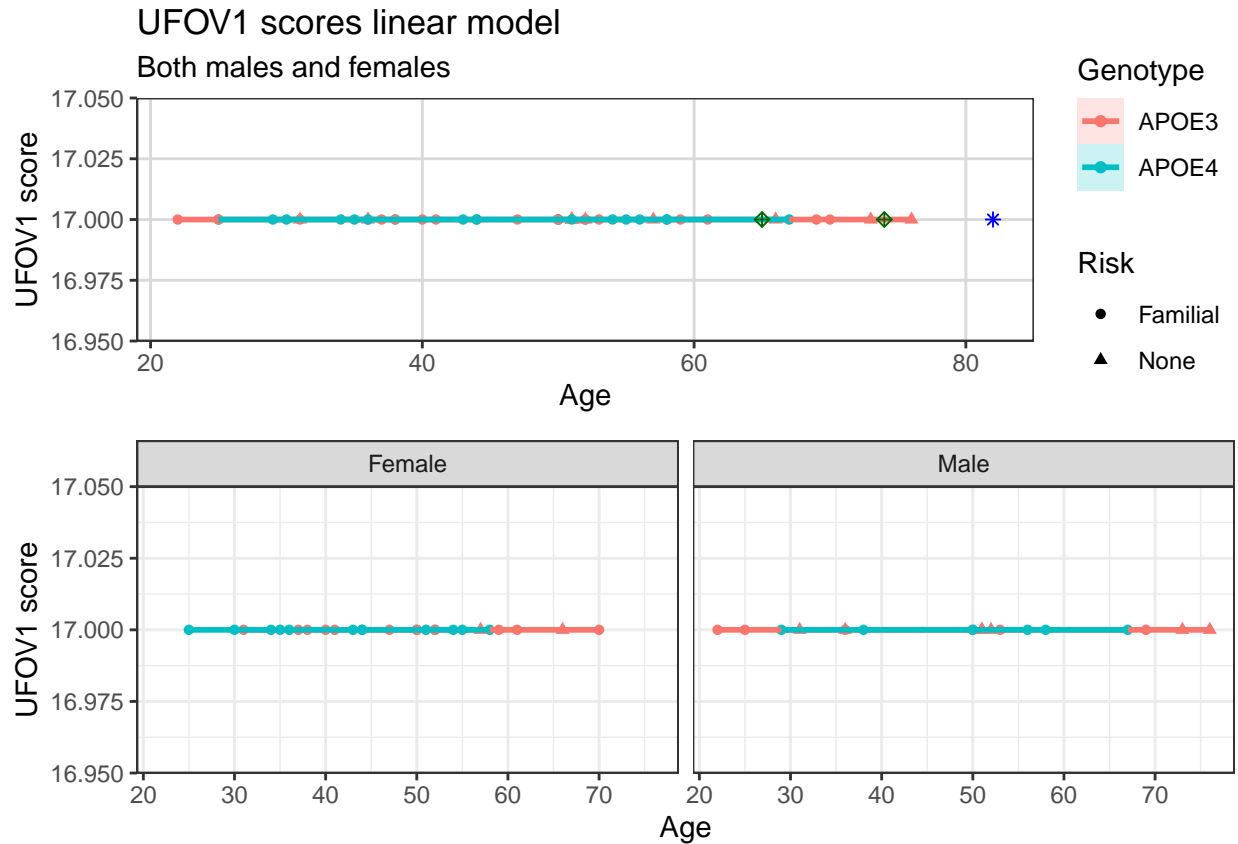# Linear models with AD subject

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
## -4.278e-14  0.000e+00  0.000e+00  0.000e+00  8.381e-15
##
## Coefficients:
##                   Estimate Std. Error    t value Pr(>|t|)
## (Intercept)      1.700e+01  8.896e-15  1.911e+15   <2e-16 ***
## age              2.449e-16  1.735e-16  1.411e+00    0.166
## GenotypeAPOE4    1.597e-14  1.255e-14  1.273e+00    0.210
## sexMale          1.597e-14  1.080e-14  1.479e+00    0.147
```

```
## age:GenotypeAPOE4        -2.449e-16  2.630e-16 -9.310e-01    0.358
## age:sexMale              -2.449e-16  2.110e-16 -1.160e+00    0.253
## GenotypeAPOE4:sexMale    -1.597e-14  1.842e-14 -8.670e-01    0.391
## age:GenotypeAPOE4:sexMale 2.449e-16  3.722e-16  6.580e-01    0.514
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.31e-15 on 39 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.4983, Adjusted R-squared:  0.4083
## F-statistic: 5.534 on 7 and 39 DF,  p-value: 0.0001787


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


##
## Call:
## lm(formula = ufov1 ~ age * Genotype, data = combo_m)
##
## Residuals:
##        Min         1Q     Median         3Q        Max
## -3.761e-15 -8.569e-16 -3.016e-16  0.000e+00  1.179e-14
##
## Coefficients:
##                    Estimate Std. Error    t value Pr(>|t|)
## (Intercept)       1.700e+01  2.865e-15  5.934e+15   <2e-16 ***
## age              -1.128e-16  5.623e-17 -2.006e+00   0.0621 .
## GenotypeAPOE4     -6.581e-15  6.311e-15 -1.043e+00   0.3125
## age:GenotypeAPOE4  1.128e-16  1.232e-16  9.150e-01   0.3737
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.421e-15 on 16 degrees of freedom
##   (3 observations deleted due to missingness)
## Multiple R-squared:  0.4854, Adjusted R-squared:  0.389
```

```
## F-statistic: 5.032 on 3 and 16 DF,  p-value: 0.01207


## Analysis of Variance Table
##
## Response: ufov1
##                   Df     Sum Sq    Mean Sq F value Pr(>F)
## age                1 1.2440e-29 1.2438e-29  0.2328 0.6322
## Genotype           1 4.4320e-29 4.4323e-29  0.8295 0.3680
## sex                1 5.5240e-29 5.5244e-29  1.0339 0.3155
## age:Genotype       1 1.7180e-29 1.7178e-29  0.3215 0.5740
## age:sex            1 4.1650e-29 4.1648e-29  0.7794 0.3827
## Genotype:sex       1 4.4520e-29 4.4523e-29  0.8332 0.3669
## age:Genotype:sex   1 2.3130e-29 2.3135e-29  0.4330 0.5144
## Residuals         39 2.0839e-27 5.3434e-29


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


## Analysis of Variance Table
##
## Response: ufov1
##              Df     Sum Sq    Mean Sq F value  Pr(>F)
## age           1 3.8418e-29 3.8418e-29  3.2818 0.08886 .
## Genotype      1 4.2900e-30 4.2900e-30  0.3665 0.55342
## age:Genotype  1 9.8040e-30 9.8040e-30  0.8375 0.37369
## Residuals    16 1.8730e-28 1.1706e-29
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
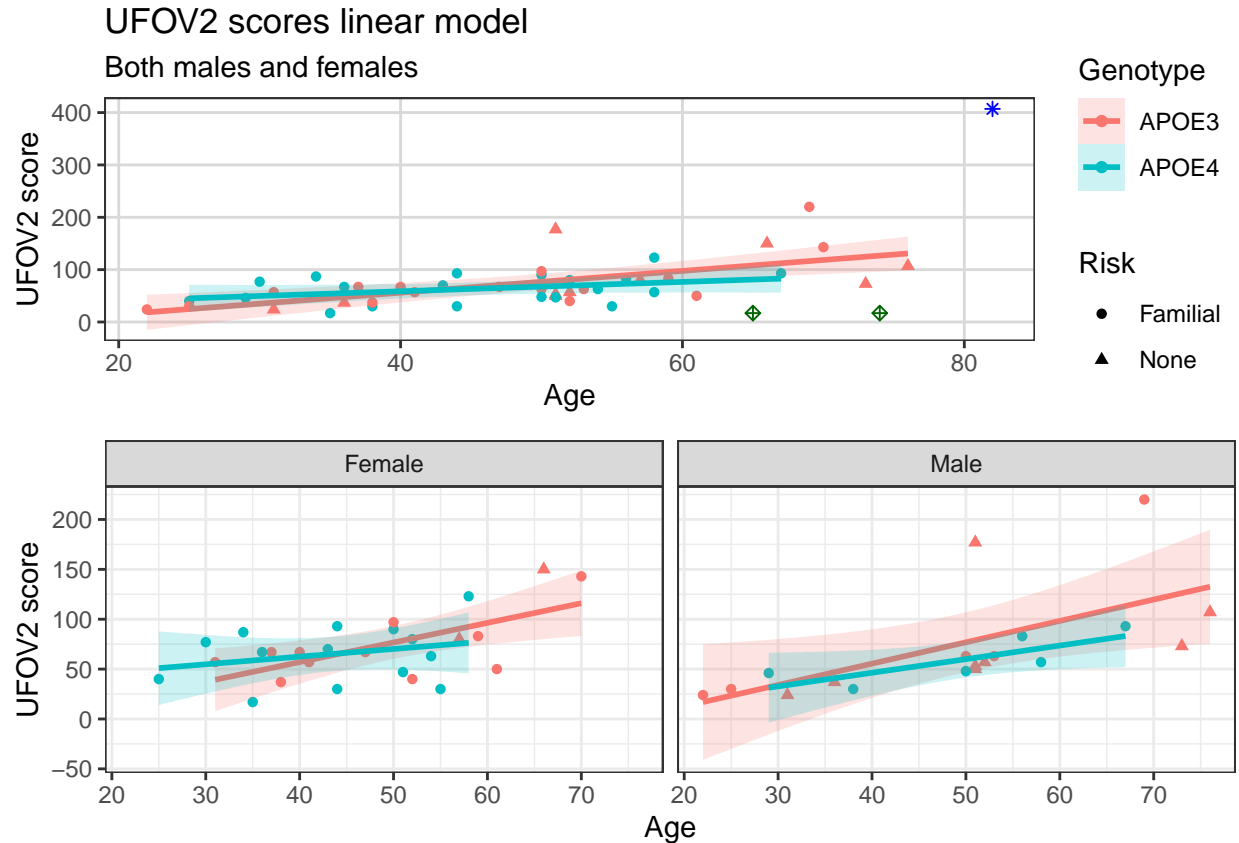
UFOV2 scores linear model
Both males and females


```
## 
## Call:
## lm(formula = ufov2 ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -53.124 -19.247  -6.845  15.627 102.440 
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             -21.6677    42.4724  -0.510   0.6129
## age                       1.9671     0.8284   2.375   0.0227 *
## GenotypeAPOE4            53.4227    59.8971   0.892   0.3781
## sexMale                  -8.5117    52.2628  -0.163   0.8715
## age:GenotypeAPOE4        -1.1989     1.2558  -0.955   0.3458
## age:sexMale               0.1740     1.0150   0.171   0.8648
## GenotypeAPOE4:sexMale   -31.5077    88.3451  -0.357   0.7233
## age:GenotypeAPOE4:sexMale  0.4221     1.7811   0.237   0.8139
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 34.9 on 38 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.3735, Adjusted R-squared:  0.2581 
## F-statistic: 3.236 on 7 and 38 DF,  p-value: 0.008606
```

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


##
## Call:
## lm(formula = ufov2 ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -53.124 -22.231 -12.196   8.462 102.440
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -30.1794    37.4808  -0.805  0.43329
## age                 2.1411     0.7219   2.966  0.00961 **
## GenotypeAPOE4      21.9150    79.9222   0.274  0.78767
## age:GenotypeAPOE4  -0.7768     1.5545  -0.500  0.62454
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 42.95 on 15 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.4078, Adjusted R-squared:  0.2894
## F-statistic: 3.444 on 3 and 15 DF,  p-value: 0.04392


## Analysis of Variance Table
##
## Response: ufov2
##              Df Sum Sq Mean Sq F value    Pr(>F)
## age           1  24088 24088.4 19.7778 7.337e-05 ***
## Genotype      1    310   310.2  0.2547    0.6167
## sex           1    437   437.5  0.3592    0.5525
## age:Genotype  1   2160  2159.7  1.7733    0.1909
## age:sex       1    217   217.2  0.1783    0.6752
## Genotype:sex  1    308   308.0  0.2529    0.6179
```

```
## age:Genotype:sex  1      68     68.4  0.0562      0.8139
## Residuals         38  46282   1217.9
## ---
## 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 17467.8 17467.8  9.4689 0.007667 **
## Genotype      1  1129.8  1129.8  0.6125 0.446044
## age:Genotype  1   460.6   460.6  0.2497 0.624540
## Residuals    15 27671.4  1844.8
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


UFOV3 scores linear model
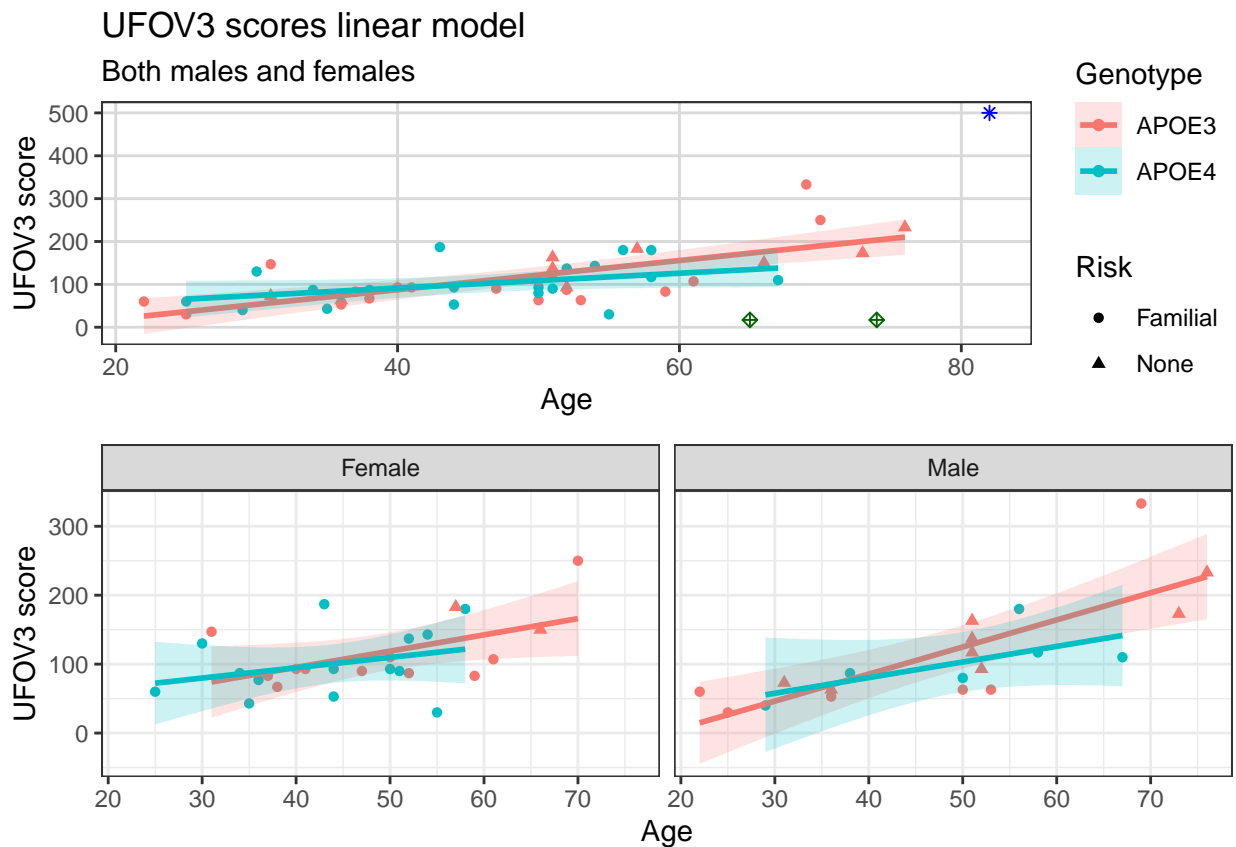
```
## 
## Call:
## lm(formula = ufov3 ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -87.202 -23.335  -6.866  23.533 133.460
## 
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  0.9899    58.5994   0.017   0.9866
## age                          2.3577     1.1429   2.063   0.0458 *
## GenotypeAPOE4               33.9436    82.6402   0.411   0.6835
## sexMale                    -72.5864    71.1289  -1.020   0.3138
## age:GenotypeAPOE4           -0.8619     1.7326  -0.497   0.6217
## age:sexMale                  1.5718     1.3901   1.131   0.2651
## GenotypeAPOE4:sexMale       27.3858   121.3139   0.226   0.8226
## age:GenotypeAPOE4:sexMale   -0.8005     2.4516  -0.327   0.7458
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 48.15 on 39 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.4652, Adjusted R-squared:  0.3693
## F-statistic: 4.847 on 7 and 39 DF,  p-value: 0.0005319


## 
## 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  69459   69459 29.9590 2.786e-06 ***
## Genotype          1    569     569  0.2454    0.6231
## sex               1    118     118  0.0511    0.8224
## age:Genotype      1   4740    4740  2.0443    0.1607
## age:sex           1   3238    3238  1.3967    0.2444
## Genotype:sex      1    295     295  0.1274    0.7230
## age:Genotype:sex  1    247     247  0.1066    0.7458
## Residuals        39  90420    2318
## ---
## 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  59292   59292 23.3283 0.0001847 ***
## Genotype      1   1807    1807  0.7108 0.4115932
## age:Genotype  1   2130    2130  0.8380 0.3735522
## Residuals    16  40666    2542
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
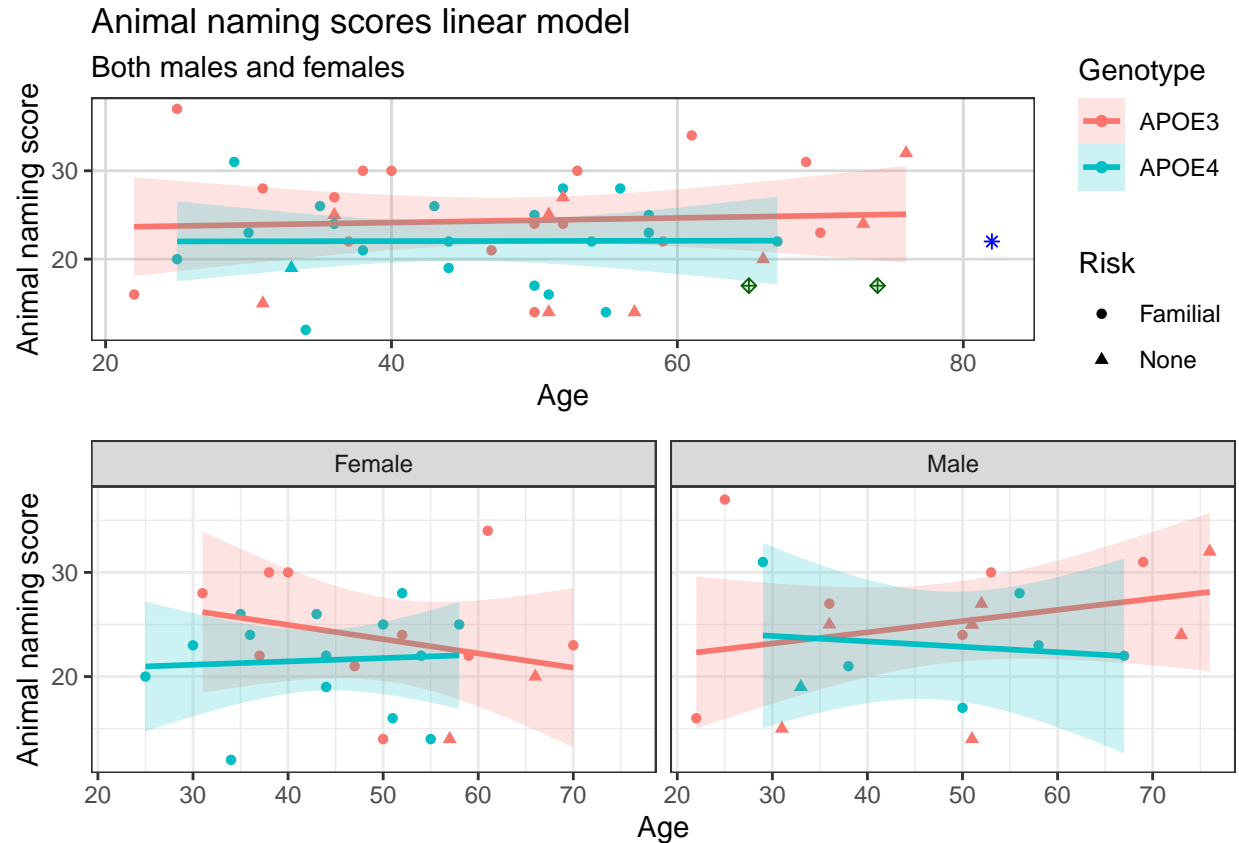
Animal naming scores linear model

```
## 
## Call:
## lm(formula = animals ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -11.4349  -3.1856   0.4171   3.4265  14.3627 
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)    
## (Intercept)              30.4309     7.4585   4.080 0.000215 ***
## age                      -0.1368     0.1433  -0.954 0.345766    
## GenotypeAPOE4           -10.2594    10.3169  -0.994 0.326142    
## sexMale                 -10.4836     8.9416  -1.172 0.248126    
## age:GenotypeAPOE4         0.1689     0.2143   0.788 0.435420    
## age:sexMale               0.2444     0.1730   1.413 0.165569    
## GenotypeAPOE4:sexMale    15.7712    14.1332   1.116 0.271294    
## age:GenotypeAPOE4:sexMale -0.3285    0.2897  -1.134 0.263774    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 5.89 on 39 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.1114, Adjusted R-squared:  -0.04813 
## F-statistic: 0.6982 on 7 and 39 DF,  p-value: 0.6732
```

9

```
## 
## 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
## -11.4349  -3.8021   0.0252   3.6283  14.3627
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        19.9473     5.2391   3.807  0.00141 **
## age                 0.1076     0.1028   1.046  0.31001
## GenotypeAPOE4       5.5118    10.2617   0.537  0.59814
## age:GenotypeAPOE4  -0.1596     0.2071  -0.771  0.45149
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 6.257 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.09217,    Adjusted R-squared:  -0.06803
## F-statistic: 0.5753 on 3 and 17 DF,  p-value: 0.639


## Analysis of Variance Table
## 
## Response: animals
##               Df  Sum Sq Mean Sq F value Pr(>F)
## age            1    8.79   8.790  0.2534 0.6175
## Genotype       1   57.35  57.346  1.6530 0.2061
## sex            1   26.75  26.748  0.7710 0.3853
## age:Genotype   1    2.69   2.686  0.0774 0.7823
## age:sex        1   29.17  29.171  0.8409 0.3648
## Genotype:sex   1    0.22   0.221  0.0064 0.9367
```

```
## age:Genotype:sex  1    44.60   44.602   1.2856 0.2638
## Residuals         39 1352.99   34.692


## 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  24.26  24.257  0.6196 0.4420
## Genotype      1  20.07  20.066  0.5125 0.4838
## age:Genotype  1  23.25  23.252  0.5939 0.4515
## Residuals    17 665.57  39.151
```
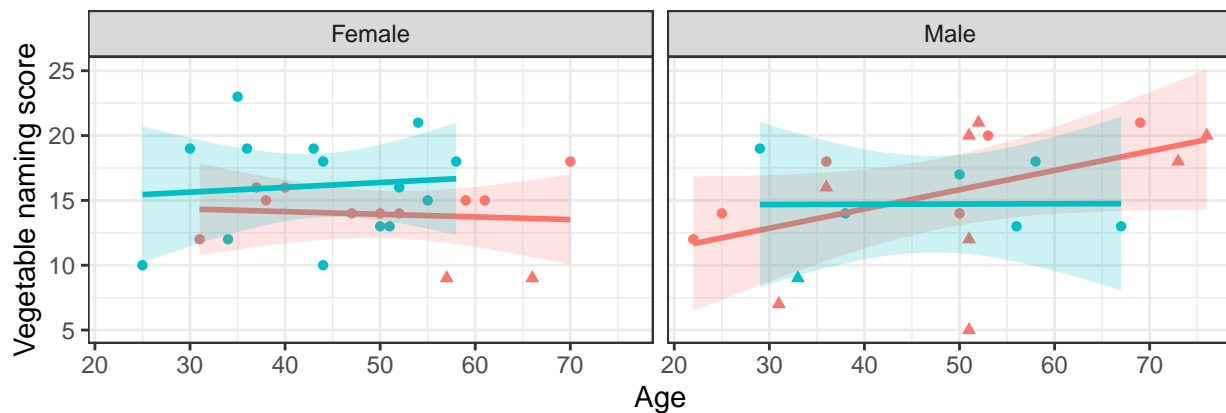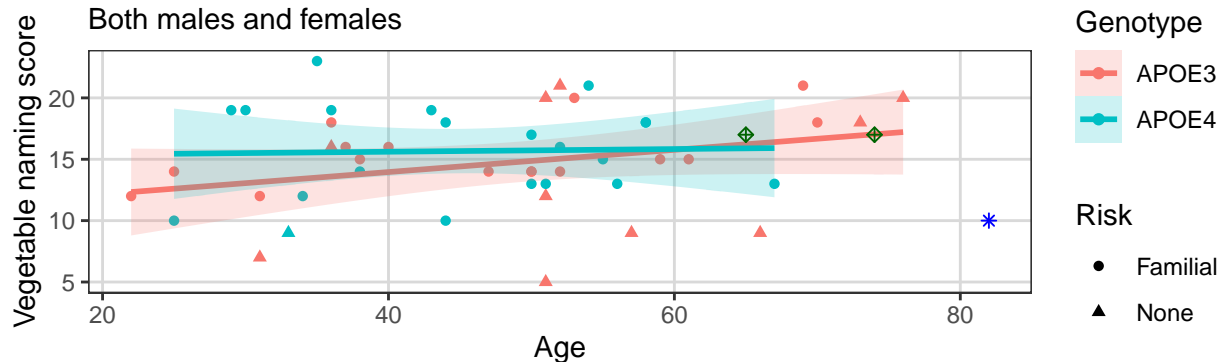

Vegetable naming scores linear model

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

```
## Residuals:
##     Min      1Q  Median      3Q     Max
## -10.975  -2.071   0.338   2.614   7.178
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)               14.94680    5.09355   2.934  0.00557 **
## age                       -0.02033    0.09788  -0.208  0.83653
## GenotypeAPOE4             -0.42280    7.04556  -0.060  0.95245
## sexMale                   -6.55676    6.10633  -1.074  0.28953
## age:GenotypeAPOE4          0.05742    0.14634   0.392  0.69689
## age:sexMale                0.16906    0.11811   1.431  0.16030
## GenotypeAPOE4:sexMale      6.64666    9.65177   0.689  0.49512
## age:GenotypeAPOE4:sexMale -0.20403    0.19784  -1.031  0.30876
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.022 on 39 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.1601, Adjusted R-squared:  0.009348
## F-statistic: 1.062 on 7 and 39 DF,  p-value: 0.4057


##
## 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
## -10.975  -1.756   0.338   3.263   4.876
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)        8.39005    3.72769   2.251   0.0379 *
## age                0.14873    0.07316   2.033   0.0580 .
## GenotypeAPOE4       6.22387    7.30134   0.852   0.4058
## age:GenotypeAPOE4 -0.14660    0.14736  -0.995   0.3337
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.452 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2021, Adjusted R-squared:  0.06128
## F-statistic: 1.435 on 3 and 17 DF,  p-value: 0.2674


## Analysis of Variance Table
##
## Response: vegetables
##                  Df Sum Sq Mean Sq F value Pr(>F)
## age               1  27.13  27.132  1.6770 0.2029
## Genotype          1  14.94  14.941  0.9235 0.3425
## sex               1   1.38   1.382  0.0854 0.7716
## age:Genotype      1  12.33  12.326  0.7618 0.3881
## age:sex           1  24.45  24.454  1.5114 0.2263
## Genotype:sex      1  22.84  22.836  1.4114 0.2420
## age:Genotype:sex  1  17.21  17.208  1.0636 0.3088
## Residuals        39 631.00  16.179


## 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  63.14  63.137  3.1855 0.09215 .
## Genotype      1   2.58   2.585  0.1304 0.72247
## age:Genotype  1  19.62  19.619  0.9898 0.33374
## Residuals    17 336.95  19.820
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
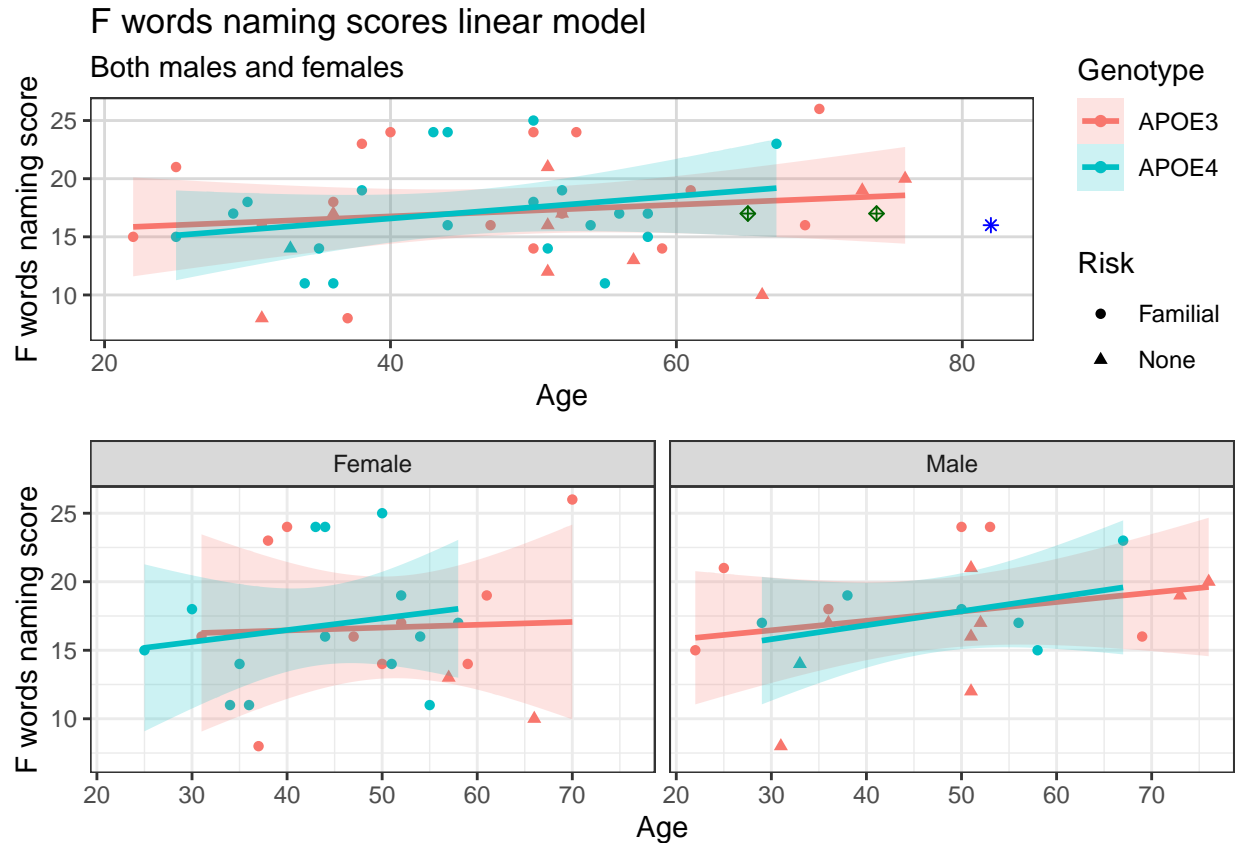
F words naming scores linear model

Both males and females


```
## 
## Call:
## lm(formula = f ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -8.5279 -2.7454 -0.4105  2.3845  8.9364 
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)  
## (Intercept)             15.62653    6.05810   2.579   0.0138 *
## age                      0.02053    0.11642   0.176   0.8609  
## GenotypeAPOE4           -2.60521    8.37975  -0.311   0.7575  
## sexMale                 -1.22630    7.26267  -0.169   0.8668  
## age:GenotypeAPOE4        0.06573    0.17405   0.378   0.7078  
## age:sexMale              0.04811    0.14048   0.342   0.7339  
## GenotypeAPOE4:sexMale    0.94189   11.47950   0.082   0.9350  
## age:GenotypeAPOE4:sexMale -0.03212   0.23530  -0.137   0.8921  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 4.784 on 39 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.0544, Adjusted R-squared:  -0.1153 
## F-statistic: 0.3205 on 7 and 39 DF,  p-value: 0.9402
```

```
##
## 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
## -8.5279 -1.9006  0.1289  2.3779  6.1681
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       14.40023    3.33976   4.312 0.000473 ***
## age                0.06863    0.06555   1.047 0.309725
## GenotypeAPOE4     -1.66332    6.54152  -0.254 0.802336
## age:GenotypeAPOE4  0.03361    0.13202   0.255 0.802123
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.989 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1004, Adjusted R-squared:  -0.0583
## F-statistic: 0.6328 on 3 and 17 DF,  p-value: 0.6039


## Analysis of Variance Table
##
## Response: f
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1  34.78  34.775  1.5194 0.2251
## Genotype      1   0.14   0.144  0.0063 0.9372
## sex           1   9.59   9.590  0.4190 0.5212
## age:Genotype  1   2.57   2.571  0.1123 0.7393
## age:sex       1   3.00   2.998  0.1310 0.7193
## Genotype:sex  1   0.85   0.847  0.0370 0.8484
```

```
## age:Genotype:sex  1    0.43    0.426   0.0186 0.8921
## Residuals          39 892.61   22.887


## 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  29.150 29.1502  1.8322 0.1936
## Genotype        1   0.020  0.0203  0.0013 0.9719
## age:Genotype    1   1.031  1.0309  0.0648 0.8021
## Residuals      17 270.465 15.9097
```
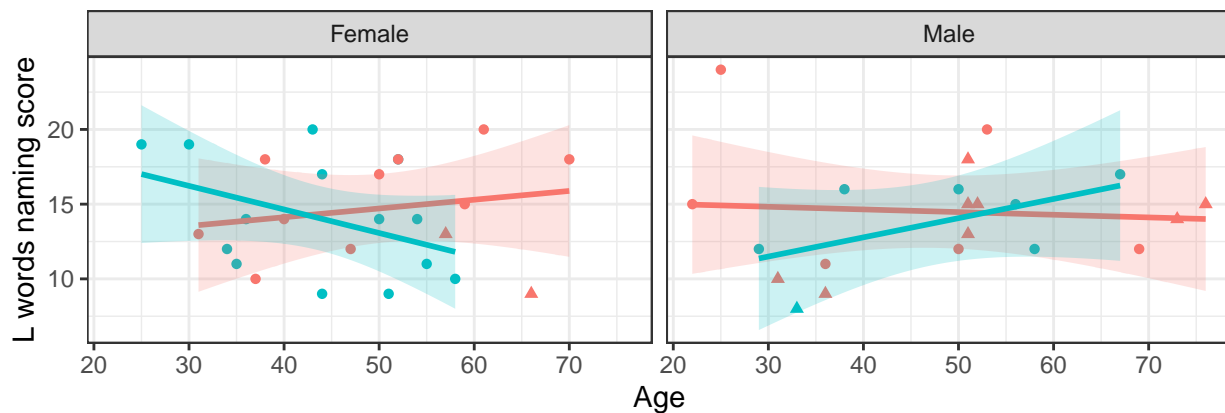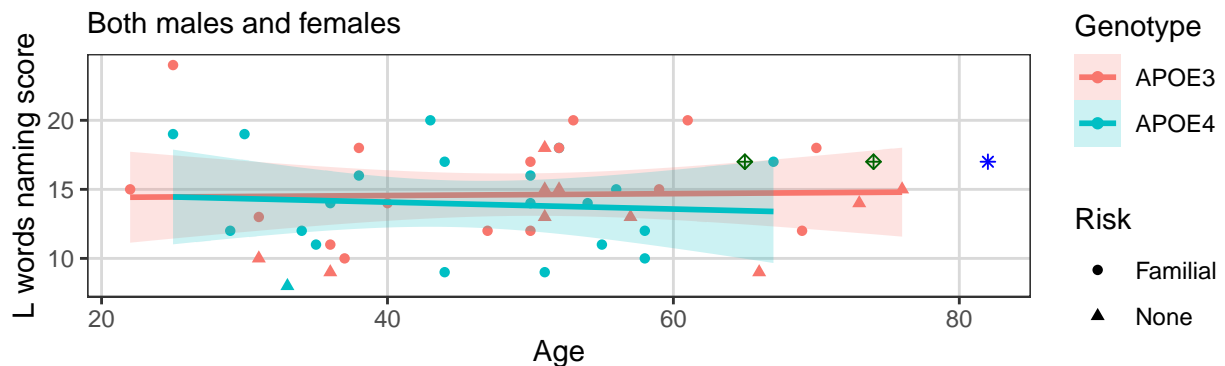
L words naming scores linear model


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

```
## Residuals:
##     Min      1Q  Median      3Q      Max
## -6.6489 -2.5022  0.0315  2.2028  9.0850
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)               11.77961    4.73434   2.488   0.0172 *
## age                        0.05863    0.09098   0.644   0.5231
## GenotypeAPOE4              9.17536    6.54868   1.401   0.1691
## sexMale                    3.58104    5.67570   0.631   0.5318
## age:GenotypeAPOE4         -0.21635    0.13602  -1.591   0.1198
## age:sexMale               -0.07645    0.10978  -0.696   0.4903
## GenotypeAPOE4:sexMale    -16.89414    8.97110  -1.883   0.0672 .
## age:GenotypeAPOE4:sexMale  0.36259    0.18389   1.972   0.0558 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.739 on 39 degrees of freedom
##   (4 observations deleted due to missingness)
## Multiple R-squared:  0.1096, Adjusted R-squared:  -0.05026
## F-statistic: 0.6855 on 7 and 39 DF,  p-value: 0.6834


##
## 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
## -5.7190 -2.4694  0.1666  0.9940  9.0850
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)       15.36065    3.22229   4.767 0.000179 ***
## age               -0.01782    0.06324  -0.282 0.781472
## GenotypeAPOE4      -7.71878    6.31143  -1.223 0.238019
## age:GenotypeAPOE4   0.14624    0.12738   1.148 0.266822
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.848 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.08715,    Adjusted R-squared:  -0.07395
## F-statistic: 0.541 on 3 and 17 DF,  p-value: 0.6607


## Analysis of Variance Table
##
## Response: l
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1   0.00   0.004  0.0003 0.98703
## Genotype         1   5.21   5.209  0.3727 0.54509
## sex              1   0.96   0.965  0.0690 0.79417
## age:Genotype     1   1.53   1.526  0.1092 0.74286
## age:sex          1   4.93   4.929  0.3526 0.55605
## Genotype:sex     1   0.10   0.096  0.0069 0.93432
## age:Genotype:sex 1  54.35  54.348  3.8881 0.05575 .
## Residuals       39 545.14  13.978
## ---
## 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   1.767  1.7673  0.1193 0.7340
## Genotype       1   2.746  2.7462  0.1854 0.6722
## age:Genotype   1  19.522 19.5222  1.3182 0.2668
## Residuals     17 251.774 14.8102
```
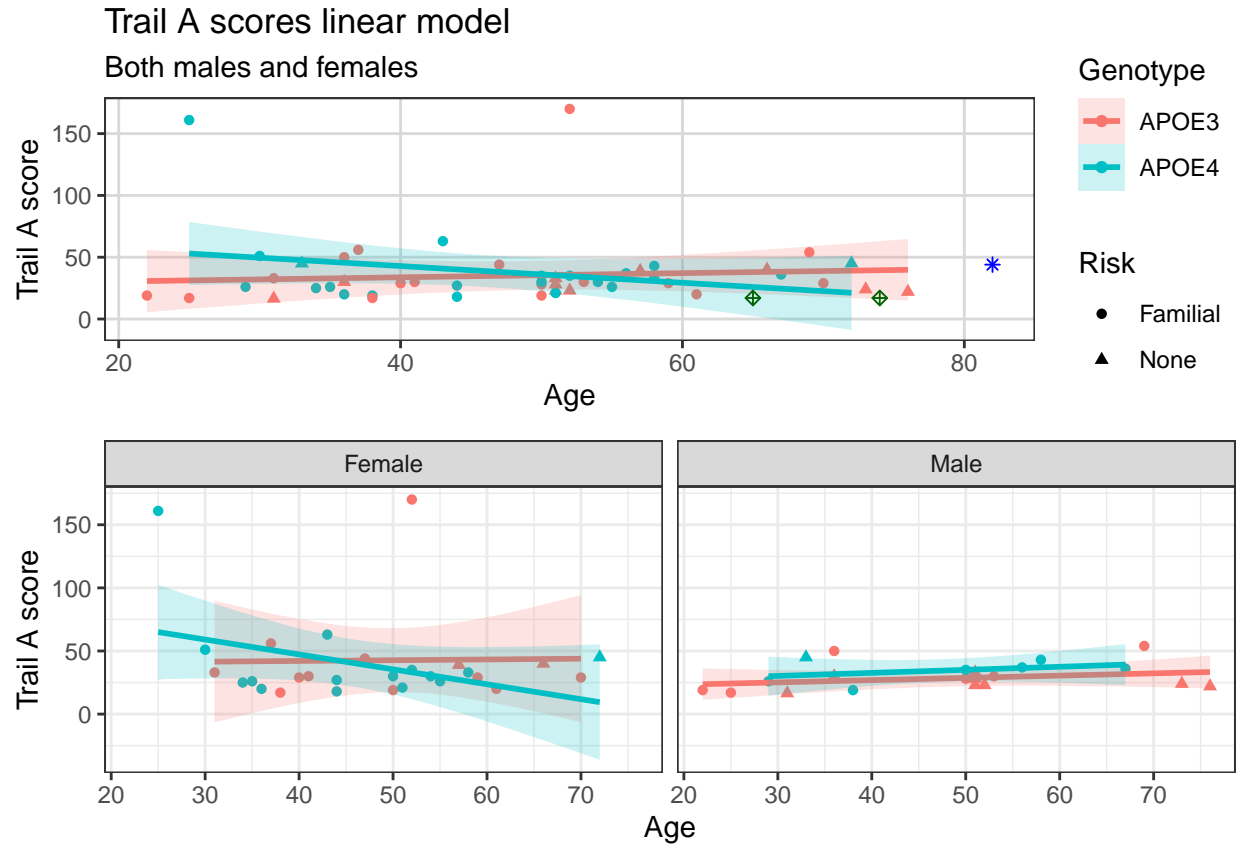
Trail A scores linear model

```
## 
## Call:
## lm(formula = trailA ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -31.996 -13.101  -4.114   1.906 127.184 
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             39.71951   35.83793   1.108    0.274
## age                      0.05955    0.69897   0.085    0.933
## GenotypeAPOE4           54.80640   46.80949   1.171    0.248
## sexMale                -19.94524   43.50065  -0.459    0.649
## age:GenotypeAPOE4       -1.24094    0.94765  -1.309    0.198
## age:sexMale              0.11894    0.85015   0.140    0.889
## GenotypeAPOE4:sexMale  -51.59434   67.25684  -0.767    0.447
## age:GenotypeAPOE4:sexMale 1.30443    1.35943   0.960    0.343
## 
## Residual standard error: 29.45 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1203, Adjusted R-squared:  -0.02986 
## F-statistic: 0.8012 on 7 and 41 DF,  p-value: 0.591
## 
## 
```

```
## 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
## -13.1816  -6.0558  -0.8773   3.8000  23.8000
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       19.77427    8.94896   2.210   0.0411 *
## age                0.17849    0.17564   1.016   0.3238
## GenotypeAPOE4      3.21205   17.52815   0.183   0.8568
## age:GenotypeAPOE4  0.06349    0.35375   0.179   0.8597
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.69 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.156,  Adjusted R-squared:  0.007051
## F-statistic: 1.047 on 3 and 17 DF,  p-value: 0.3971


## Analysis of Variance Table
##
## Response: trailA
##                 Df Sum Sq Mean Sq F value Pr(>F)
## age              1    239  238.81  0.2754 0.6026
## Genotype         1    108  107.66  0.1242 0.7264
## sex              1   1398 1398.42  1.6126 0.2113
## age:Genotype     1   1318 1318.18  1.5201 0.2246
## age:sex          1    689  689.03  0.7946 0.3779
## Genotype:sex     1    313  312.64  0.3605 0.5515
## age:Genotype:sex 1    798  798.41  0.9207 0.3429
## Residuals       41  35554  867.16


## 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  174.29 174.285  1.5257 0.2336
## Genotype     1  180.95 180.947  1.5841 0.2252
## age:Genotype 1    3.68   3.679  0.0322 0.8597
## Residuals   17 1941.90 114.229
```

Trail B scores linear model
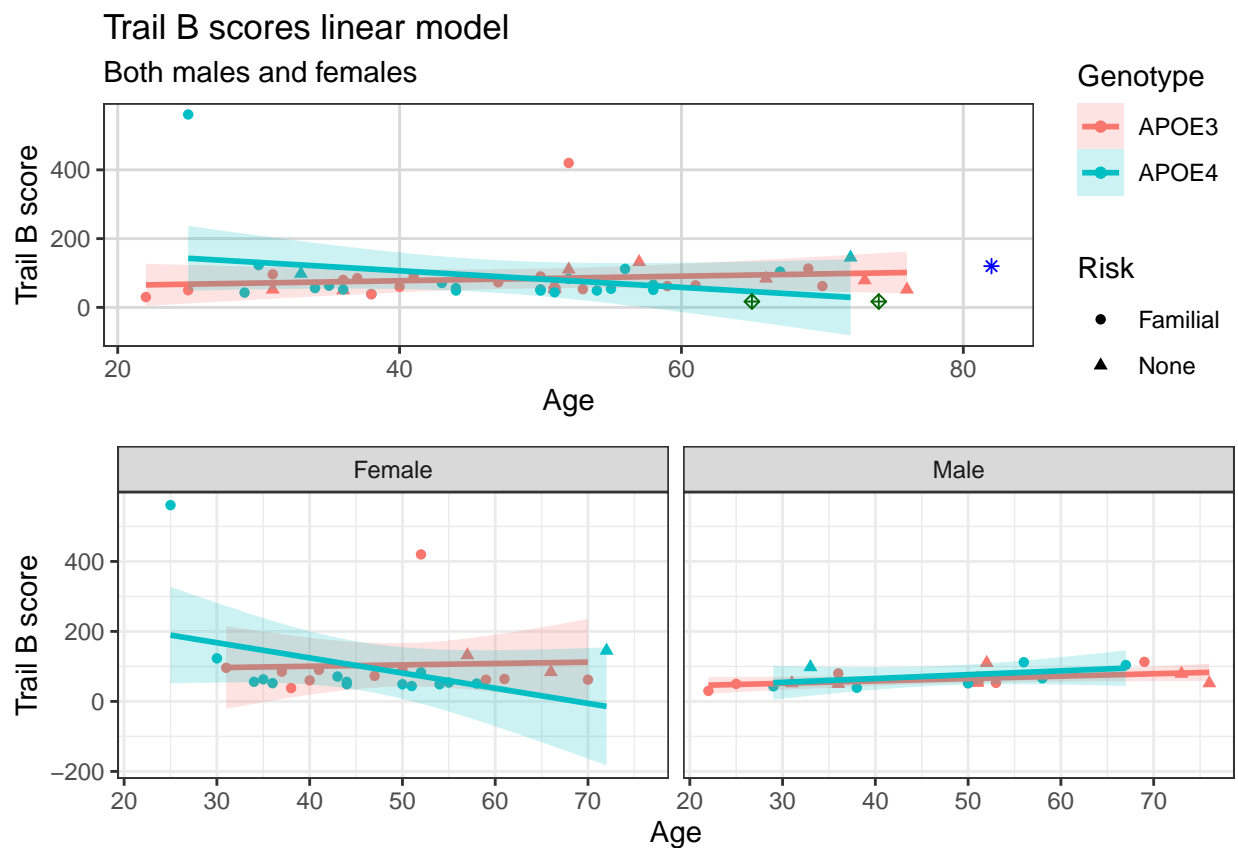

```
## 
## Call:
## lm(formula = trailB ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##    Min     1Q Median     3Q    Max
## -94.40 -32.70 -14.21   1.66 371.59
## 
```

```
## Coefficients:
##                              Estimate Std. Error t value Pr(>|t|)
## (Intercept)                   84.6102   108.0399   0.783    0.438
## age                            0.3946     2.1072   0.187    0.852
## GenotypeAPOE4                213.1730   141.1157   1.511    0.139
## sexMale                      -53.2428   131.1406  -0.406    0.687
## age:GenotypeAPOE4             -4.7295     2.8569  -1.655    0.105
## age:sexMale                    0.2842     2.5629   0.111    0.912
## GenotypeAPOE4:sexMale       -222.8753   202.7580  -1.099    0.278
## age:GenotypeAPOE4:sexMale      5.1454     4.0982   1.256    0.216
##
## Residual standard error: 88.78 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1531, Adjusted R-squared:  0.008521
## F-statistic: 1.059 on 7 and 41 DF,  p-value: 0.4067


##
## 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
## -30.955 -14.343  -5.804   8.990  43.336
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        31.3674    20.0559   1.564    0.136
## age                 0.6788     0.3936   1.724    0.103
## GenotypeAPOE4      -9.7022    39.2831  -0.247    0.808
## age:GenotypeAPOE4   0.4159     0.7928   0.525    0.607
##
## Residual standard error: 23.95 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2674, Adjusted R-squared:  0.1381
## F-statistic: 2.068 on 3 and 17 DF,  p-value: 0.1424
```
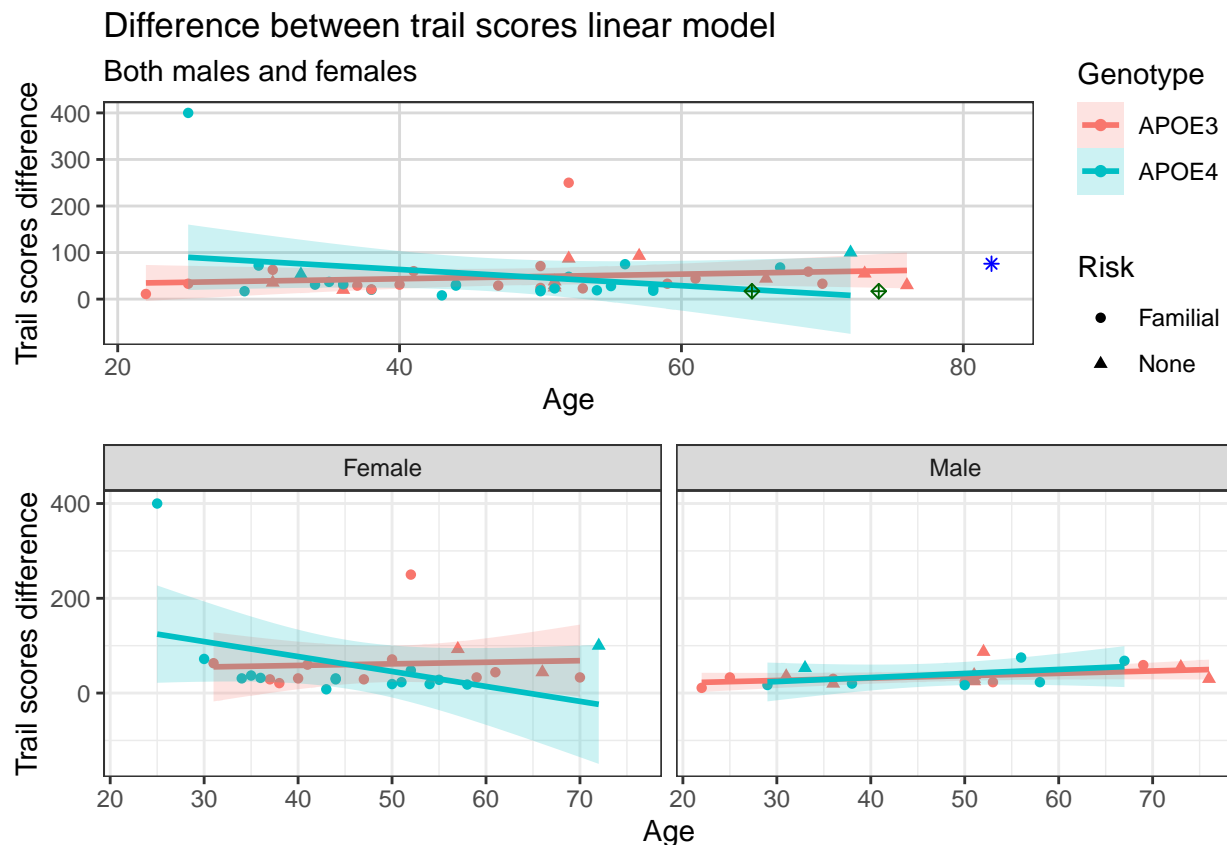
```
## Analysis of Variance Table
##
## Response: trailB
##                 Df Sum Sq Mean Sq F value Pr(>F)
## age              1   2494  2494.2  0.3165 0.5768
## Genotype         1    561   561.0  0.0712 0.7910
## sex              1  13954 13953.8  1.7706 0.1907
## age:Genotype     1  17849 17848.7  2.2648 0.1400
## age:sex          1   9722  9722.3  1.2336 0.2732
## Genotype:sex     1   1415  1415.3  0.1796 0.6739
## age:Genotype:sex 1  12423 12422.9  1.5763 0.2164
## Residuals       41 323122  7881.0


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


## Analysis of Variance Table
##
## Response: trailB
##              Df Sum Sq Mean Sq F value  Pr(>F)
## age           1 2929.8 2929.77  5.1064 0.03726 *
## Genotype      1  472.5  472.49  0.8235 0.37684
## age:Genotype  1  157.9  157.90  0.2752 0.60663
## Residuals    17 9753.6  573.74
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Difference between trail scores linear model

Both males and females


```
## 
## Call:
## lm(formula = trailDiff ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -65.037 -27.291 -11.600   8.398 275.581
## 
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 44.8907    76.2586   0.589   0.5593
## age                          0.3350     1.4873   0.225   0.8229
## GenotypeAPOE4              158.3667    99.6048   1.590   0.1195
## sexMale                    -33.2975    92.5640  -0.360   0.7209
## age:GenotypeAPOE4           -3.4885     2.0165  -1.730   0.0912 .
## age:sexMale                  0.1653     1.8090   0.091   0.9276
## GenotypeAPOE4:sexMale     -171.2809   143.1142  -1.197   0.2383
## age:GenotypeAPOE4:sexMale    3.8410     2.8927   1.328   0.1916
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 62.66 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1567, Adjusted R-squared:  0.01268
## F-statistic: 1.088 on 7 and 41 DF,  p-value: 0.3886
```

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


##
## Call:
## lm(formula = trailDiff ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -25.136 -12.108  -6.408   8.900  49.392
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        11.5932    17.0351   0.681    0.505
## age                 0.5003     0.3343   1.496    0.153
## GenotypeAPOE4     -12.9143    33.3663  -0.387    0.704
## age:GenotypeAPOE4   0.3524     0.6734   0.523    0.607
##
## Residual standard error: 20.35 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2088, Adjusted R-squared:  0.06917
## F-statistic: 1.495 on 3 and 17 DF,  p-value: 0.2516


## Analysis of Variance Table
##
## Response: trailDiff
##                 Df Sum Sq Mean Sq F value Pr(>F)
## age              1   1189  1189.5  0.3029 0.5850
## Genotype         1    177   177.1  0.0451 0.8328
## sex              1   6517  6517.4  1.6599 0.2048
## age:Genotype     1   9466  9465.8  2.4108 0.1282
## age:sex          1   5235  5234.9  1.3333 0.2549
## Genotype:sex     1    398   397.6  0.1013 0.7519
## age:Genotype:sex 1   6923  6922.6  1.7631 0.1916
## Residuals       41 160982  3926.4


## 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 1674.9 1674.91  4.0464 0.06039 .
## Genotype     1   68.6   68.65  0.1658 0.68892
## age:Genotype 1  113.4  113.37  0.2739 0.60749
## Residuals   17 7036.7  413.93
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
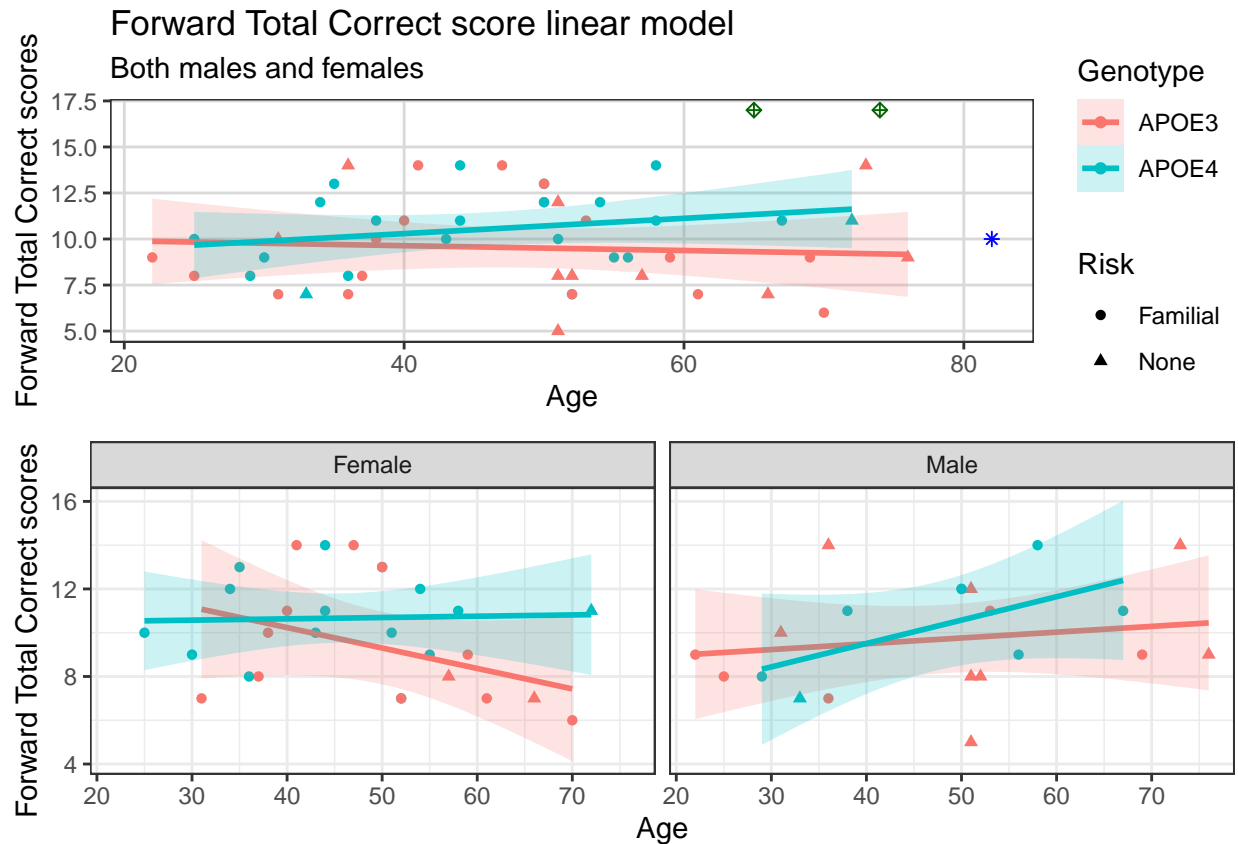

Forward Total Correct score linear model

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

```
## -4.7862 -1.5738 -0.4207  1.4243  4.6113
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              13.96810    2.95925   4.720 2.75e-05 ***
## age                      -0.09335    0.05772  -1.617   0.1135
## GenotypeAPOE4            -3.57378    3.86520  -0.925   0.3606
## sexMale                  -5.53361    3.59198  -1.541   0.1311
## age:GenotypeAPOE4         0.09933    0.07825   1.269   0.2114
## age:sexMale               0.11986    0.07020   1.707   0.0953 .
## GenotypeAPOE4:sexMale     0.37302    5.55360   0.067   0.9468
## age:GenotypeAPOE4:sexMale -0.01900   0.11225  -0.169   0.8664
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.432 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1611, Adjusted R-squared:  0.01791
## F-statistic: 1.125 on 7 and 41 DF,  p-value: 0.3664


##
## 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
## -4.7862 -1.7594 -0.3321  1.7064  4.6113
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)     8.43449    2.10903   3.999 0.000929 ***
## age             0.02650    0.04139   0.640 0.530506
## GenotypeAPOE4  -3.20076    4.13091  -0.775 0.449082
```

```
## age:GenotypeAPOE4  0.08033    0.08337   0.964 0.348758
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.519 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1427, Adjusted R-squared:  -0.008587
## F-statistic: 0.9432 on 3 and 17 DF,  p-value: 0.4417


## Analysis of Variance Table
##
## Response: fwd_total_correct
##                 Df  Sum Sq Mean Sq F value  Pr(>F)
## age              1   0.099  0.0988  0.0167 0.89777
## Genotype         1  13.191 13.1914  2.2311 0.14292
## sex              1   0.077  0.0772  0.0131 0.90958
## age:Genotype     1   6.148  6.1479  1.0398 0.31385
## age:sex          1  26.095 26.0953  4.4135 0.04185 *
## Genotype:sex     1   0.784  0.7841  0.1326 0.71760
## age:Genotype:sex 1   0.169  0.1694  0.0286 0.86644
## Residuals       41 242.415  5.9126
## ---
## 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  10.283 10.2831  1.6208 0.2201
## Genotype      1   1.779  1.7791  0.2804 0.6033
## age:Genotype  1   5.891  5.8909  0.9285 0.3488
## Residuals    17 107.856  6.3445
```
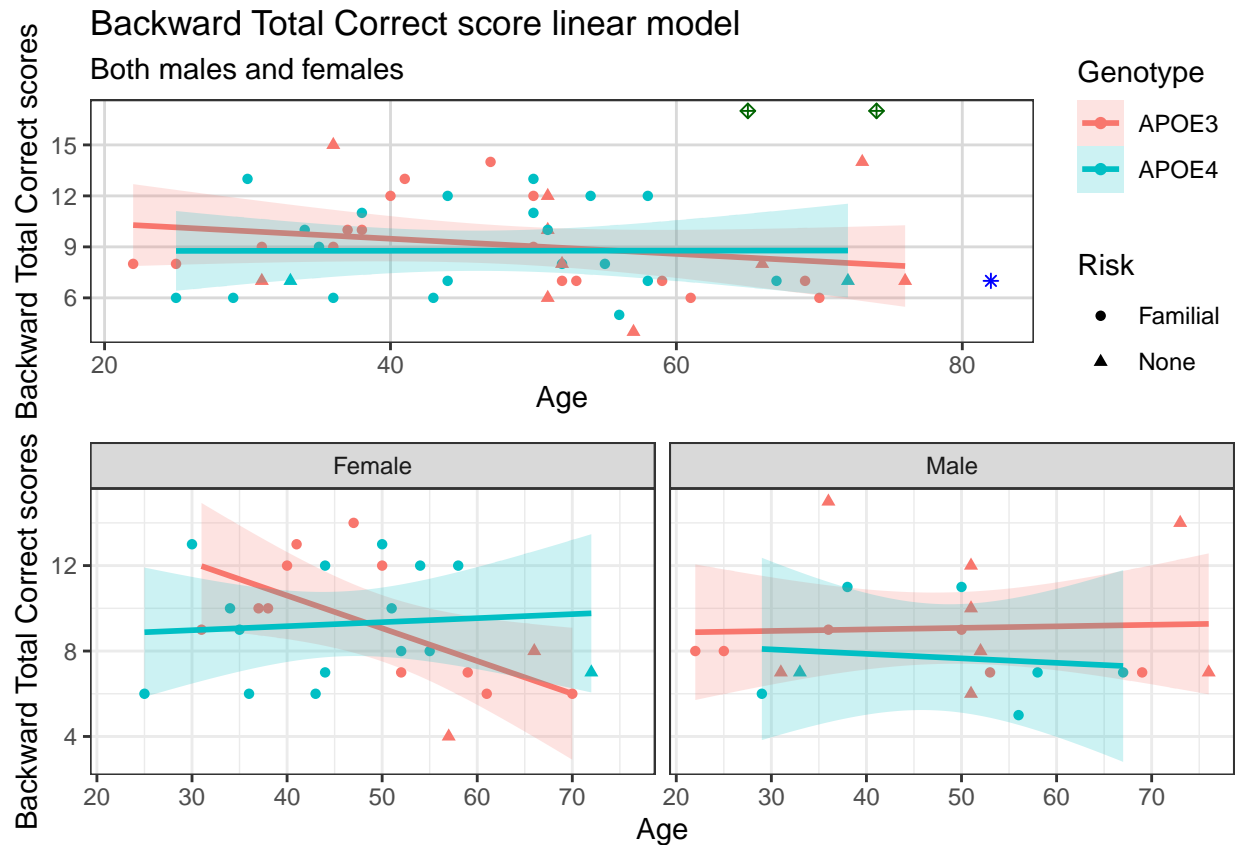
Backward Total Correct score linear model

```
##
## Call:
## lm(formula = bckwds_total_correct ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.9927 -2.0981 -0.6863  2.4986  6.0172
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             16.72528    3.28695   5.088 8.44e-06 ***
## age                     -0.15320    0.06411  -2.390   0.0215 *
## GenotypeAPOE4           -8.31578    4.29322  -1.937   0.0597 .
## sexMale                 -8.00220    3.98975  -2.006   0.0515 .
## age:GenotypeAPOE4        0.17203    0.08692   1.979   0.0545 .
## age:sexMale              0.16042    0.07797   2.057   0.0461 *
## GenotypeAPOE4:sexMale    8.29955    6.16859   1.345   0.1859
## age:GenotypeAPOE4:sexMale -0.20023   0.12468  -1.606   0.1160
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.701 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1571, Adjusted R-squared:  0.01318
## F-statistic: 1.092 on 7 and 41 DF,  p-value: 0.3864
```

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


## 
## Call:
## lm(formula = bckwds_total_correct ~ age * Genotype, data = combo_m)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.0910 -2.0981 -0.8818  0.9090  6.0172
## 
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        8.723071   2.329903   3.744  0.00162 **
## age                0.007215   0.045728   0.158  0.87650
## GenotypeAPOE4     -0.016231   4.563534  -0.004  0.99720
## age:GenotypeAPOE4 -0.028205   0.092102  -0.306  0.76314
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 2.783 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.06613,    Adjusted R-squared:  -0.09867
## F-statistic: 0.4013 on 3 and 17 DF,  p-value: 0.7539


## Analysis of Variance Table
## 
## Response: bckwds_total_correct
##                 Df  Sum Sq Mean Sq F value Pr(>F)
## age              1   6.057  6.0568  0.8303 0.3675
## Genotype         1   1.762  1.7622  0.2416 0.6257
## sex              1   4.912  4.9118  0.6733 0.4166
## age:Genotype     1   4.805  4.8048  0.6587 0.4217
## age:sex          1  15.047 15.0470  2.0628 0.1585
## Genotype:sex     1   4.343  4.3434  0.5954 0.4447
## age:Genotype:sex 1  18.813 18.8130  2.5790 0.1160
```

```
## Residuals        41 299.077  7.2946


## 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   0.012  0.0118  0.0015 0.9693
## Genotype     1   8.584  8.5838  1.1086 0.3071
## age:Genotype 1   0.726  0.7262  0.0938 0.7631
## Residuals   17 131.631  7.7430
```
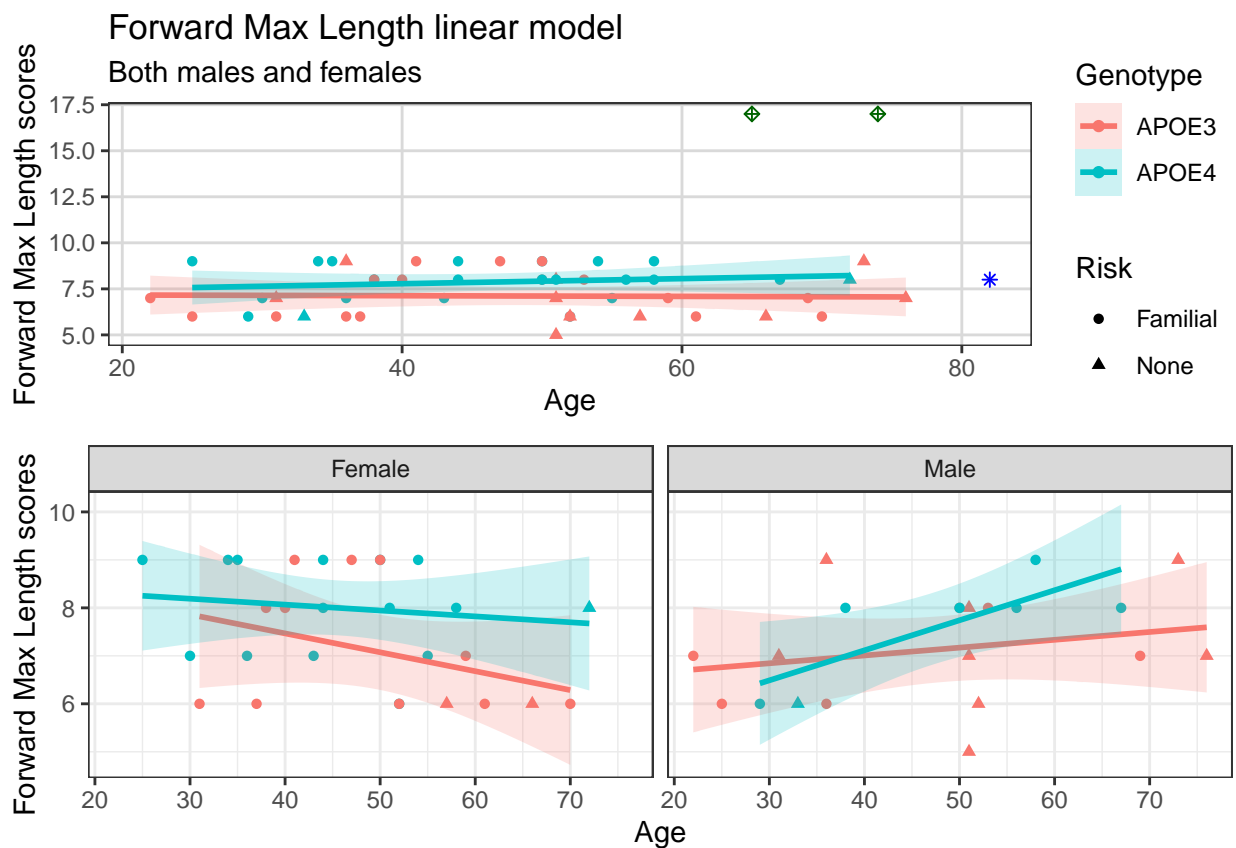

Forward Max Length linear model

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

```
##
## Residuals:
##      Min      1Q   Median       3Q      Max
## -2.18715 -0.79813  0.06712  0.81285  2.05764
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                 9.04364    1.36452   6.628 5.54e-08 ***
## age                        -0.03939    0.02661  -1.480   0.1464
## GenotypeAPOE4              -0.48462    1.78226  -0.272   0.7871
## sexMale                    -2.68878    1.65628  -1.623   0.1122
## age:GenotypeAPOE4           0.02712    0.03608   0.752   0.4566
## age:sexMale                 0.05571    0.03237   1.721   0.0927 .
## GenotypeAPOE4:sexMale      -1.25975    2.56079  -0.492   0.6254
## age:GenotypeAPOE4:sexMale   0.01918    0.05176   0.371   0.7129
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.121 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2434, Adjusted R-squared:  0.1142
## F-statistic: 1.884 on 7 and 41 DF,  p-value: 0.09717


##
## 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
## -2.1871 -0.6769 -0.1171  0.7802  2.0576
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)          6.35486    0.90117   7.052 1.94e-06 ***
## age                  0.01632    0.01769   0.923    0.369
## GenotypeAPOE4       -1.74437    1.76511  -0.988    0.337
## age:GenotypeAPOE4    0.04630    0.03562   1.300    0.211
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.076 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2508, Adjusted R-squared:  0.1186
## F-statistic: 1.897 on 3 and 17 DF,  p-value: 0.1684


## Analysis of Variance Table
##
## Response: fwd_max_length
##               Df Sum Sq Mean Sq F value  Pr(>F)
## age            1  0.009  0.0087  0.0069 0.93400
## Genotype       1  7.003  7.0032  5.5708 0.02310 *
## sex            1  0.220  0.2196  0.1747 0.67815
## age:Genotype   1  0.556  0.5558  0.4421 0.50981
## age:sex        1  8.294  8.2941  6.5978 0.01395 *
## Genotype:sex   1  0.327  0.3267  0.2599 0.61294
## age:Genotype:sex 1 0.173 0.1726  0.1373 0.71286
## Residuals     41 51.542  1.2571
## ---
## 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  3.6660  3.6660  3.1647 0.09313 .
## Genotype      1  0.9707  0.9707  0.8380 0.37277
## age:Genotype  1  1.9566  1.9566  1.6891 0.21107
## Residuals    17 19.6924  1.1584
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
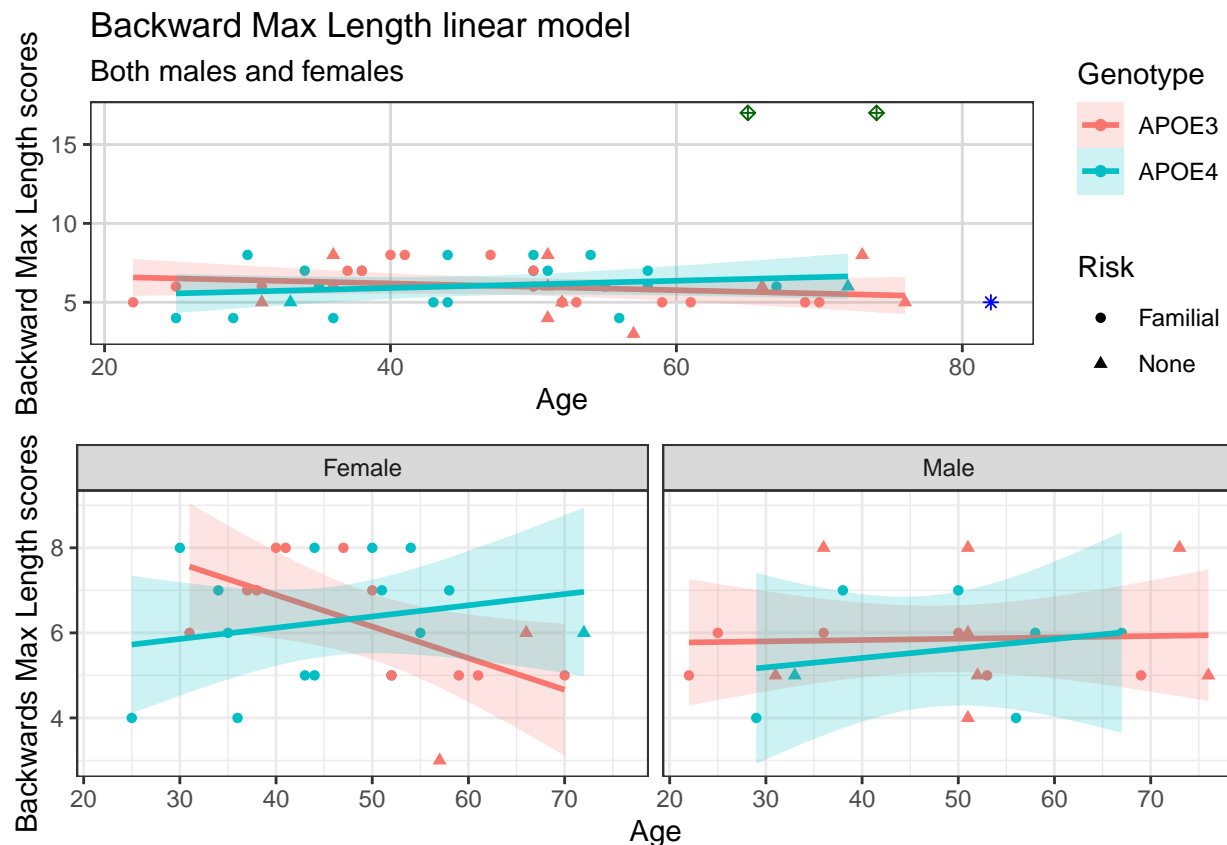
Backward Max Length linear model

```
## 
## Call:
## lm(formula = bckwds_max_length ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min      1Q   Median       3Q      Max 
## -2.62815 -0.94375 -0.00849  1.04039  2.18125 
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)    
## (Intercept)              9.86227    1.65863   5.946 5.16e-07 ***
## age                     -0.07428    0.03235  -2.296   0.0268 *  
## GenotypeAPOE4           -4.79679    2.16641  -2.214   0.0324 *  
## sexMale                 -4.15602    2.01327  -2.064   0.0454 *  
## age:GenotypeAPOE4        0.10066    0.04386   2.295   0.0269 *  
## age:sexMale              0.07741    0.03935   1.967   0.0559 .  
## GenotypeAPOE4:sexMale    3.61365    3.11275   1.161   0.2524    
## age:GenotypeAPOE4:sexMale -0.08162   0.06292  -1.297   0.2018    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.363 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1629, Adjusted R-squared:  0.02003 
## F-statistic:  1.14 on 7 and 41 DF,  p-value: 0.3577
```

```
## 
## 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
## -1.86563 -0.87188 -0.00849  0.21562  2.18125
## 
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        5.706250   1.126973   5.063  9.6e-05 ***
## age                0.003125   0.022119   0.141    0.889
## GenotypeAPOE4     -1.183137   2.207379  -0.536    0.599
## age:GenotypeAPOE4  0.019045   0.044549   0.427    0.674
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.346 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.03183,    Adjusted R-squared:  -0.139
## F-statistic: 0.1863 on 3 and 17 DF,  p-value: 0.9042


## Analysis of Variance Table
## 
## Response: bckwds_max_length
##                 Df Sum Sq Mean Sq F value Pr(>F)
## age              1  0.195  0.1947  0.1048 0.7478
## Genotype         1  0.012  0.0122  0.0066 0.9358
## sex              1  2.468  2.4679  1.3287 0.2557
## age:Genotype     1  4.488  4.4879  2.4162 0.1278
## age:sex          1  4.318  4.3182  2.3248 0.1350
## Genotype:sex     1  0.218  0.2179  0.1173 0.7337
## age:Genotype:sex 1  3.126  3.1258  1.6829 0.2018
```

```
## Residuals        41 76.155  1.8574


## 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  0.3214 0.32141  0.1774 0.6789
## Genotype      1  0.3600 0.36004  0.1987 0.6614
## age:Genotype  1  0.3311 0.33108  0.1828 0.6744
## Residuals    17 30.7970 1.81159
```


RAVLT forgetting scores linear model
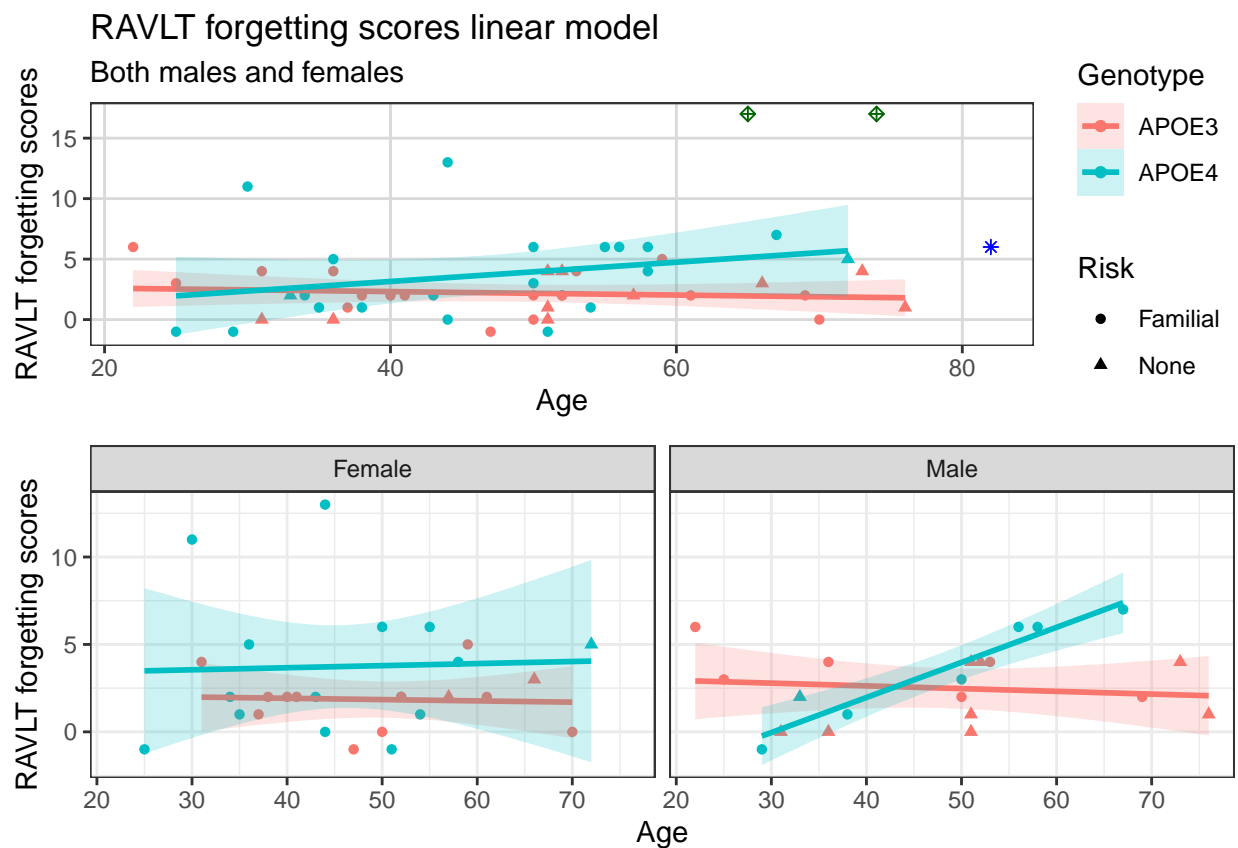
```
##
## Call:
## lm(formula = RAVLT_FORGETTING ~ age * Genotype * sex, data = geno_combined)
```

```
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.7982 -1.6974  0.0803  1.3798  9.2849
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                2.216131   3.387922   0.654    0.517
## age                       -0.007411   0.066077  -0.112    0.911
## GenotypeAPOE4              0.976811   4.425115   0.221    0.826
## sexMale                    1.040196   4.112315   0.253    0.802
## age:GenotypeAPOE4          0.019279   0.089586   0.215    0.831
## age:sexMale               -0.008253   0.080368  -0.103    0.919
## GenotypeAPOE4:sexMale    -10.295167   6.358096  -1.619    0.113
## age:GenotypeAPOE4:sexMale  0.197092   0.128513   1.534    0.133
##
## Residual standard error: 2.784 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.199,  Adjusted R-squared:  0.06229
## F-statistic: 1.456 on 7 and 41 DF,  p-value: 0.2102


##
## 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
## -2.7708 -0.9734 -0.1755  1.4387  3.0883
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        3.25633    1.45742   2.234  0.03918 *
## age               -0.01566    0.02860  -0.548  0.59109
## GenotypeAPOE4     -9.31836    2.85462  -3.264  0.00457 **
## age:GenotypeAPOE4  0.21637    0.05761   3.756  0.00158 **
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.741 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.5106, Adjusted R-squared:  0.4242
## F-statistic: 5.912 on 3 and 17 DF,  p-value: 0.005921


## Analysis of Variance Table
##
## Response: RAVLT_FORGETTING
##                  Df Sum Sq Mean Sq F value  Pr(>F)
## age               1   2.03  2.0332  0.2624 0.61125
## Genotype          1  27.47 27.4667  3.5443 0.06686 .
## sex               1   0.79  0.7867  0.1015 0.75163
## age:Genotype      1  17.87 17.8725  2.3062 0.13653
## age:sex           1  10.39 10.3924  1.3410 0.25356
## Genotype:sex      1   2.18  2.1797  0.2813 0.59873
## age:Genotype:sex  1  18.23 18.2275  2.3520 0.13280
## Residuals        41 317.74  7.7496
## ---
## 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  6.646   6.646  2.1937 0.156877
## Genotype      1  4.353   4.353  1.4367 0.247116
## age:Genotype  1 42.734  42.734 14.1049 0.001575 **
## Residuals    17 51.505   3.030
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

RAVLT learning scores linear model

Both males and females
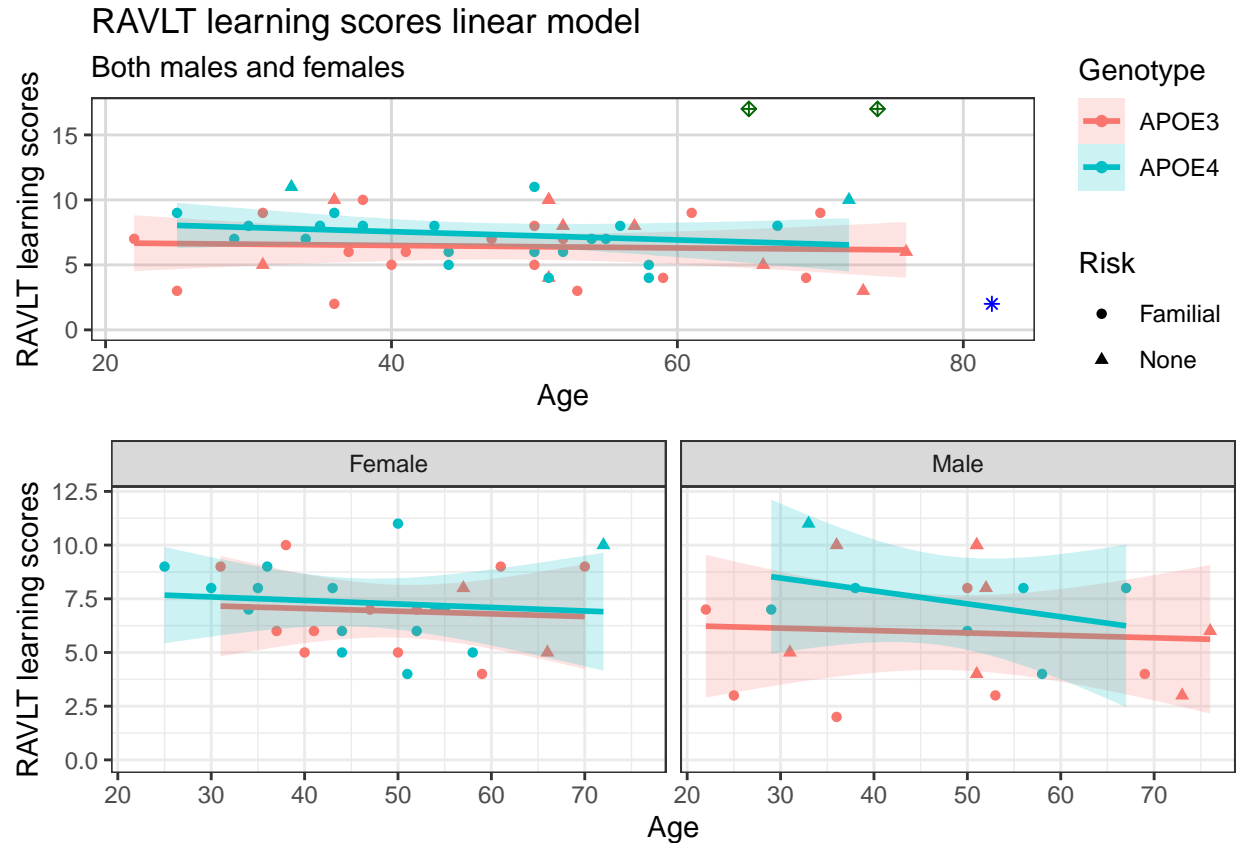
```
##
## Call:
## lm(formula = RAVLT_LEARNING ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -4.067 -1.723  0.013  1.757  4.102
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             7.544032   2.877487   2.622   0.0122 *
## age                    -0.012438   0.056122  -0.222   0.8257
## GenotypeAPOE4           0.534668   3.758413   0.142   0.8876
## sexMale                -1.071501   3.492741  -0.307   0.7606
## age:GenotypeAPOE4      -0.003931   0.076088  -0.052   0.9590
## age:sexMale             0.001173   0.068260   0.017   0.9864
## GenotypeAPOE4:sexMale   3.265207   5.400165   0.605   0.5487
## age:GenotypeAPOE4:sexMale -0.044945 0.109151  -0.412   0.6827
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.364 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.09295,    Adjusted R-squared:  -0.06191
## F-statistic: 0.6002 on 7 and 41 DF,  p-value: 0.752
```

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```
## 
## 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
## -2.7708 -0.9734 -0.1755  1.4387  3.0883
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        3.25633    1.45742   2.234  0.03918 *
## age               -0.01566    0.02860  -0.548  0.59109
## GenotypeAPOE4     -9.31836    2.85462  -3.264  0.00457 **
## age:GenotypeAPOE4  0.21637    0.05761   3.756  0.00158 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.741 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.5106, Adjusted R-squared:  0.4242
## F-statistic: 5.912 on 3 and 17 DF,  p-value: 0.005921


## Analysis of Variance Table
## 
## Response: RAVLT_LEARNING
##                 Df  Sum Sq Mean Sq F value Pr(>F)
## age              1   4.212  4.2116  0.7534 0.3905
## Genotype         1   9.752  9.7523  1.7445 0.1939
## sex              1   3.445  3.4447  0.6162 0.4370
## age:Genotype     1   0.821  0.8214  0.1469 0.7035
## age:sex          1   0.853  0.8535  0.1527 0.6980
## Genotype:sex     1   3.457  3.4570  0.6184 0.4362
## age:Genotype:sex 1   0.948  0.9479  0.1696 0.6827
```

```
## Residuals        41 229.206  5.5904


## 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  6.646   6.646  2.1937 0.156877
## Genotype      1  4.353   4.353  1.4367 0.247116
## age:Genotype  1 42.734  42.734 14.1049 0.001575 **
## Residuals    17 51.505   3.030
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

RAVLT Immediate scores linear model
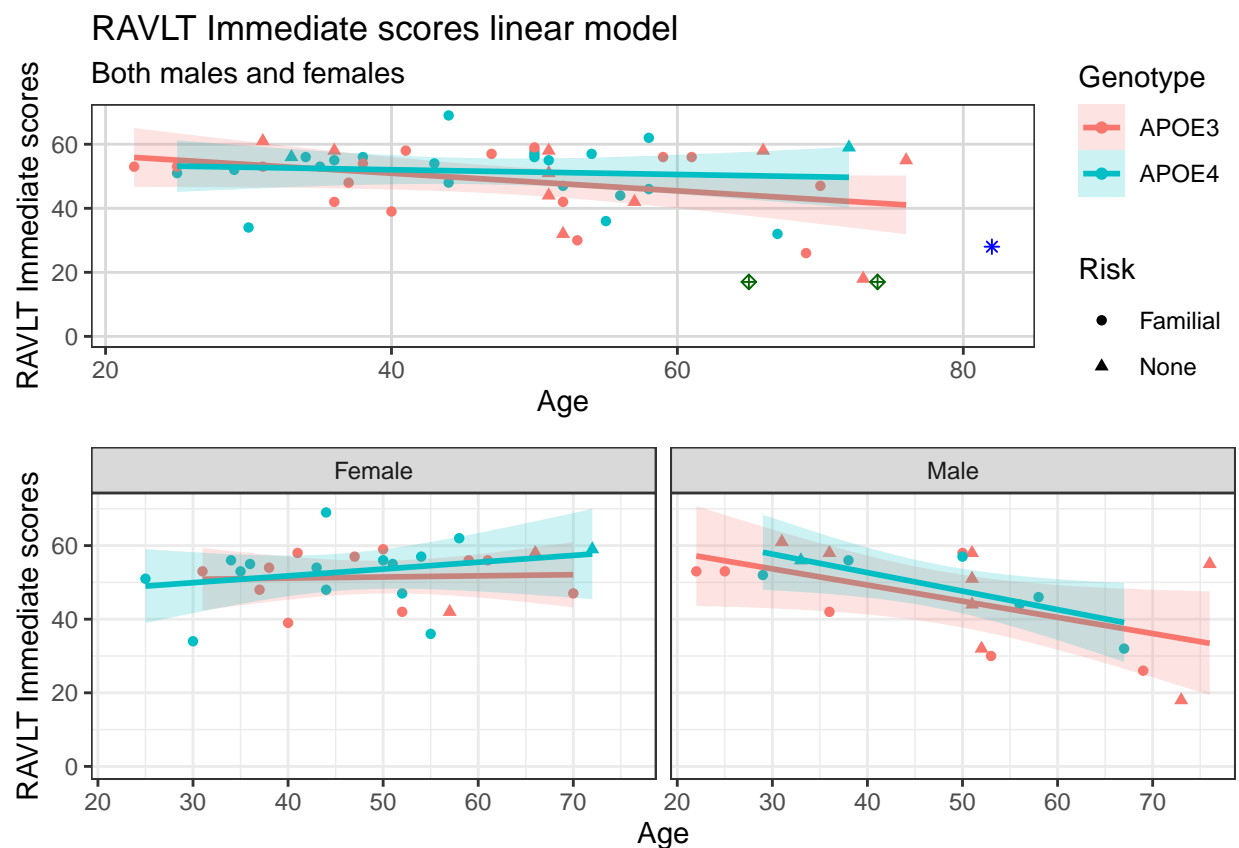

```
##
## Call:
## lm(formula = RAVLT_IMMEDIATE ~ age * Genotype * sex, data = geno_combined)
```

```
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -18.555  -6.192   2.007   5.630  21.539
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              49.90158   11.45568   4.356 8.64e-05 ***
## age                       0.03125    0.22343   0.140   0.8895
## GenotypeAPOE4            -5.54286   14.96277  -0.370   0.7130
## sexMale                  16.96501   13.90509   1.220   0.2294
## age:GenotypeAPOE4         0.15414    0.30292   0.509   0.6136
## age:sexMale              -0.47079    0.27175  -1.732   0.0907 .
## GenotypeAPOE4:sexMale    11.44738   21.49881   0.532   0.5973
## age:GenotypeAPOE4:sexMale -0.21731   0.43454  -0.500   0.6197
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.413 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2941, Adjusted R-squared:  0.1735
## F-statistic:  2.44 on 7 and 41 DF,  p-value: 0.03465


##
## 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
## -2.7708 -0.9734 -0.1755  1.4387  3.0883
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)          3.25633    1.45742    2.234  0.03918 *
## age                 -0.01566    0.02860   -0.548  0.59109
## GenotypeAPOE4        -9.31836    2.85462   -3.264  0.00457 **
## age:GenotypeAPOE4     0.21637    0.05761    3.756  0.00158 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.741 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.5106, Adjusted R-squared:  0.4242
## F-statistic: 5.912 on 3 and 17 DF,  p-value: 0.005921


## Analysis of Variance Table
##
## Response: RAVLT_IMMEDIATE
##                Df Sum Sq Mean Sq F value  Pr(>F)
## age             1  390.8  390.76  4.4102 0.04192 *
## Genotype        1   78.1   78.11  0.8816 0.35327
## sex             1  291.1  291.09  3.2853 0.07723 .
## age:Genotype    1  103.6  103.60  1.1692 0.28588
## age:sex         1  624.3  624.30  7.0459 0.01126 *
## Genotype:sex    1    3.2    3.20  0.0361 0.85032
## age:Genotype:sex 1   22.2   22.16  0.2501 0.61969
## Residuals      41 3632.8   88.60
## ---
## 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  6.646   6.646  2.1937 0.156877
## Genotype      1  4.353   4.353  1.4367 0.247116
## age:Genotype  1 42.734  42.734 14.1049 0.001575 **
## Residuals    17 51.505   3.030
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
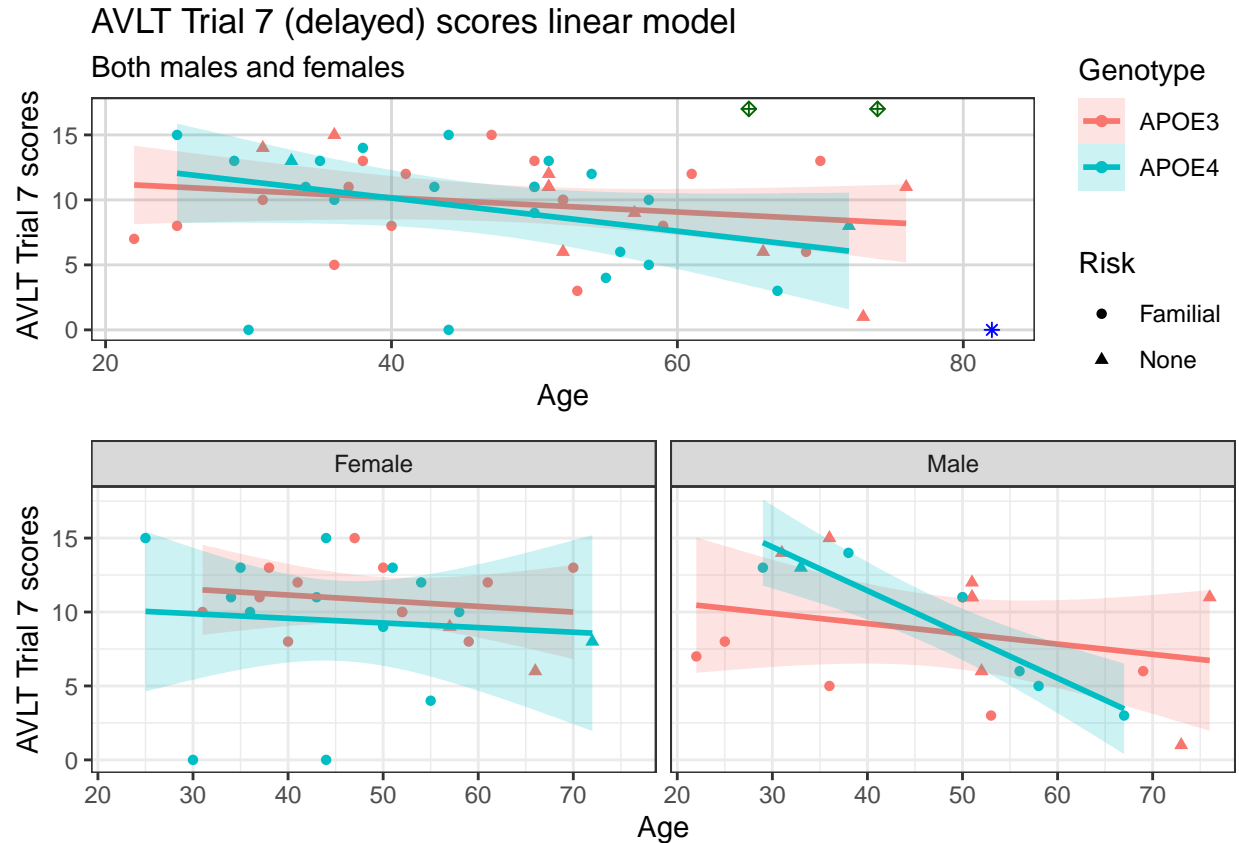
AVLT Trial 7 (delayed) scores linear model

Both males and females

```
##
## Call:
## lm(formula = AVLT_Trial7 ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -9.886 -1.698  0.302  2.545  5.552
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)             12.688351   4.670896   2.716  0.00962 **
## age                     -0.038442   0.091100  -0.422  0.67525
## GenotypeAPOE4           -1.864986   6.100863  -0.306  0.76139
## sexMale                 -0.699770   5.669609  -0.123  0.90237
## age:GenotypeAPOE4        0.007182   0.123511   0.058  0.95391
## age:sexMale             -0.030849   0.110803  -0.278  0.78210
## GenotypeAPOE4:sexMale   13.158245   8.765845   1.501  0.14100
## age:GenotypeAPOE4:sexMale -0.233882  0.177179  -1.320  0.19415
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.838 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2097, Adjusted R-squared:  0.07478
## F-statistic: 1.554 on 7 and 41 DF,  p-value: 0.1767
```

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


## 
## Call:
## lm(formula = AVLT_Trial7 ~ age * Genotype, data = combo_m)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.9304 -2.2563 -0.5142  2.5452  5.5059
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       11.98858    3.01711   3.974 0.000982 ***
## age               -0.06929    0.05922  -1.170 0.258094
## GenotypeAPOE4     11.29326    5.90955   1.911 0.073015 .
## age:GenotypeAPOE4 -0.22670    0.11927  -1.901 0.074423 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 3.603 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.3631, Adjusted R-squared:  0.2507
## F-statistic: 3.231 on 3 and 17 DF,  p-value: 0.04853


## Analysis of Variance Table
## 
## Response: AVLT_Trial7
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1  57.31  57.312  3.8907 0.05532 .
## Genotype         1   3.60   3.602  0.2445 0.62361
## sex              1  19.80  19.802  1.3443 0.25299
## age:Genotype     1   9.25   9.248  0.6278 0.43272
## age:sex          1  33.64  33.643  2.2839 0.13839
## Genotype:sex     1  10.98  10.984  0.7456 0.39288
## age:Genotype:sex 1  25.67  25.667  1.7425 0.19415
```

```
## Residuals         41 603.95  14.730
## ---
## 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  77.679  77.679  5.9826 0.02562 *
## Genotype       1   1.249   1.249  0.0962 0.76017
## age:Genotype   1  46.911  46.911  3.6130 0.07442 .
## Residuals     17 220.731  12.984
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Composite pleasantness scores linear model

```
##
```
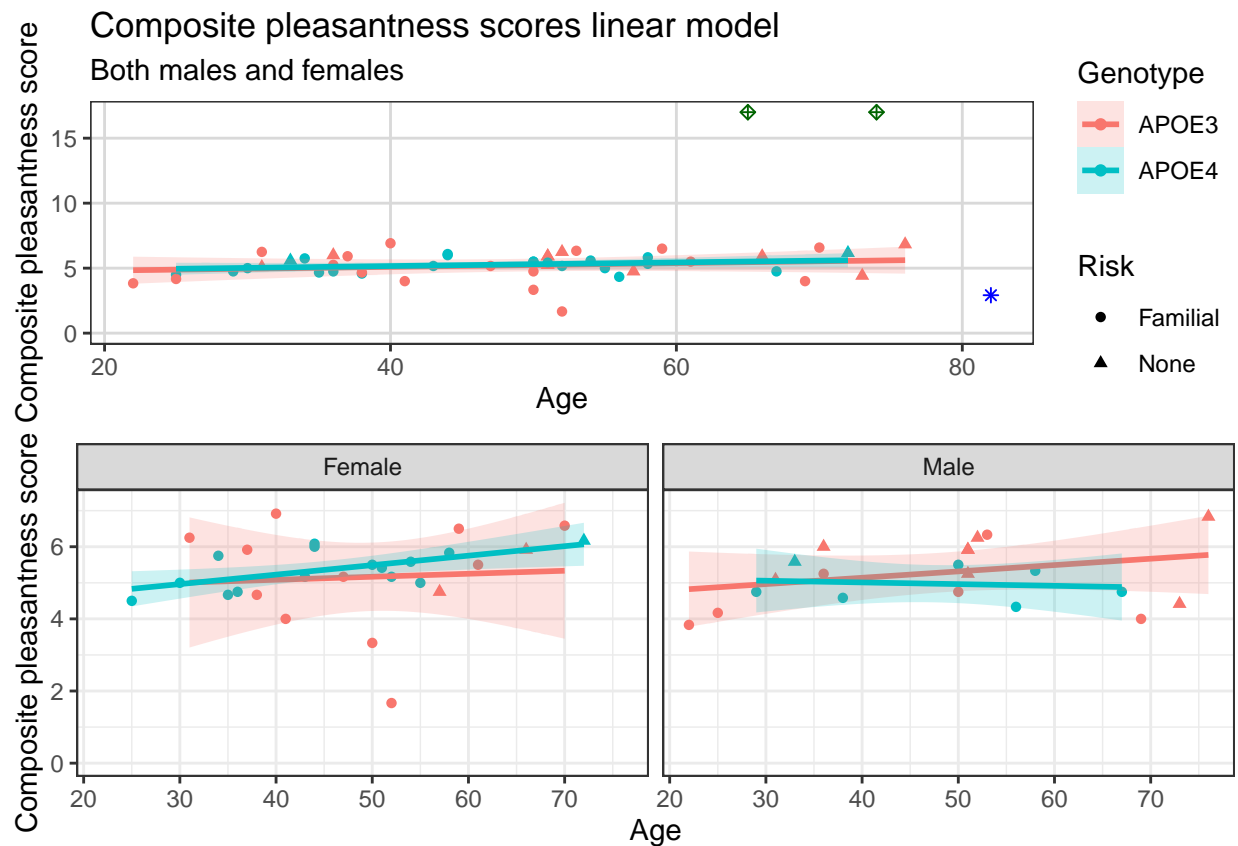
```
## Call:
## lm(formula = Composite_Pleasantness ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.5173 -0.4286  0.0243  0.6164  1.8325
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)               4.751795   1.218793   3.899 0.000351 ***
## age                       0.008310   0.023771   0.350 0.728432
## GenotypeAPOE4            -0.576938   1.591919  -0.362 0.718902
## sexMale                  -0.315086   1.479391  -0.213 0.832395
## age:GenotypeAPOE4         0.017986   0.032228   0.558 0.579817
## age:sexMale               0.009273   0.028912   0.321 0.750052
## GenotypeAPOE4:sexMale     1.339001   2.287303   0.585 0.561483
## age:GenotypeAPOE4:sexMale -0.040276   0.046232  -0.871 0.388730
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.001 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.08063,    Adjusted R-squared:  -0.07633
## F-statistic: 0.5137 on 7 and 41 DF,  p-value: 0.8189


##
## 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
## -1.6499 -0.5659  0.1016  0.5832  1.0603
##
```

```
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)         4.43671    0.70635   6.281 8.28e-06 ***
## age                 0.01758    0.01386   1.268    0.222
## GenotypeAPOE4       0.76206    1.38351   0.551    0.589
## age:GenotypeAPOE4  -0.02229    0.02792  -0.798    0.436
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8436 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.118,  Adjusted R-squared:  -0.03764
## F-statistic: 0.7582 on 3 and 17 DF,  p-value: 0.5329


## Analysis of Variance Table
##
## Response: Composite_Pleasantness
##                 Df Sum Sq Mean Sq F value Pr(>F)
## age              1  1.734 1.73438  1.7293 0.1958
## Genotype         1  0.043 0.04322  0.0431 0.8366
## sex              1  0.096 0.09573  0.0954 0.7589
## age:Genotype     1  0.000 0.00001  0.0000 0.9972
## age:sex          1  0.036 0.03584  0.0357 0.8510
## Genotype:sex     1  0.936 0.93619  0.9334 0.3396
## age:Genotype:sex 1  0.761 0.76118  0.7590 0.3887
## Residuals       41 41.120 1.00294


## 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  0.7527 0.75273  1.0577 0.3182
## Genotype      1  0.4125 0.41246  0.5796 0.4569
## age:Genotype  1  0.4535 0.45352  0.6373 0.4357
## Residuals    17 12.0982 0.71166
```
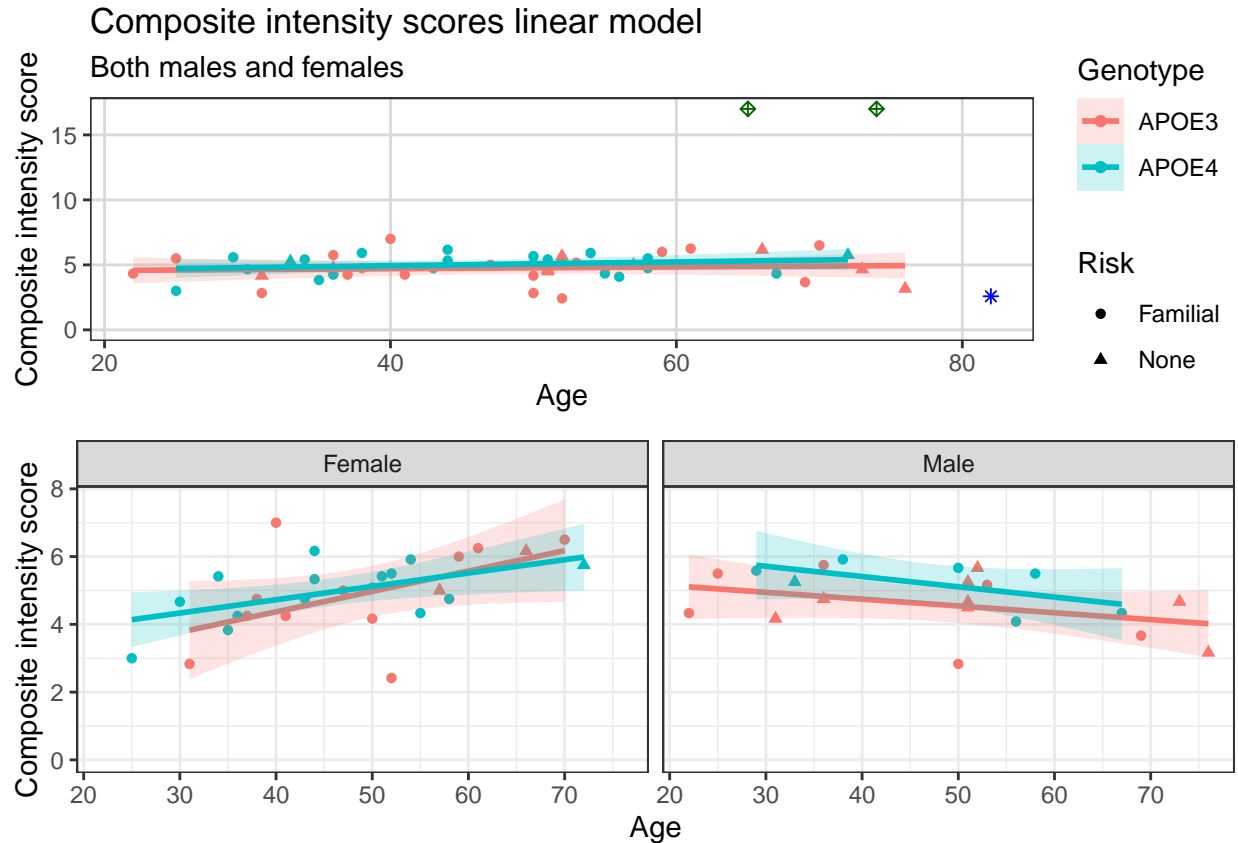
Composite intensity scores linear model

```
##
## Call:
## lm(formula = Composite_Intensity ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.67635 -0.49362  0.06027  0.50005  2.62961
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)               1.96162    1.11547   1.759  0.08612 .
## age                       0.06022    0.02176   2.768  0.00843 **
## GenotypeAPOE4             1.19227    1.45696   0.818  0.41790
## sexMale                   3.58803    1.35397   2.650  0.01138 *
## age:GenotypeAPOE4        -0.02090    0.02950  -0.708  0.48270
## age:sexMale              -0.08035    0.02646  -3.037  0.00415 **
## GenotypeAPOE4:sexMale    -0.11838    2.09339  -0.057  0.95518
## age:GenotypeAPOE4:sexMale 0.01072    0.04231   0.253  0.80118
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9166 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2955, Adjusted R-squared:  0.1752
## F-statistic: 2.456 on 7 and 41 DF,  p-value: 0.03359
```

```
## 
## 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 
## -1.70953 -0.49362 -0.02273  0.58692  1.16408 
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)    
## (Intercept)        5.54965    0.66453   8.351 2.02e-07 ***
## age               -0.02014    0.01304  -1.544    0.141    
## GenotypeAPOE4      1.07390    1.30159   0.825    0.421    
## age:GenotypeAPOE4 -0.01017    0.02627  -0.387    0.703    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.7936 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2897, Adjusted R-squared:  0.1644 
## F-statistic: 2.312 on 3 and 17 DF,  p-value: 0.1127


## Analysis of Variance Table
## 
## Response: Composite_Intensity
##                 Df Sum Sq Mean Sq F value    Pr(>F)    
## age              1  0.645  0.6447  0.7675 0.3861108    
## Genotype         1  0.980  0.9801  1.1666 0.2864093    
## sex              1  0.178  0.1783  0.2122 0.6474621    
## age:Genotype     1  0.148  0.1485  0.1767 0.6763779    
## age:sex          1 12.013 12.0132 14.2998 0.0004983 ***
## Genotype:sex     1  0.426  0.4262  0.5074 0.4803190    
## age:Genotype:sex 1  0.054  0.0540  0.0642 0.8011834    
```

```
## Residuals          41 34.444   0.8401
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


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


## Analysis of Variance Table
##
## Response: Composite_Intensity
##               Df  Sum Sq Mean Sq F value  Pr(>F)
## age            1  2.6483 2.64828  4.2044 0.05606 .
## Genotype       1  1.6254 1.62541  2.5805 0.12660
## age:Genotype   1  0.0944 0.09443  0.1499 0.70342
## Residuals     17 10.7079 0.62988
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Composite familiarity scores linear model
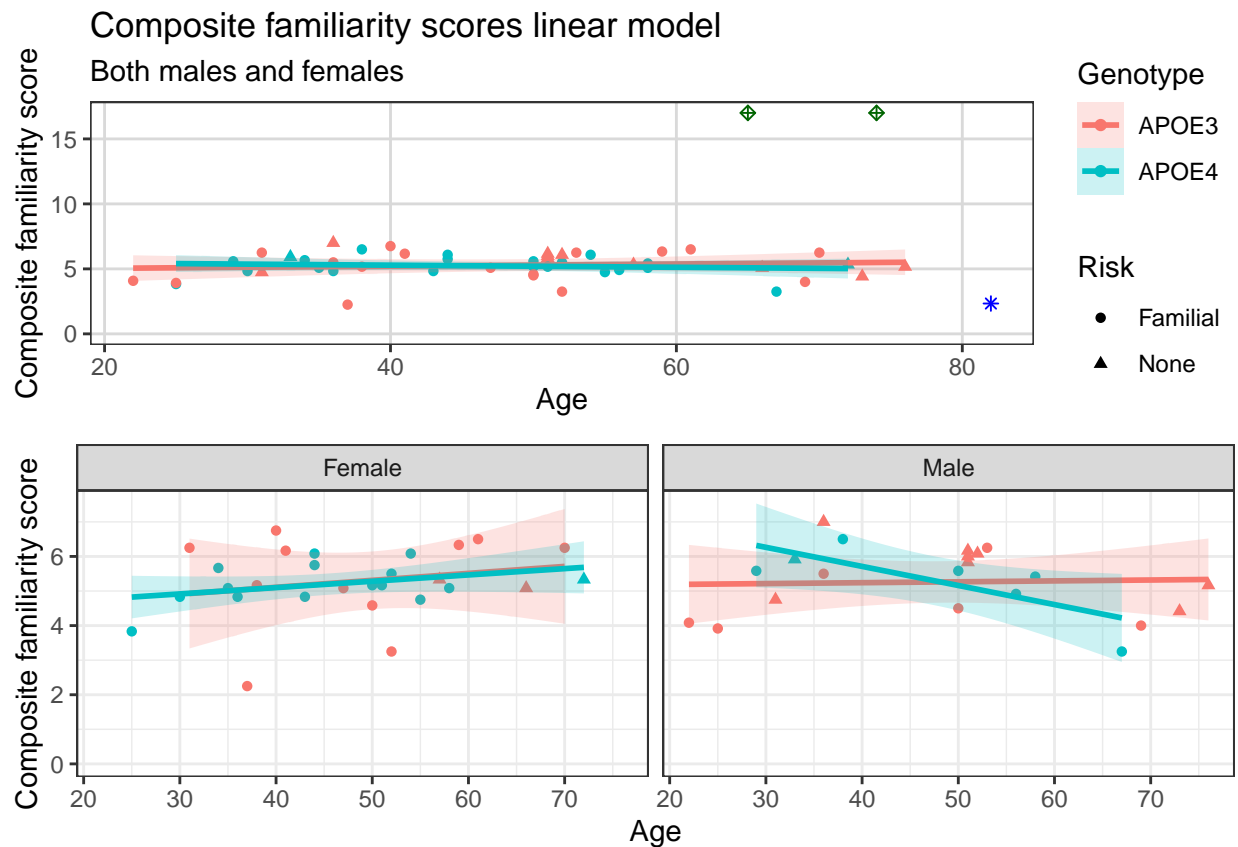
```
##
## Call:
## lm(formula = Composite_Familiarity ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.79759 -0.54794 -0.08256  0.69856  1.77001
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                4.302877   1.201535   3.581 0.000898 ***
## age                        0.020127   0.023434   0.859 0.395402
## GenotypeAPOE4              0.064319   1.569378   0.041 0.967508
## sexMale                    0.833594   1.458443   0.572 0.570737
## age:GenotypeAPOE4         -0.001837   0.031772  -0.058 0.954167
## age:sexMale               -0.017530   0.028503  -0.615 0.541946
## GenotypeAPOE4:sexMale      2.718835   2.254914   1.206 0.234831
## age:GenotypeAPOE4:sexMale -0.055959   0.045577  -1.228 0.226533
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9873 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.116,  Adjusted R-squared:  -0.03493
## F-statistic: 0.7686 on 7 and 41 DF,  p-value: 0.6167


##
## 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
## -1.31572 -0.76636  0.08816  0.69856  1.77001
```

```
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       5.136471   0.797007   6.445 6.05e-06 ***
## age               0.002598   0.015643   0.166   0.8701
## GenotypeAPOE4     2.783153   1.561080   1.783   0.0925 .
## age:GenotypeAPOE4 -0.057796   0.031506  -1.834   0.0841 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9519 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1948, Adjusted R-squared:  0.05272
## F-statistic: 1.371 on 3 and 17 DF,  p-value: 0.2854


## Analysis of Variance Table
##
## Response: Composite_Familiarity
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1  0.047 0.04653  0.0477 0.82813
## Genotype         1  0.022 0.02195  0.0225 0.88144
## sex              1  0.004 0.00419  0.0043 0.94802
## age:Genotype     1  0.573 0.57282  0.5877 0.44771
## age:sex          1  3.123 3.12282  3.2038 0.08086 .
## Genotype:sex     1  0.006 0.00645  0.0066 0.93556
## age:Genotype:sex 1  1.469 1.46936  1.5074 0.22653
## Residuals       41 39.964 0.97474
## ---
## 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  0.6715 0.67150  0.7411 0.40128
## Genotype      1  0.0060 0.00603  0.0067 0.93592
## age:Genotype  1  3.0491 3.04911  3.3653 0.08415 .
## Residuals    17 15.4030 0.90606
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
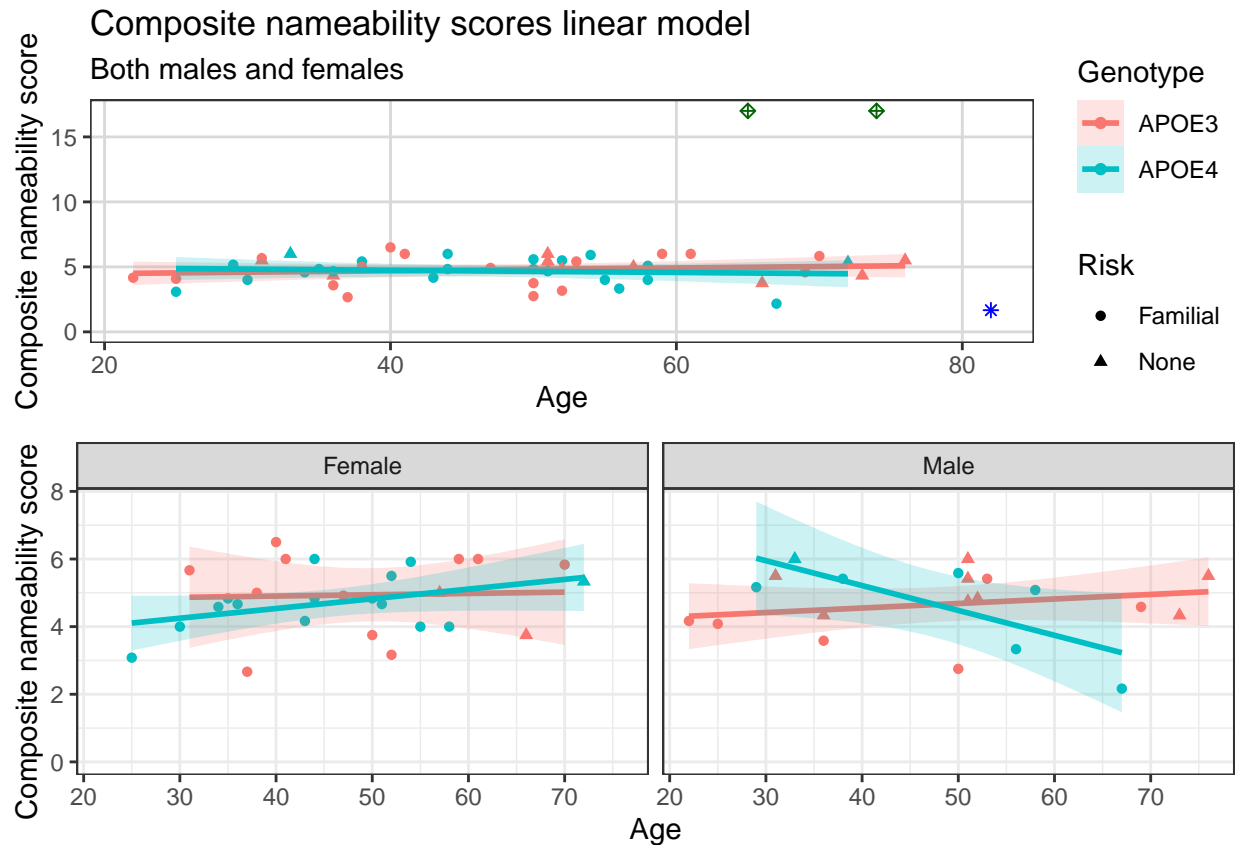
Composite nameability scores linear model

```
## 
## Call:
## lm(formula = Composite_Nameability ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min      1Q   Median      3Q      Max
## -2.22570 -0.65848  0.05292  0.71959  1.59604
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              4.749386   1.195520   3.973 0.000281 ***
## age                      0.003864   0.023317   0.166 0.869183
## GenotypeAPOE4           -1.361723   1.561522  -0.872 0.388260
## sexMale                 -0.735555   1.451142  -0.507 0.614954
## age:GenotypeAPOE4        0.024835   0.031613   0.786 0.436616
## age:sexMale              0.009533   0.028360   0.336 0.738489
## GenotypeAPOE4:sexMale    5.504584   2.243626   2.453 0.018490 *
## age:GenotypeAPOE4:sexMale -0.111787  0.045349  -2.465 0.017978 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.9823 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1963, Adjusted R-squared:  0.05909
## F-statistic: 1.431 on 7 and 41 DF,  p-value: 0.2196
```

```
##
## 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
## -1.93368 -0.65848  0.05292  0.69280  1.30292
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        4.01383    0.77074   5.208 7.11e-05 ***
## age                0.01340    0.01513   0.886   0.3882
## GenotypeAPOE4      4.14286    1.50964   2.744   0.0138 *
## age:GenotypeAPOE4 -0.08695    0.03047  -2.854   0.0110 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9205 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.3339, Adjusted R-squared:  0.2163
## F-statistic:  2.84 on 3 and 17 DF,  p-value: 0.06882


## Analysis of Variance Table
##
## Response: Composite_Nameability
##                Df Sum Sq Mean Sq F value  Pr(>F)
## age             1  0.137  0.1367  0.1417 0.70854
## Genotype        1  0.111  0.1113  0.1153 0.73588
## sex             1  0.335  0.3352  0.3474 0.55884
## age:Genotype    1  0.720  0.7205  0.7466 0.39257
## age:sex         1  2.417  2.4169  2.5046 0.12120
## Genotype:sex    1  0.080  0.0795  0.0824 0.77550
## age:Genotype:sex 1  5.864  5.8637  6.0764 0.01798 *
```

```
## Residuals          41 39.565  0.9650
## ---
## 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  0.3185  0.3185  0.3759 0.54791
## Genotype      1  0.0004  0.0004  0.0005 0.98189
## age:Genotype  1  6.9014  6.9014  8.1449 0.01098 *
## Residuals    17 14.4046  0.8473
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Odor percent correctly recognized linear model

```
##
```
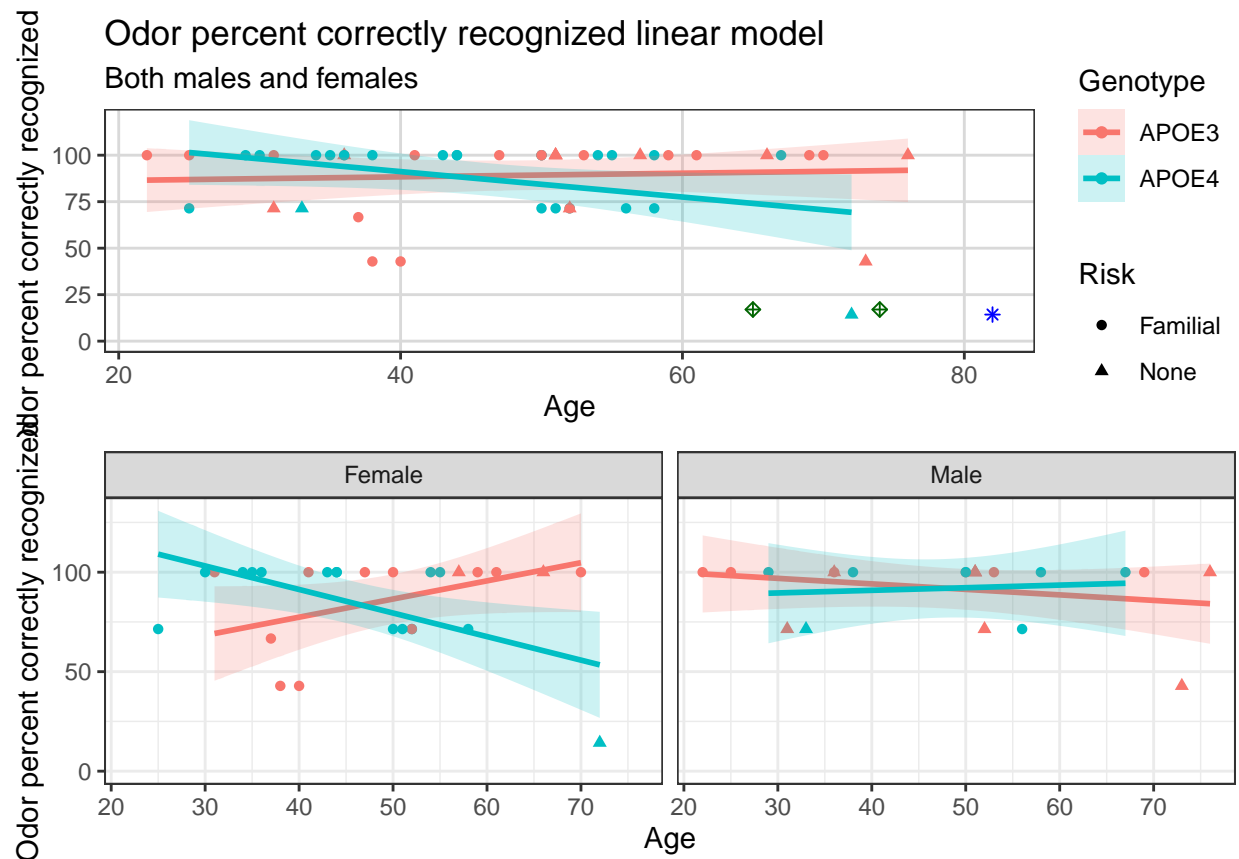
```
## Call:
## lm(formula = Recognized ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -42.142  -6.863   4.764   9.468  30.822
##
## Coefficients:
##                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)                  40.8875    22.8056   1.793  0.08037 .
## age                           0.9126     0.4448   2.052  0.04662 *
## GenotypeAPOE4                97.7702    29.7874   3.282  0.00211 **
## sexMale                      64.3087    27.6818   2.323  0.02521 *
## age:GenotypeAPOE4            -2.0962     0.6030  -3.476  0.00122 **
## age:sexMale                  -1.1893     0.5410  -2.198  0.03363 *
## GenotypeAPOE4:sexMale      -117.3431    42.7991  -2.742  0.00902 **
## age:GenotypeAPOE4:sexMale     2.5043     0.8651   2.895  0.00605 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 18.74 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.267,  Adjusted R-squared:  0.1419
## F-statistic: 2.134 on 7 and 41 DF,  p-value: 0.06127


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


##
## Call:
## lm(formula = Recognized ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -42.142   0.891   6.755   8.914  15.831
##
```

```
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)      105.1962    14.1088   7.456 9.39e-07 ***
## age               -0.2767     0.2769  -0.999    0.332
## GenotypeAPOE4    -19.5729    27.6346  -0.708    0.488
## age:GenotypeAPOE4  0.4081     0.5577   0.732    0.474
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.85 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.05932,    Adjusted R-squared:  -0.1067
## F-statistic: 0.3573 on 3 and 17 DF,  p-value: 0.7845


## Analysis of Variance Table
##
## Response: Recognized
##                 Df  Sum Sq Mean Sq F value   Pr(>F)
## age              1   312.4  312.41  0.8897 0.351093
## Genotype         1    95.2   95.24  0.2712 0.605307
## sex              1   420.4  420.38  1.1971 0.280281
## age:Genotype     1  1365.9 1365.92  3.8898 0.055351 .
## age:sex          1    94.8   94.78  0.2699 0.606183
## Genotype:sex     1    12.9   12.93  0.0368 0.848779
## age:Genotype:sex 1  2942.9 2942.86  8.3805 0.006053 **
## Residuals       41 14397.3  351.15
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


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


## Analysis of Variance Table
##
## Response: Recognized
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1  152.2 152.218  0.5361 0.4740
## Genotype      1    0.1   0.145  0.0005 0.9823
## age:Genotype  1  152.0 152.005  0.5354 0.4743
## Residuals    17 4826.8 283.931
```
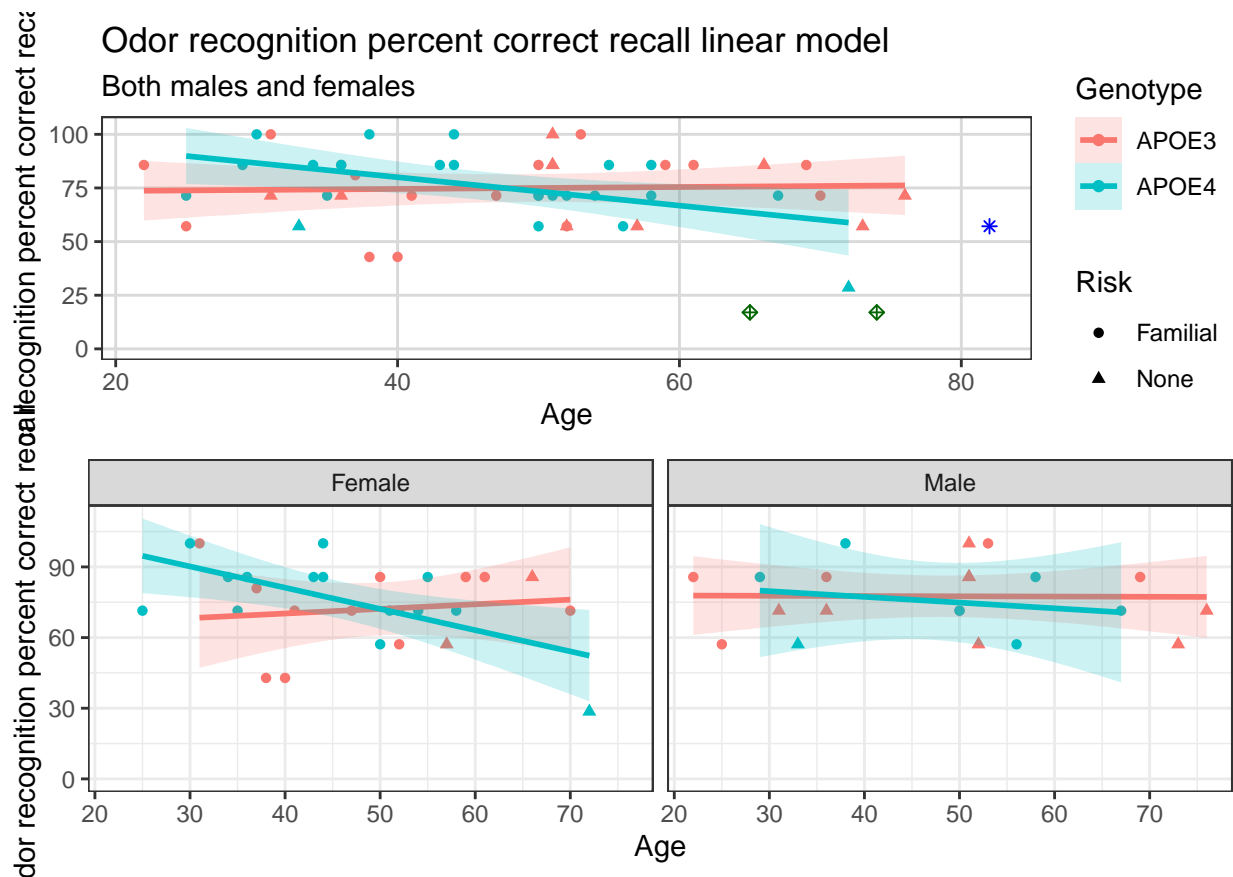
Odor recognition percent correct recall linear model

```
##
## Call:
## lm(formula = PrecentCorrectRecall ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -27.357 -14.260   1.019   9.803  31.553
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)               62.3631    19.4810   3.201  0.00264 **
## age                        0.1963     0.3800   0.517  0.60825
## GenotypeAPOE4             54.8840    25.4451   2.157  0.03692 *
## sexMale                   15.6935    23.6464   0.664  0.51061
## age:GenotypeAPOE4         -1.0979     0.5151  -2.131  0.03910 *
## age:sexMale               -0.2067     0.4621  -0.447  0.65698
## GenotypeAPOE4:sexMale    -45.9595    36.5600  -1.257  0.21583
## age:GenotypeAPOE4:sexMale  0.8658     0.7390   1.172  0.24809
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.01 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1648, Adjusted R-squared:  0.02217
## F-statistic: 1.155 on 7 and 41 DF,  p-value: 0.349
```

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


##
## Call:
## lm(formula = PrecentCorrectRecall ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min      1Q   Median      3Q      Max
## -21.8329  -6.3035   0.7008   8.1917  22.4983
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       78.05666   13.13712   5.942 1.61e-05 ***
## age               -0.01047    0.25784  -0.041    0.968
## GenotypeAPOE4      8.92447   25.73140   0.347    0.733
## age:GenotypeAPOE4 -0.23212    0.51931  -0.447    0.661
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 15.69 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared: 0.02131,    Adjusted R-squared:  -0.1514
## F-statistic: 0.1234 on 3 and 17 DF,  p-value: 0.945


## Analysis of Variance Table
##
## Response: PrecentCorrectRecall
##                 Df  Sum Sq Mean Sq F value  Pr(>F)
## age              1   445.2  445.18  1.7374 0.19479
## Genotype         1     1.5    1.53  0.0060 0.93885
## sex              1    91.7   91.70  0.3579 0.55297
## age:Genotype     1  1078.3 1078.33  4.2084 0.04665 *
## age:sex          1    44.6   44.62  0.1741 0.67865
## Genotype:sex     1    59.3   59.32  0.2315 0.63298
## age:Genotype:sex 1   351.8  351.77  1.3728 0.24809
```

```
## Residuals        41 10505.6   256.24
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


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


## Analysis of Variance Table
##
## Response: PrecentCorrectRecall
##               Df Sum Sq Mean Sq F value Pr(>F)
## age            1   21.2  21.227  0.0862 0.7726
## Genotype       1   20.7  20.727  0.0842 0.7752
## age:Genotype   1   49.2  49.179  0.1998 0.6605
## Residuals     17 4184.9 246.168
```
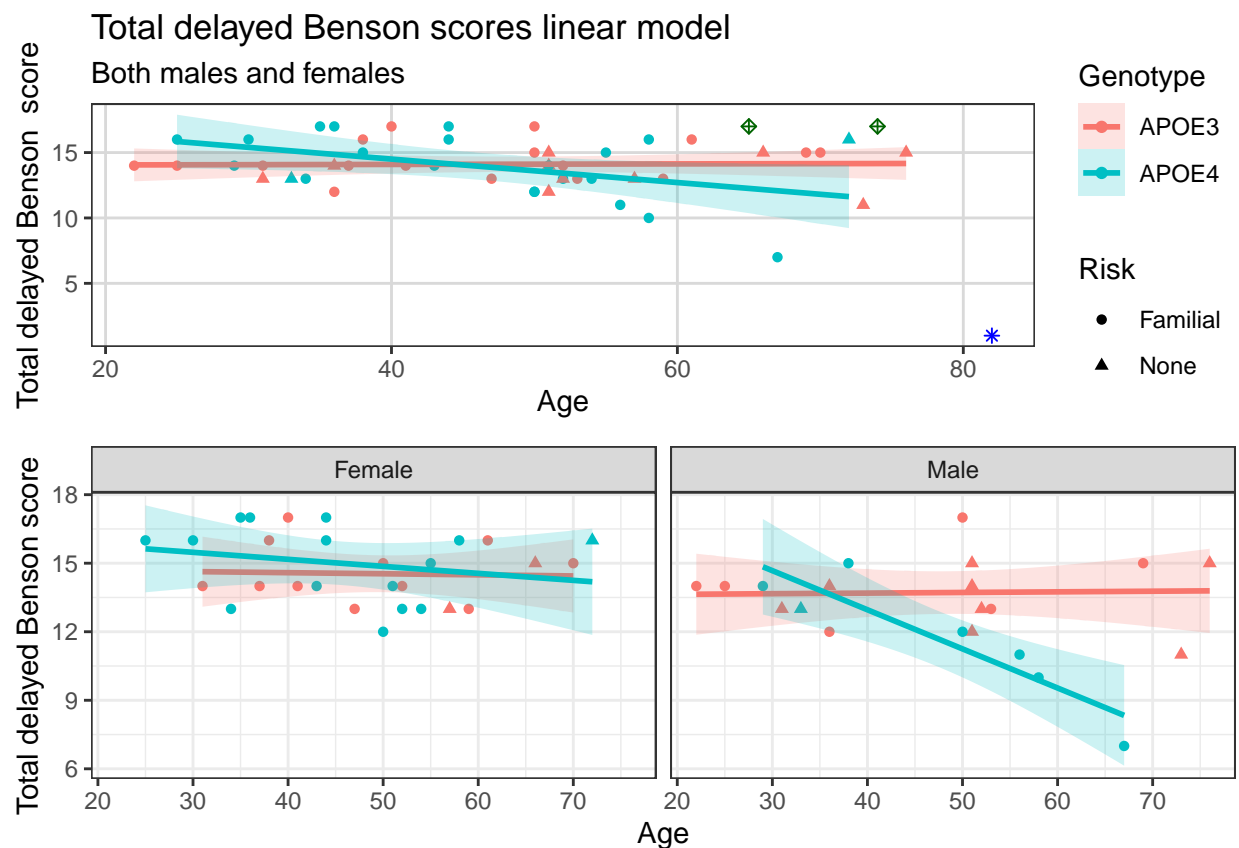

Total delayed Benson scores linear model

```
##
```

```
## Call:
## lm(formula = Delay_BensonTotal ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.8629 -1.0778  0.2906  1.2098  3.2810
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)              14.776458   1.861623   7.937 8.09e-10 ***
## age                      -0.004767   0.036309  -0.131   0.8962
## GenotypeAPOE4             1.621105   2.431548   0.667   0.5087
## sexMale                  -1.194437   2.259668  -0.529   0.5999
## age:GenotypeAPOE4        -0.025926   0.049226  -0.527   0.6013
## age:sexMale               0.007506   0.044161   0.170   0.8659
## GenotypeAPOE4:sexMale     4.607722   3.493698   1.319   0.1945
## age:GenotypeAPOE4:sexMale -0.148040   0.070616  -2.096   0.0423 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.53 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.4949, Adjusted R-squared:  0.4086
## F-statistic: 5.738 on 7 and 41 DF,  p-value: 0.0001133


##
## 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
## -2.7820 -0.8453  0.2783  0.7778  3.2810
##
```

```
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      13.582022   1.263988  10.745 5.34e-09 ***
## age               0.002739   0.024808   0.110  0.91337
## GenotypeAPOE4     6.228827   2.475748   2.516  0.02221 *
## age:GenotypeAPOE4 -0.173966   0.049966  -3.482  0.00286 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.51 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.5832, Adjusted R-squared:  0.5097
## F-statistic:  7.93 on 3 and 17 DF,  p-value: 0.001597


## Analysis of Variance Table
##
## Response: Delay_BensonTotal
##                 Df Sum Sq Mean Sq F value    Pr(>F)
## age              1  8.981   8.981  3.8380 0.0569261 .
## Genotype         1  0.774   0.774  0.3306 0.5684622
## sex              1 39.500  39.500 16.8810 0.0001856 ***
## age:Genotype     1 14.478  14.478  6.1876 0.0170244 *
## age:sex          1  3.342   3.342  1.4282 0.2389205
## Genotype:sex     1 16.625  16.625  7.1048 0.0109473 *
## age:Genotype:sex 1 10.284  10.284  4.3949 0.0422605 *
## Residuals       41 95.936   2.340
## ---
## 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  7.182  7.1816  3.1514 0.093766 .
## Genotype      1 19.405 19.4051  8.5153 0.009588 **
## age:Genotype  1 27.625 27.6249 12.1222 0.002855 **
## Residuals    17 38.741  2.2789
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
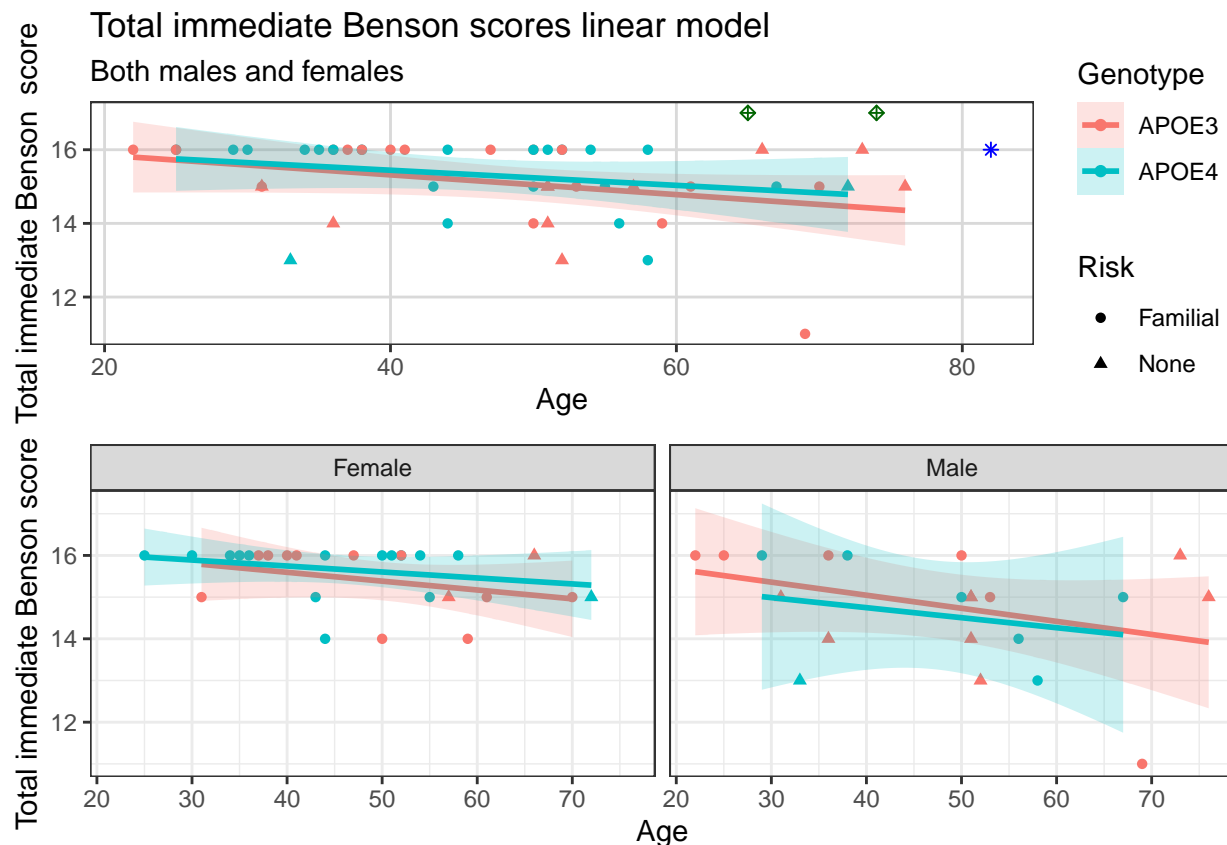
Total immediate Benson scores linear model

```
##
## Call:
## lm(formula = Im_BensonTotal ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.1360 -0.3618  0.2994  0.4839  1.9895
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)             16.4426194  1.2449736  13.207 2.32e-16 ***
## age                     -0.0211927  0.0242816  -0.873    0.388
## GenotypeAPOE4           -0.1237565  1.6261149  -0.076    0.940
## sexMale                 -0.1423879  1.5111691  -0.094    0.925
## age:GenotypeAPOE4        0.0068692  0.0329204   0.209    0.836
## age:sexMale             -0.0101731  0.0295333  -0.344    0.732
## GenotypeAPOE4:sexMale   -0.4675128  2.3364353  -0.200    0.842
## age:GenotypeAPOE4:sexMale 0.0004399 0.0472252   0.009   0.993
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.023 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2518, Adjusted R-squared:  0.1241
## F-statistic: 1.971 on 7 and 41 DF,  p-value: 0.08276
```

```
##
## 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
## -3.1360 -0.7006  0.3622  0.9028  1.9895
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)       16.300231   1.143871  14.250 6.97e-11 ***
## age               -0.031366   0.022450  -1.397    0.180
## GenotypeAPOE4     -0.591269   2.240476  -0.264    0.795
## age:GenotypeAPOE4  0.007309   0.045217   0.162    0.873
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.366 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1256, Adjusted R-squared:  -0.02868
## F-statistic: 0.8141 on 3 and 17 DF,  p-value: 0.5036


## Analysis of Variance Table
##
## Response: Im_BensonTotal
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1  5.638  5.6385  5.3880 0.02533 *
## Genotype         1  0.351  0.3514  0.3358 0.56546
## sex              1  7.560  7.5604  7.2246 0.01034 *
## age:Genotype     1  0.205  0.2046  0.1955 0.66069
## age:sex          1  0.137  0.1368  0.1307 0.71954
## Genotype:sex     1  0.549  0.5491  0.5247 0.47296
## age:Genotype:sex 1  0.000  0.0001  0.0001 0.99261
```

```
## Residuals       41 42.906  1.0465
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


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


## Analysis of Variance Table
##
## Response: Im_BensonTotal
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1  4.232  4.2323  2.2677 0.1504
## Genotype      1  0.277  0.2772  0.1485 0.7047
## age:Genotype  1  0.049  0.0488  0.0261 0.8735
## Residuals    17 31.727  1.8663
```
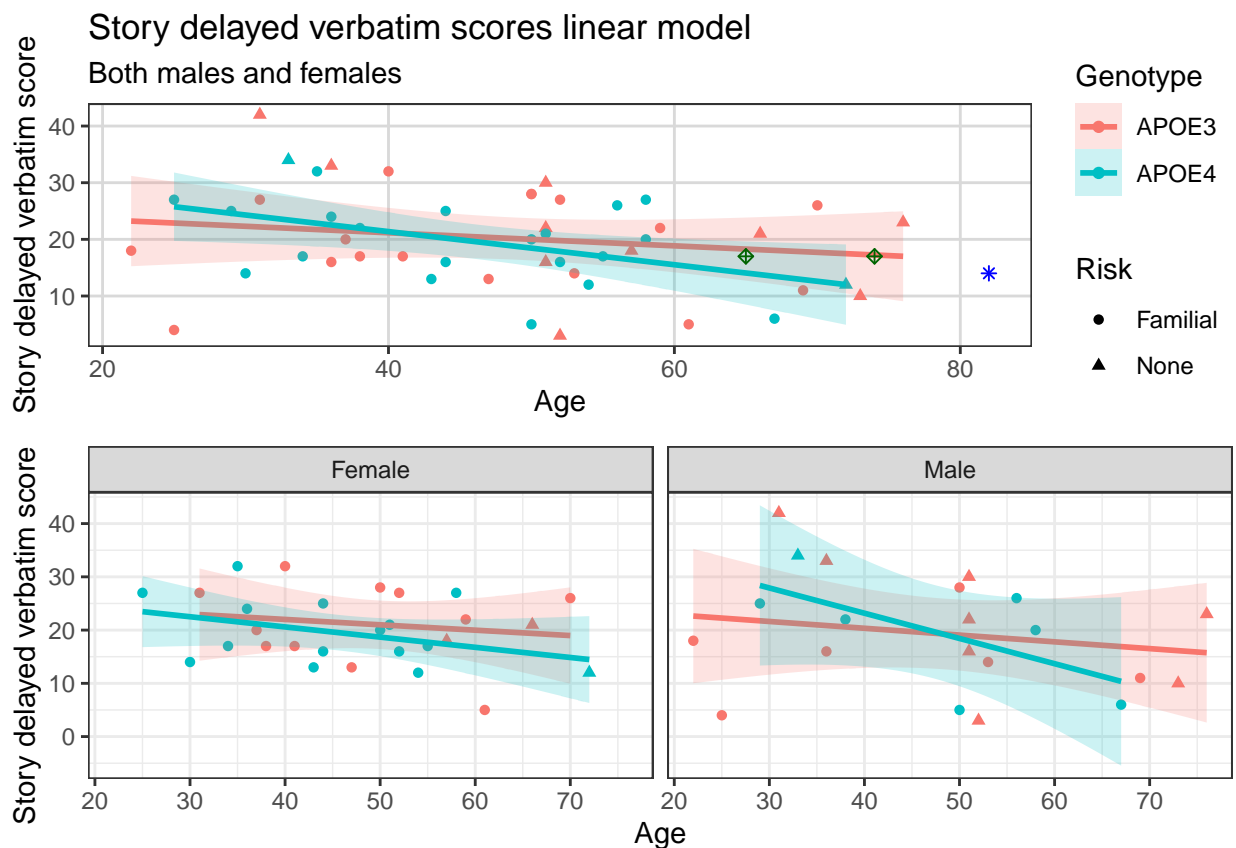

Story delayed verbatim scores linear model

```
##
```

```
## Call:
## lm(formula = Delayed_verbatim ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min     1Q  Median      3Q     Max
## -18.255  -4.852  -2.117   6.210  20.510
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                26.03471   10.49292   2.481   0.0173 *
## age                        -0.10085    0.20465  -0.493   0.6248
## GenotypeAPOE4               2.21225   13.70526   0.161   0.8726
## sexMale                    -0.59220   12.73647  -0.046   0.9631
## age:GenotypeAPOE4          -0.09052    0.27746  -0.326   0.7459
## age:sexMale                -0.02666    0.24891  -0.107   0.9152
## GenotypeAPOE4:sexMale      14.48120   19.69200   0.735   0.4663
## age:GenotypeAPOE4:sexMale  -0.25615    0.39802  -0.644   0.5235
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.622 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.129,  Adjusted R-squared:  -0.0197
## F-statistic: 0.8675 on 7 and 41 DF,  p-value: 0.5399


##
## 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
## -18.255  -4.852  -2.940   7.512  20.510
##
```

```
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        25.4425     9.0128   2.823   0.0117 *
## age                -0.1275     0.1769  -0.721   0.4808
## GenotypeAPOE4       16.6935    17.6532   0.946   0.3576
## age:GenotypeAPOE4   -0.3467     0.3563  -0.973   0.3442
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.76 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1448, Adjusted R-squared:  -0.006147
## F-statistic: 0.9593 on 3 and 17 DF,  p-value: 0.4345


## Analysis of Variance Table
##
## Response: Delayed_verbatim
##                   Df  Sum Sq Mean Sq F value  Pr(>F)
## age                1  283.11 283.113  3.8085 0.05785 .
## Genotype           1   13.55  13.550  0.1823 0.67166
## sex                1   10.85  10.855  0.1460 0.70434
## age:Genotype       1   62.54  62.536  0.8412 0.36440
## age:sex            1   36.56  36.559  0.4918 0.48709
## Genotype:sex       1   14.03  14.035  0.1888 0.66620
## age:Genotype:sex   1   30.79  30.787  0.4142 0.52345
## Residuals         41 3047.83  74.337
## ---
## 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  223.52 223.524  1.9292 0.1828
## Genotype        1    0.22   0.217  0.0019 0.9660
## age:Genotype    1  109.70 109.698  0.9468 0.3442
## Residuals      17 1969.70 115.865
```
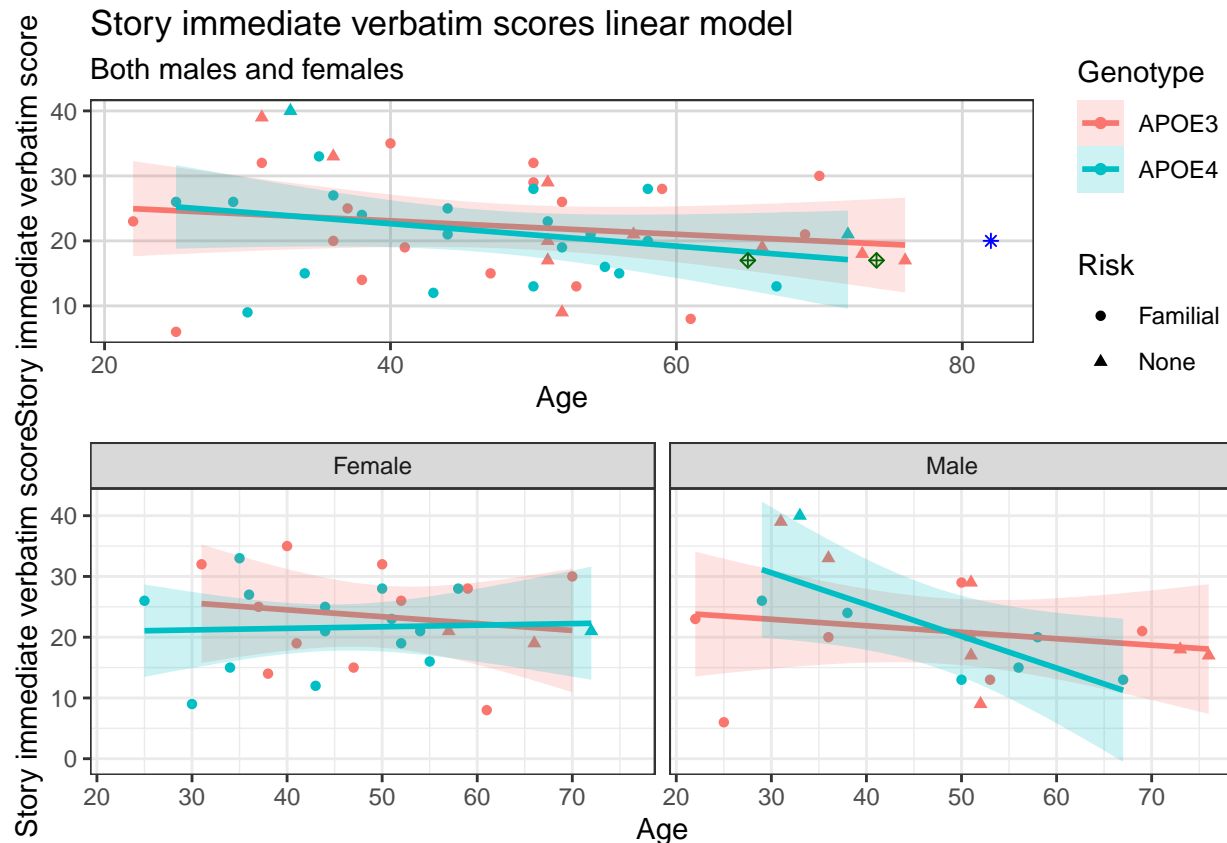
Story immediate verbatim scores linear model

Both males and females

```
##
## Call:
## lm(formula = Immediate_verbatim ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -17.4840  -5.1283  -0.7105   5.6485  16.1561
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)               29.027303   9.767971   2.972  0.00494 **
## age                       -0.113028   0.190512  -0.593  0.55625
## GenotypeAPOE4             -8.614157  12.758377  -0.675  0.50335
## sexMale                   -2.876455  11.856521  -0.243  0.80952
## age:GenotypeAPOE4          0.139093   0.258291   0.539  0.59313
## age:sexMale                0.006353   0.231716   0.027  0.97826
## GenotypeAPOE4:sexMale     28.748214  18.331498   1.568  0.12451
## age:GenotypeAPOE4:sexMale -0.555060   0.370525  -1.498  0.14178
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.026 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1426, Adjusted R-squared:  -0.003794
## F-statistic: 0.9741 on 7 and 41 DF,  p-value: 0.4629
```

```
##
## 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
## -17.484  -3.711  -0.804   4.028  16.156
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        26.1508     7.2104   3.627  0.00208 **
## age                -0.1067     0.1415  -0.754  0.46129
## GenotypeAPOE4      20.1341    14.1229   1.426  0.17208
## age:GenotypeAPOE4  -0.4160     0.2850  -1.459  0.16269
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.611 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2291, Adjusted R-squared:  0.09301
## F-statistic: 1.684 on 3 and 17 DF,  p-value: 0.2082


## Analysis of Variance Table
##
## Response: Immediate_verbatim
##                 Df  Sum Sq Mean Sq F value Pr(>F)
## age              1  142.03 142.035  2.2048 0.1452
## Genotype         1   10.68  10.683  0.1658 0.6860
## sex              1   23.81  23.813  0.3696 0.5465
## age:Genotype     1    8.24   8.239  0.1279 0.7225
## age:sex          1   95.85  95.852  1.4879 0.2295
## Genotype:sex     1   14.07  14.066  0.2183 0.6428
## age:Genotype:sex 1  144.57 144.567  2.2441 0.1418
```

```
## Residuals         41 2641.23  64.420


## 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  216.02 216.015  2.9129 0.1061
## Genotype       1    0.61   0.612  0.0082 0.9287
## age:Genotype   1  157.94 157.940  2.1298 0.1627
## Residuals     17 1260.67  74.157
```


MOCA attention digits scores linear model
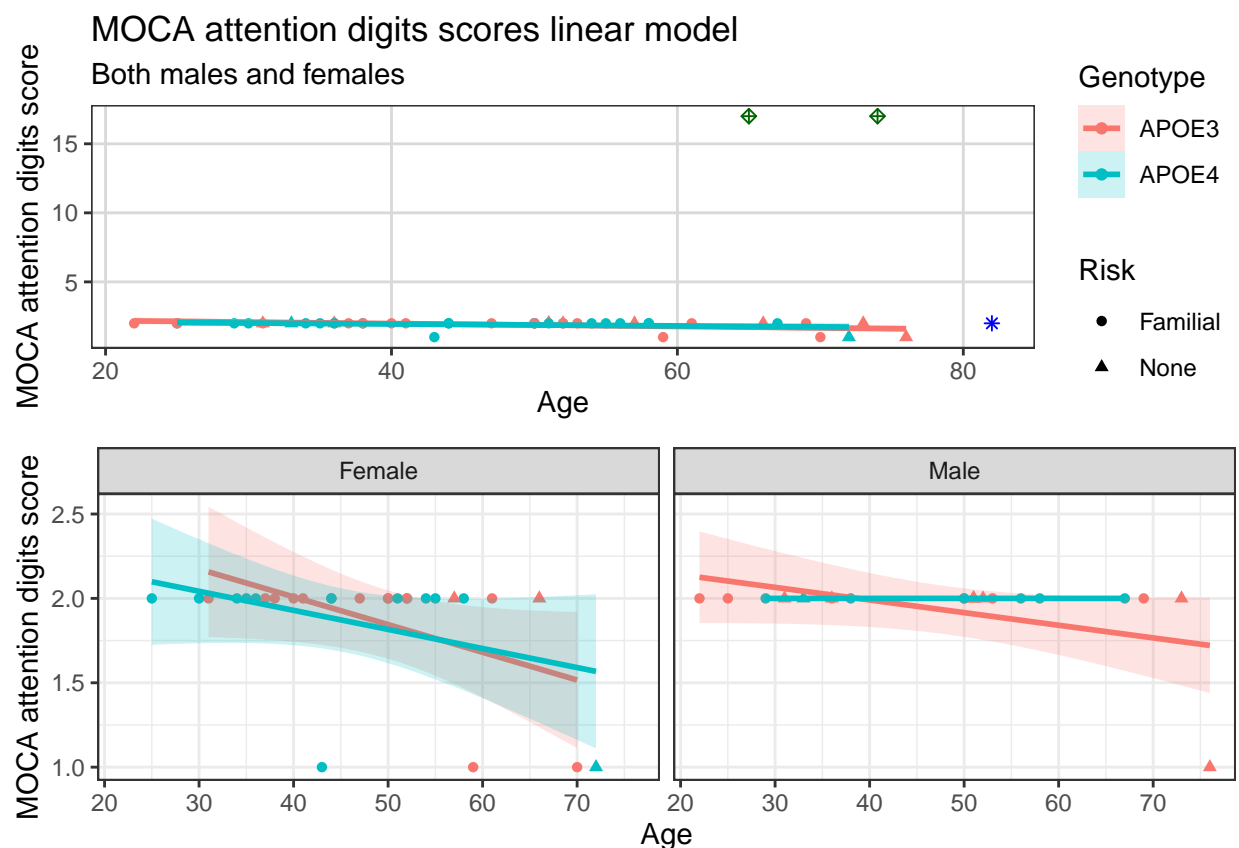
```
##
## Call:
## lm(formula = MOCA_Attention_Digits ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
```

```
##      Min      1Q  Median      3Q     Max
## -0.89530 -0.04200  0.00728  0.15511  0.41792
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)               2.666161   0.350330   7.610  2.3e-09 ***
## age                      -0.016425   0.006833  -2.404   0.0208 *
## GenotypeAPOE4            -0.284904   0.457581  -0.623   0.5370
## sexMale                  -0.376192   0.425236  -0.885   0.3815
## age:GenotypeAPOE4         0.005124   0.009264   0.553   0.5832
## age:sexMale               0.008941   0.008311   1.076   0.2883
## GenotypeAPOE4:sexMale    -0.005065   0.657462  -0.008   0.9939
## age:GenotypeAPOE4:sexMale 0.002361   0.013289   0.178   0.8599
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2879 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2433, Adjusted R-squared:  0.1141
## F-statistic: 1.883 on 7 and 41 DF,  p-value: 0.09735


##
## 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
## -0.72114 -0.02052  0.00000  0.09174  0.25640
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)     2.289969   0.172453  13.279 2.11e-10 ***
## age            -0.007485   0.003385  -2.211    0.041 *
```

```
## GenotypeAPOE4     -0.289969   0.337779  -0.858      0.403
## age:GenotypeAPOE4  0.007485   0.006817   1.098      0.288
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.206 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2428, Adjusted R-squared:  0.1092
## F-statistic: 1.817 on 3 and 17 DF,  p-value: 0.1823


## Analysis of Variance Table
##
## Response: MOCA_Attention_Digits
##                  Df Sum Sq Mean Sq F value   Pr(>F)
## age               1 0.7392 0.73920  8.9206 0.004743 **
## Genotype          1 0.0006 0.00059  0.0071 0.933371
## sex               1 0.1184 0.11841  1.4289 0.238812
## age:Genotype      1 0.0218 0.02179  0.2630 0.610832
## age:sex           1 0.1779 0.17789  2.1467 0.150502
## Genotype:sex      1 0.0319 0.03188  0.3847 0.538547
## age:Genotype:sex  1 0.0026 0.00261  0.0316 0.859886
## Residuals        41 3.3974 0.08286
## ---
## 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 0.15993 0.159926  3.7701 0.06894 .
## Genotype      1 0.02018 0.020179  0.4757 0.49969
## age:Genotype  1 0.05113 0.051134  1.2054 0.28755
## Residuals    17 0.72114 0.042420
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
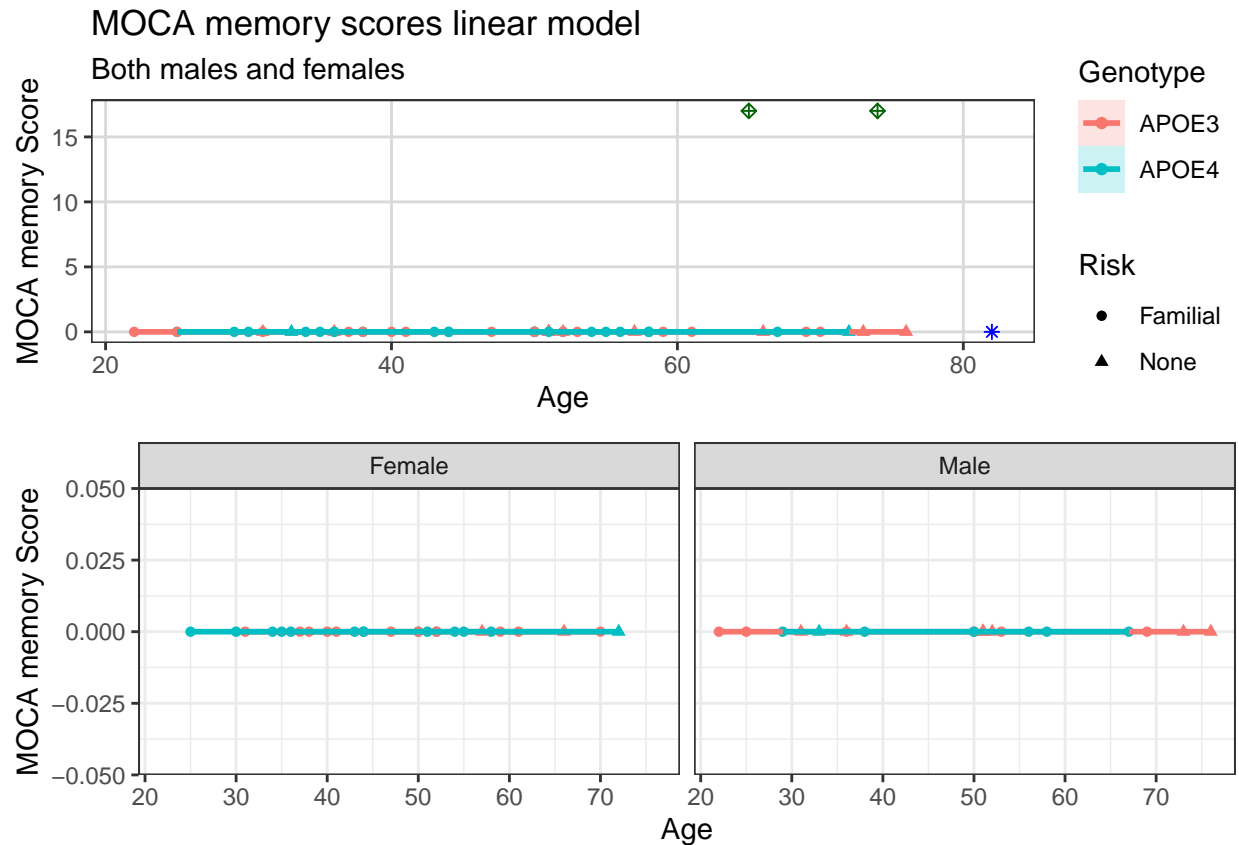
MOCA memory scores linear model

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 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:    NaN,  Adjusted R-squared:    NaN
## F-statistic:   NaN on 7 and 41 DF,  p-value: NA
##
##
```

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


##
## Call:
## lm(formula = MOCA_Memory ~ age * Genotype, data = combo_m)
##
## Residuals:
##    Min     1Q Median     3Q    Max
##      0      0      0      0      0
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)             0          0     NaN      NaN
## age                     0          0     NaN      NaN
## GenotypeAPOE4           0          0     NaN      NaN
## age:GenotypeAPOE4       0          0     NaN      NaN
##
## Residual standard error: 0 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:    NaN,  Adjusted R-squared:    NaN
## F-statistic:   NaN on 3 and 17 DF,  p-value: NA


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


## Analysis of Variance Table
##
```

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


## Analysis of Variance Table
##
## Response: MOCA_Memory
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1      0       0     NaN    NaN
## Genotype      1      0       0     NaN    NaN
## age:Genotype  1      0       0     NaN    NaN
## Residuals    17      0       0
```

MOCA naming scores linear model


```
##
## Call:
## lm(formula = MOCA_Naming ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min     1Q  Median      3Q     Max
## -2.6846  0.0000  0.0000  0.0000  0.4709
##
## Coefficients:
```

```
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)              3.36639    0.53939   6.241 1.96e-07 ***
## age                     -0.01196    0.01052  -1.137    0.262
## GenotypeAPOE4           -0.36639    0.70452  -0.520    0.606
## sexMale                 -0.36639    0.65472  -0.560    0.579
## age:GenotypeAPOE4        0.01196    0.01426   0.839    0.407
## age:sexMale              0.01196    0.01280   0.935    0.355
## GenotypeAPOE4:sexMale    0.36639    1.01226   0.362    0.719
## age:GenotypeAPOE4:sexMale -0.01196   0.02046  -0.585    0.562
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4432 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.0865, Adjusted R-squared:  -0.06947
## F-statistic: 0.5546 on 7 and 41 DF,  p-value: 0.7878


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


##
## Call:
## lm(formula = MOCA_Naming ~ age * Genotype, data = combo_m)
##
## Residuals:
##        Min         1Q     Median         3Q        Max
## -9.635e-16 -2.123e-16  0.000e+00  0.000e+00  3.020e-15
##
## Coefficients:
##                    Estimate Std. Error    t value Pr(>|t|)
## (Intercept)       3.000e+00  7.120e-16  4.214e+15  <2e-16 ***
## age              -2.889e-17  1.397e-17 -2.068e+00   0.0542 .
## GenotypeAPOE4    -1.686e-15  1.395e-15 -1.209e+00   0.2432
## age:GenotypeAPOE4 2.889e-17  2.814e-17  1.027e+00   0.3190
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 8.503e-16 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.5027, Adjusted R-squared:  0.4149
## F-statistic: 5.728 on 3 and 17 DF,  p-value: 0.006741


## Analysis of Variance Table
##
## Response: MOCA_Naming
##                 Df Sum Sq  Mean Sq F value Pr(>F)
## age              1 0.0863 0.086349  0.4396 0.5110
## Genotype         1 0.1273 0.127270  0.6479 0.4255
## sex              1 0.2082 0.208243  1.0601 0.3092
## age:Genotype     1 0.0289 0.028875  0.1470 0.7034
## age:sex          1 0.1296 0.129614  0.6598 0.4213
## Genotype:sex     1 0.1151 0.115098  0.5859 0.4484
## age:Genotype:sex 1 0.0671 0.067137  0.3418 0.5620
## Residuals       41 8.0537 0.196433


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


## Analysis of Variance Table
##
## Response: MOCA_Naming
##              Df     Sum Sq    Mean Sq F value  Pr(>F)
## age           1 2.2683e-30 2.2683e-30  3.1372 0.09445 .
## Genotype      1 4.5530e-31 4.5528e-31  0.6297 0.43841
## age:Genotype  1 7.6200e-31 7.6201e-31  1.0539 0.31900
## Residuals    17 1.2292e-29 7.2304e-31
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
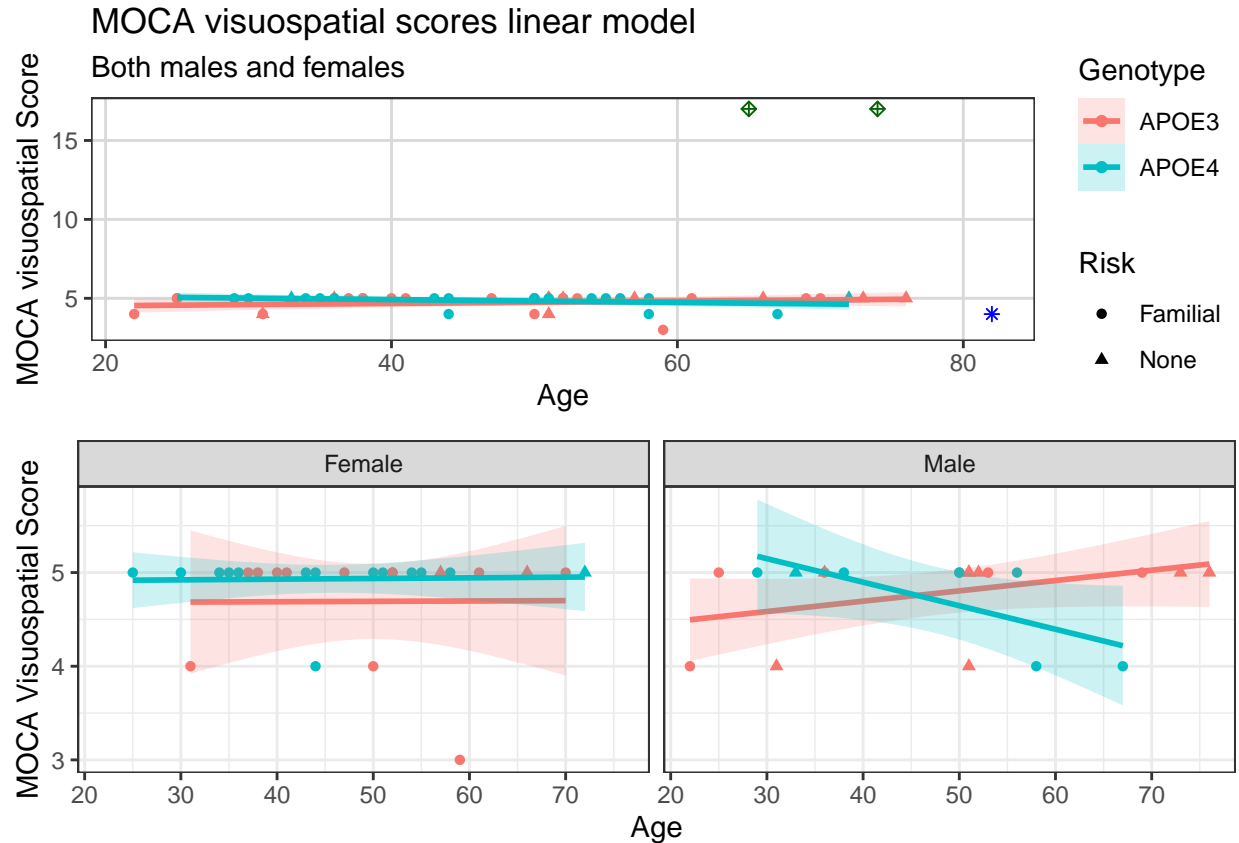
MOCA visuospatial scores linear model


```
## 
## Call:
## lm(formula = MOCA_Visuospatial ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -1.69585 -0.05841  0.07357  0.30337  0.50460 
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)    
## (Intercept)              4.672835   0.546639   8.548 1.19e-10 ***
## age                      0.000390   0.010662   0.037   0.9710    
## GenotypeAPOE4            0.227530   0.713989   0.319   0.7516    
## sexMale                 -0.419903   0.663519  -0.633   0.5304    
## age:GenotypeAPOE4        0.000334   0.014455   0.023   0.9817    
## age:sexMale              0.010644   0.012967   0.821   0.4165    
## GenotypeAPOE4:sexMale    1.421543   1.025874   1.386   0.1733    
## age:GenotypeAPOE4:sexMale -0.036486   0.020736  -1.760   0.0859 .  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.4492 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1694, Adjusted R-squared:  0.02763 
## F-statistic: 1.195 on 7 and 41 DF,  p-value: 0.3273
```

```
## 
## 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
## -0.81566 -0.17358  0.05248  0.19537  0.50460
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        4.25293    0.32559  13.062 2.72e-10 ***
## age                0.01103    0.00639   1.727   0.1024
## GenotypeAPOE4      1.64907    0.63773   2.586   0.0192 *
## age:GenotypeAPOE4 -0.03615    0.01287  -2.809   0.0121 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.3889 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.3252, Adjusted R-squared:  0.2061
## F-statistic: 2.731 on 3 and 17 DF,  p-value: 0.07606


## Analysis of Variance Table
## 
## Response: MOCA_Visuospatial
##                 Df Sum Sq Mean Sq F value  Pr(>F)
## age              1 0.0032 0.00320  0.0158 0.90047
## Genotype         1 0.1907 0.19074  0.9454 0.33659
## sex              1 0.0148 0.01481  0.0734 0.78783
## age:Genotype     1 0.5612 0.56122  2.7818 0.10297
## age:sex          1 0.0115 0.01146  0.0568 0.81278
## Genotype:sex     1 0.2813 0.28133  1.3944 0.24446
## age:Genotype:sex 1 0.6247 0.62465  3.0962 0.08594 .
```

```
## Residuals          41 8.2718 0.20175
## ---
## 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 0.02355 0.02355  0.1557 0.69804
## Genotype      1 0.02239 0.02239  0.1481 0.70513
## age:Genotype  1 1.19299 1.19299  7.8895 0.01208 *
## Residuals    17 2.57060 0.15121
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
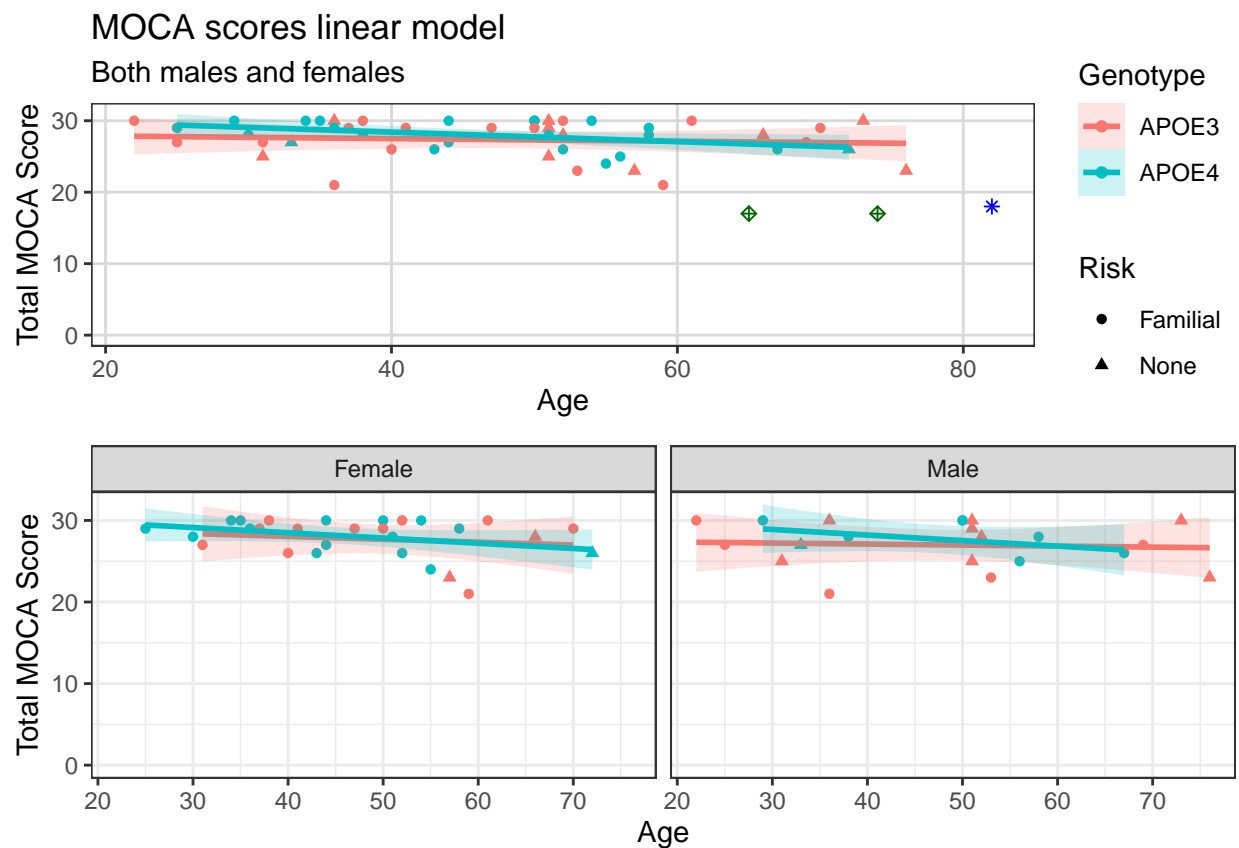

MOCA scores linear model

```
##
```

```
## Call:
## lm(formula = MOCA_TOTAL ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.374  -1.686   0.854   1.889   3.307
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                29.44483    3.16228   9.311 1.14e-11 ***
## age                        -0.03510    0.06168  -0.569    0.572
## GenotypeAPOE4               1.61407    4.13040   0.391    0.698
## sexMale                    -1.84498    3.83843  -0.481    0.633
## age:GenotypeAPOE4          -0.02915    0.08362  -0.349    0.729
## age:sexMale                 0.02268    0.07502   0.302    0.764
## GenotypeAPOE4:sexMale       1.71781    5.93464   0.289    0.774
## age:GenotypeAPOE4:sexMale  -0.02647    0.11995  -0.221    0.826
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.598 on 41 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.08757,    Adjusted R-squared:  -0.06822
## F-statistic: 0.5621 on 7 and 41 DF,  p-value: 0.782


##
## 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
## -6.1526 -1.9663  0.2573  2.4704  3.3070
##
```

```
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        27.59985    2.41352  11.436  2.1e-09 ***
## age                -0.01242    0.04737  -0.262    0.796
## GenotypeAPOE4        3.33188    4.72732   0.705    0.490
## age:GenotypeAPOE4  -0.05562    0.09541  -0.583    0.568
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.882 on 17 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.05715,    Adjusted R-squared:  -0.1092
## F-statistic: 0.3435 on 3 and 17 DF,  p-value: 0.7943


## Analysis of Variance Table
##
## Response: MOCA_TOTAL
##                  Df  Sum Sq Mean Sq F value Pr(>F)
## age               1  13.440 13.4398  1.9906 0.1658
## Genotype          1   3.726  3.7260  0.5519 0.4618
## sex               1   3.974  3.9743  0.5886 0.4473
## age:Genotype      1   4.306  4.3055  0.6377 0.4292
## age:sex           1   0.223  0.2231  0.0330 0.8566
## Genotype:sex      1   0.569  0.5688  0.0843 0.7731
## age:Genotype:sex  1   0.329  0.3288  0.0487 0.8264
## Residuals        41 276.821  6.7517


## 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  3.529  3.5295  0.4248 0.5233
## Genotype      1  2.208  2.2078  0.2657 0.6129
## age:Genotype  1  2.824  2.8238  0.3399 0.5676
## Residuals    17 141.248  8.3087
```