Linear models with AD subject
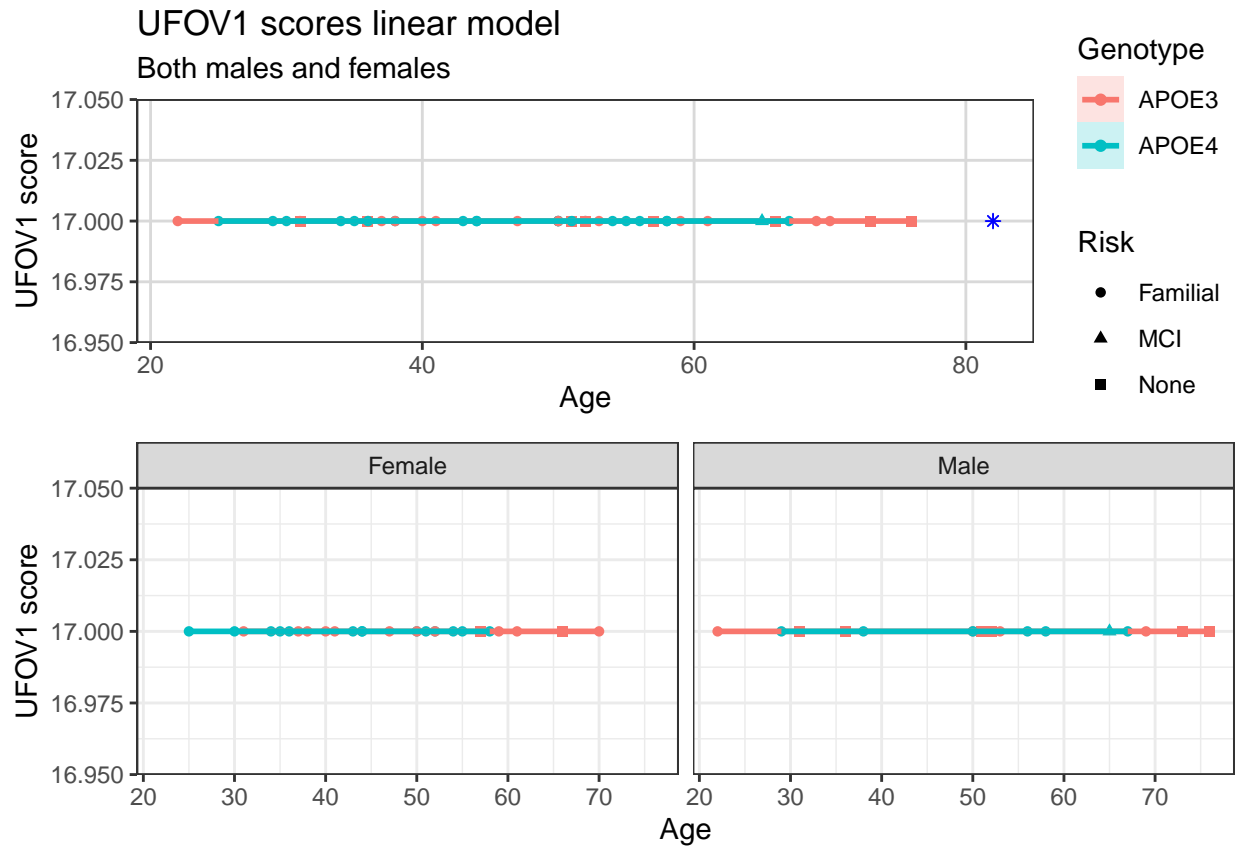

UFOV1 scores linear model
Both males and females

```
## 
## Call:
## lm(formula = ufov1 ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##       Min         1Q     Median         3Q        Max 
## -4.278e-14  0.000e+00  0.000e+00  0.000e+00  8.381e-15 
## 
## Coefficients:
##                     Estimate Std. Error   t value Pr(>|t|)    
## (Intercept)         1.700e+01  8.896e-15  1.911e+15   <2e-16 ***
## age                 2.449e-16  1.735e-16  1.411e+00    0.166    
## GenotypeAPOE4       1.597e-14  1.255e-14  1.273e+00    0.210    
## sexMale             1.597e-14  1.123e-14  1.422e+00    0.163    
## age:GenotypeAPOE4  -2.449e-16  2.630e-16 -9.310e-01    0.358    
## age:sexMale        -2.449e-16  2.173e-16 -1.127e+00    0.267    
## GenotypeAPOE4:sexMale -1.597e-14  1.829e-14 -8.730e-01   0.388    
```

```
## age:GenotypeAPOE4:sexMale  2.449e-16  3.630e-16  6.750e-01     0.504
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.31e-15 on 39 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.4983, Adjusted R-squared:  0.4083
## F-statistic: 5.534 on 7 and 39 DF,  p-value: 0.0001787


##
## Call:
## lm(formula = ufov1 ~ age * Genotype, data = combo_f)
##
## Residuals:
##        Min         1Q      Median         3Q         Max
## -6.485e-14  0.000e+00  0.000e+00  3.981e-15  1.270e-14
##
## Coefficients:
##                     Estimate Std. Error     t value Pr(>|t|)
## (Intercept)        1.700e+01  1.756e-14   9.681e+14   <2e-16 ***
## age                3.712e-16  3.425e-16   1.084e+00    0.290
## GenotypeAPOE4      2.421e-14  2.476e-14   9.780e-01    0.338
## age:GenotypeAPOE4 -3.712e-16  5.192e-16  -7.150e-01    0.482
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.443e-14 on 23 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.4991, Adjusted R-squared:  0.4337
## F-statistic: 7.639 on 3 and 23 DF,  p-value: 0.001022


##
## Call:
## lm(formula = ufov1 ~ age * Genotype, data = combo_m)
##
## Residuals:
##        Min         1Q      Median         3Q         Max
## -3.951e-15 -1.090e-15  0.000e+00  0.000e+00  1.065e-14
##
## Coefficients:
##                     Estimate Std. Error     t value Pr(>|t|)
## (Intercept)        1.700e+01  3.052e-15   5.569e+15   <2e-16 ***
## age               -1.430e-16  5.823e-17  -2.456e+00   0.0258 *
## GenotypeAPOE4     -8.385e-15  5.919e-15  -1.417e+00   0.1758
## age:GenotypeAPOE4  1.430e-16  1.113e-16   1.285e+00   0.2172
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.252e-15 on 16 degrees of freedom
##   (3 observations deleted due to missingness)
## Multiple R-squared:  0.5108, Adjusted R-squared:  0.4191
## F-statistic: 5.569 on 3 and 16 DF,  p-value: 0.008222


## Analysis of Variance Table
```
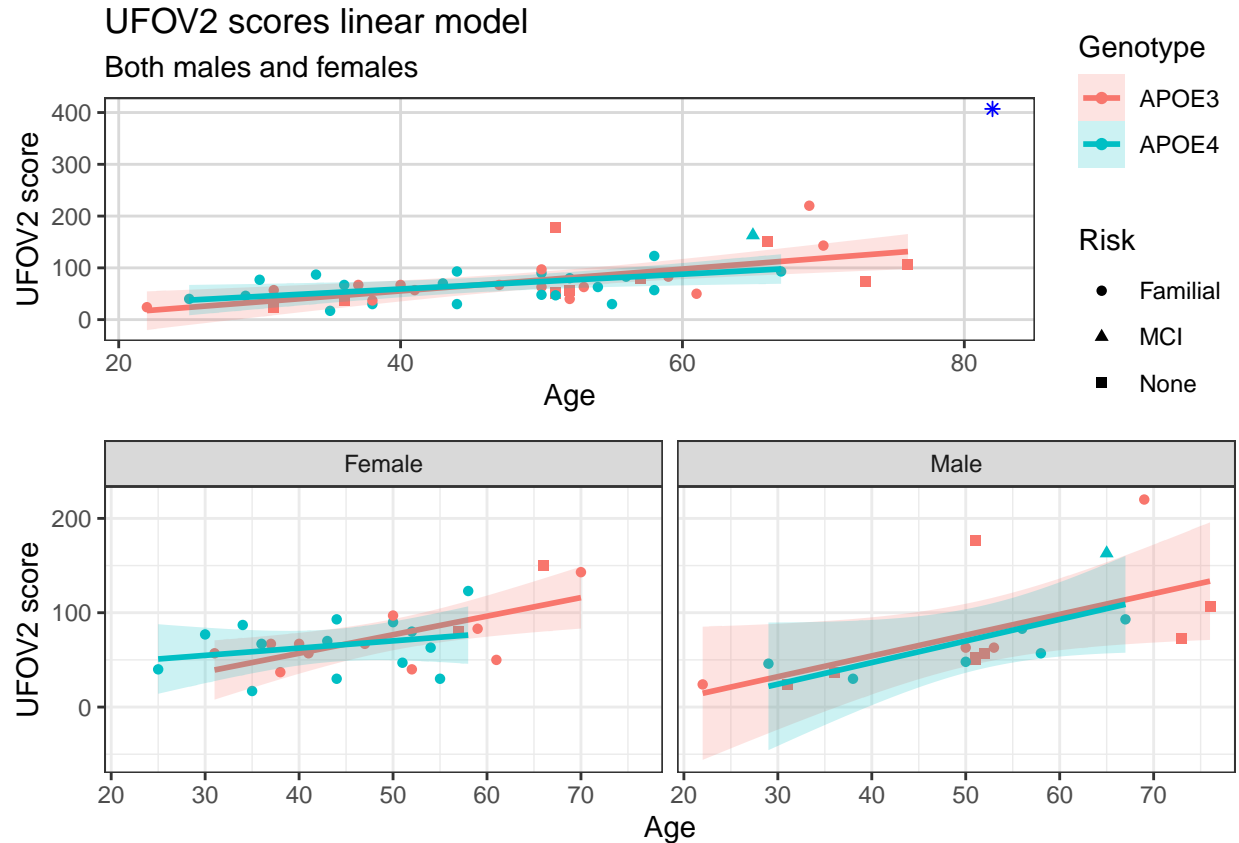
```
## 
## Response: ufov1
##                  Df     Sum Sq    Mean Sq F value Pr(>F)
## age               1 1.6370e-29 1.6366e-29  0.3063 0.5831
## Genotype          1 4.9210e-29 4.9210e-29  0.9209 0.3431
## sex               1 4.4660e-29 4.4661e-29  0.8358 0.3662
## age:Genotype      1 2.5100e-29 2.5097e-29  0.4697 0.4972
## age:sex           1 3.7810e-29 3.7811e-29  0.7076 0.4054
## Genotype:sex      1 4.1030e-29 4.1031e-29  0.7679 0.3862
## age:Genotype:sex  1 2.4310e-29 2.4314e-29  0.4550 0.5039
## Residuals        39 2.0839e-27 5.3434e-29


## Analysis of Variance Table
## 
## Response: ufov1
##               Df     Sum Sq    Mean Sq F value Pr(>F)
## age            1 5.1400e-29 5.1376e-29  0.2468 0.6241
## Genotype       1 3.0430e-28 3.0427e-28  1.4615 0.2390
## age:Genotype   1 1.0640e-28 1.0643e-28  0.5112 0.4818
## Residuals     23 4.7886e-27 2.0820e-28


## Analysis of Variance Table
## 
## Response: ufov1
##               Df     Sum Sq    Mean Sq F value  Pr(>F)
## age            1 4.8263e-29 4.8263e-29  4.5635 0.04846 *
## Genotype       1 4.8790e-30 4.8790e-30  0.4613 0.50673
## age:Genotype   1 1.7458e-29 1.7458e-29  1.6507 0.21715
## Residuals     16 1.6921e-28 1.0576e-29
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

UFOV2 scores linear model
Both males and females


```
## 
## Call:
## lm(formula = ufov2 ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -53.877 -23.247  -9.337  19.294 101.928
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             -21.6677    44.6136  -0.486   0.6300
## age                       1.9671     0.8701   2.261   0.0296 *
## GenotypeAPOE4            53.4227    62.9167   0.849   0.4011
## sexMale                 -12.1467    57.5997  -0.211   0.8341
## age:GenotypeAPOE4        -1.1989     1.3191  -0.909   0.3692
## age:sexMale               0.2341     1.1045   0.212   0.8333
## GenotypeAPOE4:sexMale   -63.9811    92.4868  -0.692   0.4933
## age:GenotypeAPOE4:sexMale  1.2858    1.8294   0.703   0.4864
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 36.66 on 38 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.3648, Adjusted R-squared:  0.2478
## F-statistic: 3.118 on 7 and 38 DF,  p-value: 0.01062
```

```
##
## Call:
## lm(formula = ufov2 ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -48.328 -13.739   5.208  20.070  46.684
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -21.6677    34.6186  -0.626  0.53755
## age                 1.9671     0.6752   2.913  0.00782 **
## GenotypeAPOE4      53.4227    48.8212   1.094  0.28517
## age:GenotypeAPOE4  -1.1989     1.0236  -1.171  0.25350
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 28.45 on 23 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.3143, Adjusted R-squared:  0.2248
## F-statistic: 3.514 on 3 and 23 DF,  p-value: 0.03126


##
## Call:
## lm(formula = ufov2 ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -53.877 -24.550 -13.248   4.311 101.928
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -33.81441   46.22909  -0.731   0.4758
## age                 2.20126    0.86314   2.550   0.0222 *
## GenotypeAPOE4     -10.55840   86.01618  -0.123   0.9039
## age:GenotypeAPOE4   0.08692    1.60832   0.054   0.9576
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 46.52 on 15 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.3851, Adjusted R-squared:  0.2621
## F-statistic: 3.131 on 3 and 15 DF,  p-value: 0.05705


## Analysis of Variance Table
##
## Response: ufov2
##              Df Sum Sq Mean Sq F value    Pr(>F)
## age           1  26912 26912.2 20.0262 6.738e-05 ***
## Genotype      1     32    31.7  0.0236    0.8788
## sex           1     79    79.4  0.0591    0.8092
## age:Genotype  1    769   769.0  0.5722    0.4540
## age:sex       1    872   872.0  0.6489    0.4255
## Genotype:sex  1      3     2.9  0.0021    0.9634
```
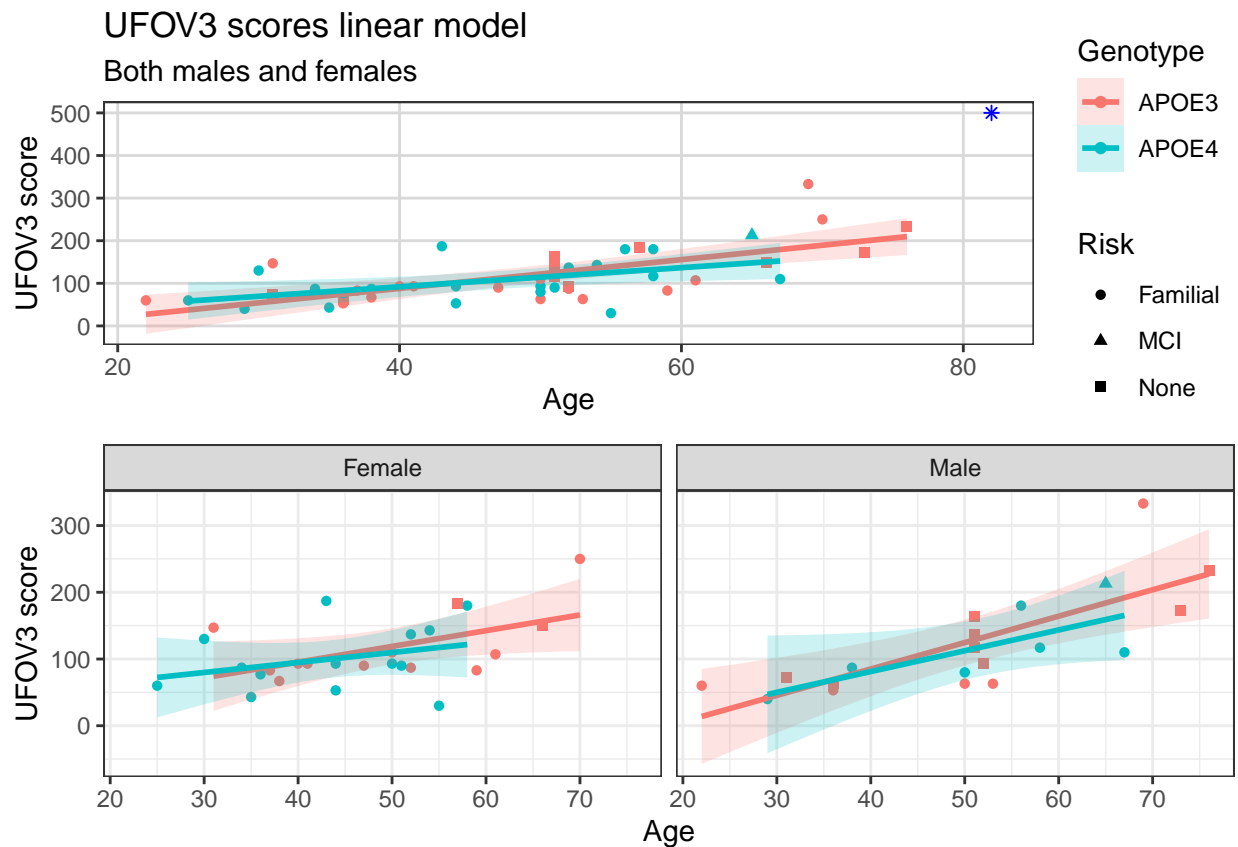
```
## age:Genotype:sex  1     664    663.9  0.4940     0.4864
## Residuals        38   51066   1343.8
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: ufov2
##              Df  Sum Sq Mean Sq F value   Pr(>F)
## age           1  7389.6  7389.6  9.1324 0.006069 **
## Genotype      1    29.4    29.4  0.0363 0.850521
## age:Genotype  1  1110.0  1110.0  1.3718 0.253496
## Residuals    23 18610.7   809.2
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: ufov2
##              Df Sum Sq Mean Sq F value   Pr(>F)
## age           1  20153 20153.2  9.3142 0.008072 **
## Genotype      1    163   162.6  0.0752 0.787714
## age:Genotype  1      6     6.3  0.0029 0.957611
## Residuals    15  32456  2163.7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


UFOV3 scores linear model

```
##
## Call:
## lm(formula = ufov3 ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -87.202 -27.969  -6.914  25.789 133.207
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 0.98990   59.90589   0.017   0.9869
## age                         2.35768    1.16839   2.018   0.0505 .
## GenotypeAPOE4              33.94364   84.48270   0.402   0.6900
## sexMale                   -74.19710   75.65221  -0.981   0.3328
## age:GenotypeAPOE4          -0.86188    1.77126  -0.487   0.6293
## age:sexMale                 1.59884    1.46356   1.092   0.2813
## GenotypeAPOE4:sexMale      -4.19316  123.14253  -0.034   0.9730
## age:GenotypeAPOE4:sexMale   0.02161    2.44471   0.009   0.9930
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 49.22 on 39 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.4514, Adjusted R-squared:  0.3529
## F-statistic: 4.584 on 7 and 39 DF,  p-value: 0.0008194


##
## Call:
## lm(formula = ufov3 ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -87.202 -22.691  -7.748  25.789  87.747
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)         0.9899    56.6034   0.017   0.9862
## age                 2.3577     1.1040   2.136   0.0436 *
## GenotypeAPOE4      33.9436    79.8254   0.425   0.6746
## age:GenotypeAPOE4  -0.8619     1.6736  -0.515   0.6115
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 46.51 on 23 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.2343, Adjusted R-squared:  0.1345
## F-statistic: 2.346 on 3 and 23 DF,  p-value: 0.09922


##
## Call:
## lm(formula = ufov3 ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
```

```
## -87.202 -22.691  -7.748  25.789  87.747
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)         0.9899    56.6034   0.017   0.9862
## age                 2.3577     1.1040   2.136   0.0436 *
## GenotypeAPOE4      33.9436    79.8254   0.425   0.6746
## age:GenotypeAPOE4  -0.8619     1.6736  -0.515   0.6115
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 46.51 on 23 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.2343, Adjusted R-squared:  0.1345
## F-statistic: 2.346 on 3 and 23 DF,  p-value: 0.09922


## Analysis of Variance Table
##
## Response: ufov3
##               Df Sum Sq Mean Sq F value   Pr(>F)
## age            1  70361   70361 29.0386 3.65e-06 ***
## Genotype       1    275     275  0.1135   0.7380
## sex            1      6       6  0.0023   0.9619
## age:Genotype   1   2454    2454  1.0126   0.3205
## age:sex        1   4624    4624  1.9083   0.1750
## Genotype:sex   1     25      25  0.0103   0.9199
## age:Genotype:sex 1    0       0  0.0001   0.9930
## Residuals     39  94497    2423
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: ufov3
##              Df Sum Sq Mean Sq F value  Pr(>F)
## age           1  14427 14427.3  6.6694 0.01665 *
## Genotype      1    226   225.7  0.1043 0.74960
## age:Genotype  1    574   573.7  0.2652 0.61148
## Residuals    23  49754  2163.2
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: ufov3
##              Df Sum Sq Mean Sq F value    Pr(>F)
## age           1  59023   59023 21.1066 0.0002993 ***
## Genotype      1    816     816  0.2918 0.5965060
## age:Genotype  1    603     603  0.2155 0.6487670
## Residuals    16  44743    2796
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
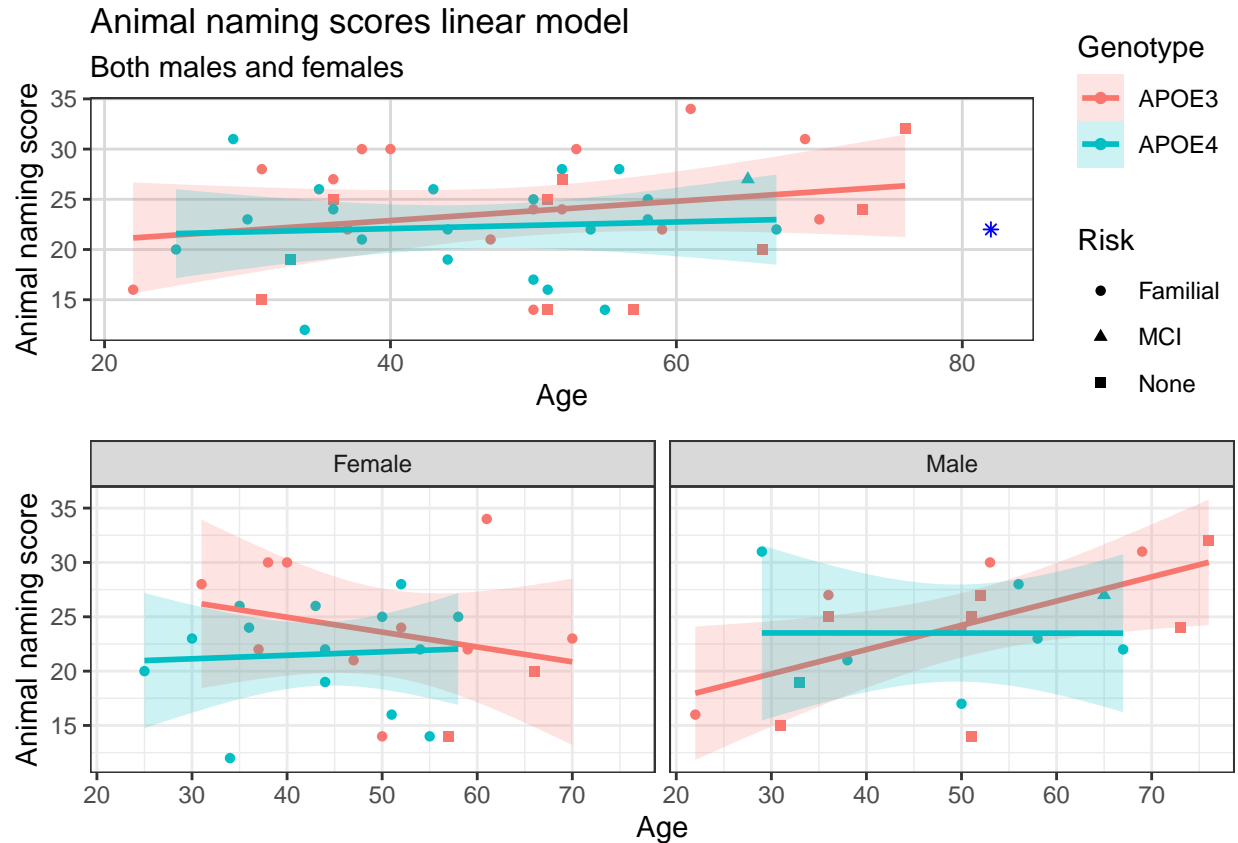
Animal naming scores linear model
Both males and females


```
## 
## Call:
## lm(formula = animals ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -10.4367  -2.7922   0.5633   3.3675  11.9135 
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)    
## (Intercept)              30.4309     6.7451   4.512 5.77e-05 ***
## age                      -0.1368     0.1296  -1.055   0.2978    
## GenotypeAPOE4           -10.2594     9.3300  -1.100   0.2782    
## sexMale                 -17.3713     8.3959  -2.069   0.0452 *  
## age:GenotypeAPOE4         0.1689     0.1938   0.871   0.3889    
## age:sexMale               0.3599     0.1609   2.236   0.0311 *  
## GenotypeAPOE4:sexMale    20.7331    12.7425   1.627   0.1118    
## age:GenotypeAPOE4:sexMale -0.3926     0.2564  -1.531   0.1338    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 5.327 on 39 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.1787, Adjusted R-squared:  0.03126 
## F-statistic: 1.212 on 7 and 39 DF,  p-value: 0.3194
```

```
##
## Call:
## lm(formula = animals ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -9.5912 -2.8969  0.5498  3.1605 11.9135
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        30.4309     7.0785   4.299 0.000291 ***
## age                -0.1368     0.1360  -1.006 0.325525
## GenotypeAPOE4     -10.2594     9.7912  -1.048 0.306094
## age:GenotypeAPOE4   0.1689     0.2034   0.830 0.415242
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.59 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.07662,    Adjusted R-squared:  -0.0493
## F-statistic: 0.6085 on 3 and 22 DF,  p-value: 0.6166


##
## Call:
## lm(formula = animals ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -10.4367  -2.5077   0.5633   3.5104   7.4862
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       13.05961    4.66023   2.802   0.0122 *
## age                0.22308    0.08891   2.509   0.0225 *
## GenotypeAPOE4     10.47370    8.09004   1.295   0.2128
## age:GenotypeAPOE4 -0.22375    0.15651  -1.430   0.1709
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.965 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2736, Adjusted R-squared:  0.1454
## F-statistic: 2.134 on 3 and 17 DF,  p-value: 0.1336


## Analysis of Variance Table
##
## Response: animals
##               Df  Sum Sq Mean Sq F value Pr(>F)
## age            1   52.06  52.059  1.8349 0.1833
## Genotype       1   18.53  18.533  0.6532 0.4239
## sex            1   13.90  13.902  0.4900 0.4881
## age:Genotype   1   10.57  10.572  0.3726 0.5451
## age:sex        1   69.81  69.807  2.4604 0.1248
## Genotype:sex   1    9.32   9.315  0.3283 0.5699
```

```
## age:Genotype:sex  1   66.53  66.527  2.3448 0.1338
## Residuals        39 1106.52  28.372


## Analysis of Variance Table
##
## Response: animals
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1   2.94   2.941  0.0941 0.7619
## Genotype      1  32.55  32.553  1.0418 0.3185
## age:Genotype  1  21.55  21.546  0.6895 0.4152
## Residuals    22 687.42  31.246


## Analysis of Variance Table
##
## Response: animals
##              Df Sum Sq Mean Sq F value  Pr(>F)
## age           1 105.42 105.417  4.2761 0.05422 .
## Genotype      1   2.05   2.051  0.0832 0.77648
## age:Genotype  1  50.39  50.389  2.0440 0.17093
## Residuals    17 419.09  24.653
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
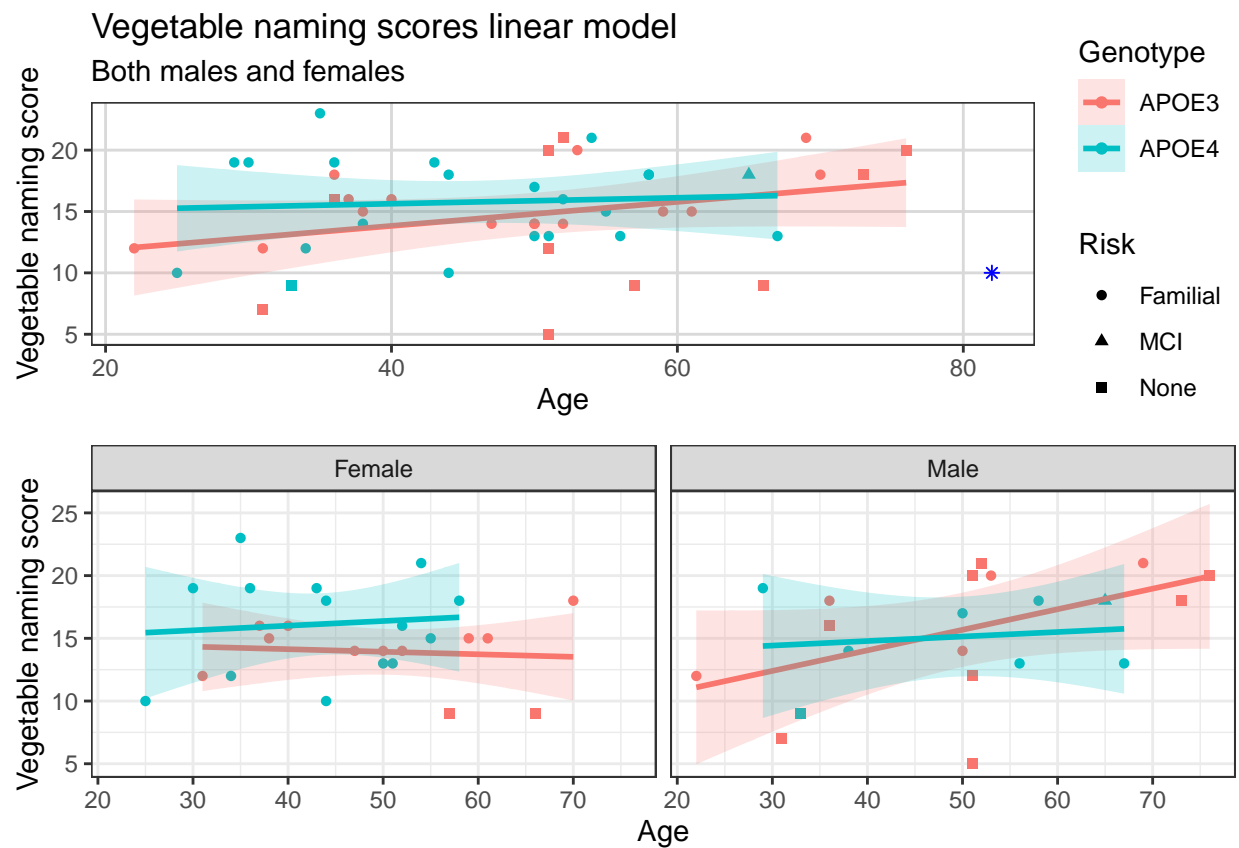

Vegetable naming scores linear model

```
##
## Call:
```

```
## lm(formula = vegetables ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min      1Q   Median      3Q     Max
## -10.8436  -2.5570   0.8258   2.5922   7.1777
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)               14.94680    5.10544   2.928  0.00567 **
## age                       -0.02033    0.09811  -0.207  0.83691
## GenotypeAPOE4             -0.42280    7.06201  -0.060  0.95257
## sexMale                   -7.46397    6.35495  -1.175  0.24731
## age:GenotypeAPOE4          0.05742    0.14668   0.391  0.69756
## age:sexMale                0.18427    0.12181   1.513  0.13840
## GenotypeAPOE4:sexMale      6.28283    9.64503   0.651  0.51860
## age:GenotypeAPOE4:sexMale -0.18536    0.19408  -0.955  0.34542
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.032 on 39 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.163,  Adjusted R-squared:  0.01277
## F-statistic: 1.085 on 7 and 39 DF,  p-value: 0.3914


##
## Call:
## lm(formula = vegetables ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.1561 -3.1131  0.4681  1.8608  7.1777
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       14.94680    4.62956   3.229  0.00386 **
## age               -0.02033    0.08897  -0.229  0.82135
## GenotypeAPOE4     -0.42280    6.40375  -0.066  0.94796
## age:GenotypeAPOE4  0.05742    0.13301   0.432  0.67013
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.656 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1053, Adjusted R-squared:  -0.01672
## F-statistic: 0.8629 on 3 and 22 DF,  p-value: 0.475


##
## Call:
## lm(formula = vegetables ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min      1Q   Median      3Q     Max
## -10.8436  -2.3590   0.9105   2.6154   4.9924
##
```

```
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        7.48283    4.19686   1.783   0.0925 .
## age                0.16394    0.08007   2.048   0.0564 .
## GenotypeAPOE4      5.86003    7.28564   0.804   0.4323
## age:GenotypeAPOE4 -0.12793    0.14094  -0.908   0.3767
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.471 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2044, Adjusted R-squared:  0.06404
## F-statistic: 1.456 on 3 and 17 DF,  p-value: 0.2617


## Analysis of Variance Table
##
## Response: vegetables
##                 Df Sum Sq Mean Sq F value Pr(>F)
## age              1  30.22 30.2166  1.8589 0.1806
## Genotype         1  17.76 17.7645  1.0929 0.3023
## sex              1   1.48  1.4826  0.0912 0.7642
## age:Genotype     1  11.30 11.3043  0.6954 0.4094
## age:sex          1  29.69 29.6882  1.8264 0.1843
## Genotype:sex     1  18.17 18.1729  1.1180 0.2969
## age:Genotype:sex 1  14.83 14.8276  0.9122 0.3454
## Residuals       39 633.95 16.2551


## Analysis of Variance Table
##
## Response: vegetables
##              Df  Sum Sq Mean Sq F value Pr(>F)
## age           1   2.124  2.1236  0.1589 0.6940
## Genotype      1  29.987 29.9871  2.2435 0.1484
## age:Genotype  1   2.491  2.4914  0.1864 0.6701
## Residuals    22 294.052 13.3660


## Analysis of Variance Table
##
## Response: vegetables
##              Df Sum Sq Mean Sq F value  Pr(>F)
## age           1  69.65  69.649  3.4835 0.07933 .
## Genotype      1   1.22   1.221  0.0610 0.80780
## age:Genotype  1  16.47  16.473  0.8239 0.37673
## Residuals    17 339.90  19.994
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
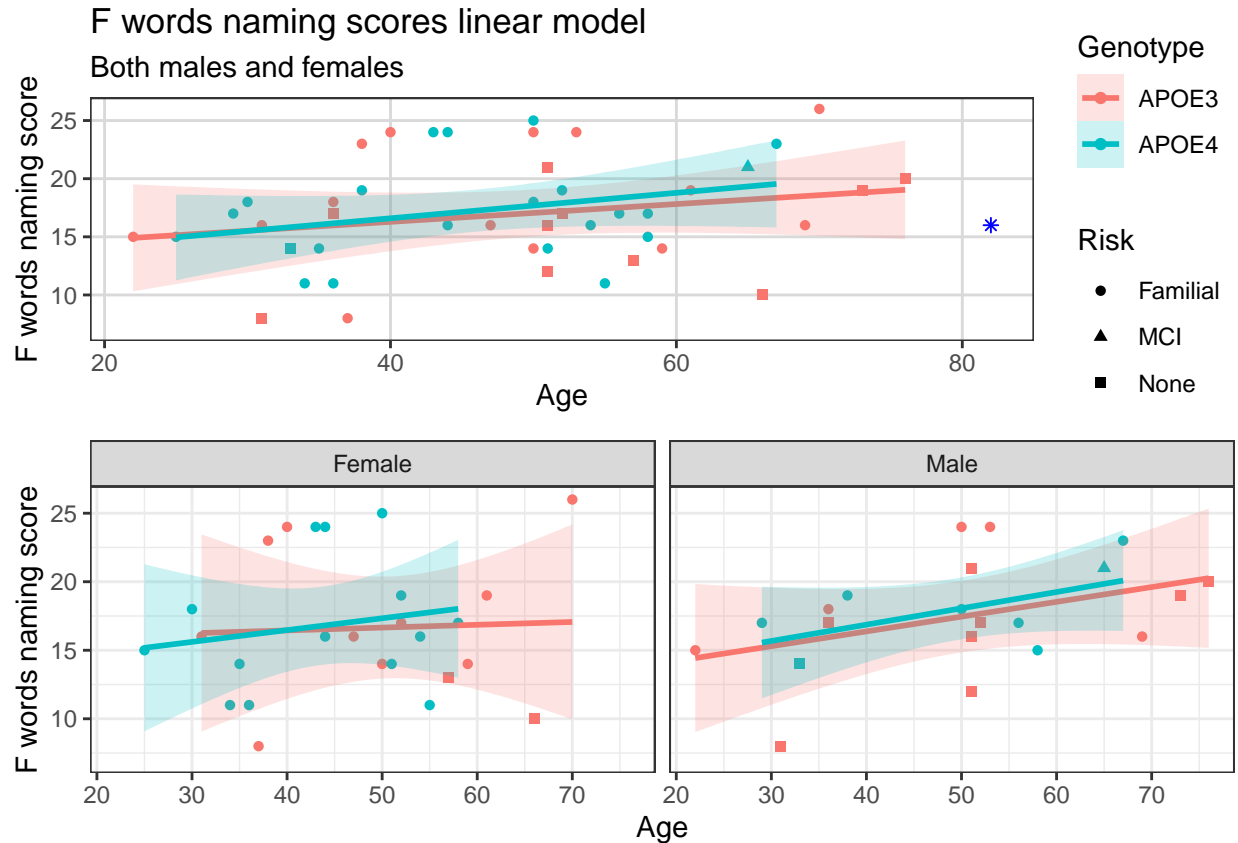
F words naming scores linear model

Both males and females


```
## 
## Call:
## lm(formula = f ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min     1Q  Median     3Q     Max
## -8.3861 -2.7454 -0.2629  2.2455  8.9364
## 
## Coefficients:
##                        Estimate Std. Error t value Pr(>|t|)
## (Intercept)            15.62653    5.96015   2.622   0.0124 *
## age                     0.02053    0.11454   0.179   0.8587
## GenotypeAPOE4          -2.60521    8.24427  -0.316   0.7537
## sexMale                -3.56840    7.41885  -0.481   0.6332
## age:GenotypeAPOE4       0.06573    0.17124   0.384   0.7032
## age:sexMale             0.08737    0.14220   0.614   0.5425
## GenotypeAPOE4:sexMale   2.65105   11.25971   0.235   0.8151
## age:GenotypeAPOE4:sexMale -0.05452  0.22657  -0.241   0.8111
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 4.707 on 39 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.08473,    Adjusted R-squared:  -0.07955
## F-statistic: 0.5158 on 7 and 39 DF,  p-value: 0.8171
```

```
##
## Call:
## lm(formula = f ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min    1Q Median    3Q    Max
## -8.386 -3.275 -0.704  2.324  8.936
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       15.62653    6.73398   2.321    0.030 *
## age                0.02053    0.12941   0.159    0.875
## GenotypeAPOE4     -2.60521    9.31465  -0.280    0.782
## age:GenotypeAPOE4  0.06573    0.19347   0.340    0.737
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.318 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.01734,    Adjusted R-squared:  -0.1167
## F-statistic: 0.1294 on 3 and 22 DF,  p-value: 0.9416


##
## Call:
## lm(formula = f ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -7.4031 -1.7742 -0.0596  2.0574  6.5468
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       12.05813    3.54006   3.406  0.00336 **
## age                0.10790    0.06754   1.598  0.12853
## GenotypeAPOE4      0.04584    6.14546   0.007  0.99414
## age:GenotypeAPOE4  0.01121    0.11889   0.094  0.92598
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.772 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1957, Adjusted R-squared:  0.05373
## F-statistic: 1.379 on 3 and 17 DF,  p-value: 0.2832


## Analysis of Variance Table
##
## Response: f
##               Df Sum Sq Mean Sq F value Pr(>F)
## age            1  59.15  59.153  2.6702 0.1103
## Genotype       1   3.52   3.515  0.1587 0.6925
## sex            1   6.90   6.902  0.3116 0.5799
## age:Genotype   1   1.13   1.135  0.0512 0.8221
## age:sex        1   7.99   7.992  0.3608 0.5516
## Genotype:sex   1   0.00   0.003  0.0001 0.9910
```

```
## age:Genotype:sex  1    1.28    1.283  0.0579 0.8111
## Residuals         39 863.98   22.153


## Analysis of Variance Table
##
## Response: f
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1   6.42  6.4201  0.2270 0.6384
## Genotype      1   1.29  1.2913  0.0457 0.8328
## age:Genotype  1   3.26  3.2637  0.1154 0.7373
## Residuals    22 622.14 28.2791


## Analysis of Variance Table
##
## Response: f
##              Df  Sum Sq Mean Sq F value  Pr(>F)
## age           1  56.907  56.907  4.0003 0.06173 .
## Genotype      1   1.799   1.799  0.1265 0.72651
## age:Genotype  1   0.126   0.126  0.0089 0.92598
## Residuals    17 241.835  14.226
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
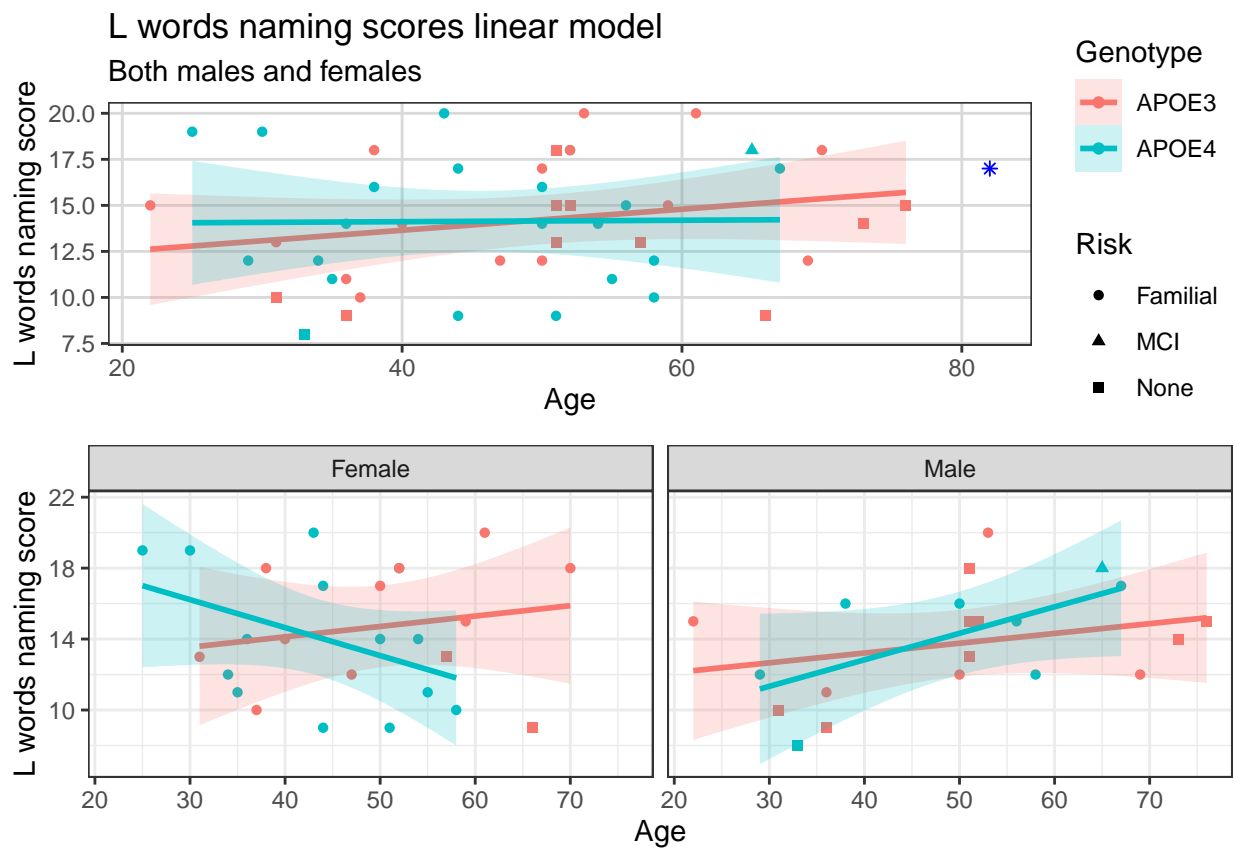

L words naming scores linear model
Both males and females


```
##
## Call:
```

```
## lm(formula = l ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -6.6489 -2.3282 -0.2007  2.2028  6.0694
##
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                11.779609   4.265405   2.762  0.00872 **
## age                         0.058626   0.081969   0.715  0.47873
## GenotypeAPOE4               9.175357   5.900041   1.555  0.12799
## sexMale                    -0.775688   5.309326  -0.146  0.88460
## age:GenotypeAPOE4          -0.216350   0.122546  -1.765  0.08532 .
## age:sexMale                -0.003405   0.101768  -0.033  0.97348
## GenotypeAPOE4:sexMale     -13.324298   8.058057  -1.654  0.10625
## age:GenotypeAPOE4:sexMale   0.310524   0.162144   1.915  0.06283 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.368 on 39 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.1671, Adjusted R-squared:  0.01762
## F-statistic: 1.118 on 7 and 39 DF,  p-value: 0.3717


##
## Call:
## lm(formula = l ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -6.6489 -2.4316 -0.1816  2.6548  5.8272
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       11.77961    4.62413   2.547   0.0184 *
## age                0.05863    0.08886   0.660   0.5163
## GenotypeAPOE4      9.17536    6.39624   1.434   0.1655
## age:GenotypeAPOE4 -0.21635    0.13285  -1.629   0.1177
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.652 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1273, Adjusted R-squared:  0.008292
## F-statistic:  1.07 on 3 and 22 DF,  p-value: 0.3822


##
## Call:
## lm(formula = l ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -3.9919 -1.9919 -0.2007  1.4344  6.0694
##
```

```
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       11.00392    2.77994   3.958  0.00101 **
## age                0.05522    0.05303   1.041  0.31235
## GenotypeAPOE4     -4.14894    4.82591  -0.860  0.40190
## age:GenotypeAPOE4  0.09417    0.09336   1.009  0.32726
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.962 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2271, Adjusted R-squared:  0.09072
## F-statistic: 1.665 on 3 and 17 DF,  p-value: 0.2121


## Analysis of Variance Table
##
## Response: l
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1  10.55  10.554  0.9302 0.34076
## Genotype         1   0.05   0.047  0.0041 0.94925
## sex              1   3.38   3.382  0.2981 0.58821
## age:Genotype     1   4.27   4.265  0.3759 0.54335
## age:sex          1  22.23  22.229  1.9592 0.16950
## Genotype:sex     1   6.69   6.693  0.5899 0.44709
## age:Genotype:sex 1  41.61  41.613  3.6677 0.06283 .
## Residuals       39 442.49  11.346
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: l
##              Df  Sum Sq Mean Sq F value Pr(>F)
## age           1   2.184   2.184  0.1638 0.6896
## Genotype      1   5.244   5.244  0.3932 0.5371
## age:Genotype  1  35.364  35.364  2.6520 0.1177
## Residuals    22 293.362  13.335


## Analysis of Variance Table
##
## Response: l
##              Df  Sum Sq Mean Sq F value  Pr(>F)
## age           1  33.504  33.504  3.8192 0.06732 .
## Genotype      1   1.391   1.391  0.1586 0.69539
## age:Genotype  1   8.926   8.926  1.0175 0.32726
## Residuals    17 149.131   8.772
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
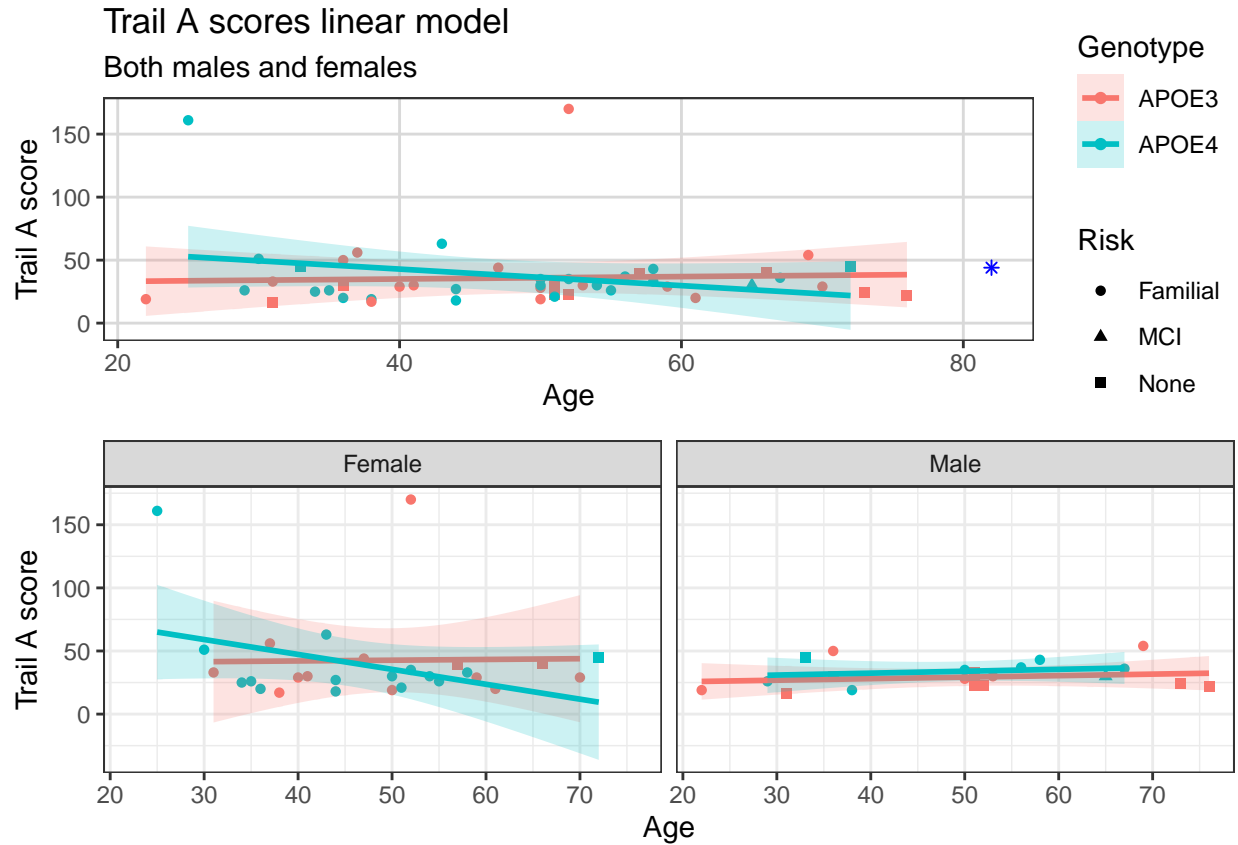
Trail A scores linear model

Both males and females


```
## 
## Call:
## lm(formula = trailA ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -31.996 -13.101  -4.778   2.143 127.184
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              39.71951   35.83149   1.109    0.274
## age                       0.05955    0.69885   0.085    0.933
## GenotypeAPOE4            54.80640   46.80108   1.171    0.248
## sexMale                 -16.47492   45.24983  -0.364    0.718
## age:GenotypeAPOE4        -1.24094    0.94748  -1.310    0.198
## age:sexMale               0.06076    0.87540   0.069    0.945
## GenotypeAPOE4:sexMale   -51.65428   67.02007  -0.771    0.445
## age:GenotypeAPOE4:sexMale  1.27171    1.32627   0.959    0.343
## 
## Residual standard error: 29.44 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.113,  Adjusted R-squared:  -0.03848
## F-statistic: 0.7459 on 7 and 41 DF,  p-value: 0.6348


## 
```

```
## Call:
## lm(formula = trailA ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -31.996 -17.497  -8.325   1.588 127.184
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       39.71951   45.54415   0.872    0.392
## age                0.05955    0.88828   0.067    0.947
## GenotypeAPOE4     54.80640   59.48723   0.921    0.366
## age:GenotypeAPOE4 -1.24094    1.20431  -1.030    0.313
##
## Residual standard error: 37.42 on 24 degrees of freedom
## Multiple R-squared:  0.08166,    Adjusted R-squared:  -0.03314
## F-statistic: 0.7113 on 3 and 24 DF,  p-value: 0.5547


##
## Call:
## lm(formula = trailA ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -13.138  -6.501  -1.260   2.424  22.454
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       23.24459    9.99841   2.325   0.0327 *
## age                0.12031    0.19074   0.631   0.5366
## GenotypeAPOE4      3.15212   17.35700   0.182   0.8580
## age:GenotypeAPOE4  0.03077    0.33578   0.092   0.9281
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.65 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.08712,    Adjusted R-squared:  -0.07397
## F-statistic: 0.5408 on 3 and 17 DF,  p-value: 0.6608


## Analysis of Variance Table
##
## Response: trailA
##                 Df Sum Sq Mean Sq F value Pr(>F)
## age              1    479  479.02  0.5526 0.4615
## Genotype         1     33   33.37  0.0385 0.8454
## sex              1   1196 1195.88  1.3796 0.2470
## age:Genotype     1   1027 1027.14  1.1849 0.2827
## age:sex          1    687  687.21  0.7928 0.3785
## Genotype:sex     1    306  306.38  0.3534 0.5554
## age:Genotype:sex 1    797  796.99  0.9194 0.3433
## Residuals       41  35541  866.85


## Analysis of Variance Table
```
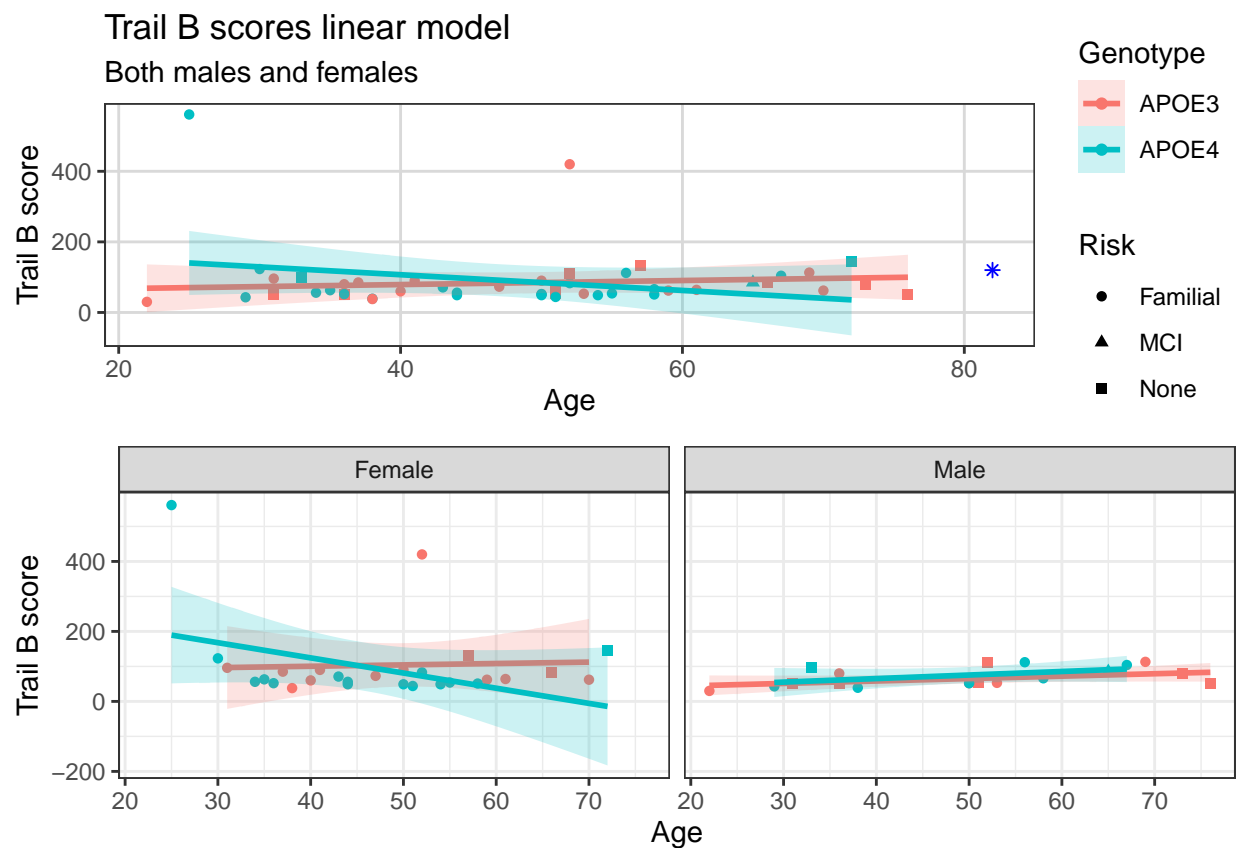
```
##
## Response: trailA
##             Df Sum Sq Mean Sq F value Pr(>F)
## age          1   1355 1355.46  0.9678 0.3350
## Genotype     1    146  146.26  0.1044 0.7494
## age:Genotype 1   1487 1486.98  1.0618 0.3131
## Residuals   24  33612 1400.49


## Analysis of Variance Table
##
## Response: trailA
##             Df Sum Sq Mean Sq F value Pr(>F)
## age          1  74.69  74.690  0.6582 0.4284
## Genotype     1 108.47 108.472  0.9559 0.3419
## age:Genotype 1   0.95   0.953  0.0084 0.9281
## Residuals   17 1929.12 113.478
```

Trail B scores linear model

Both males and females


```
##
## Call:
## lm(formula = trailB ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -94.40 -32.70 -14.21   0.13 371.59
##
```

```
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 84.6102   108.0466   0.783    0.438
## age                          0.3946     2.1073   0.187    0.852
## GenotypeAPOE4              213.1730   141.1245   1.511    0.139
## sexMale                    -54.0403   136.4468  -0.396    0.694
## age:GenotypeAPOE4           -4.7295     2.8570  -1.655    0.105
## age:sexMale                  0.2976     2.6397   0.113    0.911
## GenotypeAPOE4:sexMale     -219.0175   202.0930  -1.084    0.285
## age:GenotypeAPOE4:sexMale    5.0504     3.9993   1.263    0.214
##
## Residual standard error: 88.78 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1499, Adjusted R-squared:  0.004731
## F-statistic: 1.033 on 7 and 41 DF,  p-value: 0.4236


##
## Call:
## lm(formula = trailB ~ age * Genotype, data = combo_f)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -94.40 -46.97 -31.10  -4.23 371.59
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        84.6102   139.0641   0.608    0.549
## age                 0.3946     2.7123   0.145    0.886
## GenotypeAPOE4     213.1730   181.6377   1.174    0.252
## age:GenotypeAPOE4  -4.7295     3.6772  -1.286    0.211
##
## Residual standard error: 114.3 on 24 degrees of freedom
## Multiple R-squared:  0.1136, Adjusted R-squared:  0.002848
## F-statistic: 1.026 on 3 and 24 DF,  p-value: 0.3988


##
## Call:
## lm(formula = trailB ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -31.173 -14.254  -5.578  11.395  43.438
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        30.5699    22.5281   1.357    0.193
## age                 0.6922     0.4298   1.610    0.126
## GenotypeAPOE4      -5.8445    39.1083  -0.149    0.883
## age:GenotypeAPOE4   0.3210     0.7566   0.424    0.677
##
## Residual standard error: 24 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2622, Adjusted R-squared:  0.132
## F-statistic: 2.014 on 3 and 17 DF,  p-value: 0.1502
```
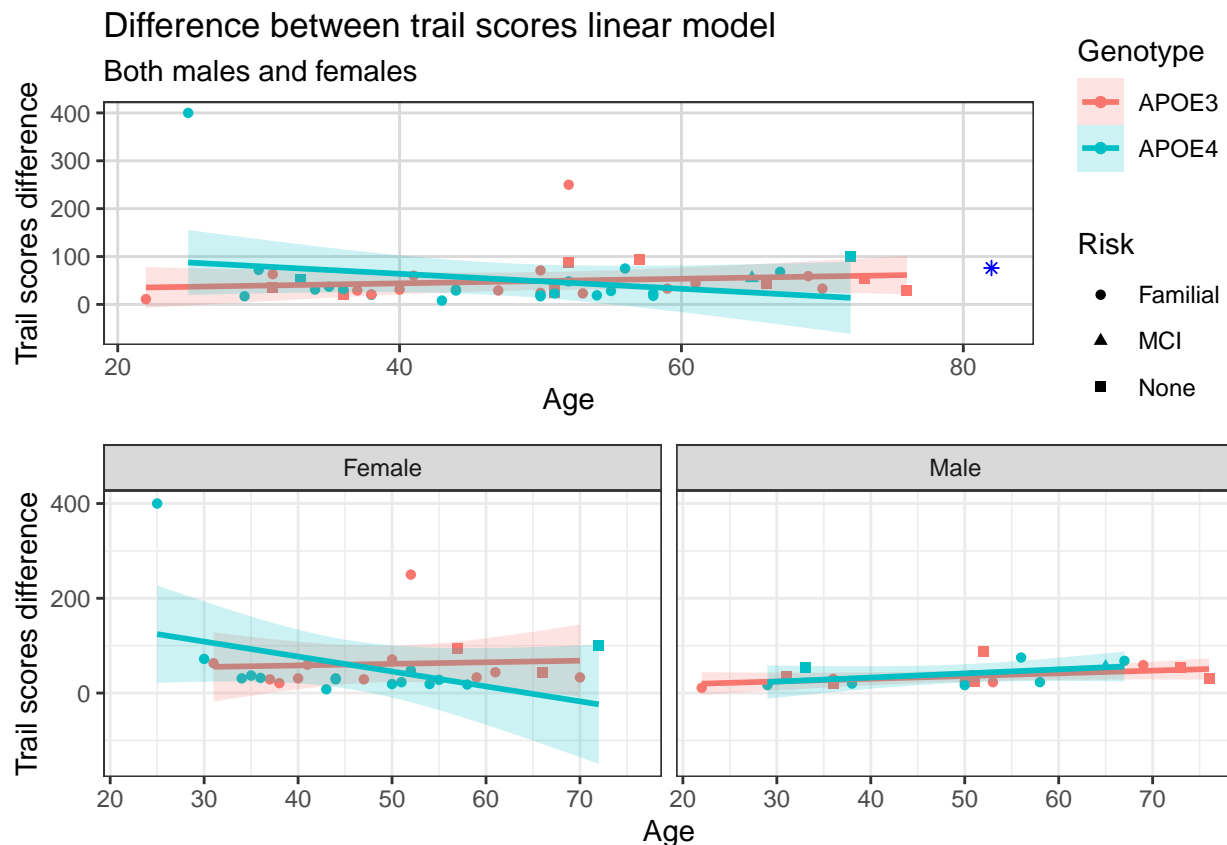
```
## Analysis of Variance Table
##
## Response: trailB
##                  Df Sum Sq Mean Sq F value Pr(>F)
## age               1   3654  3654.5  0.4636 0.4998
## Genotype          1    279   279.2  0.0354 0.8516
## sex               1  11966 11965.6  1.5181 0.2249
## age:Genotype      1  14602 14602.2  1.8526 0.1809
## age:sex           1  11773 11773.2  1.4937 0.2286
## Genotype:sex      1   2128  2127.7  0.2699 0.6062
## age:Genotype:sex  1  12570 12570.1  1.5948 0.2138
## Residuals        41 323162  7882.0


## Analysis of Variance Table
##
## Response: trailB
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1  17358 17357.6  1.3294 0.2603
## Genotype      1   1222  1221.6  0.0936 0.7623
## age:Genotype  1  21599 21598.8  1.6542 0.2107
## Residuals    24 313369 13057.0


## Analysis of Variance Table
##
## Response: trailB
##              Df Sum Sq Mean Sq F value  Pr(>F)
## age           1 2871.0 2871.05  4.9836 0.03933 *
## Genotype      1  505.3  505.34  0.8772 0.36209
## age:Genotype  1  103.7  103.69  0.1800 0.67671
## Residuals    17 9793.7  576.10
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Difference between trail scores linear model
Both males and females


```
## 
## Call:
## lm(formula = trailDiff ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -65.037 -27.291 -11.086   7.724 275.581
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)               44.8907    76.2348   0.589   0.5592
## age                        0.3350     1.4869   0.225   0.8229
## GenotypeAPOE4            158.3667    99.5736   1.590   0.1194
## sexMale                  -37.5654    96.2732  -0.390   0.6984
## age:GenotypeAPOE4         -3.4885     2.0158  -1.731   0.0911 .
## age:sexMale                0.2368     1.8625   0.127   0.8994
## GenotypeAPOE4:sexMale   -167.3633   142.5914  -1.174   0.2473
## age:GenotypeAPOE4:sexMale   3.7787     2.8218   1.339   0.1879
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 62.64 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1559, Adjusted R-squared:  0.01179
## F-statistic: 1.082 on 7 and 41 DF,  p-value: 0.3924
```

```
##
## Call:
## lm(formula = trailDiff ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -65.037 -35.382 -24.791   2.961 275.581
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)         44.891     97.470   0.461    0.649
## age                  0.335      1.901   0.176    0.862
## GenotypeAPOE4      158.367    127.309   1.244    0.226
## age:GenotypeAPOE4   -3.489      2.577  -1.354    0.188
##
## Residual standard error: 80.09 on 24 degrees of freedom
## Multiple R-squared:  0.1215, Adjusted R-squared:  0.01166
## F-statistic: 1.106 on 3 and 24 DF,  p-value: 0.366


##
## Call:
## lm(formula = trailDiff ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -25.327 -11.489  -6.328  10.447  49.939
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)         7.3253    18.9586   0.386    0.704
## age                 0.5718     0.3617   1.581    0.132
## GenotypeAPOE4      -8.9966    32.9117  -0.273    0.788
## age:GenotypeAPOE4   0.2902     0.6367   0.456    0.654
##
## Residual standard error: 20.2 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2449, Adjusted R-squared:  0.1117
## F-statistic: 1.838 on 3 and 17 DF,  p-value: 0.1785


## Analysis of Variance Table
##
## Response: trailDiff
##                 Df Sum Sq Mean Sq F value Pr(>F)
## age              1   1487  1487.3  0.3790 0.5415
## Genotype         1    120   119.5  0.0305 0.8623
## sex              1   5596  5595.9  1.4261 0.2393
## age:Genotype     1   7884  7883.7  2.0091 0.1639
## age:sex          1   6772  6771.6  1.7257 0.1963
## Genotype:sex     1    819   819.3  0.2088 0.6501
## age:Genotype:sex 1   7037  7036.8  1.7933 0.1879
## Residuals       41 160881  3923.9


## Analysis of Variance Table
```
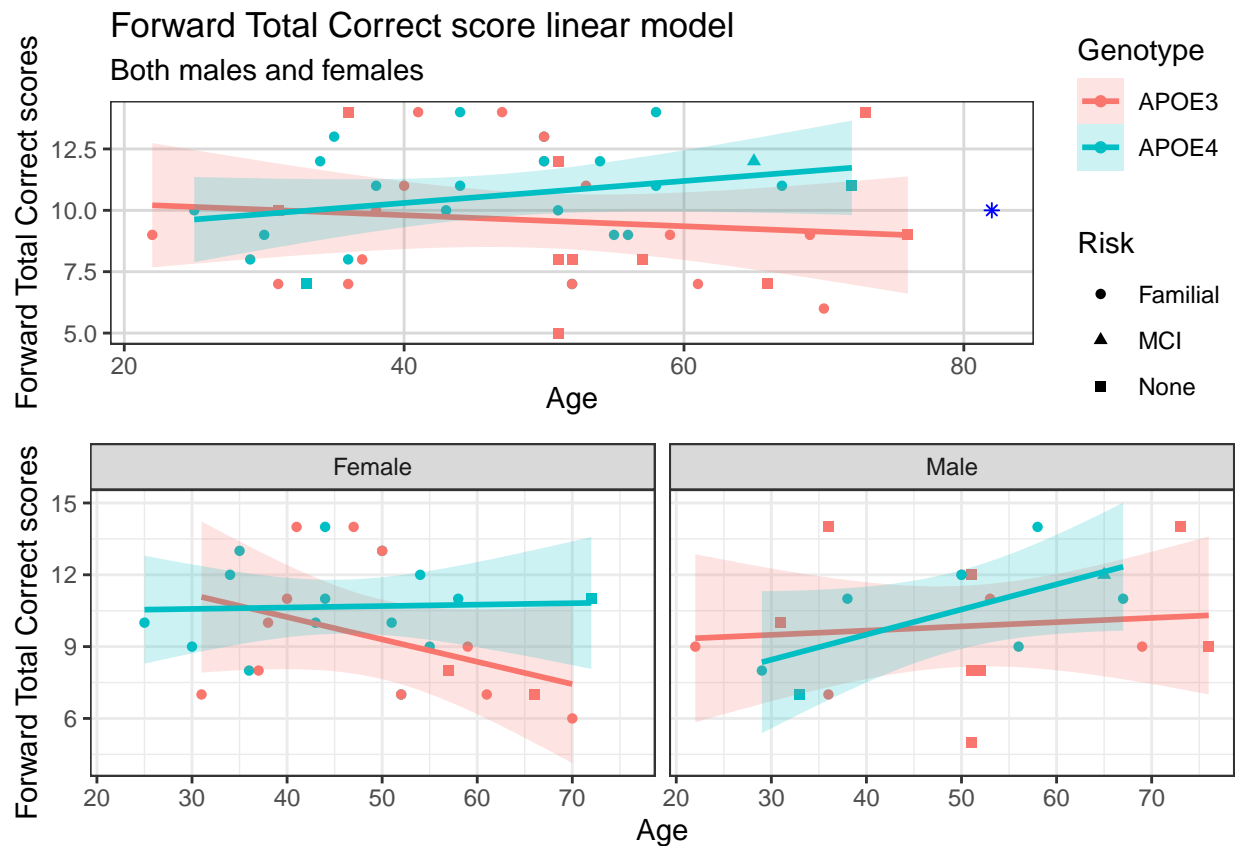
```
##
## Response: trailDiff
##           Df Sum Sq Mean Sq F value Pr(>F)
## age        1   9012  9012.1  1.4050 0.2475
## Genotype   1    522   522.4  0.0814 0.7778
## age:Genotype 1 11751 11751.5 1.8321 0.1885
## Residuals 24 153945  6414.4


## Analysis of Variance Table
##
## Response: trailDiff
##           Df Sum Sq Mean Sq F value  Pr(>F)
## age        1 2019.6 2019.59  4.9499 0.03992 *
## Genotype   1  145.6  145.56  0.3568 0.55818
## age:Genotype 1  84.8   84.76  0.2077 0.65431
## Residuals 17 6936.0  408.00
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Forward Total Correct score linear model
Both males and females


```
##
## Call:
## lm(formula = fwd_total_correct ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
```

```
## -4.8625 -1.5738 -0.3497  1.4475  4.4194
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)               13.96810    2.94998   4.735 2.62e-05 ***
## age                       -0.09335    0.05754  -1.623    0.112
## GenotypeAPOE4             -3.57378    3.85309  -0.928    0.359
## sexMale                   -5.00749    3.72538  -1.344    0.186
## age:GenotypeAPOE4          0.09933    0.07801   1.273    0.210
## age:sexMale                0.11104    0.07207   1.541    0.131
## GenotypeAPOE4:sexMale     -0.08333    5.51771  -0.015    0.988
## age:GenotypeAPOE4:sexMale -0.01204    0.10919  -0.110    0.913
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.424 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1659, Adjusted R-squared:  0.0235
## F-statistic: 1.165 on 7 and 41 DF,  p-value: 0.3436


##
## Call:
## lm(formula = fwd_total_correct ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.0742 -1.4685 -0.4823  1.3126  4.4194
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       13.96810    2.88167   4.847 6.12e-05 ***
## age               -0.09335    0.05620  -1.661    0.110
## GenotypeAPOE4     -3.57378    3.76387  -0.949    0.352
## age:GenotypeAPOE4  0.09933    0.07620   1.304    0.205
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.368 on 24 degrees of freedom
## Multiple R-squared:  0.1743, Adjusted R-squared:  0.07109
## F-statistic: 1.689 on 3 and 24 DF,  p-value: 0.196


##
## Call:
## lm(formula = fwd_total_correct ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.8625 -1.7678 -0.3479  1.7073  4.4028
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    8.96061    2.34747   3.817  0.00138 **
## age            0.01768    0.04478   0.395  0.69785
## GenotypeAPOE4 -3.65711    4.07515  -0.897  0.38203
```

```
## age:GenotypeAPOE4  0.08730    0.07884   1.107  0.28358
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.501 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1548, Adjusted R-squared:  0.005592
## F-statistic: 1.037 on 3 and 17 DF,  p-value: 0.4011


## Analysis of Variance Table
##
## Response: fwd_total_correct
##                 Df  Sum Sq Mean Sq F value  Pr(>F)
## age              1   0.031  0.0307  0.0052 0.94270
## Genotype         1  13.317 13.3165  2.2664 0.13987
## sex              1   0.532  0.5320  0.0905 0.76501
## age:Genotype     1   9.248  9.2475  1.5739 0.21675
## age:sex          1  23.442 23.4419  3.9897 0.05244 .
## Genotype:sex     1   1.277  1.2770  0.2173 0.64354
## age:Genotype:sex 1   0.071  0.0714  0.0122 0.91276
## Residuals       41 240.899  5.8756
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: fwd_total_correct
##              Df  Sum Sq Mean Sq F value Pr(>F)
## age           1   9.401  9.4014  1.6768 0.2077
## Genotype      1   9.476  9.4760  1.6901 0.2059
## age:Genotype  1   9.528  9.5278  1.6994 0.2047
## Residuals    24 134.559  5.6066


## Analysis of Variance Table
##
## Response: fwd_total_correct
##              Df  Sum Sq Mean Sq F value Pr(>F)
## age           1   9.508  9.5083  1.5200 0.2344
## Genotype      1   2.291  2.2912  0.3663 0.5530
## age:Genotype  1   7.670  7.6699  1.2261 0.2836
## Residuals    17 106.340  6.2553
```
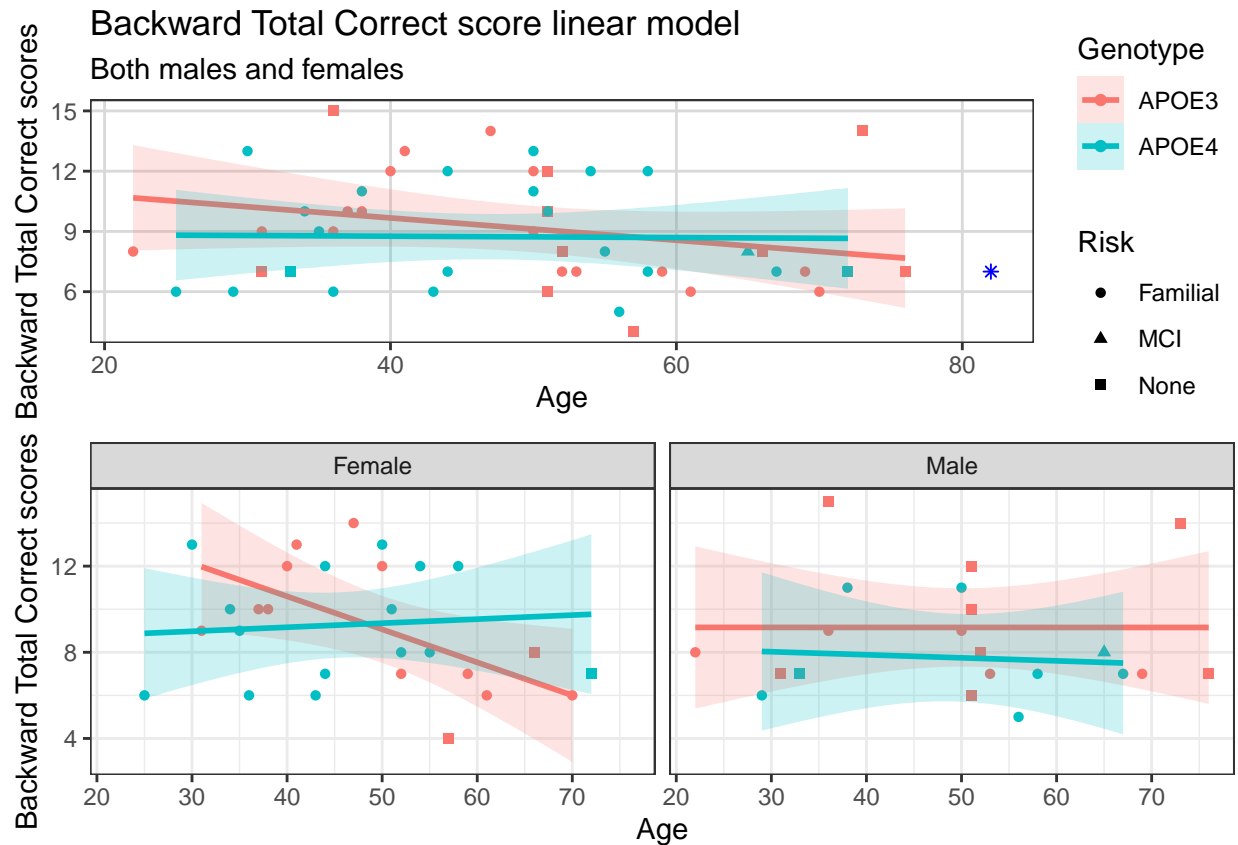
Backward Total Correct score linear model

Both males and females

Backward Total Correct scores

Genotype
— APOE3
— APOE4

Risk
● Familial
▲ MCI
■ None

Female | Male

Backward Total Correct scores

Age

```
## 
## Call:
## lm(formula = bckwds_total_correct ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -3.9927 -2.1526 -0.6299  2.4986  5.8455 
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)    
## (Intercept)             16.72528    3.28290   5.095 8.27e-06 ***
## age                     -0.15320    0.06403  -2.393   0.0214 *  
## GenotypeAPOE4           -8.31578    4.28795  -1.939   0.0594 .  
## sexMale                 -7.56896    4.14582  -1.826   0.0752 .  
## age:GenotypeAPOE4        0.17203    0.08681   1.982   0.0542 .  
## age:sexMale              0.15315    0.08020   1.910   0.0632 .  
## GenotypeAPOE4:sexMale    7.60899    6.14042   1.239   0.2223    
## age:GenotypeAPOE4:sexMale -0.18611   0.12151  -1.532   0.1333    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 2.698 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1592, Adjusted R-squared:  0.01561 
## F-statistic: 1.109 on 7 and 41 DF,  p-value: 0.3761
```

```
## 
## Call:
## lm(formula = bckwds_total_correct ~ age * Genotype, data = combo_f)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.9927 -1.8785 -0.3773  2.5130  4.4753
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        16.7253     3.2146   5.203 2.49e-05 ***
## age                -0.1532     0.0627  -2.444   0.0223 *
## GenotypeAPOE4      -8.3158     4.1987  -1.981   0.0592 .
## age:GenotypeAPOE4   0.1720     0.0850   2.024   0.0543 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 2.641 on 24 degrees of freedom
## Multiple R-squared:  0.203,  Adjusted R-squared:  0.1034
## F-statistic: 2.038 on 3 and 24 DF,  p-value: 0.1353


## 
## Call:
## lm(formula = bckwds_total_correct ~ age * Genotype, data = combo_m)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.1538 -2.1526 -0.6299  0.8462  5.8455
## 
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        9.156e+00  2.604e+00   3.516  0.00265 **
## age               -4.933e-05  4.969e-02  -0.001  0.99922
## GenotypeAPOE4     -7.068e-01  4.521e+00  -0.156  0.87762
## age:GenotypeAPOE4 -1.408e-02  8.747e-02  -0.161  0.87399
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 2.775 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.07135,    Adjusted R-squared:  -0.09253
## F-statistic: 0.4354 on 3 and 17 DF,  p-value: 0.7305


## Analysis of Variance Table
## 
## Response: bckwds_total_correct
##                 Df  Sum Sq Mean Sq F value Pr(>F)
## age              1   8.405  8.4046  1.1550 0.2888
## Genotype         1   2.758  2.7583  0.3791 0.5415
## sex              1   3.842  3.8417  0.5280 0.4716
## age:Genotype     1   6.460  6.4603  0.8878 0.3516
## age:sex          1  11.799 11.7986  1.6214 0.2101
## Genotype:sex     1   6.141  6.1412  0.8440 0.3636
## age:Genotype:sex 1  17.070 17.0695  2.3458 0.1333
```

```
## Residuals        41 298.342  7.2766


## Analysis of Variance Table
##
## Response: bckwds_total_correct
##              Df  Sum Sq Mean Sq F value  Pr(>F)
## age           1  14.050 14.0497  2.0137 0.16874
## Genotype      1   0.035  0.0348  0.0050 0.94424
## age:Genotype  1  28.576 28.5761  4.0958 0.05426 .
## Residuals    24 167.447  6.9769
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: bckwds_total_correct
##              Df  Sum Sq Mean Sq F value Pr(>F)
## age           1   0.064  0.0638  0.0083 0.9285
## Genotype      1   9.793  9.7935  1.2719 0.2751
## age:Genotype  1   0.200  0.1996  0.0259 0.8740
## Residuals    17 130.896  7.6997
```
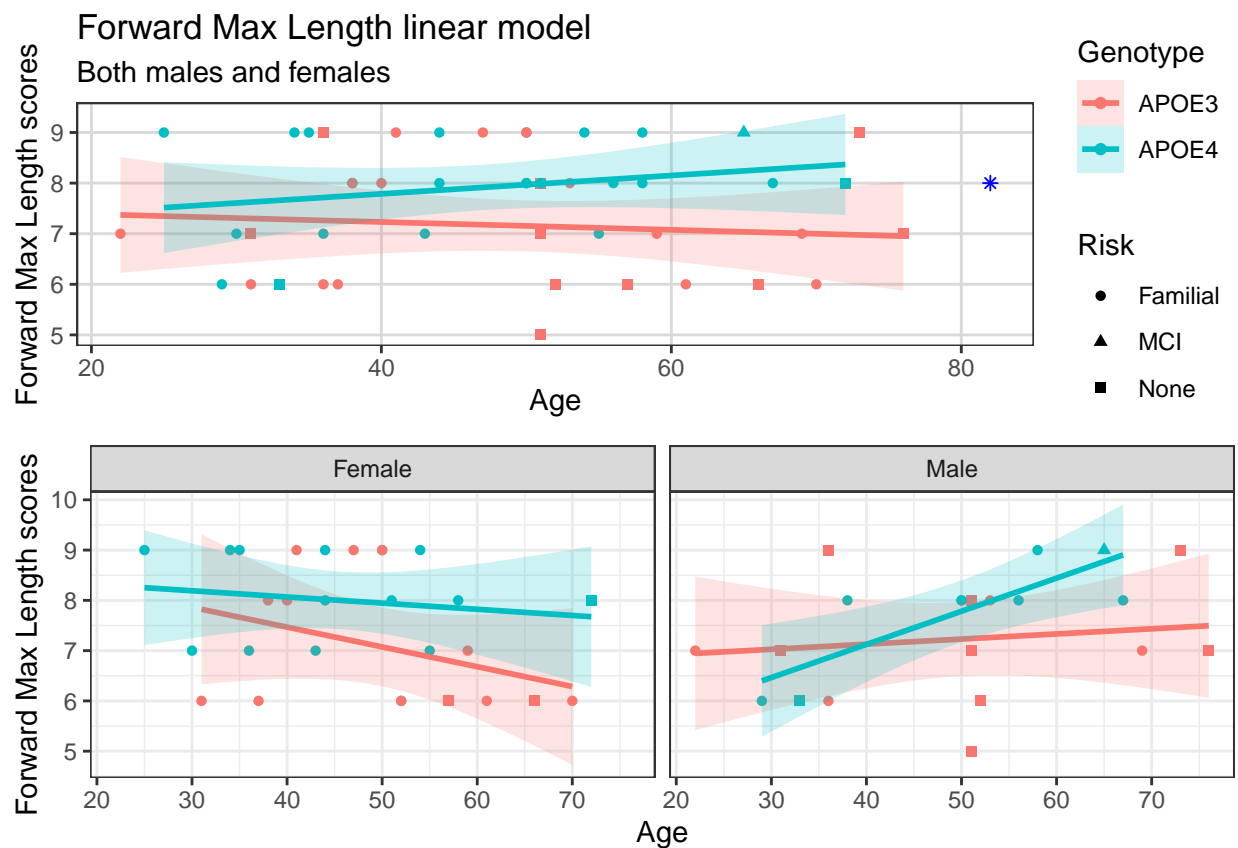


```
##
## Call:
## lm(formula = fwd_max_length ~ age * Genotype * sex, data = geno_combined)
```

```
##
## Residuals:
##      Min      1Q   Median      3Q      Max
## -2.24017 -0.79813  0.05522  0.75983  1.92611
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)                9.04364    1.35561   6.671 4.81e-08 ***
## age                       -0.03939    0.02644  -1.490    0.144
## GenotypeAPOE4             -0.48462    1.77062  -0.274    0.786
## sexMale                   -2.32295    1.71193  -1.357    0.182
## age:GenotypeAPOE4          0.02712    0.03585   0.757    0.454
## age:sexMale                0.04958    0.03312   1.497    0.142
## GenotypeAPOE4:sexMale     -1.75054    2.53556  -0.690    0.494
## age:GenotypeAPOE4:sexMale  0.02865    0.05018   0.571    0.571
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.114 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2546, Adjusted R-squared:  0.1273
## F-statistic:     2 on 7 and 41 DF,  p-value: 0.07842


##
## Call:
## lm(formula = fwd_max_length ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q      Max
## -1.9206 -0.9116  0.1101  0.8615  1.9261
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        9.04364    1.40196   6.451 1.14e-06 ***
## age               -0.03939    0.02734  -1.441    0.163
## GenotypeAPOE4     -0.48462    1.83117  -0.265    0.794
## age:GenotypeAPOE4  0.02712    0.03707   0.731    0.472
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.152 on 24 degrees of freedom
## Multiple R-squared:  0.2205, Adjusted R-squared:  0.123
## F-statistic: 2.263 on 3 and 24 DF,  p-value: 0.107


##
## Call:
## lm(formula = fwd_max_length ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min      1Q  Median      3Q      Max
## -2.24017 -0.49482 -0.03645  0.73946  1.91262
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)       6.72069    0.99282   6.769 3.28e-06 ***
## age               0.01019    0.01894   0.538    0.598
## GenotypeAPOE4     -2.23516    1.72351  -1.297    0.212
## age:GenotypeAPOE4  0.05576    0.03334   1.672    0.113
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.058 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2992, Adjusted R-squared:  0.1756
## F-statistic:  2.42 on 3 and 17 DF,  p-value: 0.1017


## Analysis of Variance Table
##
## Response: fwd_max_length
##                Df Sum Sq Mean Sq F value  Pr(>F)
## age             1  0.000  0.0000  0.0000 0.99829
## Genotype        1  7.131  7.1310  5.7474 0.02115 *
## sex             1  0.012  0.0122  0.0098 0.92149
## age:Genotype    1  1.437  1.4365  1.1578 0.28822
## age:sex         1  8.036  8.0364  6.4771 0.01479 *
## Genotype:sex    1  0.354  0.3540  0.2853 0.59611
## age:Genotype:sex 1 0.404  0.4044  0.3259 0.57119
## Residuals      41 50.870  1.2407
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: fwd_max_length
##              Df Sum Sq Mean Sq F value  Pr(>F)
## age           1  3.827  3.8272  2.8840 0.10240
## Genotype      1  4.471  4.4706  3.3689 0.07886 .
## age:Genotype  1  0.710  0.7101  0.5351 0.47156
## Residuals    24 31.849  1.3271
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: fwd_max_length
##              Df  Sum Sq Mean Sq F value Pr(>F)
## age           1  3.5726  3.5726  3.1929 0.0918 .
## Genotype      1  1.4196  1.4196  1.2687 0.2757
## age:Genotype  1  3.1296  3.1296  2.7971 0.1127
## Residuals    17 19.0211  1.1189
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
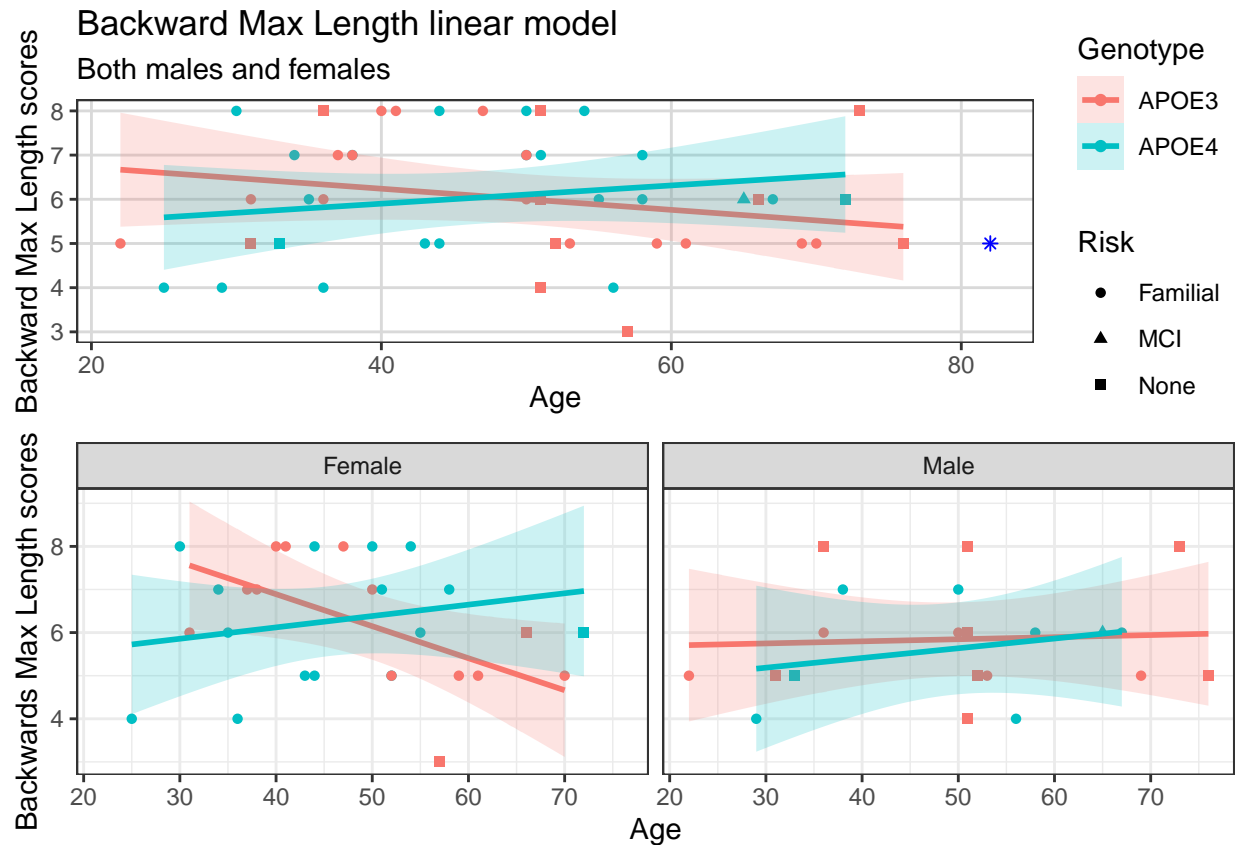
Backward Max Length linear model

Both males and females


```
## 
## Call:
## lm(formula = bckwds_max_length ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.62815 -0.96487 -0.01952  1.04039  2.22224
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)               9.86227    1.65799   5.948 5.12e-07 ***
## age                      -0.07428    0.03234  -2.297   0.0268 *
## GenotypeAPOE4            -4.79679    2.16558  -2.215   0.0324 *
## sexMale                 -4.25942    2.09380  -2.034   0.0484 *
## age:GenotypeAPOE4         0.10066    0.04384   2.296   0.0269 *
## age:sexMale               0.07914    0.04051   1.954   0.0576 .
## GenotypeAPOE4:sexMale     3.70303    3.10115   1.194   0.2393
## age:GenotypeAPOE4:sexMale -0.08298    0.06137  -1.352   0.1838
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.362 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1636, Adjusted R-squared:  0.02079
## F-statistic: 1.146 on 7 and 41 DF,  p-value: 0.3546
```

```
##
## Call:
## lm(formula = bckwds_max_length ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.62815 -1.04963 -0.01416  1.05755  2.14311
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)         9.86227    1.67307   5.895 4.42e-06 ***
## age                -0.07428    0.03263  -2.276   0.0320 *
## GenotypeAPOE4      -4.79679    2.18527  -2.195   0.0381 *
## age:GenotypeAPOE4   0.10066    0.04424   2.275   0.0321 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.375 on 24 degrees of freedom
## Multiple R-squared:  0.2002, Adjusted R-squared:  0.1003
## F-statistic: 2.003 on 3 and 24 DF,  p-value: 0.1404


##
## Call:
## lm(formula = bckwds_max_length ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.85064 -0.86036 -0.01952  0.22224  2.22224
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        5.602846   1.262096   4.439  0.00036 ***
## age                0.004859   0.024078   0.202  0.84247
## GenotypeAPOE4     -1.093761   2.190967  -0.499  0.62403
## age:GenotypeAPOE4  0.017685   0.042385   0.417  0.68172
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.345 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.03367,    Adjusted R-squared:  -0.1369
## F-statistic: 0.1975 on 3 and 17 DF,  p-value: 0.8967


## Analysis of Variance Table
##
## Response: bckwds_max_length
##               Df Sum Sq Mean Sq F value Pr(>F)
## age            1  0.208  0.2082  0.1122 0.7394
## Genotype       1  0.010  0.0100  0.0054 0.9420
## sex            1  2.358  2.3583  1.2706 0.2662
## age:Genotype   1  4.666  4.6655  2.5137 0.1205
## age:sex        1  3.910  3.9098  2.1066 0.1543
## Genotype:sex   1  0.338  0.3382  0.1822 0.6717
## age:Genotype:sex 1 3.393 3.3932  1.8282 0.1838
```

```
## Residuals        41 76.096  1.8560


## Analysis of Variance Table
##
## Response: bckwds_max_length
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1  1.567  1.5667  0.8290 0.3716
## Genotype      1  0.005  0.0050  0.0026 0.9596
## age:Genotype  1  9.785  9.7847  5.1773 0.0321 *
## Residuals    24 45.358  1.8899
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: bckwds_max_length
##              Df  Sum Sq Mean Sq F value Pr(>F)
## age           1  0.5273 0.52731  0.2916 0.5962
## Genotype      1  0.2290 0.22897  0.1266 0.7263
## age:Genotype  1  0.3148 0.31479  0.1741 0.6817
## Residuals    17 30.7385 1.80814
```
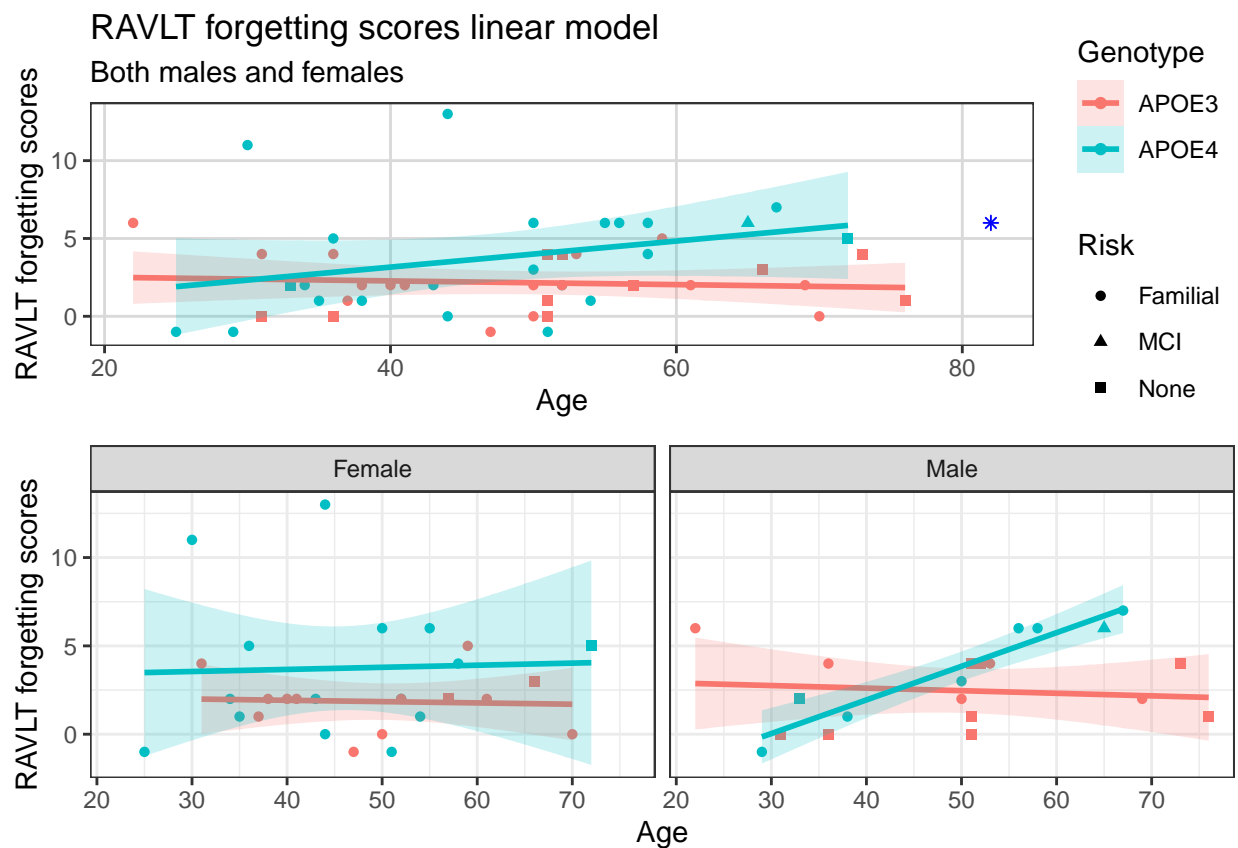
RAVLT forgetting scores linear model


```
##
## Call:
## lm(formula = RAVLT_FORGETTING ~ age * Genotype * sex, data = geno_combined)
```

```
##
## Residuals:
##     Min     1Q Median     3Q    Max
## -4.7982 -1.6974  0.0655  1.3798  9.2849
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              2.216131   3.391478   0.653    0.517
## age                     -0.007411   0.066146  -0.112    0.911
## GenotypeAPOE4            0.976811   4.429759   0.221    0.827
## sexMale                  0.975331   4.282931   0.228    0.821
## age:GenotypeAPOE4        0.019279   0.089680   0.215    0.831
## age:sexMale             -0.007165   0.082857  -0.086    0.932
## GenotypeAPOE4:sexMale   -9.845258   6.343501  -1.552    0.128
## age:GenotypeAPOE4:sexMale 0.185741  0.125533   1.480    0.147
##
## Residual standard error: 2.787 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2167, Adjusted R-squared:  0.08297
## F-statistic:  1.62 on 7 and 41 DF,  p-value: 0.157


##
## Call:
## lm(formula = RAVLT_FORGETTING ~ age * Genotype, data = combo_f)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -4.798 -1.819  0.084  1.300  9.285
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       2.216131   4.053364   0.547    0.590
## age              -0.007411   0.079056  -0.094    0.926
## GenotypeAPOE4     0.976811   5.294277   0.185    0.855
## age:GenotypeAPOE4 0.019279   0.107182   0.180    0.859
##
## Residual standard error: 3.331 on 24 degrees of freedom
## Multiple R-squared:  0.08647,    Adjusted R-squared:  -0.02773
## F-statistic: 0.7572 on 3 and 24 DF,  p-value: 0.5291


##
## Call:
## lm(formula = RAVLT_FORGETTING ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min     1Q  Median     3Q    Max
## -2.7396 -0.8459 -0.1857  1.3923  3.1292
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        3.19146    1.64426   1.941  0.06903 .
## age               -0.01458    0.03137  -0.465  0.64806
## GenotypeAPOE4     -8.86845    2.85440  -3.107  0.00641 **
## age:GenotypeAPOE4  0.20502    0.05522   3.713  0.00173 **
```
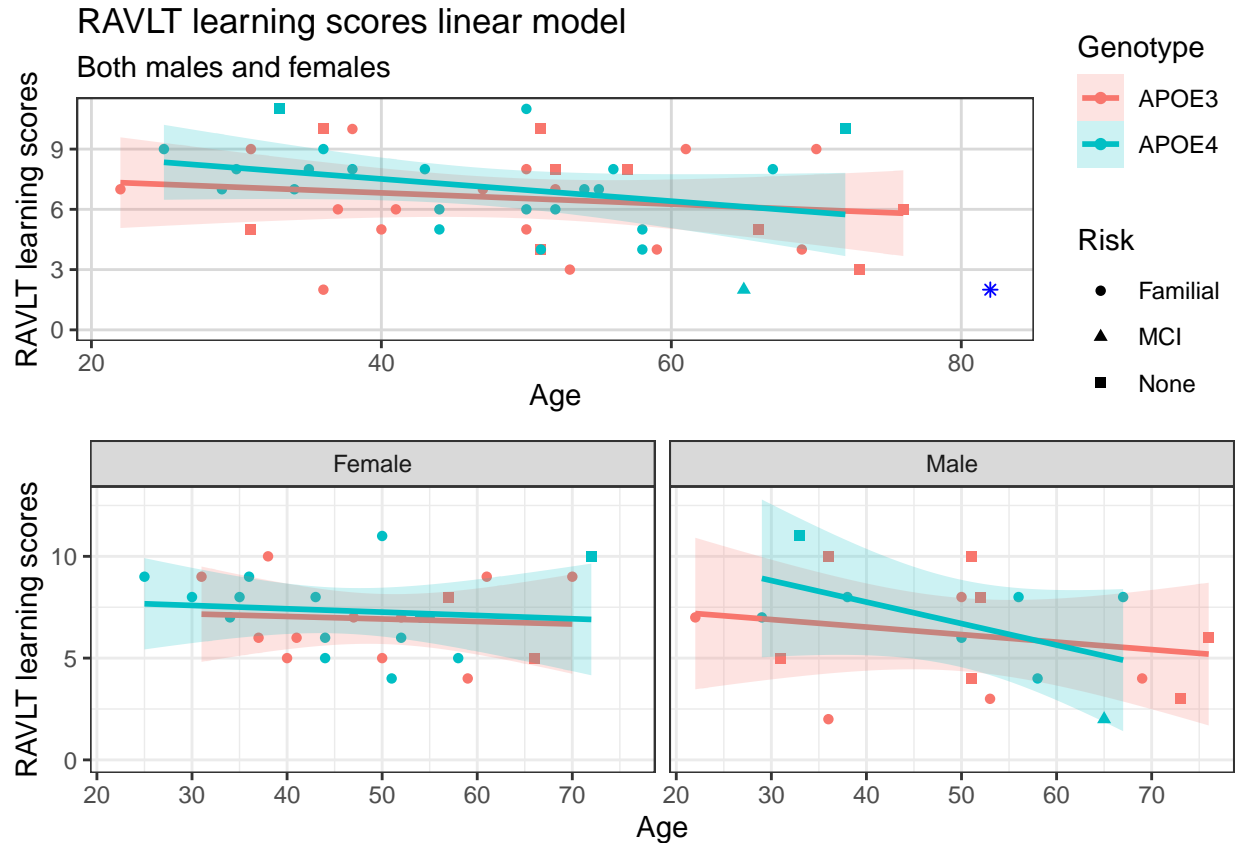
```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.752 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.5461, Adjusted R-squared:  0.466
## F-statistic: 6.819 on 3 and 17 DF,  p-value: 0.003207


## Analysis of Variance Table
##
## Response: RAVLT_FORGETTING
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1   4.18   4.184  0.5388 0.46710
## Genotype         1  33.80  33.798  4.3522 0.04322 *
## sex              1   1.02   1.023  0.1317 0.71855
## age:Genotype     1  18.65  18.653  2.4019 0.12888
## age:sex          1  11.68  11.683  1.5044 0.22699
## Genotype:sex     1   1.74   1.745  0.2246 0.63804
## age:Genotype:sex 1  17.00  17.002  2.1893 0.14662
## Residuals       41 318.40   7.766
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: RAVLT_FORGETTING
##              Df  Sum Sq Mean Sq F value Pr(>F)
## age           1   0.519  0.5190  0.0468 0.8306
## Genotype      1  24.321 24.3208  2.1925 0.1517
## age:Genotype  1   0.359  0.3589  0.0324 0.8588
## Residuals    24 266.230 11.0929


## Analysis of Variance Table
##
## Response: RAVLT_FORGETTING
##              Df Sum Sq Mean Sq F value   Pr(>F)
## age           1 11.872  11.872  3.8684 0.065745 .
## Genotype      1  8.603   8.603  2.8031 0.112378
## age:Genotype  1 42.305  42.305 13.7849 0.001729 **
## Residuals    17 52.172   3.069
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

RAVLT learning scores linear model

```
##
## Call:
## lm(formula = RAVLT_LEARNING ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.6736 -1.8582 -0.1784  1.8433  3.8802
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             7.544032   2.881013   2.619   0.0123 *
## age                    -0.012438   0.056190  -0.221   0.8259
## GenotypeAPOE4           0.534668   3.763018   0.142   0.8877
## sexMale                 0.458705   3.638290   0.126   0.9003
## age:GenotypeAPOE4      -0.003931   0.076182  -0.052   0.9591
## age:sexMale            -0.024483   0.070386  -0.348   0.7297
## GenotypeAPOE4:sexMale   3.442406   5.388716   0.639   0.5265
## age:GenotypeAPOE4:sexMale -0.064800 0.106638  -0.608   0.5468
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.367 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1208, Adjusted R-squared:  -0.02927
## F-statistic: 0.805 on 7 and 41 DF,  p-value: 0.588
```

```
##
## Call:
## lm(formula = RAVLT_LEARNING ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.2438 -1.4496 -0.0689  1.3756  3.7398
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       7.544032   2.451877   3.077  0.00517 **
## age              -0.012438   0.047821  -0.260  0.79700
## GenotypeAPOE4     0.534668   3.202504   0.167  0.86881
## age:GenotypeAPOE4 -0.003931   0.064834  -0.061  0.95215
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.015 on 24 degrees of freedom
## Multiple R-squared:  0.02026,    Adjusted R-squared:  -0.1022
## F-statistic: 0.1654 on 3 and 24 DF,  p-value: 0.9186


##
## Call:
## lm(formula = RAVLT_FORGETTING ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.7396 -0.8459 -0.1857  1.3923  3.1292
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        3.19146    1.64426   1.941  0.06903 .
## age               -0.01458    0.03137  -0.465  0.64806
## GenotypeAPOE4     -8.86845    2.85440  -3.107  0.00641 **
## age:GenotypeAPOE4  0.20502    0.05522   3.713  0.00173 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.752 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.5461, Adjusted R-squared:  0.466
## F-statistic: 6.819 on 3 and 17 DF,  p-value: 0.003207


## Analysis of Variance Table
##
## Response: RAVLT_LEARNING
##                 Df  Sum Sq Mean Sq F value Pr(>F)
## age              1  15.240 15.2396  2.7194 0.1068
## Genotype         1   2.649  2.6487  0.4726 0.4956
## sex              1   4.420  4.4195  0.7886 0.3797
## age:Genotype     1   1.192  1.1920  0.2127 0.6471
## age:sex          1   5.786  5.7858  1.0324 0.3155
## Genotype:sex     1   0.224  0.2244  0.0400 0.8424
## age:Genotype:sex 1   2.069  2.0693  0.3693 0.5468
```

```
## Residuals        41 229.768   5.6041


## Analysis of Variance Table
##
## Response: RAVLT_LEARNING
##             Df Sum Sq Mean Sq F value Pr(>F)
## age          1  1.192  1.1921  0.2937 0.5929
## Genotype     1  0.807  0.8072  0.1989 0.6596
## age:Genotype 1  0.015  0.0149  0.0037 0.9521
## Residuals   24 97.414  4.0589


## Analysis of Variance Table
##
## Response: RAVLT_FORGETTING
##             Df Sum Sq Mean Sq F value   Pr(>F)
## age          1 11.872  11.872  3.8684 0.065745 .
## Genotype     1  8.603   8.603  2.8031 0.112378
## age:Genotype 1 42.305  42.305 13.7849 0.001729 **
## Residuals   17 52.172   3.069
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
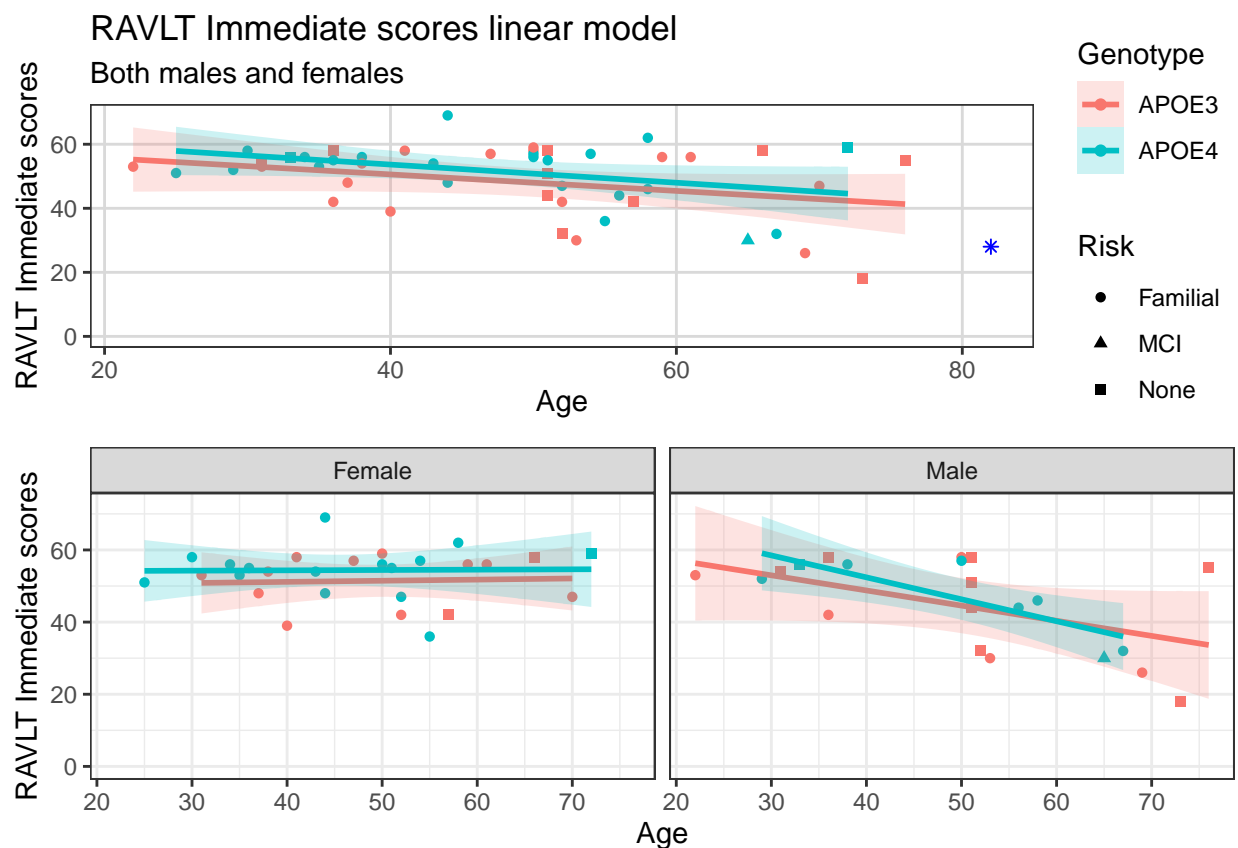


```
##
## Call:
## lm(formula = RAVLT_IMMEDIATE ~ age * Genotype * sex, data = geno_combined)
```

```
##
## Residuals:
##     Min     1Q  Median      3Q     Max
## -18.488  -6.386   1.327   4.543  21.346
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              49.90158   10.98903   4.541 4.84e-05 ***
## age                       0.03125    0.21433   0.146    0.885
## GenotypeAPOE4             4.07270   14.35325   0.284    0.778
## sexMale                  15.66262   13.87750   1.129    0.266
## age:GenotypeAPOE4        -0.02190    0.29058  -0.075    0.940
## age:sexMale              -0.45112    0.26847  -1.680    0.101
## GenotypeAPOE4:sexMale     7.08450   20.55414   0.345    0.732
## age:GenotypeAPOE4:sexMale -0.16624   0.40675  -0.409    0.685
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.03 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.3618, Adjusted R-squared:  0.2528
## F-statistic:  3.32 on 7 and 41 DF,  p-value: 0.006832


##
## Call:
## lm(formula = RAVLT_IMMEDIATE ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min     1Q  Median      3Q     Max
## -18.488  -3.678   1.633   4.279  14.614
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       49.90158    9.13739   5.461  1.3e-05 ***
## age                0.03125    0.17821   0.175    0.862
## GenotypeAPOE4      4.07270   11.93475   0.341    0.736
## age:GenotypeAPOE4 -0.02190    0.24162  -0.091    0.929
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.508 on 24 degrees of freedom
## Multiple R-squared:  0.04385,    Adjusted R-squared:  -0.07566
## F-statistic: 0.3669 on 3 and 24 DF,  p-value: 0.7775


##
## Call:
## lm(formula = RAVLT_FORGETTING ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min     1Q  Median      3Q     Max
## -2.7396 -0.8459 -0.1857  1.3923  3.1292
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)           3.19146    1.64426    1.941   0.06903 .
## age                   -0.01458    0.03137   -0.465   0.64806
## GenotypeAPOE4         -8.86845    2.85440   -3.107   0.00641 **
## age:GenotypeAPOE4      0.20502    0.05522    3.713   0.00173 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.752 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.5461, Adjusted R-squared:  0.466
## F-statistic: 6.819 on 3 and 17 DF,  p-value: 0.003207


## Analysis of Variance Table
##
## Response: RAVLT_IMMEDIATE
##                 Df Sum Sq Mean Sq F value    Pr(>F)
## age              1  687.3  687.34  8.4303 0.005918 **
## Genotype         1   98.9   98.91  1.2131 0.277135
## sex              1  545.1  545.14  6.6861 0.013369 *
## age:Genotype     1    0.3    0.27  0.0033 0.954635
## age:sex          1  546.4  546.44  6.7020 0.013267 *
## Genotype:sex     1    3.0    2.99  0.0366 0.849134
## age:Genotype:sex 1   13.6   13.62  0.1670 0.684881
## Residuals       41 3342.8   81.53
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: RAVLT_IMMEDIATE
##              Df  Sum Sq Mean Sq F value Pr(>F)
## age           1    0.05   0.053  0.0009 0.9759
## Genotype      1   61.54  61.536  1.0916 0.3065
## age:Genotype  1    0.46   0.463  0.0082 0.9285
## Residuals    24 1352.91  56.371


## Analysis of Variance Table
##
## Response: RAVLT_FORGETTING
##              Df Sum Sq Mean Sq F value    Pr(>F)
## age           1 11.872  11.872  3.8684 0.065745 .
## Genotype      1  8.603   8.603  2.8031 0.112378
## age:Genotype  1 42.305  42.305 13.7849 0.001729 **
## Residuals    17 52.172   3.069
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
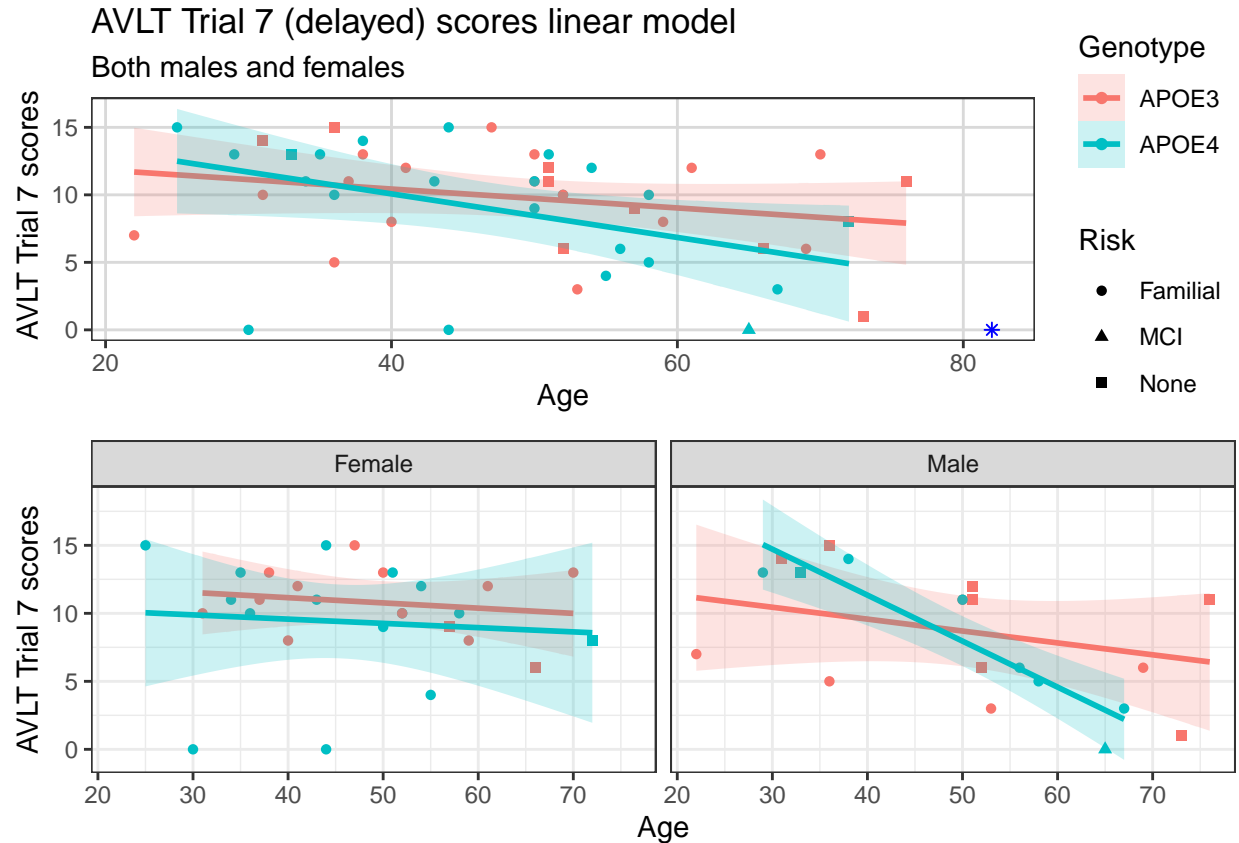
AVLT Trial 7 (delayed) scores linear model

Both males and females

```
##
## Call:
## lm(formula = AVLT_Trial7 ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -9.8856 -2.0572  0.7927  2.3884  5.5521
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)             12.688351   4.690759   2.705   0.0099 **
## age                     -0.038442   0.091487  -0.420   0.6765
## GenotypeAPOE4           -1.864986   6.126807  -0.304   0.7624
## sexMale                  0.382261   5.923730   0.065   0.9489
## age:GenotypeAPOE4        0.007182   0.124036   0.058   0.9541
## age:sexMale             -0.048990   0.114600  -0.427   0.6713
## GenotypeAPOE4:sexMale   13.658103   8.773708   1.557   0.1272
## age:GenotypeAPOE4:sexMale -0.257906   0.173624  -1.485   0.1451
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.854 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2846, Adjusted R-squared:  0.1624
## F-statistic:  2.33 on 7 and 41 DF,  p-value: 0.04252
```

```
## 
## Call:
## lm(formula = AVLT_Trial7 ~ age * Genotype, data = combo_f)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -9.8856 -1.4968  0.8449  2.3915  5.5521
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      12.688351   4.863049   2.609   0.0154 *
## age              -0.038442   0.094848  -0.405   0.6888
## GenotypeAPOE4    -1.864986   6.351843  -0.294   0.7716
## age:GenotypeAPOE4 0.007182   0.128592   0.056   0.9559
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 3.996 on 24 degrees of freedom
## Multiple R-squared:  0.04427,    Adjusted R-squared:  -0.0752
## F-statistic: 0.3705 on 3 and 24 DF,  p-value: 0.775


## 
## Call:
## lm(formula = AVLT_Trial7 ~ age * Genotype, data = combo_m)
## 
## Residuals:
##    Min     1Q Median     3Q    Max
## -5.688 -2.524  0.073  2.388  5.077
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      13.07061    3.42128   3.820  0.00137 **
## age              -0.08743    0.06527  -1.340  0.19803
## GenotypeAPOE4    11.79312    5.93926   1.986  0.06345 .
## age:GenotypeAPOE4 -0.25072   0.11490  -2.182  0.04342 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 3.645 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.4638, Adjusted R-squared:  0.3691
## F-statistic: 4.901 on 3 and 17 DF,  p-value: 0.01238


## Analysis of Variance Table
## 
## Response: AVLT_Trial7
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1  95.00  95.000  6.3947 0.01539 *
## Genotype         1  14.88  14.883  1.0018 0.32275
## sex              1  27.11  27.106  1.8246 0.18417
## age:Genotype     1  14.60  14.602  0.9829 0.32730
## age:sex          1  54.63  54.635  3.6776 0.06213 .
## Genotype:sex     1   3.29   3.288  0.2213 0.64052
## age:Genotype:sex 1  32.78  32.780  2.2065 0.14508
```

```
## Residuals        41 609.09   14.856
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: AVLT_Trial7
##               Df Sum Sq Mean Sq F value Pr(>F)
## age            1   2.13  2.1281  0.1333 0.7183
## Genotype       1  15.57 15.5710  0.9752 0.3332
## age:Genotype   1   0.05  0.0498  0.0031 0.9559
## Residuals     24 383.22 15.9673

## Analysis of Variance Table
##
## Response: AVLT_Trial7
##               Df  Sum Sq Mean Sq F value    Pr(>F)
## age            1 129.904 129.904  9.7768  0.006141 **
## Genotype       1   2.186   2.186  0.1645  0.690119
## age:Genotype   1  63.270  63.270  4.7618  0.043421 *
## Residuals     17 225.879  13.287
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
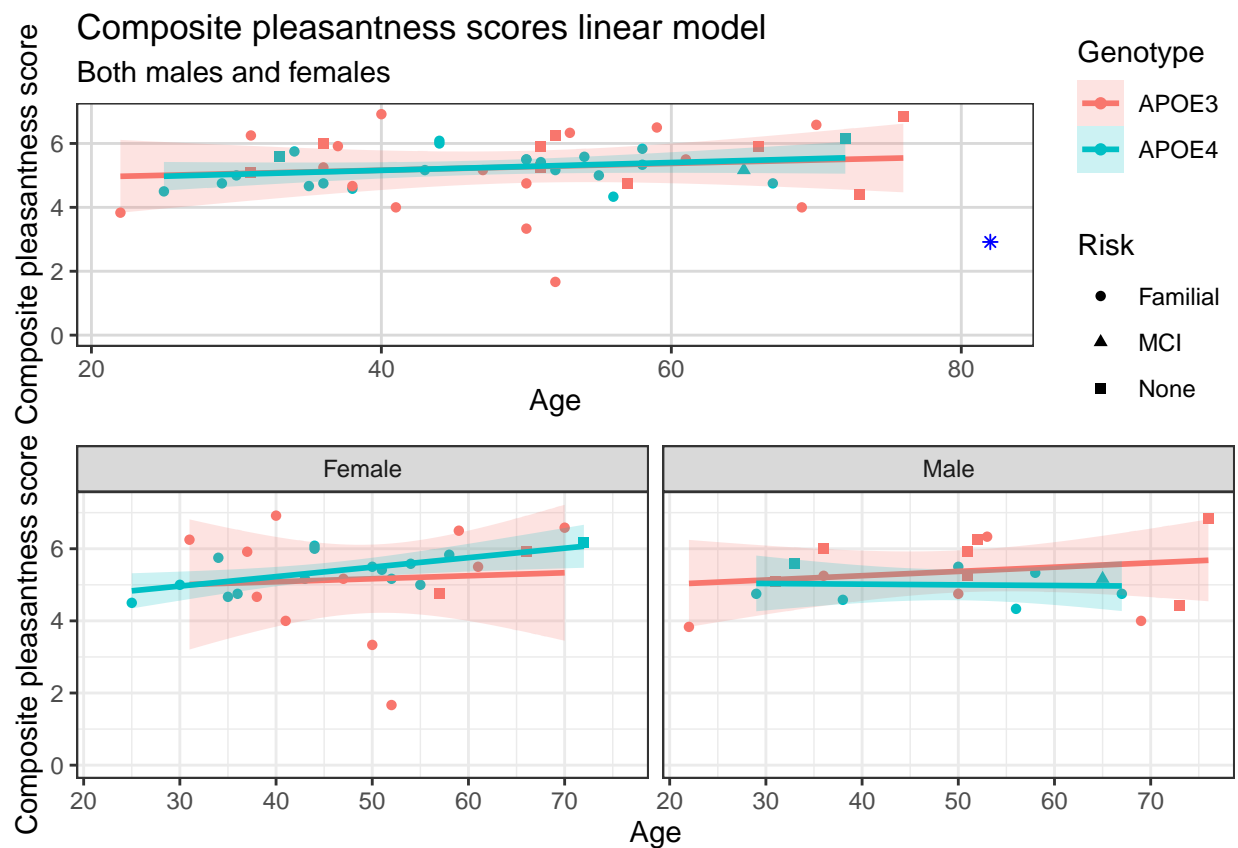

Composite pleasantness scores linear model

```
##
```

```
## Call:
## lm(formula = Composite_Pleasantness ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.5173 -0.4009  0.0243  0.6164  1.8325
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                4.751795   1.210013   3.927 0.000322 ***
## age                        0.008310   0.023600   0.352 0.726543
## GenotypeAPOE4             -0.576938   1.580451  -0.365 0.716953
## sexMale                    0.025213   1.528066   0.017 0.986915
## age:GenotypeAPOE4          0.017986   0.031996   0.562 0.577080
## age:sexMale                0.003567   0.029562   0.121 0.904541
## GenotypeAPOE4:sexMale      0.891535   2.263237   0.394 0.695681
## age:GenotypeAPOE4:sexMale -0.031714   0.044788  -0.708 0.482886
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9943 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.06971,    Adjusted R-squared:  -0.08912
## F-statistic: 0.4389 on 7 and 41 DF,  p-value: 0.8719


##
## Call:
## lm(formula = Composite_Pleasantness ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.5173 -0.3819  0.0173  0.6713  1.8325
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        4.75180    1.33830   3.551  0.00163 **
## age                0.00831    0.02610   0.318  0.75295
## GenotypeAPOE4     -0.57694    1.74801  -0.330  0.74422
## age:GenotypeAPOE4  0.01799    0.03539   0.508  0.61591
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.1 on 24 degrees of freedom
## Multiple R-squared:  0.06088,    Adjusted R-squared:  -0.05652
## F-statistic: 0.5186 on 3 and 24 DF,  p-value: 0.6735


##
## Call:
## lm(formula = Composite_Pleasantness ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.5965 -0.4380  0.0454  0.5339  1.1536
##
```

```
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        4.77701    0.77223   6.186 9.96e-06 ***
## age                0.01188    0.01473   0.806    0.431
## GenotypeAPOE4      0.31460    1.34058   0.235    0.817
## age:GenotypeAPOE4 -0.01373    0.02593  -0.529    0.603
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8228 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.08939,    Adjusted R-squared:  -0.07131
## F-statistic: 0.5563 on 3 and 17 DF,  p-value: 0.651


## Analysis of Variance Table
##
## Response: Composite_Pleasantness
##                  Df Sum Sq Mean Sq F value Pr(>F)
## age               1  1.110 1.10966  1.1225 0.2956
## Genotype          1  0.001 0.00087  0.0009 0.9765
## sex               1  0.063 0.06262  0.0633 0.8025
## age:Genotype      1  0.009 0.00883  0.0089 0.9252
## age:sex           1  0.138 0.13846  0.1401 0.7101
## Genotype:sex      1  1.221 1.22090  1.2351 0.2729
## age:Genotype:sex  1  0.496 0.49567  0.5014 0.4829
## Residuals        41 40.530 0.98854


## Analysis of Variance Table
##
## Response: Composite_Pleasantness
##              Df  Sum Sq Mean Sq F value Pr(>F)
## age           1  1.0221 1.02210  0.8452 0.3671
## Genotype      1  0.5468 0.54678  0.4522 0.5077
## age:Genotype  1  0.3124 0.31238  0.2583 0.6159
## Residuals    24 29.0223 1.20926


## Analysis of Variance Table
##
## Response: Composite_Pleasantness
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1 0.2714 0.27138  0.4009 0.5351
## Genotype      1 0.6686 0.66860  0.9877 0.3342
## age:Genotype  1 0.1897 0.18968  0.2802 0.6034
## Residuals    17 11.5079 0.67694
```
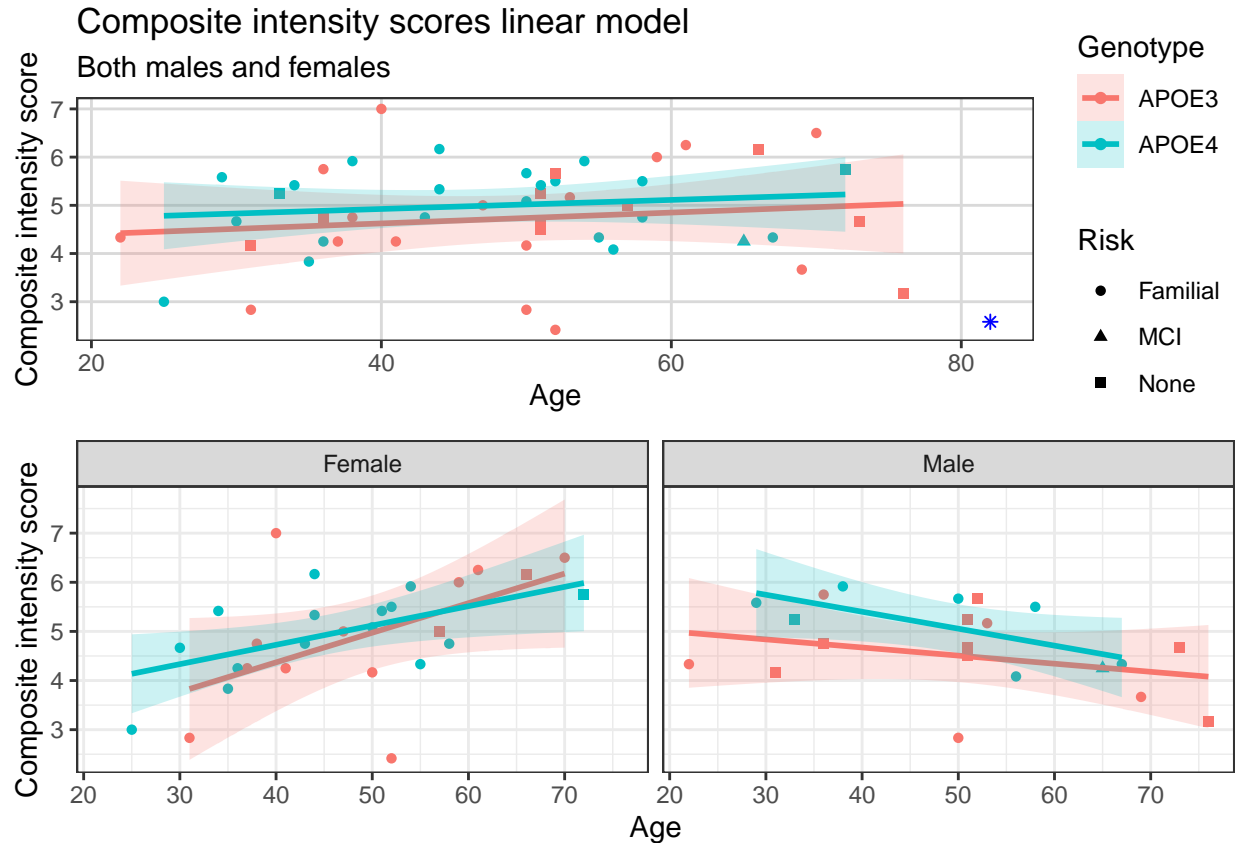
Composite intensity scores linear model


```
##
## Call:
## lm(formula = Composite_Intensity ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.6763 -0.5278  0.0115  0.5000  2.6296
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              1.961616   1.113084   1.762  0.08547 .
## age                      0.060219   0.021709   2.774  0.00830 **
## GenotypeAPOE4            1.192275   1.453849   0.820  0.41691
## sexMale                  3.370435   1.405660   2.398  0.02113 *
## age:GenotypeAPOE4       -0.020895   0.029433  -0.710  0.48177
## age:sexMale             -0.076707   0.027194  -2.821  0.00735 **
## GenotypeAPOE4:sexMale    0.257163   2.081940   0.124  0.90230
## age:GenotypeAPOE4:sexMale 0.002866  0.041200   0.070  0.94488
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9146 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2982, Adjusted R-squared:  0.1784
## F-statistic: 2.489 on 7 and 41 DF,  p-value: 0.03161
```

```
## 
## Call:
## lm(formula = Composite_Intensity ~ age * Genotype, data = combo_f)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -2.6763 -0.4668  0.1342  0.4582  2.6296 
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        1.96162    1.21029   1.621   0.1181  
## age                0.06022    0.02361   2.551   0.0175 *
## GenotypeAPOE4      1.19227    1.58082   0.754   0.4581  
## age:GenotypeAPOE4 -0.02090    0.03200  -0.653   0.5200  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.9945 on 24 degrees of freedom
## Multiple R-squared:  0.2904, Adjusted R-squared:  0.2017 
## F-statistic: 3.274 on 3 and 24 DF,  p-value: 0.03846


## 
## Call:
## lm(formula = Composite_Intensity ~ age * Genotype, data = combo_m)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -1.67435 -0.52775  0.00881  0.61101  1.19196 
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)    
## (Intercept)        5.33205    0.73978   7.208 1.47e-06 ***
## age               -0.01649    0.01411  -1.168    0.259    
## GenotypeAPOE4      1.44944    1.28424   1.129    0.275    
## age:GenotypeAPOE4 -0.01803    0.02484  -0.726    0.478    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.7882 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2849, Adjusted R-squared:  0.1587 
## F-statistic: 2.258 on 3 and 17 DF,  p-value: 0.1186


## Analysis of Variance Table
## 
## Response: Composite_Intensity
##                 Df Sum Sq Mean Sq F value   Pr(>F)    
## age              1  0.739  0.7388  0.8832 0.352839    
## Genotype         1  0.973  0.9726  1.1627 0.287220    
## sex              1  0.560  0.5604  0.6699 0.417828    
## age:Genotype     1  0.001  0.0009  0.0011 0.973984    
## age:sex          1 11.851 11.8508 14.1670 0.000525 ***
## Genotype:sex     1  0.448  0.4476  0.5351 0.468648    
## age:Genotype:sex 1  0.004  0.0040  0.0048 0.944877    
```

50

```
## Residuals          41 34.297  0.8365
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: Composite_Intensity
##             Df  Sum Sq Mean Sq F value   Pr(>F)
## age          1  9.0481  9.0481  9.1488 0.005852 **
## Genotype     1  0.2454  0.2454  0.2482 0.622896
## age:Genotype 1  0.4216  0.4216  0.4263 0.520021
## Residuals   24 23.7360  0.9890
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: Composite_Intensity
##             Df  Sum Sq Mean Sq F value  Pr(>F)
## age          1  2.3630 2.36303  3.8038 0.06782 .
## Genotype     1  1.5174 1.51744  2.4426 0.13650
## age:Genotype 1  0.3272 0.32715  0.5266 0.47790
## Residuals   17 10.5609 0.62123
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
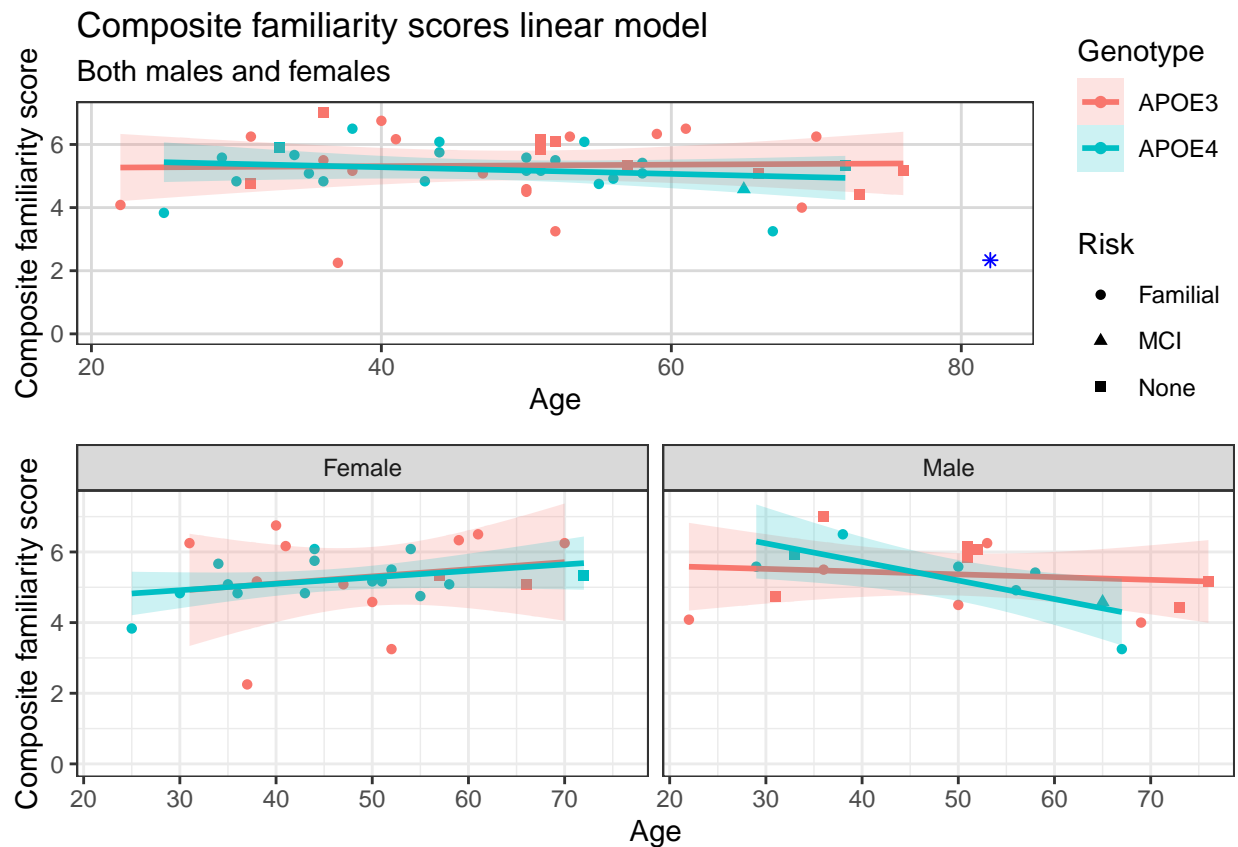

Composite familiarity scores linear model

```
## 
## Call:
## lm(formula = Composite_Familiarity ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.79759 -0.54794  0.02577  0.67665  1.64203
## 
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                4.302877   1.170078   3.677 0.000678 ***
## age                        0.020127   0.022821   0.882 0.382936
## GenotypeAPOE4              0.064319   1.528291   0.042 0.966635
## sexMale                    1.449700   1.477634   0.981 0.332300
## age:GenotypeAPOE4         -0.001837   0.030940  -0.059 0.952936
## age:sexMale               -0.027859   0.028586  -0.975 0.335488
## GenotypeAPOE4:sexMale      2.004268   2.188542   0.916 0.365127
## age:GenotypeAPOE4:sexMale -0.043005   0.043309  -0.993 0.326551
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.9614 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1357, Adjusted R-squared:  -0.01185
## F-statistic: 0.9197 on 7 and 41 DF,  p-value: 0.5014


## 
## Call:
## lm(formula = Composite_Familiarity ~ age * Genotype, data = combo_f)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.7976 -0.3462 -0.0988  0.6903  1.6420
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       4.302877   1.231153   3.495  0.00187 **
## age               0.020127   0.024012   0.838  0.41018
## GenotypeAPOE4     0.064319   1.608063   0.040  0.96843
## age:GenotypeAPOE4 -0.001837   0.032555  -0.056  0.95546
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.012 on 24 degrees of freedom
## Multiple R-squared:  0.05785,    Adjusted R-squared:  -0.05991
## F-statistic: 0.4913 on 3 and 24 DF,  p-value: 0.6917


## 
## Call:
## lm(formula = Composite_Familiarity ~ age * Genotype, data = combo_m)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.49914 -0.76289  0.03965  0.64480  1.52577
```
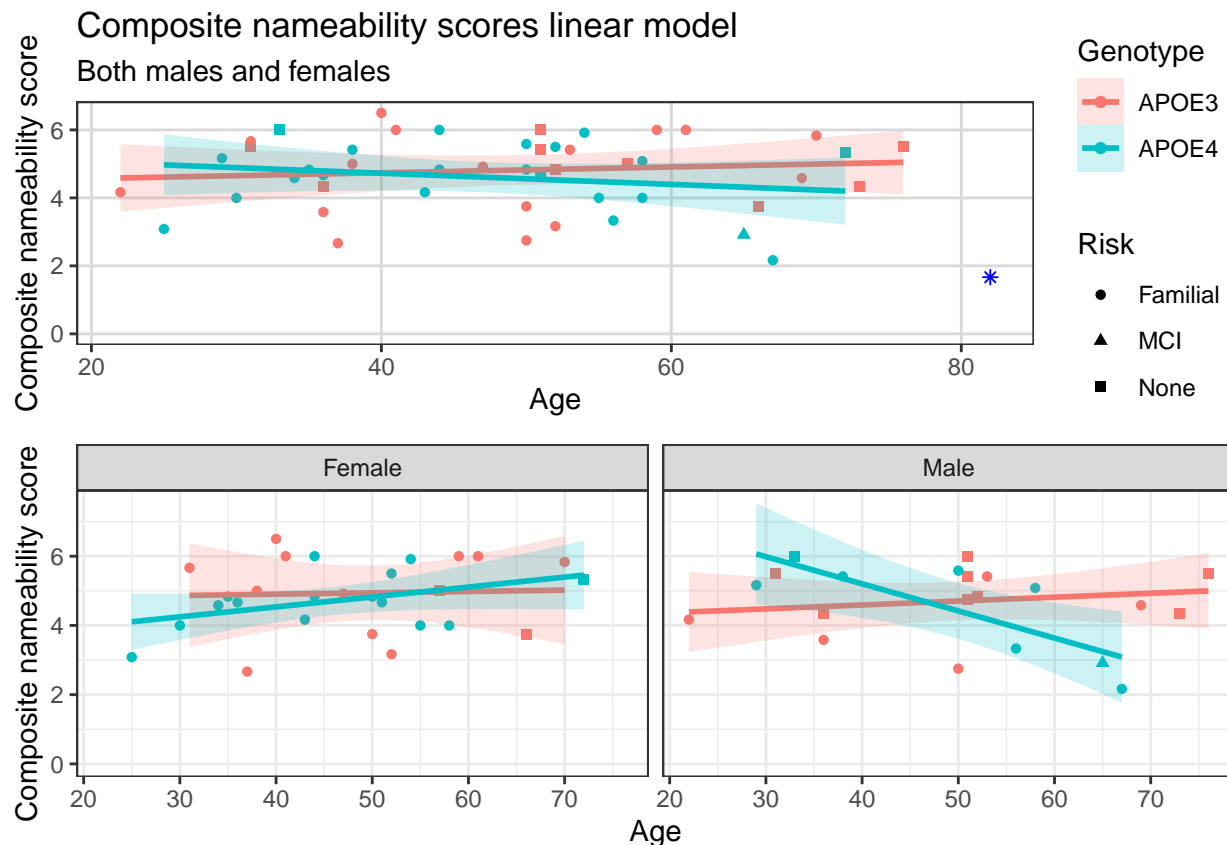
```
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)      5.752577   0.831368   6.919 2.48e-06 ***
## age             -0.007732   0.015860  -0.487    0.632
## GenotypeAPOE4    2.068587   1.443234   1.433    0.170
## age:GenotypeAPOE4 -0.044842  0.027920  -1.606    0.127
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8858 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2481, Adjusted R-squared:  0.1154
## F-statistic: 1.869 on 3 and 17 DF,  p-value: 0.1731


## Analysis of Variance Table
##
## Response: Composite_Familiarity
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1  0.058  0.0579  0.0626 0.80363
## Genotype         1  0.236  0.2355  0.2548 0.61644
## sex              1  0.025  0.0252  0.0272 0.86971
## age:Genotype     1  0.369  0.3692  0.3995 0.53088
## age:sex          1  4.327  4.3268  4.6809 0.03638 *
## Genotype:sex     1  0.025  0.0250  0.0270 0.87029
## age:Genotype:sex 1  0.911  0.9114  0.9860 0.32655
## Residuals       41 37.899  0.9244
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: Composite_Familiarity
##              Df  Sum Sq Mean Sq F value Pr(>F)
## age           1  1.5012 1.50119  1.4669 0.2376
## Genotype      1  0.0038 0.00379  0.0037 0.9520
## age:Genotype  1  0.0033 0.00326  0.0032 0.9555
## Residuals    24 24.5612 1.02338


## Analysis of Variance Table
##
## Response: Composite_Familiarity
##              Df  Sum Sq Mean Sq F value Pr(>F)
## age           1  2.2506 2.25061  2.8686 0.1086
## Genotype      1  0.1259 0.12586  0.1604 0.6938
## age:Genotype  1  2.0238 2.02382  2.5795 0.1267
## Residuals    17 13.3378 0.78458
```

Composite nameability scores linear model

```
##
## Call:
## lm(formula = Composite_Nameability ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.22570 -0.61578  0.03448  0.70114  1.59604
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             4.749386   1.196429   3.970 0.000283 ***
## age                     0.003864   0.023335   0.166 0.869281
## GenotypeAPOE4          -1.361723   1.562708  -0.871 0.388617
## sexMale                -0.608271   1.510911  -0.403 0.689345
## age:GenotypeAPOE4       0.024835   0.031637   0.785 0.436962
## age:sexMale             0.007399   0.029230   0.253 0.801444
## GenotypeAPOE4:sexMale   5.556885   2.237829   2.483 0.017204 *
## age:GenotypeAPOE4:sexMale -0.114440  0.044285  -2.584 0.013420 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9831 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2396, Adjusted R-squared:  0.1098
## F-statistic: 1.846 on 7 and 41 DF,  p-value: 0.1042
```
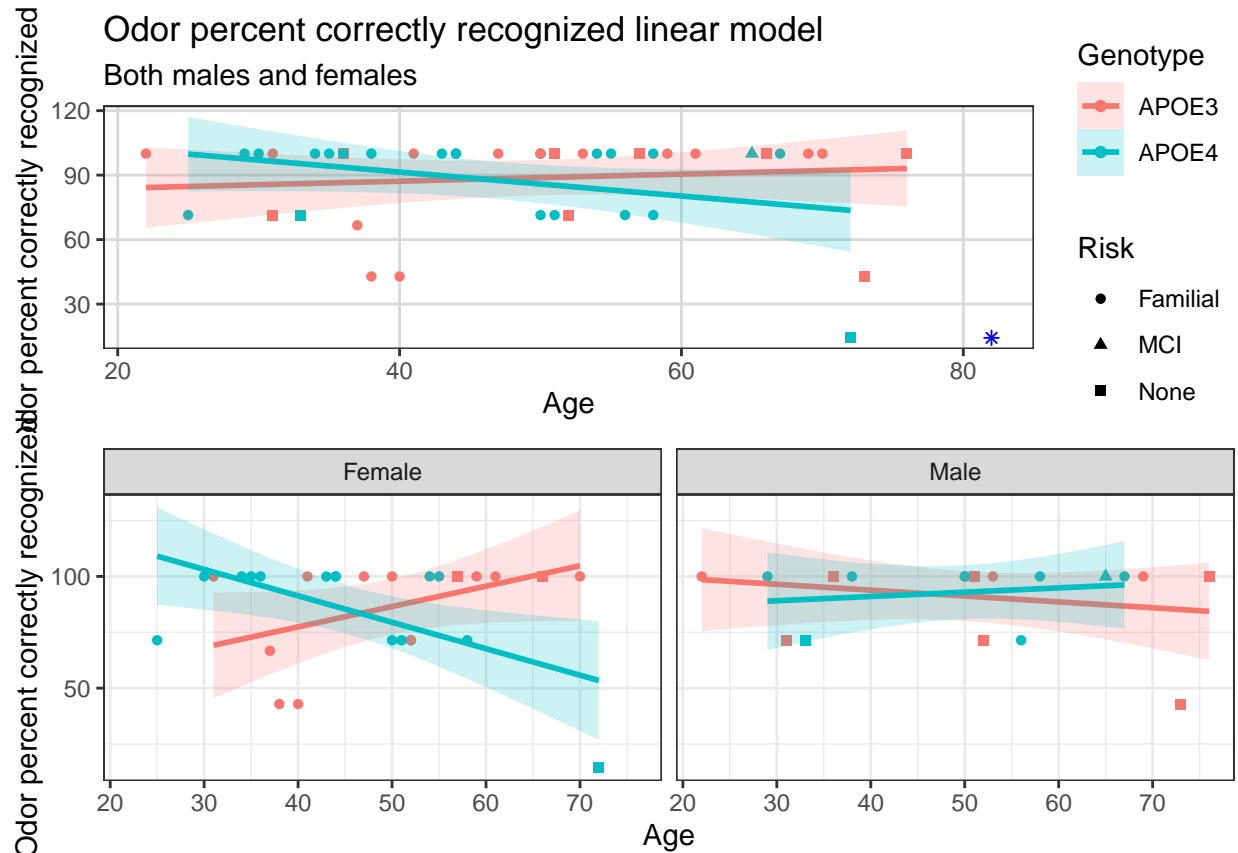
```
##
## Call:
## lm(formula = Composite_Nameability ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min      1Q  Median      3Q     Max
## -2.22570 -0.58284  0.06706  0.80147  1.59604
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       4.749386   1.246082   3.811 0.000847 ***
## age               0.003864   0.024303   0.159 0.874994
## GenotypeAPOE4    -1.361723   1.627562  -0.837 0.411035
## age:GenotypeAPOE4 0.024835   0.032950   0.754 0.458345
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.024 on 24 degrees of freedom
## Multiple R-squared:  0.08036,   Adjusted R-squared:  -0.03459
## F-statistic: 0.6991 on 3 and 24 DF,  p-value: 0.5618


##
## Call:
## lm(formula = Composite_Nameability ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min      1Q  Median      3Q     Max
## -1.95426 -0.61578  0.03448  0.67862  1.29091
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        4.14112    0.86578   4.783 0.000173 ***
## age                0.01126    0.01652   0.682 0.504486
## GenotypeAPOE4      4.19516    1.50297   2.791 0.012534 *
## age:GenotypeAPOE4 -0.08961    0.02908  -3.082 0.006763 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9224 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.4043, Adjusted R-squared:  0.2992
## F-statistic: 3.846 on 3 and 17 DF,  p-value: 0.02865
```

Odor percent correctly recognized linear model
Both males and females

```
##
## Call:
## lm(formula = Recognized ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -42.327  -6.863   4.163   9.560  30.822
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)               40.8875    22.8218   1.792  0.08058 .
## age                        0.9126     0.4451   2.050  0.04677 *
## GenotypeAPOE4             97.7702    29.8086   3.280  0.00212 **
## sexMale                   63.4836    28.8206   2.203  0.03329 *
## age:GenotypeAPOE4         -2.0962     0.6035  -3.474  0.00123 **
## age:sexMale               -1.1754     0.5576  -2.108  0.04117 *
## GenotypeAPOE4:sexMale   -118.8015    42.6865  -2.783  0.00810 **
## age:GenotypeAPOE4:sexMale   2.5514     0.8447   3.020  0.00433 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 18.75 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.266,  Adjusted R-squared:  0.1406
## F-statistic: 2.122 on 7 and 41 DF,  p-value: 0.06258
```

```
##
## Call:
## lm(formula = Recognized ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min      1Q  Median      3Q     Max
## -39.149  -7.144   2.178  13.423  30.822
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        40.8875    24.3027   1.682  0.10545
## age                 0.9126     0.4740   1.925  0.06612 .
## GenotypeAPOE4      97.7702    31.7428   3.080  0.00513 **
## age:GenotypeAPOE4  -2.0962     0.6426  -3.262  0.00330 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 19.97 on 24 degrees of freedom
## Multiple R-squared:  0.3181, Adjusted R-squared:  0.2329
## F-statistic: 3.732 on 3 and 24 DF,  p-value: 0.02473


##
## Call:
## lm(formula = Recognized ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min      1Q  Median      3Q     Max
## -42.327   1.411   5.509   9.034  15.605
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       104.3710    15.8490   6.585 4.63e-06 ***
## age                -0.2628     0.3024  -0.869    0.397
## GenotypeAPOE4     -21.0313    27.5135  -0.764    0.455
## age:GenotypeAPOE4   0.4551     0.5323   0.855    0.404
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.89 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared: 0.05532,    Adjusted R-squared:  -0.1114
## F-statistic: 0.3318 on 3 and 17 DF,  p-value: 0.8024


## Analysis of Variance Table
##
## Response: Recognized
##                  Df  Sum Sq Mean Sq F value    Pr(>F)
## age               1   166.0   166.0  0.4721  0.495885
## Genotype          1    34.8    34.8  0.0989  0.754758
## sex               1   499.8   499.8  1.4212  0.240056
## age:Genotype      1  1211.1  1211.1  3.4440  0.070681 .
## age:sex           1    13.2    13.2  0.0375  0.847332
## Genotype:sex      1    91.2    91.2  0.2595  0.613228
## age:Genotype:sex  1  3207.9  3207.9  9.1224  0.004333 **
```

```
## Residuals          41 14417.8    351.7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: Recognized
##              Df Sum Sq Mean Sq F value   Pr(>F)
## age           1  173.3   173.3  0.4346 0.516024
## Genotype      1   48.5    48.5  0.1217 0.730219
## age:Genotype  1 4243.2  4243.2 10.6406 0.003304 **
## Residuals    24 9570.5   398.8
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: Recognized
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1   63.0  63.014  0.2210 0.6443
## Genotype      1   12.4  12.381  0.0434 0.8374
## age:Genotype  1  208.5 208.467  0.7311 0.4044
## Residuals    17 4847.3 285.137
```
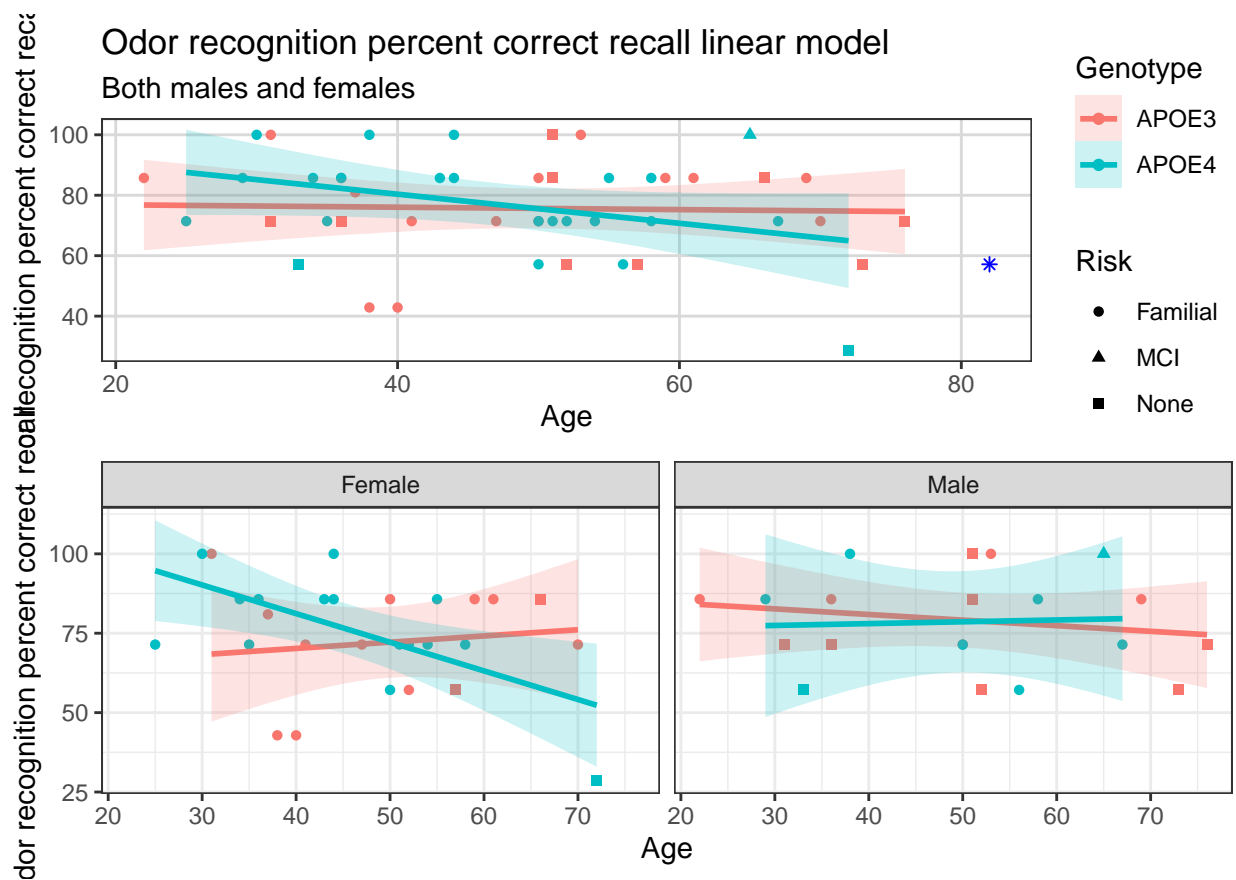

Odor recognition percent correct recall linear model
Both males and females

##

```
## Call:
## lm(formula = PrecentCorrectRecall ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -27.357 -11.060   1.069   9.934  31.553
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)                62.3631    19.5235   3.194   0.0027 **
## age                         0.1963     0.3808   0.515   0.6090
## GenotypeAPOE4              54.8840    25.5005   2.152   0.0373 *
## sexMale                    25.5973    24.6553   1.038   0.3053
## age:GenotypeAPOE4          -1.0979     0.5163  -2.127   0.0395 *
## age:sexMale                -0.3728     0.4770  -0.782   0.4390
## GenotypeAPOE4:sexMale     -67.1282    36.5172  -1.838   0.0733 .
## age:GenotypeAPOE4:sexMale   1.3321     0.7226   1.843   0.0725 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.04 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1764, Adjusted R-squared:  0.03578
## F-statistic: 1.254 on 7 and 41 DF,  p-value: 0.2966


##
## Call:
## lm(formula = PrecentCorrectRecall ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -27.357 -14.450   1.044  10.630  31.553
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        62.3631    19.7503   3.158  0.00426 **
## age                 0.1963     0.3852   0.510  0.61505
## GenotypeAPOE4      54.8840    25.7967   2.128  0.04385 *
## age:GenotypeAPOE4  -1.0979     0.5222  -2.102  0.04620 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.23 on 24 degrees of freedom
## Multiple R-squared:  0.2314, Adjusted R-squared:  0.1354
## F-statistic: 2.409 on 3 and 24 DF,  p-value: 0.09191


##
## Call:
## lm(formula = PrecentCorrectRecall ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -21.803 -10.177   1.637   8.325  22.092
##
```

```
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        87.9604    14.8066   5.941 1.61e-05 ***
## age                -0.1765     0.2825  -0.625    0.540
## GenotypeAPOE4      -12.2442    25.7040  -0.476    0.640
## age:GenotypeAPOE4    0.2342     0.4973   0.471    0.644
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 15.78 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.02391,    Adjusted R-squared:  -0.1483
## F-statistic: 0.1388 on 3 and 17 DF,  p-value: 0.9354


## Analysis of Variance Table
##
## Response: PrecentCorrectRecall
##                 Df  Sum Sq Mean Sq F value Pr(>F)
## age              1   470.0  470.00  1.8263 0.1840
## Genotype         1     5.4    5.39  0.0209 0.8857
## sex              1   336.5  336.46  1.3074 0.2595
## age:Genotype     1   468.1  468.11  1.8190 0.1848
## age:sex          1    92.4   92.37  0.3589 0.5524
## Genotype:sex     1    13.0   12.99  0.0505 0.8234
## age:Genotype:sex 1   874.5  874.55  3.3982 0.0725 .
## Residuals       41 10551.5  257.35
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: PrecentCorrectRecall
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1  704.5  704.53  2.6751 0.1150
## Genotype      1   34.7   34.65  0.1316 0.7200
## age:Genotype  1 1164.0 1164.04  4.4198 0.0462 *
## Residuals    24 6320.8  263.37
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: PrecentCorrectRecall
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1   46.6  46.589  0.1872 0.6707
## Genotype      1    1.8   1.828  0.0073 0.9327
## age:Genotype  1   55.2  55.205  0.2218 0.6436
## Residuals    17 4230.7 248.864
```
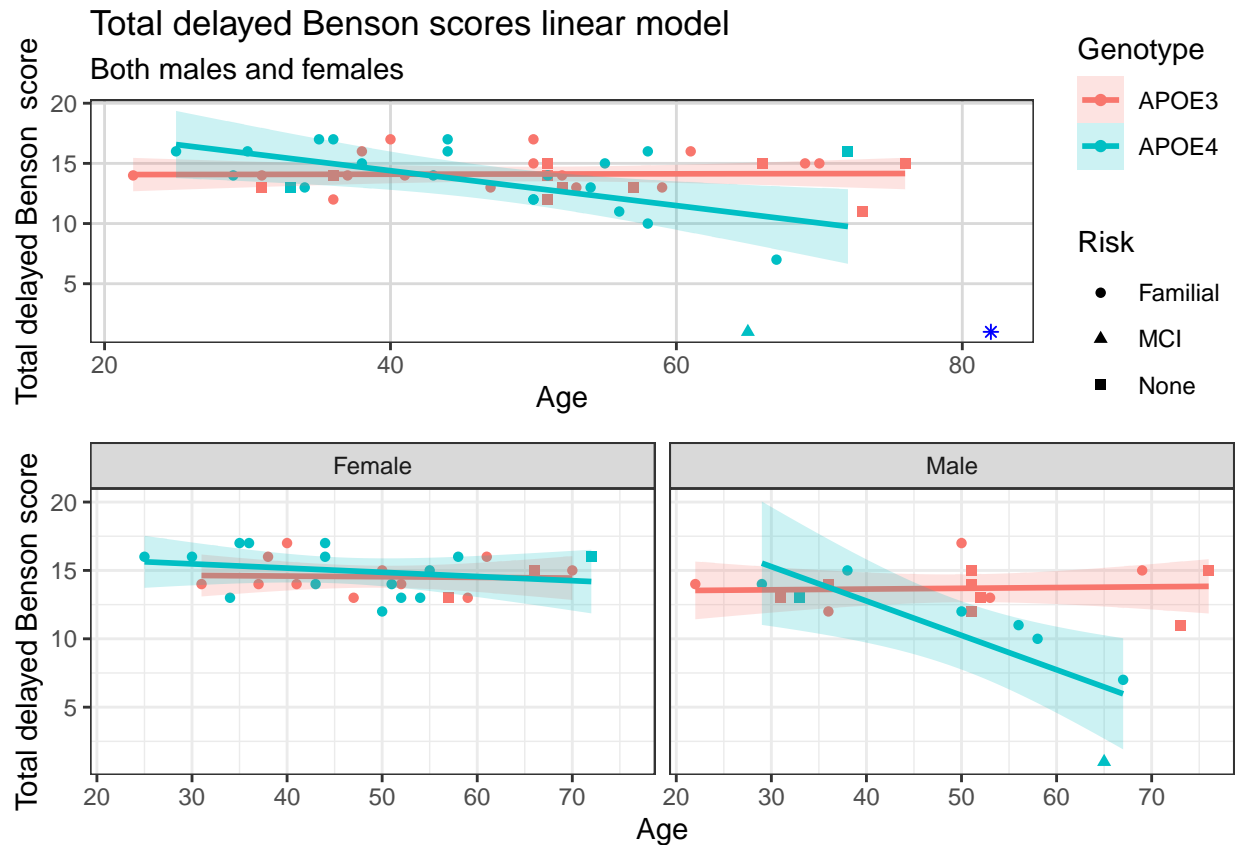
Total delayed Benson scores linear model

Both males and females

```
##
## Call:
## lm(formula = Delay_BensonTotal ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.4791 -1.4952  0.3698  1.3826  3.3081
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)             14.776458   2.231666   6.621 5.66e-08 ***
## age                     -0.004767   0.043526  -0.110  0.91332
## GenotypeAPOE4            1.621105   2.914878   0.556  0.58113
## sexMale                 -1.362040   2.818262  -0.483  0.63146
## age:GenotypeAPOE4       -0.025926   0.059011  -0.439  0.66272
## age:sexMale              0.010317   0.054522   0.189  0.85086
## GenotypeAPOE4:sexMale    7.781099   4.174162   1.864  0.06948 .
## age:GenotypeAPOE4:sexMale -0.230969  0.082603  -2.796  0.00784 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.834 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.6133, Adjusted R-squared:  0.5473
## F-statistic:  9.29 on 7 and 41 DF,  p-value: 7.733e-07
```

```
##
## Call:
## lm(formula = Delay_BensonTotal ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -2.8629 -1.1821  0.3302  1.3882  2.4142
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      14.776458   1.878744   7.865 4.26e-08 ***
## age              -0.004767   0.036642  -0.130    0.898
## GenotypeAPOE4     1.621105   2.453911   0.661    0.515
## age:GenotypeAPOE4 -0.025926   0.049679  -0.522    0.607
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.544 on 24 degrees of freedom
## Multiple R-squared:  0.05796,    Adjusted R-squared:  -0.0598
## F-statistic: 0.4922 on 3 and 24 DF,  p-value: 0.691


##
## Call:
## lm(formula = Delay_BensonTotal ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -5.4791 -1.5222  0.3858  1.3026  3.3081
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      13.414418   2.044601   6.561 4.85e-06 ***
## age               0.005549   0.039006   0.142  0.88854
## GenotypeAPOE4     9.402204   3.549376   2.649  0.01688 *
## age:GenotypeAPOE4 -0.256895   0.068665  -3.741  0.00163 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.178 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.6479, Adjusted R-squared:  0.5858
## F-statistic: 10.43 on 3 and 17 DF,  p-value: 0.0003976


## Analysis of Variance Table
##
## Response: Delay_BensonTotal
##                 Df Sum Sq Mean Sq F value    Pr(>F)
## age              1 28.627  28.627  8.5133  0.005699 **
## Genotype         1 10.046  10.046  2.9876  0.091432 .
## sex              1 68.671  68.671 20.4221 5.188e-05 ***
## age:Genotype     1 37.637  37.637 11.1929  0.001765 **
## age:sex          1 12.865  12.865  3.8260  0.057300 .
## Genotype:sex     1 34.529  34.529 10.2686  0.002620 **
## age:Genotype:sex 1 26.290  26.290  7.8183  0.007837 **
```
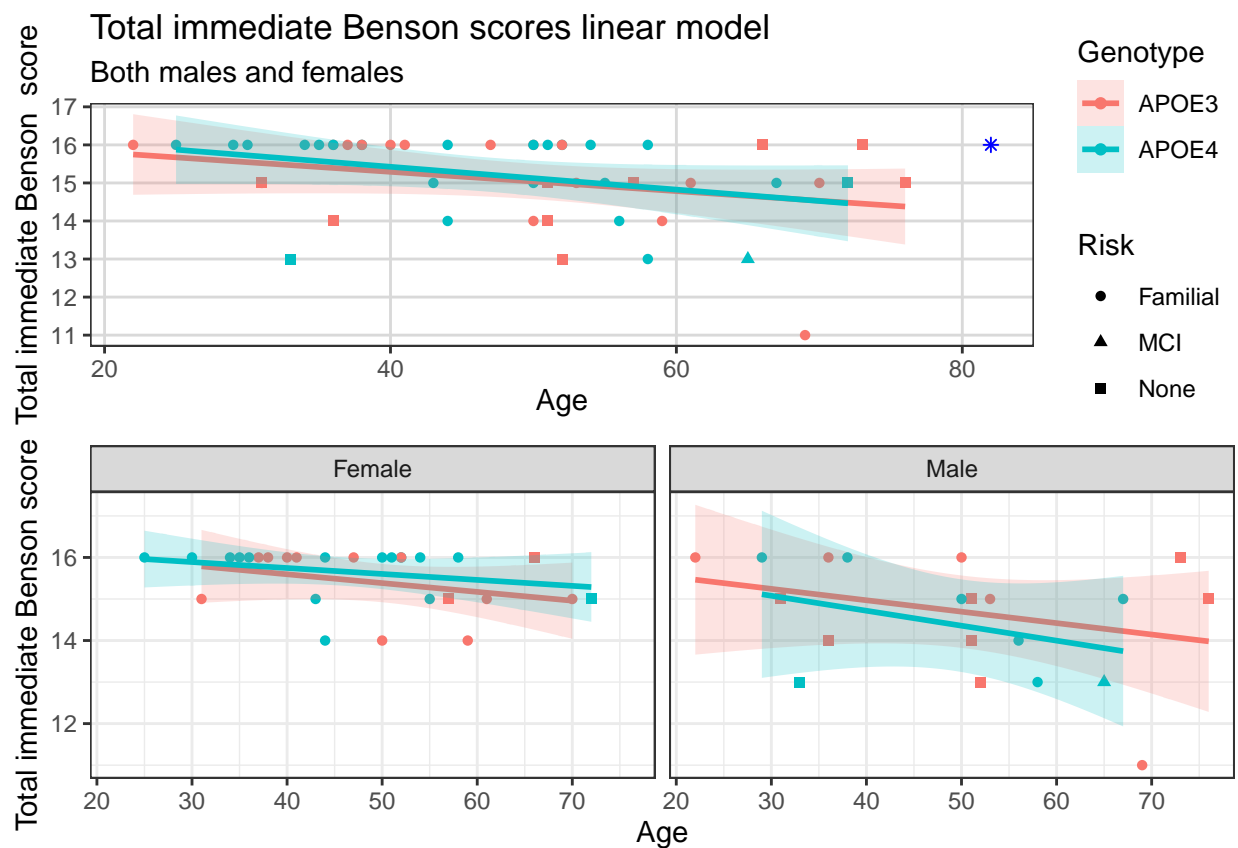
```
## Residuals          41 137.866    3.363
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Delay_BensonTotal
##                Df Sum Sq Mean Sq F value Pr(>F)
## age             1  1.904 1.90440  0.7991 0.3802
## Genotype        1  0.965 0.96547  0.4051 0.5305
## age:Genotype    1  0.649 0.64904  0.2723 0.6065
## Residuals      24 57.195 2.38314

## Analysis of Variance Table
##
## Response: Delay_BensonTotal
##                Df Sum Sq Mean Sq F value   Pr(>F)
## age             1 26.096  26.096  5.4992 0.031422 *
## Genotype        1 55.955  55.955 11.7915 0.003167 **
## age:Genotype    1 66.422  66.422 13.9974 0.001625 **
## Residuals      17 80.670   4.745
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Total immediate Benson scores linear model
Both males and females

##

```
## Call:
## lm(formula = Im_BensonTotal ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.1724 -0.5311  0.3114  0.5119  1.9375
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)               16.442619   1.254170  13.110 2.97e-16 ***
## age                       -0.021193   0.024461  -0.866    0.391
## GenotypeAPOE4             -0.123756   1.638127  -0.076    0.940
## sexMale                   -0.374450   1.583830  -0.236    0.814
## age:GenotypeAPOE4          0.006869   0.033164   0.207    0.837
## age:sexMale               -0.006282   0.030641  -0.205    0.839
## GenotypeAPOE4:sexMale      0.212720   2.345830   0.091    0.928
## age:GenotypeAPOE4:sexMale -0.015397   0.046422  -0.332    0.742
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.031 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2893, Adjusted R-squared:  0.1679
## F-statistic: 2.384 on 7 and 41 DF,  p-value: 0.03844


##
## Call:
## lm(formula = Im_BensonTotal ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.6886 -0.2479  0.1896  0.4152  0.9561
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       16.442619   0.830579  19.797 2.26e-16 ***
## age               -0.021193   0.016199  -1.308    0.203
## GenotypeAPOE4     -0.123756   1.084856  -0.114    0.910
## age:GenotypeAPOE4  0.006869   0.021963   0.313    0.757
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6825 on 24 degrees of freedom
## Multiple R-squared:  0.1377, Adjusted R-squared:  0.02996
## F-statistic: 1.278 on 3 and 24 DF,  p-value: 0.3045


##
## Call:
## lm(formula = Im_BensonTotal ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.1724 -0.8170  0.3331  0.9209  1.9375
##
```

```
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)       16.068169   1.295031  12.408 6.03e-10 ***
## age               -0.027475   0.024706  -1.112    0.282
## GenotypeAPOE4      0.088964   2.248142   0.040    0.969
## age:GenotypeAPOE4 -0.008528   0.043491  -0.196    0.847
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.38 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1287,	Adjusted R-squared:  -0.02509
## F-statistic: 0.8368 on 3 and 17 DF,  p-value: 0.4922


## Analysis of Variance Table
##
## Response: Im_BensonTotal
##                 Df Sum Sq Mean Sq F value   Pr(>F)
## age              1  6.696  6.6959  6.3050 0.016076 *
## Genotype         1  0.108  0.1076  0.1013 0.751861
## sex              1  9.718  9.7181  9.1506 0.004279 **
## age:Genotype     1  0.000  0.0002  0.0002 0.990139
## age:sex          1  0.261  0.2611  0.2459 0.622657
## Genotype:sex     1  0.823  0.8233  0.7753 0.383730
## age:Genotype:sex 1  0.117  0.1168  0.1100 0.741826
## Residuals       41 43.542  1.0620
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: Im_BensonTotal
##              Df  Sum Sq Mean Sq F value  Pr(>F)
## age           1  1.4560 1.45602  3.1260 0.08976 .
## Genotype      1  0.2841 0.28410  0.6099 0.44245
## age:Genotype  1  0.0456 0.04556  0.0978 0.75716
## Residuals    24 11.1786 0.46578
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: Im_BensonTotal
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1  4.151  4.1512  2.1806 0.1580
## Genotype      1  0.555  0.5547  0.2914 0.5963
## age:Genotype  1  0.073  0.0732  0.0384 0.8469
## Residuals    17 32.364  1.9037
```
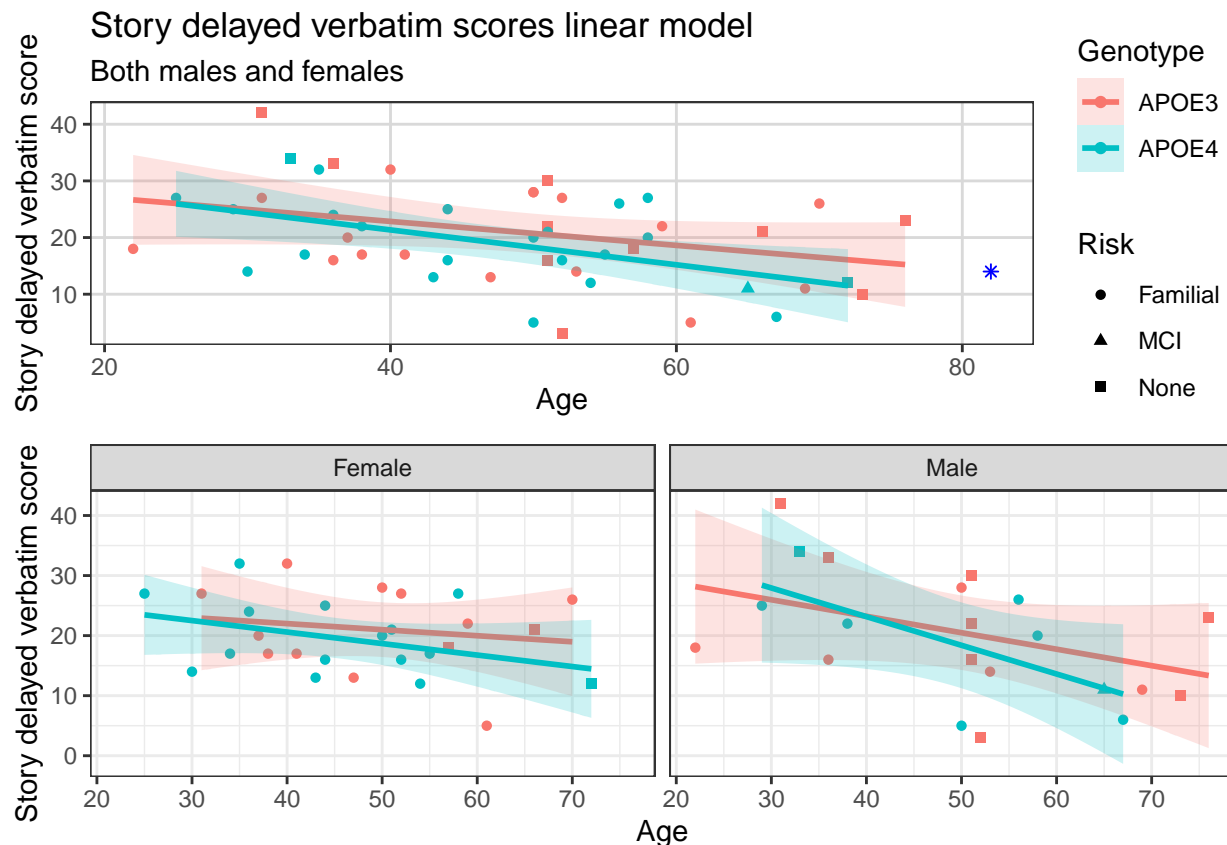
Story delayed verbatim scores linear model

Both males and females


```
## 
## Call:
## lm(formula = Delayed_verbatim ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -16.9341  -4.7404  -0.7217   6.2095  16.3060 
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)  
## (Intercept)              26.03471    9.73204   2.675   0.0107 *
## age                      -0.10085    0.18981  -0.531   0.5981  
## GenotypeAPOE4             2.21225   12.71145   0.174   0.8627  
## sexMale                   8.16198   12.29012   0.664   0.5103  
## age:GenotypeAPOE4        -0.09052    0.25734  -0.352   0.7268  
## age:sexMale              -0.17343    0.23776  -0.729   0.4699  
## GenotypeAPOE4:sexMale     5.85015   18.20304   0.321   0.7496  
## age:GenotypeAPOE4:sexMale -0.11266    0.36022  -0.313   0.7561  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 7.997 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2115, Adjusted R-squared:  0.07685 
## F-statistic: 1.571 on 7 and 41 DF,  p-value: 0.1715
```

```
## 
## Call:
## lm(formula = Delayed_verbatim ~ age * Genotype, data = combo_f)
## 
## Residuals:
##      Min      1Q  Median      3Q     Max
## -14.8829  -4.7803   0.2999   4.3620  10.4509
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       26.03471    8.15684   3.192  0.00392 **
## age               -0.10085    0.15909  -0.634  0.53213
## GenotypeAPOE4      2.21225   10.65401   0.208  0.83726
## age:GenotypeAPOE4 -0.09052    0.21569  -0.420  0.67846
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 6.702 on 24 degrees of freedom
## Multiple R-squared:  0.09303,    Adjusted R-squared:  -0.02034
## F-statistic: 0.8206 on 3 and 24 DF,  p-value: 0.4953


## 
## Call:
## lm(formula = Delayed_verbatim ~ age * Genotype, data = combo_m)
## 
## Residuals:
##     Min     1Q  Median      3Q     Max
## -16.934  -4.271  -2.116   7.517  16.306
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        34.1967     8.9441   3.823  0.00136 **
## age                -0.2743     0.1706  -1.607  0.12637
## GenotypeAPOE4       8.0624    15.5267   0.519  0.61027
## age:GenotypeAPOE4  -0.2032     0.3004  -0.676  0.50788
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 9.529 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2765, Adjusted R-squared:  0.1489
## F-statistic: 2.166 on 3 and 17 DF,  p-value: 0.1296


## Analysis of Variance Table
## 
## Response: Delayed_verbatim
##                 Df  Sum Sq Mean Sq F value   Pr(>F)
## age              1  512.72  512.72  8.0178 0.007147 **
## Genotype         1   63.34   63.34  0.9905 0.325446
## sex              1    0.65    0.65  0.0102 0.920121
## age:Genotype     1   18.99   18.99  0.2969 0.588755
## age:sex          1  100.83  100.83  1.5768 0.216337
## Genotype:sex     1    0.36    0.36  0.0056 0.940871
## age:Genotype:sex 1    6.25    6.25  0.0978 0.756063
```
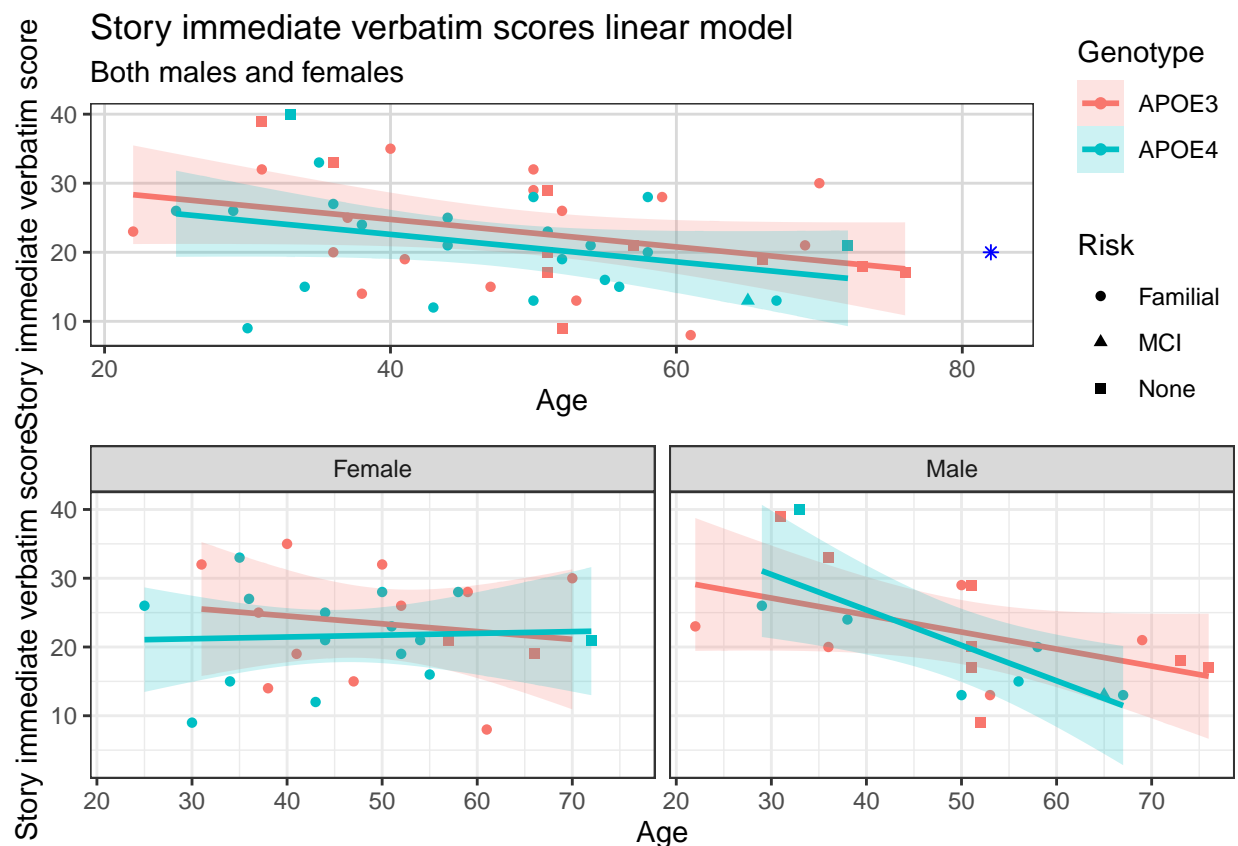
```
## Residuals         41 2621.84    63.95
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: Delayed_verbatim
##              Df  Sum Sq Mean Sq F value Pr(>F)
## age           1   72.26  72.261  1.6086 0.2169
## Genotype      1   30.42  30.416  0.6771 0.4187
## age:Genotype  1    7.91   7.912  0.1761 0.6785
## Residuals    24 1078.13  44.922


## Analysis of Variance Table
##
## Response: Delayed_verbatim
##              Df  Sum Sq Mean Sq F value  Pr(>F)
## age           1  528.10  528.10  5.8156 0.02748 *
## Genotype      1   20.45   20.45  0.2252 0.64112
## age:Genotype  1   41.55   41.55  0.4575 0.50788
## Residuals    17 1543.71   90.81
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Story immediate verbatim scores linear model
Both males and females

```
##
```

```
## Call:
## lm(formula = Immediate_verbatim ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -14.1326  -5.3932   0.1547   5.6485  12.1294
##
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  29.0273     9.0170   3.219  0.00252 **
## age                          -0.1130     0.1759  -0.643  0.52400
## GenotypeAPOE4                -8.6142    11.7775  -0.731  0.46869
## sexMale                       5.5081    11.3871   0.484  0.63117
## age:GenotypeAPOE4             0.1391     0.2384   0.583  0.56284
## age:sexMale                  -0.1342     0.2203  -0.609  0.54570
## GenotypeAPOE4:sexMale        20.0949    16.8656   1.191  0.24032
## age:GenotypeAPOE4:sexMale    -0.4073     0.3338  -1.220  0.22928
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.409 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2255, Adjusted R-squared:  0.09323
## F-statistic: 1.705 on 7 and 41 DF,  p-value: 0.1348


##
## Call:
## lm(formula = Immediate_verbatim ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -14.1326  -5.5066  -0.2027   5.7551  11.6746
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        29.0273     9.2303   3.145  0.00439 **
## age                -0.1130     0.1800  -0.628  0.53603
## GenotypeAPOE4      -8.6142    12.0561  -0.715  0.48181
## age:GenotypeAPOE4   0.1391     0.2441   0.570  0.57405
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.584 on 24 degrees of freedom
## Multiple R-squared:  0.03244,    Adjusted R-squared:  -0.0885
## F-statistic: 0.2683 on 3 and 24 DF,  p-value: 0.8476


##
## Call:
## lm(formula = Immediate_verbatim ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -12.6784  -5.0673   0.4899   3.8816  12.1294
##
```

```
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        34.5354     6.7151   5.143 8.13e-05 ***
## age                -0.2473     0.1281  -1.930   0.0705 .
## GenotypeAPOE4      11.4808    11.6573   0.985   0.3385
## age:GenotypeAPOE4  -0.2682     0.2255  -1.189   0.2506
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.154 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.4077, Adjusted R-squared:  0.3032
## F-statistic: 3.901 on 3 and 17 DF,  p-value: 0.02737


## Analysis of Variance Table
##
## Response: Immediate_verbatim
##                  Df  Sum Sq Mean Sq F value  Pr(>F)
## age               1  312.35 312.351  5.6899 0.02177 *
## Genotype          1   56.48  56.483  1.0289 0.31637
## sex               1    7.61   7.615  0.1387 0.71148
## age:Genotype      1    0.04   0.037  0.0007 0.97951
## age:sex           1  196.80 196.798  3.5849 0.06538 .
## Genotype:sex      1    0.14   0.142  0.0026 0.95969
## age:Genotype:sex  1   81.76  81.762  1.4894 0.22928
## Residuals        41 2250.73  54.896
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: Immediate_verbatim
##              Df  Sum Sq Mean Sq F value Pr(>F)
## age           1    2.05   2.050  0.0356 0.8519
## Genotype      1   25.56  25.562  0.4444 0.5114
## age:Genotype  1   18.68  18.682  0.3248 0.5741
## Residuals    24 1380.56  57.523


## Analysis of Variance Table
##
## Response: Immediate_verbatim
##              Df Sum Sq Mean Sq F value  Pr(>F)
## age           1 509.78  509.78  9.9593 0.00577 **
## Genotype      1  16.88   16.88  0.3297 0.57333
## age:Genotype  1  72.41   72.41  1.4147 0.25063
## Residuals    17 870.17   51.19
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
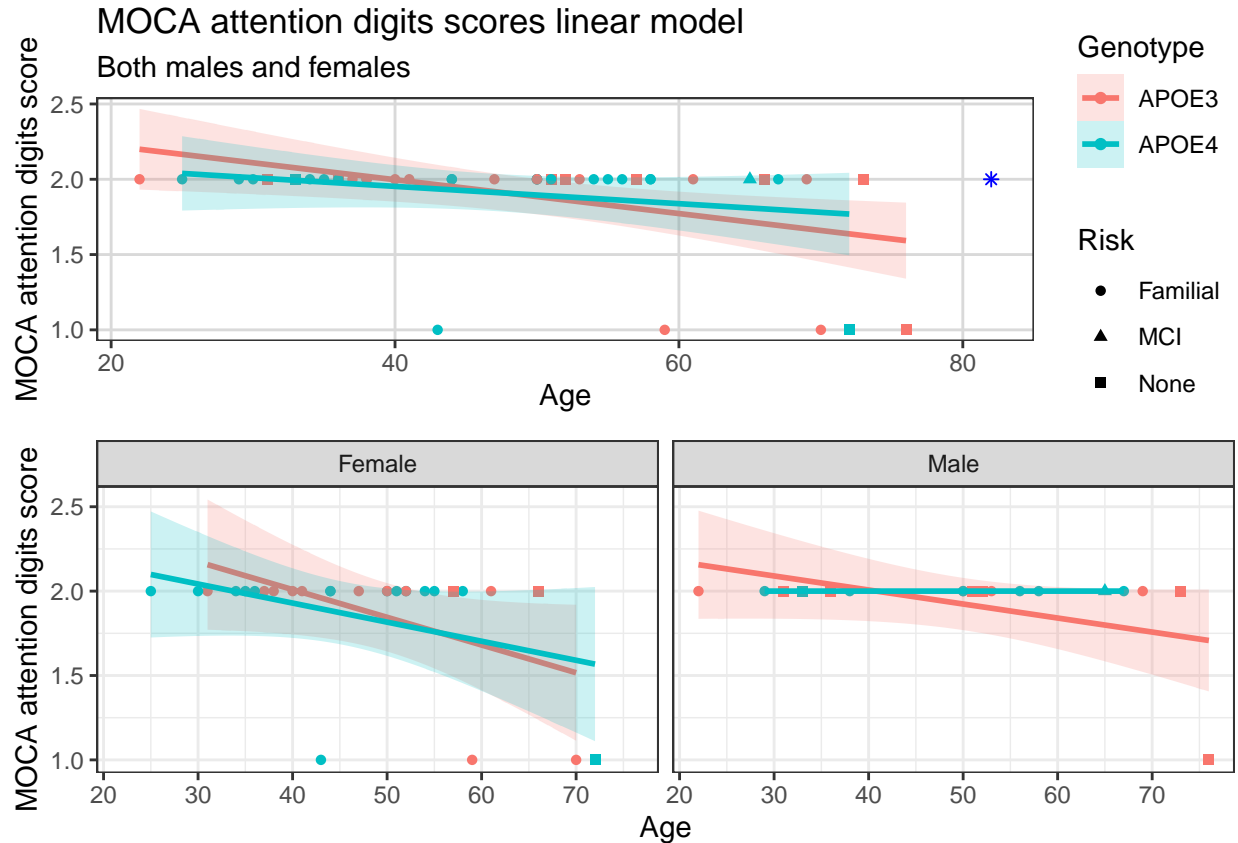
MOCA attention digits scores linear model
Both males and females

```
##
## Call:
## lm(formula = MOCA_Attention_Digits ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.89530 -0.04008  0.00728  0.15511  0.41792
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              2.666161   0.349631   7.626 2.19e-09 ***
## age                     -0.016425   0.006819  -2.409   0.0206 *
## GenotypeAPOE4           -0.284904   0.456669  -0.624   0.5362
## sexMale                 -0.326867   0.441532  -0.740   0.4633
## age:GenotypeAPOE4        0.005124   0.009245   0.554   0.5824
## age:sexMale              0.008114   0.008542   0.950   0.3477
## GenotypeAPOE4:sexMale   -0.054389   0.653959  -0.083   0.9341
## age:GenotypeAPOE4:sexMale  0.003188   0.012941   0.246   0.8067
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2873 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2463, Adjusted R-squared:  0.1176
## F-statistic: 1.914 on 7 and 41 DF,  p-value: 0.09197
```

```
##
## Call:
## lm(formula = MOCA_Attention_Digits ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.89530 -0.04627  0.06571  0.19794  0.41792
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       2.666161   0.406401   6.560 8.73e-07 ***
## age              -0.016425   0.007926  -2.072   0.0491 *
## GenotypeAPOE4    -0.284904   0.530818  -0.537   0.5964
## age:GenotypeAPOE4 0.005124   0.010746   0.477   0.6378
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3339 on 24 degrees of freedom
## Multiple R-squared:  0.2194, Adjusted R-squared:  0.1218
## F-statistic: 2.249 on 3 and 24 DF,  p-value: 0.1085


##
## Call:
## lm(formula = MOCA_Attention_Digits ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.7076  0.0000  0.0000  0.0846  0.2675
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       2.339294   0.191492  12.216 7.65e-10 ***
## age              -0.008312   0.003653  -2.275   0.0361 *
## GenotypeAPOE4    -0.339294   0.332425  -1.021   0.3217
## age:GenotypeAPOE4 0.008312   0.006431   1.292   0.2135
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.204 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.257,  Adjusted R-squared:  0.1259
## F-statistic:  1.96 on 3 and 17 DF,  p-value: 0.1583


## Analysis of Variance Table
##
## Response: MOCA_Attention_Digits
##                 Df Sum Sq Mean Sq F value    Pr(>F)
## age              1 0.6861 0.68614  8.3134 0.006241 **
## Genotype         1 0.0000 0.00001  0.0002 0.990218
## sex              1 0.1653 0.16526  2.0023 0.164615
## age:Genotype     1 0.0497 0.04971  0.6023 0.442174
## age:sex          1 0.1707 0.17072  2.0685 0.157960
## Genotype:sex     1 0.0290 0.02904  0.3518 0.556343
## age:Genotype:sex 1 0.0050 0.00501  0.0607 0.806674
```
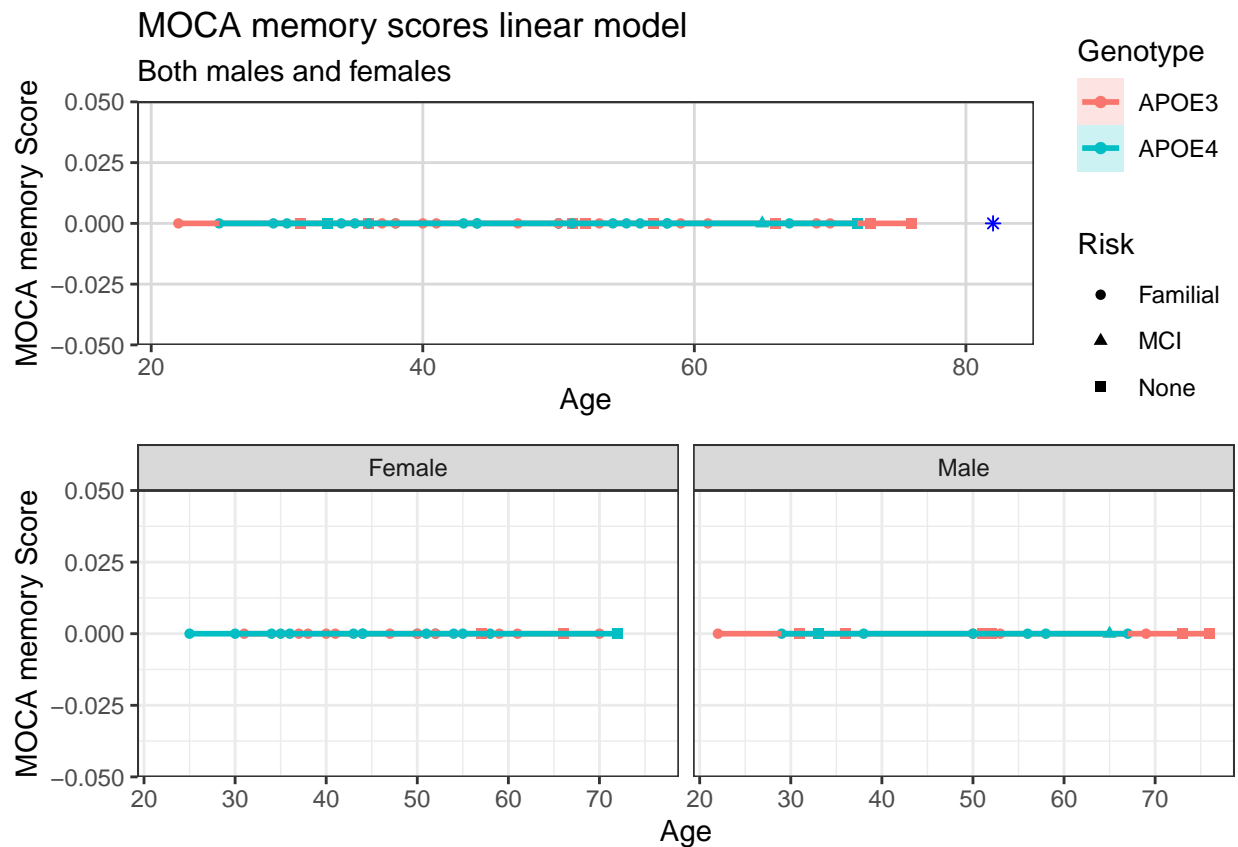
```
## Residuals          41 3.3839 0.08253
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: MOCA_Attention_Digits
##              Df  Sum Sq Mean Sq F value  Pr(>F)
## age           1 0.71650 0.71650  6.4253 0.01818 *
## Genotype      1 0.01043 0.01043  0.0935 0.76241
## age:Genotype  1 0.02535 0.02535  0.2274 0.63781
## Residuals    24 2.67630 0.11151
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: MOCA_Attention_Digits
##              Df  Sum Sq  Mean Sq F value  Pr(>F)
## age           1 0.14836 0.148364  3.5643 0.07622 .
## Genotype      1 0.02687 0.026872  0.6456 0.43279
## age:Genotype  1 0.06953 0.069529  1.6704 0.21350
## Residuals    17 0.70762 0.041624
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


MOCA memory scores linear model

```
## 
## Call:
## lm(formula = MOCA_Memory ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##    Min     1Q Median     3Q    Max
##      0      0      0      0      0
## 
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)                      0          0     NaN      NaN
## age                              0          0     NaN      NaN
## GenotypeAPOE4                    0          0     NaN      NaN
## sexMale                          0          0     NaN      NaN
## age:GenotypeAPOE4                0          0     NaN      NaN
## age:sexMale                      0          0     NaN      NaN
## GenotypeAPOE4:sexMale            0          0     NaN      NaN
## age:GenotypeAPOE4:sexMale        0          0     NaN      NaN
## 
## Residual standard error: 0 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:    NaN,  Adjusted R-squared:    NaN
## F-statistic:   NaN on 7 and 41 DF,  p-value: NA


## 
## Call:
## lm(formula = MOCA_Memory ~ age * Genotype, data = combo_f)
## 
## Residuals:
##    Min     1Q Median     3Q    Max
##      0      0      0      0      0
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)              0          0     NaN      NaN
## age                      0          0     NaN      NaN
## GenotypeAPOE4            0          0     NaN      NaN
## age:GenotypeAPOE4        0          0     NaN      NaN
## 
## Residual standard error: 0 on 24 degrees of freedom
## Multiple R-squared:    NaN,  Adjusted R-squared:    NaN
## F-statistic:   NaN on 3 and 24 DF,  p-value: NA


## 
## Call:
## lm(formula = MOCA_Memory ~ age * Genotype, data = combo_m)
## 
## Residuals:
##    Min     1Q Median     3Q    Max
##      0      0      0      0      0
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)              0          0     NaN      NaN
```

```
## age                        0            0       NaN       NaN
## GenotypeAPOE4               0            0       NaN       NaN
## age:GenotypeAPOE4           0            0       NaN       NaN
##
## Residual standard error: 0 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:    NaN,  Adjusted R-squared:    NaN
## F-statistic:   NaN on 3 and 17 DF,  p-value: NA


## Analysis of Variance Table
##
## Response: MOCA_Memory
##                   Df Sum Sq Mean Sq F value Pr(>F)
## age                1     0        0      NaN     NaN
## Genotype           1     0        0      NaN     NaN
## sex                1     0        0      NaN     NaN
## age:Genotype       1     0        0      NaN     NaN
## age:sex            1     0        0      NaN     NaN
## Genotype:sex       1     0        0      NaN     NaN
## age:Genotype:sex   1     0        0      NaN     NaN
## Residuals         41     0        0


## Analysis of Variance Table
##
## Response: MOCA_Memory
##             Df Sum Sq Mean Sq F value Pr(>F)
## age          1     0        0      NaN     NaN
## Genotype     1     0        0      NaN     NaN
## age:Genotype 1     0        0      NaN     NaN
## Residuals   24     0        0


## Analysis of Variance Table
##
## Response: MOCA_Memory
##             Df Sum Sq Mean Sq F value Pr(>F)
## age          1     0        0      NaN     NaN
## Genotype     1     0        0      NaN     NaN
## age:Genotype 1     0        0      NaN     NaN
## Residuals   17     0        0
```
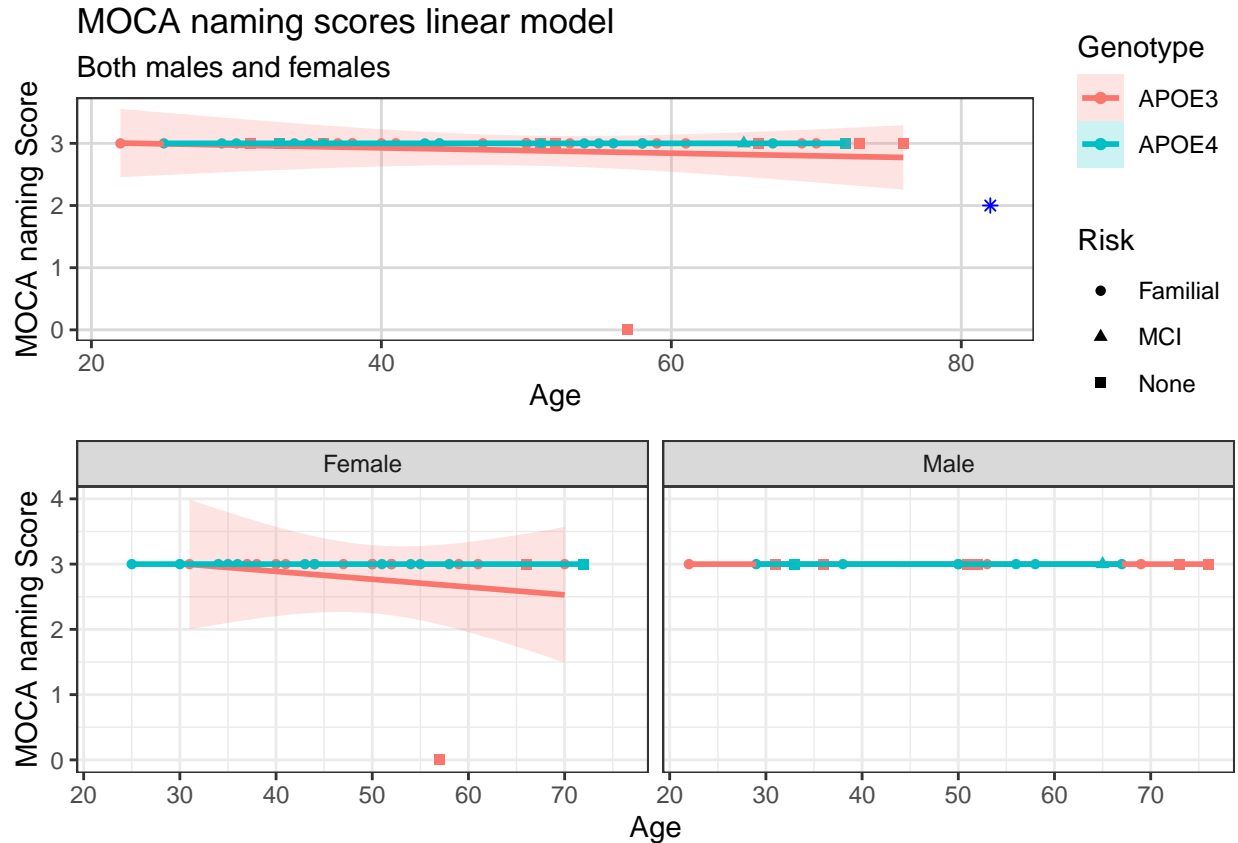
MOCA naming scores linear model
Both males and females

```
##
## Call:
## lm(formula = MOCA_Naming ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.6846  0.0000  0.0000  0.0000  0.4709
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)               3.36639    0.53939   6.241 1.96e-07 ***
## age                      -0.01196    0.01052  -1.137    0.262
## GenotypeAPOE4            -0.36639    0.70452  -0.520    0.606
## sexMale                  -0.36639    0.68116  -0.538    0.594
## age:GenotypeAPOE4         0.01196    0.01426   0.839    0.407
## age:sexMale               0.01196    0.01318   0.908    0.369
## GenotypeAPOE4:sexMale     0.36639    1.00888   0.363    0.718
## age:GenotypeAPOE4:sexMale -0.01196    0.01996  -0.599    0.552
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4432 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.0865, Adjusted R-squared:  -0.06947
## F-statistic: 0.5546 on 7 and 41 DF,  p-value: 0.7878
```

```
##
## Call:
## lm(formula = MOCA_Naming ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.6846  0.0000  0.0000  0.1420  0.4709
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        3.36639    0.70499   4.775 7.36e-05 ***
## age               -0.01196    0.01375  -0.870    0.393
## GenotypeAPOE4     -0.36639    0.92082  -0.398    0.694
## age:GenotypeAPOE4  0.01196    0.01864   0.642    0.527
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5793 on 24 degrees of freedom
## Multiple R-squared:  0.072,  Adjusted R-squared:  -0.044
## F-statistic: 0.6207 on 3 and 24 DF,  p-value: 0.6085


##
## Call:
## lm(formula = MOCA_Naming ~ age * Genotype, data = combo_m)
##
## Residuals:
##        Min         1Q     Median         3Q        Max
## -1.012e-15 -2.793e-16  0.000e+00  0.000e+00  2.728e-15
##
## Coefficients:
##                    Estimate Std. Error    t value Pr(>|t|)
## (Intercept)       3.000e+00  7.586e-16  3.955e+15   <2e-16 ***
## age              -3.664e-17  1.447e-17 -2.532e+00   0.0215 *
## GenotypeAPOE4    -2.148e-15  1.317e-15 -1.631e+00   0.1213
## age:GenotypeAPOE4 3.664e-17  2.548e-17  1.438e+00   0.1685
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.082e-16 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.4986, Adjusted R-squared:  0.4102
## F-statistic: 5.636 on 3 and 17 DF,  p-value: 0.007199


## Analysis of Variance Table
##
## Response: MOCA_Naming
##                 Df Sum Sq  Mean Sq F value Pr(>F)
## age              1 0.0739 0.073880  0.3761 0.5431
## Genotype         1 0.1400 0.140000  0.7127 0.4034
## sex              1 0.2068 0.206827  1.0529 0.3109
## age:Genotype     1 0.0269 0.026944  0.1372 0.7130
## age:sex          1 0.1105 0.110492  0.5625 0.4575
## Genotype:sex     1 0.1339 0.133933  0.6818 0.4137
## age:Genotype:sex 1 0.0705 0.070510  0.3590 0.5524
```

```
## Residuals        41 8.0537 0.196433


## Analysis of Variance Table
##
## Response: MOCA_Naming
##               Df Sum Sq Mean Sq F value Pr(>F)
## age            1 0.1987 0.19869  0.5921 0.4491
## Genotype       1 0.2880 0.28799  0.8582 0.3635
## age:Genotype   1 0.1382 0.13816  0.4117 0.5272
## Residuals     24 8.0537 0.33557


## Analysis of Variance Table
##
## Response: MOCA_Naming
##               Df     Sum Sq    Mean Sq F value  Pr(>F)
## age            1 2.7907e-30 2.7907e-30  4.2723 0.05432 .
## Genotype       1 5.3070e-31 5.3068e-31  0.8124 0.38000
## age:Genotype   1 1.3512e-30 1.3512e-30  2.0685 0.16853
## Residuals     17 1.1105e-29 6.5322e-31
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
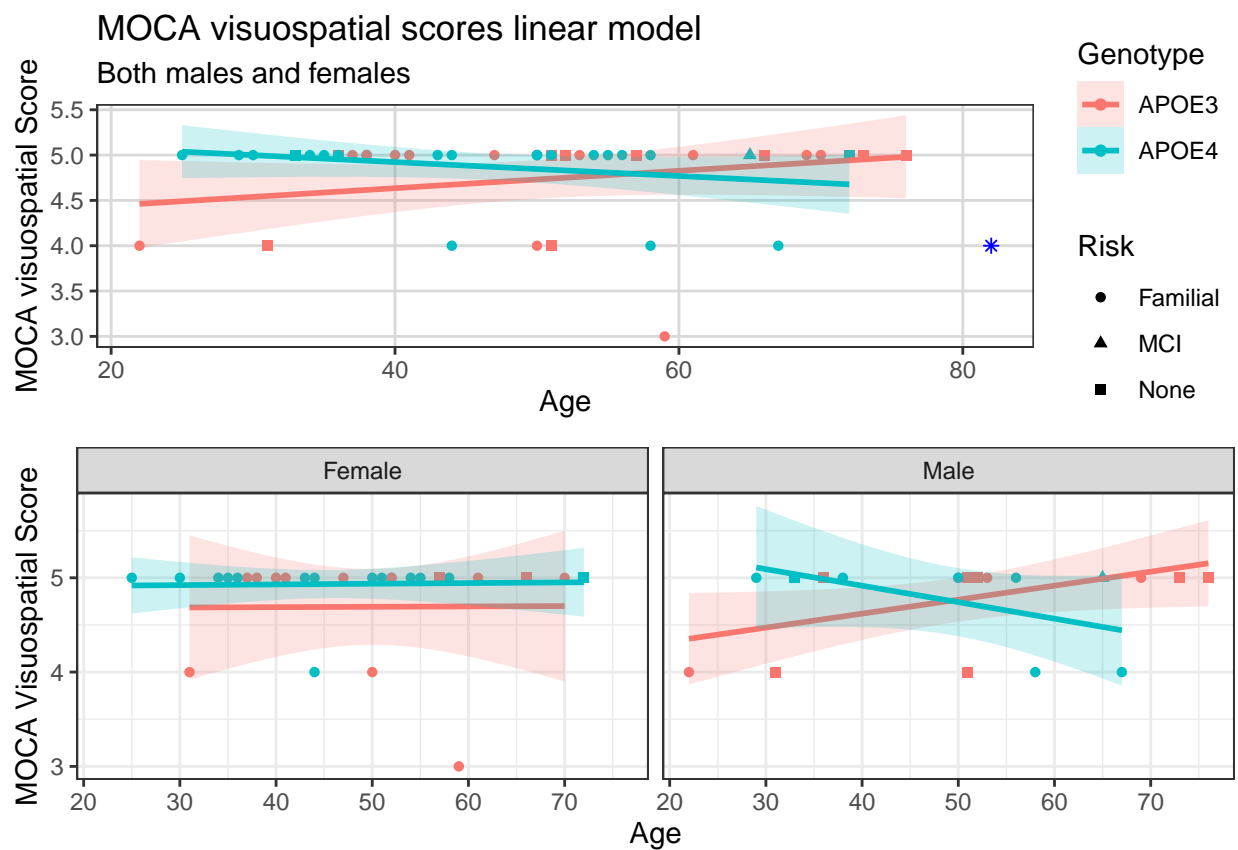

MOCA visuospatial scores linear model

```
##
## Call:
## lm(formula = MOCA_Visuospatial ~ age * Genotype * sex, data = geno_combined)
```

```
##
## Residuals:
##      Min      1Q   Median      3Q     Max
## -1.69585 -0.04972  0.07357  0.30142  0.52120
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              4.672835   0.549832   8.499 1.38e-10 ***
## age                      0.000390   0.010724   0.036    0.971
## GenotypeAPOE4            0.227530   0.718160   0.317    0.753
## sexMale                 -0.645878   0.694356  -0.930    0.358
## age:GenotypeAPOE4        0.000334   0.014539   0.023    0.982
## age:sexMale              0.014433   0.013433   1.074    0.289
## GenotypeAPOE4:sexMale    1.361597   1.028419   1.324    0.193
## age:GenotypeAPOE4:sexMale -0.032653  0.020352  -1.604    0.116
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4518 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1597, Adjusted R-squared:  0.01623
## F-statistic: 1.113 on 7 and 41 DF,  p-value: 0.3735


##
## Call:
## lm(formula = MOCA_Visuospatial ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min      1Q   Median      3Q     Max
## -1.69585  0.06036  0.07393  0.30376  0.31273
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       4.672835   0.593157   7.878 4.14e-08 ***
## age               0.000390   0.011569   0.034    0.973
## GenotypeAPOE4     0.227530   0.774749   0.294    0.772
## age:GenotypeAPOE4 0.000334   0.015685   0.021    0.983
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4874 on 24 degrees of freedom
## Multiple R-squared:  0.06647,    Adjusted R-squared:  -0.05022
## F-statistic: 0.5696 on 3 and 24 DF,  p-value: 0.6404


##
## Call:
## lm(formula = MOCA_Visuospatial ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min      1Q   Median      3Q     Max
## -0.78291 -0.15348  0.04879  0.23191  0.52120
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)        4.026957   0.371796  10.831 4.75e-09 ***
## age                0.014823   0.007093   2.090   0.0520 .
## GenotypeAPOE4       1.589126   0.645429   2.462   0.0248 *
## age:GenotypeAPOE4  -0.032319   0.012486  -2.588   0.0191 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3961 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2998, Adjusted R-squared:  0.1762
## F-statistic: 2.426 on 3 and 17 DF,  p-value: 0.1011


## Analysis of Variance Table
##
## Response: MOCA_Visuospatial
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1 0.0210 0.02099  0.1028 0.75009
## Genotype         1 0.2550 0.25504  1.2495 0.27015
## sex              1 0.0218 0.02177  0.1067 0.74563
## age:Genotype     1 0.6135 0.61350  3.0057 0.09049 .
## age:sex          1 0.0016 0.00163  0.0080 0.92912
## Genotype:sex     1 0.1521 0.15209  0.7451 0.39305
## age:Genotype:sex 1 0.5255 0.52545  2.5743 0.11629
## Residuals       41 8.3687 0.20411
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: MOCA_Visuospatial
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1 0.0066 0.00657  0.0276 0.8693
## Genotype      1 0.3993 0.39928  1.6808 0.2071
## age:Genotype  1 0.0001 0.00011  0.0005 0.9832
## Residuals    24 5.7012 0.23755


## Analysis of Variance Table
##
## Response: MOCA_Visuospatial
##              Df  Sum Sq Mean Sq F value  Pr(>F)
## age           1 0.08933 0.08933  0.5693 0.46086
## Genotype      1 0.00138 0.00138  0.0088 0.92638
## age:Genotype  1 1.05130 1.05130  6.6999 0.01913 *
## Residuals    17 2.66752 0.15691
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
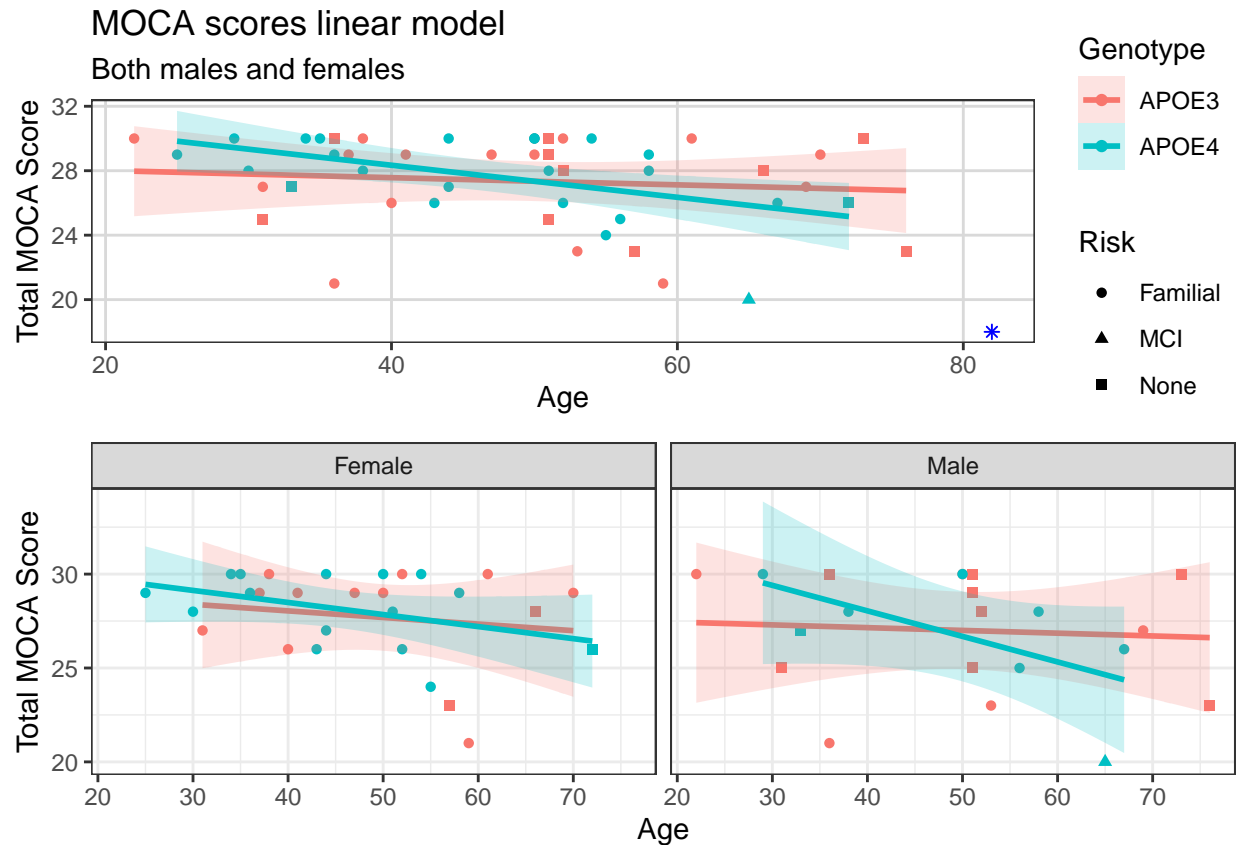
MOCA scores linear model
Both males and females

```
##
## Call:
## lm(formula = MOCA_TOTAL ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##    Min    1Q Median    3Q    Max
## -6.374 -1.718  0.854  2.013  3.338
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              29.44483    3.32985    8.843 4.77e-11 ***
## age                      -0.03510    0.06494   -0.541    0.592
## GenotypeAPOE4             1.61407    4.34926    0.371    0.712
## sexMale                  -1.70626    4.20510   -0.406    0.687
## age:GenotypeAPOE4        -0.02915    0.08805   -0.331    0.742
## age:sexMale               0.02036    0.08135    0.250    0.804
## GenotypeAPOE4:sexMale     4.12616    6.22823    0.662    0.511
## age:GenotypeAPOE4:sexMale -0.09204    0.12325   -0.747    0.459
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.736 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.148,  Adjusted R-squared:  0.002514
## F-statistic: 1.017 on 7 and 41 DF,  p-value: 0.4337
```

```
##
## Call:
## lm(formula = MOCA_TOTAL ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.374 -1.263   0.863   1.693   2.696
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        29.44483    2.89250  10.180 3.47e-10 ***
## age                -0.03510    0.05641  -0.622    0.540
## GenotypeAPOE4       1.61407    3.77802   0.427    0.673
## age:GenotypeAPOE4  -0.02915    0.07649  -0.381    0.707
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.377 on 24 degrees of freedom
## Multiple R-squared:  0.08308,    Adjusted R-squared:  -0.03153
## F-statistic: 0.7249 on 3 and 24 DF,  p-value: 0.5471


##
## Call:
## lm(formula = MOCA_TOTAL ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.2076 -1.9929  0.4633  2.5859  3.3381
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        27.73857    2.97995   9.308 4.38e-08 ***
## age                -0.01475    0.05685  -0.259    0.798
## GenotypeAPOE4       5.74023    5.17312   1.110    0.283
## age:GenotypeAPOE4  -0.12119    0.10008  -1.211    0.242
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.175 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1424, Adjusted R-squared:  -0.008976
## F-statistic: 0.9407 on 3 and 17 DF,  p-value: 0.4428


## Analysis of Variance Table
##
## Response: MOCA_TOTAL
##                 Df  Sum Sq Mean Sq F value Pr(>F)
## age              1  27.298 27.2981  3.6464 0.0632 .
## Genotype         1   0.219  0.2190  0.0293 0.8650
## sex              1   9.479  9.4795  1.2663 0.2670
## age:Genotype     1  11.060 11.0599  1.4774 0.2311
## age:sex          1   0.702  0.7017  0.0937 0.7610
## Genotype:sex     1   0.376  0.3764  0.0503 0.8237
## age:Genotype:sex 1   4.175  4.1748  0.5577 0.4595
```

```
## Residuals       41 306.935  7.4862
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## Analysis of Variance Table
##
## Response: MOCA_TOTAL
##              Df  Sum Sq Mean Sq F value Pr(>F)
## age           1  11.146 11.1460  1.9731 0.1729
## Genotype      1   0.318  0.3179  0.0563 0.8145
## age:Genotype  1   0.820  0.8203  0.1452 0.7065
## Residuals    24 135.573  5.6489


## Analysis of Variance Table
##
## Response: MOCA_TOTAL
##              Df  Sum Sq Mean Sq F value Pr(>F)
## age           1  13.275 13.2746  1.3169 0.2670
## Genotype      1   0.391  0.3911  0.0388 0.8462
## age:Genotype  1  14.781 14.7812  1.4664 0.2425
## Residuals    17 171.363 10.0802
```