Linear models with AD subject

```
##
## Call:
## lm(formula = ufov1 ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##        Min         1Q      Median         3Q        Max
## -1.034e-13  0.000e+00  0.000e+00  3.680e-16  1.876e-14
##
## Coefficients:
##                              Estimate Std. Error    t value Pr(>|t|)
## (Intercept)                 1.700e+01  2.330e-14  7.298e+14   <2e-16 ***
## age                        -1.060e-30  4.477e-16  0.000e+00    1.000
## GenotypeAPOE4               2.302e-14  3.222e-14  7.140e-01    0.480
## sexMale                    -5.587e-29  3.275e-14  0.000e+00    1.000
## age:GenotypeAPOE4          -7.202e-16  6.693e-16 -1.076e+00    0.289
## age:sexMale                 1.408e-30  6.100e-16  0.000e+00    1.000
## GenotypeAPOE4:sexMale      -2.302e-14  4.890e-14 -4.710e-01    0.641
## age:GenotypeAPOE4:sexMale   7.202e-16  9.527e-16  7.560e-01    0.455
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.84e-14 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.4971, Adjusted R-squared:  0.3993
## F-statistic: 5.083 on 7 and 36 DF,  p-value: 0.0004396


##
## Call:
## lm(formula = ufov1 ~ age * Genotype, data = combo_f)
##
## Residuals:
##        Min         1Q      Median         3Q        Max
## -2.884e-15 -1.306e-15  0.000e+00  0.000e+00  1.590e-14
##
## Coefficients:
##                     Estimate Std. Error    t value Pr(>|t|)
## (Intercept)        1.700e+01  4.581e-15  3.711e+15   <2e-16 ***
## age                4.142e-31  8.804e-17  0.000e+00    1.000
## GenotypeAPOE4     -3.539e-15  6.337e-15 -5.580e-01    0.582
## age:GenotypeAPOE4  1.107e-16  1.316e-16  8.410e-01    0.409
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.618e-15 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.4793, Adjusted R-squared:  0.4083
## F-statistic:  6.75 on 3 and 22 DF,  p-value: 0.002132
```
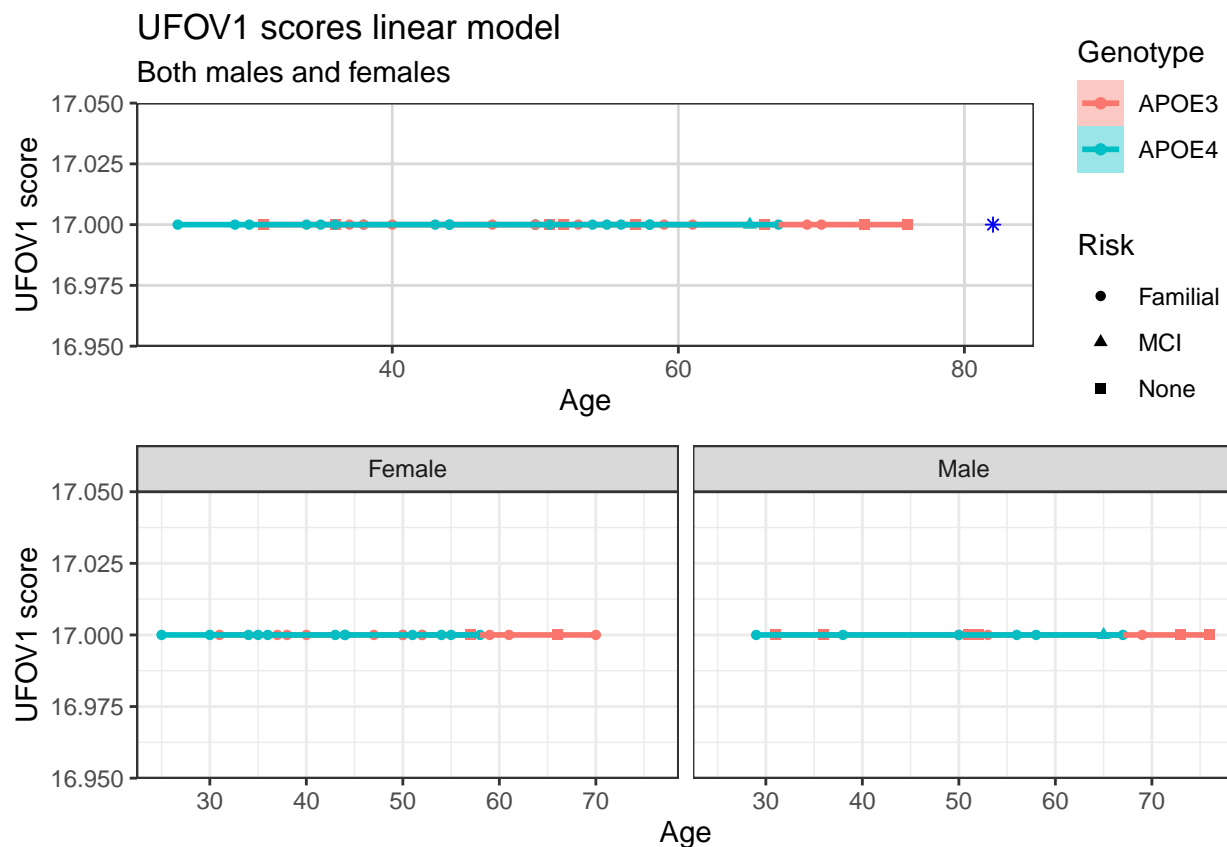
```
## 
## Call:
## lm(formula = ufov1 ~ age * Genotype, data = combo_m)
## 
## Residuals:
##    Min      1Q Median      3Q     Max
##      0       0      0       0       0
## 
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)            17          0     Inf   <2e-16 ***
## age                     0          0     NaN      NaN
## GenotypeAPOE4           0          0     NaN      NaN
## age:GenotypeAPOE4       0          0     NaN      NaN
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:    NaN,  Adjusted R-squared:    NaN
## F-statistic:   NaN on 3 and 14 DF,  p-value: NA
```


UFOV1 scores linear model

```
## 
## Call:
## lm(formula = ufov2 ~ age * Genotype * sex, data = geno_combined)
```
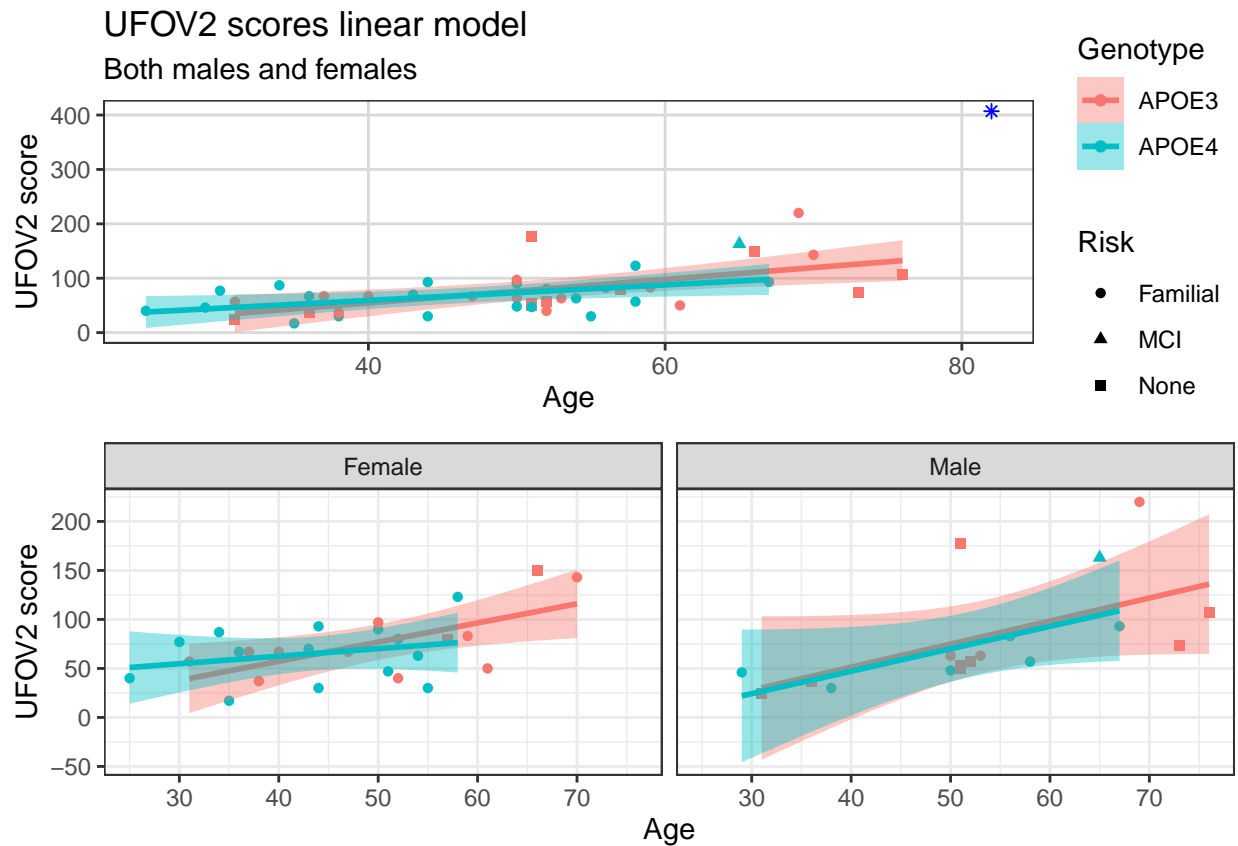
```
##
## Residuals:
##      Min      1Q  Median      3Q     Max
## -55.925 -22.865  -8.166  19.907 100.488
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)               -20.9264    47.6247  -0.439   0.6630
## age                         1.9558     0.9152   2.137   0.0395 *
## GenotypeAPOE4              52.6813    65.8760   0.800   0.4291
## sexMale                   -21.9341    66.9504  -0.328   0.7451
## age:GenotypeAPOE4          -1.1875     1.3683  -0.868   0.3912
## age:sexMale                 0.3974     1.2471   0.319   0.7518
## GenotypeAPOE4:sexMale     -54.1937    99.9676  -0.542   0.5911
## age:GenotypeAPOE4:sexMale   1.1224     1.9478   0.576   0.5680
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 37.61 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.3437, Adjusted R-squared:  0.2161
## F-statistic: 2.693 on 7 and 36 DF,  p-value: 0.02372


##
## Call:
## lm(formula = ufov2 ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min      1Q  Median      3Q     Max
## -48.376 -15.161   6.397  20.060  46.684
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -20.9264    36.8261  -0.568   0.5756
## age                 1.9558     0.7077   2.764   0.0113 *
## GenotypeAPOE4      52.6813    50.9391   1.034   0.3123
## age:GenotypeAPOE4  -1.1875     1.0580  -1.122   0.2738
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 29.08 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.3095, Adjusted R-squared:  0.2153
## F-statistic: 3.286 on 3 and 22 DF,  p-value: 0.0398


##
## Call:
## lm(formula = ufov2 ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min      1Q  Median      3Q     Max
## -55.925 -23.743 -14.257  -1.788 100.488
##
## Coefficients:
```

```
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -42.86042   60.11050  -0.713   0.4875
## age                 2.35323    1.08217   2.175   0.0473 *
## GenotypeAPOE4      -1.51239   96.05289  -0.016   0.9877
## age:GenotypeAPOE4  -0.06505    1.77079  -0.037   0.9712
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 48.04 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.3509, Adjusted R-squared:  0.2118
## F-statistic: 2.523 on 3 and 14 DF,  p-value: 0.09994
```


UFOV2 scores linear model

```
##
## Call:
## lm(formula = ufov3 ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -87.202 -33.183  -7.011  30.193 126.875
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)         2.7278    63.7665   0.043   0.9661
## age                 2.3310     1.2254   1.902   0.0652 .
```

```
## GenotypeAPOE4                  32.2058     88.2038    0.365    0.7172
## sexMale                      -110.9986     89.6424   -1.238    0.2236
## age:GenotypeAPOE4              -0.8352      1.8320   -0.456    0.6512
## age:sexMale                     2.2254      1.6698    1.333    0.1910
## GenotypeAPOE4:sexMale          32.6084    133.8503    0.244    0.8089
## age:GenotypeAPOE4:sexMale      -0.6050      2.6079   -0.232    0.8179
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 50.36 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.4451, Adjusted R-squared:  0.3372
## F-statistic: 4.125 on 7 and 36 DF,  p-value: 0.002023


##
## Call:
## lm(formula = ufov3 ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -87.202 -23.802  -8.514  26.541  87.747
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)         2.7278    60.2052   0.045   0.9643
## age                 2.3310     1.1570   2.015   0.0563 .
## GenotypeAPOE4      32.2058    83.2777   0.387   0.7027
## age:GenotypeAPOE4  -0.8352     1.7297  -0.483   0.6340
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 47.54 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2315, Adjusted R-squared:  0.1267
## F-statistic: 2.209 on 3 and 22 DF,  p-value: 0.1156


##
## Call:
## lm(formula = ufov3 ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -70.221 -34.838  -5.967  32.392 126.875
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -108.271     68.168  -1.588  0.13454
## age                  4.556      1.227   3.713  0.00232 **
## GenotypeAPOE4       64.814    108.929   0.595  0.56133
## age:GenotypeAPOE4   -1.440      2.008  -0.717  0.48506
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 54.48 on 14 degrees of freedom
```
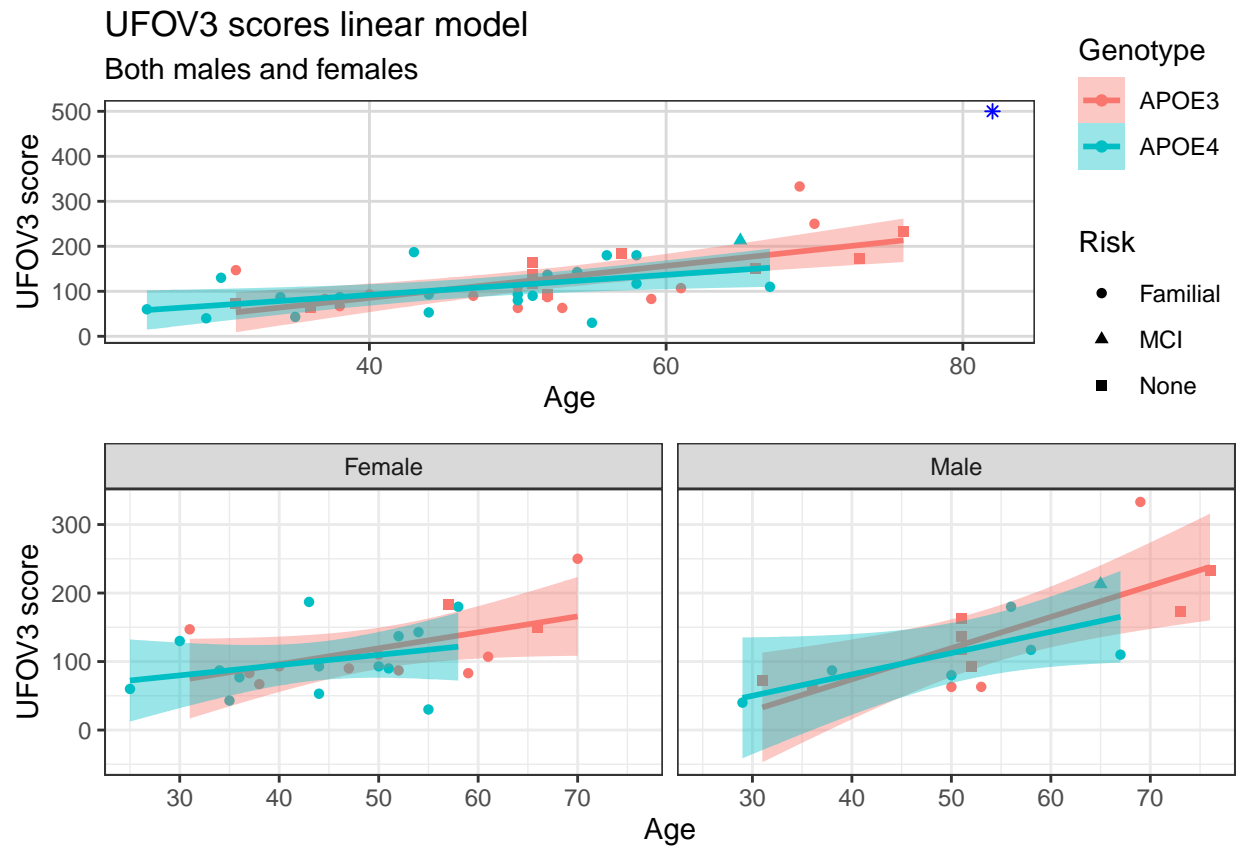
```
##     (5 observations deleted due to missingness)
## Multiple R-squared:  0.5647, Adjusted R-squared:  0.4714
## F-statistic: 6.054 on 3 and 14 DF,  p-value: 0.007318
```


UFOV3 scores linear model

Both males and females

```
##
## Call:
## lm(formula = animals ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -10.0148  -3.0936   0.8338   3.3729  11.9135
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)              30.4309     6.7929   4.480 7.27e-05 ***
## age                      -0.1368     0.1305  -1.048   0.3017
## GenotypeAPOE4           -10.2594     9.3962  -1.092   0.2821
## sexMale                 -18.9074     9.5495  -1.980   0.0554 .
## age:GenotypeAPOE4         0.1689     0.1952   0.865   0.3926
## age:sexMale               0.3817     0.1779   2.146   0.0387 *
## GenotypeAPOE4:sexMale    26.6684    14.2589   1.870   0.0696 .
## age:GenotypeAPOE4:sexMale -0.4869    0.2778  -1.753   0.0882 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```
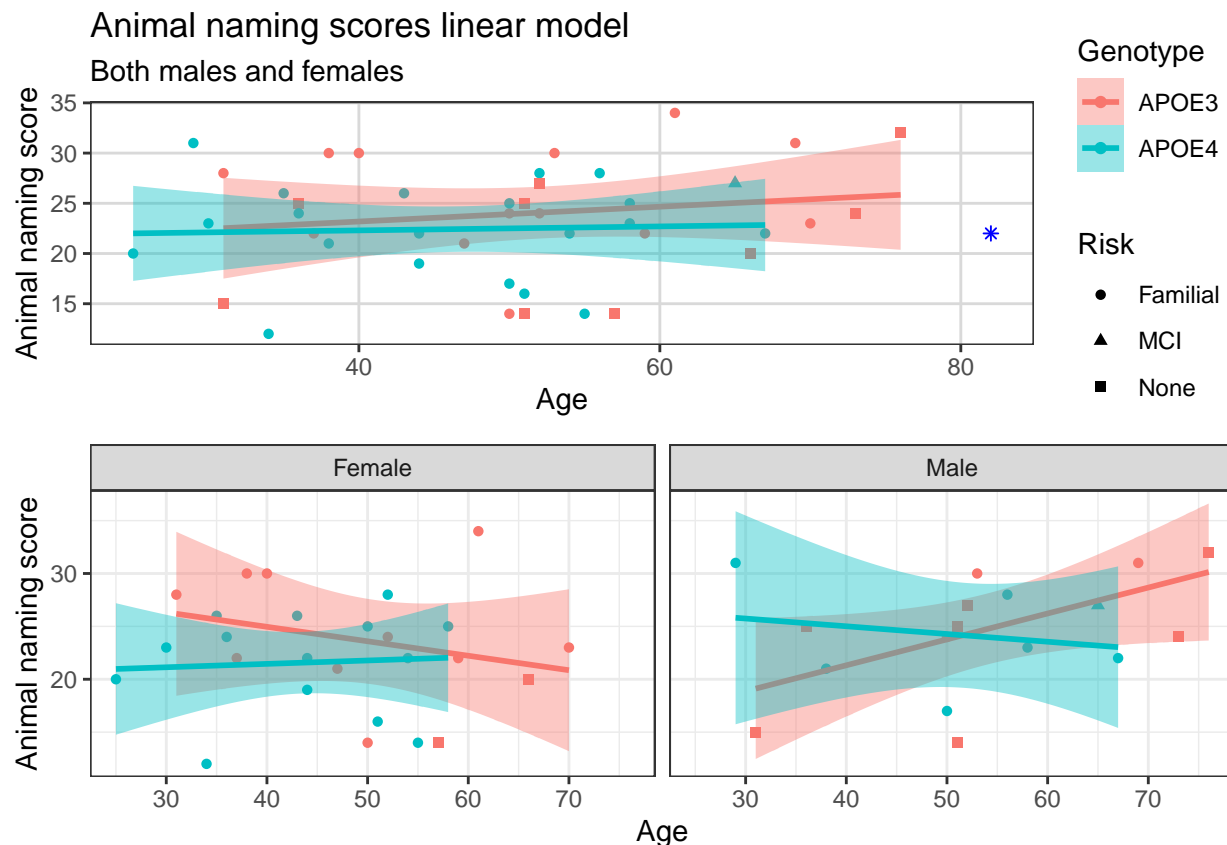
```
## Residual standard error: 5.364 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.1799, Adjusted R-squared:  0.0204
## F-statistic: 1.128 on 7 and 36 DF,  p-value: 0.3676


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


##
## Call:
## lm(formula = animals ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min      1Q  Median      3Q     Max
## -10.0148  -3.3462  0.9852  3.5483  5.4954
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        11.5235     6.2428   1.846   0.0862 .
## age                 0.2449     0.1124   2.179   0.0469 *
## GenotypeAPOE4      16.4090     9.9756   1.645   0.1222
## age:GenotypeAPOE4  -0.3180     0.1839  -1.729   0.1058
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.99 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.2655, Adjusted R-squared:  0.1081
## F-statistic: 1.687 on 3 and 14 DF,  p-value: 0.2154
```

Animal naming scores linear model
Both males and females
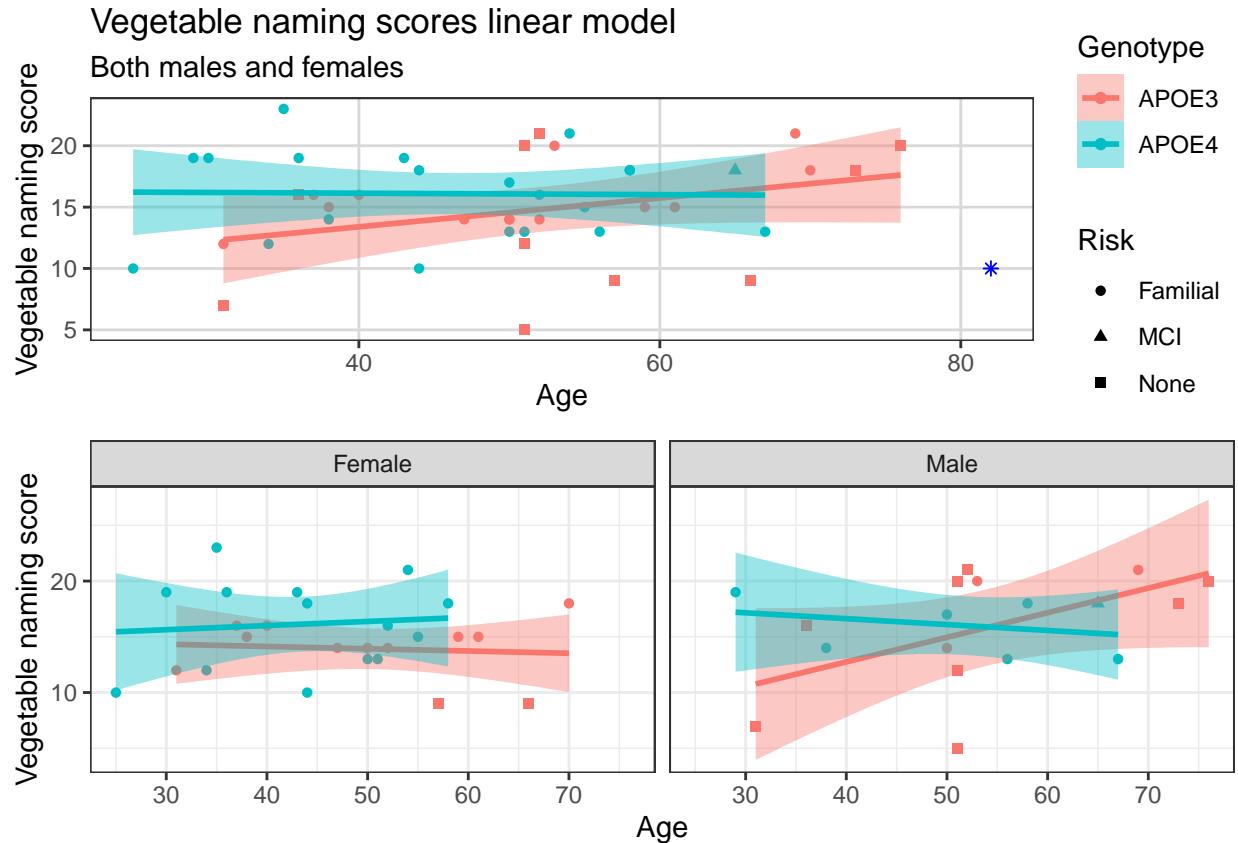
```
## 
## Call:
## lm(formula = vegetables ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -10.1764  -2.7438   0.4681   2.4165   7.1777 
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)   
## (Intercept)             14.94680    4.98763   2.997  0.00492 **
## age                     -0.02033    0.09585  -0.212  0.83321   
## GenotypeAPOE4           -0.42280    6.89905  -0.061  0.95147   
## sexMale                -11.02194    7.01158  -1.572  0.12471   
## age:GenotypeAPOE4        0.05742    0.14330   0.401  0.69098   
## age:sexMale              0.24095    0.13061   1.845  0.07330 . 
## GenotypeAPOE4:sexMale   15.23456   10.46939   1.455  0.15429   
## age:GenotypeAPOE4:sexMale -0.33082    0.20398  -1.622  0.11358   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 3.939 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.2008, Adjusted R-squared:  0.04538 
## F-statistic: 1.292 on 7 and 36 DF,  p-value: 0.2821
```

```
## 
## 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
## -10.1764 -2.5987  0.1051  2.6012  5.6030
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)         3.9249     5.4377   0.722   0.4823
## age                 0.2206     0.0979   2.254   0.0408 *
## GenotypeAPOE4      14.8118     8.6891   1.705   0.1103
## age:GenotypeAPOE4  -0.2734     0.1602  -1.707   0.1100
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 4.346 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.2731, Adjusted R-squared:  0.1173
## F-statistic: 1.753 on 3 and 14 DF,  p-value: 0.2022
```
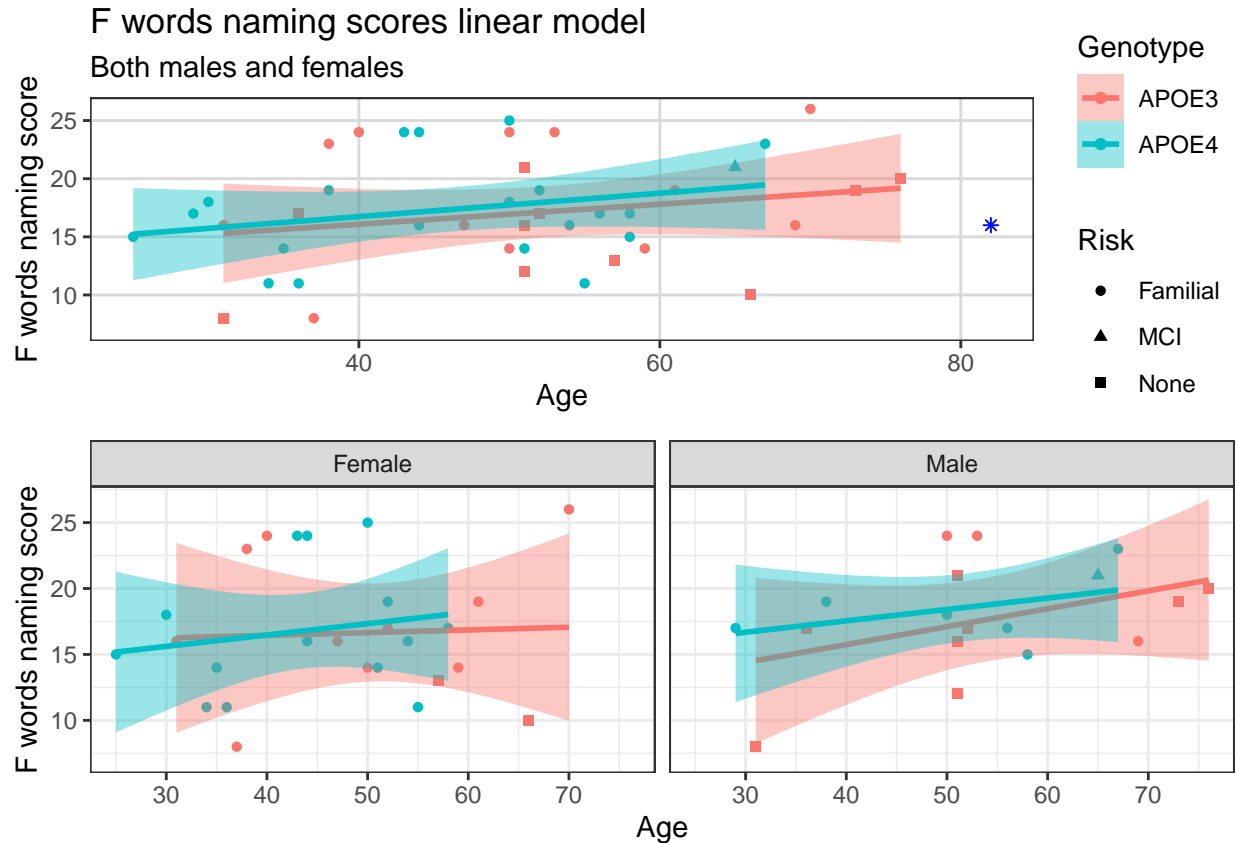
Vegetable naming scores linear model

Both males and females

```
##
## Call:
## lm(formula = f ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -8.3861 -2.9834 -0.5011  2.1887  8.9364
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              15.62653    6.15776   2.538   0.0156 *
## age                       0.02053    0.11833   0.173   0.8632
## GenotypeAPOE4            -2.60521    8.51761  -0.306   0.7615
## sexMale                 -5.31066    8.65653  -0.613   0.5434
## age:GenotypeAPOE4         0.06573    0.17691   0.372   0.7124
## age:sexMale               0.11526    0.16125   0.715   0.4793
## GenotypeAPOE4:sexMale     6.37750   12.92557   0.493   0.6247
## age:GenotypeAPOE4:sexMale -0.11506    0.25184  -0.457   0.6505
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.863 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.08292,    Adjusted R-squared:  -0.0954
## F-statistic: 0.465 on 7 and 36 DF,  p-value: 0.8532
```

```
##
## 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
## -6.526 -1.758 -0.394  1.753  6.894
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       10.31587    5.06176   2.038   0.0609 .
## age                0.13579    0.09113   1.490   0.1584
## GenotypeAPOE4      3.77229    8.08839   0.466   0.6481
## age:GenotypeAPOE4 -0.04934    0.14911  -0.331   0.7456
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.046 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.1758, Adjusted R-squared:  -0.0008475
## F-statistic: 0.9952 on 3 and 14 DF,  p-value: 0.4237
```

F words naming scores linear model
Both males and females


```
## 
## Call:
## lm(formula = l ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -6.6489 -2.0507 -0.3743  2.0933  6.1656 
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)    
## (Intercept)              11.77961    4.26614   2.761  0.00901 ** 
## age                       0.05863    0.08198   0.715  0.47916    
## GenotypeAPOE4             9.17536    5.90106   1.555  0.12873    
## sexMale                  -2.29912    5.99731  -0.383  0.70371    
## age:GenotypeAPOE4        -0.21635    0.12257  -1.765  0.08602 .  
## age:sexMale               0.02352    0.11171   0.211  0.83441    
## GenotypeAPOE4:sexMale    -8.10976    8.95493  -0.906  0.37116    
## age:GenotypeAPOE4:sexMale 0.22284    0.17448   1.277  0.20970    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 3.369 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.1495, Adjusted R-squared:  -0.01585 
## F-statistic: 0.9042 on 7 and 36 DF,  p-value: 0.5141
```

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


##
## Call:
## lm(formula = l ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.6874 -1.5603 -0.5901  1.3094  6.1656
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        9.480489   3.589600   2.641   0.0194 *
## age                0.082149   0.064624   1.271   0.2244
## GenotypeAPOE4      1.065596   5.735961   0.186   0.8553
## age:GenotypeAPOE4 0.006494   0.105746   0.061   0.9519
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.869 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.2013, Adjusted R-squared:  0.03016
## F-statistic: 1.176 on 3 and 14 DF,  p-value: 0.3541
```
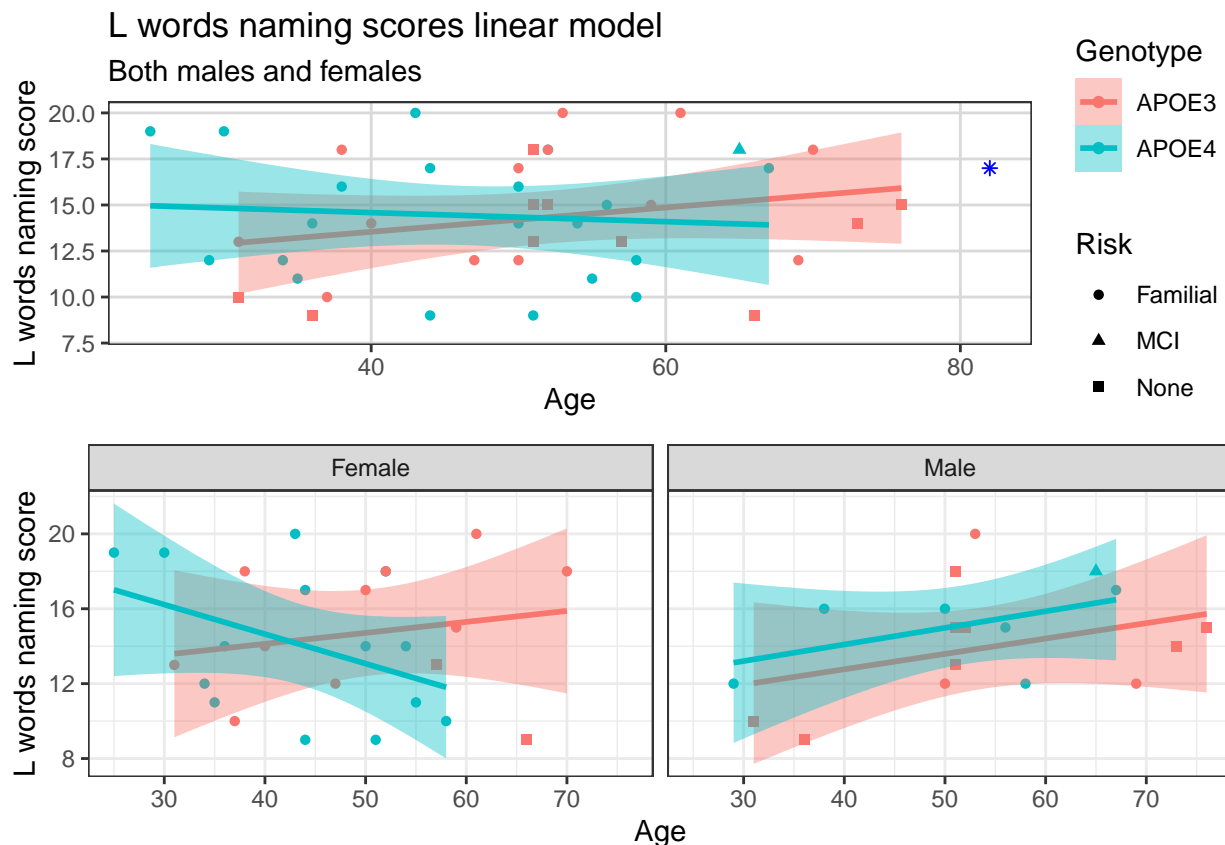
L words naming scores linear model
Both males and females


```
##
## Call:
## lm(formula = trailA ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -35.091 -13.196  -4.141   5.347 126.263
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             44.26007   38.00085   1.165    0.252
## age                     -0.01007    0.73027  -0.014    0.989
## GenotypeAPOE4           79.89275   52.56396   1.520    0.137
## sexMale                -27.39757   53.42130  -0.513    0.611
## age:GenotypeAPOE4       -1.90833    1.09177  -1.748    0.089 .
## age:sexMale              0.22257    0.99509   0.224    0.824
## GenotypeAPOE4:sexMale  -83.63851   79.76647  -1.049    0.301
## age:GenotypeAPOE4:sexMale 2.06548   1.55416   1.329    0.192
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 30.01 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.1771, Adjusted R-squared:  0.0171
## F-statistic: 1.107 on 7 and 36 DF,  p-value: 0.38
```

```
## 
## Call:
## lm(formula = trailA ~ age * Genotype, data = combo_f)
## 
## Residuals:
##     Min     1Q  Median     3Q     Max
## -35.091 -20.208  -8.131   8.920 126.263
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       44.26007   47.80039   0.926    0.365
## age               -0.01007    0.91859  -0.011    0.991
## GenotypeAPOE4     79.89275   66.11898   1.208    0.240
## age:GenotypeAPOE4 -1.90833    1.37332  -1.390    0.179
## 
## Residual standard error: 37.75 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:   0.14,  Adjusted R-squared:  0.02273
## F-statistic: 1.194 on 3 and 22 DF,  p-value: 0.3352


## 
## Call:
## lm(formula = trailA ~ age * Genotype, data = combo_m)
## 
## Residuals:
##      Min      1Q  Median      3Q     Max
## -11.0125  -6.4406  0.4063  3.3463 22.4750
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       16.8625    10.9486   1.540    0.146
## age                0.2125     0.1971   1.078    0.299
## GenotypeAPOE4     -3.7458    17.4952  -0.214    0.834
## age:GenotypeAPOE4  0.1571     0.3225   0.487    0.634
## 
## Residual standard error: 8.751 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.2281, Adjusted R-squared:  0.06275
## F-statistic: 1.379 on 3 and 14 DF,  p-value: 0.2899
```
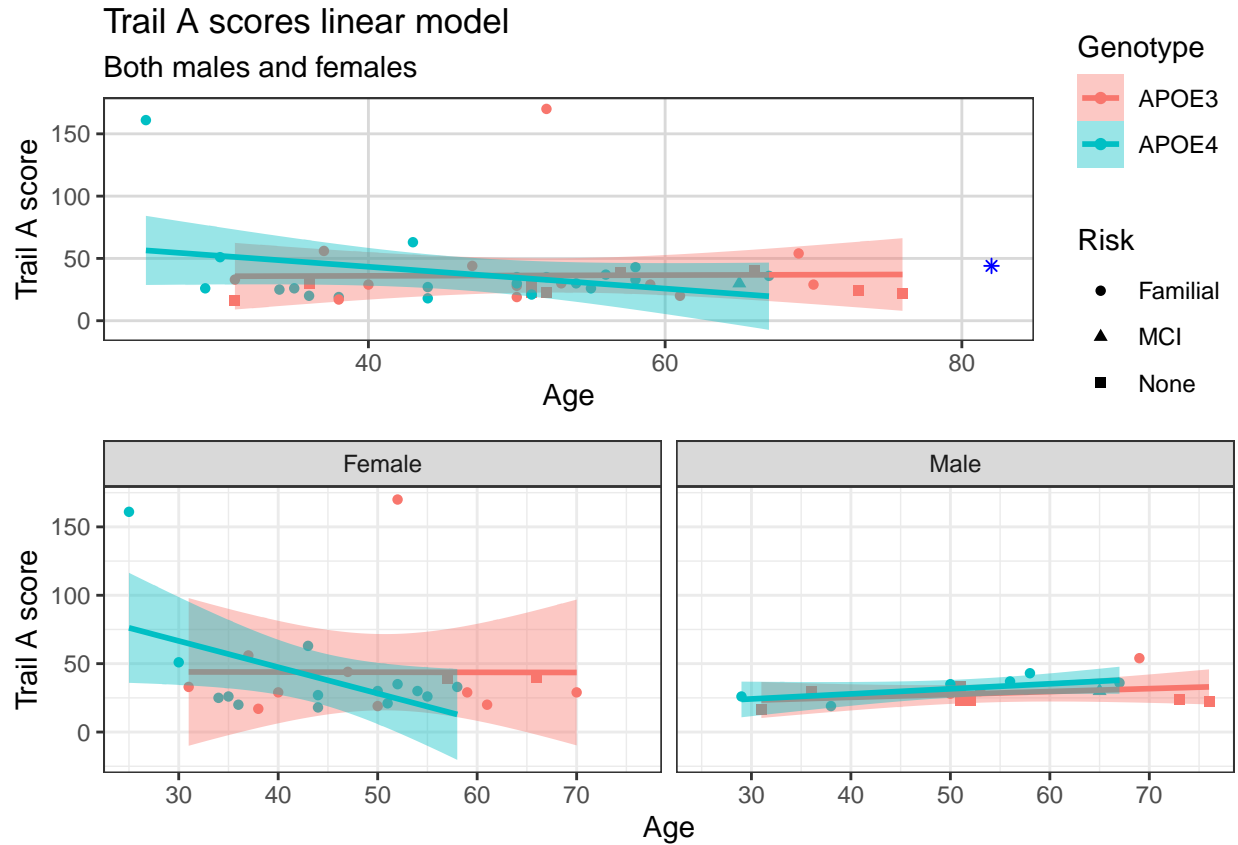
Trail A scores linear model
Both males and females

```
## 
## Call:
## lm(formula = trailB ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -114.88  -33.08  -10.92    7.85  321.36
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)               88.6378   111.2272   0.797   0.4307
## age                        0.3328     2.1375   0.156   0.8771
## GenotypeAPOE4            341.9891   153.8530   2.223   0.0326 *
## sexMale                  -57.0801   156.3624  -0.365   0.7172
## age:GenotypeAPOE4         -7.9724     3.1956  -2.495   0.0173 *
## age:sexMale                0.3263     2.9126   0.112   0.9114
## GenotypeAPOE4:sexMale   -387.6746   233.4738  -1.660   0.1055
## age:GenotypeAPOE4:sexMale   8.9658     4.5490   1.971   0.0565 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 87.84 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.2561, Adjusted R-squared:  0.1114
## F-statistic:  1.77 on 7 and 36 DF,  p-value: 0.1238
```

```
##
## Call:
## lm(formula = trailB ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -114.88  -46.08  -28.86   19.04  321.36
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        88.6378   140.5714   0.631   0.5348
## age                 0.3328     2.7014   0.123   0.9031
## GenotypeAPOE4     341.9891   194.4427   1.759   0.0925 .
## age:GenotypeAPOE4  -7.9724     4.0386  -1.974   0.0611 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 111 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2288, Adjusted R-squared:  0.1236
## F-statistic: 2.175 on 3 and 22 DF,  p-value: 0.1197


##
## Call:
## lm(formula = trailB ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -29.652 -12.429  -6.230   5.759  44.167
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        31.5577    27.2477   1.158    0.266
## age                 0.6591     0.4905   1.344    0.200
## GenotypeAPOE4     -45.6855    43.5402  -1.049    0.312
## age:GenotypeAPOE4   0.9935     0.8027   1.238    0.236
##
## Residual standard error: 21.78 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.3847, Adjusted R-squared:  0.2528
## F-statistic: 2.917 on 3 and 14 DF,  p-value: 0.07112
```
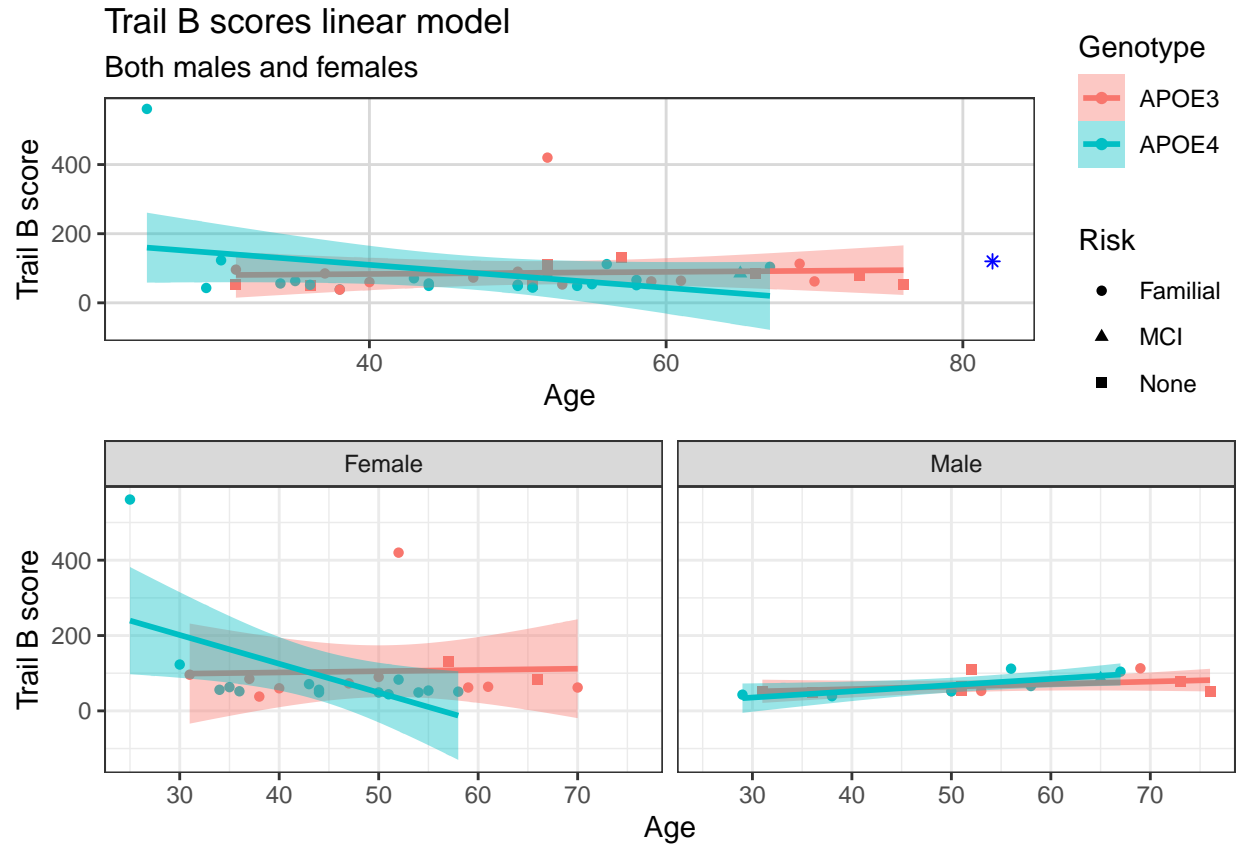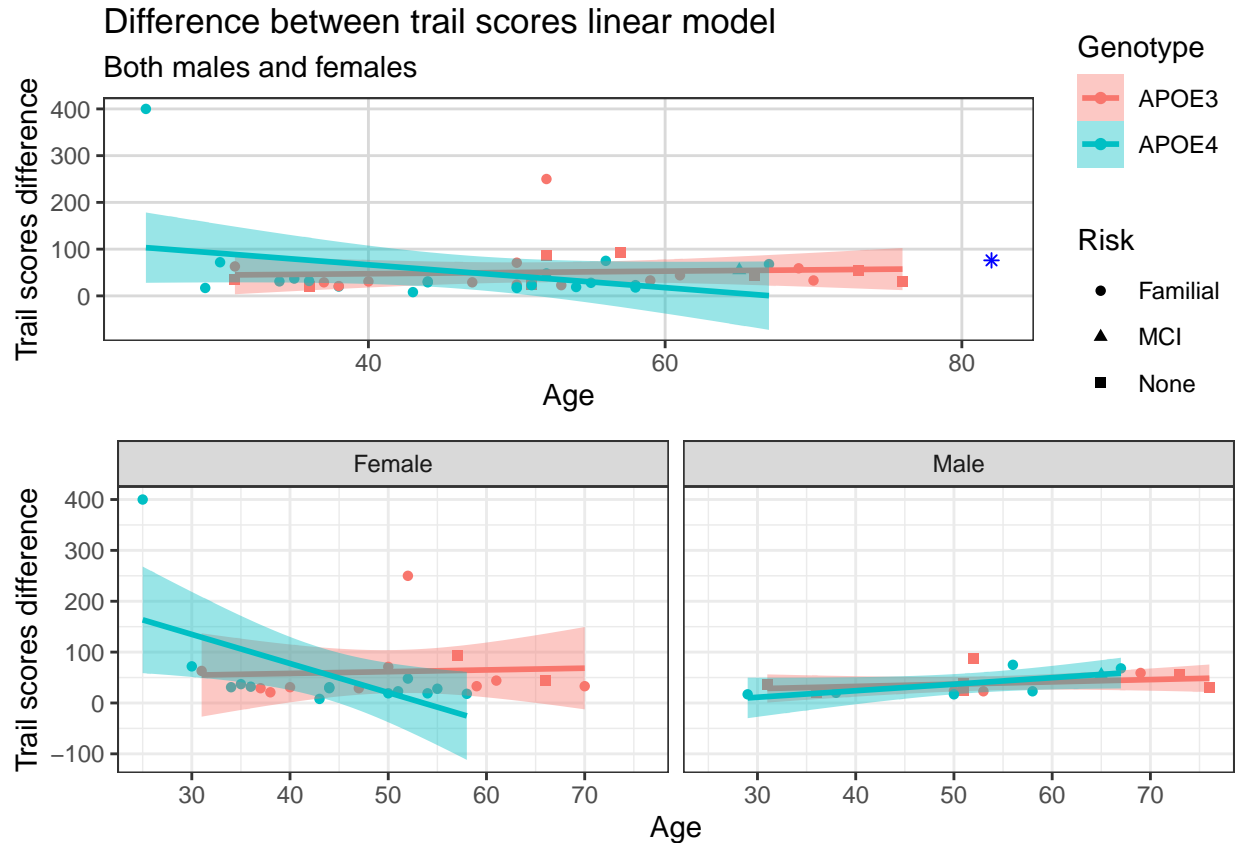
Trail B scores linear model

```
## 
## Call:
## lm(formula = trailDiff ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -80.954 -26.080  -9.124   9.335 236.555 
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)   
## (Intercept)               44.3777    77.3530   0.574  0.56974   
## age                        0.3429     1.4865   0.231  0.81889   
## GenotypeAPOE4            262.0964   106.9971   2.450  0.01930 * 
## sexMale                  -29.6826   108.7423  -0.273  0.78644   
## age:GenotypeAPOE4         -6.0640     2.2224  -2.729  0.00977 **
## age:sexMale                0.1038     2.0256   0.051  0.95943   
## GenotypeAPOE4:sexMale   -304.0361   162.3694  -1.872  0.06928 . 
## age:GenotypeAPOE4:sexMale   6.9004     3.1636   2.181  0.03578 * 
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 61.09 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.2781, Adjusted R-squared:  0.1377 
## F-statistic: 1.981 on 7 and 36 DF,  p-value: 0.08512
```

```
##
## Call:
## lm(formula = trailDiff ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min     1Q Median     3Q    Max
## -80.95 -34.44 -23.38  18.47 236.56
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        44.3777    96.7818   0.459   0.6511
## age                 0.3429     1.8599   0.184   0.8554
## GenotypeAPOE4     262.0964   133.8716   1.958   0.0631 .
## age:GenotypeAPOE4  -6.0640     2.7806  -2.181   0.0402 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 76.43 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2598, Adjusted R-squared:  0.1589
## F-statistic: 2.574 on 3 and 22 DF,  p-value: 0.07985


##
## Call:
## lm(formula = trailDiff ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min     1Q Median     3Q    Max
## -24.167 -12.888  -1.328  7.535  49.080
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        14.6952    25.5174   0.576    0.574
## age                 0.4466     0.4594   0.972    0.347
## GenotypeAPOE4     -41.9397    40.7752  -1.029    0.321
## age:GenotypeAPOE4   0.8363     0.7517   1.113    0.285
##
## Residual standard error: 20.39 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.2856, Adjusted R-squared:  0.1325
## F-statistic: 1.866 on 3 and 14 DF,  p-value: 0.1818
```
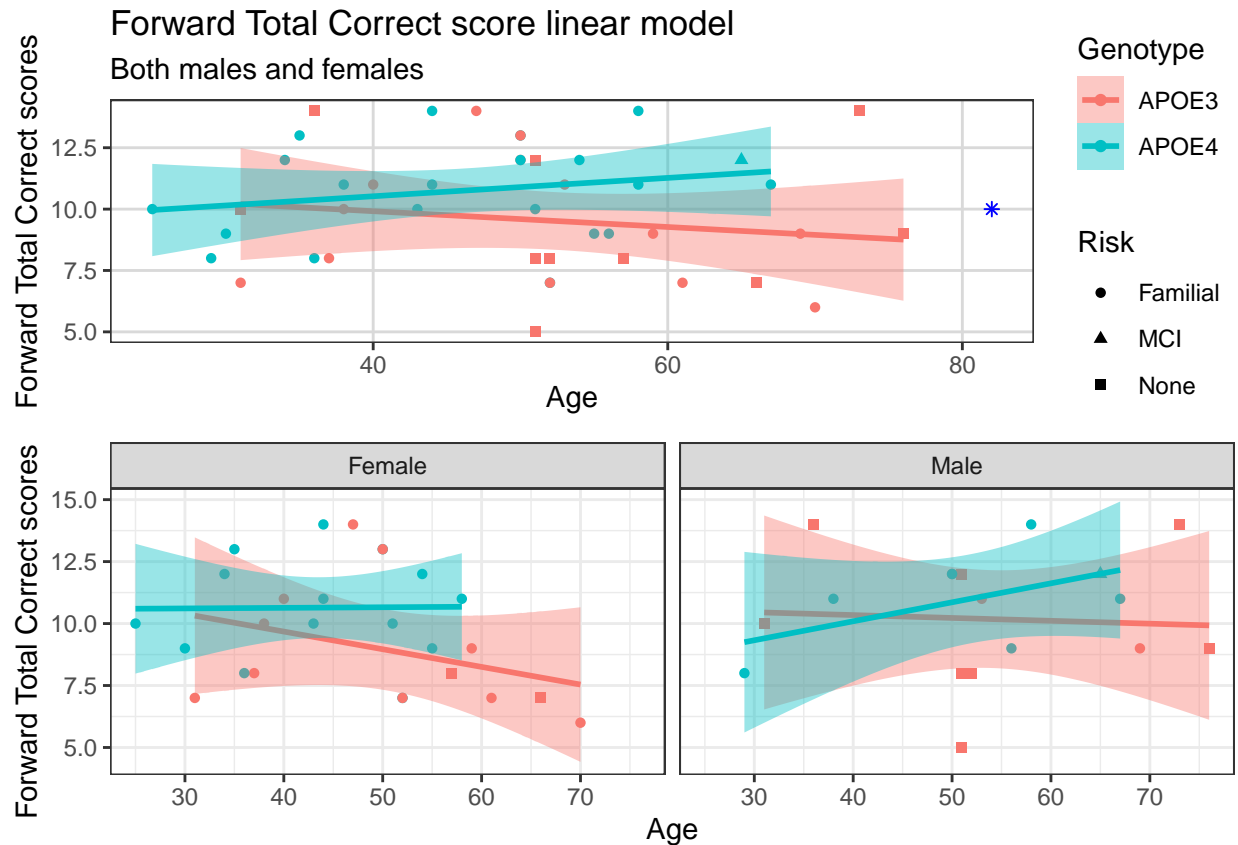
Difference between trail scores linear model

```
##
## Call:
## lm(formula = fwd_total_correct ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.2155 -1.5569 -0.4562  1.3445  4.8220
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              12.52714    3.05861   4.096 0.000228 ***
## age                      -0.07126    0.05878  -1.212 0.233275
## GenotypeAPOE4            -1.98689    4.23077  -0.470 0.641453
## sexMale                  -1.72119    4.29977  -0.400 0.691303
## age:GenotypeAPOE4         0.07361    0.08787   0.838 0.407741
## age:sexMale               0.05968    0.08009   0.745 0.461015
## GenotypeAPOE4:sexMale    -1.79158    6.42024  -0.279 0.781802
## age:GenotypeAPOE4:sexMale 0.01457    0.12509   0.116 0.907910
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.415 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.168,  Adjusted R-squared:  0.006208
## F-statistic: 1.038 on 7 and 36 DF,  p-value: 0.4222
```

```
##
## Call:
## lm(formula = fwd_total_correct ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.6625 -1.5928 -0.5322  1.3304  4.8220
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       12.52714    2.92709   4.280 0.000305 ***
## age               -0.07126    0.05625  -1.267 0.218466
## GenotypeAPOE4     -1.98689    4.04884  -0.491 0.628477
## age:GenotypeAPOE4  0.07361    0.08410   0.875 0.390860
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.312 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1915, Adjusted R-squared:  0.08121
## F-statistic: 1.737 on 3 and 22 DF,  p-value: 0.1888


##
## Call:
## lm(formula = fwd_total_correct ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.2155 -1.2268 -0.2269  1.6153  4.0392
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       10.80595    3.21569   3.360  0.00467 **
## age               -0.01158    0.05789  -0.200  0.84437
## GenotypeAPOE4     -3.77847    5.13848  -0.735  0.47428
## age:GenotypeAPOE4  0.08818    0.09473   0.931  0.36769
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.57 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.09778,    Adjusted R-squared:  -0.09556
## F-statistic: 0.5057 on 3 and 14 DF,  p-value: 0.6846
```

Forward Total Correct score linear model

```
##
## Call:
## lm(formula = bckwds_total_correct ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.8724 -2.1216 -0.4547  1.7746  5.3663
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             15.77092    3.49675   4.510 6.64e-05 ***
## age                     -0.13857    0.06720  -2.062   0.0465 *
## GenotypeAPOE4           -9.66670    4.83681  -1.999   0.0533 .
## sexMale                 -5.41156    4.91570  -1.101   0.2783
## age:GenotypeAPOE4        0.21474    0.10046   2.138   0.0394 *
## age:sexMale              0.11841    0.09157   1.293   0.2042
## GenotypeAPOE4:sexMale    8.71565    7.33993   1.187   0.2428
## age:GenotypeAPOE4:sexMale -0.22450   0.14301  -1.570   0.1252
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.761 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.1679, Adjusted R-squared:  0.006139
## F-statistic: 1.038 on 7 and 36 DF,  p-value: 0.4225
```

```
##
## Call:
## lm(formula = bckwds_total_correct ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.8724 -2.0510 -0.2881  1.6984  4.7419
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       15.77092    3.27687   4.813  8.3e-05 ***
## age               -0.13857    0.06297  -2.201   0.0386 *
## GenotypeAPOE4     -9.66670    4.53267  -2.133   0.0444 *
## age:GenotypeAPOE4  0.21474    0.09415   2.281   0.0326 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.588 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2273, Adjusted R-squared:  0.1219
## F-statistic: 2.157 on 3 and 22 DF,  p-value: 0.1219


##
## Call:
## lm(formula = bckwds_total_correct ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.3314 -2.2104 -0.5388  2.1686  5.3663
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)       10.359363   3.771179   2.747   0.0157 *
## age               -0.020157   0.067893  -0.297   0.7709
## GenotypeAPOE4     -0.951046   6.026113  -0.158   0.8769
## age:GenotypeAPOE4 -0.009756   0.111095  -0.088   0.9313
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.014 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.07575,    Adjusted R-squared:  -0.1223
## F-statistic: 0.3825 on 3 and 14 DF,  p-value: 0.7672
```
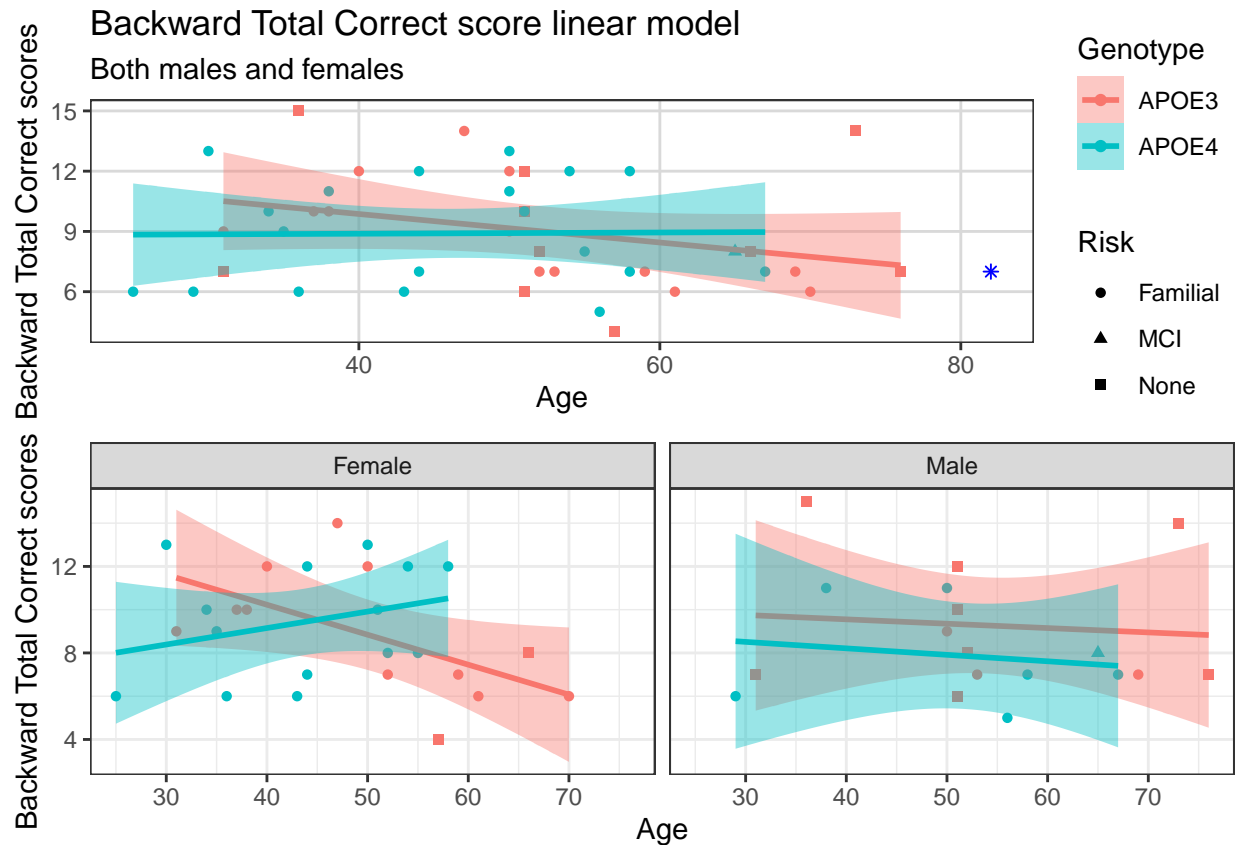
Backward Total Correct score linear model
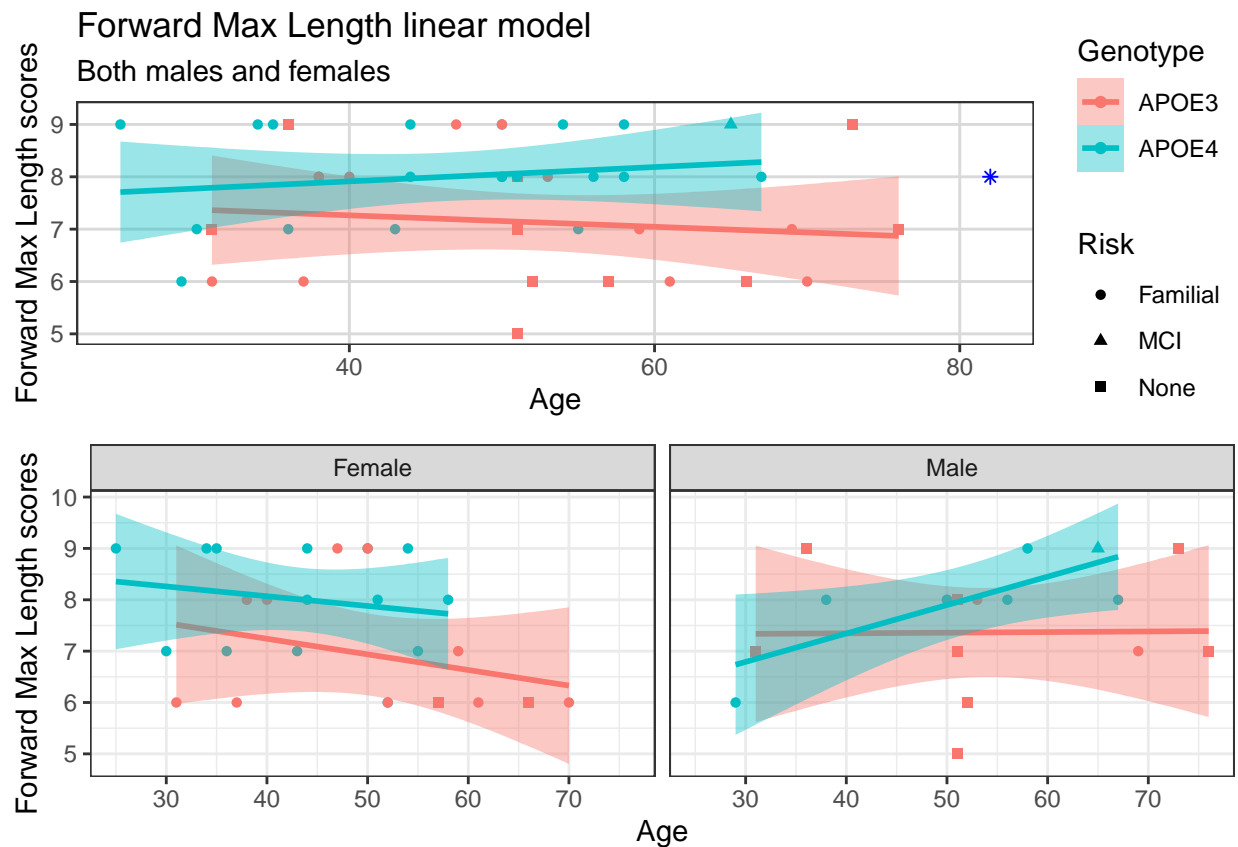
```
## 
## Call:
## lm(formula = fwd_max_length ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.36015 -0.74756  0.05477  0.71348  2.06307
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)              8.45687    1.42843   5.920 8.88e-07 ***
## age                     -0.03040    0.02745  -1.107    0.275
## GenotypeAPOE4            0.37308    1.97585   0.189    0.851
## sexMale                 -1.15788    2.00808  -0.577    0.568
## age:GenotypeAPOE4        0.01138    0.04104   0.277    0.783
## age:sexMale              0.03160    0.03741   0.845    0.404
## GenotypeAPOE4:sexMale   -2.54110    2.99838  -0.847    0.402
## age:GenotypeAPOE4:sexMale 0.04274   0.05842   0.732    0.469
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.128 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.2479, Adjusted R-squared:  0.1017
## F-statistic: 1.695 on 7 and 36 DF,  p-value: 0.1413
```

```
##
## Call:
## lm(formula = fwd_max_length ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.84107 -0.85311  0.07335  0.80224  2.06307
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        8.45687    1.45040   5.831 7.24e-06 ***
## age               -0.03040    0.02787  -1.091    0.287
## GenotypeAPOE4      0.37308    2.00624   0.186    0.854
## age:GenotypeAPOE4  0.01138    0.04167   0.273    0.787
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.145 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2503, Adjusted R-squared:  0.1481
## F-statistic: 2.449 on 3 and 22 DF,  p-value: 0.09057


##
## Call:
## lm(formula = fwd_max_length ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.36015 -0.38803 -0.06323  0.64075  1.65784
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       7.298985   1.376560   5.302 0.000112 ***
## age               0.001199   0.024782   0.048 0.962088
## GenotypeAPOE4     -2.168027   2.199658  -0.986 0.341048
## age:GenotypeAPOE4 0.054127   0.040552   1.335 0.203262
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.1 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.2393, Adjusted R-squared:  0.07631
## F-statistic: 1.468 on 3 and 14 DF,  p-value: 0.2659
```
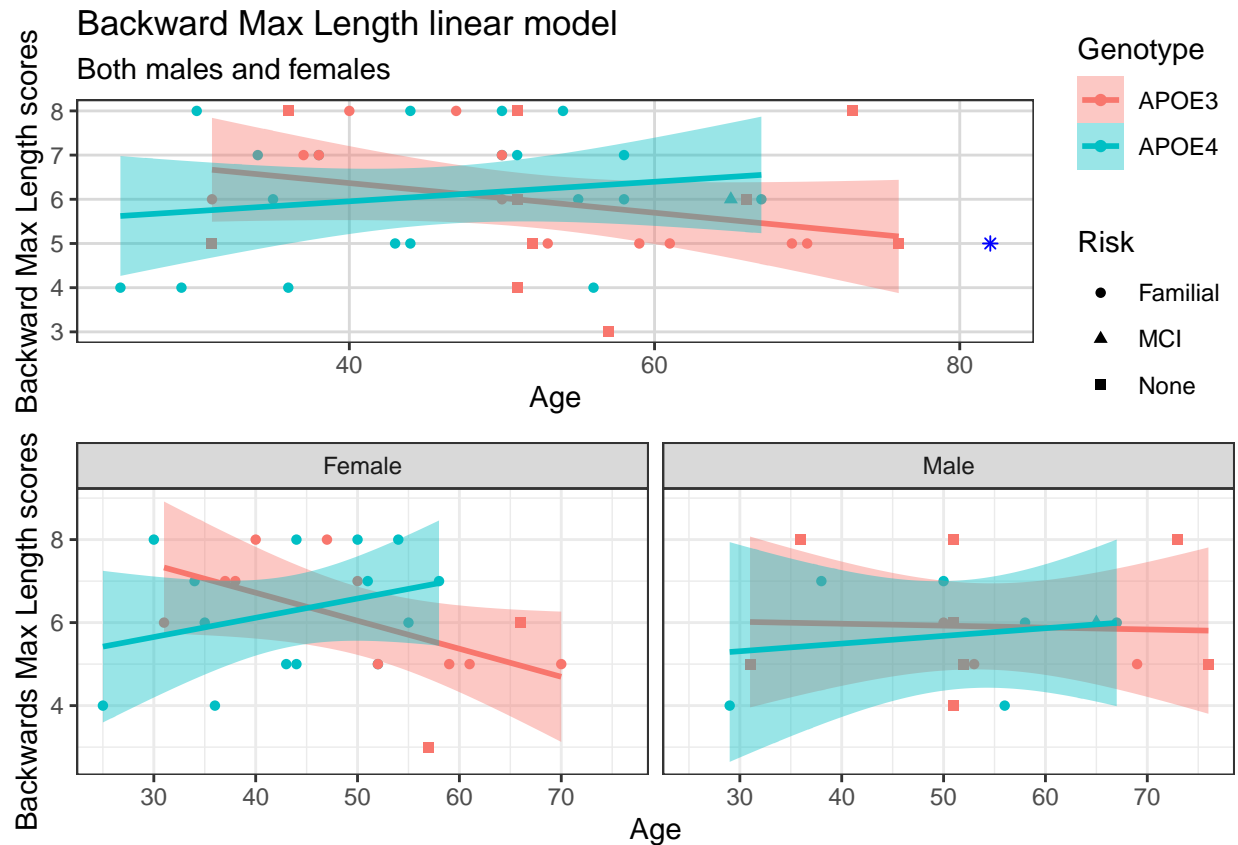
Forward Max Length linear model
Both males and females

```
## 
## Call:
## lm(formula = bckwds_max_length ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -2.57244 -0.94211  0.06055  1.17968  2.34721 
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)    
## (Intercept)              9.42045    1.79223   5.256 6.85e-06 ***
## age                     -0.06751    0.03444  -1.960   0.0578 .  
## GenotypeAPOE4           -5.15944    2.47907  -2.081   0.0446 *  
## sexMale                 -3.26270    2.51951  -1.295   0.2036    
## age:GenotypeAPOE4        0.11390    0.05149   2.212   0.0334 *  
## age:sexMale              0.06290    0.04693   1.340   0.1886    
## GenotypeAPOE4:sexMale    3.75753    3.76202   0.999   0.3246    
## age:GenotypeAPOE4:sexMale -0.09081   0.07330  -1.239   0.2234    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.415 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.1514, Adjusted R-squared:  -0.01362 
## F-statistic: 0.9174 on 7 and 36 DF,  p-value: 0.5045
```

```
##
## Call:
## lm(formula = bckwds_max_length ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min      1Q   Median      3Q      Max
## -2.57244 -1.16941  0.09631  1.13002  2.34721
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)       9.42045    1.75420   5.370 2.16e-05 ***
## age              -0.06751    0.03371  -2.003   0.0577 .
## GenotypeAPOE4    -5.15944    2.42646  -2.126   0.0449 *
## age:GenotypeAPOE4 0.11390    0.05040   2.260   0.0341 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.385 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2092, Adjusted R-squared:  0.1013
## F-statistic:  1.94 on 3 and 22 DF,  p-value: 0.1527


##
## Call:
## lm(formula = bckwds_max_length ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min      1Q   Median      3Q      Max
## -1.92251 -0.91674  0.02432  1.03307  2.17897
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       6.157749   1.828314   3.368   0.0046 **
## age              -0.004613   0.032915  -0.140   0.8906
## GenotypeAPOE4    -1.401913   2.921533  -0.480   0.6387
## age:GenotypeAPOE4 0.023095   0.053860   0.429   0.6746
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.461 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.01986,    Adjusted R-squared:  -0.1902
## F-statistic: 0.09454 on 3 and 14 DF,  p-value: 0.9618
```

Backward Max Length linear model

```
## 
## Call:
## lm(formula = RAVLT_FORGETTING ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.7899 -1.6609 -0.0937  1.1570  9.3600
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              2.183379   3.612233   0.604    0.549
## age                     -0.006909   0.069417  -0.100    0.921
## GenotypeAPOE4            1.803769   4.996553   0.361    0.720
## sexMale                 -2.781857   5.078049  -0.548    0.587
## age:GenotypeAPOE4       -0.000980   0.103780  -0.009    0.993
## age:sexMale              0.055110   0.094590   0.583    0.564
## GenotypeAPOE4:sexMale   -8.240067   7.582331  -1.087    0.284
## age:GenotypeAPOE4:sexMale 0.165571  0.147733   1.121    0.270
## 
## Residual standard error: 2.853 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.2473, Adjusted R-squared:  0.1009
## F-statistic: 1.689 on 7 and 36 DF,  p-value: 0.1428


## 
```
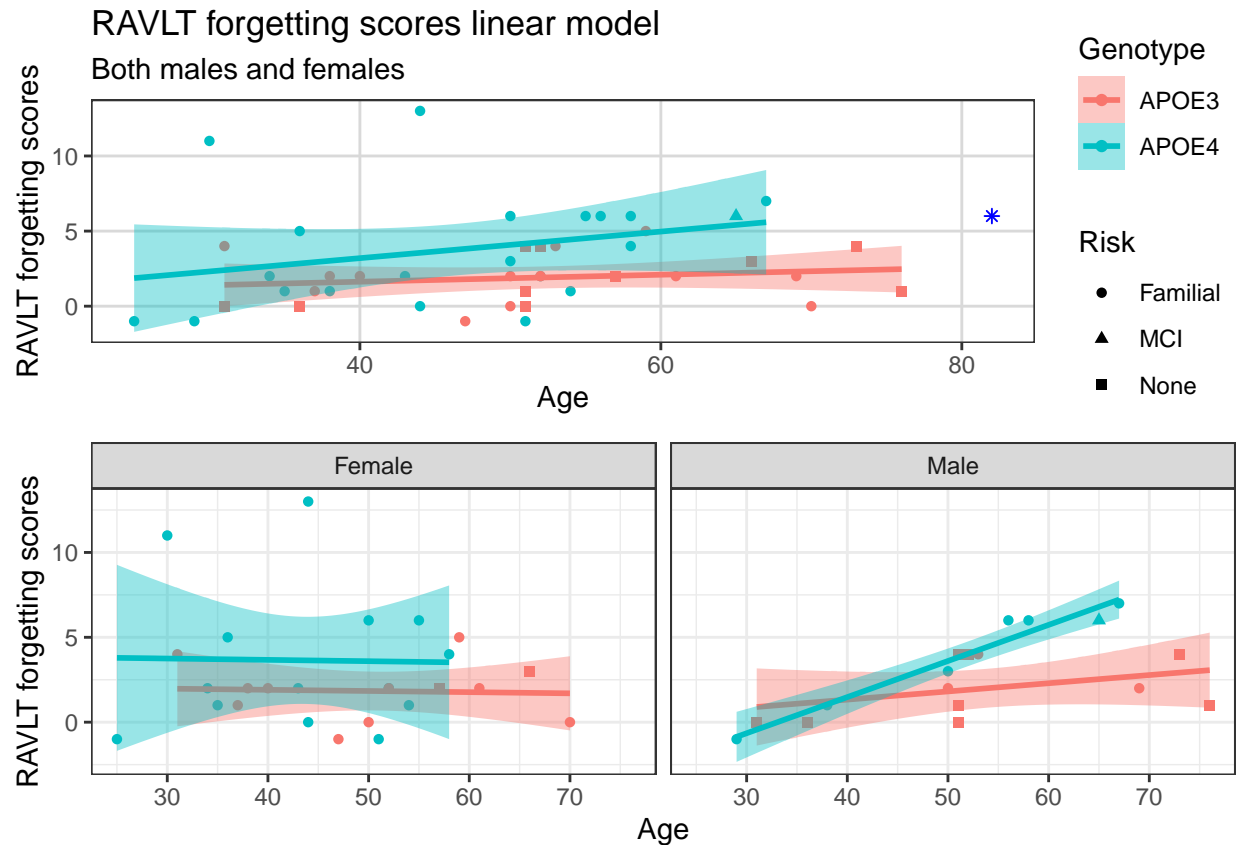
```
## Call:
## lm(formula = RAVLT_FORGETTING ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.7899 -1.8082  0.0861  1.2908  9.3600
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        2.183379   4.392554   0.497    0.624
## age               -0.006909   0.084412  -0.082    0.936
## GenotypeAPOE4      1.803769   6.075918   0.297    0.769
## age:GenotypeAPOE4 -0.000980   0.126199  -0.008    0.994
##
## Residual standard error: 3.469 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.07455,    Adjusted R-squared:  -0.05165
## F-statistic: 0.5907 on 3 and 22 DF,  p-value: 0.6276


##
## Call:
## lm(formula = RAVLT_FORGETTING ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.0648 -0.8440 -0.1792  0.9831  2.1402
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       -0.59848    1.77647  -0.337  0.74120
## age                0.04820    0.03198   1.507  0.15400
## GenotypeAPOE4     -6.43630    2.83868  -2.267  0.03973 *
## age:GenotypeAPOE4  0.16459    0.05233   3.145  0.00716 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.42 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.7263, Adjusted R-squared:  0.6676
## F-statistic: 12.38 on 3 and 14 DF,  p-value: 0.0003153
```

RAVLT forgetting scores linear model
Both males and females

```
##
## Call:
## lm(formula = RAVLT_LEARNING ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.5295 -1.7241 -0.0214  1.3725  4.3699
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)               7.93012    2.79513   2.837  0.00743 **
## age                      -0.01836    0.05371  -0.342  0.73452
## GenotypeAPOE4             2.73317    3.86632   0.707  0.48417
## sexMale                   2.97043    3.92938   0.756  0.45459
## age:GenotypeAPOE4        -0.06231    0.08030  -0.776  0.44289
## age:sexMale              -0.06411    0.07319  -0.876  0.38686
## GenotypeAPOE4:sexMale    -4.09846    5.86718  -0.699  0.48933
## age:GenotypeAPOE4:sexMale 0.07936    0.11432   0.694  0.49200
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.207 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.1637, Adjusted R-squared:  0.001057
## F-statistic: 1.006 on 7 and 36 DF,  p-value: 0.443
```

```
## 
## Call:
## lm(formula = RAVLT_LEARNING ~ age * Genotype, data = combo_f)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.8470 -1.2167 -0.0214  1.0385  4.3699
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        7.93012    2.41851   3.279  0.00343 **
## age               -0.01836    0.04648  -0.395  0.69666
## GenotypeAPOE4      2.73317    3.34536   0.817  0.42269
## age:GenotypeAPOE4 -0.06231    0.06948  -0.897  0.37958
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 1.91 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1068, Adjusted R-squared:  -0.01498
## F-statistic: 0.877 on 3 and 22 DF,  p-value: 0.4681


## 
## Call:
## lm(formula = RAVLT_LEARNING ~ age * Genotype, data = combo_m)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.5295 -1.8453  0.3431  1.8983  3.3055
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       10.90055    3.26184   3.342  0.00484 **
## age               -0.08247    0.05872  -1.404  0.18199
## GenotypeAPOE4     -1.36529    5.21222  -0.262  0.79718
## age:GenotypeAPOE4  0.01705    0.09609   0.177  0.86167
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 2.607 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.1653, Adjusted R-squared:  -0.01351
## F-statistic: 0.9244 on 3 and 14 DF,  p-value: 0.4546
```
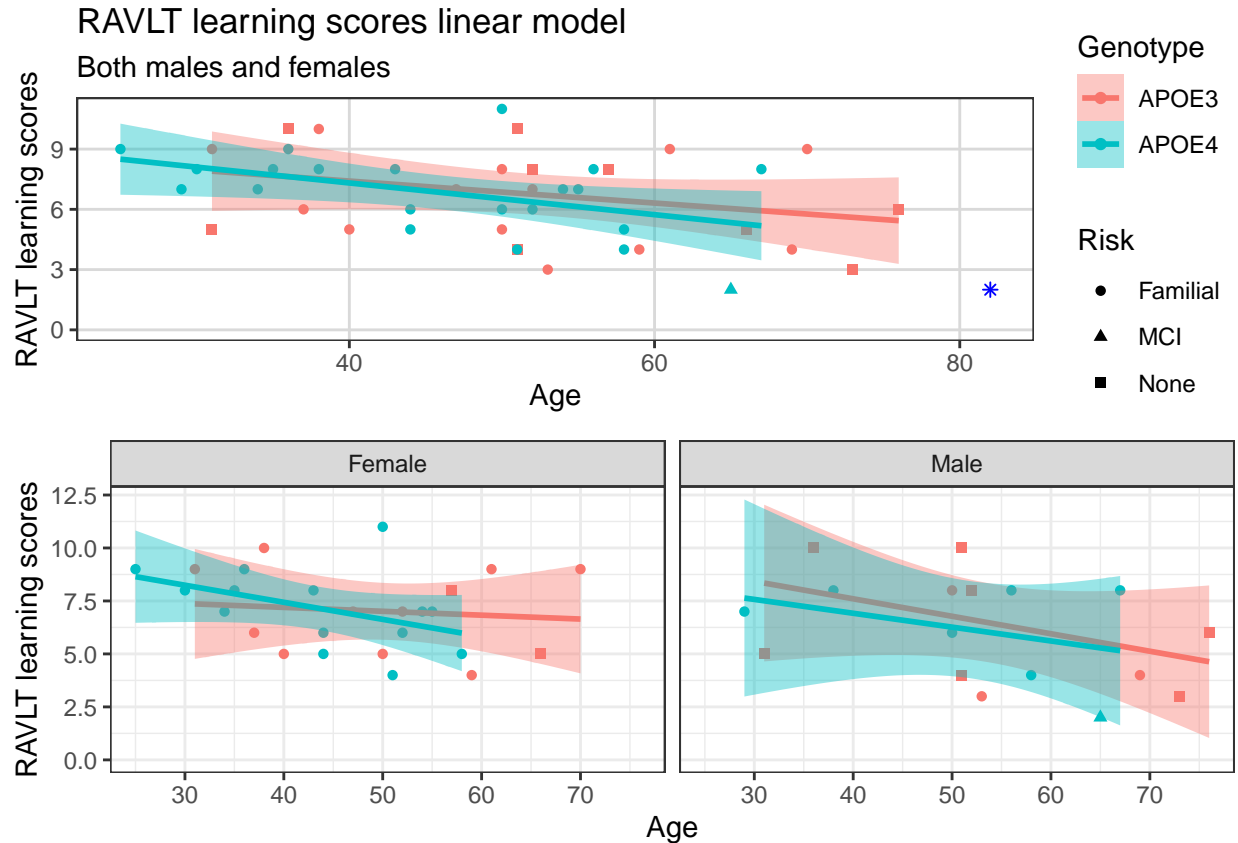
RAVLT learning scores linear model
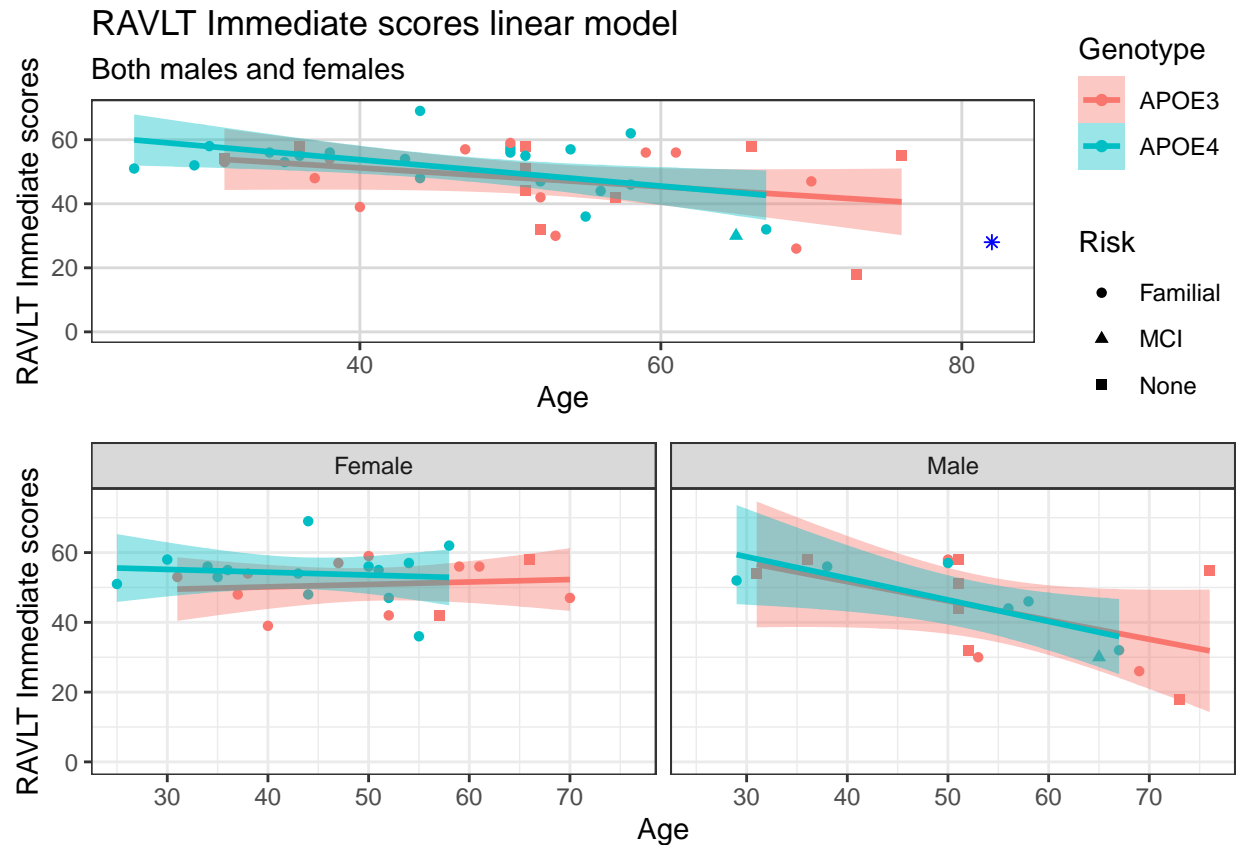
```
##
## Call:
## lm(formula = RAVLT_IMMEDIATE ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -17.152  -6.131   1.212   4.502  23.161
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              47.35620   11.80598   4.011 0.000292 ***
## age                       0.07027    0.22688   0.310 0.758547
## GenotypeAPOE4            10.24706   16.33040   0.627 0.534302
## sexMale                  26.32115   16.59676   1.586 0.121503
## age:GenotypeAPOE4        -0.15120    0.33919  -0.446 0.658437
## age:sexMale              -0.62078    0.30915  -2.008 0.052192 .
## GenotypeAPOE4:sexMale    -6.56218   24.78159  -0.265 0.792673
## age:GenotypeAPOE4:sexMale  0.08315    0.48284   0.172 0.864237
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.323 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.3698, Adjusted R-squared:  0.2472
## F-statistic: 3.017 on 7 and 36 DF,  p-value: 0.01336
```

```
##
## Call:
## lm(formula = RAVLT_IMMEDIATE ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -17.152  -5.101   1.336   4.261  14.957
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       47.35620    9.61572   4.925 6.32e-05 ***
## age                0.07027    0.18479   0.380    0.707
## GenotypeAPOE4     10.24706   13.30076   0.770    0.449
## age:GenotypeAPOE4 -0.15120    0.27626  -0.547    0.590
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.594 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.06044,    Adjusted R-squared:  -0.06768
## F-statistic: 0.4717 on 3 and 22 DF,  p-value: 0.7051


##
## Call:
## lm(formula = RAVLT_IMMEDIATE ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -15.4903  -7.3571  -0.1623   5.1774  23.1612
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       73.67735   14.42395   5.108 0.000159 ***
## age               -0.55051    0.25968  -2.120 0.052359 .
## GenotypeAPOE4      3.68488   23.04858   0.160 0.875264
## age:GenotypeAPOE4 -0.06805    0.42491  -0.160 0.875054
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.53 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.3616, Adjusted R-squared:  0.2248
## F-statistic: 2.643 on 3 and 14 DF,  p-value: 0.08995
```

RAVLT Immediate scores linear model


```
## 
## Call:
## lm(formula = AVLT_Trial7 ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -9.7644 -1.6887  0.7201  2.2410  6.2211
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              12.35689    4.87410   2.535   0.0157 *
## age                      -0.03336    0.09367  -0.356   0.7238
## GenotypeAPOE4            -2.01098    6.74201  -0.298   0.7672
## sexMale                   7.56945    6.85198   1.105   0.2766
## age:GenotypeAPOE4         0.01398    0.14003   0.100   0.9210
## age:sexMale              -0.16595    0.12763  -1.300   0.2018
## GenotypeAPOE4:sexMale     7.63547   10.23109   0.746   0.4603
## age:GenotypeAPOE4:sexMale -0.16413    0.19934  -0.823   0.4157
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 3.849 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.3372, Adjusted R-squared:  0.2083
## F-statistic: 2.616 on 7 and 36 DF,  p-value: 0.02724
```

```
##
## Call:
## lm(formula = AVLT_Trial7 ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -9.7644 -1.4222  0.7201  2.6033  5.5069
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       12.35689    5.27510   2.342   0.0286 *
## age               -0.03336    0.10137  -0.329   0.7452
## GenotypeAPOE4     -2.01098    7.29668  -0.276   0.7854
## age:GenotypeAPOE4  0.01398    0.15155   0.092   0.9274
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.166 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.02847,    Adjusted R-squared:  -0.104
## F-statistic: 0.2149 on 3 and 22 DF,  p-value: 0.885


##
## Call:
## lm(formula = AVLT_Trial7 ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.3630 -1.8827  0.5578  1.6062  6.2211
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       19.92634    4.11694   4.840 0.000262 ***
## age               -0.19931    0.07412  -2.689 0.017630 *
## GenotypeAPOE4      5.62449    6.57862   0.855 0.406964
## age:GenotypeAPOE4 -0.15016    0.12128  -1.238 0.236043
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.29 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.6078, Adjusted R-squared:  0.5238
## F-statistic: 7.233 on 3 and 14 DF,  p-value: 0.003632
```
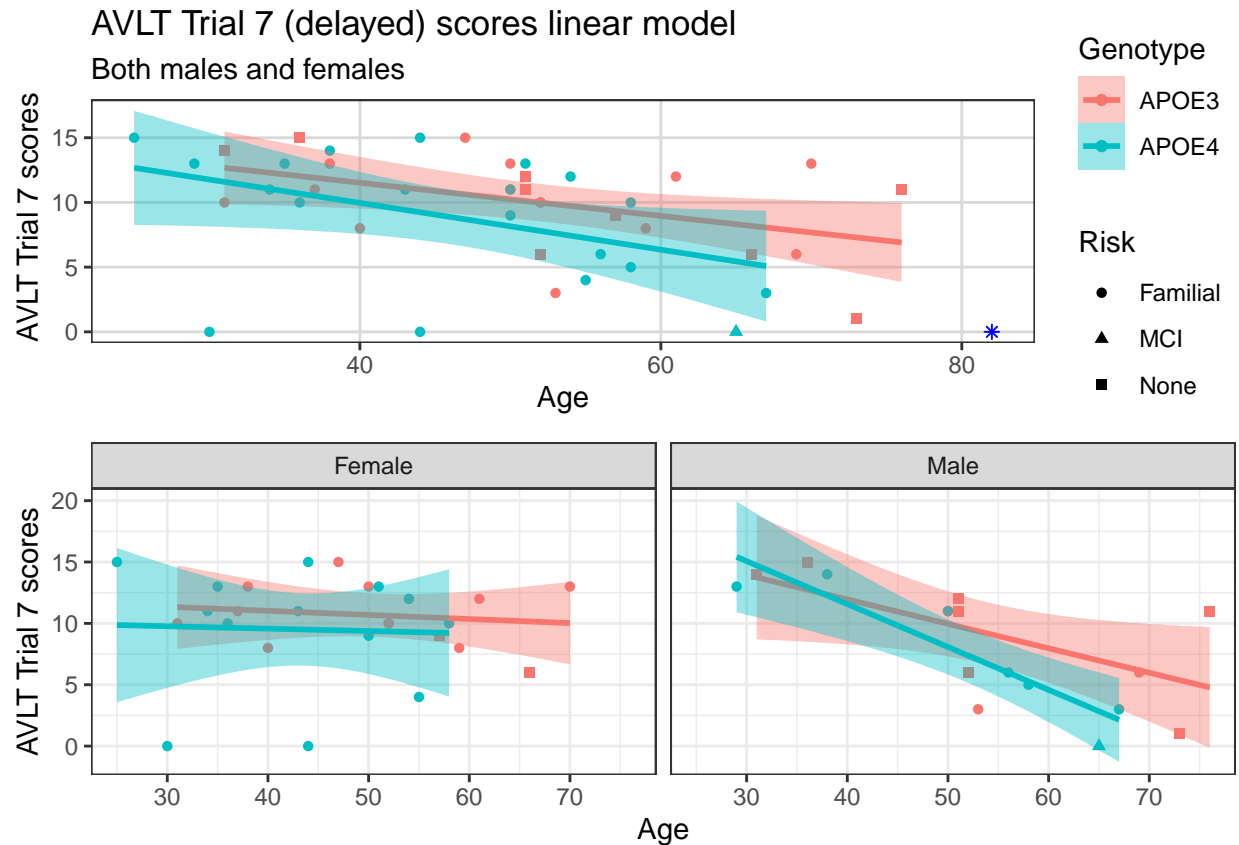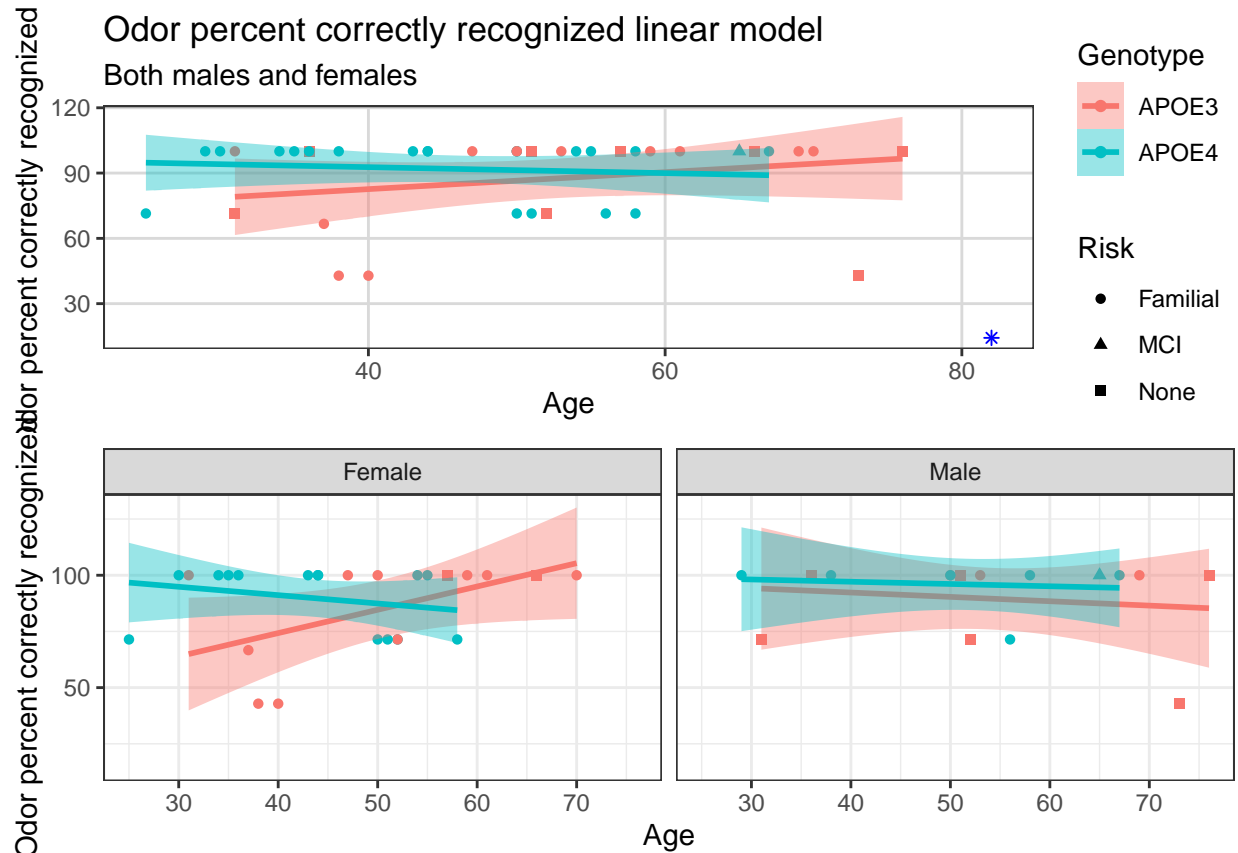
AVLT Trial 7 (delayed) scores linear model

Both males and females

```
##
## Call:
## lm(formula = Recognized ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -43.055 -13.589   5.507   9.861  35.073
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)              32.7867    21.9487   1.494   0.1439
## age                       1.0368     0.4218   2.458   0.0189 *
## GenotypeAPOE4            73.2303    30.3601   2.412   0.0211 *
## sexMale                 67.2673    30.8552   2.180   0.0359 *
## age:GenotypeAPOE4        -1.4085     0.6306  -2.234   0.0318 *
## age:sexMale              -1.2305     0.5748  -2.141   0.0391 *
## GenotypeAPOE4:sexMale   -72.1413    46.0718  -1.566   0.1261
## age:GenotypeAPOE4:sexMale  1.5014     0.8977   1.673   0.1031
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 17.33 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.1932, Adjusted R-squared:  0.0363
## F-statistic: 1.231 on 7 and 36 DF,  p-value: 0.3115
```

```
##
## Call:
## lm(formula = Recognized ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -31.401 -14.704   5.588  10.244  35.073
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)       32.7867    21.7511   1.507   0.1459
## age                1.0368     0.4180   2.480   0.0213 *
## GenotypeAPOE4     73.2303    30.0868   2.434   0.0235 *
## age:GenotypeAPOE4 -1.4085     0.6249  -2.254   0.0345 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 17.18 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.2474, Adjusted R-squared:  0.1448
## F-statistic: 2.411 on 3 and 22 DF,  p-value: 0.09415


##
## Call:
## lm(formula = Recognized ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -43.055   2.005   5.507   9.826  14.669
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      100.05403   21.98965   4.550 0.000454 ***
## age               -0.19373    0.39588  -0.489 0.632168
## GenotypeAPOE4      1.08896   35.13811   0.031 0.975714
## age:GenotypeAPOE4  0.09298    0.64779   0.144 0.887918
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 17.58 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.05591,    Adjusted R-squared:  -0.1464
## F-statistic: 0.2764 on 3 and 14 DF,  p-value: 0.8415
```
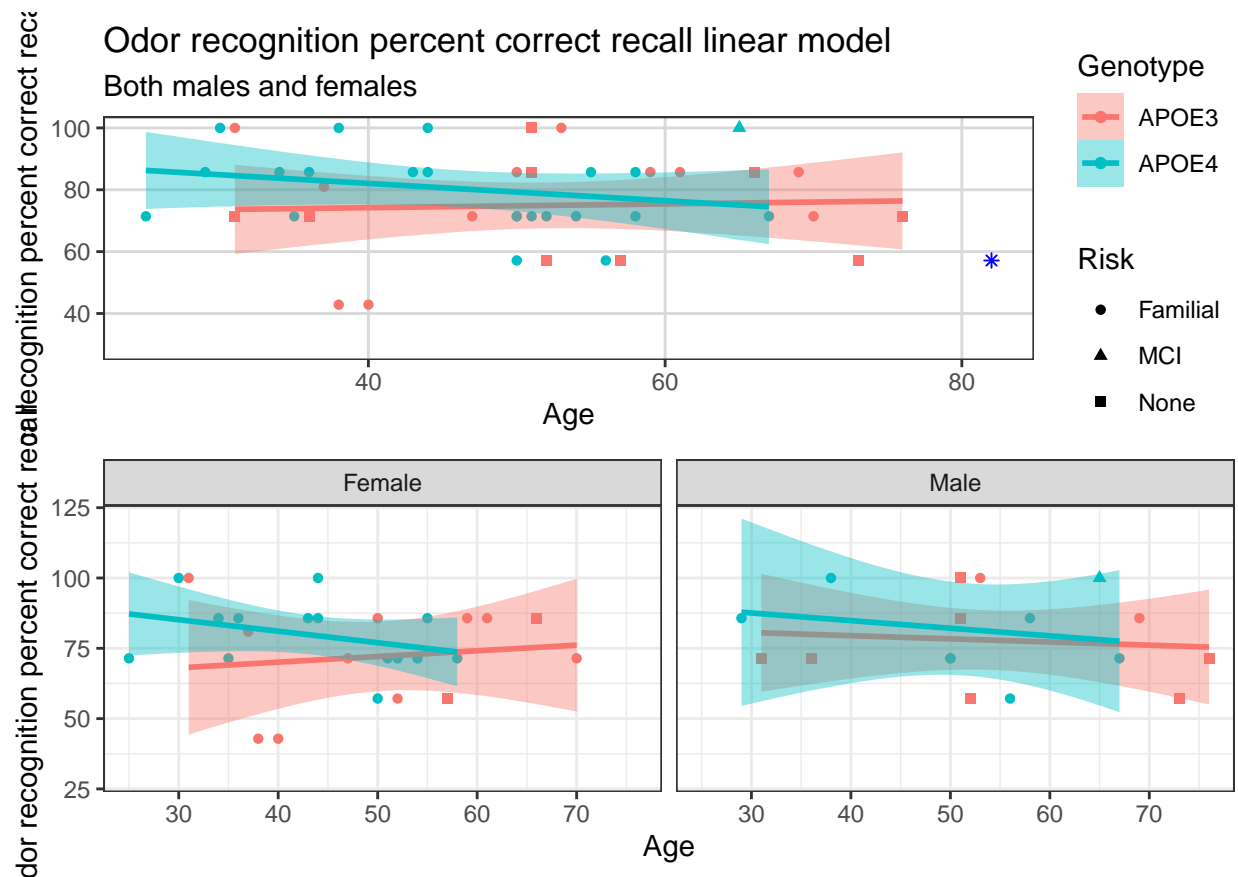
Odor percent correctly recognized linear model
Both males and females

```
## 
## Call:
## lm(formula = PrecentCorrectRecall ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -27.209  -9.483  -1.082  10.927  31.752 
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)    
## (Intercept)              61.9828    19.9966   3.100  0.00375 **
## age                       0.2021     0.3843   0.526  0.60218    
## GenotypeAPOE4            35.4588    27.6599   1.282  0.20805    
## sexMale                  22.0137    28.1111   0.783  0.43869    
## age:GenotypeAPOE4        -0.6111     0.5745  -1.064  0.29456    
## age:sexMale              -0.3148     0.5236  -0.601  0.55152    
## GenotypeAPOE4:sexMale   -23.7701    41.9743  -0.566  0.57470    
## age:GenotypeAPOE4:sexMale  0.4528     0.8178   0.554  0.58324    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 15.79 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.09351,    Adjusted R-squared:  -0.08276 
## F-statistic: 0.5305 on 7 and 36 DF,  p-value: 0.8055
```

```
##
## Call:
## lm(formula = PrecentCorrectRecall ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -27.209 -10.062   1.063  11.245  31.752
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)         61.9828    19.8082   3.129  0.00488 **
## age                  0.2021     0.3807   0.531  0.60080
## GenotypeAPOE4       35.4588    27.3993   1.294  0.20904
## age:GenotypeAPOE4   -0.6111     0.5691  -1.074  0.29455
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 15.64 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1075, Adjusted R-squared:  -0.01417
## F-statistic: 0.8836 on 3 and 22 DF,  p-value: 0.4649


##
## Call:
## lm(formula = PrecentCorrectRecall ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -23.367  -8.934  -3.058   8.986  21.976
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)         83.9964    20.0467   4.190 0.000908 ***
## age                 -0.1127     0.3609  -0.312 0.759482
## GenotypeAPOE4       11.6887    32.0334   0.365 0.720647
## age:GenotypeAPOE4   -0.1583     0.5906  -0.268 0.792560
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.02 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.04521,    Adjusted R-squared:  -0.1594
## F-statistic: 0.221 on 3 and 14 DF,  p-value: 0.8802
```

Odor recognition percent correct recall linear model
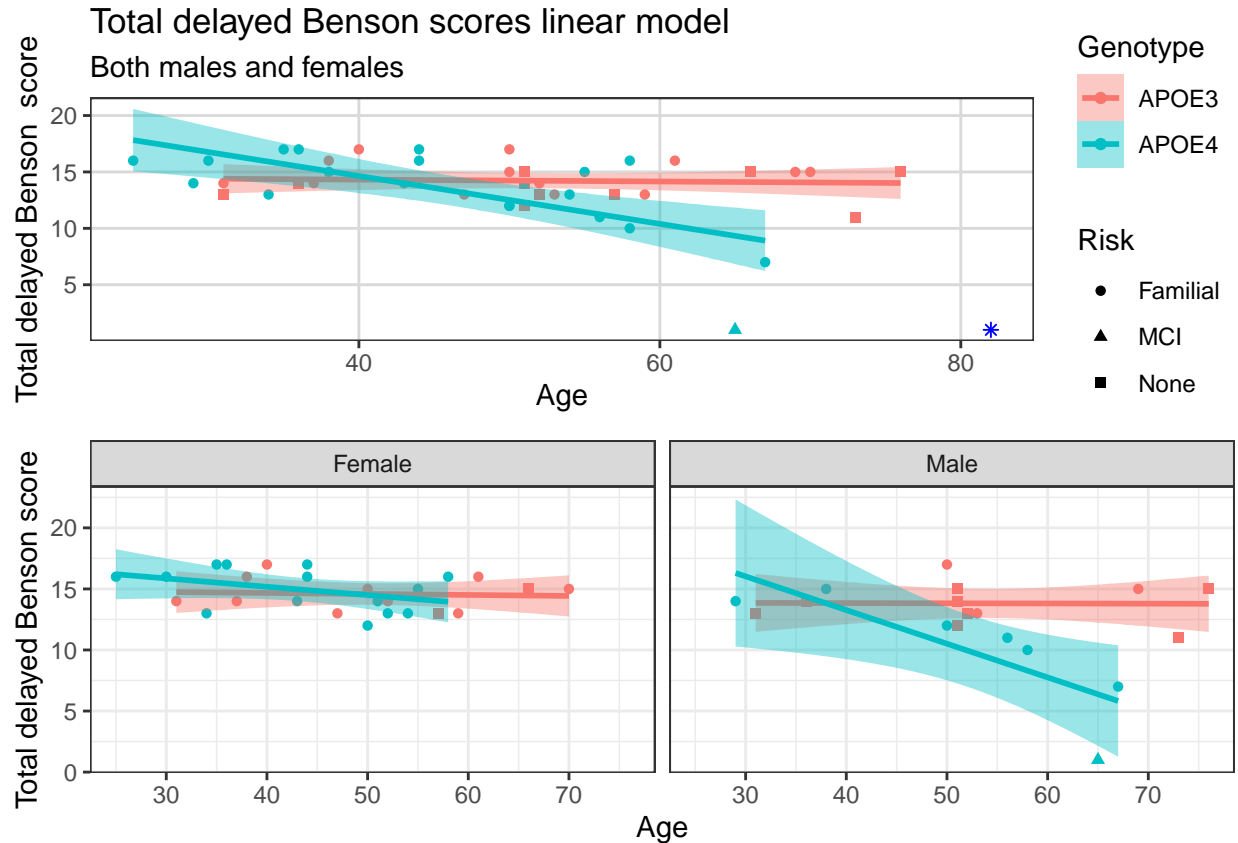Both males and females

```
##
## Call:
## lm(formula = Delay_BensonTotal ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -5.375 -1.035  0.165  1.242  3.175
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)            14.993387   2.365648   6.338 2.46e-07 ***
## age                    -0.008093   0.045461  -0.178   0.8597
## GenotypeAPOE4           2.915238   3.272237   0.891   0.3789
## sexMale                -1.088175   3.325609  -0.327   0.7454
## age:GenotypeAPOE4      -0.060190   0.067966  -0.886   0.3817
## age:sexMale             0.006479   0.061947   0.105   0.9173
## GenotypeAPOE4:sexMale   7.480620   4.965661   1.506   0.1407
## age:GenotypeAPOE4:sexMale -0.213974   0.096750  -2.212   0.0334 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.868 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.6387, Adjusted R-squared:  0.5684
## F-statistic: 9.091 on 7 and 36 DF,  p-value: 2.015e-06
```

```
##
## Call:
## lm(formula = Delay_BensonTotal ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.58701 -1.15913 -0.03085  1.25957  2.33034
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      14.993387   1.934817   7.749 9.97e-08 ***
## age              -0.008093   0.037182  -0.218    0.830
## GenotypeAPOE4     2.915238   2.676299   1.089    0.288
## age:GenotypeAPOE4 -0.060190   0.055588  -1.083    0.291
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.528 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1238, Adjusted R-squared:  0.004296
## F-statistic: 1.036 on 3 and 22 DF,  p-value: 0.3961


##
## Call:
## lm(formula = Delay_BensonTotal ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.3755 -0.8467  0.6766  1.2147  3.1755
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      13.905212   2.881968   4.825  0.00027 ***
## age              -0.001614   0.051884  -0.031  0.97562
## GenotypeAPOE4    10.395858   4.605208   2.257  0.04048 *
## age:GenotypeAPOE4 -0.274164   0.084900  -3.229  0.00606 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.303 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.6713, Adjusted R-squared:  0.6009
## F-statistic: 9.532 on 3 and 14 DF,  p-value: 0.001098
```
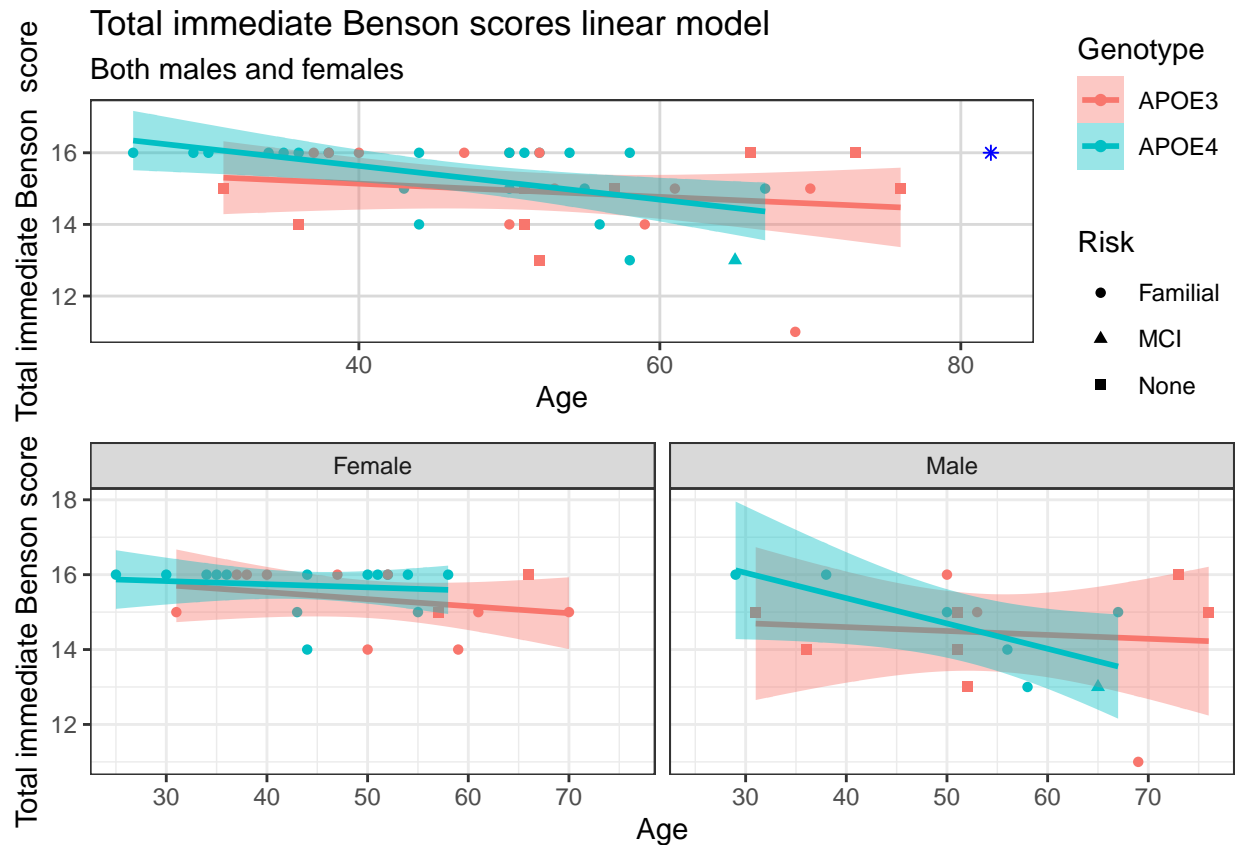
Total delayed Benson scores linear model

Both males and females

```
##
## Call:
## lm(formula = Im_BensonTotal ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.2972 -0.5185  0.2553  0.4729  1.7445
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)            16.283458   1.260877  12.914 4.44e-15 ***
## age                    -0.018752   0.024230  -0.774    0.444
## GenotypeAPOE4          -0.204361   1.744084  -0.117    0.907
## sexMale                -1.266945   1.772531  -0.715    0.479
## age:GenotypeAPOE4       0.010393   0.036225   0.287    0.776
## age:sexMale             0.008328   0.033017   0.252    0.802
## GenotypeAPOE4:sexMale   3.265183   2.646669   1.234    0.225
## age:GenotypeAPOE4:sexMale -0.067576   0.051567  -1.310    0.198
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9957 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.3443, Adjusted R-squared:  0.2168
## F-statistic:   2.7 on 7 and 36 DF,  p-value: 0.02343
```

```
##
## Call:
## lm(formula = Im_BensonTotal ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.7113 -0.1958  0.2177  0.3974  0.9542
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       16.28346    0.88865  18.324 8.23e-15 ***
## age               -0.01875    0.01708  -1.098    0.284
## GenotypeAPOE4     -0.20436    1.22921  -0.166    0.869
## age:GenotypeAPOE4  0.01039    0.02553   0.407    0.688
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7018 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.1306, Adjusted R-squared:  0.01201
## F-statistic: 1.101 on 3 and 22 DF,  p-value: 0.3697


##
## Call:
## lm(formula = Im_BensonTotal ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.2972 -0.6021  0.3048  0.5308  1.7445
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       15.01651    1.66719   9.007 3.36e-07 ***
## age               -0.01042    0.03001  -0.347    0.734
## GenotypeAPOE4      3.06082    2.66406   1.149    0.270
## age:GenotypeAPOE4 -0.05718    0.04911  -1.164    0.264
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.332 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.185,  Adjusted R-squared:  0.01036
## F-statistic: 1.059 on 3 and 14 DF,  p-value: 0.3976
```
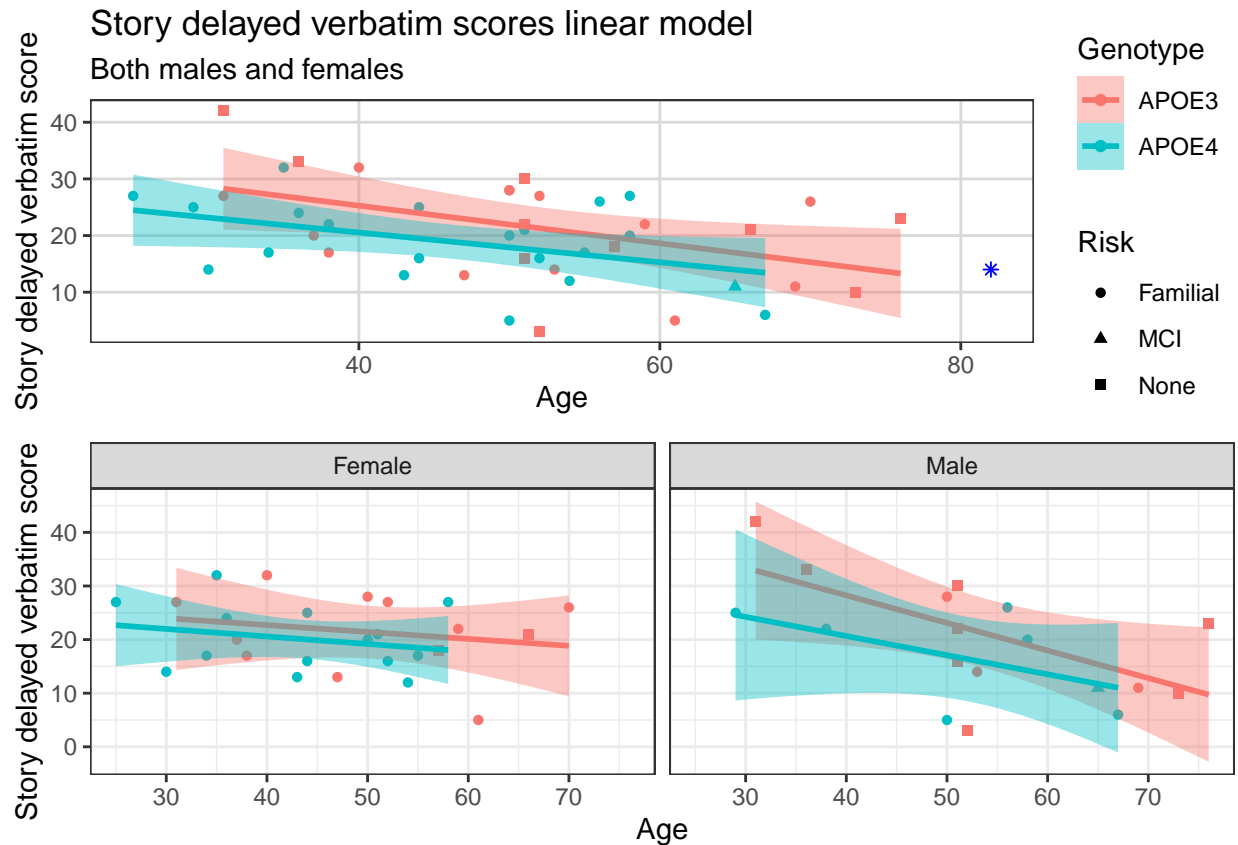
Total immediate Benson scores linear model

Both males and females

```
## 
## Call:
## lm(formula = Delayed_verbatim ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max
## -19.0730  -4.5725   0.5156   5.1753  13.2735
## 
## Coefficients:
##                        Estimate Std. Error t value Pr(>|t|)
## (Intercept)            27.86419    9.86733   2.824  0.00768 **
## age                    -0.12890    0.18962  -0.680  0.50100
## GenotypeAPOE4          -1.67533   13.64880  -0.123  0.90299
## sexMale                20.95956   13.87141   1.511  0.13952
## age:GenotypeAPOE4      -0.01127    0.28349  -0.040  0.96850
## age:sexMale            -0.38554    0.25839  -1.492  0.14439
## GenotypeAPOE4:sexMale -12.20034   20.71222  -0.589  0.55951
## age:GenotypeAPOE4:sexMale 0.16858  0.40355   0.418  0.67861
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 7.792 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.2799, Adjusted R-squared:  0.1399
## F-statistic: 1.999 on 7 and 36 DF,  p-value: 0.08233
```

```
##
## Call:
## lm(formula = Delayed_verbatim ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -15.001  -4.323   1.231   4.813  10.717
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       27.86419    8.70934   3.199  0.00414 **
## age               -0.12890    0.16737  -0.770  0.44940
## GenotypeAPOE4     -1.67533   12.04703  -0.139  0.89066
## age:GenotypeAPOE4 -0.01127    0.25022  -0.045  0.96448
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.878 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.05897,    Adjusted R-squared:  -0.06936
## F-statistic: 0.4595 on 3 and 22 DF,  p-value: 0.7134


##
## Call:
## lm(formula = Delayed_verbatim ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min      1Q   Median      3Q      Max
## -19.0730  -4.3474  -0.0894   5.5484  13.2735
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        48.8238    11.3160   4.315 0.000713 ***
## age                -0.5144     0.2037  -2.525 0.024257 *
## GenotypeAPOE4     -13.8757    18.0824  -0.767 0.455615
## age:GenotypeAPOE4   0.1573     0.3334   0.472 0.644270
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.044 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.4003, Adjusted R-squared:  0.2718
## F-statistic: 3.115 on 3 and 14 DF,  p-value: 0.06029
```

Story delayed verbatim scores linear model
Both males and females

```
##
## Call:
## lm(formula = Immediate_verbatim ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -14.2630  -3.9070   0.7528   5.3614  11.8136
##
## Coefficients:
##                           Estimate Std. Error t value Pr(>|t|)
## (Intercept)                31.0410     9.2343   3.361  0.00185 **
## age                        -0.1439     0.1775  -0.811  0.42275
## GenotypeAPOE4             -11.7033    12.7732  -0.916  0.36564
## sexMale                    12.6412    12.9816   0.974  0.33666
## age:GenotypeAPOE4           0.1967     0.2653   0.741  0.46321
## age:sexMale                -0.2532     0.2418  -1.047  0.30196
## GenotypeAPOE4:sexMale       3.3153    19.3835   0.171  0.86515
## age:GenotypeAPOE4:sexMale  -0.1386     0.3777  -0.367  0.71580
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.292 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.2534, Adjusted R-squared:  0.1083
## F-statistic: 1.746 on 7 and 36 DF,  p-value: 0.1293
```

```
##
## Call:
## lm(formula = Immediate_verbatim ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -14.2630  -5.3712   0.1534   5.5614  11.8136
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        31.0410     9.9001   3.135  0.00481 **
## age                -0.1439     0.1903  -0.756  0.45745
## GenotypeAPOE4     -11.7033    13.6941  -0.855  0.40197
## age:GenotypeAPOE4   0.1967     0.2844   0.692  0.49641
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.818 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.04778,    Adjusted R-squared:  -0.08207
## F-statistic: 0.368 on 3 and 22 DF,  p-value: 0.7768


##
## Call:
## lm(formula = Immediate_verbatim ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -14.031  -2.898   1.062   4.180   7.629
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       43.68220    7.98165   5.473 8.21e-05 ***
## age               -0.39714    0.14369  -2.764   0.0152 *
## GenotypeAPOE4     -8.38793   12.75419  -0.658   0.5214
## age:GenotypeAPOE4  0.05813    0.23513   0.247   0.8083
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.379 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.4842, Adjusted R-squared:  0.3736
## F-statistic:  4.38 on 3 and 14 DF,  p-value: 0.02259
```
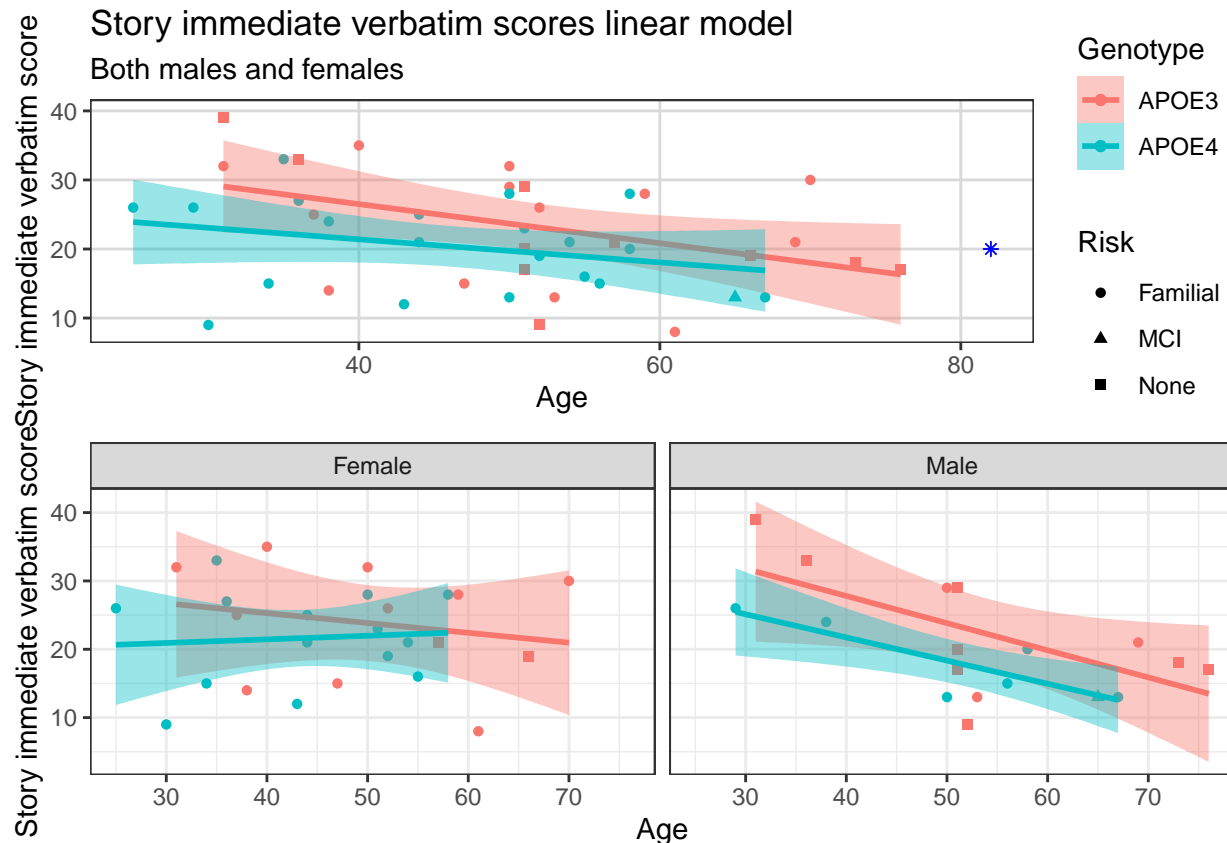
Story immediate verbatim scores linear model
Both males and females

```
##
## Call:
## lm(formula = MOCA_Attention_Digits ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.92827  0.00000  0.06538  0.07643  0.41788
##
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)              2.663443   0.353354   7.538 6.56e-09 ***
## age                     -0.016384   0.006790  -2.413   0.0211 *
## GenotypeAPOE4           -0.755392   0.488770  -1.545   0.1310
## sexMale                 -0.150112   0.496742  -0.302   0.7642
## age:GenotypeAPOE4        0.016854   0.010152   1.660   0.1056
## age:sexMale              0.005175   0.009253   0.559   0.5794
## GenotypeAPOE4:sexMale    0.242062   0.741715   0.326   0.7460
## age:GenotypeAPOE4:sexMale -0.005645  0.014451  -0.391   0.6984
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.279 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.2291, Adjusted R-squared:  0.07925
## F-statistic: 1.529 on 7 and 36 DF,  p-value: 0.189
```
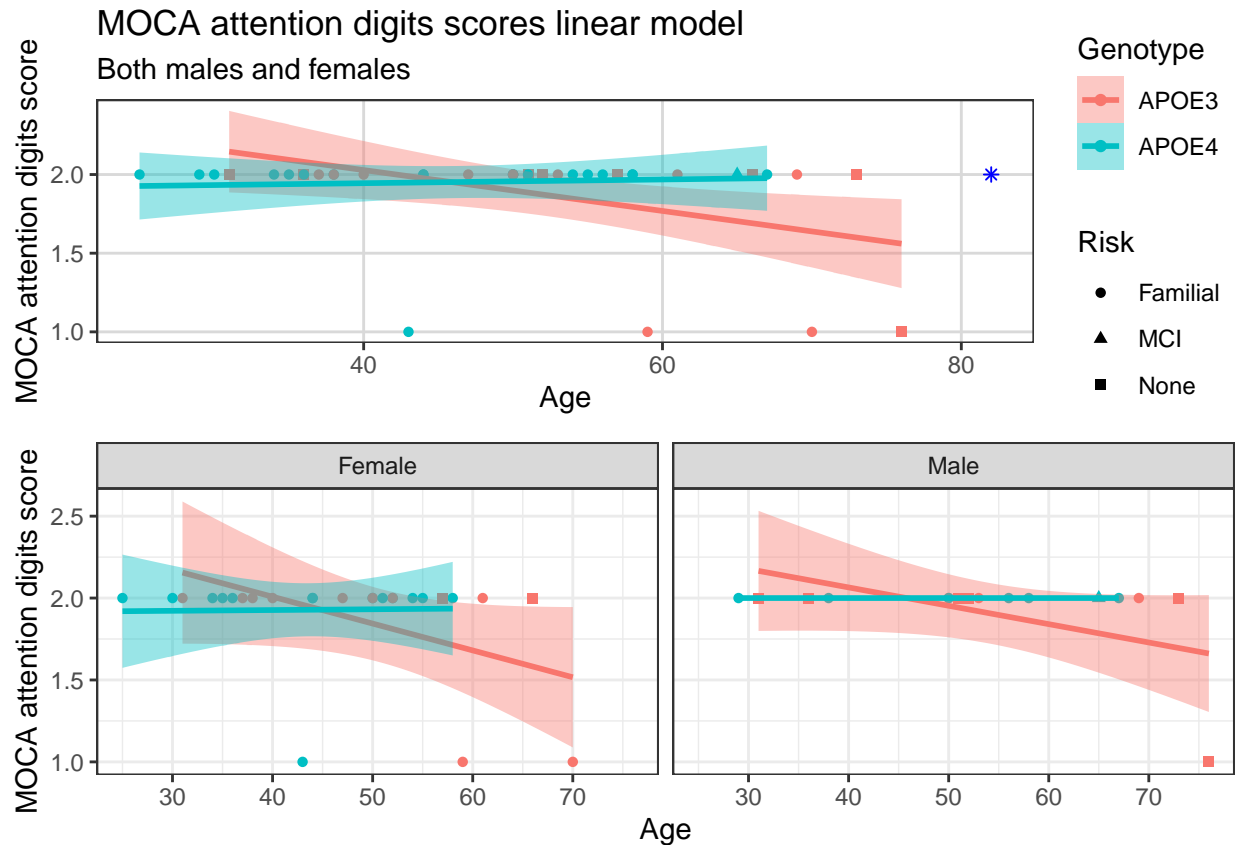
```
##
## Call:
## lm(formula = MOCA_Attention_Digits ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.92827  0.01010  0.06985  0.07961  0.41788
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        2.663443   0.395096   6.741 8.94e-07 ***
## age               -0.016384   0.007593  -2.158   0.0421 *
## GenotypeAPOE4     -0.755392   0.546508  -1.382   0.1808
## age:GenotypeAPOE4  0.016854   0.011351   1.485   0.1518
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.312 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.193,  Adjusted R-squared:  0.08296
## F-statistic: 1.754 on 3 and 22 DF,  p-value: 0.1854


##
## Call:
## lm(formula = MOCA_Attention_Digits ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.6615  0.0000  0.0000  0.0583  0.3049
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)        2.513330   0.271967   9.241 2.46e-07 ***
## age               -0.011208   0.004896  -2.289   0.0381 *
## GenotypeAPOE4     -0.513330   0.434586  -1.181   0.2572
## age:GenotypeAPOE4  0.011208   0.008012   1.399   0.1836
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2174 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.2996, Adjusted R-squared:  0.1495
## F-statistic: 1.996 on 3 and 14 DF,  p-value: 0.1609
```
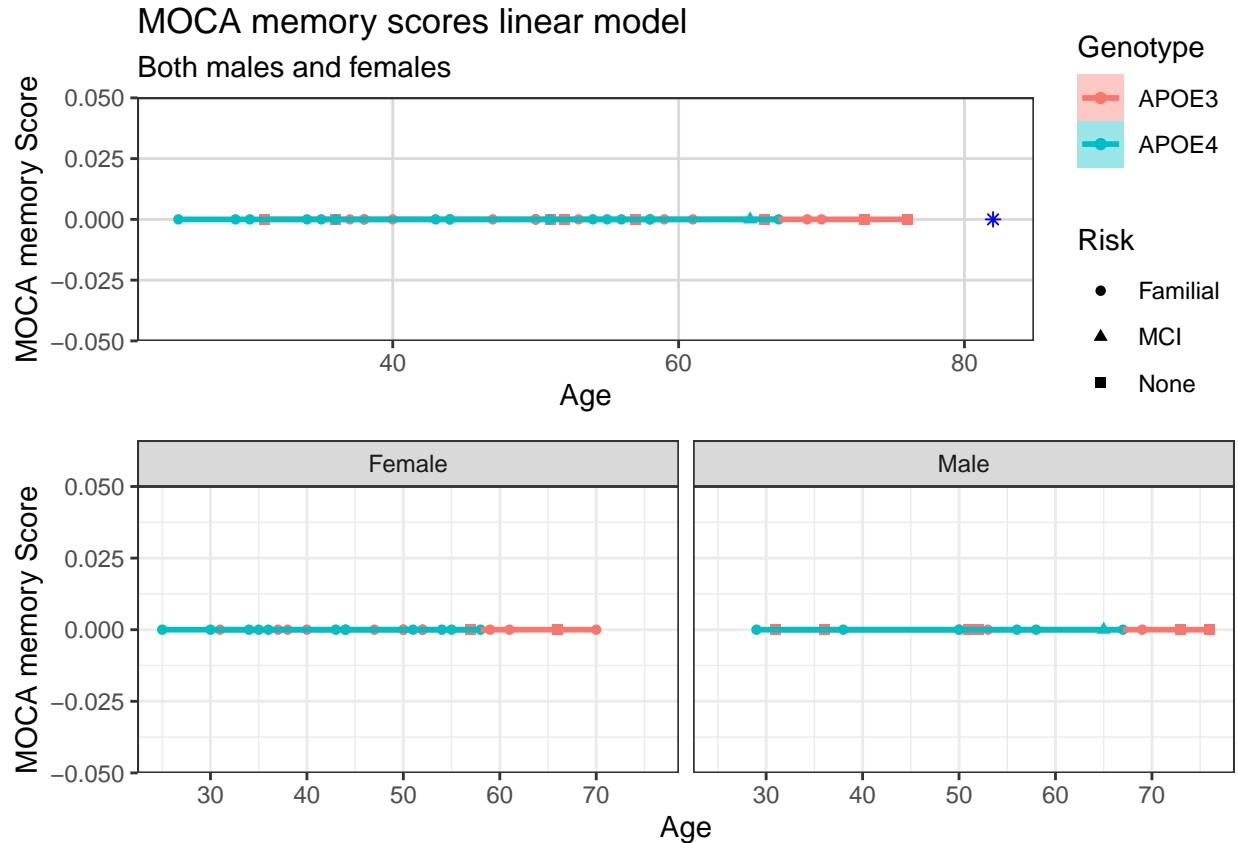
MOCA attention digits scores linear model
Both males and females

```
##
## 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 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:    NaN,  Adjusted R-squared:    NaN
## F-statistic:   NaN on 7 and 36 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 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:     NaN,  Adjusted R-squared:    NaN
## F-statistic:   NaN on 3 and 22 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 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:     NaN,  Adjusted R-squared:    NaN
## F-statistic:   NaN on 3 and 14 DF,  p-value: NA
```
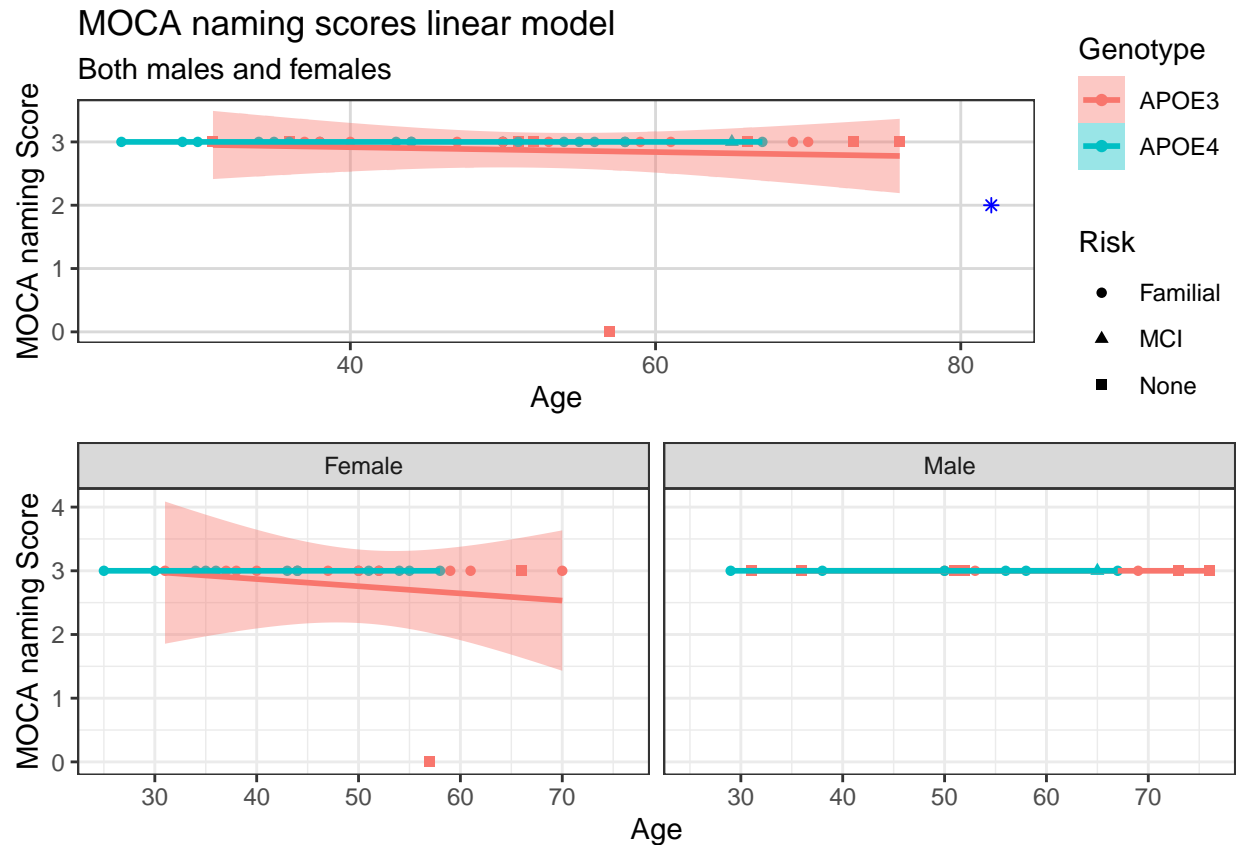
MOCA memory scores linear model

```
## 
## Call:
## lm(formula = MOCA_Naming ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.67874  0.00000  0.00000  0.00718  0.46753
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)               3.32008    0.59829   5.549 2.78e-06 ***
## age                      -0.01125    0.01150  -0.979    0.334
## GenotypeAPOE4            -0.32008    0.82758  -0.387    0.701
## sexMale                  -0.32008    0.84108  -0.381    0.706
## age:GenotypeAPOE4         0.01125    0.01719   0.655    0.517
## age:sexMale               0.01125    0.01567   0.718    0.477
## GenotypeAPOE4:sexMale     0.32008    1.25586   0.255    0.800
## age:GenotypeAPOE4:sexMale -0.01125    0.02447  -0.460    0.648
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.4725 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.08632,    Adjusted R-squared:  -0.09134
## F-statistic: 0.4859 on 7 and 36 DF,  p-value: 0.8384
```

```
##
## Call:
## lm(formula = MOCA_Naming ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min     1Q  Median     3Q     Max
## -2.6787  0.0000  0.0000  0.1890  0.4675
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        3.32008    0.76534   4.338 0.000264 ***
## age               -0.01125    0.01471  -0.765 0.452395
## GenotypeAPOE4     -0.32008    1.05864  -0.302 0.765229
## age:GenotypeAPOE4  0.01125    0.02199   0.512 0.613958
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.6044 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.07137,    Adjusted R-squared:  -0.05526
## F-statistic: 0.5636 on 3 and 22 DF,  p-value: 0.6447


##
## Call:
## lm(formula = MOCA_Naming ~ age * Genotype, data = combo_m)
##
## Residuals:
##        Min         1Q     Median         3Q        Max
## -7.707e-16 -5.437e-16 -2.830e-16  0.000e+00  5.095e-15
##
## Coefficients:
##                    Estimate Std. Error    t value Pr(>|t|)
## (Intercept)       3.000e+00  1.794e-15  1.672e+15   <2e-16 ***
## age              -1.121e-17  3.231e-17 -3.470e-01    0.734
## GenotypeAPOE4    -1.118e-15  2.867e-15 -3.900e-01    0.702
## age:GenotypeAPOE4 1.121e-17  5.286e-17  2.120e-01    0.835
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.434e-15 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.4841, Adjusted R-squared:  0.3735
## F-statistic: 4.378 on 3 and 14 DF,  p-value: 0.02262
```
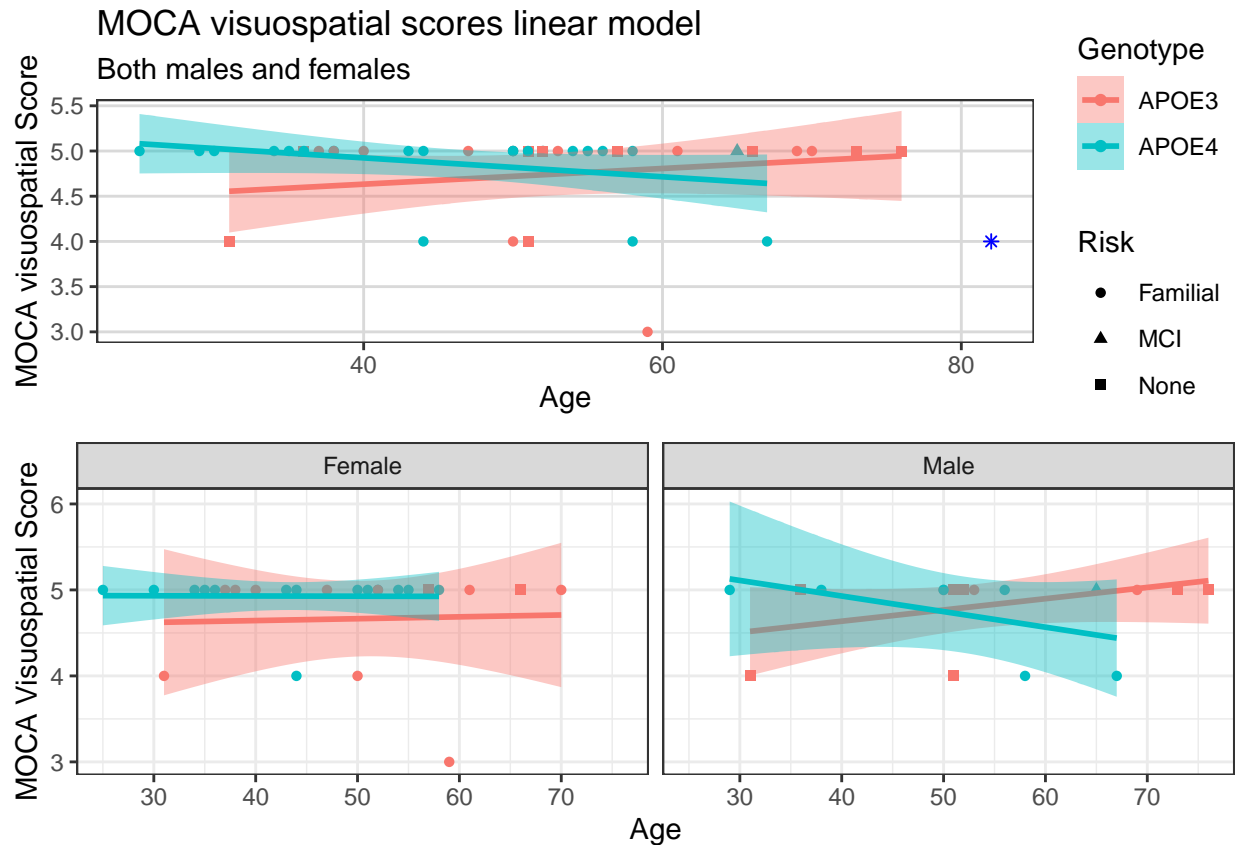
MOCA naming scores linear model


```
## 
## Call:
## lm(formula = MOCA_Visuospatial ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -1.68476 -0.02897  0.07348  0.29353  0.52383 
## 
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)    
## (Intercept)             4.556652   0.594260   7.668 4.46e-09 ***
## age                     0.002171   0.011420   0.190    0.850    
## GenotypeAPOE4           0.383320   0.821999   0.466    0.644    
## sexMale                -0.444660   0.835406  -0.532    0.598    
## age:GenotypeAPOE4      -0.002433   0.017073  -0.142    0.887    
## age:sexMale             0.010928   0.015561   0.702    0.487    
## GenotypeAPOE4:sexMale   1.158506   1.247394   0.929    0.359    
## age:GenotypeAPOE4:sexMale -0.028785   0.024304  -1.184    0.244    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.4693 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.1344, Adjusted R-squared:  -0.03393 
## F-statistic: 0.7984 on 7 and 36 DF,  p-value: 0.5938
```

```
## 
## Call:
## lm(formula = MOCA_Visuospatial ~ age * Genotype, data = combo_f)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.68476  0.06897  0.07348  0.30818  0.36301
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       4.556652   0.638152   7.140 3.69e-07 ***
## age               0.002171   0.012263   0.177    0.861
## GenotypeAPOE4     0.383320   0.882712   0.434    0.668
## age:GenotypeAPOE4 -0.002433   0.018334  -0.133    0.896
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.5039 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.07473,    Adjusted R-squared:  -0.05144
## F-statistic: 0.5923 on 3 and 22 DF,  p-value: 0.6266


## 
## Call:
## lm(formula = MOCA_Visuospatial ~ age * Genotype, data = combo_m)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.7801 -0.1232  0.1142  0.2298  0.5238
## 
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       4.111993   0.511639   8.037 1.3e-06 ***
## age               0.013100   0.009211   1.422   0.1769
## GenotypeAPOE4     1.541825   0.817568   1.886   0.0802 .
## age:GenotypeAPOE4 -0.031217   0.015072  -2.071   0.0573 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.4089 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.2475, Adjusted R-squared:  0.08626
## F-statistic: 1.535 on 3 and 14 DF,  p-value: 0.2492
```

```
## 
## Call:
## lm(formula = MOCA_TOTAL ~ age * Genotype * sex, data = geno_combined)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.3382 -1.4054  0.7695  2.0000  3.2864
## 
## Coefficients:
##                          Estimate Std. Error t value Pr(>|t|)
## (Intercept)             29.0735294  3.3564874   8.662 2.49e-10 ***
## age                     -0.0294118  0.0645021  -0.456    0.651
## GenotypeAPOE4            1.6245010  4.6427979   0.350    0.728
## sexMale                 -0.2218228  4.7185237  -0.047    0.963
## age:GenotypeAPOE4       -0.0258623  0.0964326  -0.268    0.790
## age:sexMale              0.0001221  0.0878934   0.001    0.999
## GenotypeAPOE4:sexMale    4.9460929  7.0455035   0.702    0.487
## age:GenotypeAPOE4:sexMale -0.1127712  0.1372736  -0.822    0.417
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 2.651 on 36 degrees of freedom
##   (7 observations deleted due to missingness)
## Multiple R-squared:  0.1752, Adjusted R-squared:  0.01477
## F-statistic: 1.092 on 7 and 36 DF,  p-value: 0.3888
```

```
##
## Call:
## lm(formula = MOCA_TOTAL ~ age * Genotype, data = combo_f)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.3382 -1.2399  0.9412  1.6775  2.7206
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       29.07353    3.12680   9.298 4.46e-09 ***
## age               -0.02941    0.06009  -0.489    0.629
## GenotypeAPOE4      1.62450    4.32509   0.376    0.711
## age:GenotypeAPOE4 -0.02586    0.08983  -0.288    0.776
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.469 on 22 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.06173,    Adjusted R-squared:  -0.06621
## F-statistic: 0.4825 on 3 and 22 DF,  p-value: 0.6978


##
## Call:
## lm(formula = MOCA_TOTAL ~ age * Genotype, data = combo_m)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.5073 -2.0288  0.4203  2.2886  3.2864
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       28.85171    3.64458   7.916 1.55e-06 ***
## age               -0.02929    0.06561  -0.446    0.662
## GenotypeAPOE4      6.57059    5.82381   1.128    0.278
## age:GenotypeAPOE4 -0.13863    0.10737  -1.291    0.218
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.913 on 14 degrees of freedom
##   (5 observations deleted due to missingness)
## Multiple R-squared:  0.2333, Adjusted R-squared:  0.06905
## F-statistic:  1.42 on 3 and 14 DF,  p-value: 0.2786
```

MOCA scores linear model
Both males and females