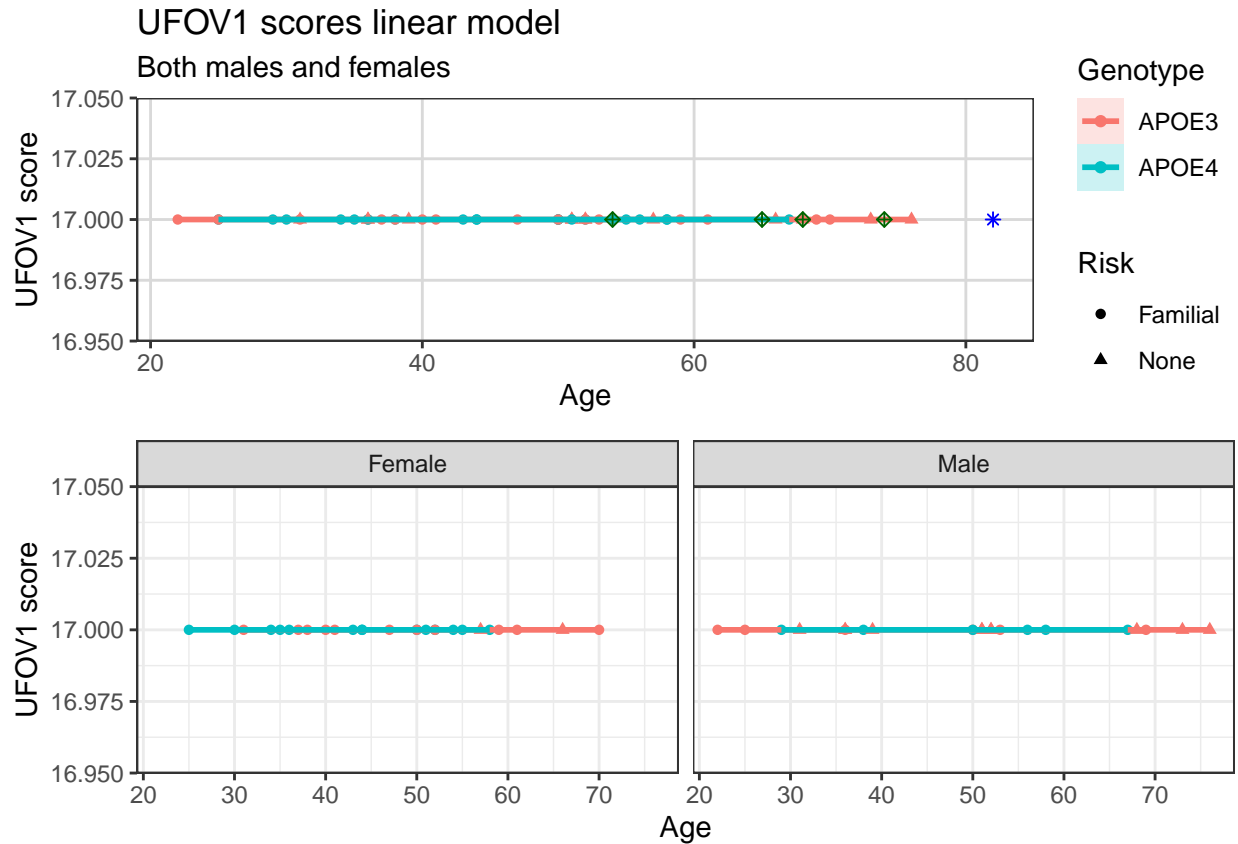# Linear models with AD subject

Anna MacFarlane

Note: blue stars on upper plots denote subject with AD, and green squares indicate subjects with MCI


```
##
## Call:
## lm(formula = ufov1 ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##        Min         1Q     Median         3Q        Max
## -1.729e-14  0.000e+00  0.000e+00  0.000e+00  8.825e-14
##
## Coefficients:
##                     Estimate Std. Error    t value Pr(>|t|)
## (Intercept)        1.700e+01  1.768e-14  9.613e+14   <2e-16 ***
## age               -5.052e-16  3.449e-16 -1.465e+00    0.150
## GenotypeAPOE4     -3.295e-14  2.494e-14 -1.321e+00    0.194
## sexMale           -3.295e-14  2.094e-14 -1.574e+00    0.123
```

```
## age:GenotypeAPOE4          5.052e-16  5.229e-16  9.660e-01    0.339
## age:sexMale                5.052e-16  4.095e-16  1.234e+00    0.224
## GenotypeAPOE4:sexMale      3.295e-14  3.630e-14  9.080e-01    0.369
## age:GenotypeAPOE4:sexMale -5.052e-16  7.342e-16 -6.880e-01    0.495
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.453e-14 on 42 degrees of freedom
##   (3 observations deleted due to missingness)
## Multiple R-squared:  0.5058, Adjusted R-squared:  0.4234
## F-statistic:  6.14 on 7 and 42 DF,  p-value: 5.639e-05


##
## 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
## -6.796e-15 -2.775e-15 -1.022e-15  0.000e+00  2.666e-14
##
## Coefficients:
##                    Estimate Std. Error    t value Pr(>|t|)
## (Intercept)       1.700e+01  5.336e-15  3.186e+15   <2e-16 ***
## age              -2.062e-16  1.050e-16 -1.964e+00   0.0644 .
## GenotypeAPOE4    -1.195e-14  1.256e-14 -9.520e-01   0.3531
## age:GenotypeAPOE4 2.062e-16  2.453e-16  8.410e-01   0.4109
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.915e-15 on 19 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.5264, Adjusted R-squared:  0.4516
```

```
## F-statistic: 7.039 on 3 and 19 DF,  p-value: 0.002253


## Analysis of Variance Table
##
## Response: ufov1
##                  Df      Sum Sq     Mean Sq F value Pr(>F)
## age               1 4.9500e-29 4.9534e-29  0.2346 0.6306
## Genotype          1 1.5940e-28 1.5941e-28  0.7550 0.3898
## sex               1 2.6910e-28 2.6913e-28  1.2747 0.2653
## age:Genotype      1 6.5000e-29 6.5028e-29  0.3080 0.5819
## age:sex           1 1.8890e-28 1.8887e-28  0.8946 0.3497
## Genotype:sex      1 1.9580e-28 1.9579e-28  0.9273 0.3411
## age:Genotype:sex  1 1.0000e-28 9.9965e-29  0.4735 0.4952
## Residuals        42 8.8677e-27 2.1114e-28


## 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 1.5461e-28 1.5461e-28  3.2334 0.08806 .
## Genotype      1 1.3770e-29 1.3767e-29  0.2879 0.59779
## age:Genotype  1 3.3810e-29 3.3805e-29  0.7070 0.41091
## Residuals    19 9.0853e-28 4.7817e-29
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
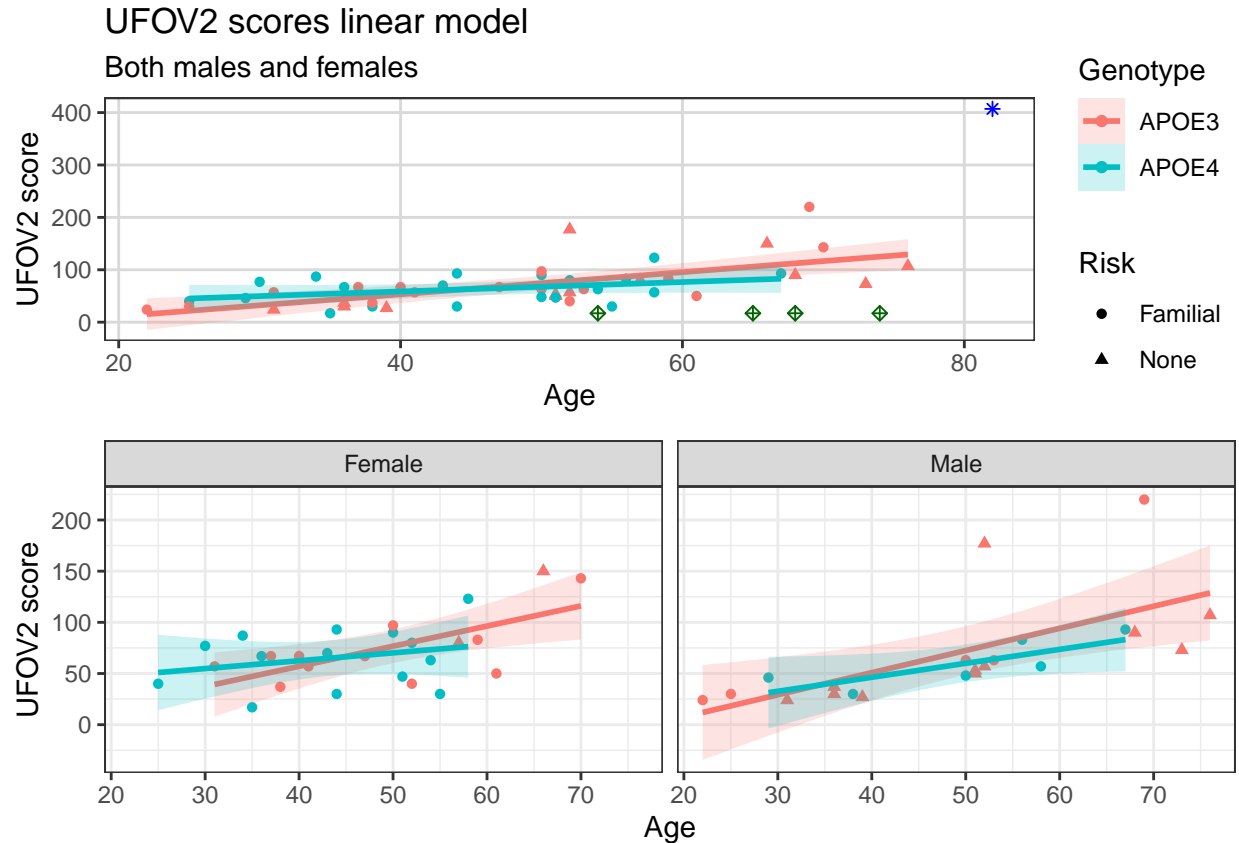
UFOV2 scores linear model
Both males and females


```
## 
## Call:
## lm(formula = ufov2 ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -49.226 -19.802  -7.377  14.859 106.426 
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             -21.6677    41.2824  -0.525    0.603
## age                       1.9671     0.8052   2.443    0.019 *
## GenotypeAPOE4            53.4227    58.2187   0.918    0.364
## sexMale                 -14.0105    49.3732  -0.284    0.778
## age:GenotypeAPOE4        -1.1989     1.2206  -0.982    0.332
## age:sexMale               0.1959     0.9612   0.204    0.839
## GenotypeAPOE4:sexMale   -26.0089    85.0344  -0.306    0.761
## age:GenotypeAPOE4:sexMale  0.4002    1.7169   0.233    0.817
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 33.92 on 41 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.3929, Adjusted R-squared:  0.2892 
## F-statistic:  3.79 on 7 and 41 DF,  p-value: 0.002939
```

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```
##
## 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
## -49.23  -21.01  -12.07   11.16  106.43
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        -35.6782    31.8062  -1.122  0.27672
## age                  2.1631     0.6165   3.509  0.00251 **
## GenotypeAPOE4       27.4138    72.7885   0.377  0.71086
## age:GenotypeAPOE4   -0.7987     1.4179  -0.563  0.58019
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 39.84 on 18 degrees of freedom
##   (3 observations deleted due to missingness)
## Multiple R-squared:  0.4335, Adjusted R-squared:  0.3391
## F-statistic: 4.592 on 3 and 18 DF,  p-value: 0.0148


## Analysis of Variance Table
##
## Response: ufov2
##              Df Sum Sq Mean Sq F value    Pr(>F)
## age           1  26916 26915.6 23.3916 1.895e-05 ***
## Genotype      1     79    79.0  0.0687    0.7946
## sex           1    912   912.2  0.7928    0.3785
## age:Genotype  1   2221  2220.9  1.9301    0.1722
## age:sex       1    218   217.7  0.1892    0.6659
## Genotype:sex  1    117   117.5  0.1021    0.7510
```

```
## age:Genotype:sex  1      63    62.5  0.0543    0.8169
## Residuals       41  47177  1150.7
## ---
## 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 20713.2 20713.2 13.0518 0.00199 **
## Genotype     1   644.3   644.3  0.4060 0.53202
## age:Genotype 1   503.5   503.5  0.3173 0.58019
## Residuals   18 28566.0  1587.0
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


UFOV3 scores linear model
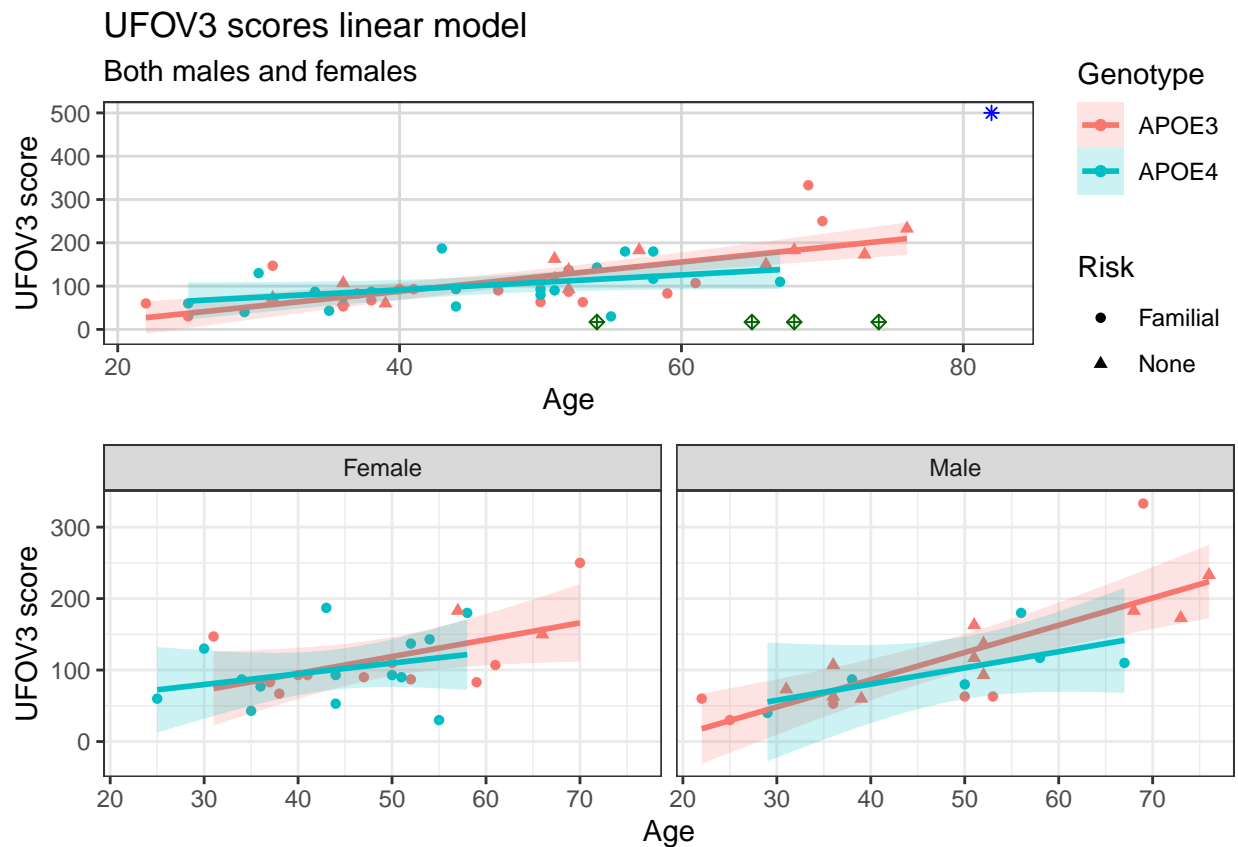
```
##
## Call:
## lm(formula = ufov3 ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -87.202 -22.987  -7.996  23.418 135.966
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)                0.9899    57.0573   0.017   0.9862
## age                        2.3577     1.1128   2.119   0.0401 *
## GenotypeAPOE4             33.9436    80.4655   0.422   0.6753
## sexMale                  -66.9719    67.5613  -0.991   0.3272
## age:GenotypeAPOE4         -0.8619     1.6870  -0.511   0.6121
## age:sexMale                1.4541     1.3211   1.101   0.2773
## GenotypeAPOE4:sexMale     21.7712   117.1353   0.186   0.8534
## age:GenotypeAPOE4:sexMale -0.6828     2.3688  -0.288   0.7746
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 46.88 on 42 degrees of freedom
##   (3 observations deleted due to missingness)
## Multiple R-squared:  0.4781, Adjusted R-squared:  0.3911
## F-statistic: 5.496 on 7 and 42 DF,  p-value: 0.000156


##
## 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  75634   75634 34.4095 6.191e-07 ***
## Genotype          1    608     608  0.2766    0.6017
## sex               1    102     102  0.0466    0.8301
## age:Genotype      1   4737    4737  2.1551    0.1495
## age:sex           1   2999    2999  1.3644    0.2494
## Genotype:sex      1    303     303  0.1380    0.7121
## age:Genotype:sex  1    183     183  0.0831    0.7746
## Residuals        42  92318    2198
## ---
## 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  65288   65288 29.1437 3.29e-05 ***
## Genotype      1   1879    1879  0.8386   0.3713
## age:Genotype  1   1897    1897  0.8466   0.3690
## Residuals    19  42564    2240
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Animal naming scores linear model

Both males and females
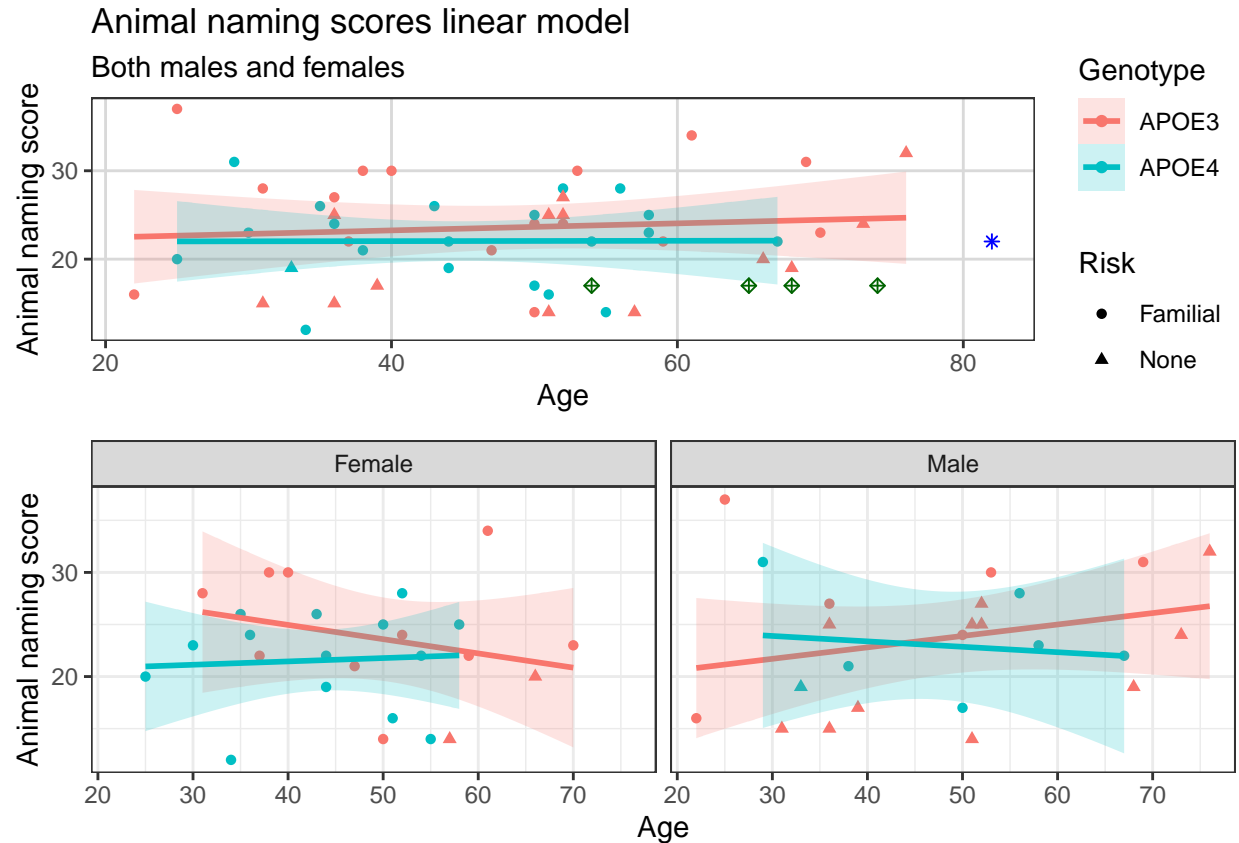

```
## 
## Call:
## lm(formula = animals ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -10.0096  -4.3996   0.4872   4.1431  15.8464 
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)    
## (Intercept)              30.4309     7.6063   4.001 0.000251 ***
## age                      -0.1368     0.1462  -0.936 0.354702    
## GenotypeAPOE4           -10.2594    10.5213  -0.975 0.335087    
## sexMale                 -12.0233     8.9075  -1.350 0.184308    
## age:GenotypeAPOE4         0.1689     0.2185   0.773 0.443991    
## age:sexMale               0.2466     0.1723   1.431 0.159715    
## GenotypeAPOE4:sexMale    17.3110    14.2805   1.212 0.232206    
## age:GenotypeAPOE4:sexMale -0.3307    0.2930  -1.129 0.265450    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 6.007 on 42 degrees of freedom
##   (3 observations deleted due to missingness)
## Multiple R-squared:  0.0782, Adjusted R-squared:  -0.07544 
## F-statistic: 0.509 on 7 and 42 DF,  p-value: 0.8225
```

```
## 
## 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
## -10.0096  -5.0409   0.3287   4.7319  15.8464
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       18.40757    4.96521   3.707  0.00139 **
## age                0.10984    0.09772   1.124  0.27430
## GenotypeAPOE4      7.05151   10.34285   0.682  0.50320
## age:GenotypeAPOE4 -0.16185    0.20910  -0.774  0.44797
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 6.434 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.06552,    Adjusted R-squared:  -0.07465
## F-statistic: 0.4674 on 3 and 20 DF,  p-value: 0.7083


## Analysis of Variance Table
## 
## Response: animals
##               Df  Sum Sq Mean Sq F value Pr(>F)
## age            1   12.24  12.240  0.3393 0.5634
## Genotype       1   24.90  24.896  0.6900 0.4109
## sex            1    5.63   5.632  0.1561 0.6948
## age:Genotype   1    3.66   3.663  0.1015 0.7516
## age:sex        1   28.10  28.095  0.7787 0.3826
## Genotype:sex   1    8.06   8.062  0.2235 0.6389
```

```
## age:Genotype:sex  1    45.96   45.961   1.2739 0.2655
## Residuals         42 1515.37   36.080


## 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  31.25   31.251  0.7549 0.3952
## Genotype       1   2.00    1.999  0.0483 0.8283
## age:Genotype   1  24.80   24.802  0.5991 0.4480
## Residuals     20 827.95   41.397
```
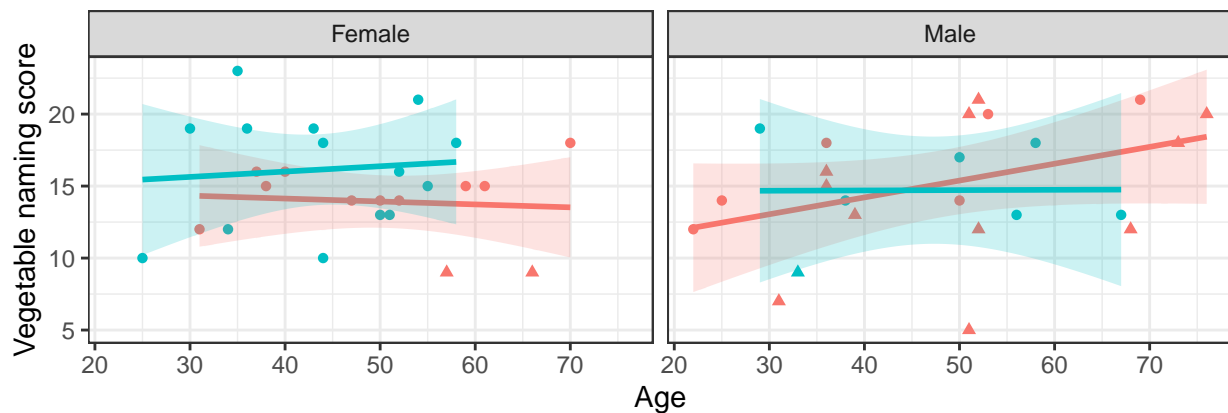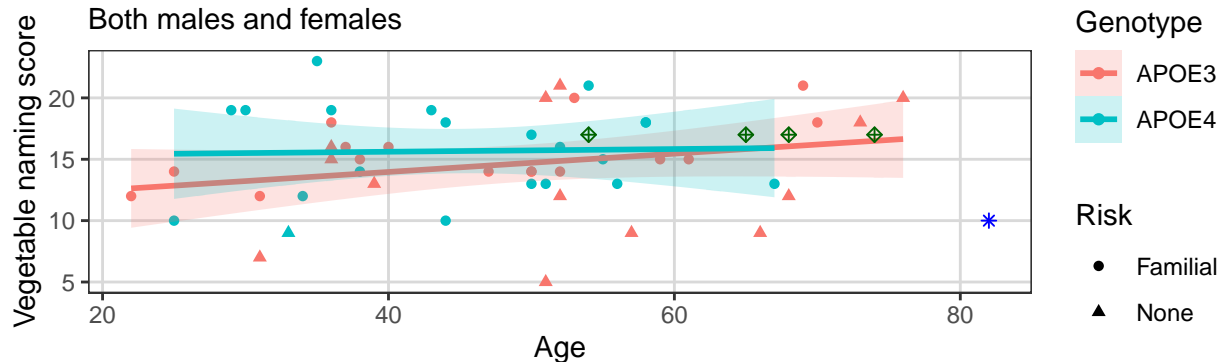

Vegetable naming scores linear model

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

```
## Residuals:
##      Min      1Q   Median      3Q      Max
## -10.5000  -2.1764   0.4681   2.7307   7.1777
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)               14.94680    5.05988   2.954  0.00512 **
## age                       -0.02033    0.09724  -0.209  0.83539
## GenotypeAPOE4             -0.42280    6.99898  -0.060  0.95212
## sexMale                   -5.41489    5.92543  -0.914  0.36602
## age:GenotypeAPOE4          0.05742    0.14537   0.395  0.69483
## age:sexMale                0.13735    0.11462   1.198  0.23751
## GenotypeAPOE4:sexMale      5.50480    9.49968   0.579  0.56537
## age:GenotypeAPOE4:sexMale -0.17232    0.19492  -0.884  0.38170
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.996 on 42 degrees of freedom
##   (3 observations deleted due to missingness)
## Multiple R-squared:  0.1242, Adjusted R-squared:  -0.02176
## F-statistic: 0.8509 on 7 and 42 DF,  p-value: 0.5524


##
## 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
## -10.5000  -1.7386   0.5904   3.2956   5.3830
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)          9.5319     3.3484    2.847  0.00997 **
## age                  0.1170     0.0659    1.776  0.09100 .
## GenotypeAPOE4         5.0820     6.9749    0.729  0.47468
## age:GenotypeAPOE4    -0.1149     0.1410   -0.815  0.42477
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.339 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1383, Adjusted R-squared:  0.009038
## F-statistic:  1.07 on 3 and 20 DF,  p-value: 0.3842


## Analysis of Variance Table
##
## Response: vegetables
##               Df Sum Sq Mean Sq F value Pr(>F)
## age            1  20.34 20.3375  1.2738 0.2655
## Genotype       1  18.63 18.6347  1.1671 0.2862
## sex            1   0.41  0.4141  0.0259 0.8728
## age:Genotype   1   7.92  7.9235  0.4963 0.4850
## age:sex        1  17.03 17.0282  1.0665 0.3076
## Genotype:sex   1  18.28 18.2825  1.1451 0.2907
## age:Genotype:sex 1 12.48 12.4784  0.7815 0.3817
## Residuals     42 670.58 15.9662


## 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  47.23  47.233  2.5088 0.1289
## Genotype      1   0.70   0.696  0.0370 0.8494
## age:Genotype  1  12.50  12.500  0.6640 0.4248
## Residuals    20 376.53  18.826
```
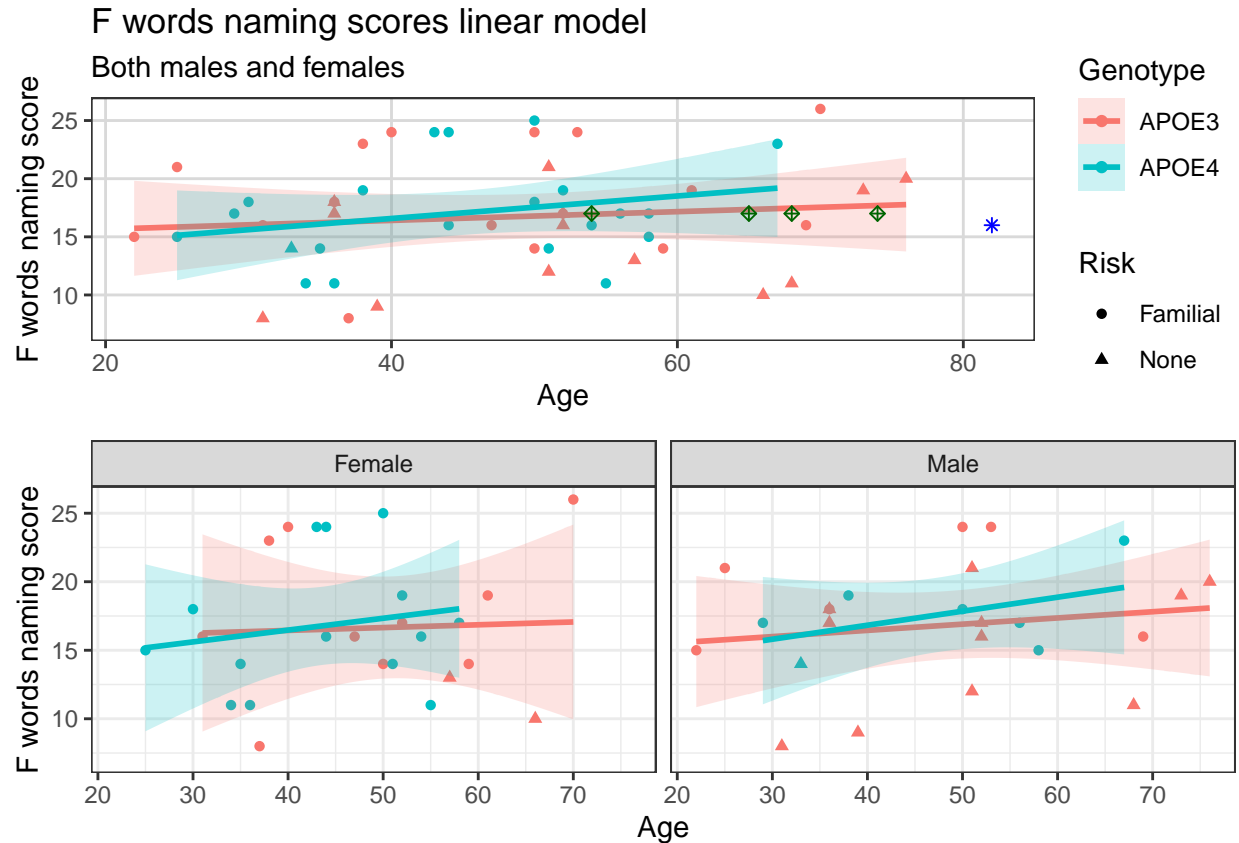
F words naming scores linear model

Both males and females


```
## 
## Call:
## lm(formula = f ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -8.3861 -2.7916 -0.2203  2.3138  8.9364 
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)   
## (Intercept)             15.626530   6.205877   2.518   0.0157 * 
## age                      0.020529   0.119259   0.172   0.8642   
## GenotypeAPOE4           -2.605214   8.584162  -0.303   0.7630   
## sexMale                 -0.991706   7.267463  -0.136   0.8921   
## age:GenotypeAPOE4        0.065726   0.178296   0.369   0.7143   
## age:sexMale              0.024847   0.140581   0.177   0.8606   
## GenotypeAPOE4:sexMale    0.707301  11.651235   0.061   0.9519   
## age:GenotypeAPOE4:sexMale -0.008861  0.239072  -0.037   0.9706   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 4.901 on 42 degrees of freedom
##   (3 observations deleted due to missingness)
## Multiple R-squared:  0.03496,    Adjusted R-squared:  -0.1259 
## F-statistic: 0.2174 on 7 and 42 DF,  p-value: 0.9793
```

```
##
## 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
## -8.0415 -1.8520  0.4414  2.0320  7.0964
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)      14.63482    3.39285   4.313 0.000338 ***
## age               0.04538    0.06678   0.680 0.504594
## GenotypeAPOE4    -1.89791    7.06753  -0.269 0.791034
## age:GenotypeAPOE4 0.05686    0.14288   0.398 0.694856
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.397 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.05928,    Adjusted R-squared:  -0.08183
## F-statistic: 0.4201 on 3 and 20 DF,  p-value: 0.7406


## Analysis of Variance Table
##
## Response: f
##              Df  Sum Sq Mean Sq F value Pr(>F)
## age           1   24.54 24.5412  1.0218 0.3179
## Genotype      1    3.37  3.3652  0.1401 0.7101
## sex           1    1.95  1.9493  0.0812 0.7771
## age:Genotype  1    5.67  5.6699  0.2361 0.6296
## age:sex       1    0.76  0.7597  0.0316 0.8597
## Genotype:sex  1    0.23  0.2254  0.0094 0.9233
```

```
## age:Genotype:sex  1    0.03  0.0330  0.0014 0.9706
## Residuals        42 1008.74 24.0175


## 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  18.11 18.1078  0.9368 0.3447
## Genotype      1   3.19  3.1929  0.1652 0.6887
## age:Genotype  1   3.06  3.0617  0.1584 0.6949
## Residuals    20 386.60 19.3298
```
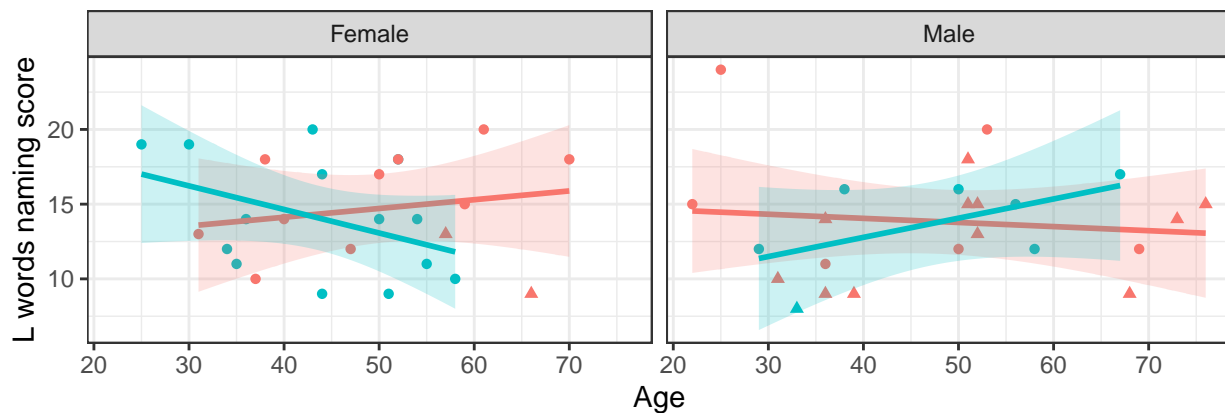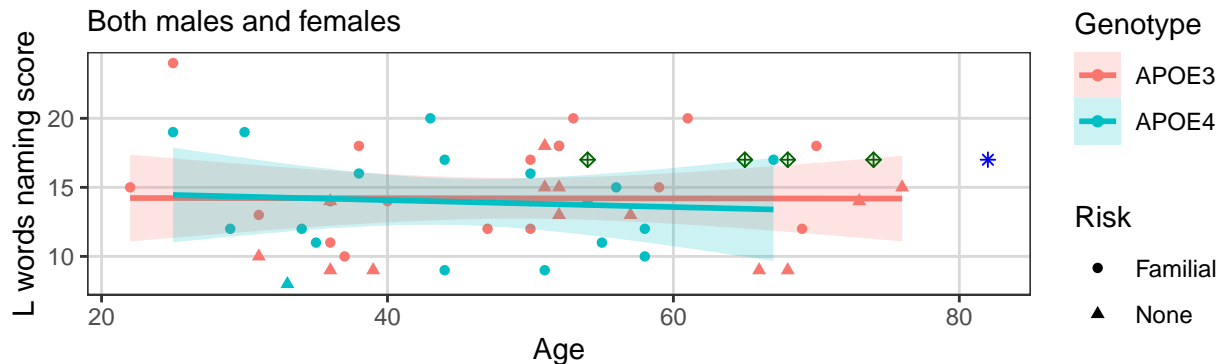

L words naming scores linear model

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

```
## Residuals:
##    Min     1Q Median     3Q    Max
## -6.649 -2.951  0.021  2.084  9.537
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)               11.77961    4.77021   2.469   0.0177 *
## age                        0.05863    0.09167   0.640   0.5259
## GenotypeAPOE4              9.17536    6.59830   1.391   0.1717
## sexMale                    3.37128    5.58621   0.604   0.5494
## age:GenotypeAPOE4         -0.21635    0.13705  -1.579   0.1219
## age:sexMale               -0.08614    0.10806  -0.797   0.4298
## GenotypeAPOE4:sexMale    -16.68438    8.95584  -1.863   0.0695 .
## age:GenotypeAPOE4:sexMale  0.37229    0.18377   2.026   0.0492 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.767 on 42 degrees of freedom
##   (3 observations deleted due to missingness)
## Multiple R-squared:  0.1058, Adjusted R-squared:  -0.04326
## F-statistic: 0.7097 on 7 and 42 DF,  p-value: 0.6639


##
## 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
## -5.1602 -3.1077  0.3106  1.4443  9.5371
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)        15.15089    3.00191   5.047 6.17e-05 ***
## age               -0.02752    0.05908  -0.466    0.646
## GenotypeAPOE4      -7.50903    6.25317  -1.201    0.244
## age:GenotypeAPOE4   0.15594    0.12642   1.234    0.232
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.89 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.07154,    Adjusted R-squared:  -0.06772
## F-statistic: 0.5137 on 3 and 20 DF,  p-value: 0.6775


## Analysis of Variance Table
##
## Response: l
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1   0.36   0.363  0.0256 0.87362
## Genotype         1   1.00   0.998  0.0703 0.79216
## sex              1   5.73   5.725  0.4034 0.52876
## age:Genotype     1   0.59   0.593  0.0418 0.83895
## age:sex          1   2.64   2.641  0.1861 0.66838
## Genotype:sex     1   1.94   1.938  0.1366 0.71359
## age:Genotype:sex 1  58.24  58.241  4.1042 0.04916 *
## Residuals       42 596.00  14.190
## ---
## 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   0.244  0.2439  0.0161 0.9003
## Genotype      1   0.053  0.0526  0.0035 0.9536
## age:Genotype  1  23.024 23.0240  1.5216 0.2317
## Residuals    20 302.638 15.1319
```
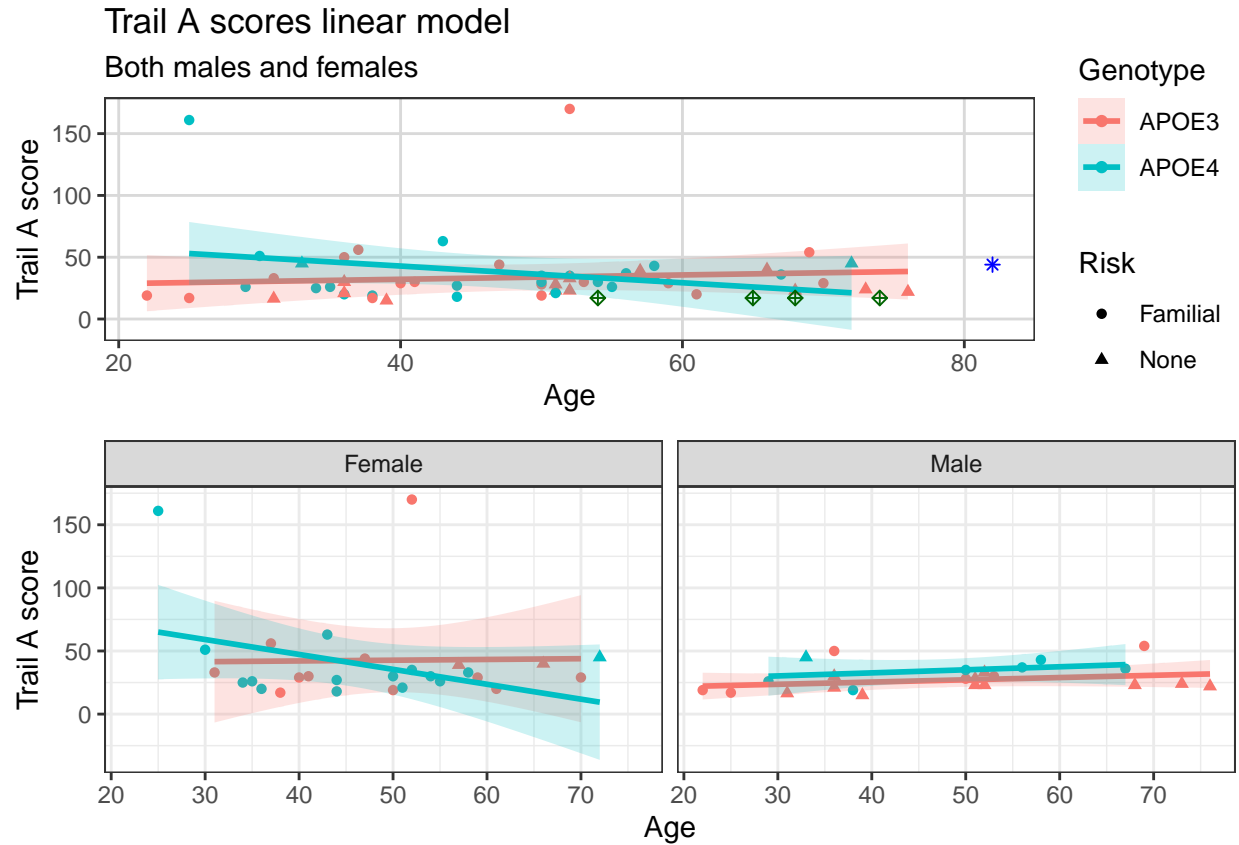
Trail A scores linear model

Both males and females


```
##
## Call:
## lm(formula = trailA ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -31.996 -12.396  -4.059   2.004 127.184
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              39.71951   34.69318   1.145    0.258
## age                       0.05955    0.67665   0.088    0.930
## GenotypeAPOE4            54.80640   45.31429   1.209    0.233
## sexMale                 -21.46856   41.08006  -0.523    0.604
## age:GenotypeAPOE4        -1.24094    0.91738  -1.353    0.183
## age:sexMale               0.11879    0.80331   0.148    0.883
## GenotypeAPOE4:sexMale   -50.07103   64.44642  -0.777    0.441
## age:GenotypeAPOE4:sexMale  1.30458    1.30379   1.001    0.322
##
## Residual standard error: 28.51 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1339, Adjusted R-squared:  -0.003905
## F-statistic: 0.9717 on 7 and 44 DF,  p-value: 0.4636


##
```

```
## 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
## -13.182  -6.099  -3.187   3.055  25.329
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        18.25095    7.99151   2.284   0.0335 *
## age                 0.17833    0.15728   1.134   0.2703
## GenotypeAPOE4       4.73537   16.64683   0.284   0.7790
## age:GenotypeAPOE4   0.06365    0.33654   0.189   0.8519
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.36 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.187,  Adjusted R-squared:  0.06506
## F-statistic: 1.534 on 3 and 20 DF,  p-value: 0.2367


## Analysis of Variance Table
##
## Response: trailA
##                 Df Sum Sq Mean Sq F value Pr(>F)
## age              1    196  195.53  0.2406 0.6262
## Genotype         1    272  271.52  0.3341 0.5662
## sex              1   1787 1787.20  2.1992 0.1452
## age:Genotype     1   1379 1378.79  1.6967 0.1995
## age:sex          1    658  658.45  0.8103 0.3729
## Genotype:sex     1    422  422.20  0.5195 0.4749
## age:Genotype:sex 1    814  813.64  1.0012 0.3225
## Residuals       44  35757  812.65


## 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  191.33 191.329  1.7841 0.1966
## Genotype     1  298.20 298.198  2.7807 0.1110
## age:Genotype 1    3.84   3.836  0.0358 0.8519
## Residuals   20 2144.79 107.240
```

Trail B scores linear model
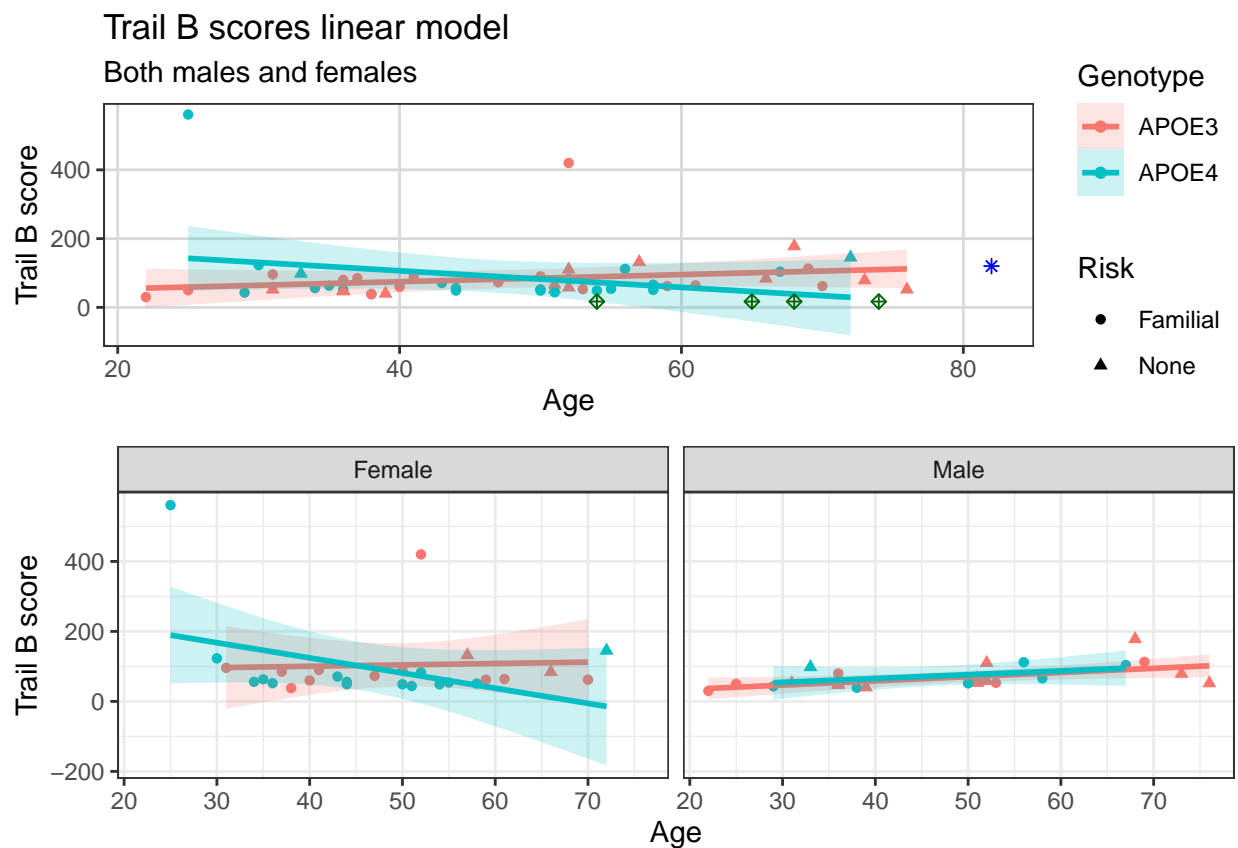

```
##
## Call:
## lm(formula = trailB ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -94.40 -34.62 -14.81   5.73 371.59
##
```

```
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)                84.6102   105.7377   0.800   0.4279
## age                         0.3946     2.0623   0.191   0.8492
## GenotypeAPOE4             213.1730   138.1087   1.544   0.1299
## sexMale                   -73.9504   125.2036  -0.591   0.5578
## age:GenotypeAPOE4          -4.7295     2.7960  -1.692   0.0978 .
## age:sexMale                 0.8027     2.4483   0.328   0.7446
## GenotypeAPOE4:sexMale    -202.1676   196.4195  -1.029   0.3090
## age:GenotypeAPOE4:sexMale   4.6269     3.9737   1.164   0.2505
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 86.88 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1562, Adjusted R-squared:  0.02196
## F-statistic: 1.164 on 7 and 44 DF,  p-value: 0.3429


##
## 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
## -49.654 -18.807  -6.881  11.988  85.924
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        10.6598    23.6447   0.451   0.6570
## age                 1.1973     0.4654   2.573   0.0182 *
## GenotypeAPOE4      11.0054    49.2535   0.223   0.8255
## age:GenotypeAPOE4  -0.1026     0.9957  -0.103   0.9190
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Residual standard error: 30.64 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.2933,	Adjusted R-squared:  0.1872
## F-statistic: 2.766 on 3 and 20 DF,  p-value: 0.06857


## Analysis of Variance Table
##
## Response: trailB
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1    430   429.9  0.0569 0.81250
## Genotype         1    673   673.1  0.0892 0.76664
## sex              1  12784 12783.7  1.6935 0.19991
## age:Genotype     1  23691 23691.1  3.1384 0.08339 .
## age:sex          1  12689 12689.4  1.6810 0.20155
## Genotype:sex     1    983   982.7  0.1302 0.71997
## age:Genotype:sex 1  10234 10234.4  1.3558 0.25054
## Residuals       44 332144  7548.7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## 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  7594.6  7594.6  8.0898 0.01002 *
## Genotype      1   186.3   186.3  0.1985 0.66075
## age:Genotype  1    10.0    10.0  0.0106 0.91896
## Residuals    20 18775.7   938.8
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
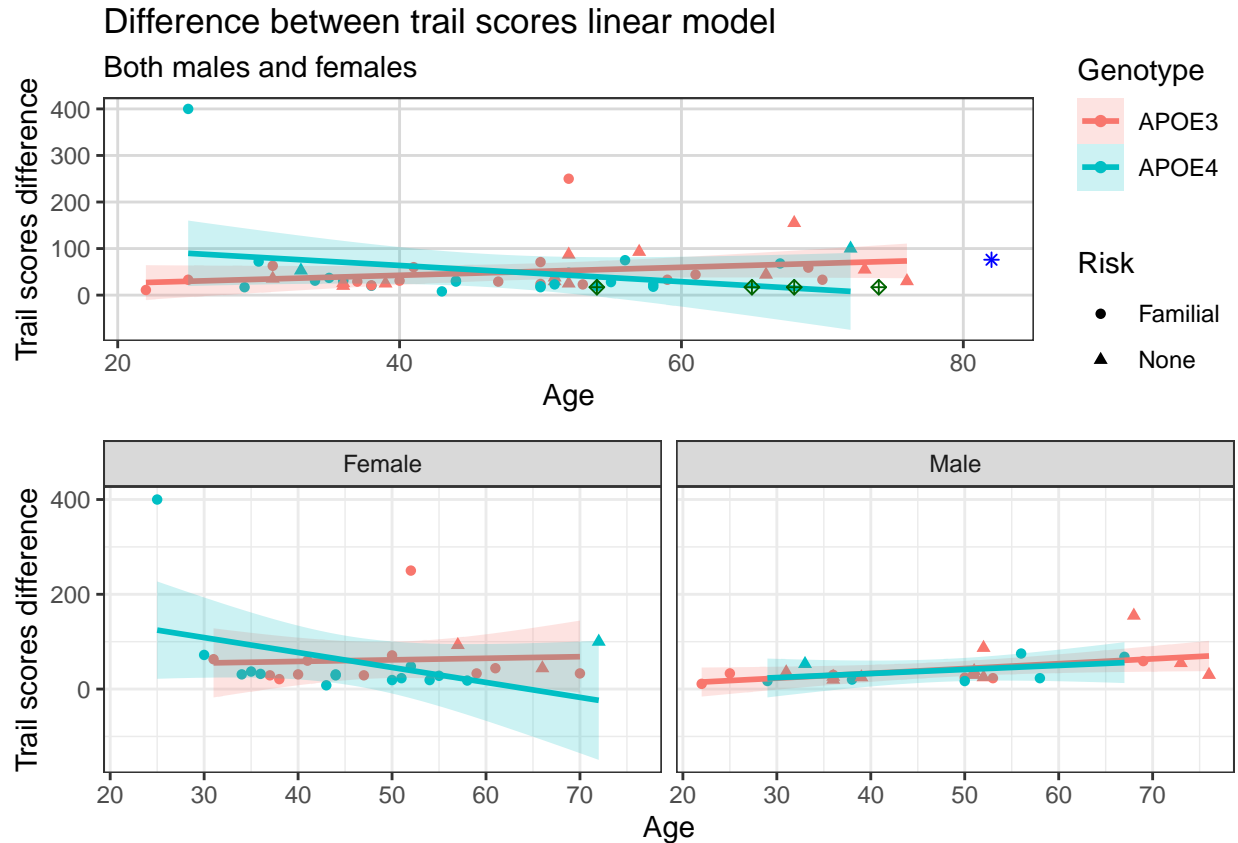
Difference between trail scores linear model

Both males and females


```
##
## Call:
## lm(formula = trailDiff ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -65.037 -27.540 -11.438   7.975 275.581
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)                44.891     75.928   0.591   0.5574
## age                         0.335      1.481   0.226   0.8221
## GenotypeAPOE4             158.367     99.173   1.597   0.1175
## sexMale                   -52.482     89.906  -0.584   0.5624
## age:GenotypeAPOE4          -3.489      2.008  -1.738   0.0893 .
## age:sexMale                 0.684      1.758   0.389   0.6991
## GenotypeAPOE4:sexMale    -152.097    141.044  -1.078   0.2867
## age:GenotypeAPOE4:sexMale   3.322      2.853   1.164   0.2506
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 62.39 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1564, Adjusted R-squared:  0.02216
## F-statistic: 1.165 on 7 and 44 DF,  p-value: 0.342
```

```
##
## 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
## -39.850 -15.621  -6.392  11.675  93.302
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)         -7.5912    22.7097  -0.334   0.7417
## age                  1.0190     0.4470   2.280   0.0337 *
## GenotypeAPOE4        6.2700    47.3057   0.133   0.8959
## age:GenotypeAPOE4   -0.1663     0.9564  -0.174   0.8637
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 29.43 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.2382, Adjusted R-squared:  0.1239
## F-statistic: 2.084 on 3 and 20 DF,  p-value: 0.1345


## Analysis of Variance Table
##
## Response: trailDiff
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1     46    45.6  0.0117 0.91434
## Genotype         1     90    89.6  0.0230 0.88009
## sex              1   5011  5011.2  1.2874 0.26266
## age:Genotype     1  13639 13639.2  3.5041 0.06787 .
## age:sex          1   7567  7566.8  1.9440 0.17024
## Genotype:sex     1    117   116.6  0.0300 0.86336
## age:Genotype:sex 1   5277  5276.7  1.3556 0.25057
## Residuals       44 171265  3892.4
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## 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  5375.1  5375.1  6.2068 0.02163 *
## Genotype       1    13.1    13.1  0.0151 0.90336
## age:Genotype   1    26.2    26.2  0.0302 0.86374
## Residuals     20 17320.1   866.0
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
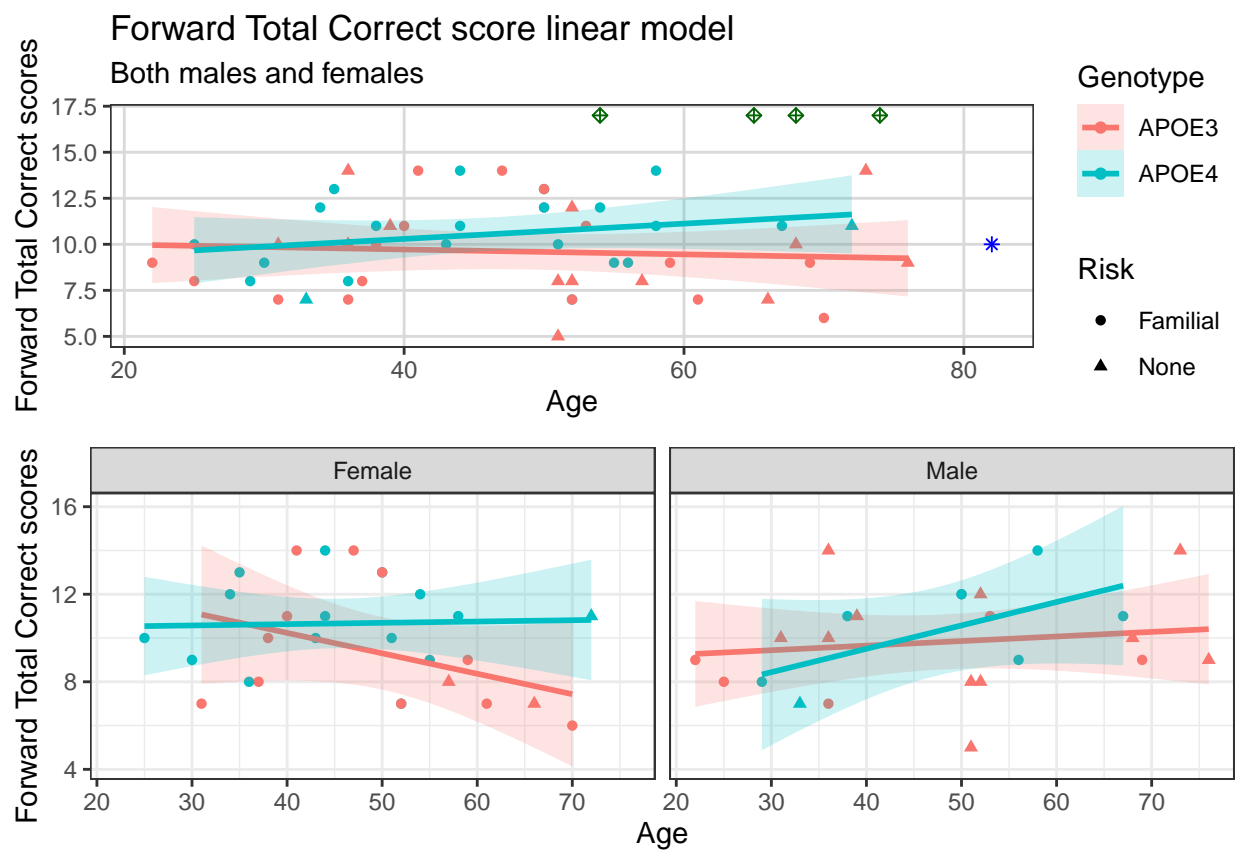

Forward Total Correct score linear model

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

```
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.8814 -1.4685 -0.3033  1.4078  4.4325
## 
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)              13.968103   2.870200   4.867  1.5e-05 ***
## age                      -0.093352   0.055980  -1.668   0.1025
## GenotypeAPOE4            -3.573782   3.748894  -0.953   0.3457
## sexMale                  -5.153839   3.398592  -1.516   0.1366
## age:GenotypeAPOE4         0.099333   0.075896   1.309   0.1974
## age:sexMale               0.114276   0.066459   1.719   0.0926 .
## GenotypeAPOE4:sexMale    -0.006756   5.331713  -0.001   0.9990
## age:GenotypeAPOE4:sexMale -0.013417   0.107864  -0.124   0.9016
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 2.358 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1561, Adjusted R-squared:  0.02184
## F-statistic: 1.163 on 7 and 44 DF,  p-value: 0.3434


## 
## 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
## -4.8814 -1.4932 -0.2558  1.4948  4.4325
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)          8.81426    1.81123    4.866 9.35e-05 ***
## age                   0.02092    0.03565    0.587    0.564
## GenotypeAPOE4        -3.58054    3.77291   -0.949    0.354
## age:GenotypeAPOE4     0.08592    0.07628    1.126    0.273
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.347 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1322, Adjusted R-squared:  0.002042
## F-statistic: 1.016 on 3 and 20 DF,  p-value: 0.4065


## Analysis of Variance Table
##
## Response: fwd_total_correct
##                 Df  Sum Sq Mean Sq F value  Pr(>F)
## age              1   0.055  0.0552  0.0099 0.92108
## Genotype         1  11.639 11.6393  2.0926 0.15510
## sex              1   0.332  0.3317  0.0596 0.80821
## age:Genotype     1   6.349  6.3491  1.1415 0.29117
## age:sex          1  25.613 25.6126  4.6049 0.03744 *
## Genotype:sex     1   1.194  1.1938  0.2146 0.64545
## age:Genotype:sex 1   0.086  0.0861  0.0155 0.90157
## Residuals       44 244.732  5.5621
## ---
## 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   8.558  8.5581  1.5536 0.2270
## Genotype      1   1.238  1.2380  0.2247 0.6406
## age:Genotype  1   6.989  6.9891  1.2687 0.2733
## Residuals    20 110.173  5.5087
```
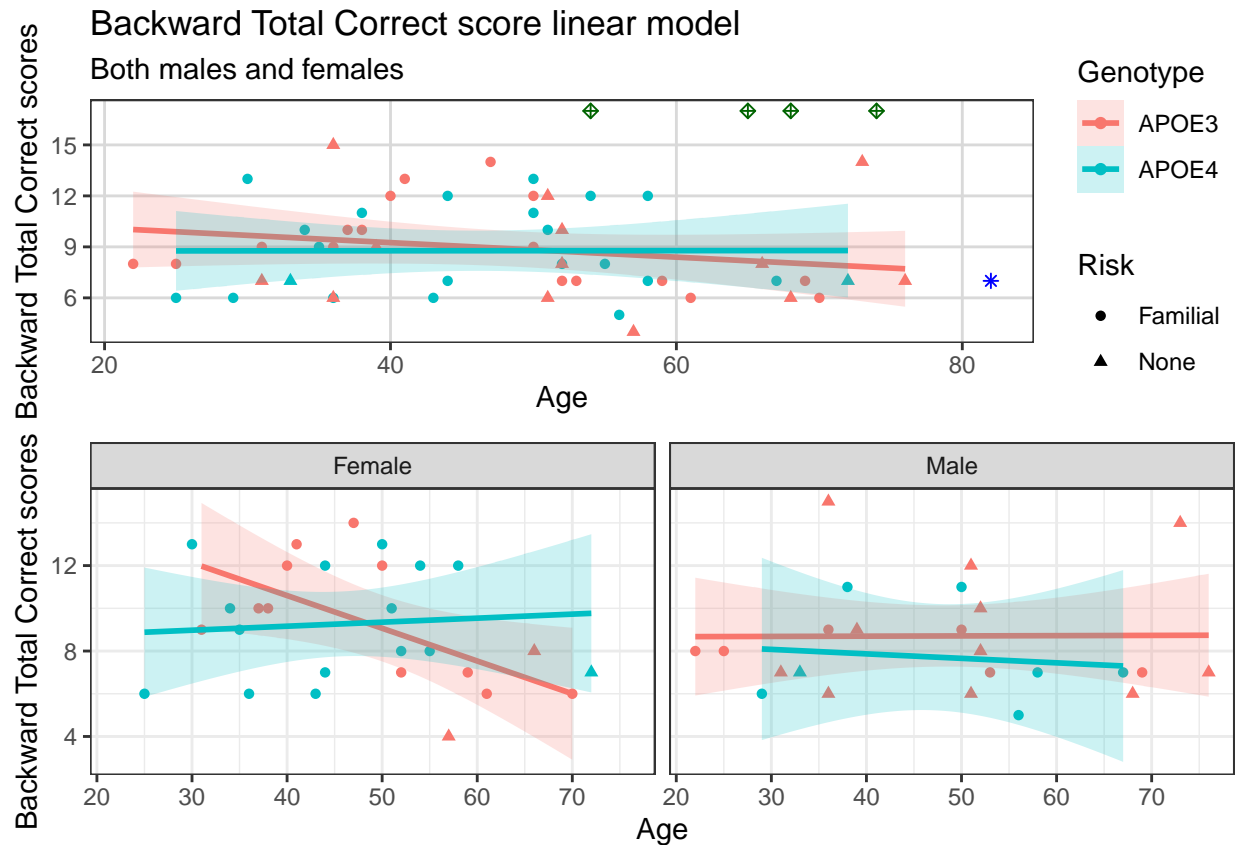
Backward Total Correct score linear model
Both males and females

```
## 
## Call:
## lm(formula = bckwds_total_correct ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -3.9927 -1.7440 -0.6763  1.6768  6.3087 
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)    
## (Intercept)             16.72528    3.26075   5.129 6.28e-06 ***
## age                     -0.15320    0.06360  -2.409   0.0203 *  
## GenotypeAPOE4           -8.31578    4.25900  -1.953   0.0573 .  
## sexMale                 -8.07699    3.86104  -2.092   0.0422 *  
## age:GenotypeAPOE4        0.17203    0.08622   1.995   0.0522 .  
## age:sexMale              0.15440    0.07550   2.045   0.0469 *  
## GenotypeAPOE4:sexMale    8.37434    6.05720   1.383   0.1738    
## age:GenotypeAPOE4:sexMale -0.19421   0.12254  -1.585   0.1202    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 2.679 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1496, Adjusted R-squared:  0.01434 
## F-statistic: 1.106 on 7 and 44 DF,  p-value: 0.3764
```

```
##
## 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
## -2.7295 -1.7328 -0.6763  0.5540  6.3087
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        8.648285   2.102225   4.114 0.000539 ***
## age                0.001194   0.041374   0.029 0.977262
## GenotypeAPOE4      0.058555   4.379072   0.013 0.989464
## age:GenotypeAPOE4 -0.022185   0.088530  -0.251 0.804688
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.724 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.0352, Adjusted R-squared:  -0.1095
## F-statistic: 0.2432 on 3 and 20 DF,  p-value: 0.8651


## Analysis of Variance Table
##
## Response: bckwds_total_correct
##                 Df  Sum Sq Mean Sq F value Pr(>F)
## age              1   6.908  6.9081  0.9623 0.3320
## Genotype         1   0.376  0.3760  0.0524 0.8200
## sex              1   8.663  8.6633  1.2068 0.2779
## age:Genotype     1   4.801  4.8007  0.6687 0.4179
## age:sex          1  14.534 14.5345  2.0247 0.1618
## Genotype:sex     1   2.263  2.2632  0.3153 0.5773
## age:Genotype:sex 1  18.032 18.0320  2.5119 0.1202
```

```
## Residuals        44 315.865  7.1787


## 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   0.044  0.0437  0.0059 0.9396
## Genotype      1   4.906  4.9055  0.6610 0.4258
## age:Genotype  1   0.466  0.4660  0.0628 0.8047
## Residuals    20 148.418  7.4209
```
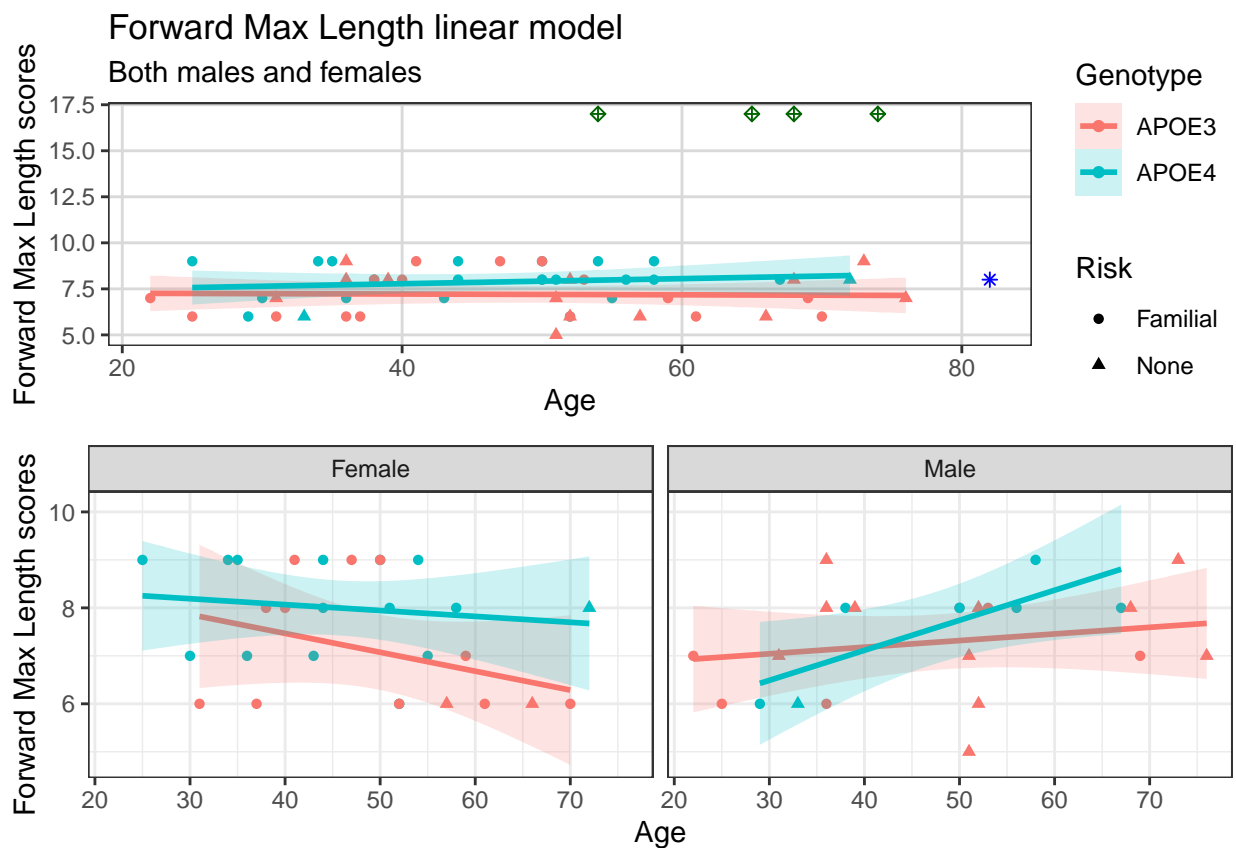

Forward Max Length linear model

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

```
##
## Residuals:
##      Min      1Q  Median      3Q      Max
## -2.33227 -0.80007  0.06752  0.77658  1.92611
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 9.04364    1.34219   6.738 2.77e-08 ***
## age                        -0.03939    0.02618  -1.505    0.139
## GenotypeAPOE4              -0.48462    1.75309  -0.276    0.784
## sexMale                    -2.41517    1.58928  -1.520    0.136
## age:GenotypeAPOE4           0.02712    0.03549   0.764    0.449
## age:sexMale                 0.05319    0.03108   1.712    0.094 .
## GenotypeAPOE4:sexMale      -1.53336    2.49327  -0.615    0.542
## age:GenotypeAPOE4:sexMale   0.02170    0.05044   0.430    0.669
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.103 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.2242, Adjusted R-squared:  0.1007
## F-statistic: 1.816 on 7 and 44 DF,  p-value: 0.1081


##
## 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
## -2.33227 -0.67698  0.00583  0.70056  1.87473
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)          6.62847    0.80324   8.252 7.19e-08 ***
## age                  0.01380    0.01581   0.873    0.393
## GenotypeAPOE4       -2.01798    1.67321  -1.206    0.242
## age:GenotypeAPOE4    0.04882    0.03383   1.443    0.164
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.041 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.2156, Adjusted R-squared:  0.09798
## F-statistic: 1.833 on 3 and 20 DF,  p-value: 0.1737


## Analysis of Variance Table
##
## Response: fwd_max_length
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1  0.009  0.0089  0.0073 0.93210
## Genotype         1  5.699  5.6992  4.6857 0.03588 *
## sex              1  0.015  0.0153  0.0126 0.91118
## age:Genotype     1  0.562  0.5620  0.4621 0.50022
## age:sex          1  8.245  8.2448  6.7786 0.01253 *
## Genotype:sex     1  0.708  0.7080  0.5821 0.44956
## age:Genotype:sex 1  0.225  0.2251  0.1851 0.66914
## Residuals       44 53.517  1.2163
## ---
## 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  3.2529  3.2529  3.0025 0.09853 .
## Genotype       1  0.4475  0.4475  0.4130 0.52773
## age:Genotype   1  2.2565  2.2565  2.0828 0.16445
## Residuals     20 21.6681  1.0834
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
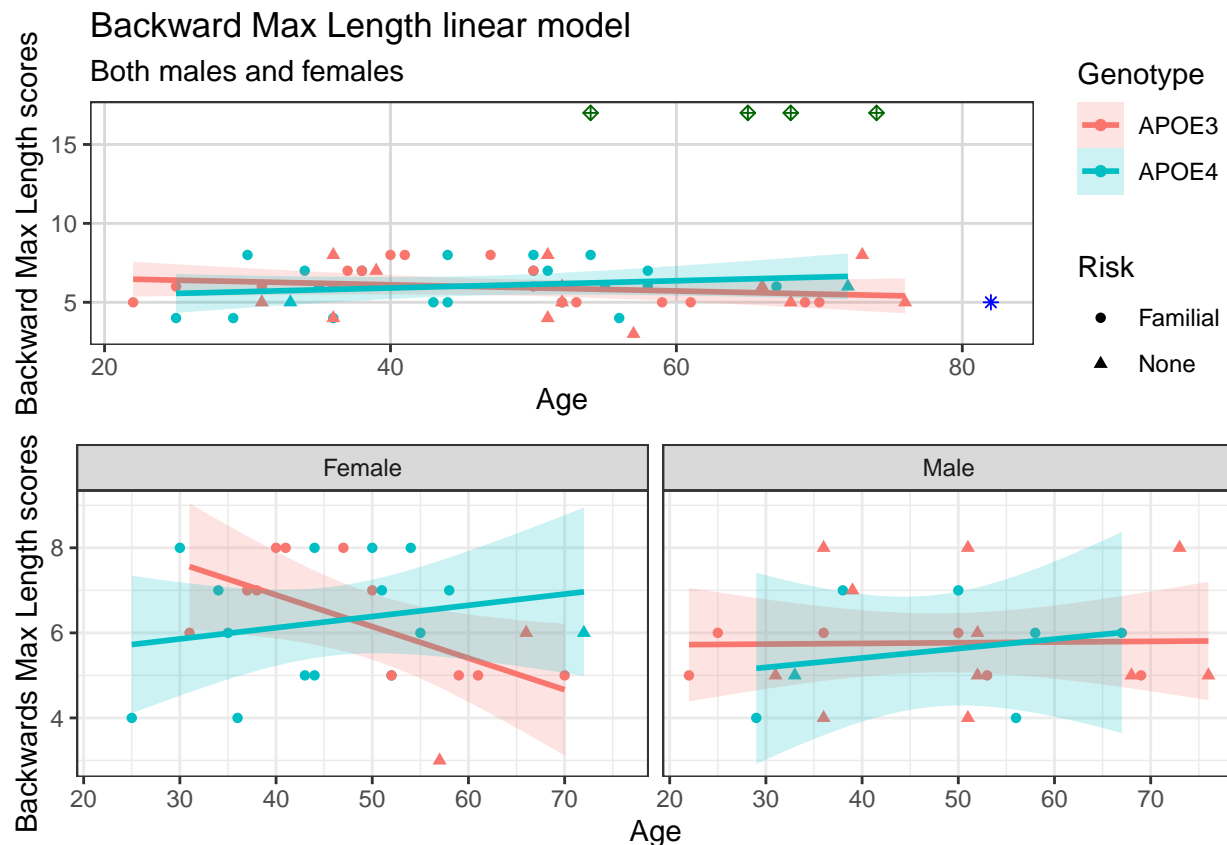
Backward Max Length linear model

Both males and females


```
## 
## Call:
## lm(formula = bckwds_max_length ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min      1Q   Median      3Q      Max
## -2.62815 -0.84809 -0.02401  1.05755  2.25488
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)              9.86227    1.65657   5.953 3.95e-07 ***
## age                     -0.07428    0.03231  -2.299   0.0263 *
## GenotypeAPOE4           -4.79679    2.16372  -2.217   0.0318 *
## sexMale                 -4.17480    1.96154  -2.128   0.0389 *
## age:GenotypeAPOE4        0.10066    0.04380   2.298   0.0264 *
## age:sexMale              0.07588    0.03836   1.978   0.0542 .
## GenotypeAPOE4:sexMale    3.63243    3.07727   1.180   0.2442
## age:GenotypeAPOE4:sexMale -0.08009   0.06225  -1.287   0.2050
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.361 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1594, Adjusted R-squared:  0.02564
## F-statistic: 1.192 on 7 and 44 DF,  p-value: 0.3274
```

```
## 
## 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
## -1.7691 -0.7967 -0.1316  0.5169  2.2549
## 
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        5.687473   1.037743   5.481  2.3e-05 ***
## age                0.001601   0.020424   0.078    0.938
## GenotypeAPOE4     -1.164360   2.161685  -0.539    0.596
## age:GenotypeAPOE4  0.020569   0.043702   0.471    0.643
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.345 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared: 0.02142,    Adjusted R-squared:  -0.1254
## F-statistic: 0.1459 on 3 and 20 DF,  p-value: 0.9311


## Analysis of Variance Table
## 
## Response: bckwds_max_length
##                 Df Sum Sq Mean Sq F value Pr(>F)
## age              1  0.233  0.2331  0.1258 0.7245
## Genotype         1  0.123  0.1231  0.0664 0.7978
## sex              1  3.170  3.1705  1.7111 0.1976
## age:Genotype     1  4.378  4.3779  2.3628 0.1314
## age:sex          1  4.384  4.3835  2.3658 0.1312
## Genotype:sex     1  0.101  0.1014  0.0547 0.8161
## age:Genotype:sex 1  3.067  3.0669  1.6552 0.2050
```

```
## Residuals           44 81.525   1.8528


## 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  0.217 0.21702  0.1200 0.7326
## Genotype      1  0.174 0.17416  0.0963 0.7595
## age:Genotype  1  0.401 0.40058  0.2215 0.6430
## Residuals    20 36.167 1.80833
```


RAVLT forgetting scores linear model

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

```
##
## Residuals:
##     Min      1Q  Median     3Q     Max
## -4.7982 -1.6988  0.0729  1.4142  9.2849
##
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 2.216131   3.314601   0.669    0.507
## age                        -0.007411   0.064647  -0.115    0.909
## GenotypeAPOE4               0.976811   4.329346   0.226    0.823
## sexMale                     0.881568   3.924806   0.225    0.823
## age:GenotypeAPOE4           0.019279   0.087647   0.220    0.827
## age:sexMale                -0.006810   0.076749  -0.089    0.930
## GenotypeAPOE4:sexMale     -10.136538   6.157238  -1.646    0.107
## age:GenotypeAPOE4:sexMale   0.195649   0.124564   1.571    0.123
##
## Residual standard error: 2.724 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1974, Adjusted R-squared:  0.06975
## F-statistic: 1.546 on 7 and 44 DF,  p-value: 0.1771


##
## 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
## -2.6569 -0.9842 -0.1236  1.4204  3.2152
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        3.09770    1.33835   2.315  0.03138 *
## age               -0.01422    0.02634  -0.540  0.59524
## GenotypeAPOE4     -9.15973    2.78788  -3.286  0.00370 **
## age:GenotypeAPOE4  0.21493    0.05636   3.813  0.00109 **
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.734 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.4767, Adjusted R-squared:  0.3982
## F-statistic: 6.074 on 3 and 20 DF,  p-value: 0.00412


## Analysis of Variance Table
##
## Response: RAVLT_FORGETTING
##                  Df Sum Sq Mean Sq F value  Pr(>F)
## age               1   1.77  1.7709  0.2387 0.62754
## Genotype          1  29.21 29.2137  3.9383 0.05346 .
## sex               1   0.64  0.6418  0.0865 0.77003
## age:Genotype      1  18.29 18.2909  2.4658 0.12351
## age:sex           1  10.23 10.2314  1.3793 0.24654
## Genotype:sex      1   1.84  1.8400  0.2481 0.62093
## age:Genotype:sex  1  18.30 18.2997  2.4670 0.12342
## Residuals        44 326.38  7.4178
## ---
## 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  5.625   5.625  1.8703 0.186616
## Genotype      1  5.440   5.440  1.8087 0.193717
## age:Genotype  1 43.738  43.738 14.5419 0.001088 **
## Residuals    20 60.155   3.008
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

RAVLT learning scores linear model
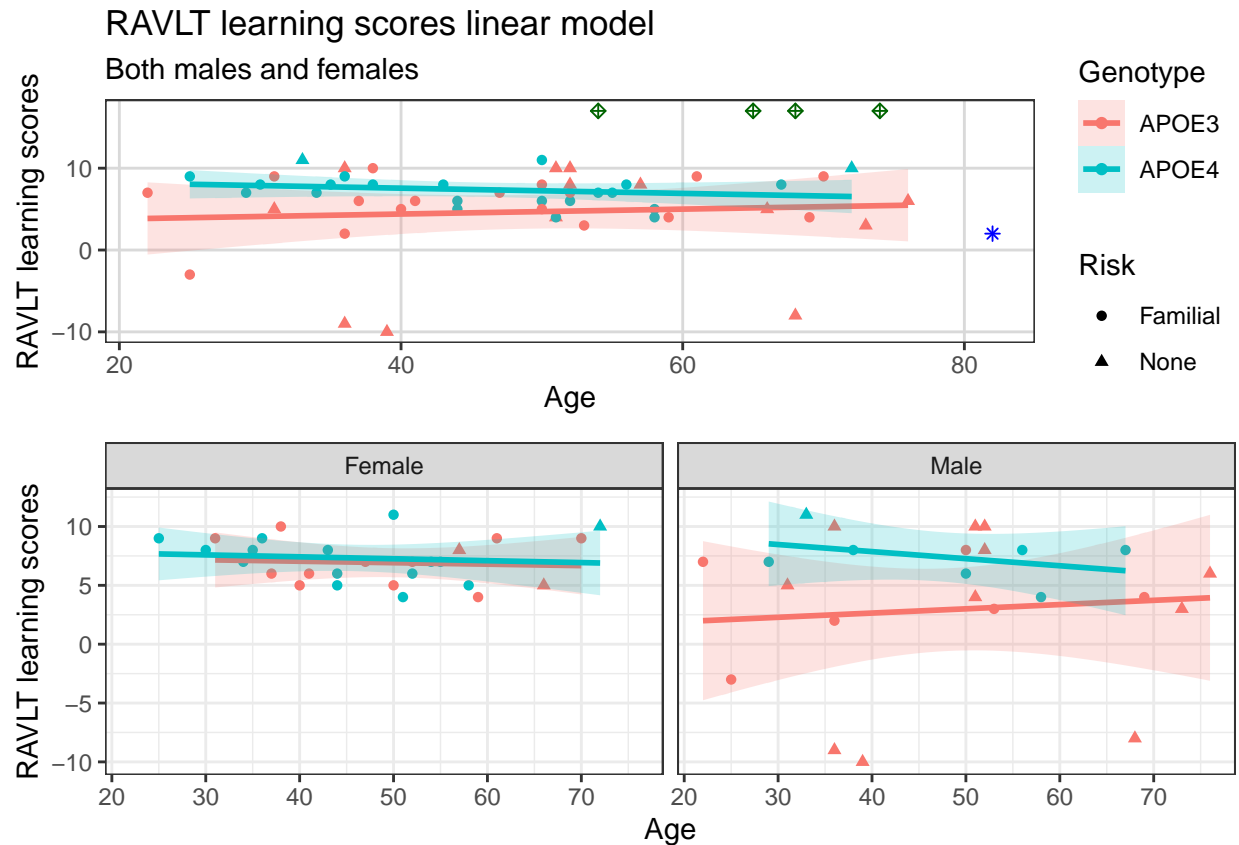
```
## 
## Call:
## lm(formula = RAVLT_LEARNING ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -12.6083  -1.4009   0.0717   2.0973   7.4998 
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              7.544032   5.234726   1.441    0.157
## age                     -0.012438   0.102097  -0.122    0.904
## GenotypeAPOE4            0.534668   6.837307   0.078    0.938
## sexMale                 -6.341253   6.198419  -1.023    0.312
## age:GenotypeAPOE4       -0.003931   0.138420  -0.028    0.977
## age:sexMale              0.048478   0.121209   0.400    0.691
## GenotypeAPOE4:sexMale    8.534958   9.724082   0.878    0.385
## age:GenotypeAPOE4:sexMale -0.092250  0.196724  -0.469    0.641
## 
## Residual standard error: 4.301 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.2128, Adjusted R-squared:  0.08753 
## F-statistic: 1.699 on 7 and 44 DF,  p-value: 0.1342


## 
```

```
## 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
## -2.6569 -0.9842 -0.1236  1.4204  3.2152
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        3.09770    1.33835   2.315  0.03138 *
## age               -0.01422    0.02634  -0.540  0.59524
## GenotypeAPOE4     -9.15973    2.78788  -3.286  0.00370 **
## age:GenotypeAPOE4  0.21493    0.05636   3.813  0.00109 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.734 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.4767, Adjusted R-squared:  0.3982
## F-statistic: 6.074 on 3 and 20 DF,  p-value: 0.00412


## Analysis of Variance Table
##
## Response: RAVLT_LEARNING
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1   0.05   0.048  0.0026 0.95950
## Genotype         1  92.90  92.896  5.0210 0.03014 *
## sex              1  68.55  68.553  3.7053 0.06072 .
## age:Genotype     1   5.67   5.673  0.3066 0.58256
## age:sex          1   0.02   0.015  0.0008 0.97724
## Genotype:sex     1  48.77  48.765  2.6358 0.11162
## age:Genotype:sex 1   4.07   4.068  0.2199 0.64143
## Residuals       44 814.06  18.501
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


## 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  5.625   5.625  1.8703 0.186616
## Genotype     1  5.440   5.440  1.8087 0.193717
## age:Genotype 1 43.738  43.738 14.5419 0.001088 **
## Residuals   20 60.155   3.008
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


RAVLT Immediate scores linear model

```
##
## Call:
```
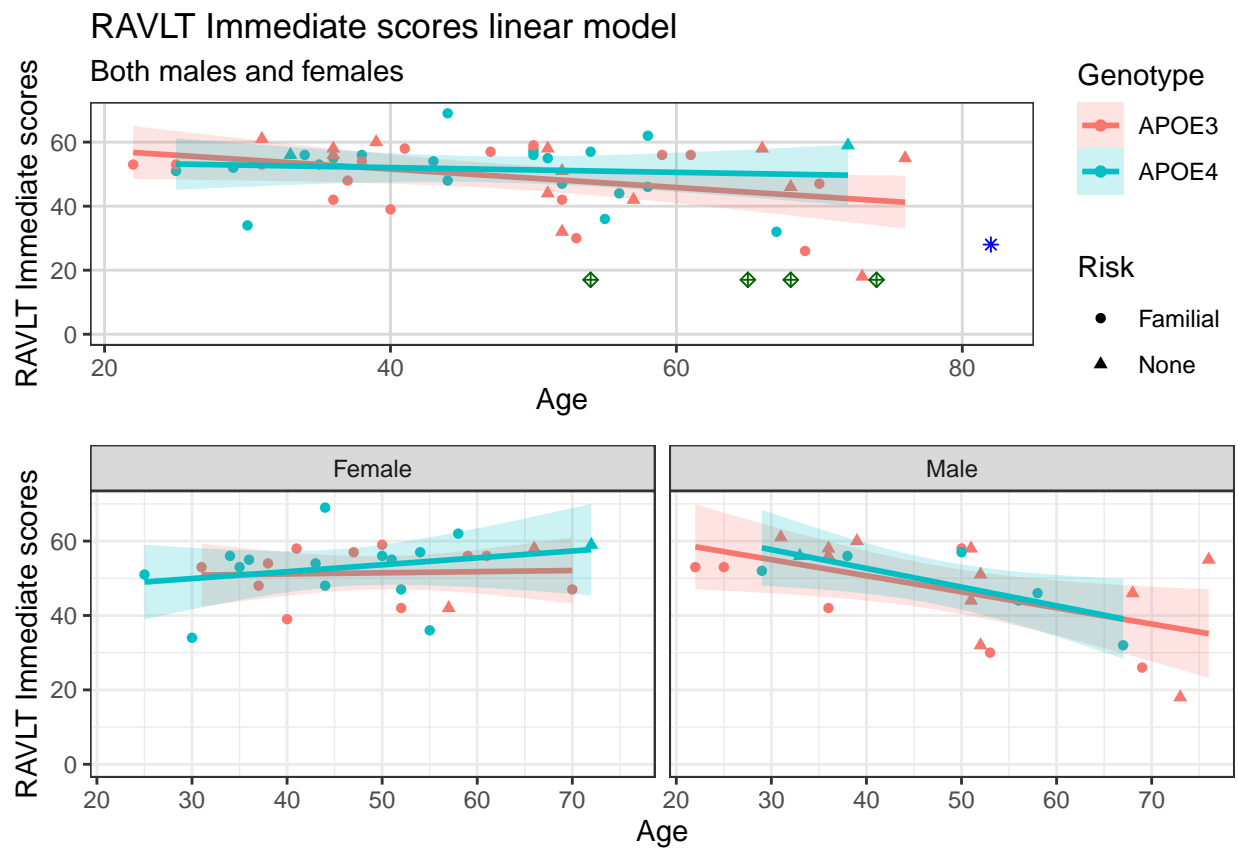
```
## lm(formula = RAVLT_IMMEDIATE ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min     1Q Median     3Q    Max
## -18.555  -5.644   2.141   5.601  19.888
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                49.90158   11.33101   4.404  6.7e-05 ***
## age                         0.03125    0.22100   0.141   0.8882
## GenotypeAPOE4              -5.54286   14.79994  -0.375   0.7098
## sexMale                    18.07291   13.41701   1.347   0.1849
## age:GenotypeAPOE4           0.15414    0.29962   0.514   0.6095
## age:sexMale                -0.46365    0.26237  -1.767   0.0841 .
## GenotypeAPOE4:sexMale      10.33948   21.04861   0.491   0.6257
## age:GenotypeAPOE4:sexMale  -0.22445    0.42583  -0.527   0.6008
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.311 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.2801, Adjusted R-squared:  0.1656
## F-statistic: 2.446 on 7 and 44 DF,  p-value: 0.03294


##
## Call:
## lm(formula = RAVLT_IMMEDIATE ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min     1Q Median     3Q    Max
## -18.555  -4.659   2.141   4.526  16.484
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       49.90158   10.07593   4.953 4.69e-05 ***
## age                0.03125    0.19652   0.159    0.875
## GenotypeAPOE4     -5.54286   13.16062  -0.421    0.677
## age:GenotypeAPOE4  0.15414    0.26643   0.579    0.568
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.279 on 24 degrees of freedom
## Multiple R-squared:  0.05022,    Adjusted R-squared:  -0.0685
## F-statistic: 0.423 on 3 and 24 DF,  p-value: 0.7382


##
## Call:
## lm(formula = RAVLT_FORGETTING ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min     1Q Median     3Q    Max
## -2.6569 -0.9842 -0.1236  1.4204  3.2152
##
## Coefficients:
```

```
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        3.09770    1.33835   2.315  0.03138 *
## age               -0.01422    0.02634  -0.540  0.59524
## GenotypeAPOE4      -9.15973    2.78788  -3.286  0.00370 **
## age:GenotypeAPOE4  0.21493    0.05636   3.813  0.00109 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.734 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.4767, Adjusted R-squared:  0.3982
## F-statistic: 6.074 on 3 and 20 DF,  p-value: 0.00412


## Analysis of Variance Table
##
## Response: RAVLT_IMMEDIATE
##                Df Sum Sq Mean Sq F value  Pr(>F)
## age             1  463.8  463.75  5.3497 0.02546 *
## Genotype        1   49.2   49.21  0.5676 0.45521
## sex             1  214.3  214.30  2.4721 0.12304
## age:Genotype    1  117.6  117.59  1.3565 0.25043
## age:sex         1  615.0  614.99  7.0944 0.01076 *
## Genotype:sex    1    0.4    0.39  0.0045 0.94705
## age:Genotype:sex 1   24.1   24.08  0.2778 0.60077
## Residuals      44 3814.2   86.69
## ---
## 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   41.16  41.165  0.6005 0.4459
## Genotype      1   22.89  22.885  0.3339 0.5688
## age:Genotype  1   22.94  22.942  0.3347 0.5683
## Residuals    24 1645.11  68.546


## Analysis of Variance Table
##
## Response: RAVLT_FORGETTING
##              Df Sum Sq Mean Sq F value   Pr(>F)
## age           1  5.625   5.625  1.8703 0.186616
## Genotype      1  5.440   5.440  1.8087 0.193717
## age:Genotype  1 43.738  43.738 14.5419 0.001088 **
## Residuals    20 60.155   3.008
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
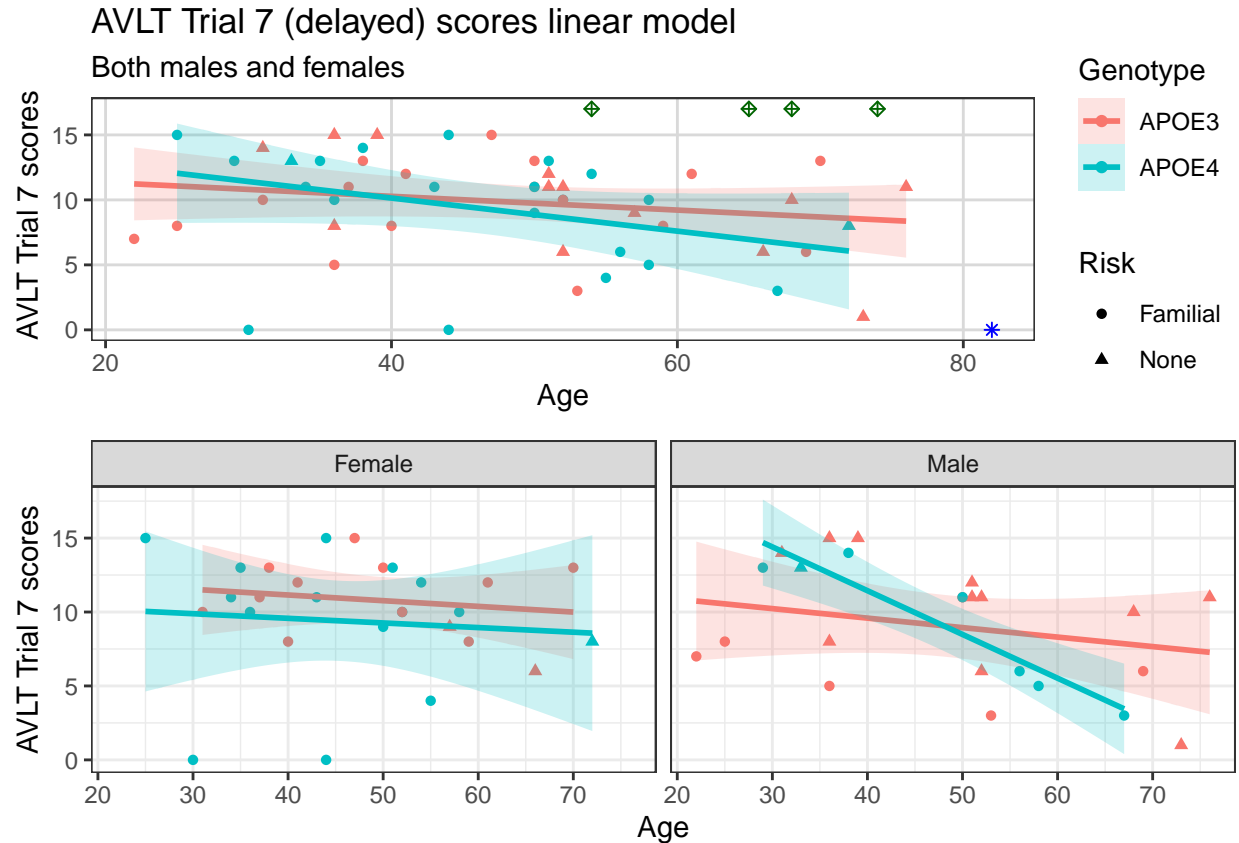
AVLT Trial 7 (delayed) scores linear model

Both males and females

```
##
## Call:
## lm(formula = AVLT_Trial7 ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -9.8856 -1.7556  0.5521  2.3047  5.5521
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)              12.688351   4.654492   2.726  0.00917 **
## age                      -0.038442   0.090780  -0.423  0.67402
## GenotypeAPOE4            -1.864986   6.079437  -0.307  0.76047
## sexMale                  -0.533661   5.511366  -0.097  0.92330
## age:GenotypeAPOE4         0.007182   0.123077   0.058  0.95373
## age:sexMale              -0.025741   0.107774  -0.239  0.81234
## GenotypeAPOE4:sexMale    12.992136   8.646233   1.503  0.14008
## age:GenotypeAPOE4:sexMale -0.238990   0.174918  -1.366  0.17879
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.825 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1918, Adjusted R-squared:  0.0632
## F-statistic: 1.491 on 7 and 44 DF,  p-value: 0.1953
```

```
##
## 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
## -6.4694 -2.0206 -0.4823  2.2867  5.3484
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      12.15469    2.78444   4.365   0.0003 ***
## age              -0.06418    0.05480  -1.171   0.2553
## GenotypeAPOE4    11.12715    5.80017   1.918   0.0694 .
## age:GenotypeAPOE4 -0.23181    0.11726  -1.977   0.0620 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.608 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.323,  Adjusted R-squared:  0.2215
## F-statistic: 3.181 on 3 and 20 DF,  p-value: 0.04627


## Analysis of Variance Table
##
## Response: AVLT_Trial7
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1  56.39  56.392  3.8553 0.05593 .
## Genotype         1   5.54   5.539  0.3787 0.54147
## sex              1  14.94  14.944  1.0217 0.31765
## age:Genotype     1  10.41  10.414  0.7120 0.40335
## age:sex          1  30.90  30.895  2.1122 0.15322
## Genotype:sex     1   7.22   7.223  0.4938 0.48593
## age:Genotype:sex 1  27.31  27.305  1.8668 0.17879
```

```
## Residuals         44 643.59  14.627
## ---
## 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  73.300  73.300  5.6303 0.02779 *
## Genotype     1   0.069   0.069  0.0053 0.94276
## age:Genotype 1  50.878  50.878  3.9080 0.06201 .
## Residuals   20 260.378  13.019
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Composite pleasantness scores linear model

```
##
```
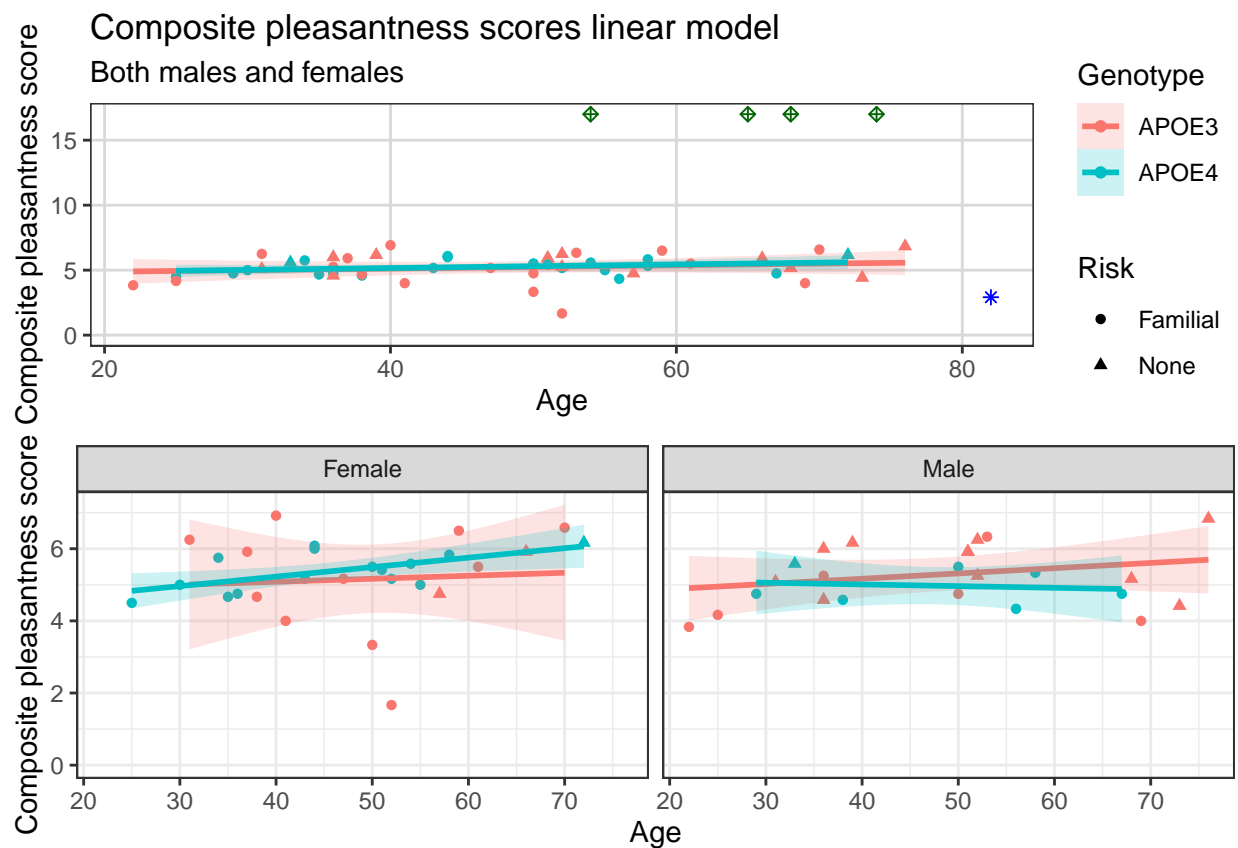
```
## Call:
## lm(formula = Composite_Pleasantness ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -3.5173 -0.4306  0.0173  0.6293  1.8325
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                4.751795   1.197881   3.967 0.000265 ***
## age                        0.008310   0.023363   0.356 0.723766
## GenotypeAPOE4             -0.576938   1.564605  -0.369 0.714087
## sexMale                   -0.165531   1.418406  -0.117 0.907627
## age:GenotypeAPOE4          0.017986   0.031675   0.568 0.573034
## age:sexMale                0.006263   0.027737   0.226 0.822396
## GenotypeAPOE4:sexMale      1.189446   2.225196   0.535 0.595662
## age:GenotypeAPOE4:sexMale -0.037267   0.045017  -0.828 0.412230
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9843 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.07377,    Adjusted R-squared:  -0.07359
## F-statistic: 0.5006 on 7 and 44 DF,  p-value: 0.8289


##
## 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
## -1.59183 -0.53691 -0.02439  0.58716  1.13949
##
```

```
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        4.58626    0.63650   7.205 5.64e-07 ***
## age                0.01457    0.01253   1.163    0.258
## GenotypeAPOE4       0.61251    1.32586   0.462    0.649
## age:GenotypeAPOE4 -0.01928    0.02680  -0.719    0.480
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8248 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.09531,    Adjusted R-squared:  -0.04039
## F-statistic: 0.7023 on 3 and 20 DF,  p-value: 0.5617


## Analysis of Variance Table
##
## Response: Composite_Pleasantness
##                 Df Sum Sq Mean Sq F value Pr(>F)
## age              1  1.572 1.57179  1.6224 0.2094
## Genotype         1  0.028 0.02827  0.0292 0.8651
## sex              1  0.072 0.07195  0.0743 0.7865
## age:Genotype     1  0.007 0.00739  0.0076 0.9308
## age:sex          1  0.064 0.06393  0.0660 0.7985
## Genotype:sex     1  0.988 0.98774  1.0195 0.3181
## age:Genotype:sex 1  0.664 0.66395  0.6853 0.4122
## Residuals       44 42.628 0.96882


## 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 0.6260 0.62599  0.9202 0.3489
## Genotype      1 0.4554 0.45541  0.6694 0.4229
## age:Genotype  1 0.3520 0.35198  0.5174 0.4803
## Residuals    20 13.6057 0.68028
```
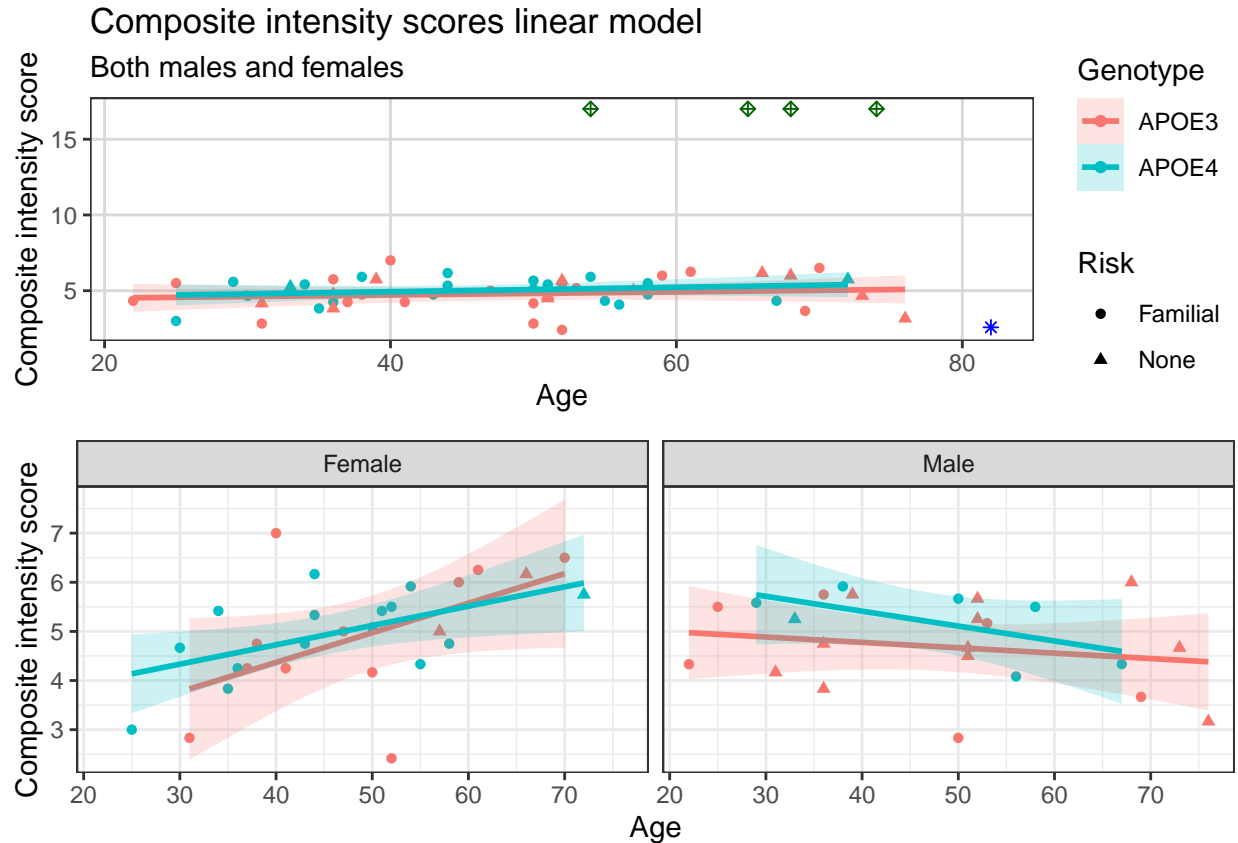
Composite intensity scores linear model

```
##
## Call:
## lm(formula = Composite_Intensity ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.67635 -0.65145  0.03548  0.53906  2.62961
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              1.961616   1.148352   1.708   0.0946 .
## age                      0.060219   0.022397   2.689   0.0101 *
## GenotypeAPOE4            1.192275   1.499913   0.795   0.4309
## sexMale                  3.253126   1.359759   2.392   0.0211 *
## age:GenotypeAPOE4       -0.020895   0.030365  -0.688   0.4950
## age:sexMale             -0.071175   0.026590  -2.677   0.0104 *
## GenotypeAPOE4:sexMale    0.216528   2.133191   0.102   0.9196
## age:GenotypeAPOE4:sexMale 0.001545  0.043156   0.036   0.9716
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9436 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.2463, Adjusted R-squared:  0.1264
## F-statistic: 2.054 on 7 and 44 DF,  p-value: 0.06925
```

```
## 
## 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 
## -1.83361 -0.65739 -0.02982  0.57061  1.53027 
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)    
## (Intercept)        5.21474    0.67804   7.691 2.13e-07 ***
## age               -0.01096    0.01334  -0.821    0.421    
## GenotypeAPOE4      1.40880    1.41241   0.997    0.330    
## age:GenotypeAPOE4 -0.01935    0.02855  -0.678    0.506    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.8786 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1578, Adjusted R-squared:  0.0315 
## F-statistic: 1.249 on 3 and 20 DF,  p-value: 0.3184


## Analysis of Variance Table
## 
## Response: Composite_Intensity
##                 Df Sum Sq Mean Sq F value   Pr(>F)    
## age              1  1.122  1.1223  1.2605 0.267650    
## Genotype         1  0.774  0.7736  0.8688 0.356366    
## sex              1  0.060  0.0599  0.0673 0.796510    
## age:Genotype     1  0.046  0.0460  0.0516 0.821303    
## age:sex          1 10.558 10.5580 11.8581 0.001272 **
## Genotype:sex     1  0.240  0.2403  0.2699 0.605993    
## age:Genotype:sex 1  0.001  0.0011  0.0013 0.971608    
```

```
## Residuals          44 39.176   0.8904
## ---
## 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  1.3505 1.35052  1.7494 0.2009
## Genotype      1  1.1885 1.18849  1.5395 0.2290
## age:Genotype  1  0.3545 0.35454  0.4593 0.5057
## Residuals    20 15.4398 0.77199
```
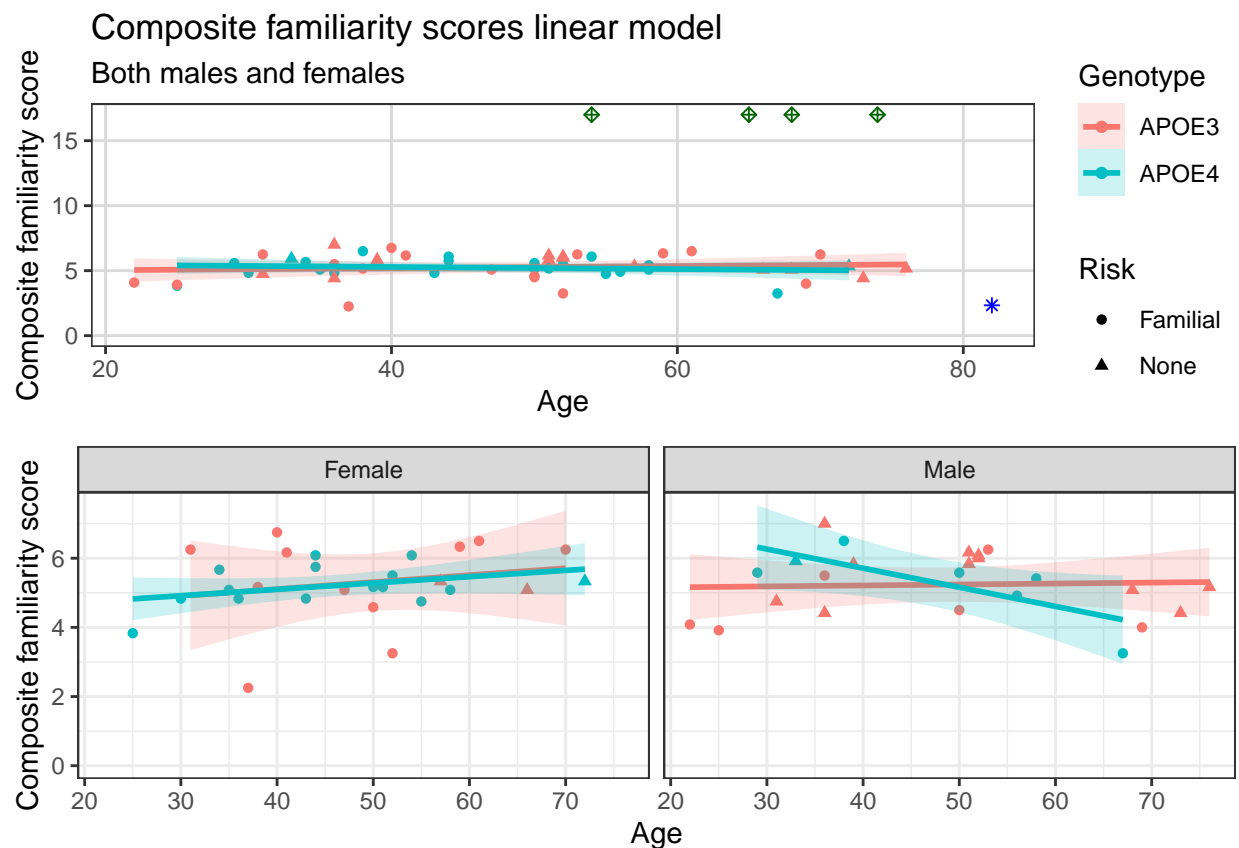

Composite familiarity scores linear model

```
##
```

```
## Call:
## lm(formula = Composite_Familiarity ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.7976 -0.5667 -0.0988  0.6831  1.7983
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                4.302877   1.175034   3.662 0.000668 ***
## age                        0.020127   0.022918   0.878 0.384580
## GenotypeAPOE4              0.064319   1.534763   0.042 0.966762
## sexMale                    0.800096   1.391353   0.575 0.568187
## age:GenotypeAPOE4         -0.001837   0.031071  -0.059 0.953115
## age:sexMale               -0.017384   0.027208  -0.639 0.526174
## GenotypeAPOE4:sexMale      2.752333   2.182755   1.261 0.213974
## age:GenotypeAPOE4:sexMale -0.056104   0.044158  -1.271 0.210574
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9655 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1137, Adjusted R-squared:  -0.02735
## F-statistic: 0.8061 on 7 and 44 DF,  p-value: 0.5868


##
## 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
## -1.29226 -0.75137 -0.02832  0.68308  1.79827
##
```

```
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       5.102973   0.700003   7.290 4.75e-07 ***
## age               0.002743   0.013777   0.199   0.8442
## GenotypeAPOE4      2.816652   1.458153   1.932   0.0677 .
## age:GenotypeAPOE4 -0.057942   0.029479  -1.966   0.0634 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9071 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1856, Adjusted R-squared:  0.06347
## F-statistic:  1.52 on 3 and 20 DF,  p-value: 0.2401


## Analysis of Variance Table
##
## Response: Composite_Familiarity
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1  0.053 0.05265  0.0565 0.81325
## Genotype         1  0.008 0.00807  0.0087 0.92629
## sex              1  0.000 0.00000  0.0000 0.99966
## age:Genotype     1  0.560 0.55965  0.6003 0.44259
## age:sex          1  3.118 3.11827  3.3450 0.07419 .
## Genotype:sex     1  0.016 0.01642  0.0176 0.89503
## age:Genotype:sex 1  1.505 1.50482  1.6142 0.21057
## Residuals       44 41.017 0.93221
## ---
## 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  0.5514  0.5514  0.6702 0.42263
## Genotype      1  0.0208  0.0208  0.0253 0.87522
## age:Genotype  1  3.1788  3.1788  3.8633 0.06339 .
## Residuals    20 16.4562  0.8228
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
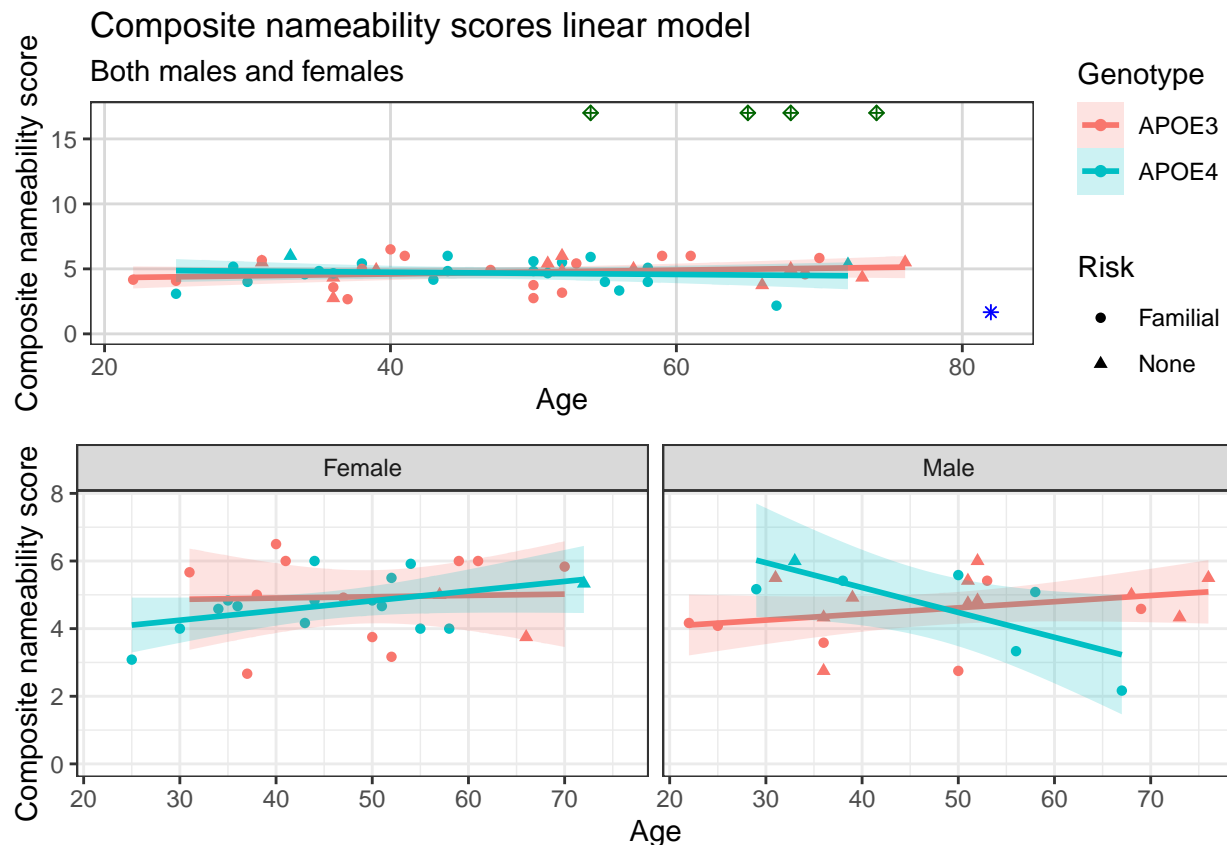
Composite nameability scores linear model

Both males and females


```
## 
## Call:
## lm(formula = Composite_Nameability ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -2.22570 -0.70061  0.05871  0.75594  1.59604 
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)    
## (Intercept)              4.749386   1.196529   3.969 0.000263 ***
## age                      0.003864   0.023337   0.166 0.869237    
## GenotypeAPOE4           -1.361723   1.562840  -0.871 0.388313    
## sexMale                 -1.041360   1.416806  -0.735 0.466236    
## age:GenotypeAPOE4        0.024835   0.031639   0.785 0.436694    
## age:sexMale              0.014282   0.027705   0.516 0.608781    
## GenotypeAPOE4:sexMale    5.810390   2.222685   2.614 0.012201 *  
## age:GenotypeAPOE4:sexMale -0.116537  0.044966  -2.592 0.012912 *  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.9832 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.2015, Adjusted R-squared:  0.07449 
## F-statistic: 1.586 on 7 and 44 DF,  p-value: 0.1647
```

```
##
## 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
## -1.86536 -0.70061  0.05871  0.56241  1.34835
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        3.70803    0.71920   5.156 4.81e-05 ***
## age                0.01815    0.01415   1.282  0.21450
## GenotypeAPOE4      4.44867    1.49815   2.969  0.00758 **
## age:GenotypeAPOE4 -0.09170    0.03029  -3.028  0.00665 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.932 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.316,  Adjusted R-squared:  0.2134
## F-statistic:  3.08 on 3 and 20 DF,  p-value: 0.05085


## Analysis of Variance Table
##
## Response: Composite_Nameability
##               Df Sum Sq Mean Sq F value  Pr(>F)
## age            1  0.419  0.4187  0.4332 0.51387
## Genotype       1  0.012  0.0119  0.0123 0.91207
## sex            1  0.598  0.5978  0.6185 0.43583
## age:Genotype   1  1.069  1.0688  1.1057 0.29876
## age:sex        1  1.965  1.9647  2.0325 0.16102
## Genotype:sex   1  0.180  0.1797  0.1859 0.66845
## age:Genotype:sex 1 6.493  6.4926  6.7167 0.01291 *
```

```
## Residuals          44 42.532   0.9666
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Composite_Nameability
##               Df  Sum Sq Mean Sq F value Pr(>F)
## age            1  1.4049 1.40486  1.3401 0.2584
## Genotype       1  0.1982 0.19822  0.1891 0.6676
## age:Genotype   1  0.5956 0.59557  0.5681 0.4583
## Residuals     24 25.1605 1.04835

## Analysis of Variance Table
##
## Response: Composite_Nameability
##               Df  Sum Sq Mean Sq F value    Pr(>F)
## age            1  0.0214  0.0214  0.0246 0.876960
## Genotype       1  0.0433  0.0433  0.0498 0.825652
## age:Genotype   1  7.9622  7.9622  9.1671 0.006648 **
## Residuals     20 17.3713  0.8686
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Odor percent correctly recognized linear model

```
##
```

56
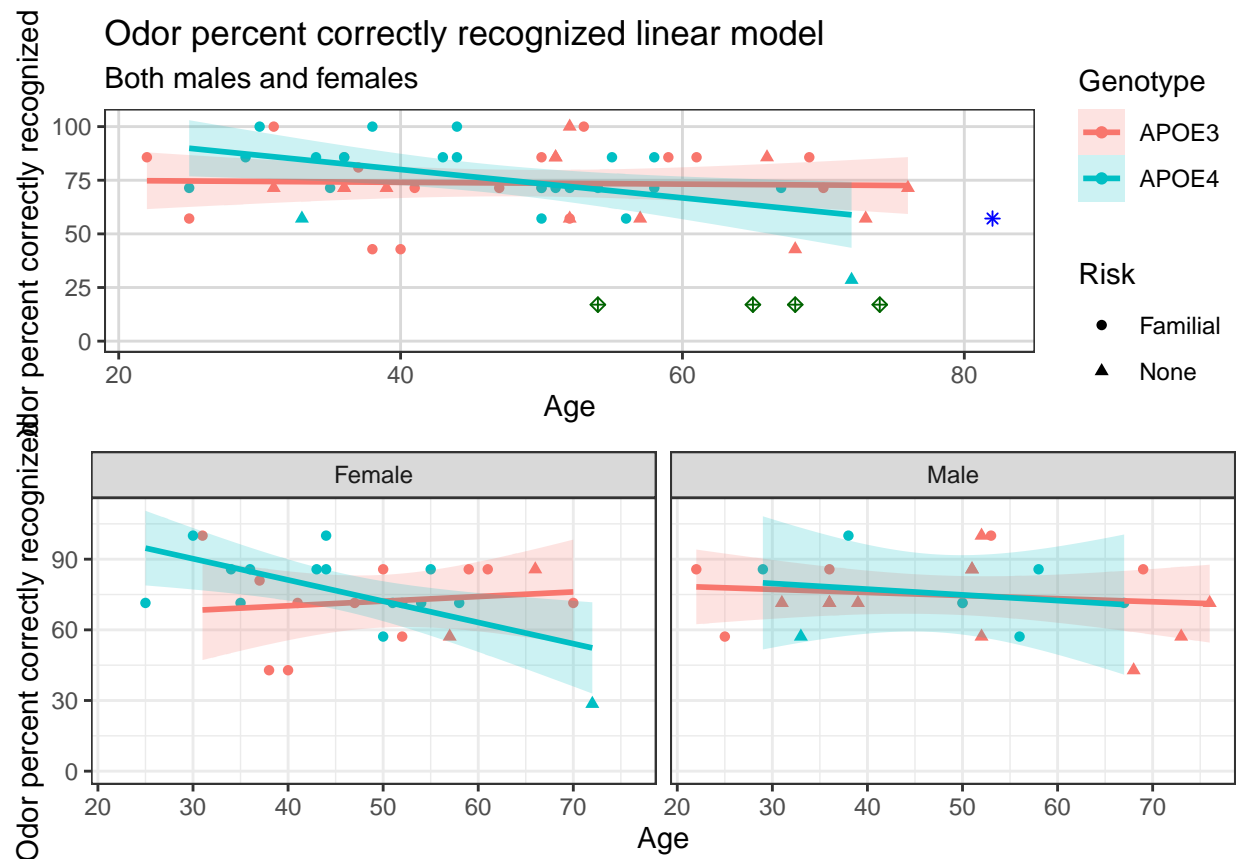
```
## Call:
## lm(formula = Recognized ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -29.3313 -14.2916   0.8143  11.2883  31.5527
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 62.3631    19.7433   3.159  0.00286 **
## age                          0.1963     0.3851   0.510  0.61282
## GenotypeAPOE4               54.8840    25.7876   2.128  0.03895 *
## sexMale                     18.7756    23.3780   0.803  0.42622
## age:GenotypeAPOE4           -1.0979     0.5221  -2.103  0.04121 *
## age:sexMale                 -0.3279     0.4572  -0.717  0.47702
## GenotypeAPOE4:sexMale      -49.0416    36.6754  -1.337  0.18804
## age:GenotypeAPOE4:sexMale    0.9870     0.7420   1.330  0.19030
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.22 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1509, Adjusted R-squared:  0.01583
## F-statistic: 1.117 on 7 and 44 DF,  p-value: 0.3697


##
## Call:
## lm(formula = Recognized ~ 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 = Recognized ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -29.331  -7.819  -1.418  11.288  25.837
##
```

```
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       81.1387    12.5140   6.484 2.54e-06 ***
## age               -0.1316     0.2463  -0.534    0.599
## GenotypeAPOE4      5.8424    26.0674   0.224    0.825
## age:GenotypeAPOE4 -0.1110     0.5270  -0.211    0.835
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.22 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.02754,    Adjusted R-squared:  -0.1183
## F-statistic: 0.1888 on 3 and 20 DF,  p-value: 0.9028


## Analysis of Variance Table
##
## Response: Recognized
##                  Df  Sum Sq Mean Sq F value  Pr(>F)
## age               1   678.1  678.14  2.5767 0.11560
## Genotype          1    31.2   31.15  0.1184 0.73244
## sex               1    18.7   18.69  0.0710 0.79113
## age:Genotype      1   847.5  847.47  3.2201 0.07961 .
## age:sex           1     6.1    6.09  0.0231 0.87982
## Genotype:sex      1    10.9   10.93  0.0415 0.83944
## age:Genotype:sex  1   465.7  465.70  1.7695 0.19030
## Residuals        44 11580.0  263.18
## ---
## 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  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: Recognized
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1  135.7 135.684  0.5160 0.4809
## Genotype      1    1.6   1.623  0.0062 0.9382
## age:Genotype  1   11.7  11.659  0.0443 0.8354
## Residuals    20 5259.2 262.960
```
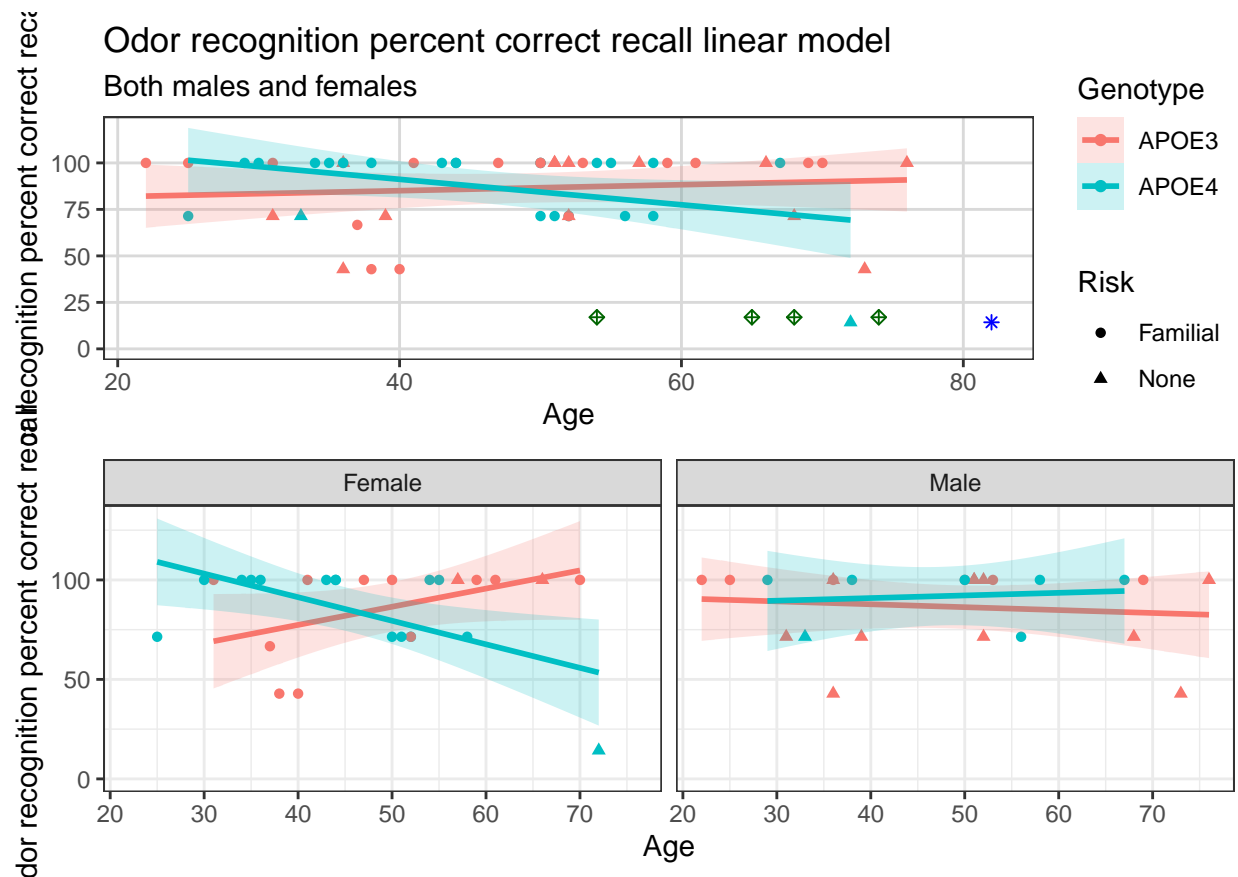
Odor recognition percent correct recall linear model
Both males and females

```
## 
## Call:
## lm(formula = PrecentCorrectRecall ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -45.481  -9.096   5.421  13.438  30.822
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)               40.8875    24.1641   1.692  0.09770 .
## age                        0.9126     0.4713   1.936  0.05926 .
## GenotypeAPOE4             97.7702    31.5617   3.098  0.00339 **
## sexMale                   52.6985    28.6126   1.842  0.07225 .
## age:GenotypeAPOE4         -2.0962     0.6390  -3.281  0.00203 **
## age:sexMale               -1.0584     0.5595  -1.892  0.06514 .
## GenotypeAPOE4:sexMale   -105.7329    44.8874  -2.356  0.02302 *
## age:GenotypeAPOE4:sexMale  2.3734     0.9081   2.614  0.01222 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 19.86 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.2168, Adjusted R-squared:  0.09215
## F-statistic:  1.74 on 7 and 44 DF,  p-value: 0.1245
```

```
## 
## Call:
## lm(formula = PrecentCorrectRecall ~ 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 = PrecentCorrectRecall ~ age * Genotype, data = combo_m)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -45.481 -15.051   9.502  13.739  17.493
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        93.5860    15.2163   6.150 5.21e-06 ***
## age                -0.1458     0.2995  -0.487    0.632
## GenotypeAPOE4      -7.9627    31.6966  -0.251    0.804
## age:GenotypeAPOE4   0.2772     0.6408   0.433    0.670
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 19.72 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared: 0.03132,    Adjusted R-squared:  -0.114
## F-statistic: 0.2155 on 3 and 20 DF,  p-value: 0.8845


## Analysis of Variance Table
## 
## Response: PrecentCorrectRecall
##                 Df  Sum Sq Mean Sq F value  Pr(>F)
## age              1   181.9  181.95  0.4615 0.50047
## Genotype         1     0.2    0.15  0.0004 0.98444
## sex              1    95.2   95.24  0.2416 0.62550
## age:Genotype     1  1598.5 1598.46  4.0546 0.05019 .
## age:sex          1    71.5   71.52  0.1814 0.67223
## Genotype:sex     1   160.1  160.14  0.4062 0.52721
## age:Genotype:sex 1  2693.0 2693.01  6.8310 0.01222 *
```

```
## Residuals        44 17346.3  394.23
## ---
## 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  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: PrecentCorrectRecall
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1   44.6   44.61  0.1147 0.7383
## Genotype      1  134.0  134.03  0.3447 0.5637
## age:Genotype  1   72.7   72.74  0.1871 0.6700
## Residuals    20 7775.8  388.79
```
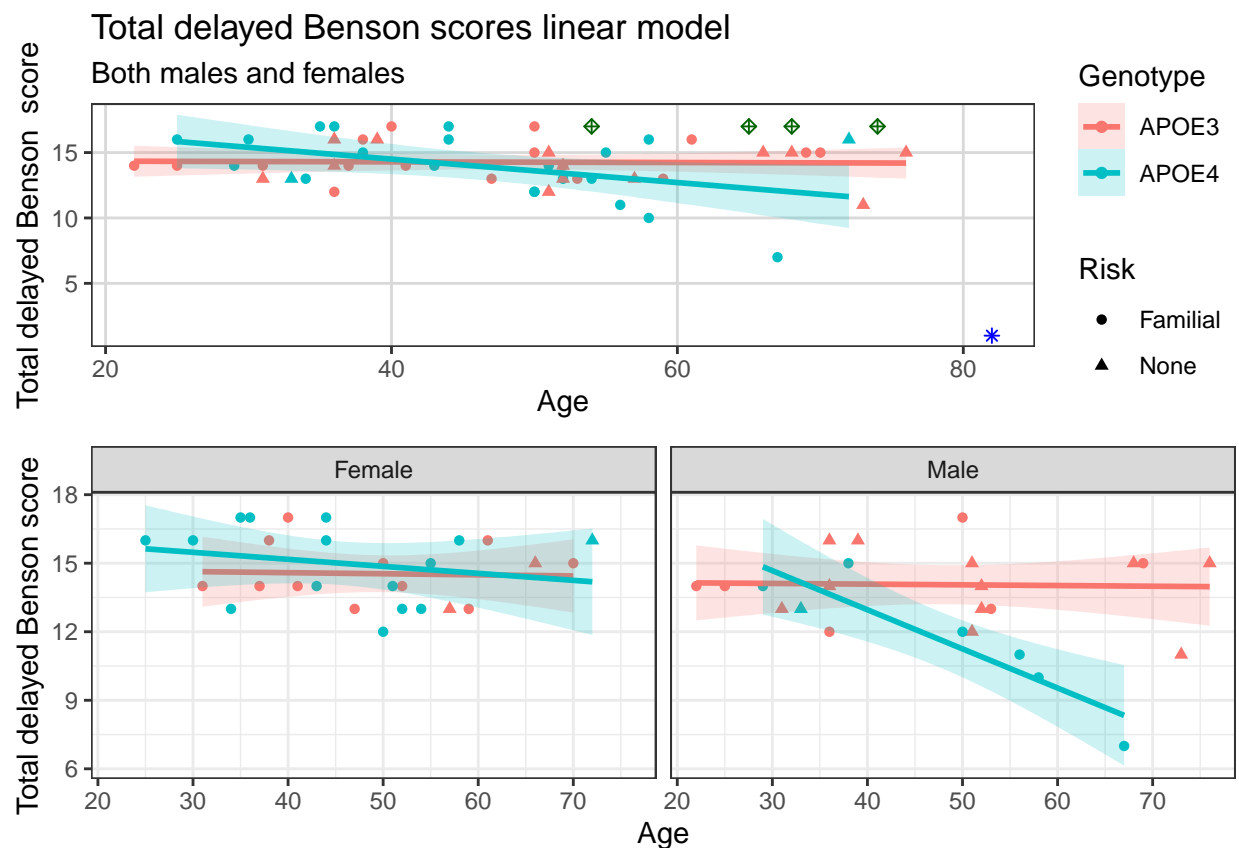

Total delayed Benson scores linear model

##

```
## Call:
## lm(formula = Delay_BensonTotal ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min      1Q   Median      3Q      Max
## -2.98321 -1.08618  0.03648  1.00992  2.94656
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)               14.776458   1.889012   7.822 7.27e-10 ***
## age                       -0.004767   0.036843  -0.129   0.8976
## GenotypeAPOE4              1.621105   2.467322   0.657   0.5146
## sexMale                   -0.570368   2.236772  -0.255   0.7999
## age:GenotypeAPOE4         -0.025926   0.049950  -0.519   0.6063
## age:sexMale                0.001714   0.043740   0.039   0.9689
## GenotypeAPOE4:sexMale      3.983654   3.509048   1.135   0.2624
## age:GenotypeAPOE4:sexMale -0.142247   0.070990  -2.004   0.0513 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.552 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.4648, Adjusted R-squared:  0.3796
## F-statistic: 5.458 on 7 and 44 DF,  p-value: 0.0001472


##
## 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
## -2.98321 -1.06336 -0.07175  1.00228  2.94656
##
```

```
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)       14.206090   1.205590  11.784 1.87e-10 ***
## age               -0.003053   0.023727  -0.129  0.89890
## GenotypeAPOE4      5.604759   2.511322   2.232  0.03723 *
## age:GenotypeAPOE4 -0.168173   0.050770  -3.312  0.00348 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.562 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.5627, Adjusted R-squared:  0.4971
## F-statistic: 8.579 on 3 and 20 DF,  p-value: 0.0007339


## Analysis of Variance Table
##
## Response: Delay_BensonTotal
##                 Df  Sum Sq Mean Sq F value    Pr(>F)
## age              1   9.663  9.6629  4.0107 0.0513972 .
## Genotype         1   2.089  2.0889  0.8670 0.3568619
## sex              1  30.850 30.8504 12.8049 0.0008564 ***
## age:Genotype     1  13.865 13.8652  5.7550 0.0207457 *
## age:sex          1   3.504  3.5036  1.4542 0.2342973
## Genotype:sex     1  22.406 22.4059  9.2999 0.0038718 **
## age:Genotype:sex 1   9.673  9.6734  4.0151 0.0512763 .
## Residuals       44 106.007  2.4093
## ---
## 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  7.916  7.9162  3.2436 0.086804 .
## Genotype      1 28.118 28.1180 11.5209 0.002879 **
## age:Genotype  1 26.779 26.7787 10.9721 0.003476 **
## Residuals    20 48.812  2.4406
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
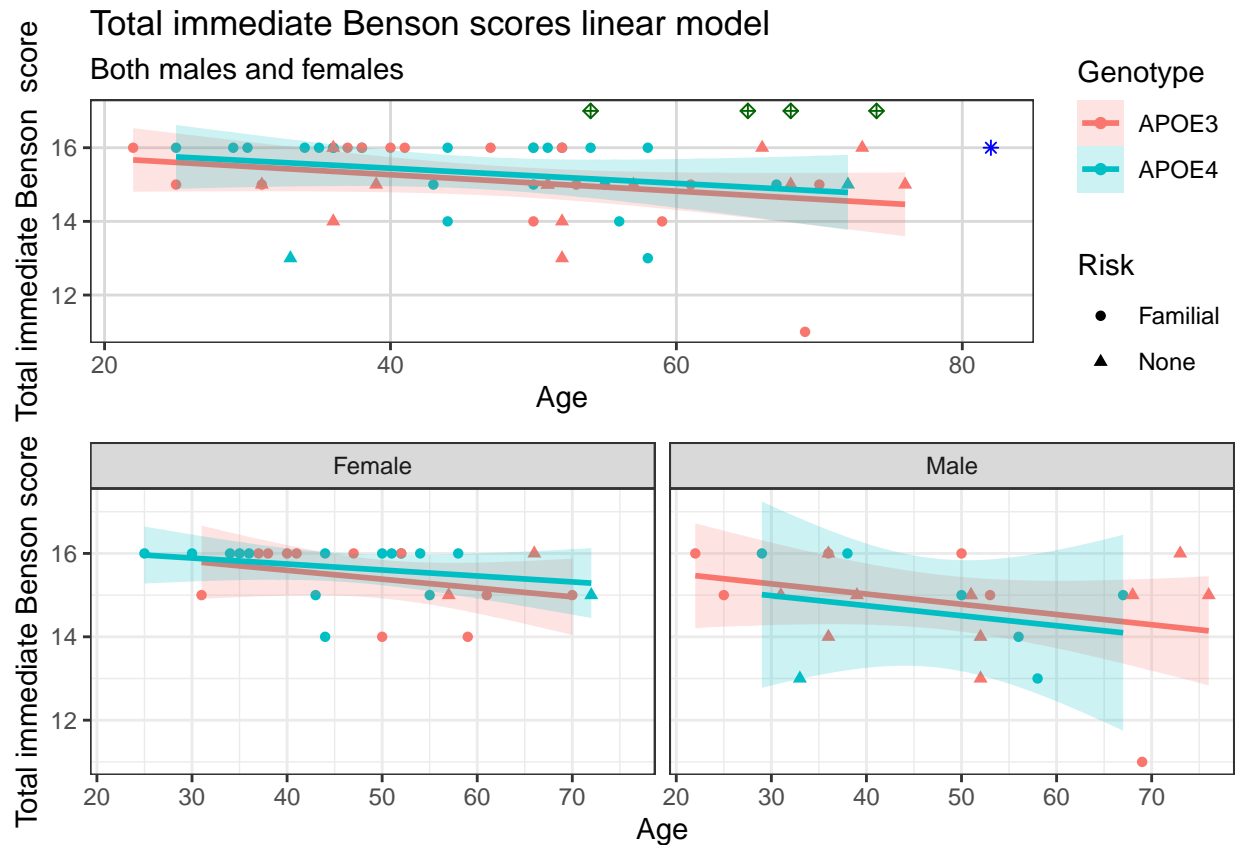
Total immediate Benson scores linear model

Both males and females

```
##
## Call:
## lm(formula = Im_BensonTotal ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.3144 -0.3697  0.2443  0.5172  1.7837
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)             16.442619   1.217782  13.502   <2e-16 ***
## age                     -0.021193   0.023751  -0.892    0.377
## GenotypeAPOE4           -0.123756   1.590599  -0.078    0.938
## sexMale                 -0.436378   1.441971  -0.303    0.764
## age:GenotypeAPOE4        0.006869   0.032201   0.213    0.832
## age:sexMale             -0.003327   0.028197  -0.118    0.907
## GenotypeAPOE4:sexMale   -0.173523   2.262164  -0.077    0.939
## age:GenotypeAPOE4:sexMale -0.006406   0.045765  -0.140    0.889
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.001 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.233,  Adjusted R-squared:  0.111
## F-statistic:  1.91 on 7 and 44 DF,  p-value: 0.09076
```

```
## 
## 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
## -3.3144 -0.4777  0.2688  0.8765  1.7837
## 
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)       16.006242   0.989431  16.177 5.93e-13 ***
## age               -0.024520   0.019473  -1.259    0.222
## GenotypeAPOE4     -0.297280   2.061048  -0.144    0.887
## age:GenotypeAPOE4  0.000463   0.041668   0.011    0.991
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.282 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared: 0.09925,    Adjusted R-squared:  -0.03587
## F-statistic: 0.7345 on 3 and 20 DF,  p-value: 0.5436


## Analysis of Variance Table
## 
## Response: Im_BensonTotal
##                 Df Sum Sq Mean Sq F value   Pr(>F)
## age              1  4.814  4.8141  4.8079 0.033661 *
## Genotype         1  0.449  0.4490  0.4484 0.506586
## sex              1  7.356  7.3558  7.3464 0.009544 **
## age:Genotype     1  0.062  0.0618  0.0617 0.804963
## age:sex          1  0.031  0.0310  0.0309 0.861243
## Genotype:sex     1  0.655  0.6550  0.6542 0.422978
## age:Genotype:sex 1  0.020  0.0196  0.0196 0.889315
```

```
## Residuals          44 44.056  1.0013
## ---
## 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  3.247  3.2468  1.9751 0.1753
## Genotype       1  0.375  0.3755  0.2284 0.6379
## age:Genotype   1  0.000  0.0002  0.0001 0.9912
## Residuals     20 32.878  1.6439
```
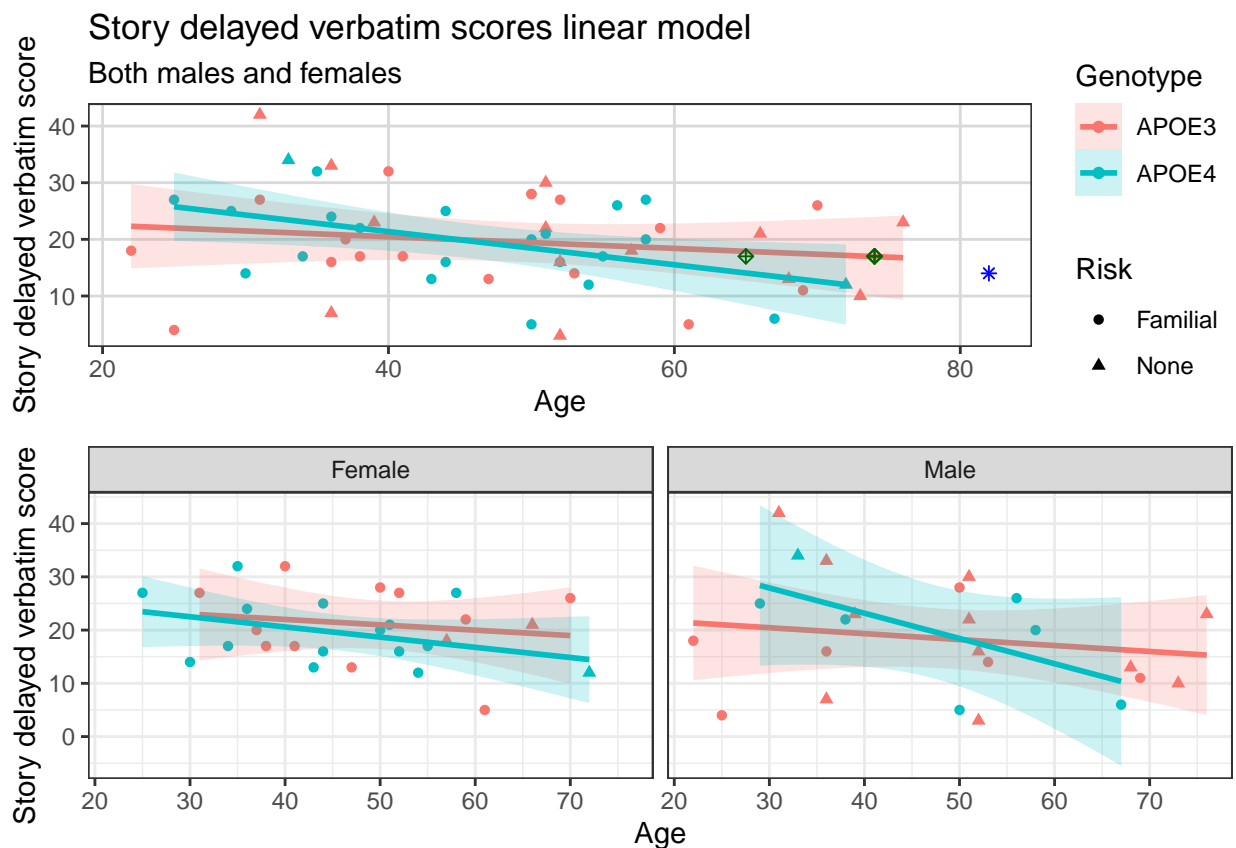

Story delayed verbatim scores linear model

```
##
```

66

```
## Call:
## lm(formula = Delayed_verbatim ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -17.004  -4.780  -2.054   5.577  21.665
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)               26.03471   10.45192   2.491   0.0166 *
## age                       -0.10085    0.20385  -0.495   0.6233
## GenotypeAPOE4              2.21225   13.65172   0.162   0.8720
## sexMale                   -2.24151   12.37608  -0.181   0.8571
## age:GenotypeAPOE4         -0.09052    0.27638  -0.328   0.7448
## age:sexMale               -0.01072    0.24201  -0.044   0.9649
## GenotypeAPOE4:sexMale     16.13051   19.41560   0.831   0.4106
## age:GenotypeAPOE4:sexMale -0.27209    0.39279  -0.693   0.4921
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.588 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1269, Adjusted R-squared:  -0.01206
## F-statistic: 0.9132 on 7 and 44 DF,  p-value: 0.5054


##
## 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
## -17.004  -4.548  -2.662   7.555  21.665
##
```

```
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        23.7932     8.0332   2.962  0.00771 **
## age                -0.1116     0.1581  -0.706  0.48854
## GenotypeAPOE4       18.3428    16.7336   1.096  0.28603
## age:GenotypeAPOE4  -0.3626     0.3383  -1.072  0.29655
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.41 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1338, Adjusted R-squared:  0.003865
## F-statistic:  1.03 on 3 and 20 DF,  p-value: 0.4006


## Analysis of Variance Table
##
## Response: Delayed_verbatim
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1  270.8 270.833  3.6719 0.06185 .
## Genotype         1    2.3   2.328  0.0316 0.85979
## sex              1   29.4  29.411  0.3988 0.53100
## age:Genotype     1   72.4  72.450  0.9823 0.32706
## age:sex          1   32.8  32.758  0.4441 0.50861
## Genotype:sex     1   28.3  28.319  0.3839 0.53869
## age:Genotype:sex 1   35.4  35.393  0.4798 0.49213
## Residuals       44 3245.3  73.758
## ---
## 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           1 204.03  204.03  1.8828 0.1852
## Genotype      1   6.23    6.23  0.0575 0.8129
## age:Genotype  1 124.49  124.49  1.1489 0.2965
## Residuals    20 2167.21  108.36
```
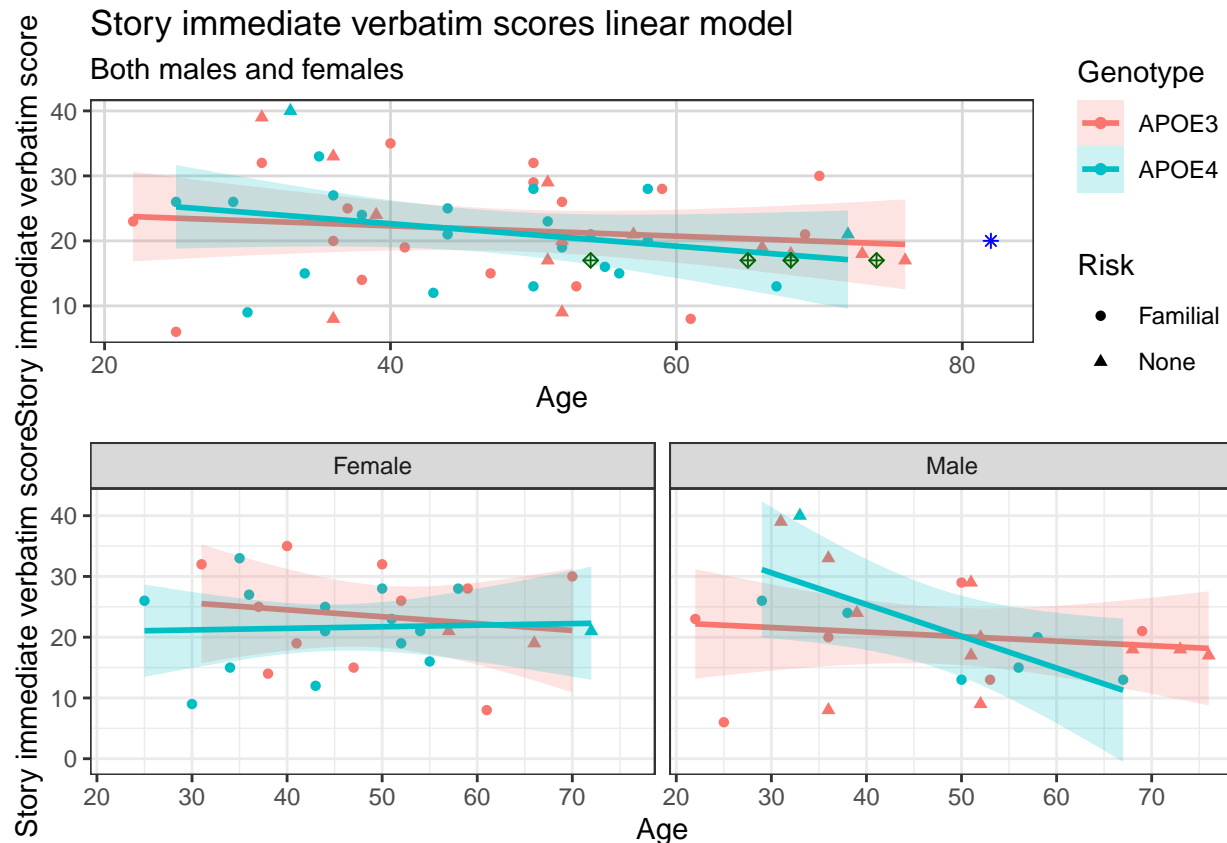
Story immediate verbatim scores linear model

```
## 
## Call:
## lm(formula = Immediate_verbatim ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -15.9716  -5.1945  -0.4724   5.6431  17.4768 
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)    
## (Intercept)              29.0273     9.7709   2.971   0.0048 ** 
## age                      -0.1130     0.1906  -0.593   0.5561    
## GenotypeAPOE4            -8.6142    12.7623  -0.675   0.5032    
## sexMale                  -5.1876    11.5697  -0.448   0.6561    
## age:GenotypeAPOE4         0.1391     0.2584   0.538   0.5930    
## age:sexMale               0.0383     0.2262   0.169   0.8663    
## GenotypeAPOE4:sexMale    31.0593    18.1506   1.711   0.0941 .  
## age:GenotypeAPOE4:sexMale -0.5870     0.3672  -1.599   0.1171    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 8.029 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1375, Adjusted R-squared:  0.0003282 
## F-statistic: 1.002 on 7 and 44 DF,  p-value: 0.4426
```

```
## 
## 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
## -15.9716  -3.5536  -0.5715   3.3130  17.4768
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       23.83972    6.58364   3.621   0.0017 **
## age               -0.07473    0.12957  -0.577   0.5706
## GenotypeAPOE4     22.44519   13.71414   1.637   0.1173
## age:GenotypeAPOE4 -0.44792    0.27725  -1.616   0.1219
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 8.531 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:    0.2,  Adjusted R-squared:  0.08003
## F-statistic: 1.667 on 3 and 20 DF,  p-value: 0.2061


## Analysis of Variance Table
## 
## Response: Immediate_verbatim
##                 Df  Sum Sq Mean Sq F value Pr(>F)
## age              1  118.01 118.009  1.8307 0.1830
## Genotype         1    1.38   1.383  0.0215 0.8842
## sex              1   46.64  46.641  0.7236 0.3996
## age:Genotype     1   15.64  15.639  0.2426 0.6248
## age:sex          1   79.25  79.246  1.2294 0.2735
## Genotype:sex     1   26.65  26.646  0.4134 0.5236
## age:Genotype:sex 1  164.73 164.732  2.5556 0.1171
```

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```
## Residuals         44 2836.22   64.460


## 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  167.19  167.195  2.2972 0.1453
## Genotype     1    6.81    6.808  0.0935 0.7629
## age:Genotype 1  189.96  189.962  2.6100 0.1219
## Residuals   20 1455.66   72.783
```
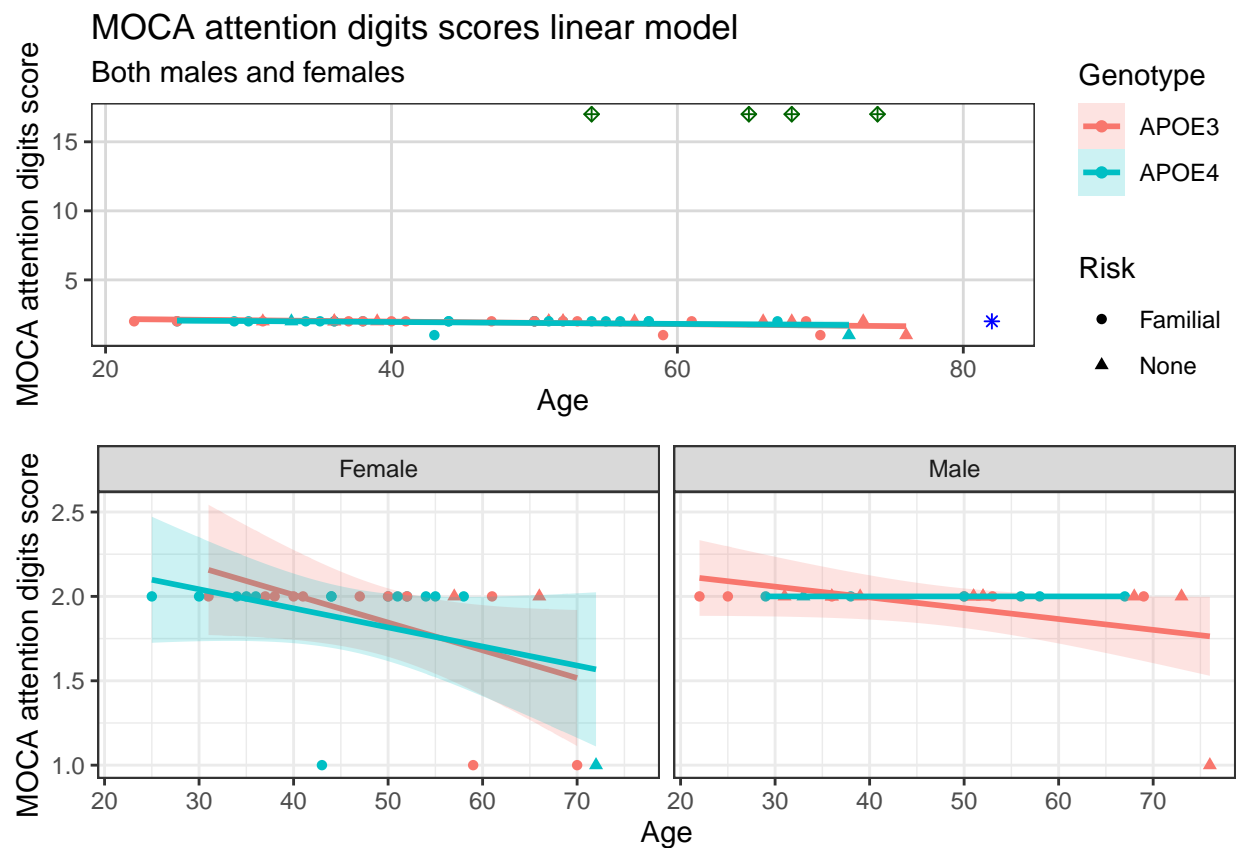


```
##
## Call:
## lm(formula = MOCA_Attention_Digits ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
```

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```
##      Min       1Q   Median        3Q       Max
## -0.89530 -0.02515  0.00514  0.16229  0.41792
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)               2.666161   0.340270   7.835 6.96e-10 ***
## age                      -0.016425   0.006637  -2.475   0.0172 *
## GenotypeAPOE4            -0.284904   0.444442  -0.641   0.5248
## sexMale                  -0.416052   0.402912  -1.033   0.3074
## age:GenotypeAPOE4         0.005124   0.008998   0.569   0.5719
## age:sexMale               0.010021   0.007879   1.272   0.2101
## GenotypeAPOE4:sexMale     0.034796   0.632089   0.055   0.9563
## age:GenotypeAPOE4:sexMale 0.001281   0.012788   0.100   0.9207
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2796 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.2389, Adjusted R-squared:  0.1178
## F-statistic: 1.973 on 7 and 44 DF,  p-value: 0.08066


##
## 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
## -0.76335 -0.01954  0.00000  0.07813  0.21743
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       2.250109   0.150764  14.925 2.64e-12 ***
## age              -0.006405   0.002967  -2.158   0.0432 *
```

```
## GenotypeAPOE4      -0.250109   0.314052  -0.796    0.4352
## age:GenotypeAPOE4  0.006405   0.006349   1.009    0.3251
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1954 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.2035, Adjusted R-squared:  0.08398
## F-statistic: 1.703 on 3 and 20 DF,  p-value: 0.1986


## Analysis of Variance Table
##
## Response: MOCA_Attention_Digits
##                   Df Sum Sq Mean Sq F value   Pr(>F)
## age                1 0.6891 0.68912  8.8152 0.004821 **
## Genotype           1 0.0030 0.00300  0.0384 0.845493
## sex                1 0.1396 0.13958  1.7855 0.188343
## age:Genotype       1 0.0102 0.01020  0.1304 0.719718
## age:sex            1 0.2107 0.21067  2.6948 0.107804
## Genotype:sex       1 0.0262 0.02624  0.3356 0.565333
## age:Genotype:sex   1 0.0008 0.00078  0.0100 0.920680
## Residuals         44 3.4396 0.07817
## ---
## 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 0.14166 0.141658  3.7115 0.06837 .
## Genotype       1 0.01448 0.014484  0.3795 0.54482
## age:Genotype   1 0.03884 0.038839  1.0176 0.32514
## Residuals     20 0.76335 0.038168
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
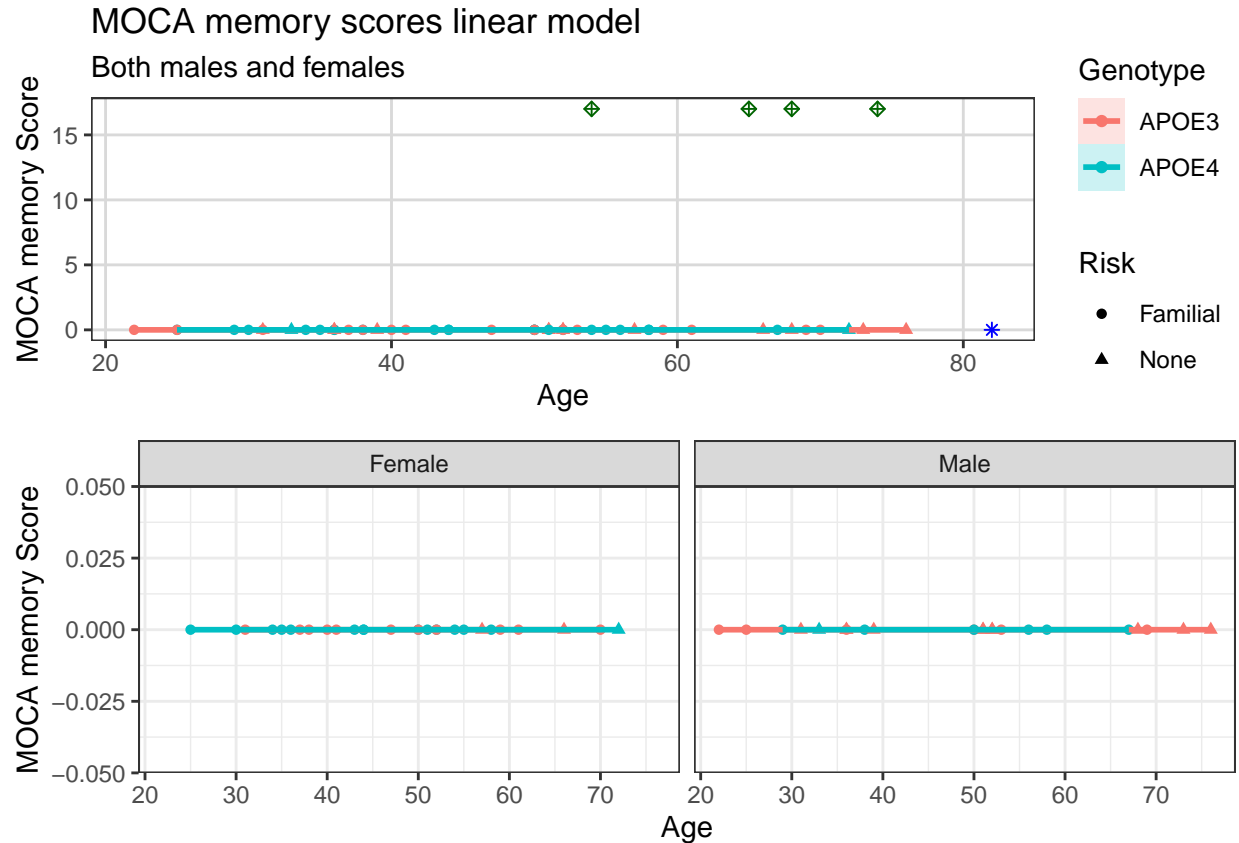
MOCA memory scores linear model

Both males and females


```
## 
## 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 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:    NaN,  Adjusted R-squared:    NaN
## F-statistic:   NaN on 7 and 44 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 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:    NaN,  Adjusted R-squared:    NaN
## F-statistic:   NaN on 3 and 20 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        44      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  20      0       0
```

MOCA naming scores linear model


```
##
## 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    0.52067   6.465 6.97e-08 ***
## age                        -0.01196    0.01016  -1.178    0.245
## GenotypeAPOE4              -0.36639    0.68007  -0.539    0.593
## sexMale                    -0.36639    0.61653  -0.594    0.555
## age:GenotypeAPOE4           0.01196    0.01377   0.869    0.390
## age:sexMale                 0.01196    0.01206   0.992    0.327
## GenotypeAPOE4:sexMale       0.36639    0.96721   0.379    0.707
## age:GenotypeAPOE4:sexMale  -0.01196    0.01957  -0.611    0.544
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4278 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.08759,    Adjusted R-squared:  -0.05756
## F-statistic: 0.6034 on 7 and 44 DF,  p-value: 0.7497


##
## 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
## -4.339e-16 -1.410e-16 -3.262e-17  0.000e+00  1.702e-15
##
## Coefficients:
##                    Estimate Std. Error    t value Pr(>|t|)
## (Intercept)       3.000e+00  3.321e-16  9.034e+15   <2e-16 ***
## age              -1.317e-17  6.535e-18 -2.015e+00   0.0576 .
## GenotypeAPOE4    -7.631e-16  6.917e-16 -1.103e+00   0.2831
## age:GenotypeAPOE4 1.317e-17  1.398e-17  9.420e-01   0.3577
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 4.303e-16 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.5505, Adjusted R-squared:  0.4831
## F-statistic: 8.166 on 3 and 20 DF,  p-value: 0.000957


## Analysis of Variance Table
##
## Response: MOCA_Naming
##                 Df Sum Sq  Mean Sq F value Pr(>F)
## age              1 0.0804 0.080384  0.4392 0.5110
## Genotype         1 0.1078 0.107839  0.5892 0.4468
## sex              1 0.2352 0.235211  1.2850 0.2631
## age:Genotype     1 0.0237 0.023655  0.1292 0.7209
## age:sex          1 0.1387 0.138672  0.7576 0.3888
## Genotype:sex     1 0.1190 0.119020  0.6502 0.4244
## age:Genotype:sex 1 0.0684 0.068401  0.3737 0.5441
## Residuals       44 8.0537 0.183040


## 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 5.7460e-31 5.7456e-31  3.1030 0.09343 .
## Genotype      1 9.4000e-32 9.4010e-32  0.5077 0.48437
## age:Genotype  1 1.6410e-31 1.6414e-31  0.8865 0.35767
## Residuals    20 3.7032e-30 1.8516e-31
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
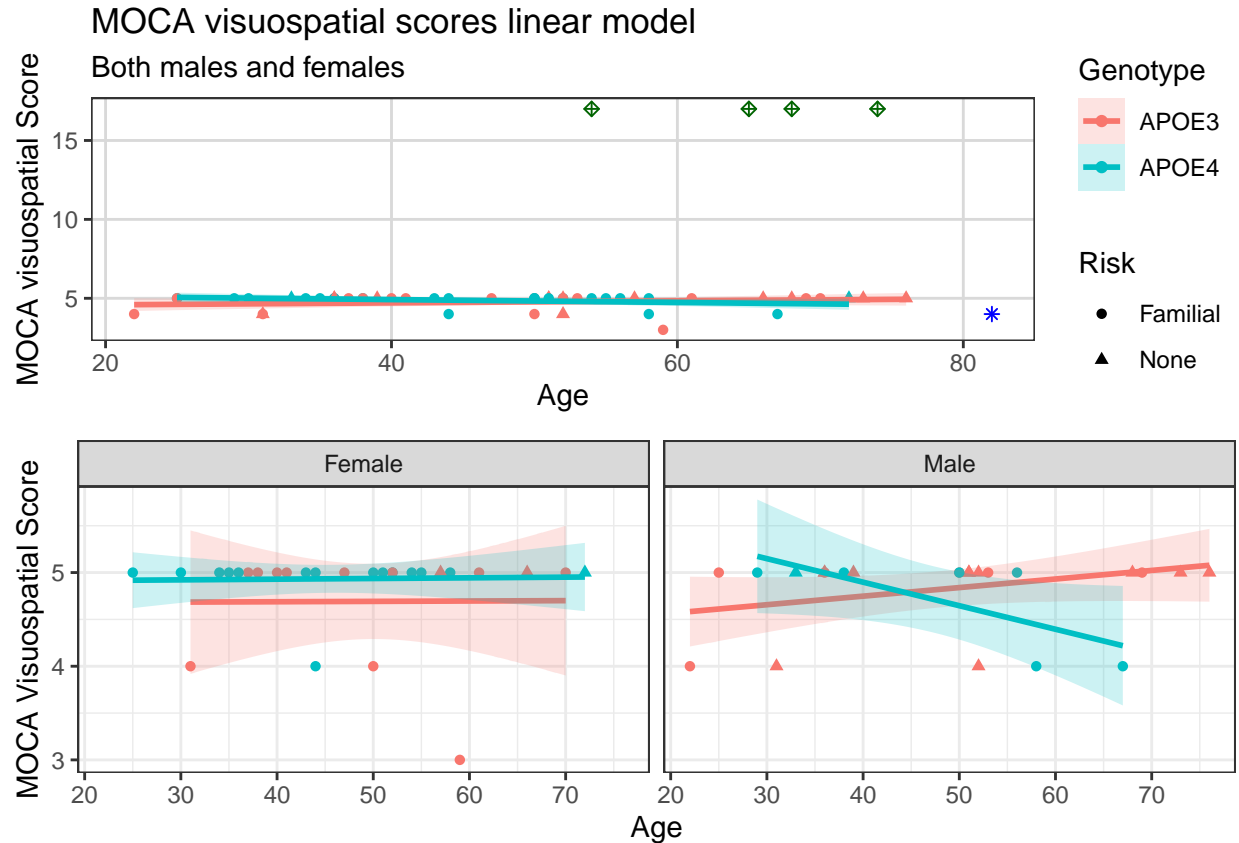
MOCA visuospatial scores linear model


```
##
## Call:
## lm(formula = MOCA_Visuospatial ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.69585 -0.02288  0.07393  0.29137  0.50460
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              4.672835   0.534034   8.750 3.47e-11 ***
## age                      0.000390   0.010416   0.037   0.9703
## GenotypeAPOE4            0.227530   0.697525   0.326   0.7458
## sexMale                 -0.291105   0.632347  -0.460   0.6475
## age:GenotypeAPOE4        0.000334   0.014121   0.024   0.9812
## age:sexMale              0.008769   0.012365   0.709   0.4820
## GenotypeAPOE4:sexMale    1.292744   0.992027   1.303   0.1993
## age:GenotypeAPOE4:sexMale -0.034611  0.020069  -1.725   0.0916 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4388 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.1592, Adjusted R-squared:  0.02547
## F-statistic:  1.19 on 7 and 44 DF,  p-value: 0.3281
```

```
## 
## 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
## -0.85801 -0.10177  0.09265  0.26793  0.50460
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       4.381730   0.287256  15.254 1.77e-12 ***
## age               0.009159   0.005654   1.620   0.1209
## GenotypeAPOE4     1.520274   0.598372   2.541   0.0195 *
## age:GenotypeAPOE4 -0.034277   0.012097  -2.834   0.0103 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.3722 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.2999, Adjusted R-squared:  0.1949
## F-statistic: 2.856 on 3 and 20 DF,  p-value: 0.06292


## Analysis of Variance Table
## 
## Response: MOCA_Visuospatial
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1 0.0021 0.00211  0.0110 0.91703
## Genotype         1 0.1241 0.12405  0.6443 0.42649
## sex              1 0.0005 0.00047  0.0024 0.96092
## age:Genotype     1 0.5207 0.52068  2.7041 0.10722
## age:sex          1 0.0181 0.01807  0.0938 0.76079
## Genotype:sex     1 0.3665 0.36648  1.9032 0.17469
## age:Genotype:sex 1 0.5727 0.57269  2.9742 0.09162 .
```

```
## Residuals          44 8.4724 0.19255
## ---
## 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 0.01727 0.01727  0.1247 0.72773
## Genotype    1 0.05742 0.05742  0.4144 0.52706
## age:Genotype 1 1.11246 1.11246  8.0288 0.01027 *
## Residuals  20 2.77118 0.13856
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
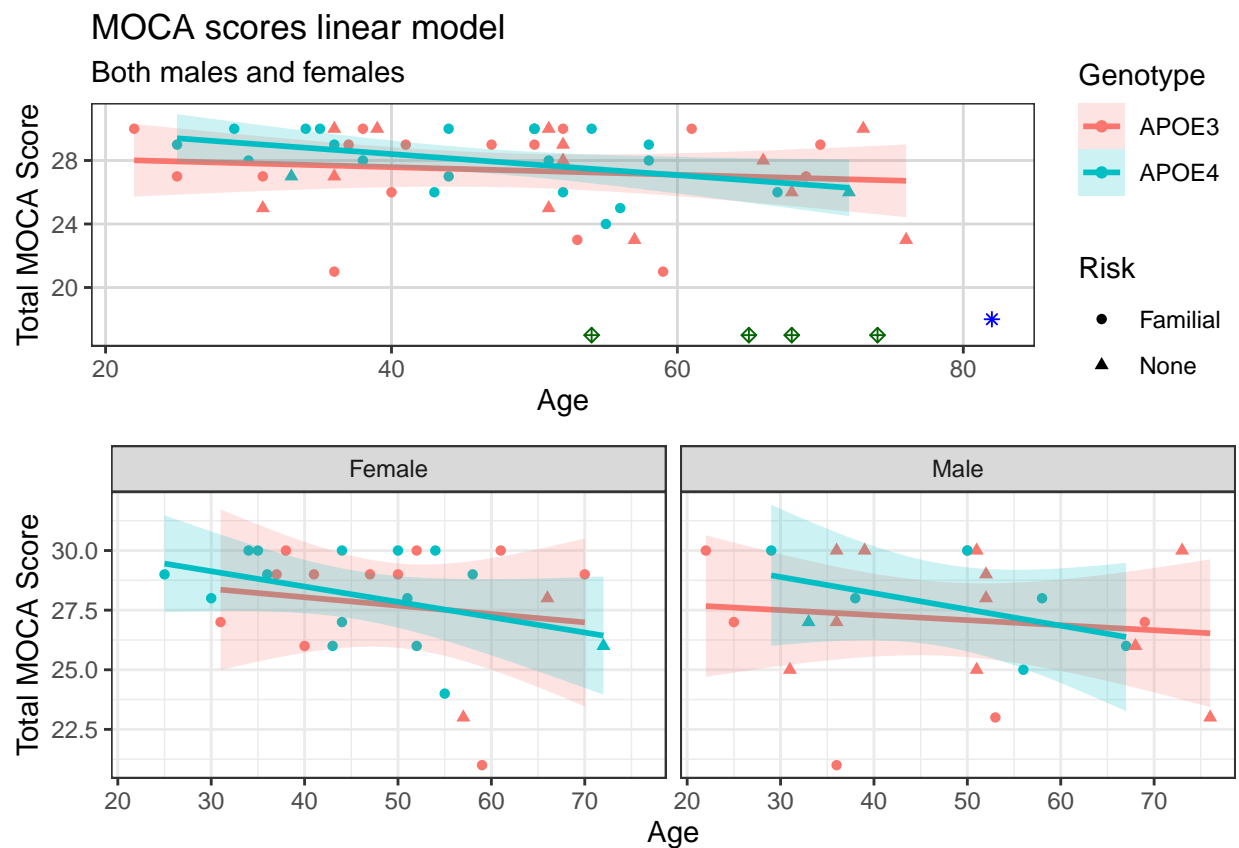

MOCA scores linear model

```
##
```

```
## Call:
## lm(formula = MOCA_TOTAL ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min     1Q  Median     3Q    Max
## -6.3758 -1.4390  0.5873  1.9073  3.4049
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                29.44483    3.09858   9.503 3.15e-12 ***
## age                        -0.03510    0.06043  -0.581    0.564
## GenotypeAPOE4               1.61407    4.04719   0.399    0.692
## sexMale                    -1.30941    3.66901  -0.357    0.723
## age:GenotypeAPOE4          -0.02915    0.08193  -0.356    0.724
## age:sexMale                 0.01400    0.07175   0.195    0.846
## GenotypeAPOE4:sexMale       1.18223    5.75595   0.205    0.838
## age:GenotypeAPOE4:sexMale  -0.01780    0.11645  -0.153    0.879
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.546 on 44 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.08598,    Adjusted R-squared:  -0.05943
## F-statistic: 0.5913 on 7 and 44 DF,  p-value: 0.7594


##
## 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
## -6.3758 -1.7796 -0.0128  2.3642  3.4049
##
```

```
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       28.13542    2.11096  13.328 2.08e-11 ***
## age               -0.02110    0.04155  -0.508    0.617
## GenotypeAPOE4       2.79630    4.39728   0.636    0.532
## age:GenotypeAPOE4 -0.04694    0.08890  -0.528    0.603
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.735 on 20 degrees of freedom
##   (1 observation deleted due to missingness)
## Multiple R-squared:  0.05853,   Adjusted R-squared:  -0.08269
## F-statistic: 0.4145 on 3 and 20 DF,  p-value: 0.7445


## Analysis of Variance Table
##
## Response: MOCA_TOTAL
##                  Df  Sum Sq Mean Sq F value Pr(>F)
## age               1  16.020 16.0200  2.4713 0.1231
## Genotype          1   3.413  3.4133  0.5265 0.4719
## sex               1   3.366  3.3658  0.5192 0.4750
## age:Genotype      1   3.490  3.4902  0.5384 0.4670
## age:sex           1   0.073  0.0725  0.0112 0.9163
## Genotype:sex      1   0.317  0.3169  0.0489 0.8260
## age:Genotype:sex  1   0.151  0.1514  0.0234 0.8792
## Residuals        44 285.227  6.4824


## 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  5.625  5.6253  0.7518 0.3962
## Genotype      1  1.592  1.5920  0.2128 0.6496
## age:Genotype  1  2.086  2.0864  0.2788 0.6033
## Residuals    20 149.655  7.4827
```