio p.value
##  APOE22 - APOE33    0.0300 0.1120 17   0.268  0.9613
##  APOE22 - APOE44    0.1254 0.1185 17   1.058  0.5519
##  APOE33 - APOE44    0.0954 0.0609 17   1.565  0.2870
##
## Sex = male:
##  contrast          estimate      SE df t.ratio p.value
##  APOE22 - APOE33    0.0845 0.1173 17   0.720  0.7553
##  APOE22 - APOE44    0.0069 0.0822 17   0.084  0.9961
##  APOE33 - APOE44   -0.0776 0.1092 17  -0.710  0.7608
##
## P value adjustment: tukey method for comparing a family of 3 estimates
## [1] "slopes"

## $emtrends
##  Genotype CPu.trend     SE df lower.CL upper.CL
##  APOE22      0.0223 0.0627 17   -0.110   0.1547
##  APOE33     -0.0349 0.0514 17   -0.143   0.0735
##  APOE44     -0.0438 0.0356 17   -0.119   0.0313
##
## Results are averaged over the levels of: Sex
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##  APOE33 - APOE44  0.00892 0.0625 17   0.143  0.9889
##
## Results are averaged over the levels of: Sex
## P value adjustment: tukey method for comparing a family of 3 estimates

## $emtrends
## Sex = female:
##  Genotype CPu.trend     SE df lower.CL upper.CL
##  APOE22      0.0841 0.1070 17  -0.1415   0.3098
##  APOE33      0.0541 0.0332 17  -0.0159   0.1241
##  APOE44     -0.0413 0.0511 17  -0.1491   0.0665
##
## Sex = male:
##  Genotype CPu.trend     SE df lower.CL upper.CL
##  APOE22     -0.0395 0.0656 17  -0.1778   0.0988
##  APOE33     -0.1239 0.0973 17  -0.3293   0.0814
##  APOE44     -0.0464 0.0496 17  -0.1510   0.0582
##
## Confidence level used: 0.95
##
```

```
## $contrasts
## Sex = female:
##  contrast          estimate      SE df t.ratio p.value
##  APOE22 - APOE33     0.0300 0.1120 17   0.268  0.9613
##  APOE22 - APOE44     0.1254 0.1185 17   1.058  0.5519
##  APOE33 - APOE44     0.0954 0.0609 17   1.565  0.2870
##
## Sex = male:
##  contrast          estimate      SE df t.ratio p.value
##  APOE22 - APOE33     0.0845 0.1173 17   0.720  0.7553
##  APOE22 - APOE44     0.0069 0.0822 17   0.084  0.9961
##  APOE33 - APOE44    -0.0776 0.1092 17  -0.710  0.7608
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```