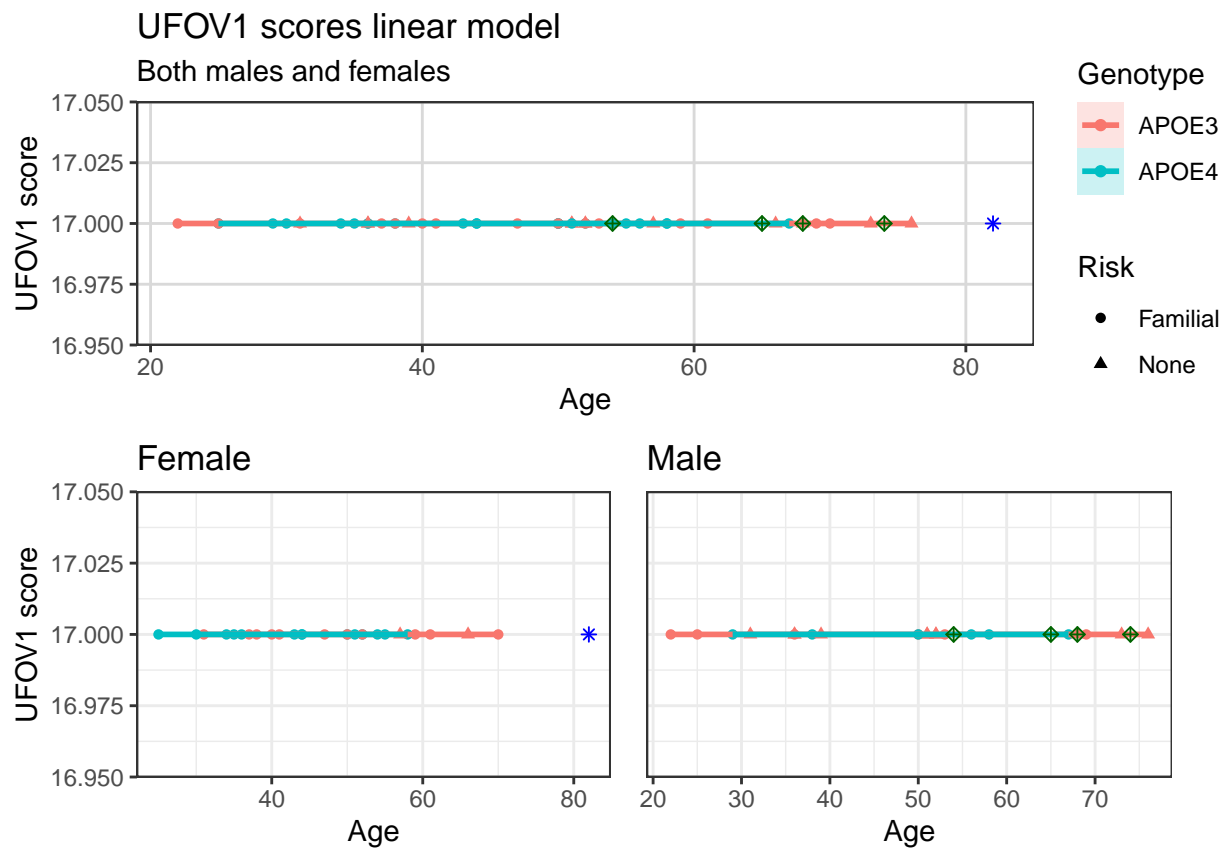


Linear Models with AD and MCI

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



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

```

## GenotypeAPOE4          -3.295e-14  2.494e-14 -1.321e+00    0.194
## sexMale                 -3.295e-14  2.094e-14 -1.574e+00    0.123
## age:GenotypeAPOE4       5.052e-16  5.229e-16  9.660e-01    0.339
## age:sexMale             5.052e-16  4.095e-16  1.234e+00    0.224
## GenotypeAPOE4:sexMale   3.295e-14  3.630e-14  9.080e-01    0.369
## age:GenotypeAPOE4:sexMale -5.052e-16  7.342e-16 -6.880e-01    0.495
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.453e-14 on 42 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.5058, Adjusted R-squared:  0.4234
## F-statistic:  6.14 on 7 and 42 DF,  p-value: 5.639e-05

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

##
## Call:
## lm(formula = ufov1 ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.796e-15 -2.775e-15 -1.022e-15  0.000e+00  2.666e-14
##
## Coefficients:
##              Estimate Std. Error  t value Pr(>|t|)
## (Intercept)   1.700e+01  5.336e-15  3.186e+15  <2e-16 ***
## age          -2.062e-16  1.050e-16 -1.964e+00  0.0644 .
## GenotypeAPOE4 -1.195e-14  1.256e-14 -9.520e-01  0.3531
## age:GenotypeAPOE4  2.062e-16  2.453e-16  8.410e-01  0.4109
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.915e-15 on 19 degrees of freedom

```

```

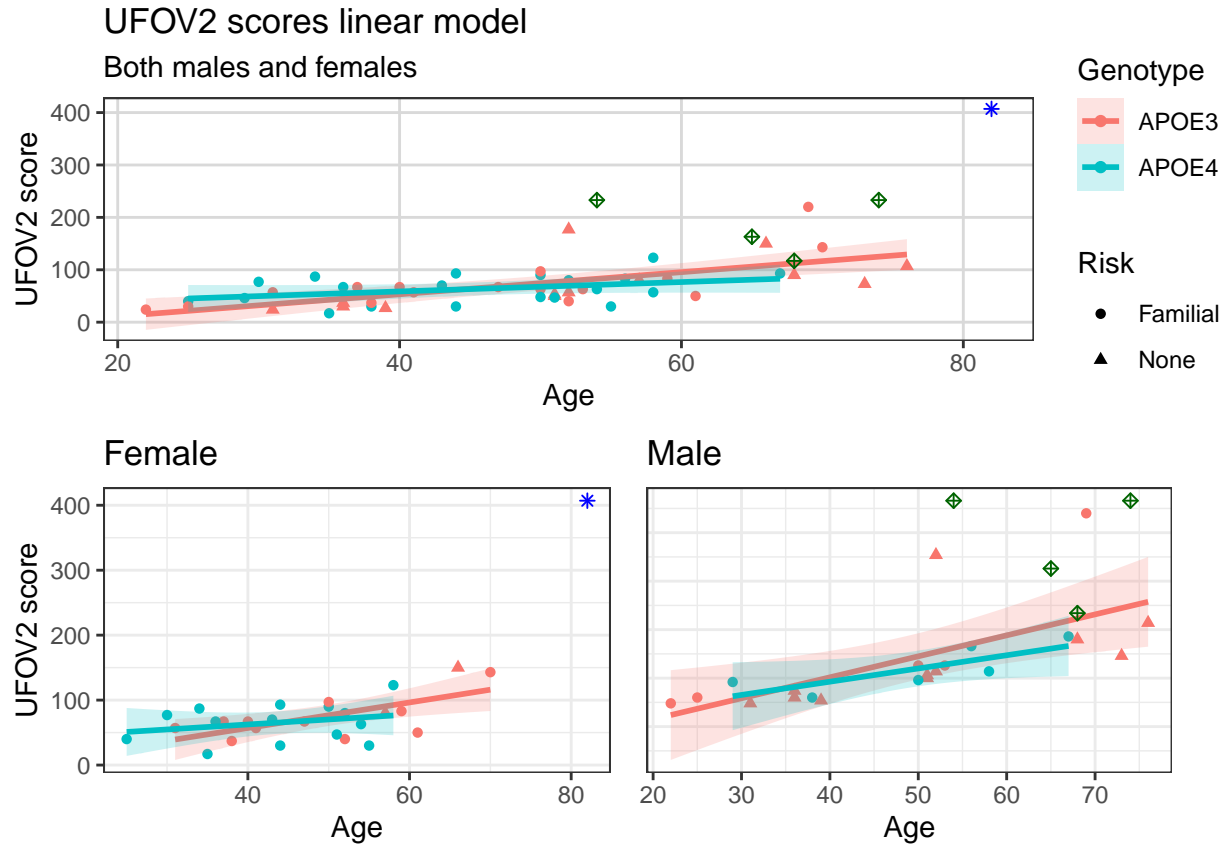
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.5264, Adjusted R-squared: 0.4516
## F-statistic: 7.039 on 3 and 19 DF, p-value: 0.002253

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

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

## Analysis of Variance Table
##
## Response: ufov1
##          Df      Sum Sq    Mean Sq F value Pr(>F)
## age       1 1.5461e-28 1.5461e-28  3.2334 0.08806 .
## Genotype  1 1.3770e-29 1.3767e-29  0.2879 0.59779
## age:Genotype 1 3.3810e-29 3.3805e-29  0.7070 0.41091
## Residuals 19 9.0853e-28 4.7817e-29
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```



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

```
##
## Call:
## lm(formula = ufov2 ~ age * Genotype, data = combo_f)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-48.328	-13.739	5.208	20.070	46.684

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-21.6677	34.6186	-0.626	0.53755
age	1.9671	0.6752	2.913	0.00782 **
GenotypeAPOE4	53.4227	48.8212	1.094	0.28517
age:GenotypeAPOE4	-1.1989	1.0236	-1.171	0.25350

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 28.45 on 23 degrees of freedom
## (1 observation deleted due to missingness)
## Multiple R-squared:  0.3143, Adjusted R-squared:  0.2248
## F-statistic: 3.514 on 3 and 23 DF,  p-value: 0.03126
```

```
##
## Call:
## lm(formula = ufov2 ~ age * Genotype, data = combo_m)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-49.23	-21.01	-12.07	11.16	106.43

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-35.6782	31.8062	-1.122	0.27672
age	2.1631	0.6165	3.509	0.00251 **
GenotypeAPOE4	27.4138	72.7885	0.377	0.71086
age:GenotypeAPOE4	-0.7987	1.4179	-0.563	0.58019

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 39.84 on 18 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.4335, Adjusted R-squared:  0.3391
## F-statistic: 4.592 on 3 and 18 DF,  p-value: 0.0148
```

Analysis of Variance Table

```
##
```

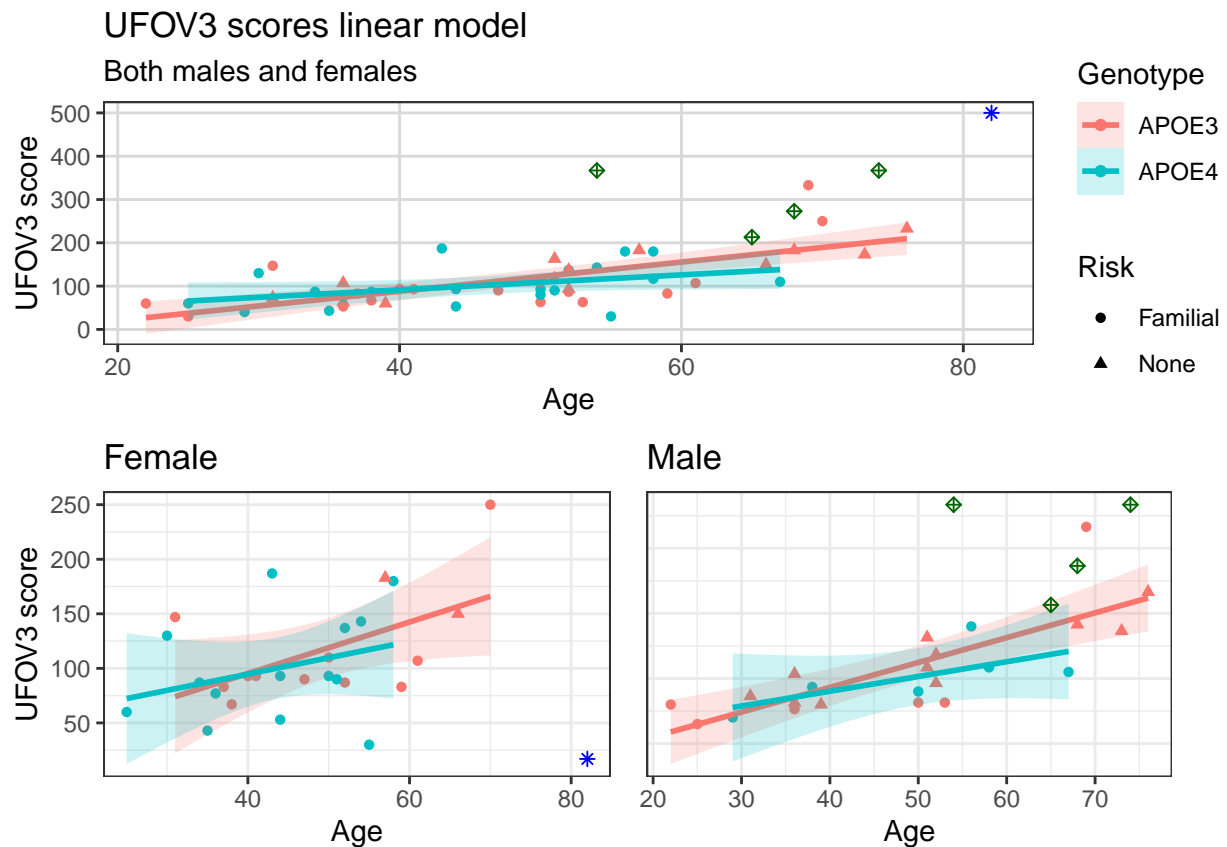
```
## Response: ufov2
```

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

```
## age:Genotype:sex 1      63      62.5  0.0543    0.8169
## Residuals      41 47177  1150.7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

## Analysis of Variance Table
##
## Response: ufov2
##          Df Sum Sq Mean Sq F value    Pr(>F)
## age       1 20713.2  20713.2  13.0518 0.00199 **
## Genotype   1   644.3    644.3   0.4060 0.53202
## age:Genotype 1   503.5    503.5   0.3173 0.58019
## Residuals 18 28566.0   1587.0
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



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

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

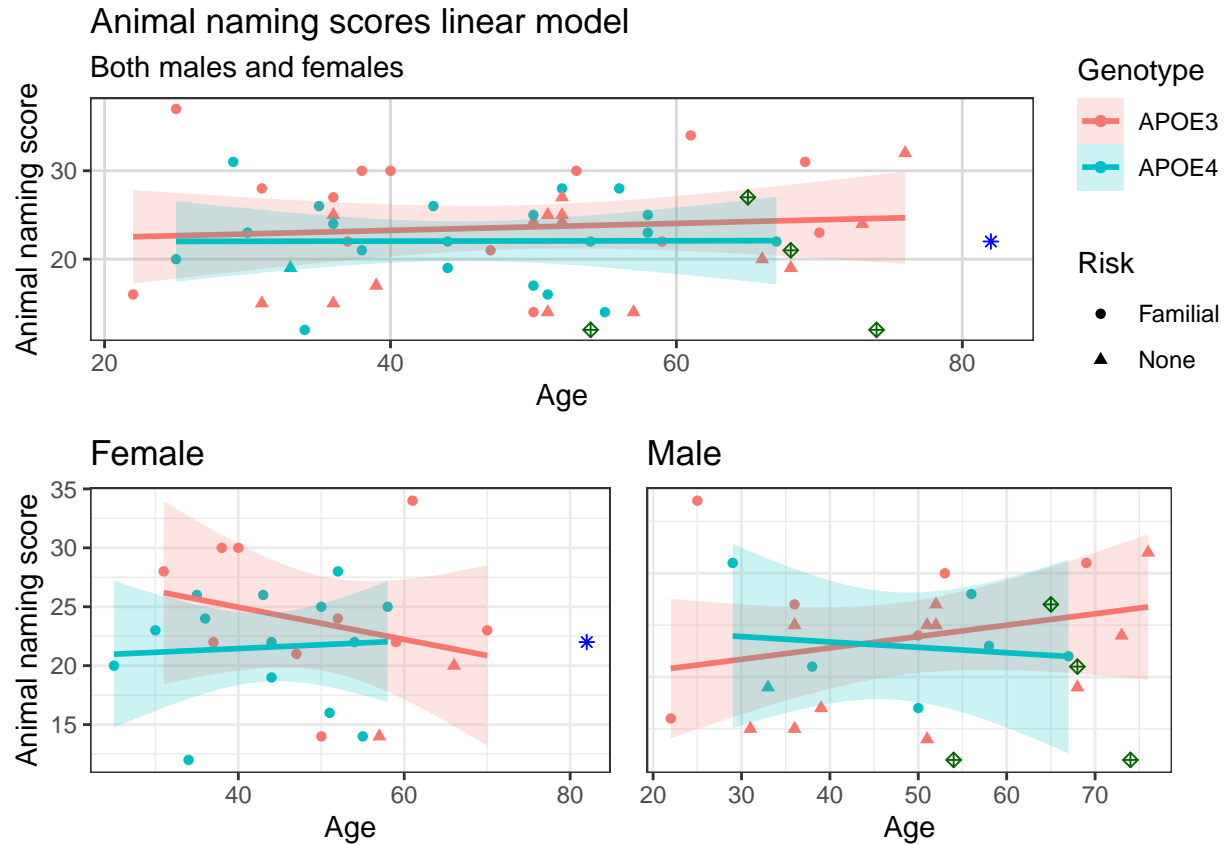
##
## Call:
## lm(formula = ufov3 ~ age * Genotype, data = combo_f)
##
## Residuals:
```

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

```
## Analysis of Variance Table
##
## Response: ufov3
##              Df Sum Sq Mean Sq F value    Pr(>F)
## age           1  75634    75634 34.4095 6.191e-07 ***
## Genotype       1    608     608  0.2766  0.6017
## sex           1    102     102  0.0466  0.8301
## age:Genotype   1   4737    4737  2.1551  0.1495
## age:sex        1   2999    2999  1.3644  0.2494
## Genotype:sex   1    303     303  0.1380  0.7121
## age:Genotype:sex 1    183     183  0.0831  0.7746
## Residuals     42  92318    2198
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## Analysis of Variance Table
##
## Response: ufov3
##              Df Sum Sq Mean Sq F value    Pr(>F)
## age           1  65288    65288 29.1437 3.29e-05 ***
## Genotype       1   1879    1879  0.8386  0.3713
## age:Genotype   1   1897    1897  0.8466  0.3690
## Residuals     19 42564    2240
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

	Min	1Q	Median	3Q	Max
	-10.0096	-4.3996	0.4872	4.1431	15.8464

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	30.4309	7.6063	4.001	0.000251 ***
age	-0.1368	0.1462	-0.936	0.354702
GenotypeAPOE4	-10.2594	10.5213	-0.975	0.335087
sexMale	-12.0233	8.9075	-1.350	0.184308
age:GenotypeAPOE4	0.1689	0.2185	0.773	0.443991
age:sexMale	0.2466	0.1723	1.431	0.159715
GenotypeAPOE4:sexMale	17.3110	14.2805	1.212	0.232206
age:GenotypeAPOE4:sexMale	-0.3307	0.2930	-1.129	0.265450

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.007 on 42 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.0782, Adjusted R-squared:  -0.07544
## F-statistic: 0.509 on 7 and 42 DF,  p-value: 0.8225
```

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

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

``` ## Analysis of Variance Table ```

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

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

```
## Analysis of Variance Table
```

```
##
```

```
## Response: animals
```

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

```
## Analysis of Variance Table
```

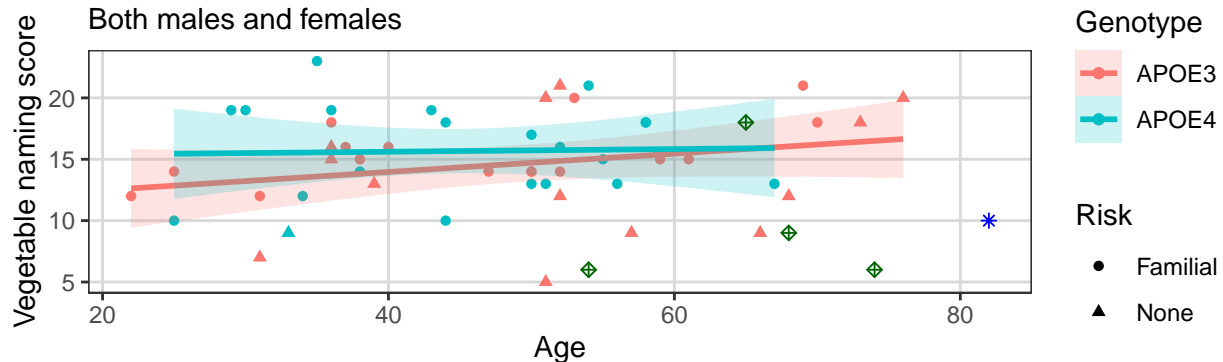
```
##
```

```
## Response: animals
```

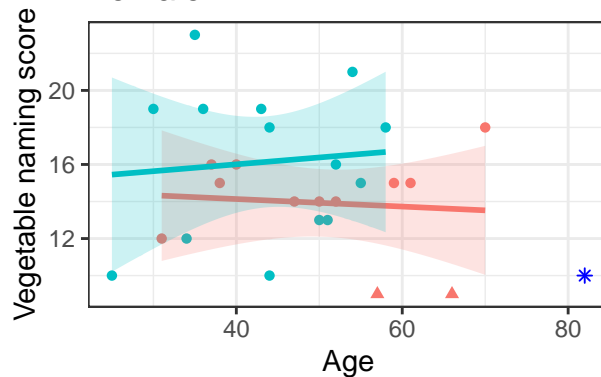
```
##          Df Sum Sq Mean Sq F value Pr(>F)
## age         1  31.25   31.251   0.7549 0.3952
## Genotype     1   2.00    1.999   0.0483 0.8283
## age:Genotype 1  24.80   24.802   0.5991 0.4480
## Residuals   20 827.95   41.397
```

Vegetable naming scores linear model

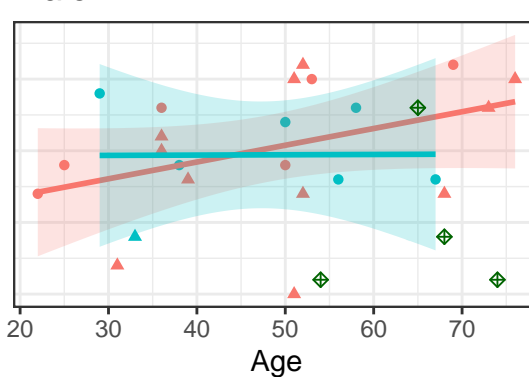
Both males and females



Female



Male



```
##
```

```
## Call:
```

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

```
##
```

```

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

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

##
## Call:
## lm(formula = vegetables ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -10.5000  -1.7386   0.5904   3.2956   5.3830
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)

```

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

Analysis of Variance Table

##

Response: vegetables

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

Analysis of Variance Table

##

Response: vegetables

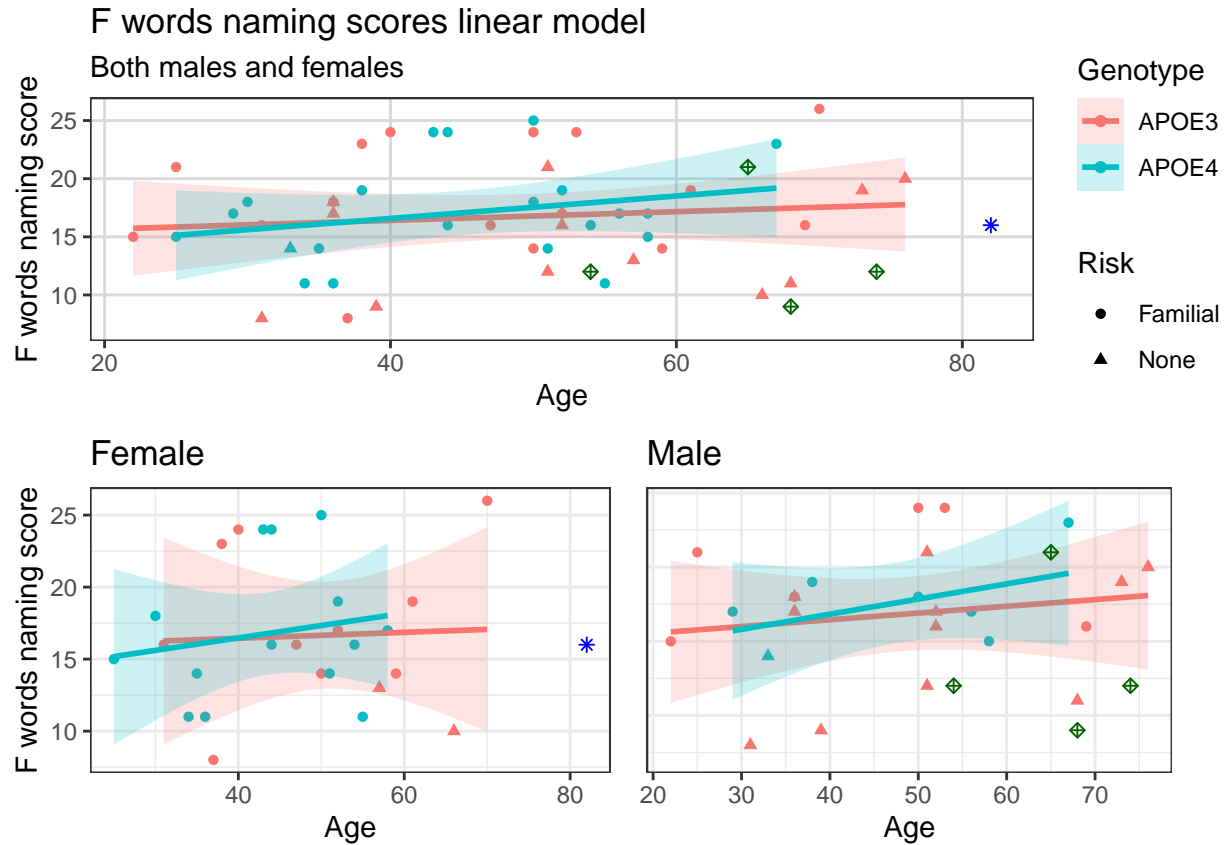
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	2.124	2.1236	0.1589	0.6940
## Genotype	1	29.987	29.9871	2.2435	0.1484
## age:Genotype	1	2.491	2.4914	0.1864	0.6701
## Residuals	22	294.052	13.3660		

Analysis of Variance Table

##

Response: vegetables

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	47.23	47.233	2.5088	0.1289
## Genotype	1	0.70	0.696	0.0370	0.8494
## age:Genotype	1	12.50	12.500	0.6640	0.4248
## Residuals	20	376.53	18.826		



```
##
## Call:
## lm(formula = f ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -8.3861 -2.7916 -0.2203  2.3138  8.9364
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    15.62653    6.205877   2.518  0.0157 *
## age             0.020529  0.119259   0.172  0.8642
## GenotypeAPOE4   -2.605214  8.584162  -0.303  0.7630
## sexMale        -0.991706  7.267463  -0.136  0.8921
## age:GenotypeAPOE4  0.065726  0.178296   0.369  0.7143
## age:sexMale      0.024847  0.140581   0.177  0.8606
## GenotypeAPOE4:sexMale  0.707301 11.651235   0.061  0.9519
## age:GenotypeAPOE4:sexMale -0.008861  0.239072  -0.037  0.9706
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.901 on 42 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.03496,    Adjusted R-squared:  -0.1259
## F-statistic: 0.2174 on 7 and 42 DF,  p-value: 0.9793
```

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

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

Analysis of Variance Table

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

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

```
## Analysis of Variance Table
```

```
##
```

```
## Response: f
```

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

```
## Analysis of Variance Table
```

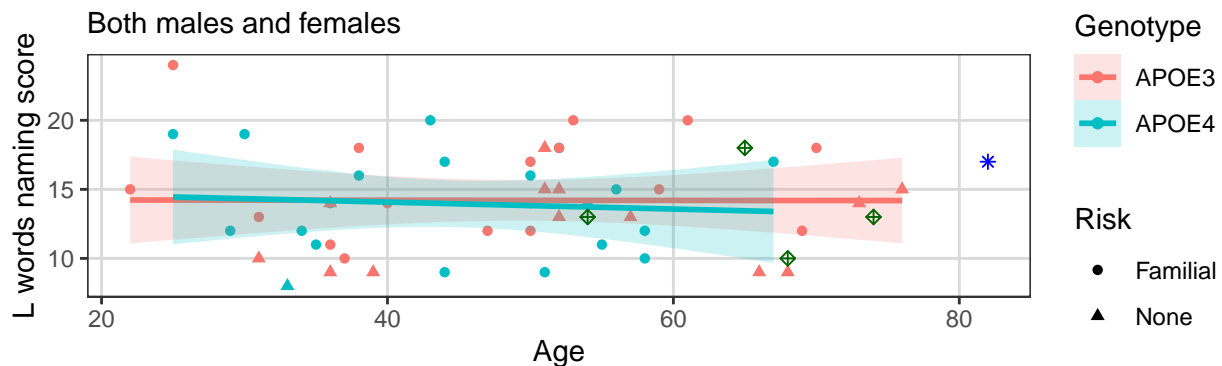
```
##
```

```
## Response: f
```

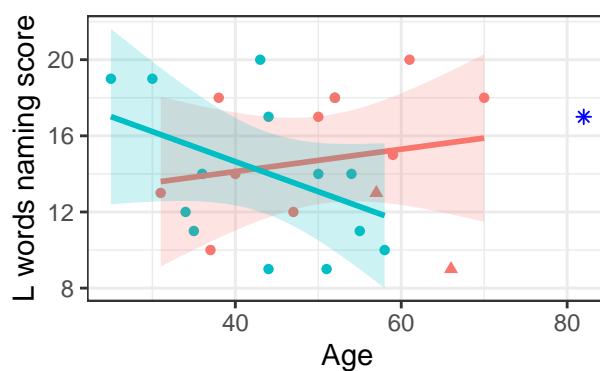
```
##          Df Sum Sq Mean Sq F value Pr(>F)
## age       1  18.11  18.1078   0.9368 0.3447
## Genotype   1   3.19   3.1929   0.1652 0.6887
## age:Genotype 1   3.06   3.0617   0.1584 0.6949
## Residuals 20 386.60 19.3298
```

L words naming scores linear model

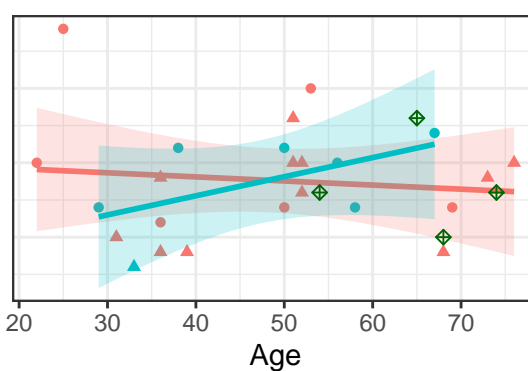
Both males and females



Female



Male



```
##
```

```
## Call:
```

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

```
##
```



```

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

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

##
## Call:
## lm(formula = l ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.1602 -3.1077  0.3106  1.4443  9.5371
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)

```

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

Analysis of Variance Table

##

Response: l

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	0.36	0.363	0.0256	0.87362
## Genotype	1	1.00	0.998	0.0703	0.79216
## sex	1	5.73	5.725	0.4034	0.52876
## age:Genotype	1	0.59	0.593	0.0418	0.83895
## age:sex	1	2.64	2.641	0.1861	0.66838
## Genotype:sex	1	1.94	1.938	0.1366	0.71359
## age:Genotype:sex	1	58.24	58.241	4.1042	0.04916 *
## Residuals	42	596.00	14.190		

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

Analysis of Variance Table

##

Response: l

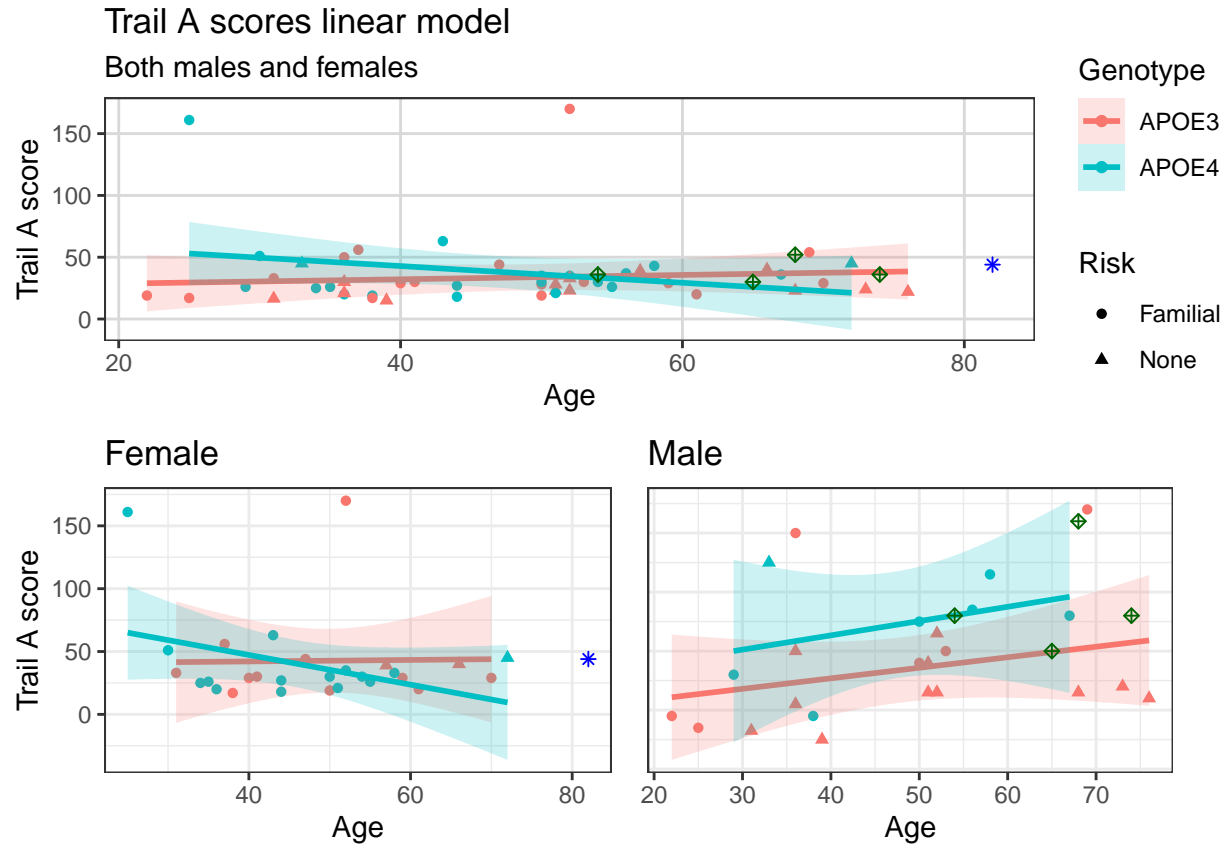
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	2.184	2.184	0.1638	0.6896
## Genotype	1	5.244	5.244	0.3932	0.5371
## age:Genotype	1	35.364	35.364	2.6520	0.1177
## Residuals	22	293.362	13.335		

Analysis of Variance Table

##

Response: l

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	0.244	0.2439	0.0161	0.9003
## Genotype	1	0.053	0.0526	0.0035	0.9536
## age:Genotype	1	23.024	23.0240	1.5216	0.2317
## Residuals	20	302.638	15.1319		



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

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

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

Analysis of Variance Table

```
##
```

```
## Response: trailA
```

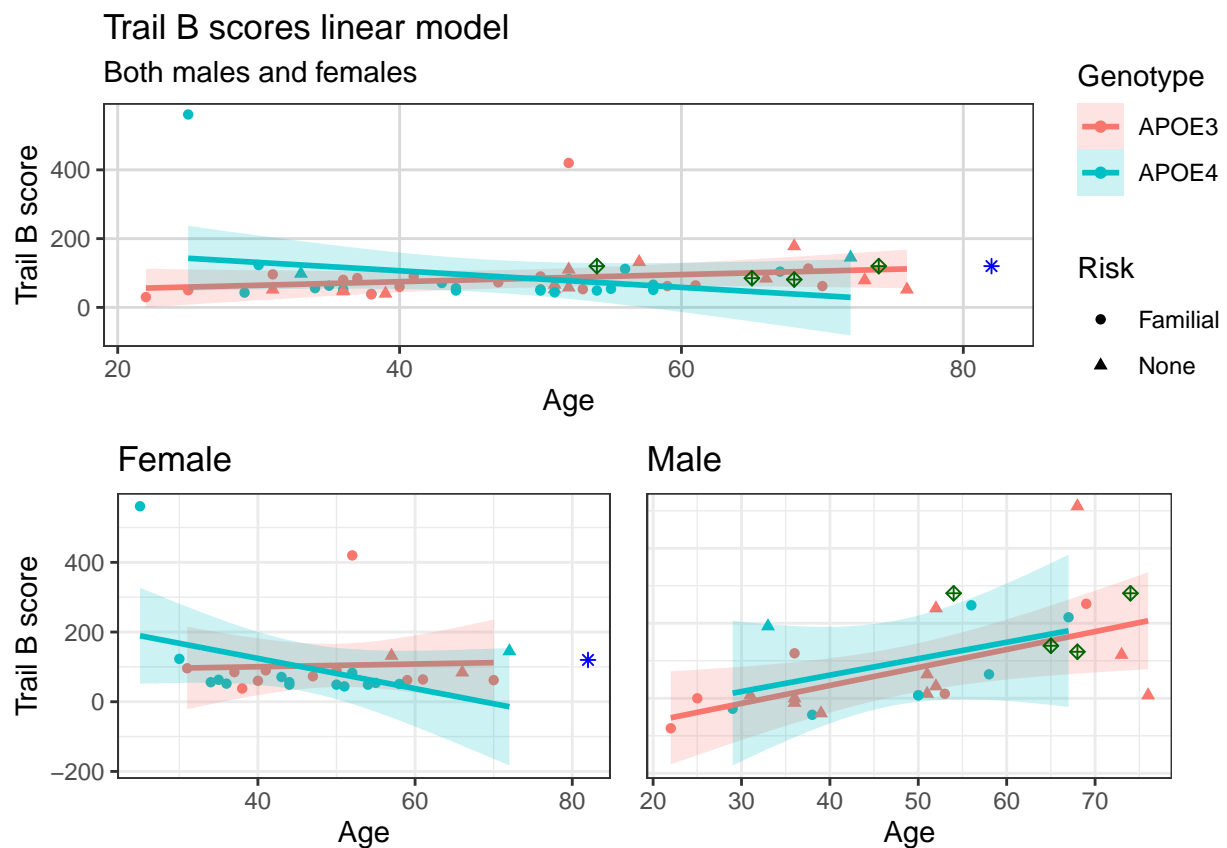
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	196	195.53	0.2406	0.6262
Genotype	1	272	271.52	0.3341	0.5662
sex	1	1787	1787.20	2.1992	0.1452
age:Genotype	1	1379	1378.79	1.6967	0.1995
age:sex	1	658	658.45	0.8103	0.3729
Genotype:sex	1	422	422.20	0.5195	0.4749
age:Genotype:sex	1	814	813.64	1.0012	0.3225
Residuals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

Analysis of Variance Table

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

```
## Analysis of Variance Table
```

```
##
## Response: trailA
##           Df Sum Sq Mean Sq F value Pr(>F)
## age       1   191.33  191.329   1.7841  0.1966
## Genotype   1   298.20  298.198   2.7807  0.1110
## age:Genotype 1    3.84    3.836   0.0358  0.8519
## Residuals 20  2144.79  107.240
```



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

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

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

##
## Call:
## lm(formula = trailB ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -49.654 -18.807  -6.881   11.988   85.924
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      10.6598    23.6447   0.451   0.6570
## age              1.1973    0.4654   2.573   0.0182 *
## GenotypeAPOE4     11.0054    49.2535   0.223   0.8255
## age:GenotypeAPOE4 -0.1026    0.9957  -0.103   0.9190
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```

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

## Analysis of Variance Table
##
## Response: trailB
##
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	430	429.9	0.0569	0.81250
Genotype	1	673	673.1	0.0892	0.76664
sex	1	12784	12783.7	1.6935	0.19991
age:Genotype	1	23691	23691.1	3.1384	0.08339 .
age:sex	1	12689	12689.4	1.6810	0.20155
Genotype:sex	1	983	982.7	0.1302	0.71997
age:Genotype:sex	1	10234	10234.4	1.3558	0.25054
Residuals	44	332144	7548.7		

```

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

## Analysis of Variance Table
##
## Response: trailB
##
```

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

```

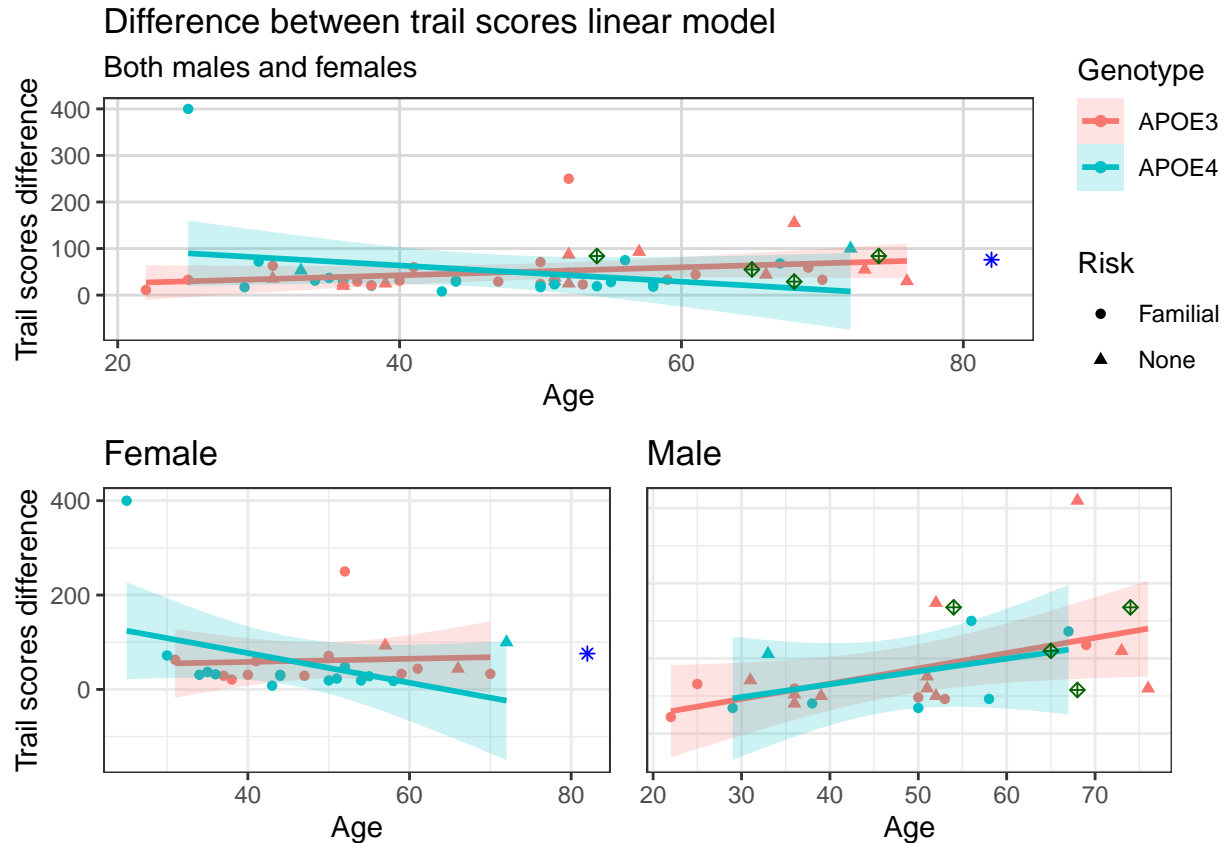
## Analysis of Variance Table
##
## Response: trailB
##
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	7594.6	7594.6	8.0898	0.01002 *
Genotype	1	186.3	186.3	0.1985	0.66075
age:Genotype	1	10.0	10.0	0.0106	0.91896
Residuals	20	18775.7	938.8		

```

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

```



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



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

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

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

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

```
## Analysis of Variance Table
```

```
##
```

```
## Response: trailDiff
```

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

```
## Analysis of Variance Table
```

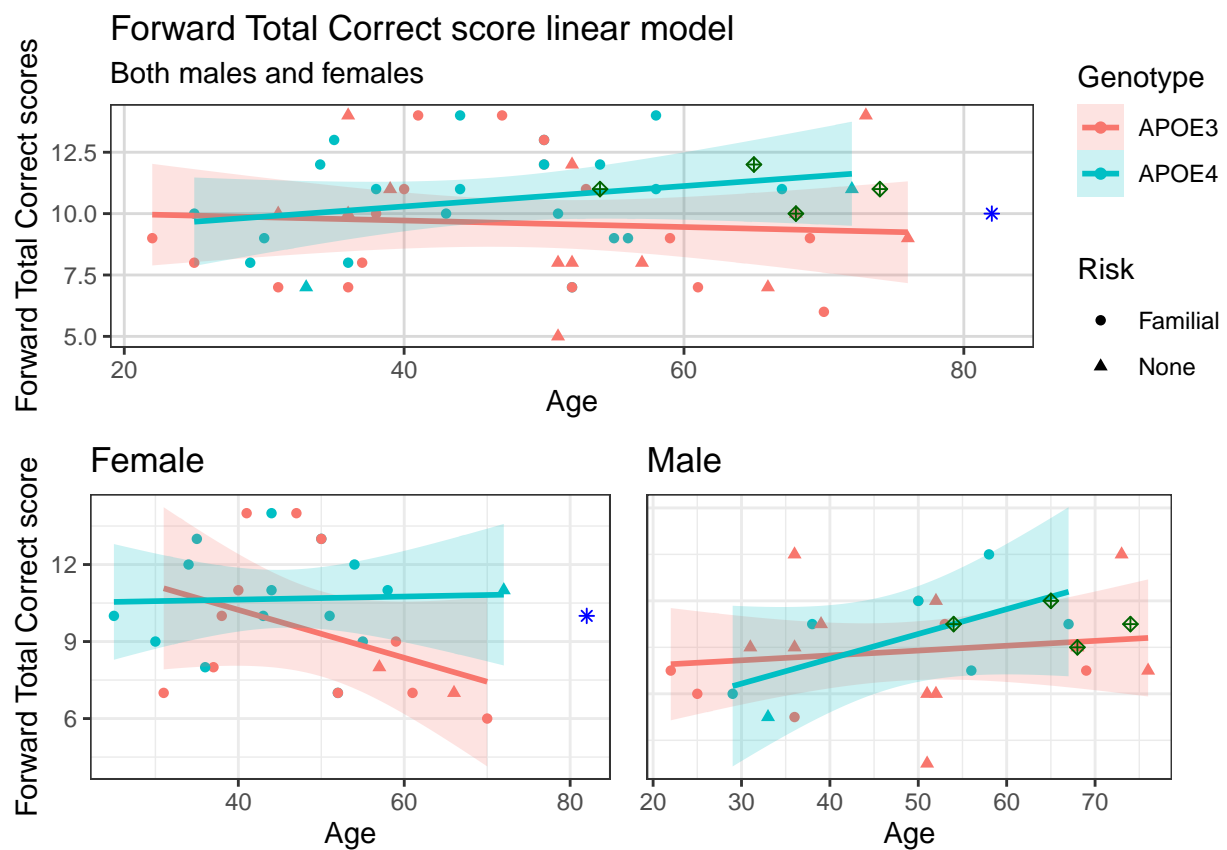
```
##
```

```
## Response: trailDiff
```

```
##          Df Sum Sq Mean Sq F value Pr(>F)
## age       1  5375.1   5375.1   6.2068 0.02163 *
## Genotype   1    13.1     13.1   0.0151  0.90336
## age:Genotype 1    26.2     26.2   0.0302  0.86374
## Residuals 20 17320.1     866.0
```

```
## ---
```

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



```
##
```

```
## Call:
```

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

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

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

##
## Call:
## lm(formula = fwd_total_correct ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.8814 -1.4932 -0.2558  1.4948  4.4325
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```

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

Analysis of Variance Table

##

Response: fwd_total_correct

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	0.055	0.0552	0.0099	0.92108
## Genotype	1	11.639	11.6393	2.0926	0.15510
## sex	1	0.332	0.3317	0.0596	0.80821
## age:Genotype	1	6.349	6.3491	1.1415	0.29117
## age:sex	1	25.613	25.6126	4.6049	0.03744 *
## Genotype:sex	1	1.194	1.1938	0.2146	0.64545
## age:Genotype:sex	1	0.086	0.0861	0.0155	0.90157
## Residuals	44	244.732	5.5621		

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

Analysis of Variance Table

##

Response: fwd_total_correct

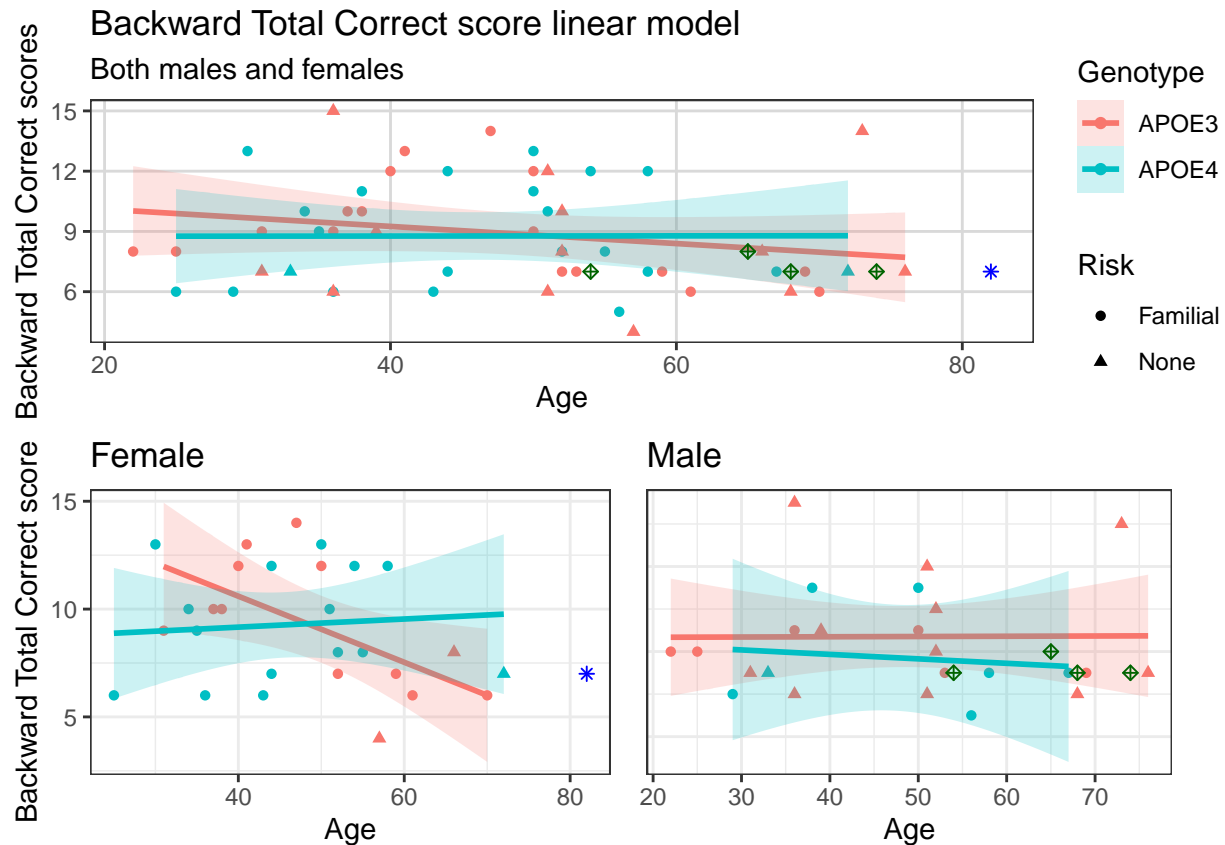
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	9.401	9.4014	1.6768	0.2077
## Genotype	1	9.476	9.4760	1.6901	0.2059
## age:Genotype	1	9.528	9.5278	1.6994	0.2047
## Residuals	24	134.559	5.6066		

Analysis of Variance Table

##

Response: fwd_total_correct

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	8.558	8.5581	1.5536	0.2270
## Genotype	1	1.238	1.2380	0.2247	0.6406
## age:Genotype	1	6.989	6.9891	1.2687	0.2733
## Residuals	20	110.173	5.5087		



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

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

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

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

```
## Residuals      44 315.865  7.1787
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: bckwds_total_correct
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)
```

```
## age         1  14.050  14.0497   2.0137 0.16874
```

```
## Genotype    1   0.035   0.0348   0.0050 0.94424
```

```
## age:Genotype 1  28.576  28.5761   4.0958 0.05426 .
```

```
## Residuals   24 167.447   6.9769
```

```
## ---
```

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

```
## Analysis of Variance Table
```

```
##
```

```
## Response: bckwds_total_correct
```

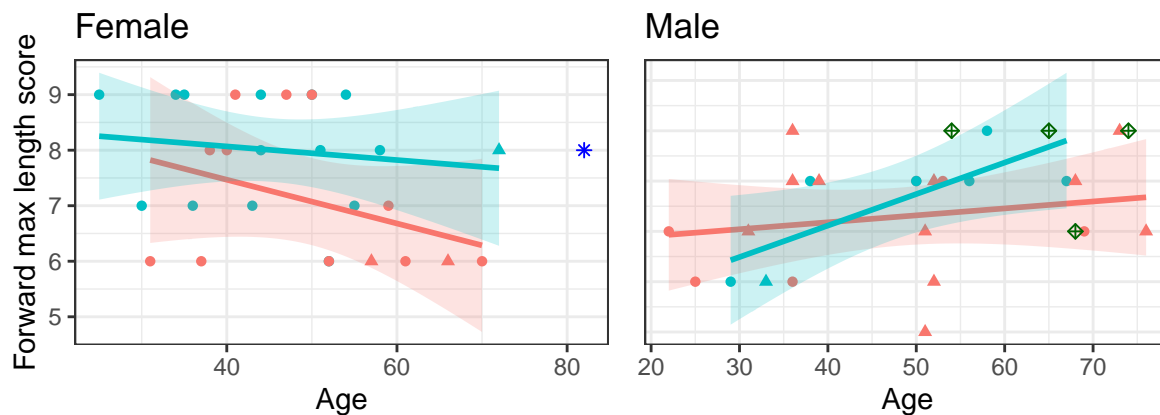
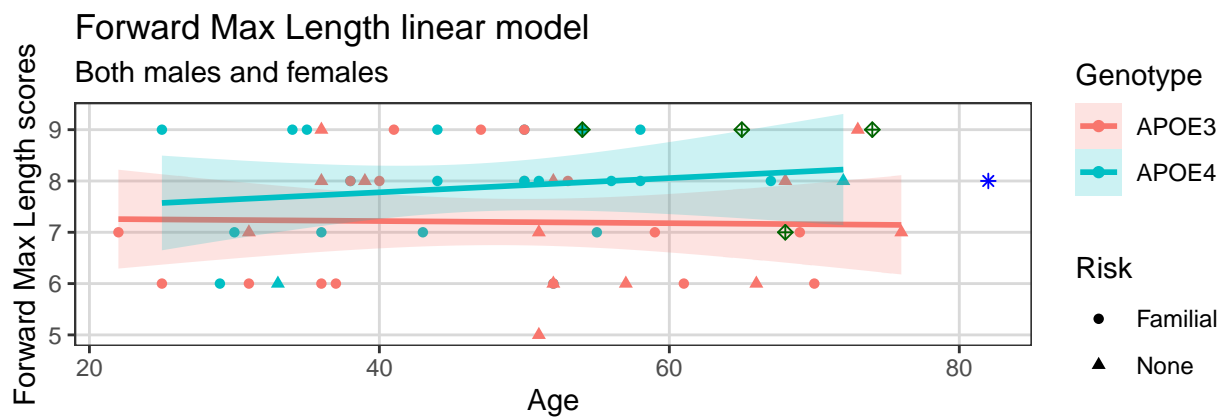
```
##           Df Sum Sq Mean Sq F value Pr(>F)
```

```
## age         1   0.044   0.0437   0.0059 0.9396
```

```
## Genotype    1   4.906   4.9055   0.6610 0.4258
```

```
## age:Genotype 1   0.466   0.4660   0.0628 0.8047
```

```
## Residuals   20 148.418   7.4209
```



```
##
```

```
## Call:
```

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

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

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

##
## Call:
## lm(formula = fwd_max_length ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.33227 -0.67698  0.00583  0.70056  1.87473
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```



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

Analysis of Variance Table

##

Response: fwd_max_length

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	0.009	0.0089	0.0073	0.93210
Genotype	1	5.699	5.6992	4.6857	0.03588 *
sex	1	0.015	0.0153	0.0126	0.91118
age:Genotype	1	0.562	0.5620	0.4621	0.50022
age:sex	1	8.245	8.2448	6.7786	0.01253 *
Genotype:sex	1	0.708	0.7080	0.5821	0.44956
age:Genotype:sex	1	0.225	0.2251	0.1851	0.66914
Residuals	44	53.517	1.2163		

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

Analysis of Variance Table

##

Response: fwd_max_length

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	3.827	3.8272	2.8840	0.10240
Genotype	1	4.471	4.4706	3.3689	0.07886 .
age:Genotype	1	0.710	0.7101	0.5351	0.47156
Residuals	24	31.849	1.3271		

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

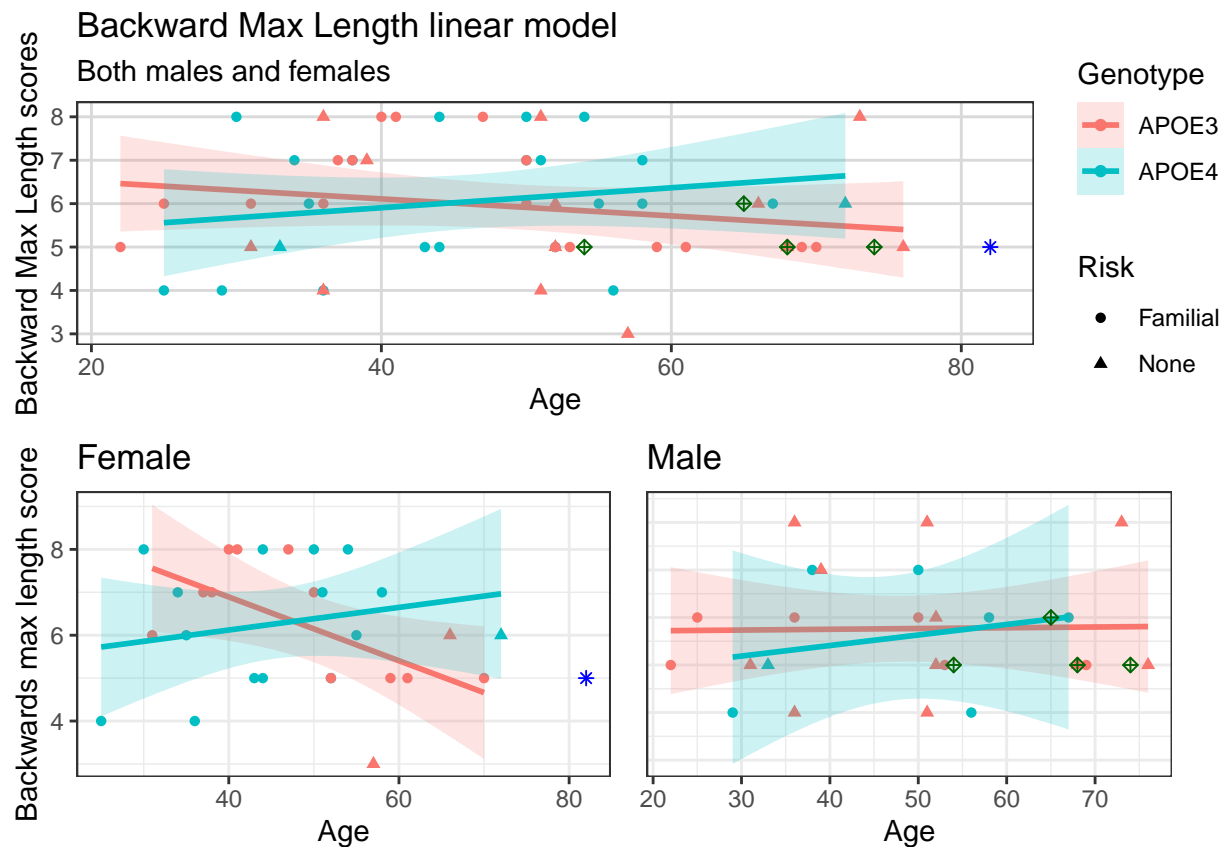
Analysis of Variance Table

##

Response: fwd_max_length

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	3.2529	3.2529	3.0025	0.09853 .
Genotype	1	0.4475	0.4475	0.4130	0.52773
age:Genotype	1	2.2565	2.2565	2.0828	0.16445
Residuals	20	21.6681	1.0834		

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



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

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

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

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

```
## Residuals      44 81.525  1.8528
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: bckwds_max_length
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)
```

```
## age         1  1.567   1.5667   0.8290 0.3716
```

```
## Genotype     1  0.005   0.0050   0.0026 0.9596
```

```
## age:Genotype 1  9.785   9.7847   5.1773 0.0321 *
```

```
## Residuals   24 45.358   1.8899
```

```
## ---
```

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

```
## Analysis of Variance Table
```

```
##
```

```
## Response: bckwds_max_length
```

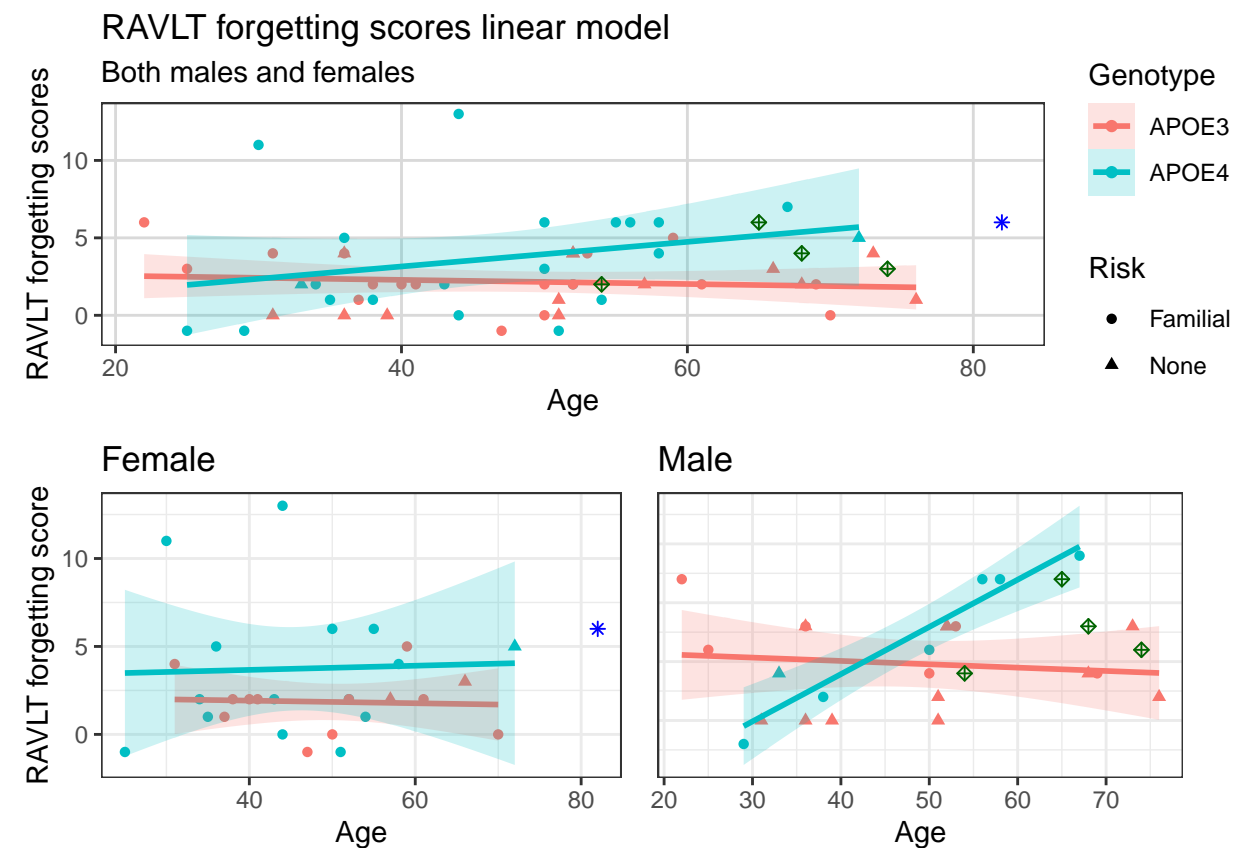
```
##           Df Sum Sq Mean Sq F value Pr(>F)
```

```
## age         1  0.217   0.21702   0.1200 0.7326
```

```
## Genotype     1  0.174   0.17416   0.0963 0.7595
```

```
## age:Genotype 1  0.401   0.40058   0.2215 0.6430
```

```
## Residuals   20 36.167   1.80833
```



```
##
```

```
## Call:
```

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

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

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

##
## Call:
## lm(formula = RAVLT_FORGETTING ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.6569 -0.9842 -0.1236  1.4204  3.2152
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.09770   1.33835   2.315  0.03138 *
## age             -0.01422   0.02634  -0.540  0.59524
## GenotypeAPOE4    -9.15973   2.78788  -3.286  0.00370 **
## age:GenotypeAPOE4  0.21493   0.05636   3.813  0.00109 **
```

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

```
## Analysis of Variance Table
```

```
##
```

```
## Response: RAVLT_FORGETTING
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	1.77	1.7709	0.2387	0.62754
Genotype	1	29.21	29.2137	3.9383	0.05346 .
sex	1	0.64	0.6418	0.0865	0.77003
age:Genotype	1	18.29	18.2909	2.4658	0.12351
age:sex	1	10.23	10.2314	1.3793	0.24654
Genotype:sex	1	1.84	1.8400	0.2481	0.62093
age:Genotype:sex	1	18.30	18.2997	2.4670	0.12342
Residuals	44	326.38	7.4178		

```
## ---
```

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

```
## Analysis of Variance Table
```

```
##
```

```
## Response: RAVLT_FORGETTING
```

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

```
## Analysis of Variance Table
```

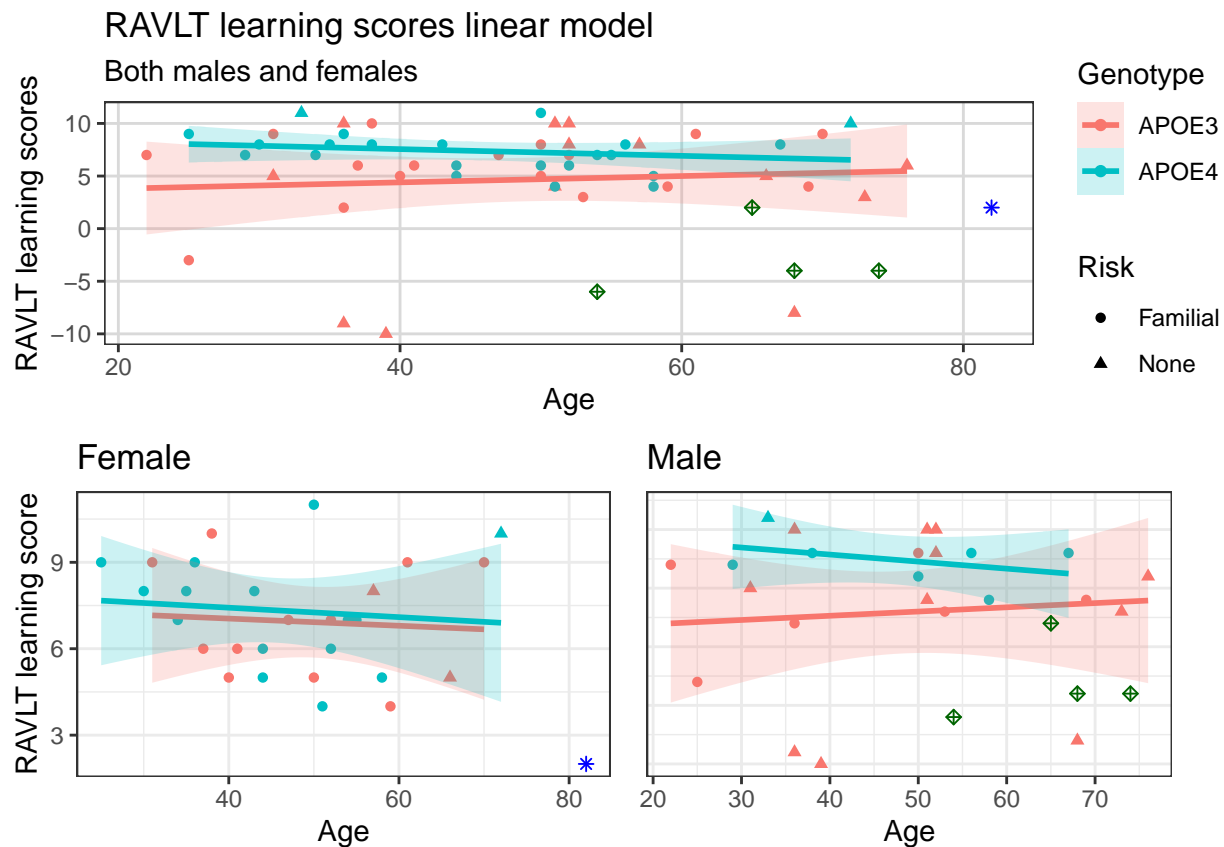
```
##
```

```
## Response: RAVLT_FORGETTING
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	5.625	5.625	1.8703	0.186616
Genotype	1	5.440	5.440	1.8087	0.193717
age:Genotype	1	43.738	43.738	14.5419	0.001088 **
Residuals	20	60.155	3.008		

```
## ---
```

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



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

	Min	1Q	Median	3Q	Max
	-12.6083	-1.4009	0.0717	2.0973	7.4998

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	7.544032	5.234726	1.441	0.157
age	-0.012438	0.102097	-0.122	0.904
GenotypeAPOE4	0.534668	6.837307	0.078	0.938
sexMale	-6.341253	6.198419	-1.023	0.312
age:GenotypeAPOE4	-0.003931	0.138420	-0.028	0.977
age:sexMale	0.048478	0.121209	0.400	0.691
GenotypeAPOE4:sexMale	8.534958	9.724082	0.878	0.385
age:GenotypeAPOE4:sexMale	-0.092250	0.196724	-0.469	0.641

```
##
## Residual standard error: 4.301 on 44 degrees of freedom
## (1 observation deleted due to missingness)
## Multiple R-squared: 0.2128, Adjusted R-squared: 0.08753
## F-statistic: 1.699 on 7 and 44 DF, p-value: 0.1342
##
```

```

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

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

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

```

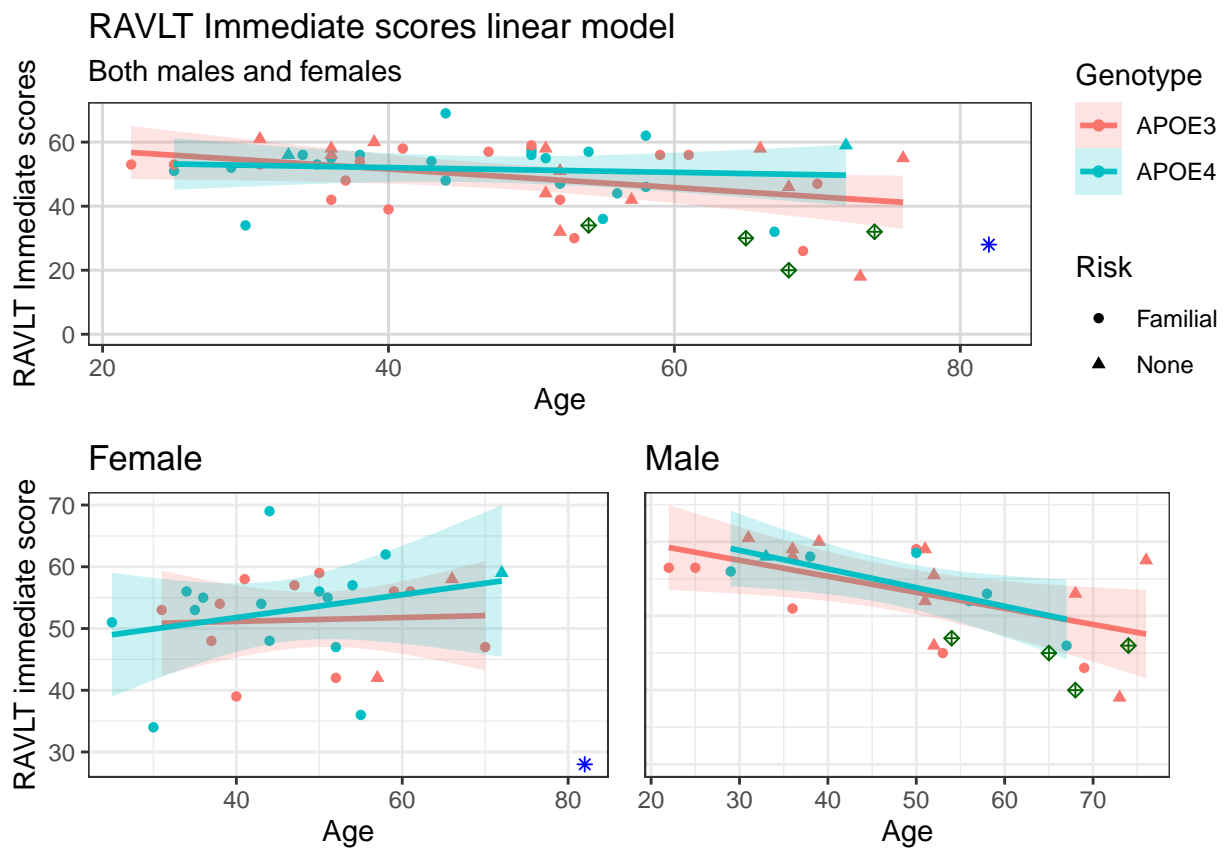


```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

## Analysis of Variance Table
##
## Response: RAVLT_FORGETTING
##           Df Sum Sq Mean Sq F value  Pr(>F)
## age        1  5.625   5.625   1.8703 0.186616
## Genotype    1  5.440   5.440   1.8087 0.193717
## age:Genotype 1 43.738  43.738  14.5419 0.001088 **
## Residuals   20 60.155   3.008

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



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

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

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

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

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

Analysis of Variance Table

##

Response: RAVLT_IMMEDIATE

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	463.8	463.75	5.3497	0.02546 *
Genotype	1	49.2	49.21	0.5676	0.45521
sex	1	214.3	214.30	2.4721	0.12304
age:Genotype	1	117.6	117.59	1.3565	0.25043
age:sex	1	615.0	614.99	7.0944	0.01076 *
Genotype:sex	1	0.4	0.39	0.0045	0.94705
age:Genotype:sex	1	24.1	24.08	0.2778	0.60077
Residuals	44	3814.2	86.69		

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

Analysis of Variance Table

##

Response: RAVLT_IMMEDIATE

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	41.16	41.165	0.6005	0.4459
Genotype	1	22.89	22.885	0.3339	0.5688
age:Genotype	1	22.94	22.942	0.3347	0.5683
Residuals	24	1645.11	68.546		

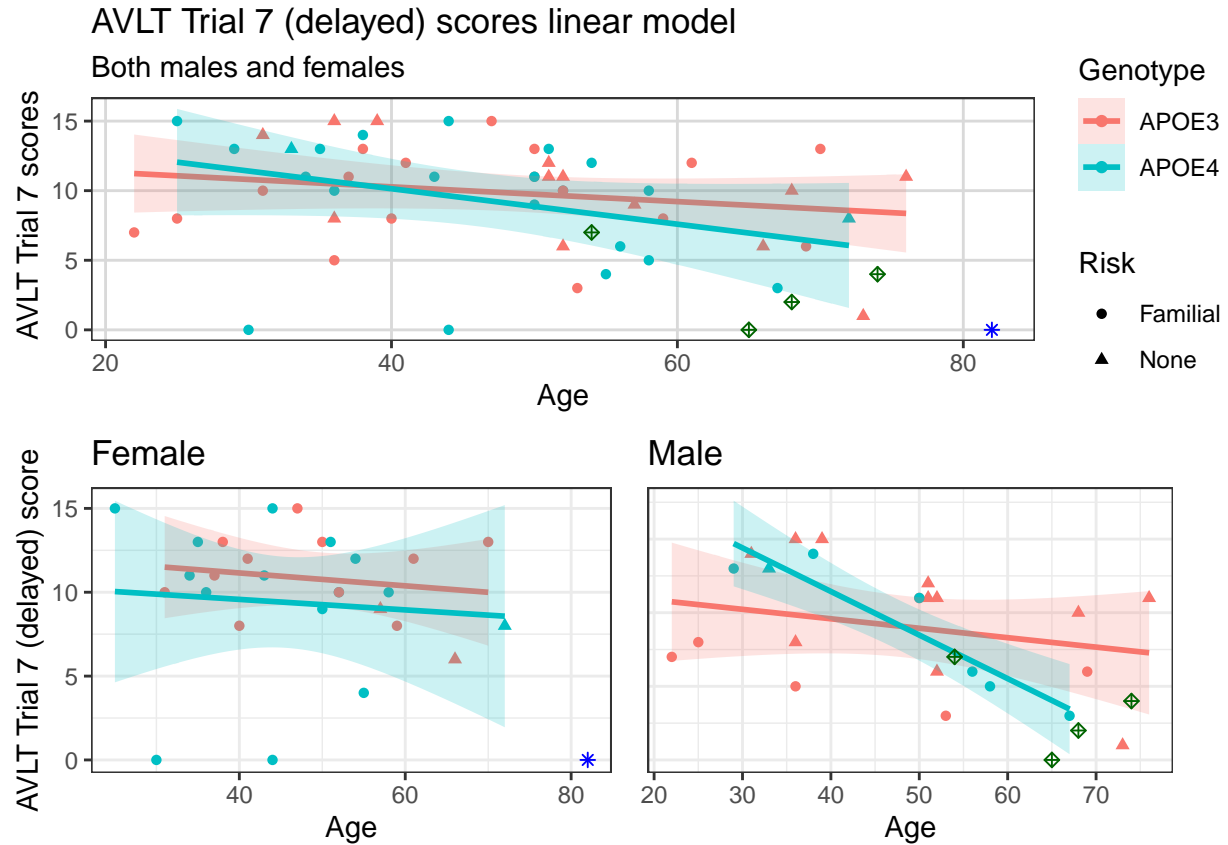
Analysis of Variance Table

##

Response: RAVLT_FORGETTING

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	5.625	5.625	1.8703	0.186616
Genotype	1	5.440	5.440	1.8087	0.193717
age:Genotype	1	43.738	43.738	14.5419	0.001088 **
Residuals	20	60.155	3.008		

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



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

```
##
## Call:
## lm(formula = AVL_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 = AVL_Trial7 ~ age * Genotype, data = combo_m)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-6.4694	-2.0206	-0.4823	2.2867	5.3484

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	12.15469	2.78444	4.365	0.0003 ***
age	-0.06418	0.05480	-1.171	0.2553
GenotypeAPOE4	11.12715	5.80017	1.918	0.0694 .
age:GenotypeAPOE4	-0.23181	0.11726	-1.977	0.0620 .

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.608 on 20 degrees of freedom
## (1 observation deleted due to missingness)
## Multiple R-squared:  0.323,    Adjusted R-squared:  0.2215
## F-statistic: 3.181 on 3 and 20 DF,  p-value: 0.04627

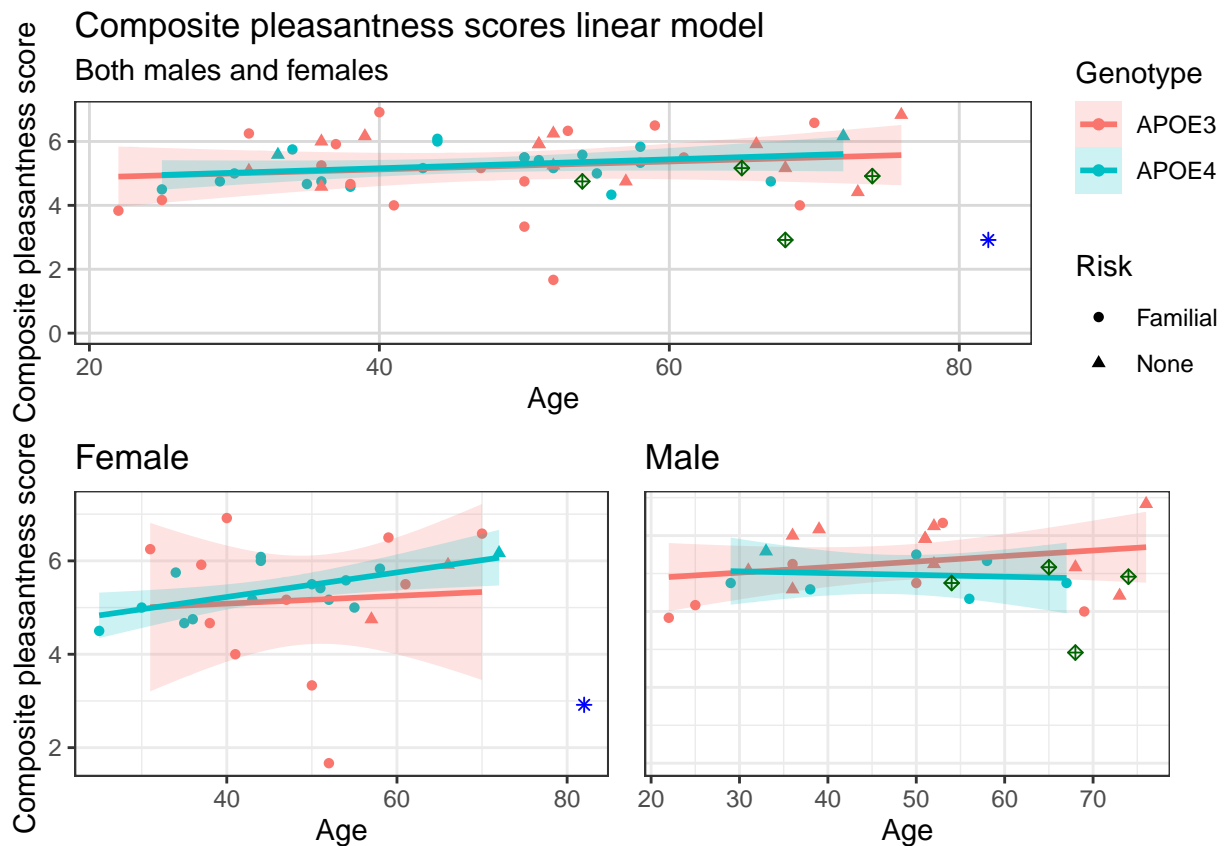
## Analysis of Variance Table
##
## Response: AVL_Trial7
```

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

```
## Residuals      44 643.59  14.627
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Analysis of Variance Table
##
## Response: AVL_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: AVL_Trial7
##           Df Sum Sq Mean Sq F value Pr(>F)
## age        1  73.300   73.300   5.6303 0.02779 *
## Genotype    1   0.069    0.069   0.0053 0.94276
## age:Genotype 1  50.878   50.878   3.9080 0.06201 .
## Residuals  20 260.378   13.019
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
##
```

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

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

##
## Call:
## lm(formula = Composite_Pleasantness ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.59183 -0.53691 -0.02439  0.58716  1.13949
##
```

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

Analysis of Variance Table

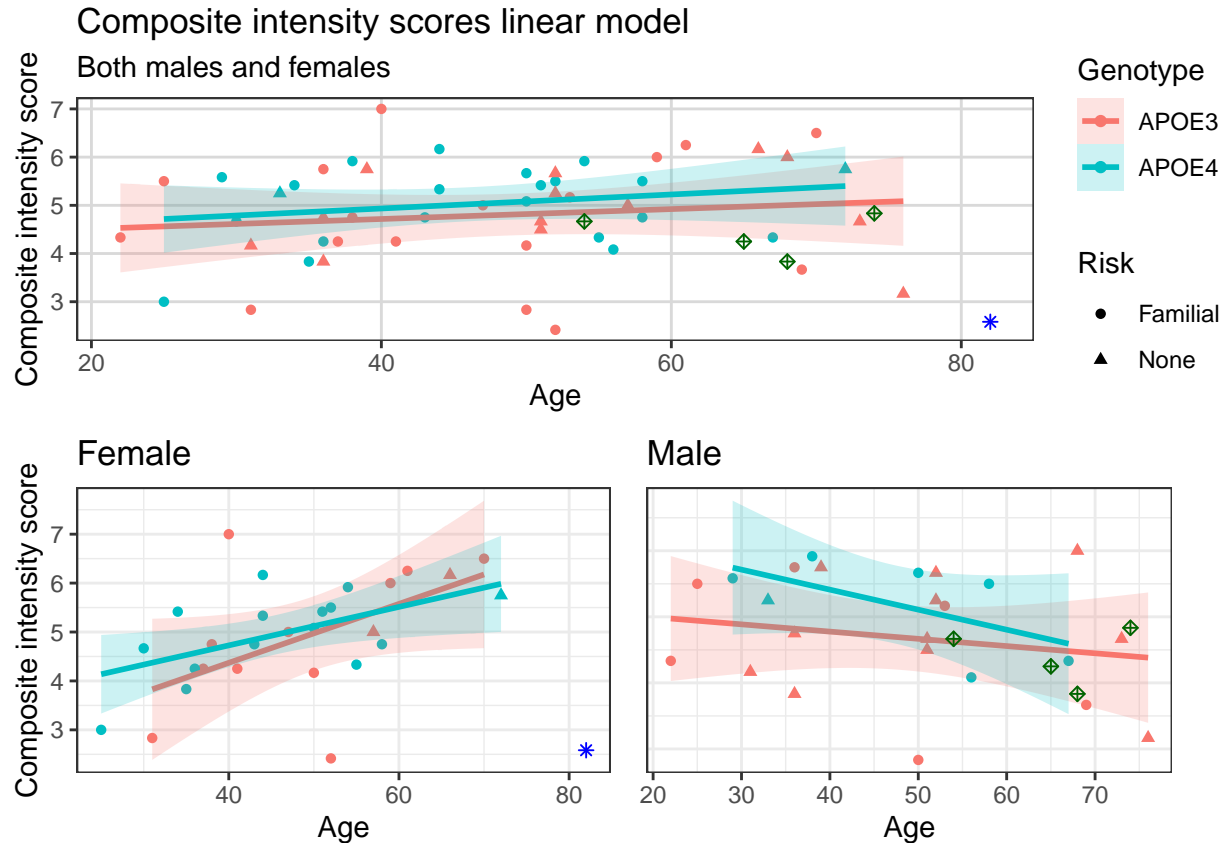
```
##
## Response: Composite_Pleasantness
##              Df Sum Sq Mean Sq F value Pr(>F)
## age            1  1.572  1.57179   1.6224 0.2094
## Genotype        1  0.028  0.02827   0.0292 0.8651
## sex             1  0.072  0.07195   0.0743 0.7865
## age:Genotype    1  0.007  0.00739   0.0076 0.9308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

Analysis of Variance Table

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

Analysis of Variance Table

```
##
## Response: Composite_Pleasantness
##              Df Sum Sq Mean Sq F value Pr(>F)
## age            1  0.6260  0.62599   0.9202 0.3489
## Genotype        1  0.4554  0.45541   0.6694 0.4229
## age:Genotype    1  0.3520  0.35198   0.5174 0.4803
## Residuals      20 13.6057  0.68028
```

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

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

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

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

```
## Residuals      44 39.176  0.8904
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: Composite_Intensity
```

```
##          Df Sum Sq Mean Sq F value    Pr(>F)
## age         1  9.0481   9.0481   9.1488 0.005852 **
## Genotype     1  0.2454   0.2454   0.2482 0.622896
## age:Genotype 1  0.4216   0.4216   0.4263 0.520021
## Residuals   24 23.7360   0.9890
```

```
## ---
```

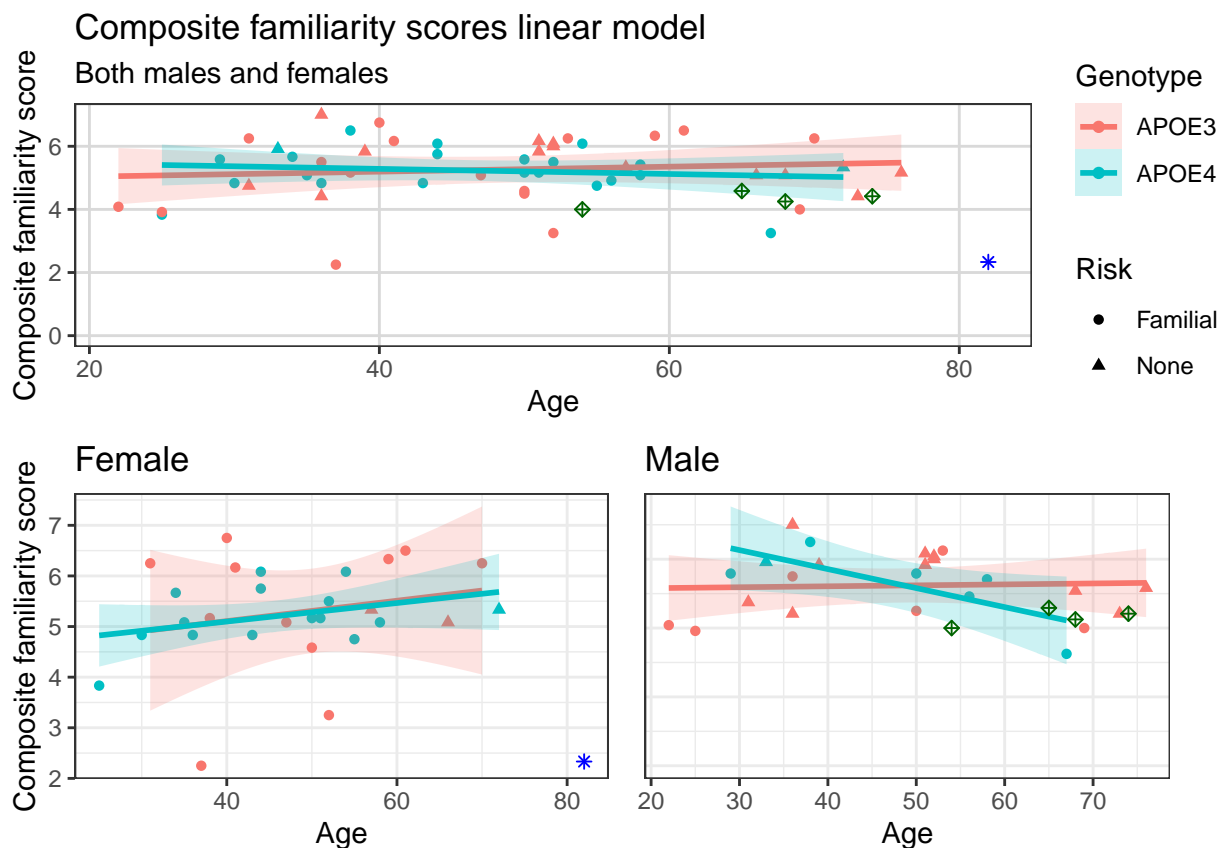
```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: Composite_Intensity
```

```
##          Df Sum Sq Mean Sq F value    Pr(>F)
## age         1  1.3505   1.35052   1.7494 0.2009
## Genotype     1  1.1885   1.18849   1.5395 0.2290
## age:Genotype 1  0.3545   0.35454   0.4593 0.5057
## Residuals   20 15.4398   0.77199
```



```
##
```

```

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

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

##
## Call:
## lm(formula = Composite_Familiarity ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.29226 -0.75137 -0.02832  0.68308  1.79827
##

```

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

Analysis of Variance Table

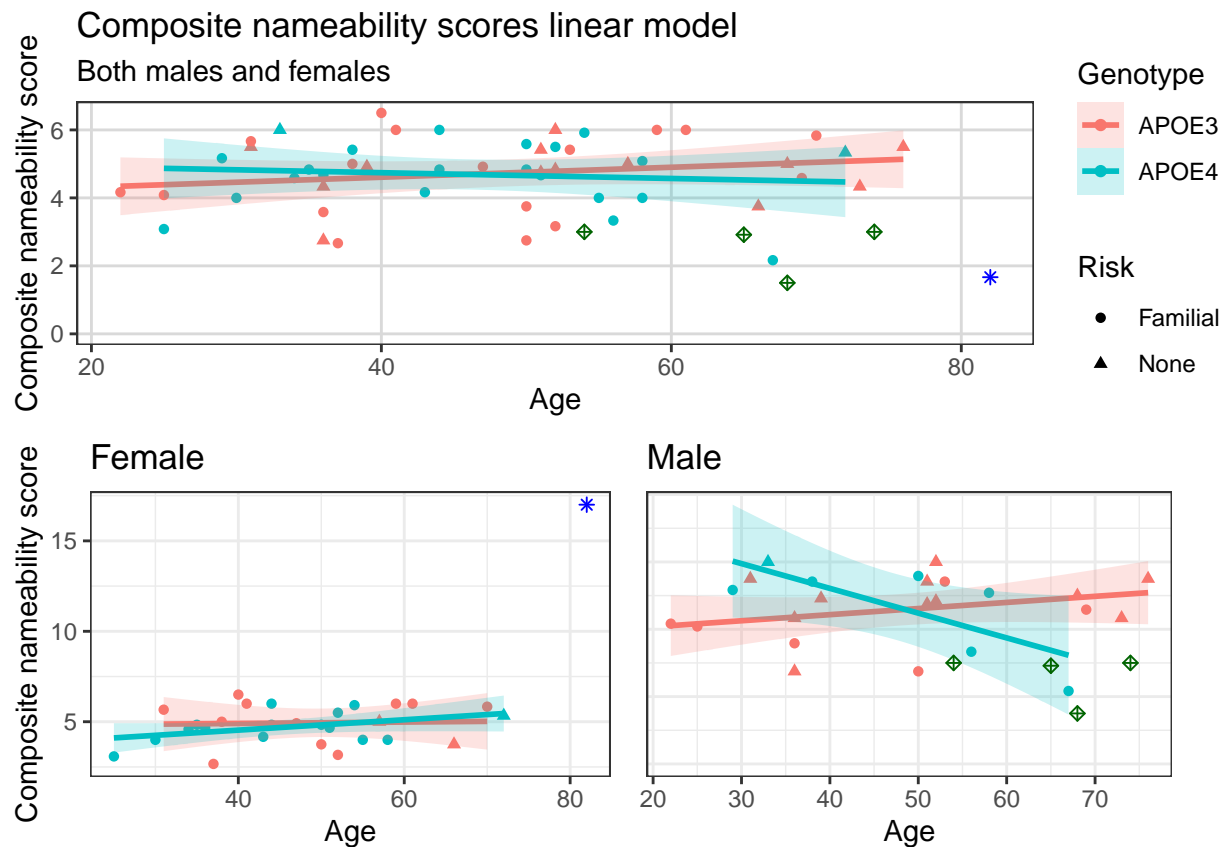
```
##
## Response: Composite_Familiarity
##               Df Sum Sq Mean Sq F value  Pr(>F)
## age            1  0.053  0.05265   0.0565 0.81325
## Genotype       1  0.008  0.00807   0.0087 0.92629
## sex            1  0.000  0.00000   0.0000 0.99966
## age:Genotype   1  0.560  0.55965   0.6003 0.44259
## age:sex        1  3.118  3.11827   3.3450 0.07419 .
## Genotype:sex   1  0.016  0.01642   0.0176 0.89503
## age:Genotype:sex 1  1.505  1.50482   1.6142 0.21057
## Residuals     44 41.017  0.93221
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Analysis of Variance Table

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

Analysis of Variance Table

```
##
## Response: Composite_Familiarity
##               Df Sum Sq Mean Sq F value  Pr(>F)
## age            1  0.5514  0.5514   0.6702 0.42263
## Genotype       1  0.0208  0.0208   0.0253 0.87522
## age:Genotype   1  3.1788  3.1788   3.8633 0.06339 .
## Residuals     20 16.4562  0.8228
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



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

```
##
## Call:
## lm(formula = Composite_Nameability ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.22570 -0.58284  0.06706  0.80147  1.59604
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    4.749386    1.246082   3.811 0.000847 ***
## age             0.003864    0.024303   0.159 0.874994
## GenotypeAPOE4   -1.361723    1.627562  -0.837 0.411035
## age:GenotypeAPOE4 0.024835    0.032950   0.754 0.458345
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.024 on 24 degrees of freedom
## Multiple R-squared:  0.08036, Adjusted R-squared:  -0.03459
## F-statistic: 0.6991 on 3 and 24 DF, p-value: 0.5618

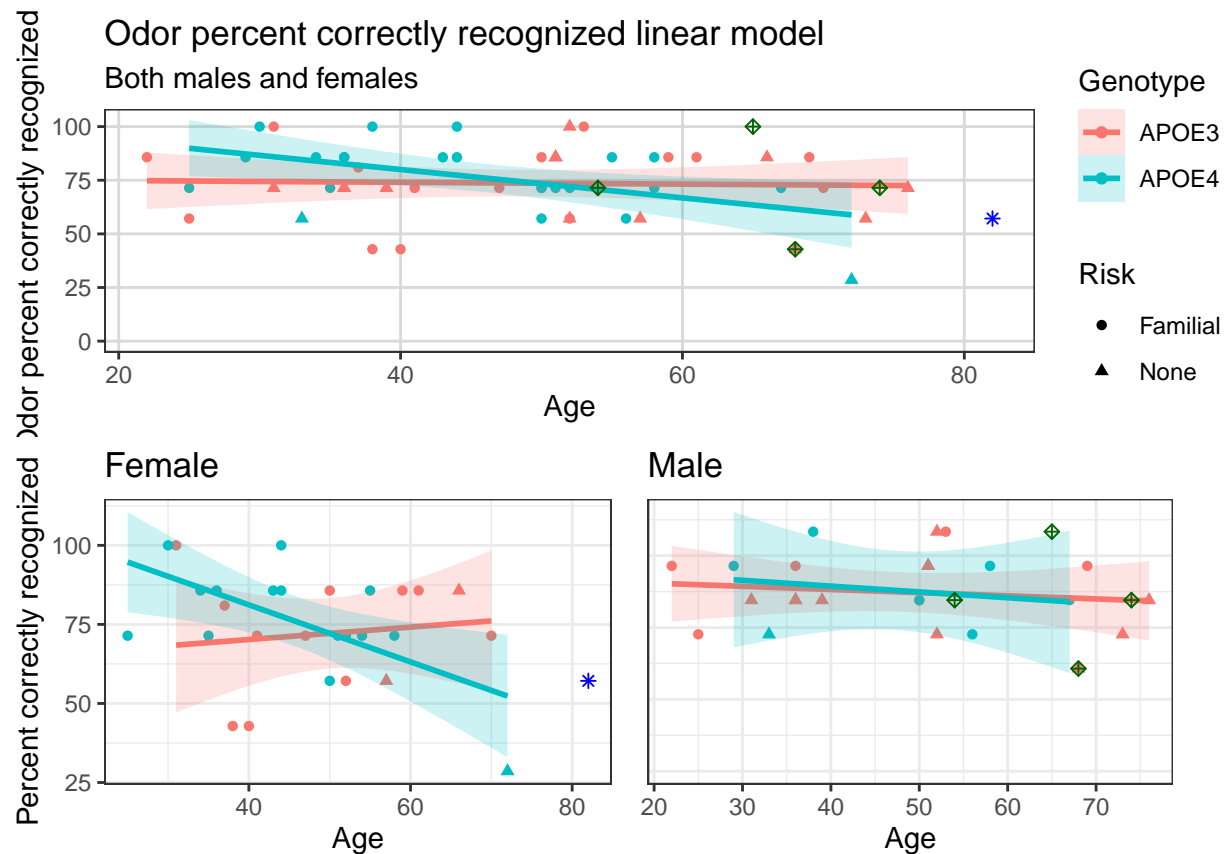
##
## Call:
## lm(formula = Composite_Nameability ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.86536 -0.70061  0.05871  0.56241  1.34835
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    3.70803    0.71920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

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

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

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

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



```
##
```



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

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

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

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

Analysis of Variance Table

##

Response: Recognized

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	678.1	678.14	2.5767	0.11560
Genotype	1	31.2	31.15	0.1184	0.73244
sex	1	18.7	18.69	0.0710	0.79113
age:Genotype	1	847.5	847.47	3.2201	0.07961 .
age:sex	1	6.1	6.09	0.0231	0.87982
Genotype:sex	1	10.9	10.93	0.0415	0.83944
age:Genotype:sex	1	465.7	465.70	1.7695	0.19030
Residuals	44	11580.0	263.18		

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

Analysis of Variance Table

##

Response: Recognized

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	704.5	704.53	2.6751	0.1150
Genotype	1	34.7	34.65	0.1316	0.7200
age:Genotype	1	1164.0	1164.04	4.4198	0.0462 *
Residuals	24	6320.8	263.37		

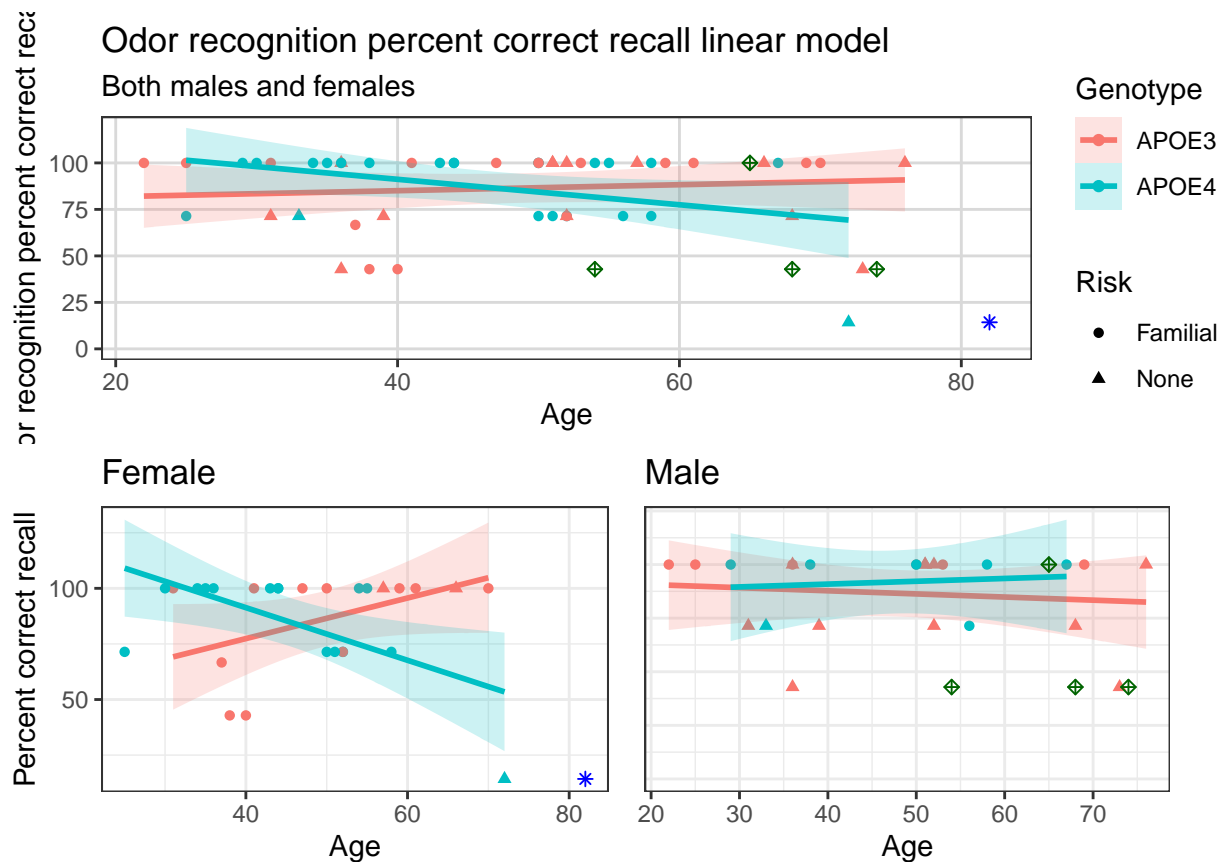
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Analysis of Variance Table

##

Response: Recognized

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	135.7	135.684	0.5160	0.4809
Genotype	1	1.6	1.623	0.0062	0.9382
age:Genotype	1	11.7	11.659	0.0443	0.8354
Residuals	20	5259.2	262.960		



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

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

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

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

```
## Residuals      44 17346.3  394.23
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: PrecentCorrectRecall
```

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## age         1   173.3    173.3   0.4346 0.516024
## Genotype     1    48.5     48.5   0.1217 0.730219
## age:Genotype  1 4243.2   4243.2 10.6406 0.003304 **
## Residuals   24  9570.5     398.8
## ---
```

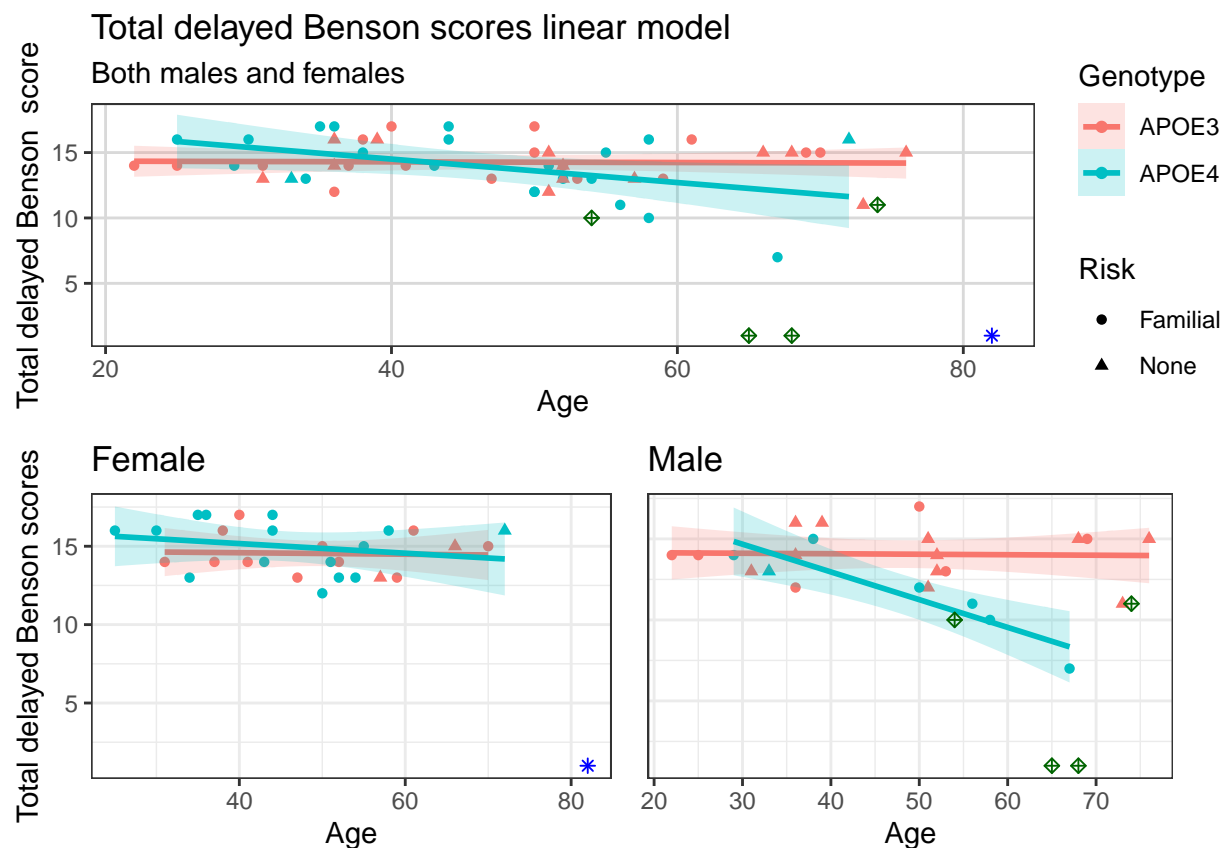
```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: PrecentCorrectRecall
```

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



```
##
```

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

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

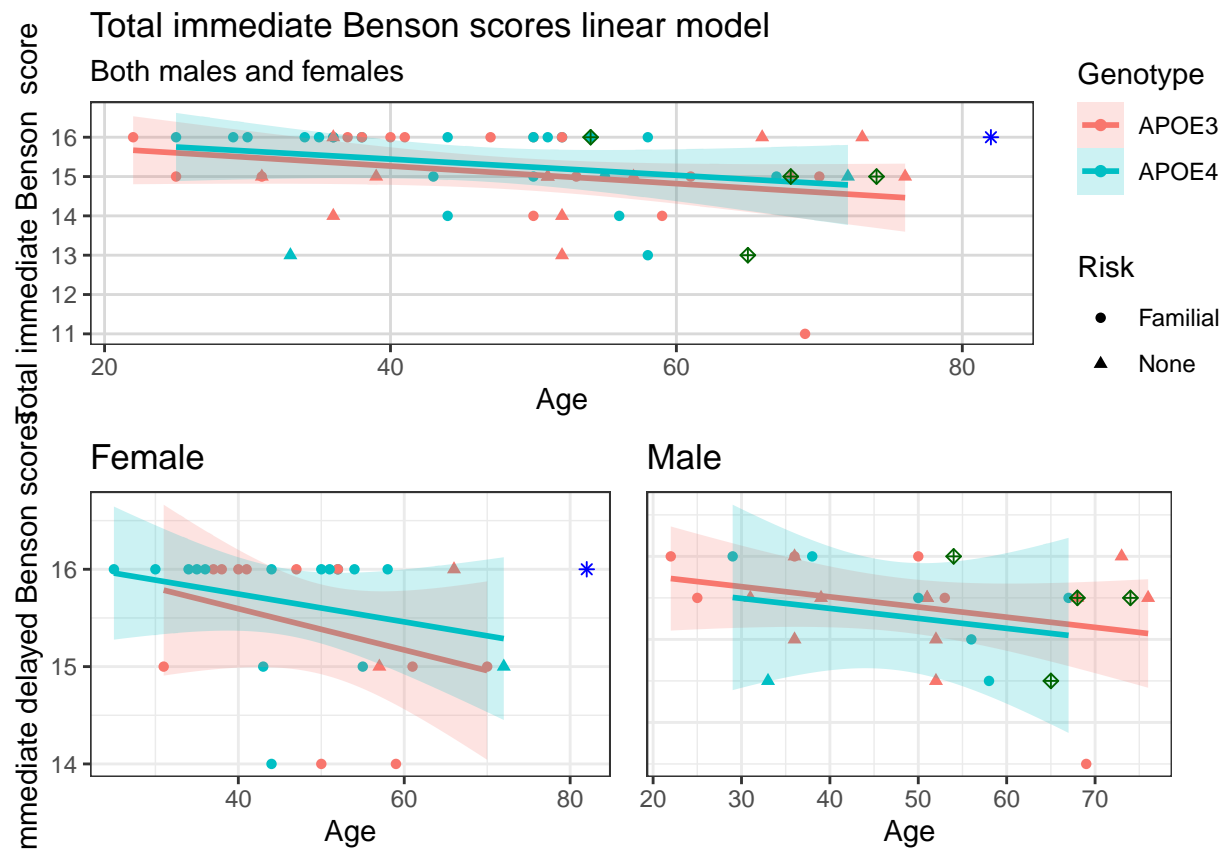
##
## Call:
## lm(formula = Delay_BensonTotal ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.98321 -1.06336 -0.07175  1.00228  2.94656
##
```

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

```
## Analysis of Variance Table
##
## Response: Delay_BensonTotal
##               Df Sum Sq Mean Sq F value    Pr(>F)
## age             1   9.663   9.6629   4.0107 0.0513972 .
## Genotype         1   2.089   2.0889   0.8670 0.3568619
## sex             1  30.850  30.8504  12.8049 0.0008564 ***
## age:Genotype     1  13.865  13.8652   5.7550 0.0207457 *
## age:sex          1   3.504   3.5036   1.4542 0.2342973
## Genotype:sex     1  22.406  22.4059   9.2999 0.0038718 **
## age:Genotype:sex 1   9.673   9.6734   4.0151 0.0512763 .
## Residuals       44 106.007   2.4093
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## Analysis of Variance Table
##
## Response: Delay_BensonTotal
##               Df Sum Sq Mean Sq F value    Pr(>F)
## age             1   7.916   7.9162   3.2436 0.086804 .
## Genotype         1  28.118  28.1180  11.5209 0.002879 **
## age:Genotype     1  26.779  26.7787  10.9721 0.003476 **
## Residuals       20  48.812   2.4406
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



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



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

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

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

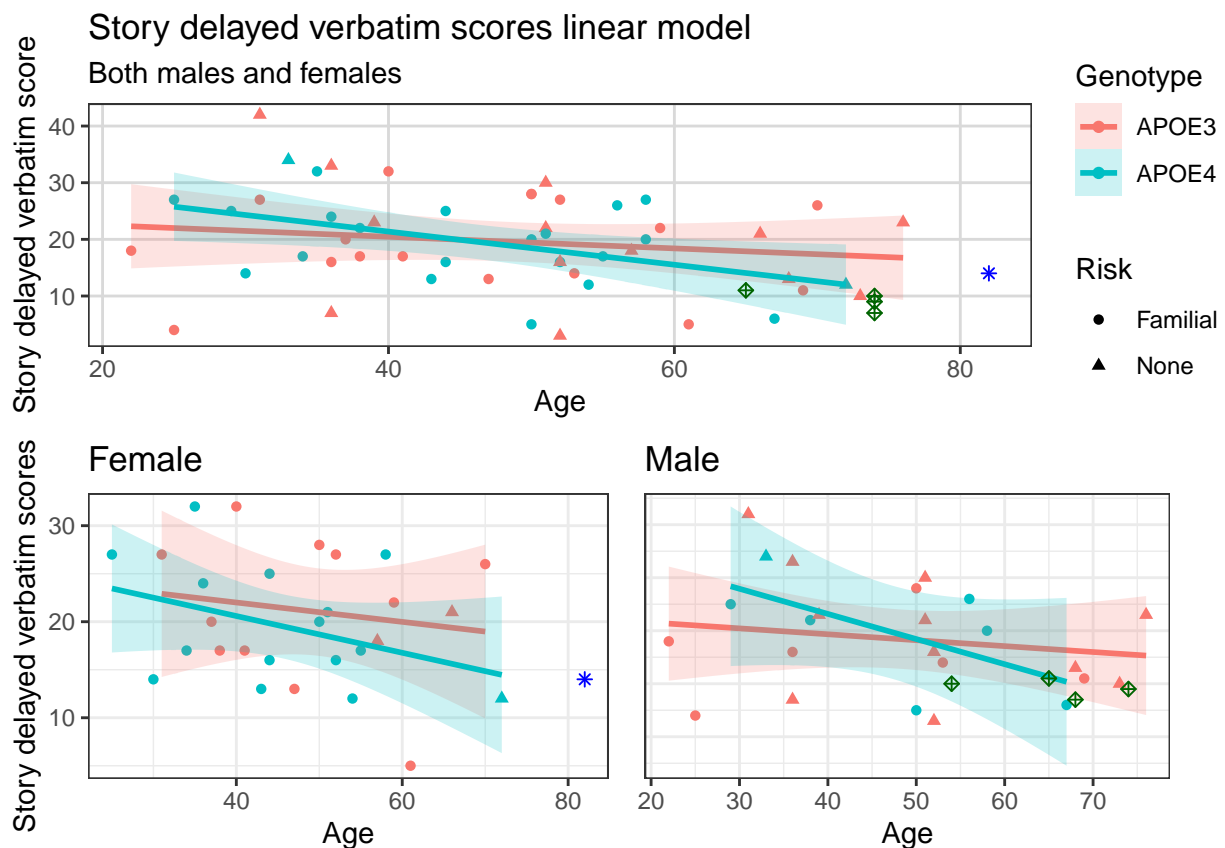
```
## Residuals      44 44.056  1.0013
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Analysis of Variance Table
##
```

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

```
## Analysis of Variance Table
##
```

```
## Response: Im_BensonTotal
##           Df Sum Sq Mean Sq F value Pr(>F)
## age        1   3.247   3.2468   1.9751 0.1753
## Genotype    1   0.375   0.3755   0.2284 0.6379
## age:Genotype 1   0.000   0.0002   0.0001 0.9912
## Residuals   20 32.878   1.6439
```



```
##
```

```

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

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

##
## Call:
## lm(formula = Delayed_verbatim ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -17.004  -4.548  -2.662   7.555  21.665
##

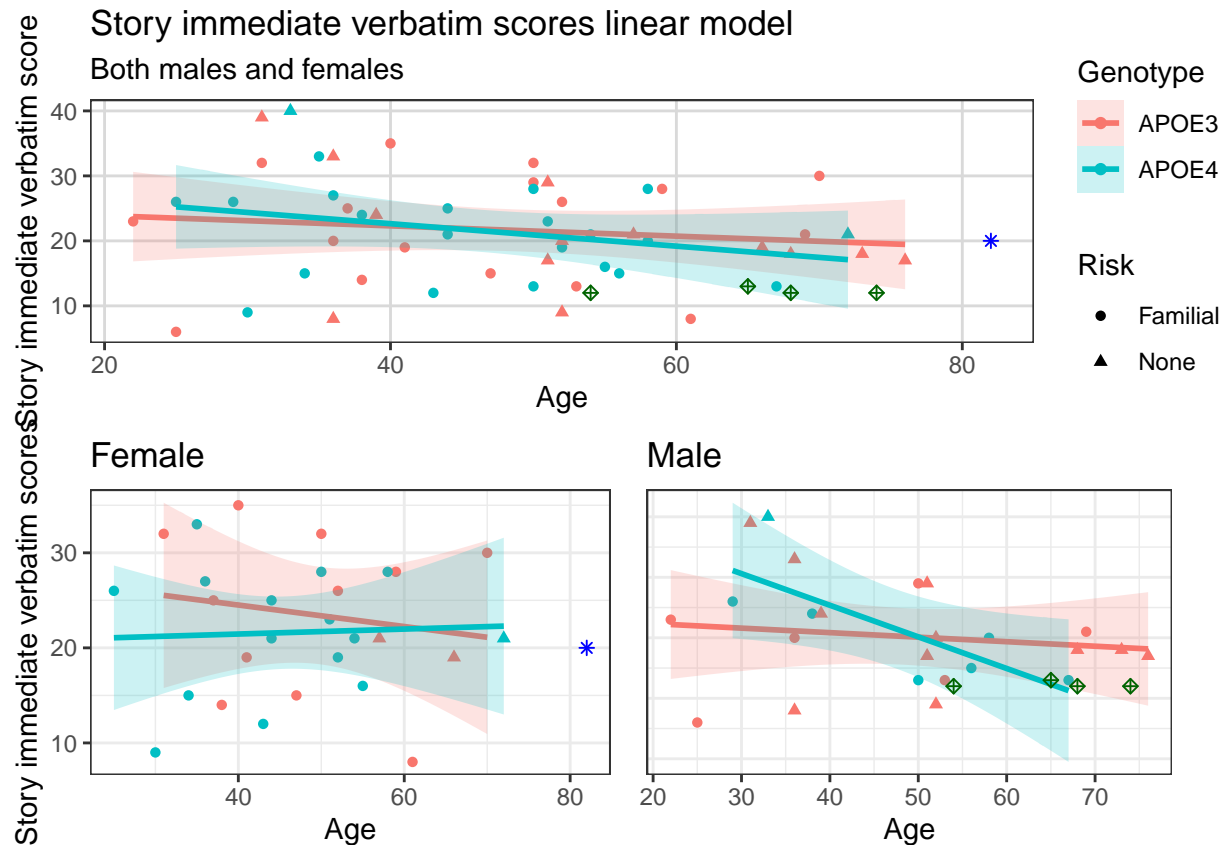
```

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

```
## Analysis of Variance Table
##
## Response: Delayed_verbatim
##               Df Sum Sq Mean Sq F value  Pr(>F)
## age             1  270.8  270.833   3.6719 0.06185 .
## Genotype         1    2.3    2.328   0.0316 0.85979
## sex              1   29.4   29.411   0.3988 0.53100
## age:Genotype     1   72.4   72.450   0.9823 0.32706
## age:sex          1   32.8   32.758   0.4441 0.50861
## Genotype:sex     1   28.3   28.319   0.3839 0.53869
## age:Genotype:sex 1   35.4   35.393   0.4798 0.49213
## Residuals       44 3245.3   73.758
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## Analysis of Variance Table
##
## Response: Delayed_verbatim
##               Df Sum Sq Mean Sq F value Pr(>F)
## age             1  204.03  204.03   1.8828 0.1852
## Genotype         1    6.23    6.23   0.0575 0.8129
## age:Genotype     1  124.49  124.49   1.1489 0.2965
## Residuals       20 2167.21  108.36
```



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

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

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

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

```
## Residuals      44 2836.22  64.460
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: Immediate_verbatim
```

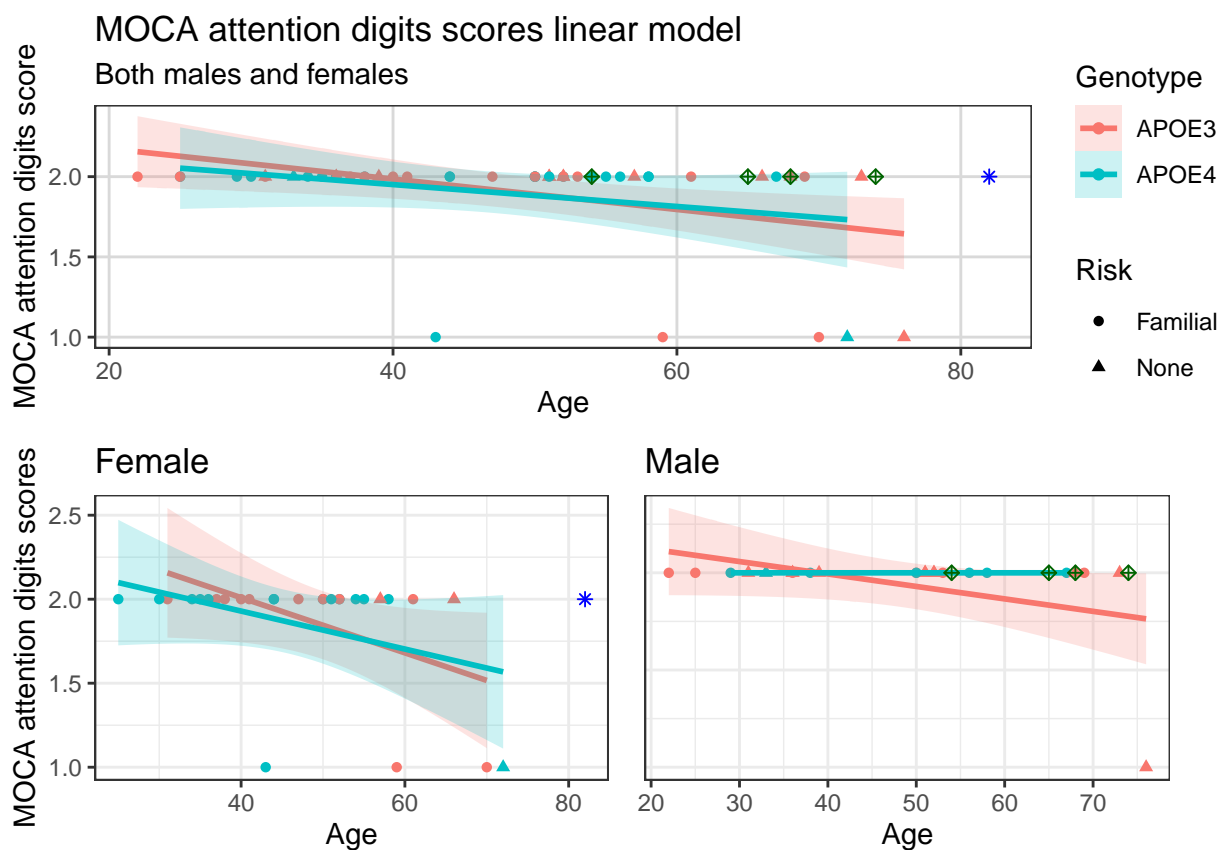
```
##          Df Sum Sq Mean Sq F value Pr(>F)
## age       1    2.05   2.050    0.0356 0.8519
## Genotype   1   25.56  25.562    0.4444 0.5114
## age:Genotype 1   18.68  18.682    0.3248 0.5741
## Residuals 24 1380.56   57.523
```

```
## Analysis of Variance Table
```

```
##
```

```
## Response: Immediate_verbatim
```

```
##          Df Sum Sq Mean Sq F value Pr(>F)
## age       1  167.19  167.195    2.2972 0.1453
## Genotype   1    6.81    6.808    0.0935 0.7629
## age:Genotype 1  189.96  189.962    2.6100 0.1219
## Residuals 20 1455.66   72.783
```



```
##
```

```
## Call:
```

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

```
##
```

```
## Residuals:
```

```

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

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

##
## Call:
## lm(formula = MOCA_Attention_Digits ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min      1Q   Median      3Q      Max
## -0.76335 -0.01954  0.00000  0.07813  0.21743
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.250109   0.150764  14.925 2.64e-12 ***
## age             -0.006405   0.002967  -2.158  0.0432 *

```



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

```
## Analysis of Variance Table
```

```
##
```

```
## Response: MOCA_Attention_Digits
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	0.6891	0.68912	8.8152	0.004821 **
Genotype	1	0.0030	0.00300	0.0384	0.845493
sex	1	0.1396	0.13958	1.7855	0.188343
age:Genotype	1	0.0102	0.01020	0.1304	0.719718
age:sex	1	0.2107	0.21067	2.6948	0.107804
Genotype:sex	1	0.0262	0.02624	0.3356	0.565333
age:Genotype:sex	1	0.0008	0.00078	0.0100	0.920680
Residuals	44	3.4396	0.07817		

```
## ---
```

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

```
## Analysis of Variance Table
```

```
##
```

```
## Response: MOCA_Attention_Digits
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	0.71650	0.71650	6.4253	0.01818 *
Genotype	1	0.01043	0.01043	0.0935	0.76241
age:Genotype	1	0.02535	0.02535	0.2274	0.63781
Residuals	24	2.67630	0.11151		

```
## ---
```

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

```
## Analysis of Variance Table
```

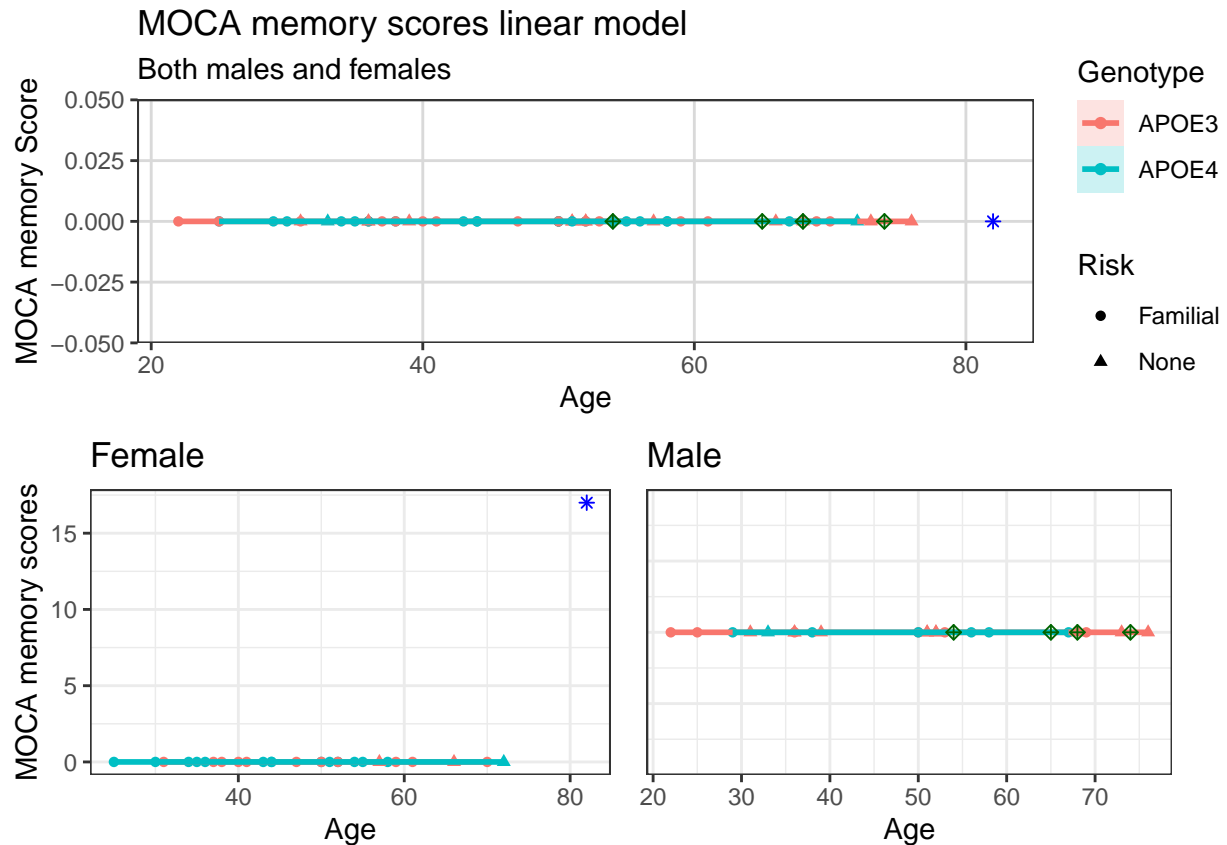
```
##
```

```
## Response: MOCA_Attention_Digits
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	0.14166	0.141658	3.7115	0.06837 .
Genotype	1	0.01448	0.014484	0.3795	0.54482
age:Genotype	1	0.03884	0.038839	1.0176	0.32514
Residuals	20	0.76335	0.038168		

```
## ---
```

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



```
##
## Call:
## lm(formula = MOCA_Memory ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
##       0        0         0        0        0
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)          0          0      NaN    NaN
## age                0          0      NaN    NaN
## GenotypeAPOE4        0          0      NaN    NaN
## sexMale             0          0      NaN    NaN
## age:GenotypeAPOE4    0          0      NaN    NaN
## age:sexMale          0          0      NaN    NaN
## GenotypeAPOE4:sexMale 0          0      NaN    NaN
## age:GenotypeAPOE4:sexMale 0        0      NaN    NaN
##
## Residual standard error: 0 on 44 degrees of freedom
## (1 observation deleted due to missingness)
## Multiple R-squared:  NaN, Adjusted R-squared:  NaN
## F-statistic:  NaN on 7 and 44 DF, p-value: NA
##
```

```
## Call:
## lm(formula = MOCA_Memory ~ age * Genotype, data = combo_f)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	0	0	0	0	0

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0	0	NaN	NaN
age	0	0	NaN	NaN
GenotypeAPOE4	0	0	NaN	NaN
age:GenotypeAPOE4	0	0	NaN	NaN

```
##
## Residual standard error: 0 on 24 degrees of freedom
## Multiple R-squared:  NaN, Adjusted R-squared:  NaN
## F-statistic:  NaN on 3 and 24 DF, p-value: NA
```

```
##
## Call:
## lm(formula = MOCA_Memory ~ age * Genotype, data = combo_m)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	0	0	0	0	0

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0	0	NaN	NaN
age	0	0	NaN	NaN
GenotypeAPOE4	0	0	NaN	NaN
age:GenotypeAPOE4	0	0	NaN	NaN

```
##
## Residual standard error: 0 on 20 degrees of freedom
## (1 observation deleted due to missingness)
## Multiple R-squared:  NaN, Adjusted R-squared:  NaN
## F-statistic:  NaN on 3 and 20 DF, p-value: NA
```

```
## Analysis of Variance Table
##
## Response: MOCA_Memory
```

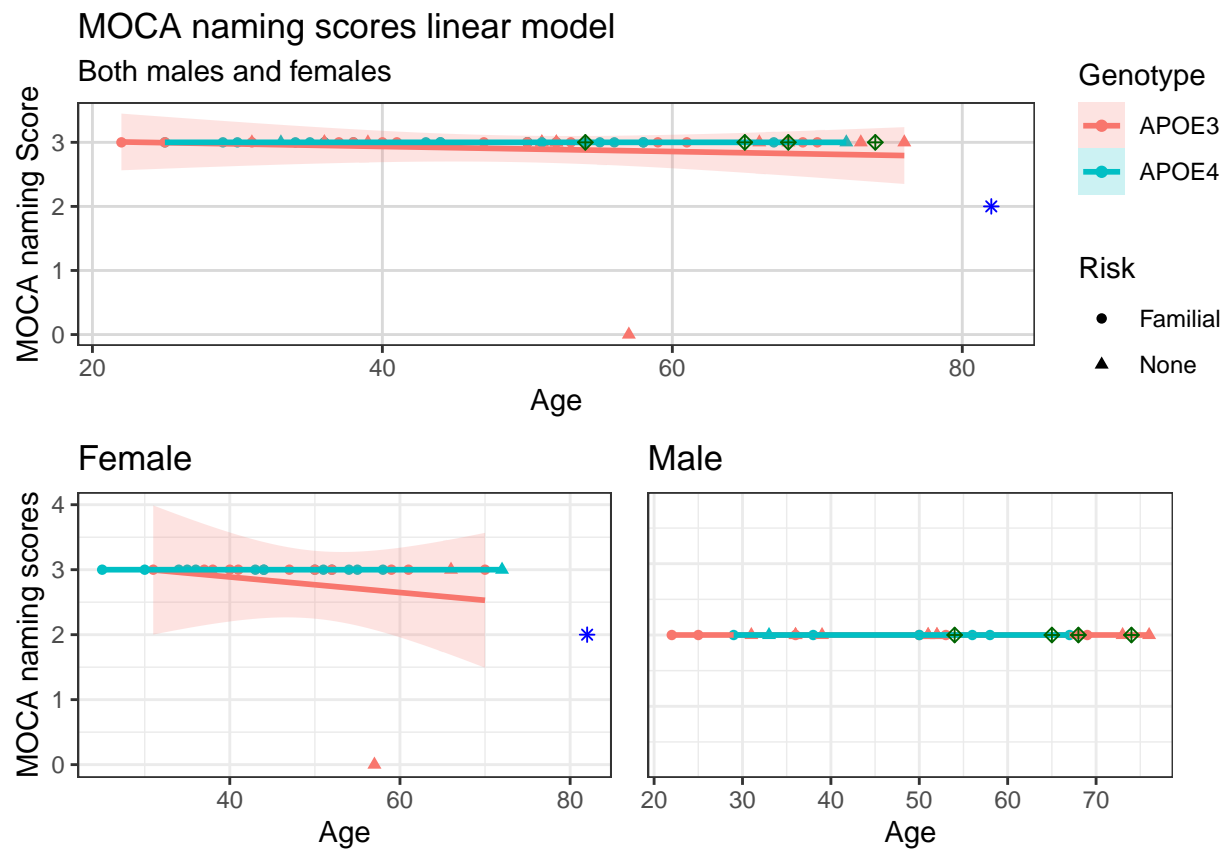
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	0	0	NaN	NaN
Genotype	1	0	0	NaN	NaN
sex	1	0	0	NaN	NaN
age:Genotype	1	0	0	NaN	NaN
age:sex	1	0	0	NaN	NaN
Genotype:sex	1	0	0	NaN	NaN
age:Genotype:sex	1	0	0	NaN	NaN
Residuals	44	0	0		

```
## Analysis of Variance Table
##
```

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

```
## Analysis of Variance Table
```

```
##
## Response: MOCA_Memory
##           Df Sum Sq Mean Sq F value Pr(>F)
## age       1     0      0      NaN   NaN
## Genotype   1     0      0      NaN   NaN
## age:Genotype 1     0      0      NaN   NaN
## Residuals 20     0      0
```



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

```

##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.36639    0.52067   6.465 6.97e-08 ***
## age              -0.01196    0.01016  -1.178   0.245
## GenotypeAPOE4     -0.36639    0.68007  -0.539   0.593
## sexMale           -0.36639    0.61653  -0.594   0.555
## age:GenotypeAPOE4  0.01196    0.01377   0.869   0.390
## age:sexMale        0.01196    0.01206   0.992   0.327
## GenotypeAPOE4:sexMale 0.36639    0.96721   0.379   0.707
## age:GenotypeAPOE4:sexMale -0.01196    0.01957  -0.611   0.544
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4278 on 44 degrees of freedom
## (1 observation deleted due to missingness)
## Multiple R-squared:  0.08759, Adjusted R-squared:  -0.05756
## F-statistic: 0.6034 on 7 and 44 DF, p-value: 0.7497

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

##
## Call:
## lm(formula = MOCA_Naming ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.339e-16 -1.410e-16 -3.262e-17  0.000e+00  1.702e-15
##
## Coefficients:
##               Estimate Std. Error    t value Pr(>|t|)
## (Intercept)      3.000e+00  3.321e-16  9.034e+15  <2e-16 ***
## age              -1.317e-17  6.535e-18 -2.015e+00   0.0576 .
## GenotypeAPOE4     -7.631e-16  6.917e-16 -1.103e+00   0.2831
## age:GenotypeAPOE4  1.317e-17  1.398e-17  9.420e-01   0.3577
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

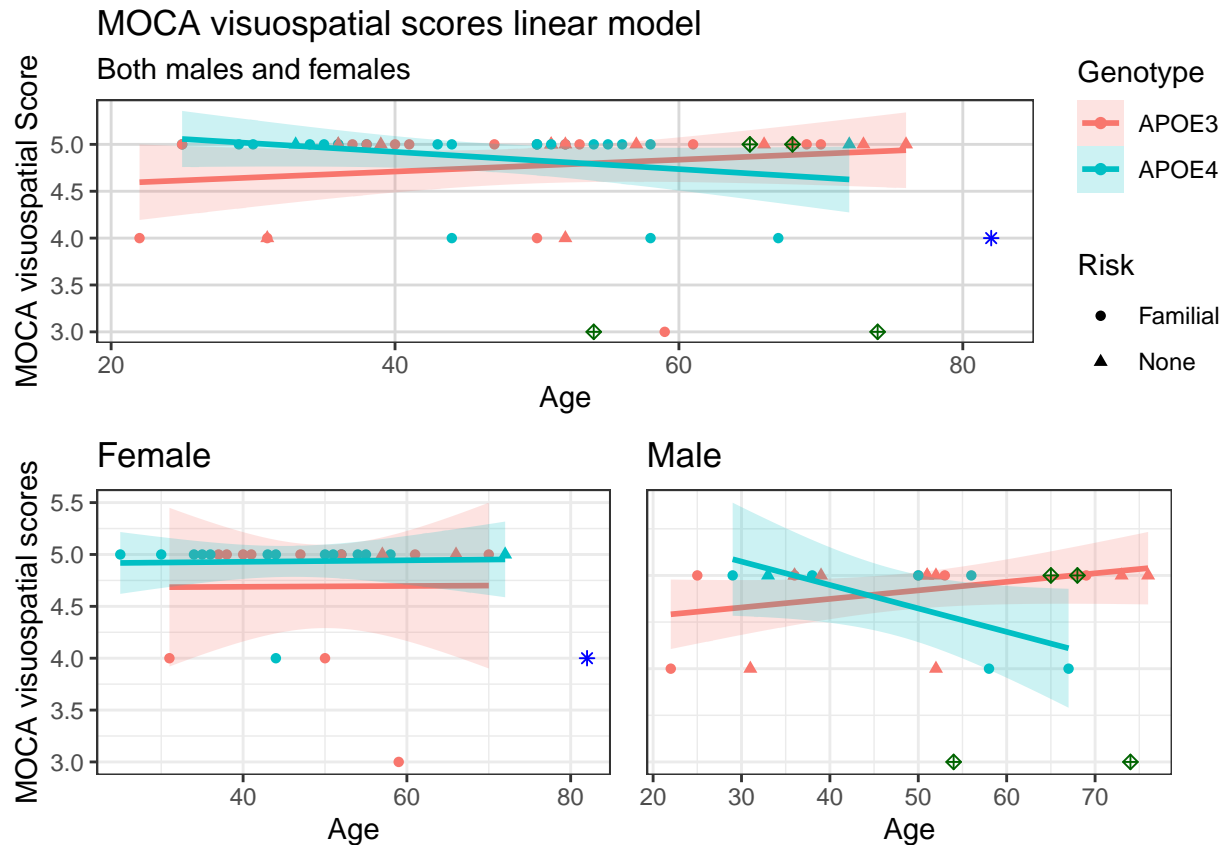
##
## Residual standard error: 4.303e-16 on 20 degrees of freedom
## (1 observation deleted due to missingness)
## Multiple R-squared: 0.5505, Adjusted R-squared: 0.4831
## F-statistic: 8.166 on 3 and 20 DF, p-value: 0.000957

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

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

## Analysis of Variance Table
##
## Response: MOCA_Naming
##      Df Sum Sq Mean Sq F value Pr(>F)
## age      1 5.7460e-31 5.7456e-31  3.1030 0.09343 .
## Genotype  1 9.4000e-32 9.4010e-32  0.5077 0.48437
## age:Genotype  1 1.6410e-31 1.6414e-31  0.8865 0.35767
## Residuals    20 3.7032e-30 1.8516e-31
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```



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

	Min	1Q	Median	3Q	Max
	-1.69585	-0.02288	0.07393	0.29137	0.50460

```
##
## Coefficients:
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	4.672835	0.534034	8.750	3.47e-11 ***
age	0.000390	0.010416	0.037	0.9703
GenotypeAPOE4	0.227530	0.697525	0.326	0.7458
sexMale	-0.291105	0.632347	-0.460	0.6475
age:GenotypeAPOE4	0.000334	0.014121	0.024	0.9812
age:sexMale	0.008769	0.012365	0.709	0.4820
GenotypeAPOE4:sexMale	1.292744	0.992027	1.303	0.1993
age:GenotypeAPOE4:sexMale	-0.034611	0.020069	-1.725	0.0916 .

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4388 on 44 degrees of freedom
## (1 observation deleted due to missingness)
## Multiple R-squared:  0.1592, Adjusted R-squared:  0.02547
## F-statistic: 1.19 on 7 and 44 DF, p-value: 0.3281
```

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

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

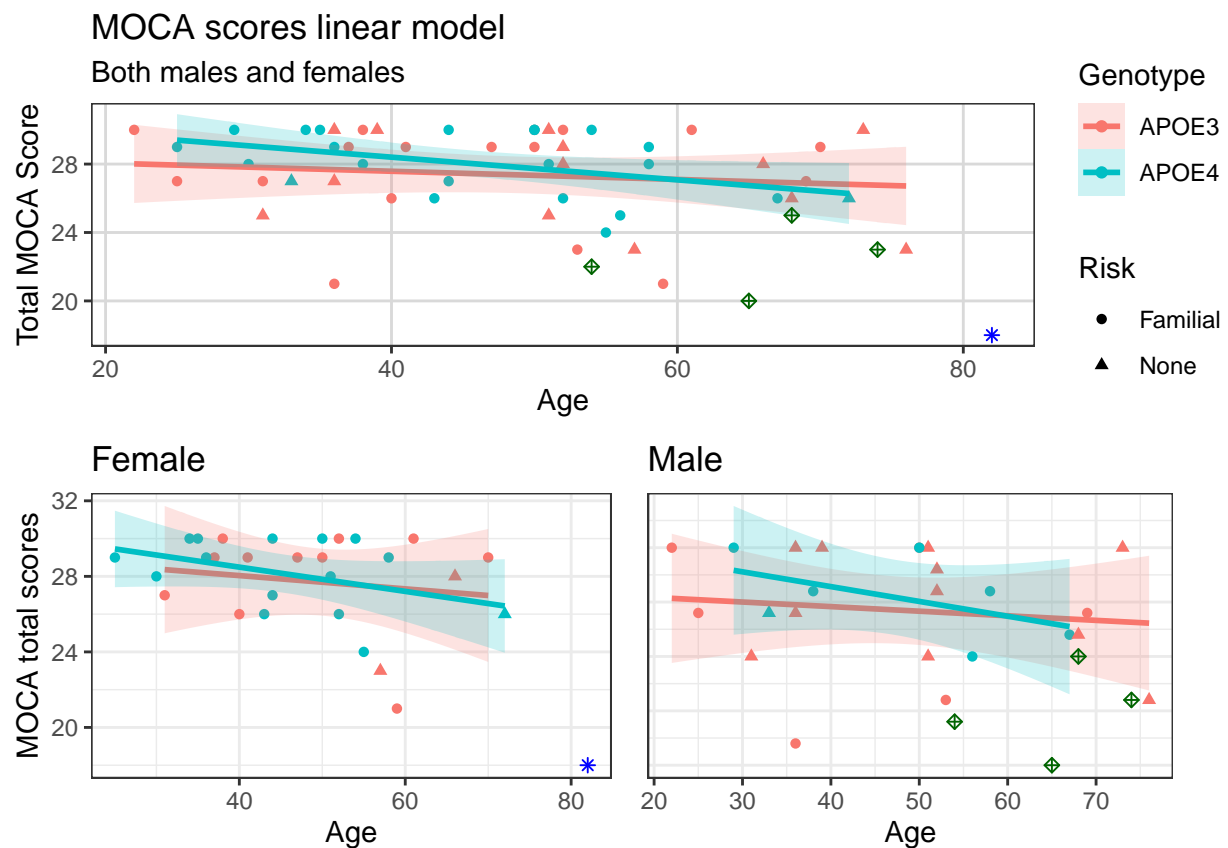
## Analysis of Variance Table
##
## Response: MOCA_Visuospatial
##              Df Sum Sq Mean Sq F value  Pr(>F)
## age           1  0.0021  0.00211   0.0110  0.91703
## Genotype      1  0.1241  0.12405   0.6443  0.42649
## sex           1  0.0005  0.00047   0.0024  0.96092
## age:Genotype  1  0.5207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



```
## Residuals      44 8.4724 0.19255
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

## Analysis of Variance Table
##
## Response: MOCA_Visuospatial
##           Df Sum Sq Mean Sq F value Pr(>F)
## age        1  0.01727  0.01727   0.1247 0.72773
## Genotype    1  0.05742  0.05742   0.4144 0.52706
## age:Genotype 1  1.11246  1.11246   8.0288 0.01027 *
## Residuals   20  2.77118  0.13856
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



##

```

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

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

##
## Call:
## lm(formula = MOCA_TOTAL ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.3758 -1.7796 -0.0128  2.3642  3.4049
##

```

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

```
## Analysis of Variance Table
```

```
##
```

```
## Response: MOCA_TOTAL
```

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

```
## Analysis of Variance Table
```

```
##
```

```
## Response: MOCA_TOTAL
```

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

```
## Analysis of Variance Table
```

```
##
```

```
## Response: MOCA_TOTAL
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## age         1   5.625   5.6253   0.7518 0.3962
## Genotype     1   1.592   1.5920   0.2128 0.6496
## age:Genotype  1   2.086   2.0864   0.2788 0.6033
## Residuals    20 149.655   7.4827
```