

Absolute Winding Number by CPu Probe Day d8

alexandra badea

10/28/2021

Contents

Aim	1
Day d8 Probe by CPu Vol	1
Day d8 Probe By CPu FA	4
Day d8 Probe By CPu DEG	6
Day d8 Probe By CPu CLUS	9

Aim

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

Day d8 Probe by CPu Vol

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

## model term    df1 df2 F.ratio p.value
## Genotype      2  17  2.731  0.0936
## Sex            1  17  6.020  0.0252
## Genotype:Sex   2  17  2.770  0.0909

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype   2  17  2.118  0.1509
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype   2  17  6.748  0.0070

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17  1.849  0.1916
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
```

```

## Sex          1  17   6.331  0.0222
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex          1  17   0.004  0.9505

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

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## CPu           1 135.382  135.382  42.2452 5.448e-06 ***
## Genotype       2   66.790   33.395  10.4207  0.001112 **
## Sex           1   10.988   10.988   3.4286  0.081525 .
## CPu:Genotype   2    1.821    0.910   0.2841  0.756206
## CPu:Sex        1    2.550    2.550   0.7956  0.384860
## Genotype:Sex   2   13.922    6.961   2.1721  0.144526
## CPu:Genotype:Sex 2   13.867    6.933   2.1635  0.145511
## Residuals     17   54.479    3.205
## ---
## 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)
## CPu           1 102.193  102.193  34.7079 0.0006047 ***
## Genotype       2    3.233    1.617   0.5491 0.6004717
## CPu:Genotype   2   11.320    5.660   1.9222 0.2160810
## Residuals      7   20.611    2.944
## ---
## 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)
## CPu           1  27.858   27.858   8.2254 0.016726 *
## Genotype       2  72.227   36.114  10.6628 0.003315 **
## CPu:Genotype   2    4.081    2.041   0.6025 0.566141
## Residuals     10  33.869    3.387
## ---
## 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    1.483 1.09 17   1.360  0.1916
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male   16.281 6.47 17   2.516  0.0222

```

```

##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male  -0.182 2.88 17  -0.063  0.9505

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33  -12.45 6.38 17  -1.953  0.1545
## APOE22 - APOE44   -2.01 2.79 17  -0.720  0.7553
## APOE33 - APOE44   10.45 6.87 17   1.521  0.3062
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    2.34 1.55 17   1.513  0.3099
## APOE22 - APOE44   -3.67 1.30 17  -2.817  0.0303
## APOE33 - APOE44   -6.02 1.74 17  -3.467  0.0079
##
## 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      1376  935 17   -597.3    3350
## APOE33      8289 3917 17    25.6    16552
## APOE44      2195 1706 17  -1405.4    5795
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33  -6913 4027 17  -1.717  0.2278
## APOE22 - APOE44   -819 1946 17  -0.421  0.9076
## APOE33 - APOE44   6094 4272 17   1.426  0.3500
##
## 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      3129 1572 17    -188    6446
## APOE33     17467 7637 17    1355   33578
## APOE44      2486 2759 17   -3336    8308
##
## Sex = male:
## Genotype CPu.trend    SE df lower.CL upper.CL
## APOE22     -377 1014 17   -2516    1763
## APOE33     -889 1745 17   -4570    2793
## APOE44      1904 2008 17   -2333    6140
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:

```

```
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33  -14337 7797 17  -1.839  0.1871
## APOE22 - APOE44    643 3176 17   0.203  0.9777
## APOE33 - APOE44  14981 8120 17   1.845  0.1853
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    512 2018 17   0.254  0.9652
## APOE22 - APOE44  -2280 2250 17  -1.014  0.5785
## APOE33 - APOE44  -2792 2660 17  -1.050  0.5570
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

Day d8 Probe By CPu FA

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

## model term    df1 df2 F.ratio p.value
## Genotype      2  17  17.469  0.0001
## Sex           1  17   1.263  0.2767
## Genotype:Sex   2  17   0.718  0.5021

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype   2  17   8.463  0.0028
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype   2  17  10.161  0.0013

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17   2.366  0.1424
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.075  0.7872
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.742  0.4011

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

## Analysis of Variance Table
##
## Response: Probe_d8
##          Df Sum Sq Mean Sq F value    Pr(>F)
## CPu        1  13.682   13.682   3.7891  0.06831 .
## Genotype    2 188.273   94.136  26.0704 6.623e-06 ***
## Sex         1   9.697    9.697   2.6854  0.11964
## CPu:Genotype 2   4.238    2.119   0.5868  0.56696
## CPu:Sex      1  14.786   14.786   4.0949  0.05903 .
## Genotype:Sex 2   3.088    1.544   0.4276  0.65888
```

```

## CPu:Genotype:Sex  2    4.650    2.325    0.6439    0.53760
## Residuals        17   61.385    3.611
## ---
## 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)
## CPu         1  44.699   44.699  11.8338 0.01084 *
## Genotype     2  55.934   27.967   7.4041 0.01874 *
## CPu:Genotype  2  10.283    5.141   1.3611 0.31671
## Residuals     7  26.441    3.777
## ---
## 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)
## CPu         1   7.300    7.300   2.0892 0.178947
## Genotype     2  94.226   47.113  13.4825 0.001449 **
## CPu:Genotype  2   1.566    0.783   0.2240 0.803204
## Residuals    10  34.944    3.494
## ---
## 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    2.124 1.38 17   1.538  0.1424
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male  -0.458 1.67 17  -0.274  0.7872
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male    1.310 1.52 17   0.861  0.4011

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    4.17 1.68 17   2.490  0.0578
## APOE22 - APOE44   -3.32 1.59 17  -2.087  0.1224
## APOE33 - APOE44   -7.49 1.82 17  -4.113  0.0020
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    1.59 1.37 17   1.156  0.4941
## APOE22 - APOE44   -4.14 1.30 17  -3.187  0.0141
## APOE33 - APOE44   -5.73 1.34 17  -4.289  0.0014
##

```

```

## 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      -72.9 63.2 17    -206    60.5
##   APOE33     -149.2 98.5 17    -357    58.6
##   APOE44       25.8 71.8 17     -126   177.4
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##   contrast      estimate    SE df t.ratio p.value
##   APOE22 - APOE33      76.4 117.0 17    0.652 0.7935
##   APOE22 - APOE44     -98.7  95.7 17   -1.032 0.5677
##   APOE33 - APOE44    -175.1 121.9 17   -1.436 0.3453
##
## 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     -150.50 102.1 17     -366    64.9
##   APOE33     -343.48 154.4 17     -669   -17.6
##   APOE44      -37.30  97.6 17     -243   168.6
##
## Sex = male:
##   Genotype CPu.trend   SE df lower.CL upper.CL
##   APOE22       4.76  74.5 17     -153   162.0
##   APOE33      45.03 122.2 17     -213   302.9
##   APOE44      89.00 105.4 17     -133   311.4
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##   contrast      estimate    SE df t.ratio p.value
##   APOE22 - APOE33     193.0 185 17    1.042 0.5613
##   APOE22 - APOE44    -113.2 141 17   -0.801 0.7072
##   APOE33 - APOE44    -306.2 183 17   -1.676 0.2428
##
## Sex = male:
##   contrast      estimate    SE df t.ratio p.value
##   APOE22 - APOE33     -40.3 143 17   -0.281 0.9574
##   APOE22 - APOE44     -84.2 129 17   -0.652 0.7935
##   APOE33 - APOE44     -44.0 161 17   -0.272 0.9600
##
## P value adjustment: tukey method for comparing a family of 3 estimates

```

Day d8 Probe By CPu DEG

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

```

## [1] "omnibus test"

## model term    df1 df2 F.ratio p.value
## Genotype      2  17  22.458 <.0001
## Sex           1  17   2.165  0.1595
## Genotype:Sex   2  17   1.264  0.3077

## Sex = female:
## model term df1 df2 F.ratio p.value
## Genotype   2  17  13.805  0.0003
##
## Sex = male:
## model term df1 df2 F.ratio p.value
## Genotype   2  17  10.404  0.0011

## Genotype = APOE22:
## model term df1 df2 F.ratio p.value
## Sex        1  17   4.737  0.0439
##
## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex        1  17   0.095  0.7612
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex        1  17   1.076  0.3142

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

## Analysis of Variance Table
##
## Response: Probe_d8
##          Df Sum Sq Mean Sq F value    Pr(>F)
## CPu        1   0.018    0.018   0.0058  0.94018
## Genotype    2 206.960  103.480  33.5721 1.248e-06 ***
## Sex         1  14.260   14.260   4.6264  0.04616 *
## CPu:Genotype 2   1.603    0.801   0.2600  0.77408
## CPu:Sex      1  10.326   10.326   3.3500  0.08480 .
## Genotype:Sex 2   3.205    1.602   0.5199  0.60375
## CPu:Genotype:Sex 2  11.027    5.514   1.7888  0.19723
## Residuals   17  52.399    3.082
## ---
## 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)
## CPu        1 18.681   18.681   6.4913 0.038226 *
## Genotype    2 89.609   44.804  15.5682 0.002649 **
## CPu:Genotype 2  8.921    4.461   1.5499 0.277165
## Residuals    7 20.146    2.878
## ---
## 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)
## CPu         1 24.933   24.933   7.7303 0.019440 *
## Genotype     2 75.550   37.775  11.7118 0.002397 **
## CPu:Genotype  2  5.299    2.649   0.8214 0.467429
## Residuals    10 32.254    3.225
## ---
## 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      2.64 1.21 17   2.177  0.0439
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male     -0.48 1.55 17  -0.309  0.7612
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male      1.22 1.17 17   1.037  0.3142
##
## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33     3.965 1.47 17   2.693  0.0389
## APOE22 - APOE44    -3.102 1.25 17  -2.476  0.0595
## APOE33 - APOE44    -7.067 1.35 17  -5.218  0.0002
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33     0.847 1.31 17   0.646  0.7969
## APOE22 - APOE44    -4.524 1.13 17  -4.005  0.0025
## APOE33 - APOE44    -5.371 1.40 17  -3.838  0.0036
##
## 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    5.61e-05 3.71e-05 17 -2.23e-05 1.34e-04
## APOE33    6.82e-07 3.76e-05 17 -7.87e-05 8.01e-05
## APOE44    2.37e-05 3.14e-05 17 -4.27e-05 9.00e-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  5.54e-05 5.29e-05 17   1.048  0.5580
## APOE22 - APOE44  3.24e-05 4.86e-05 17   0.666  0.7858
## APOE33 - APOE44 -2.30e-05 4.90e-05 17  -0.469  0.8868
##

```



```

## 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      1.20e-04 5.22e-05 17   9.88e-06 2.30e-04
##      APOE33      8.34e-05 3.75e-05 17   4.20e-06 1.63e-04
##      APOE44      2.06e-05 3.57e-05 17  -5.48e-05 9.60e-05
##
## Sex = male:
##      Genotype CPu.trend      SE df  lower.CL upper.CL
##      APOE22     -7.95e-06 5.28e-05 17  -1.19e-04 1.03e-04
##      APOE33     -8.20e-05 6.52e-05 17  -2.20e-04 5.56e-05
##      APOE44      2.67e-05 5.17e-05 17  -8.24e-05 1.36e-04
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##      contrast      estimate      SE df t.ratio p.value
##      APOE22 - APOE33  3.67e-05 6.43e-05 17    0.571  0.8374
##      APOE22 - APOE44  9.95e-05 6.33e-05 17    1.572  0.2843
##      APOE33 - APOE44  6.28e-05 5.18e-05 17    1.212  0.4627
##
## Sex = male:
##      contrast      estimate      SE df t.ratio p.value
##      APOE22 - APOE33  7.41e-05 8.39e-05 17    0.883  0.6580
##      APOE22 - APOE44 -3.47e-05 7.39e-05 17   -0.469  0.8864
##      APOE33 - APOE44 -1.09e-04 8.32e-05 17   -1.307  0.4108
##
## P value adjustment: tukey method for comparing a family of 3 estimates

```

Day d8 Probe By CPu CLUS

```

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

##      model term    df1 df2 F.ratio p.value
##      Genotype      2   17  20.826 <.0001
##      Sex            1   17   2.961  0.1034
##      Genotype:Sex    2   17   1.647  0.2219

## Sex = female:
##      model term df1 df2 F.ratio p.value
##      Genotype    2   17  12.277  0.0005
##
## Sex = male:
##      model term df1 df2 F.ratio p.value
##      Genotype    2   17  11.385  0.0007

## Genotype = APOE22:
##      model term df1 df2 F.ratio p.value
##      Sex        1   17   4.560  0.0476
##

```

```

## Genotype = APOE33:
## model term df1 df2 F.ratio p.value
## Sex          1  17   0.106  0.7483
##
## Genotype = APOE44:
## model term df1 df2 F.ratio p.value
## Sex          1  17   1.162  0.2960

## model term          df1 df2 F.ratio p.value
## CPu                  1  17   0.175  0.6811
## Genotype              2  17  22.106 <.0001
## Sex                   1  17   9.571  0.0066
## CPu:Genotype          2  17   1.380  0.2784
## CPu:Sex               1  17   8.547  0.0095
## Genotype:Sex          2  17   1.118  0.3498
## CPu:Genotype:Sex      2  17   1.844  0.1884

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

## Analysis of Variance Table
##
## Response: Probe_d8
##              Df Sum Sq Mean Sq F value    Pr(>F)
## CPu            1   3.630    3.630   1.1724  0.29402
## Genotype        2 199.270   99.635  32.1837 1.66e-06 ***
## Sex             1  13.596   13.596   4.3916  0.05139 .
## CPu:Genotype    2    1.032    0.516   0.1667  0.84780
## CPu:Sex         1  13.840   13.840   4.4707  0.04956 *
## Genotype:Sex    2    4.382    2.191   0.7077  0.50675
## CPu:Genotype:Sex 2   11.420    5.710   1.8444  0.18839
## Residuals      17   52.629    3.096
## ---
## 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)
## CPu            1  20.604   20.604   5.1554 0.057431 .
## Genotype        2  85.490   42.745  10.6953 0.007443 **
## CPu:Genotype    2    3.287    1.643   0.4112 0.677890
## Residuals       7  27.976    3.997
## ---
## 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)
## CPu            1   9.405    9.405   3.8151 0.0793237 .
## Genotype        2  93.363   46.682  18.9359 0.0003977 ***
## CPu:Genotype    2  10.615    5.307   2.1529 0.1668916
## Residuals      10  24.653    2.465

```

```

## ---
## 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      3.55 1.66 17   2.135  0.0476
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female - male     -0.48 1.47 17  -0.326  0.7483
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female - male      1.22 1.13 17   1.078  0.2960

## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    4.503 1.83 17   2.456  0.0618
## APOE22 - APOE44   -2.216 1.68 17  -1.316  0.4058
## APOE33 - APOE44   -6.719 1.36 17  -4.954  0.0003
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 - APOE33    0.477 1.25 17   0.382  0.9230
## APOE22 - APOE44   -4.543 1.09 17  -4.149  0.0018
## APOE33 - APOE44   -5.021 1.27 17  -3.965  0.0027
##
## 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      0.0273 0.0287 17  -0.0334  0.0879
## APOE33     -0.0261 0.0236 17  -0.0758  0.0236
## APOE44      0.0158 0.0163 17  -0.0186  0.0502
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33    0.0533 0.0372 17   1.435  0.3457
## APOE22 - APOE44    0.0115 0.0330 17   0.347  0.9361
## APOE33 - APOE44   -0.0419 0.0286 17  -1.462  0.3332
##
## 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      0.07990 0.0490 17 -0.023476  0.1833
## APOE33      0.03128 0.0152 17 -0.000803  0.0634
## APOE44      0.02441 0.0234 17 -0.024992  0.0738

```

```

##
## Sex = male:
##   Genotype CPu.trend      SE df  lower.CL upper.CL
##   APOE22      -0.02540 0.0300 17 -0.088761  0.0380
##   APOE33      -0.08344 0.0446 17 -0.177496  0.0106
##   APOE44       0.00718 0.0227 17 -0.040725  0.0551
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
##   contrast      estimate      SE df t.ratio p.value
##   APOE22 - APOE33  0.04862 0.0513 17   0.948  0.6186
##   APOE22 - APOE44  0.05549 0.0543 17   1.022  0.5736
##   APOE33 - APOE44  0.00687 0.0279 17   0.246  0.9672
##
## Sex = male:
##   contrast      estimate      SE df t.ratio p.value
##   APOE22 - APOE33  0.05805 0.0538 17   1.080  0.5389
##   APOE22 - APOE44 -0.03258 0.0377 17  -0.865  0.6687
##   APOE33 - APOE44 -0.09062 0.0500 17  -1.811  0.1957
##
## 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      0.0273 0.0287 17  -0.0334  0.0879
##   APOE33     -0.0261 0.0236 17  -0.0758  0.0236
##   APOE44      0.0158 0.0163 17  -0.0186  0.0502
##
## Results are averaged over the levels of: Sex
## Confidence level used: 0.95
##
## $contrasts
##   contrast      estimate      SE df t.ratio p.value
##   APOE22 - APOE33  0.0533 0.0372 17   1.435  0.3457
##   APOE22 - APOE44  0.0115 0.0330 17   0.347  0.9361
##   APOE33 - APOE44 -0.0419 0.0286 17  -1.462  0.3332
##
## 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      0.07990 0.0490 17 -0.023476  0.1833
##   APOE33      0.03128 0.0152 17 -0.000803  0.0634
##   APOE44      0.02441 0.0234 17 -0.024992  0.0738
##
## Sex = male:
##   Genotype CPu.trend      SE df  lower.CL upper.CL
##   APOE22     -0.02540 0.0300 17 -0.088761  0.0380
##   APOE33     -0.08344 0.0446 17 -0.177496  0.0106

```

```

## APOE44      0.00718 0.0227 17 -0.040725  0.0551
##
## Confidence level used: 0.95
##
## $contrasts
## Sex = female:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33  0.04862 0.0513 17   0.948  0.6186
## APOE22 - APOE44  0.05549 0.0543 17   1.022  0.5736
## APOE33 - APOE44  0.00687 0.0279 17   0.246  0.9672
##
## Sex = male:
## contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33  0.05805 0.0538 17   1.080  0.5389
## APOE22 - APOE44 -0.03258 0.0377 17  -0.865  0.6687
## APOE33 - APOE44 -0.09062 0.0500 17  -1.811  0.1957
##
## P value adjustment: tukey method for comparing a family of 3 estimates

```

