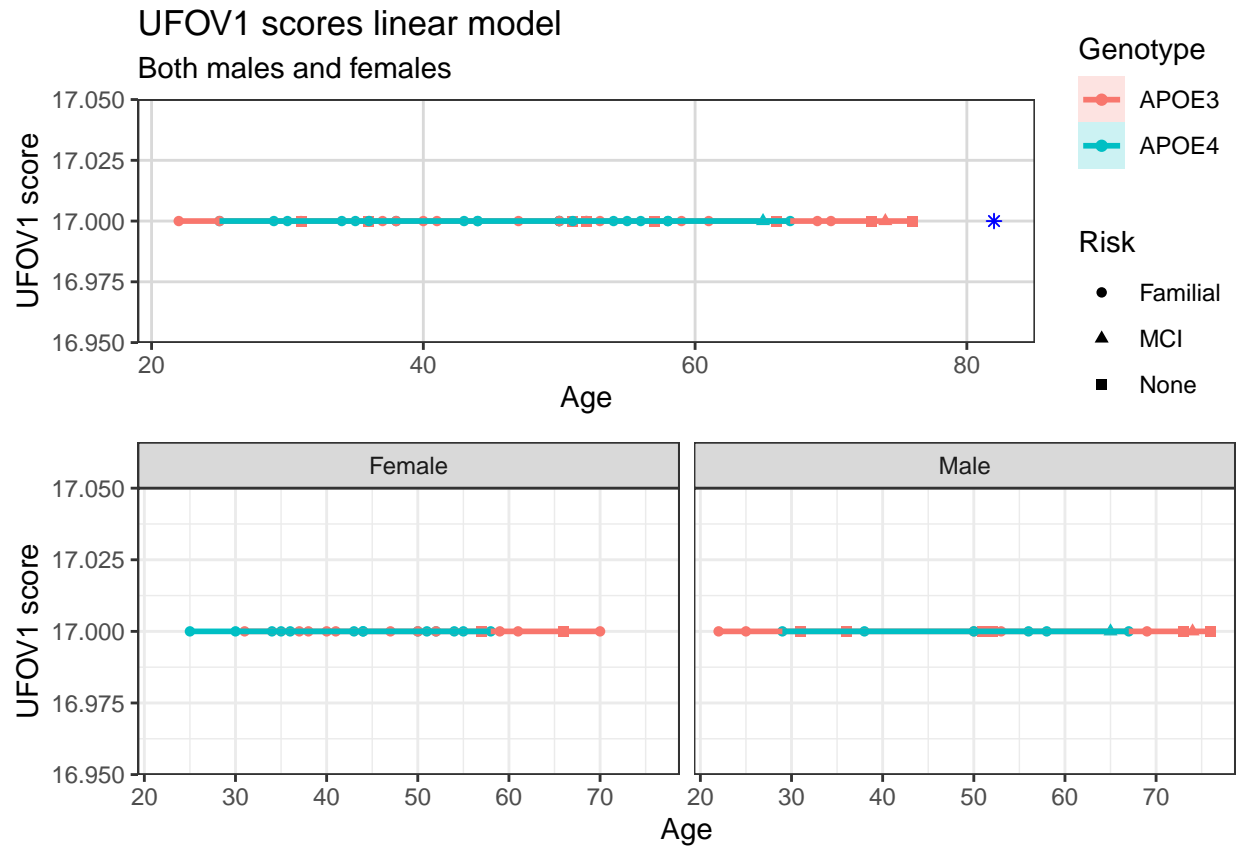


Linear models with AD subject



```
##
## Call:
## lm(formula = ufov1 ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
```

	Min	1Q	Median	3Q	Max
	-4.279e-15	0.000e+00	0.000e+00	0.000e+00	2.184e-14

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

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	1.700e+01	4.430e-15	3.838e+15	<2e-16 ***
age	-1.250e-16	8.639e-17	-1.447e+00	0.155
GenotypeAPOE4	-8.155e-15	6.247e-15	-1.305e+00	0.199
sexMale	-8.155e-15	5.308e-15	-1.536e+00	0.132
age:GenotypeAPOE4	1.250e-16	1.310e-16	9.550e-01	0.345
age:sexMale	1.250e-16	1.026e-16	1.218e+00	0.230
GenotypeAPOE4:sexMale	8.155e-15	8.932e-15	9.130e-01	0.367

```

## age:GenotypeAPOE4:sexMale -1.250e-16  1.775e-16 -7.040e-01    0.485
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.64e-15 on 41 degrees of freedom
## (4 observations deleted due to missingness)
## Multiple R-squared:  0.4939, Adjusted R-squared:  0.4075
## F-statistic: 5.717 on 7 and 41 DF,  p-value: 0.0001172

##
## 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
## -2.506e-14  0.000e+00  0.000e+00  2.006e-15  7.622e-15
##
## Coefficients:
##              Estimate Std. Error  t value Pr(>|t|)
## (Intercept)   1.700e+01  5.472e-15  3.107e+15  <2e-16 ***
## age           2.160e-16  1.036e-16  2.084e+00   0.0516 .
## GenotypeAPOE4  1.302e-14  1.195e-14  1.090e+00   0.2901
## age:GenotypeAPOE4 -2.160e-16  2.241e-16 -9.640e-01   0.3479
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.811e-15 on 18 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.5068, Adjusted R-squared:  0.4247
## F-statistic: 6.167 on 3 and 18 DF,  p-value: 0.00453

## Analysis of Variance Table

```

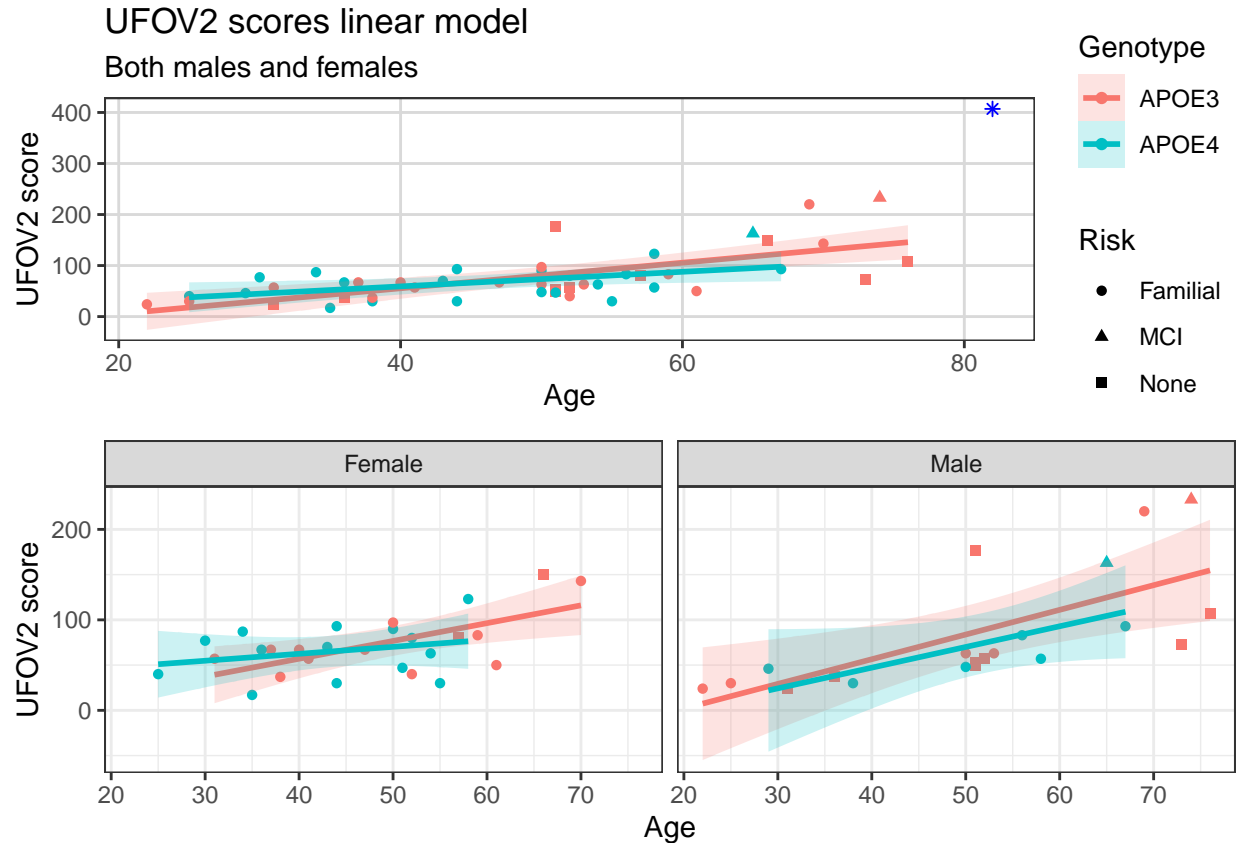
```

##
## Response: ufov1
##           Df      Sum Sq    Mean Sq F value Pr(>F)
## age        1 3.7500e-30 3.7480e-30  0.2829 0.5977
## Genotype    1 1.1270e-29 1.1270e-29  0.8507 0.3617
## sex         1 1.3320e-29 1.3317e-29  1.0052 0.3219
## age:Genotype 1 5.2100e-30 5.2053e-30  0.3929 0.5342
## age:sex      1 1.1520e-29 1.1521e-29  0.8697 0.3565
## Genotype:sex 1 1.1060e-29 1.1061e-29  0.8349 0.3662
## age:Genotype:sex 1 6.5700e-30 6.5746e-30  0.4963 0.4851
## Residuals   41 5.4315e-28 1.3248e-29

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

## Analysis of Variance Table
##
## Response: ufov1
##           Df      Sum Sq    Mean Sq F value Pr(>F)
## age        1 1.6474e-28 1.6474e-28  3.5509 0.07577 .
## Genotype    1 1.7290e-29 1.7295e-29  0.3728 0.54913
## age:Genotype 1 4.3100e-29 4.3099e-29  0.9290 0.34790
## Residuals   18 8.3509e-28 4.6394e-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
## -73.500 -25.192  -5.872  19.950  90.500
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -21.6677    47.0946  -0.460   0.6479
## age              1.9671     0.9185   2.142   0.0384 *
## GenotypeAPOE4    53.4227    66.4155   0.804   0.4259
## sexMale        -30.9221    57.2060  -0.541   0.5918
## age:GenotypeAPOE4 -1.1989     1.3925  -0.861   0.3944
## age:sexMale       0.7601     1.0991   0.692   0.4932
## GenotypeAPOE4:sexMale -45.2057    95.4314  -0.474   0.6383
## age:GenotypeAPOE4:sexMale 0.7598     1.8915   0.402   0.6901
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 38.7 on 40 degrees of freedom
## (5 observations deleted due to missingness)
## Multiple R-squared:  0.4426, Adjusted R-squared:  0.3451
## F-statistic: 4.538 on 7 and 40 DF, p-value: 0.0008414
```

```
##
## 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
	-73.50	-31.34	-12.58	16.59	90.50

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

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-52.5898	41.3579	-1.272	0.22064
age	2.7273	0.7687	3.548	0.00247 **
GenotypeAPOE4	8.2170	87.2728	0.094	0.92609
age:GenotypeAPOE4	-0.4391	1.6304	-0.269	0.79094

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 49.28 on 17 degrees of freedom
## (4 observations deleted due to missingness)
## Multiple R-squared:  0.4754, Adjusted R-squared:  0.3828
## F-statistic: 5.135 on 3 and 17 DF,  p-value: 0.01038
```

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

```
##
```

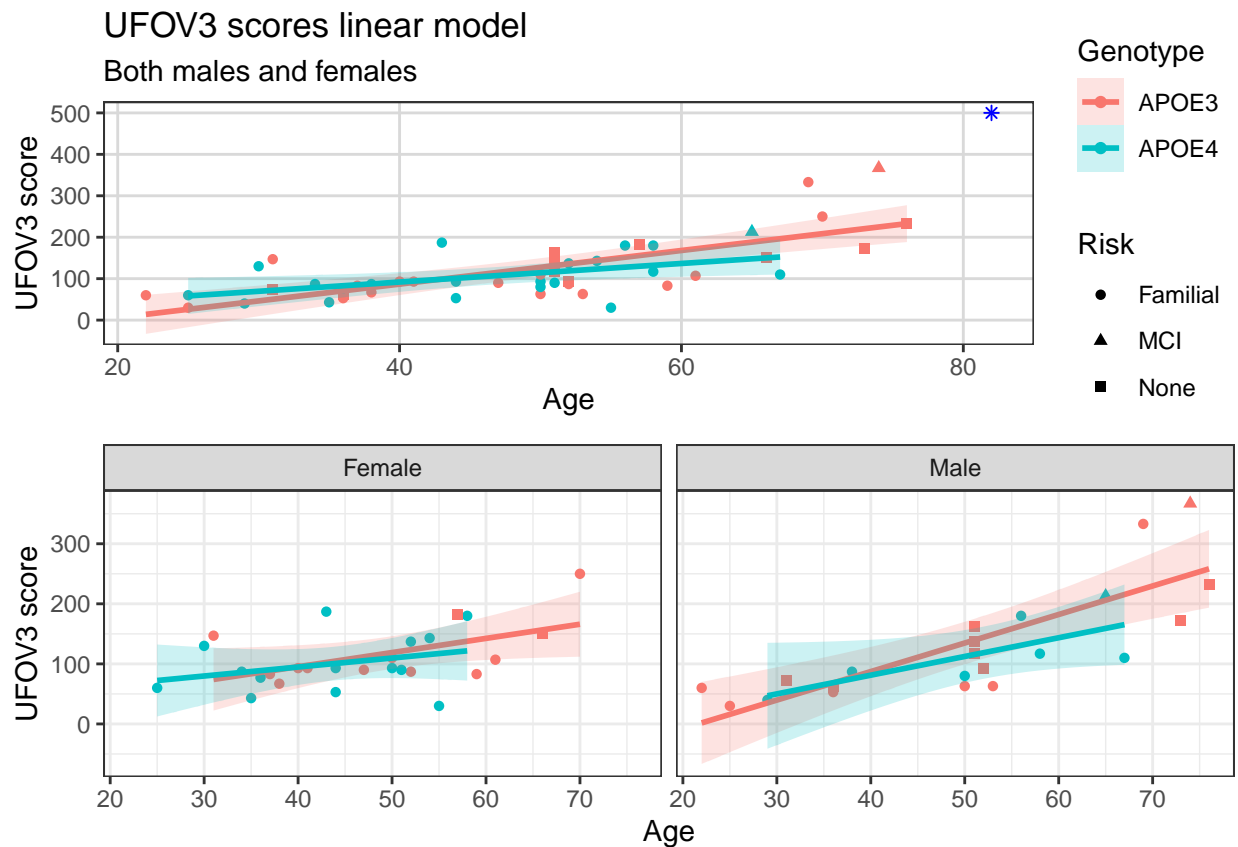
```
## Response: ufov2
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	42522	42522	28.3963	4.131e-06 ***
Genotype	1	242	242	0.1619	0.6896
sex	1	11	11	0.0071	0.9333
age:Genotype	1	2344	2344	1.5651	0.2182
age:sex	1	2041	2041	1.3629	0.2499
Genotype:sex	1	169	169	0.1126	0.7390

```
## age:Genotype:sex 1      242      242 0.1613      0.6901
## Residuals      40 59899      1497
## ---
## 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  36265   36265  14.9318 0.001245 **
## Genotype   1    976     976   0.4020 0.534517
## age:Genotype 1    176     176   0.0725 0.790937
## Residuals 17  41288    2429
## ---
## 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 -25.251  -6.914   27.294 118.250
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.9899     63.6050   0.016   0.9877
## age              2.3577      1.2405   1.901   0.0644 .
## GenotypeAPOE4     33.9436     89.6993   0.378   0.7071
## sexMale          -103.7913     76.2129  -1.362   0.1807
## age:GenotypeAPOE4  -0.8619      1.8806  -0.458   0.6492
## age:sexMale        2.3930      1.4735   1.624   0.1120
## GenotypeAPOE4:sexMale 25.4010    128.2619   0.198   0.8440
## age:GenotypeAPOE4:sexMale -0.7726     2.5483  -0.303   0.7633
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 52.26 on 41 degrees of freedom
## (4 observations deleted due to missingness)
## Multiple R-squared:  0.5381, Adjusted R-squared:  0.4592
## F-statistic: 6.823 on 7 and 41 DF,  p-value: 2.189e-05

##
## 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

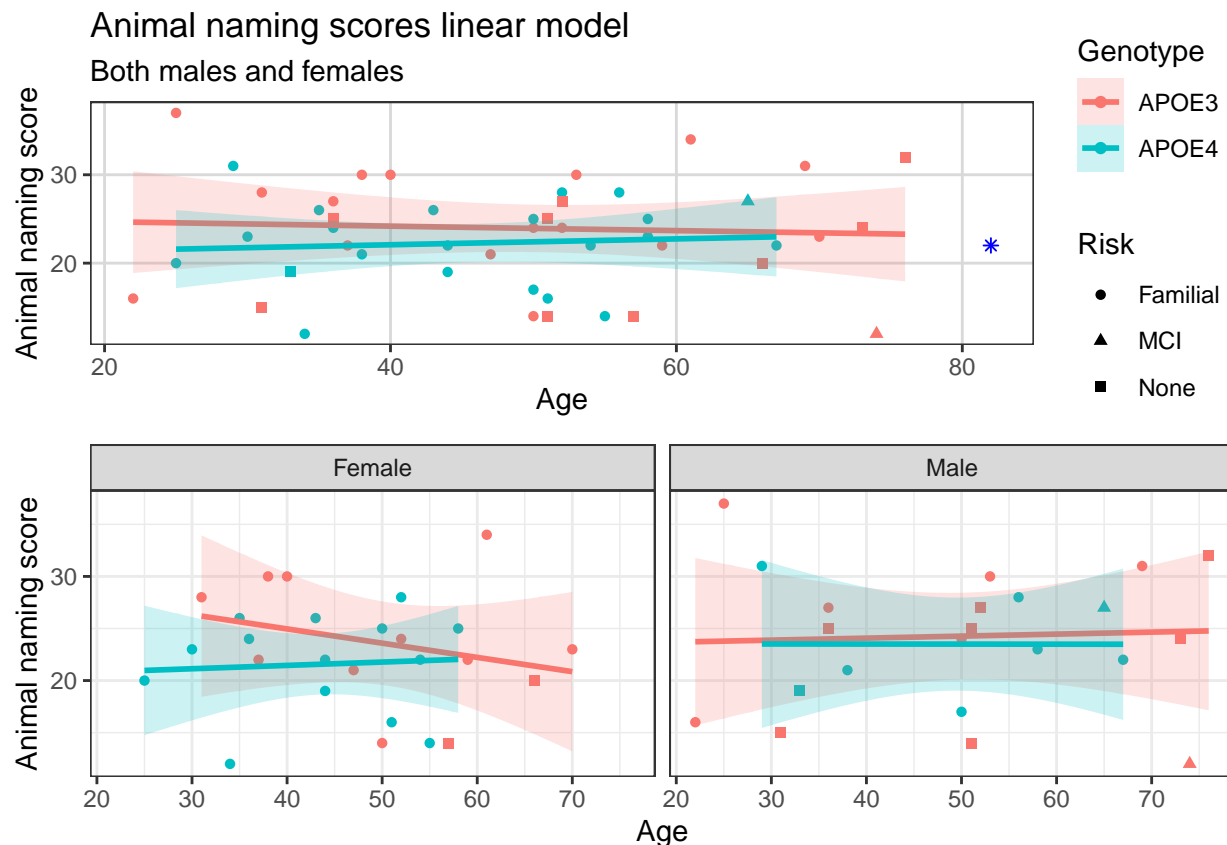
```
##
## Response: ufov3
##              Df Sum Sq Mean Sq F value    Pr(>F)
## age            1 112572  112572  41.2129 1.094e-07 ***
## Genotype       1    881    881    0.3226  0.57316
## sex            1    317    317    0.1161  0.73499
## age:Genotype   1   7145   7145    2.6159  0.11347
## age:sex        1   8912   8912    3.2628  0.07821 .
## Genotype:sex   1    386    386    0.1414  0.70880
## age:Genotype:sex 1    251    251    0.0919  0.76330
## Residuals     41 111990    2731
## ---
## 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 104835  104835  30.3206 3.145e-05 ***
## Genotype       1   2918    2918   0.8440  0.3704
## age:Genotype   1   2467    2467   0.7136  0.4093
## Residuals     18   62236    3458
## ---
## 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
## -12.7278  -3.0016   0.6824   3.5104  13.2137
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    30.4309     7.8429   3.880 0.000371 ***
## age           -0.1368     0.1507  -0.908 0.369387
## GenotypeAPOE4 -10.2594    10.8486  -0.946 0.349845
## sexMale        -7.1249     9.2881  -0.767 0.447415
## age:GenotypeAPOE4  0.1689     0.2253   0.749 0.457867
## age:sexMale      0.1560     0.1778   0.878 0.385238
## GenotypeAPOE4:sexMale 10.4867    14.5084   0.723 0.473904
## age:GenotypeAPOE4:sexMale -0.1888     0.2923  -0.646 0.522095
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.194 on 41 degrees of freedom
## (4 observations deleted due to missingness)
## Multiple R-squared:  0.05446,    Adjusted R-squared:  -0.107
## F-statistic: 0.3374 on 7 and 41 DF,  p-value: 0.9321
```

```
##
## 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
## -12.7278 -3.5094  0.7141  4.0074 13.2137
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    23.30602     5.48381   4.250 0.000433 ***
## age           0.01921     0.10386   0.185 0.855194
## GenotypeAPOE4  0.22729    10.61742   0.021 0.983144
## age:GenotypeAPOE4 -0.01989     0.20529  -0.097 0.923846
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.826 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.005238,    Adjusted R-squared:  -0.1518
## F-statistic: 0.03335 on 3 and 19 DF,  p-value: 0.9916
```

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

```
##
```

```
## Response: animals
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	0.17	0.169	0.0044	0.9474
Genotype	1	33.25	33.251	0.8668	0.3573
sex	1	19.44	19.440	0.5068	0.4806
age:Genotype	1	4.10	4.099	0.1068	0.7454
age:sex	1	12.00	12.003	0.3129	0.5789
Genotype:sex	1	5.63	5.634	0.1469	0.7035

```
## age:Genotype:sex 1 15.99 15.992 0.4169 0.5221
## Residuals      41 1572.76 38.360
```

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

```
##
```

```
## Response: animals
```

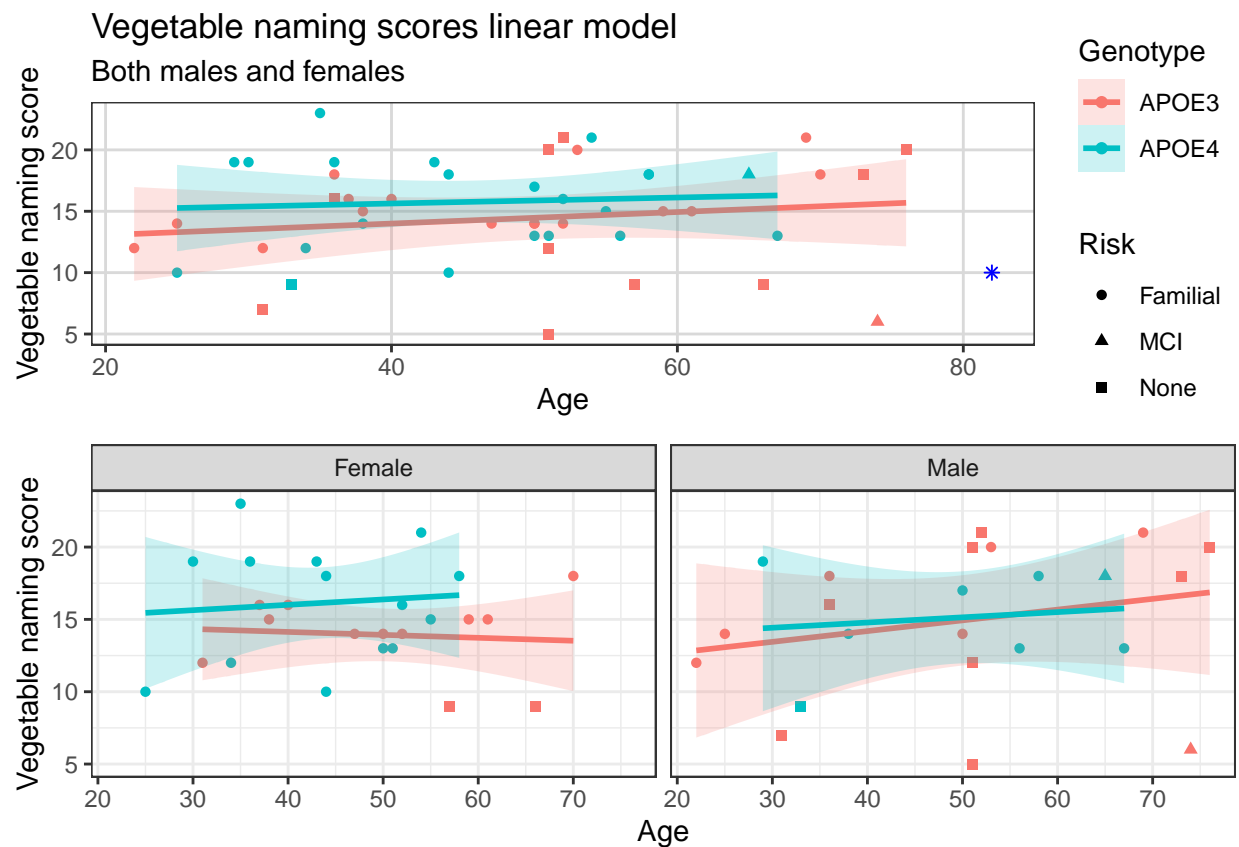
```
##          Df Sum Sq Mean Sq F value Pr(>F)
## age         1   2.94   2.941   0.0941 0.7619
## Genotype     1  32.55  32.553   1.0418 0.3185
## age:Genotype 1  21.55  21.546   0.6895 0.4152
## Residuals   22 687.42  31.246
```

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

```
##
```

```
## Response: animals
```

```
##          Df Sum Sq Mean Sq F value Pr(>F)
## age         1   1.22   1.215   0.0261 0.8734
## Genotype     1   3.01   3.010   0.0646 0.8021
## age:Genotype 1   0.44   0.437   0.0094 0.9238
## Residuals   19 885.34  46.597
```



```
##
```

```
## Call:
```

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

```
##
```

```

## Residuals:
##      Min       1Q   Median       3Q      Max
## -10.7167  -2.7550   0.9243   2.8810   7.1777
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    14.94680     5.53061   2.703  0.00997 **
## age           -0.02033     0.10628  -0.191  0.84924
## GenotypeAPOE4  -0.42280     7.65011  -0.055  0.95619
## sexMale        -3.72875     6.54967  -0.569  0.57226
## age:GenotypeAPOE4  0.05742     0.15890   0.361  0.71966
## age:sexMale      0.09464     0.12535   0.755  0.45456
## GenotypeAPOE4:sexMale  2.54761    10.23094   0.249  0.80460
## age:GenotypeAPOE4:sexMale -0.09573     0.20616  -0.464  0.64486
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.368 on 41 degrees of freedom
## (4 observations deleted due to missingness)
## Multiple R-squared:  0.07206, Adjusted R-squared:  -0.08637
## F-statistic: 0.4549 on 7 and 41 DF, p-value: 0.8611

##
## 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
## -10.717  -2.557   1.358   3.621   5.918
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)

```

```
## (Intercept)      11.21806    4.07147    2.755    0.0126 *
## age              0.07431    0.07711    0.964    0.3473
## GenotypeAPOE4    2.12481    7.88293    0.270    0.7904
## age:GenotypeAPOE4 -0.03830    0.15242   -0.251    0.8043
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.068 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.05053,    Adjusted R-squared:  -0.09939
## F-statistic: 0.337 on 3 and 19 DF,  p-value: 0.7988
```

Analysis of Variance Table

##

Response: vegetables

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	8.76	8.7581	0.4591	0.5018
## Genotype	1	25.48	25.4750	1.3355	0.2545
## sex	1	0.03	0.0305	0.0016	0.9683
## age:Genotype	1	1.09	1.0937	0.0573	0.8119
## age:sex	1	9.91	9.9066	0.5193	0.4752
## Genotype:sex	1	11.36	11.3576	0.5954	0.4448
## age:Genotype:sex	1	4.11	4.1130	0.2156	0.6449
## Residuals	41	782.08	19.0752		

Analysis of Variance Table

##

Response: vegetables

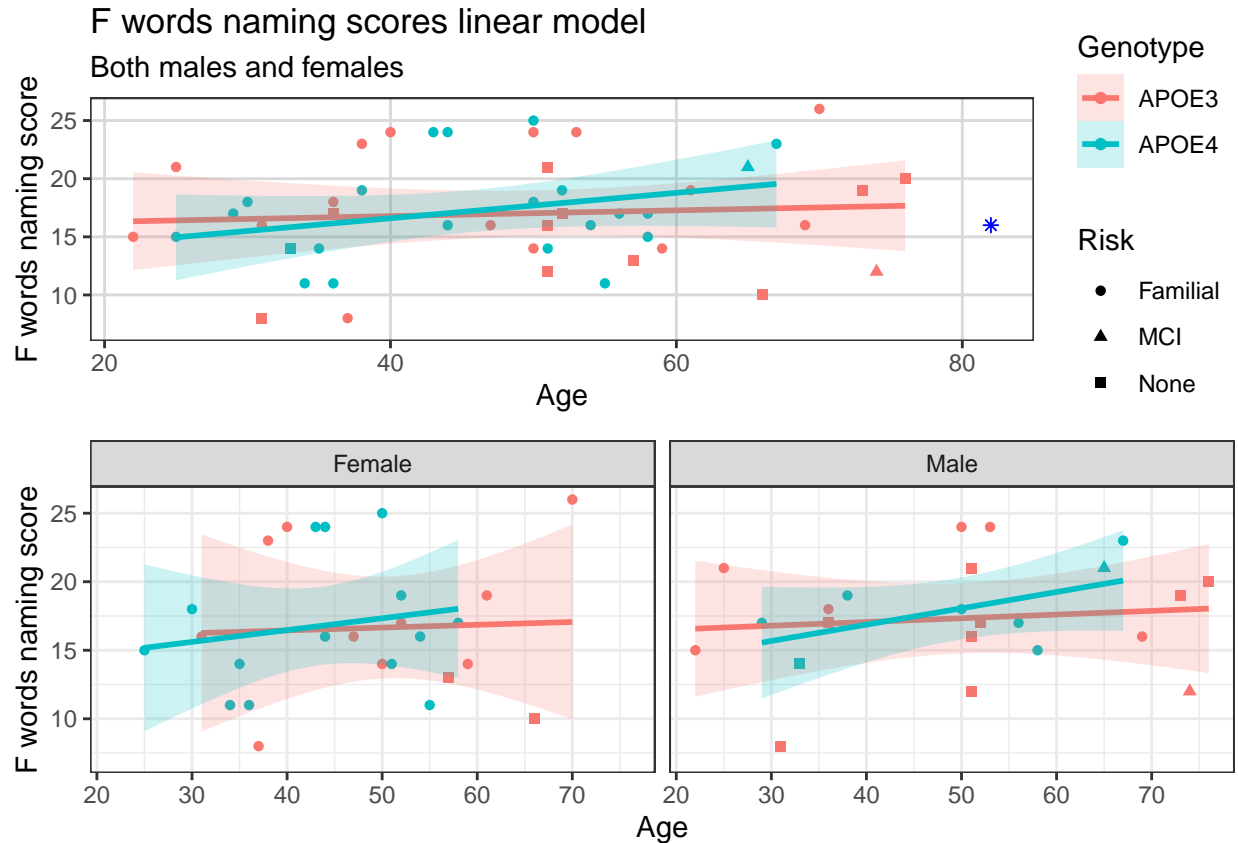
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	2.124	2.1236	0.1589	0.6940
## Genotype	1	29.987	29.9871	2.2435	0.1484
## age:Genotype	1	2.491	2.4914	0.1864	0.6701
## Residuals	22	294.052	13.3660		

Analysis of Variance Table

##

Response: vegetables

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	24.09	24.0862	0.9377	0.3450
## Genotype	1	0.26	0.2615	0.0102	0.9207
## age:Genotype	1	1.62	1.6221	0.0632	0.8043
## Residuals	19	488.03	25.6858		



```
##
## Call:
## lm(formula = f ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -8.8187 -2.6530 -0.2629  2.3698  8.9364
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    15.62653    6.060818   2.578  0.0136 *
## age             0.020529   0.116472   0.176  0.8610
## GenotypeAPOE4   -2.605214   8.383512  -0.311  0.7576
## sexMale         0.352637   7.177573   0.049  0.9611
## age:GenotypeAPOE4  0.065726   0.174129   0.377  0.7078
## age:sexMale      0.006554   0.137362   0.048  0.9622
## GenotypeAPOE4:sexMale -1.269982  11.211749  -0.113  0.9104
## age:GenotypeAPOE4:sexMale 0.026303  0.225919   0.116  0.9079
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.786 on 41 degrees of freedom
## (4 observations deleted due to missingness)
## Multiple R-squared:  0.04673,    Adjusted R-squared:  -0.116
## F-statistic: 0.2871 on 7 and 41 DF,  p-value: 0.9553
```

```
##
## 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
## -8.8188 -1.8111  0.0458  2.1661  6.6667
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    15.97917     3.28181   4.869 0.000107 ***
## age             0.02708     0.06215   0.436 0.667930
## GenotypeAPOE4   -3.87520     6.35404  -0.610 0.549167
## age:GenotypeAPOE4 0.09203     0.12286   0.749 0.462985
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.085 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.07732,    Adjusted R-squared:  -0.06837
## F-statistic: 0.5307 on 3 and 19 DF,  p-value: 0.6667
```

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

```
##
## Response: f
##              Df Sum Sq Mean Sq F value Pr(>F)
## age            1  23.72  23.7247   1.0357 0.3148
## Genotype       1   2.19   2.1852   0.0954 0.7590
## sex            1   7.37   7.3681   0.3216 0.5737
## age:Genotype   1  11.93  11.9288   0.5207 0.4746
## age:sex        1   0.53   0.5257   0.0229 0.8803
## Genotype:sex   1   0.00   0.0002   0.0000 0.9975
```

```
## age:Genotype:sex 1 0.31 0.3105 0.0136 0.9079
## Residuals      41 939.22 22.9079
```

```
## 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
```

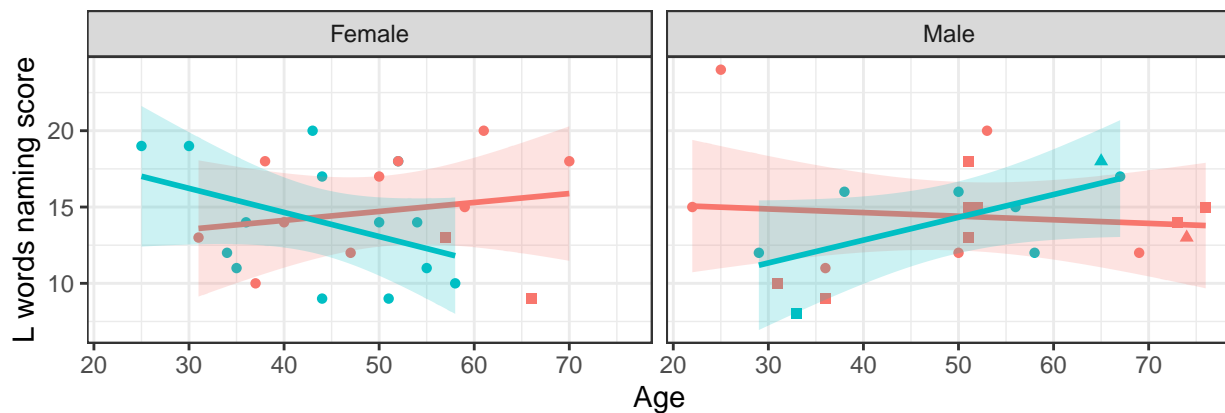
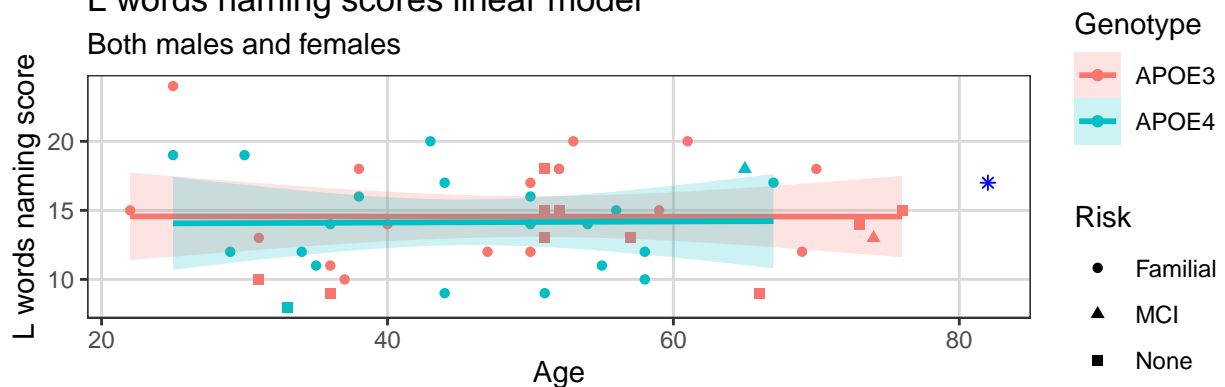
```
##
```

```
## Response: f
```

```
##          Df Sum Sq Mean Sq F value Pr(>F)
## age       1  14.71  14.7084   0.8814 0.3596
## Genotype   1   2.50   2.4978   0.1497 0.7032
## age:Genotype 1   9.36   9.3642   0.5611 0.4630
## Residuals 19 317.08 16.6885
```

L words naming scores linear model

Both males and females



```
##
```

```
## Call:
```

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

```
##
```



```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6.6489 -2.4000 -0.0611  2.1166  9.0097
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    11.77961     4.63329   2.542  0.0149 *
## age             0.05863     0.08904   0.658  0.5139
## GenotypeAPOE4    9.17536     6.40891   1.432  0.1598
## sexMale         3.80095     5.48701   0.693  0.4924
## age:GenotypeAPOE4 -0.21635     0.13312  -1.625  0.1118
## age:sexMale     -0.08224     0.10501  -0.783  0.4380
## GenotypeAPOE4:sexMale -17.90093     8.57100  -2.089  0.0430 *
## age:GenotypeAPOE4:sexMale 0.38936     0.17271   2.254  0.0296 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.659 on 41 degrees of freedom
## (4 observations deleted due to missingness)
## Multiple R-squared:  0.1251, Adjusted R-squared:  -0.02425
## F-statistic: 0.8377 on 7 and 41 DF,  p-value: 0.5627

##
## 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
## -5.7306 -2.1757  0.1356  1.3241  9.0097
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)      15.58056      2.94609      5.289 4.19e-05 ***
## age              -0.02361      0.05580     -0.423      0.677
## GenotypeAPOE4    -8.72558      5.70403     -1.530      0.143
## age:GenotypeAPOE4 0.17301      0.11029      1.569      0.133
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.667 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.1226, Adjusted R-squared:  -0.01598
## F-statistic: 0.8846 on 3 and 19 DF,  p-value: 0.4668
```

Analysis of Variance Table

##

Response: l

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	0.12	0.119	0.0089	0.92539
## Genotype	1	2.02	2.023	0.1511	0.69949
## sex	1	0.18	0.181	0.0135	0.90809
## age:Genotype	1	0.06	0.060	0.0045	0.94686
## age:sex	1	6.48	6.482	0.4842	0.49044
## Genotype:sex	1	1.59	1.593	0.1190	0.73192
## age:Genotype:sex	1	68.04	68.041	5.0824	0.02958 *
## Residuals	41	548.89	13.388		

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

Analysis of Variance Table

##

Response: l

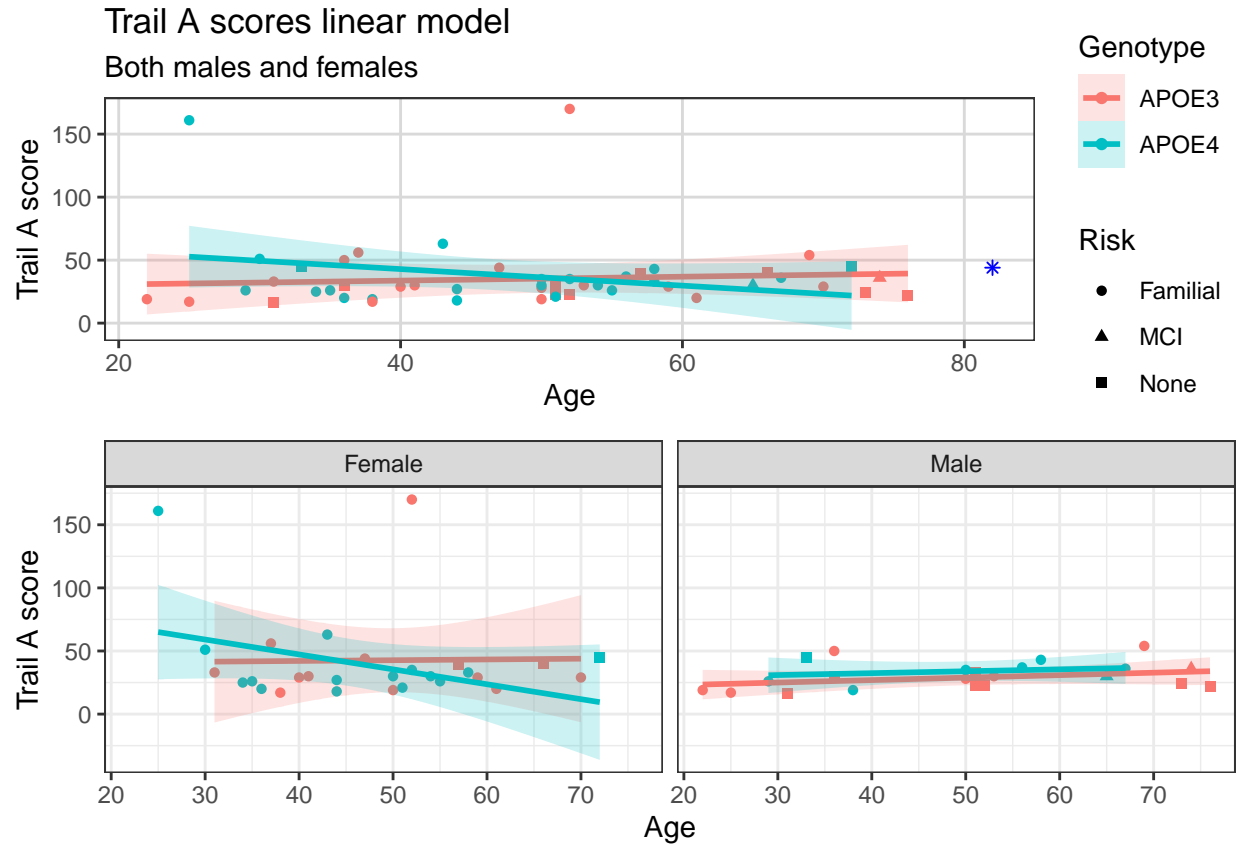
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	2.184	2.184	0.1638	0.6896
## Genotype	1	5.244	5.244	0.3932	0.5371
## age:Genotype	1	35.364	35.364	2.6520	0.1177
## Residuals	22	293.362	13.335		

Analysis of Variance Table

##

Response: l

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	2.496	2.496	0.1856	0.6715
## Genotype	1	0.102	0.102	0.0076	0.9316
## age:Genotype	1	33.094	33.094	2.4607	0.1332
## Residuals	19	255.526	13.449		



```
##
## Call:
## lm(formula = trailA ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -31.996 -12.631  -4.433   2.278 127.184
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    39.71951    35.02480   1.134   0.263
## age             0.05955     0.68311   0.087   0.931
## GenotypeAPOE4   54.80640    45.74743   1.198   0.237
## sexMale        -20.58224    41.96748  -0.490   0.626
## age:GenotypeAPOE4 -1.24094     0.92615  -1.340   0.187
## age:sexMale       0.13571     0.81140   0.167   0.868
## GenotypeAPOE4:sexMale -47.54696    64.00468  -0.743   0.462
## age:GenotypeAPOE4:sexMale  1.19676     1.26762   0.944   0.350
##
## Residual standard error: 28.78 on 43 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.1198, Adjusted R-squared:  -0.02348
## F-statistic: 0.8361 on 7 and 43 DF,  p-value: 0.5635
##
```

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

```
##
## Call:
## lm(formula = trailA ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -13.138  -6.254  -0.900   3.124  23.834
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    19.13727     8.24911   2.320   0.0316 *
## age             0.19525     0.15623   1.250   0.2265
## GenotypeAPOE4    7.25943    15.97144   0.455   0.6546
## age:GenotypeAPOE4 -0.04418     0.30881  -0.143   0.8877
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.27 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.1406, Adjusted R-squared:  0.004902
## F-statistic: 1.036 on 3 and 19 DF, p-value: 0.3991
```

Analysis of Variance Table

```
##
```

```
## Response: trailA
```

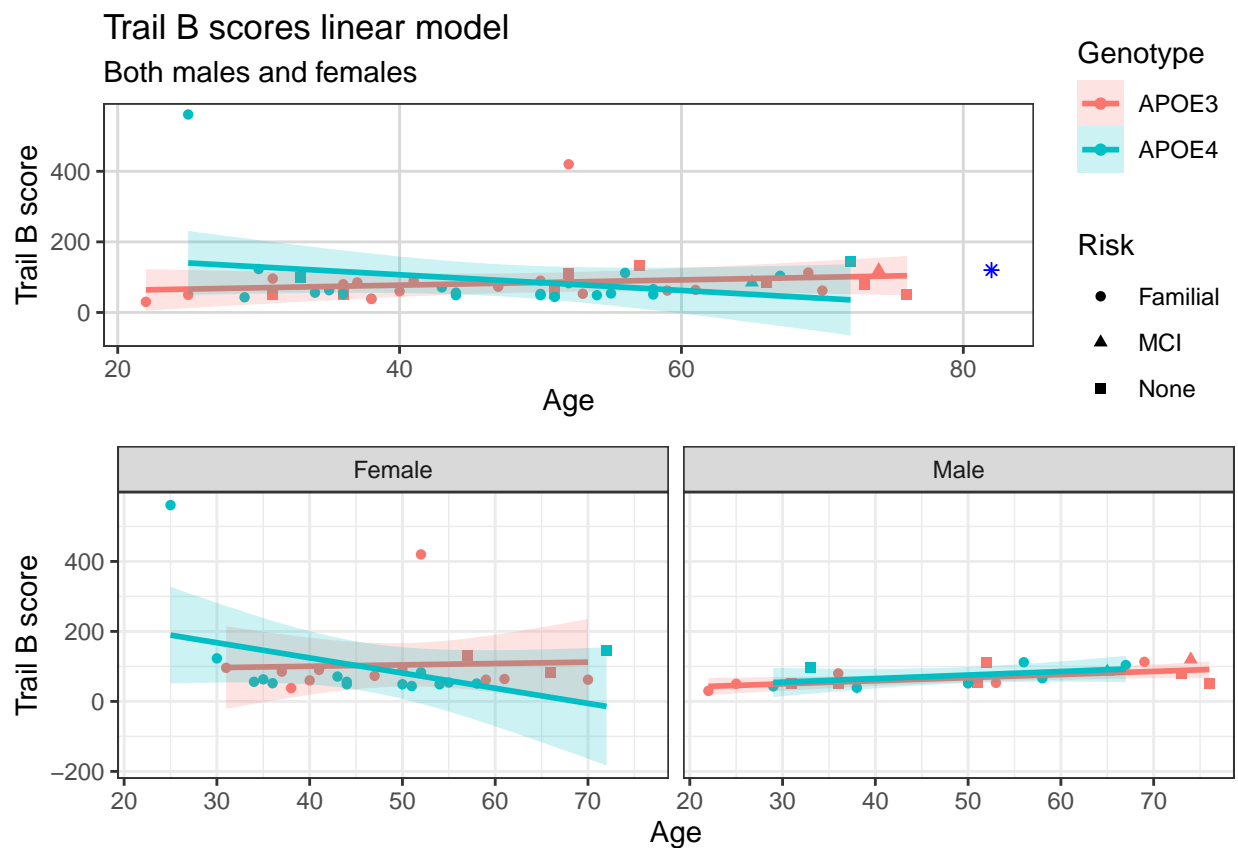
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	257	256.95	0.3102	0.5804
Genotype	1	83	83.27	0.1005	0.7527
sex	1	1363	1363.38	1.6461	0.2064
age:Genotype	1	1308	1307.54	1.5787	0.2157
age:sex	1	760	759.84	0.9174	0.3435
Genotype:sex	1	339	338.59	0.4088	0.5260
age:Genotype:sex	1	738	738.25	0.8913	0.3504
Residuals	43	35615	828.26		

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  191.67  191.667   1.8178  0.1934
## Genotype     1  133.92  133.922   1.2701  0.2738
## age:Genotype  1   2.16    2.158   0.0205  0.8877
## Residuals    19 2003.36  105.440
```



```
##
## Call:
## lm(formula = trailB ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -94.40  -35.88  -14.21    4.54   371.59
##
```

```
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      84.6102   105.6970   0.800   0.4278
## age              0.3946    2.0615   0.191   0.8491
## GenotypeAPOE4    213.1730   138.0555   1.544   0.1299
## sexMale          -61.3500   126.6485  -0.484   0.6306
## age:GenotypeAPOE4 -4.7295    2.7949  -1.692   0.0978
## age:sexMale       0.4976    2.4486   0.203   0.8399
## GenotypeAPOE4:sexMale -211.7078  193.1518  -1.096   0.2791
## age:GenotypeAPOE4:sexMale 4.8505    3.8254   1.268   0.2116
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 86.85 on 43 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.1523, Adjusted R-squared:  0.01426
## F-statistic: 1.103 on 7 and 43 DF,  p-value: 0.3784

##
## 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
## -39.062 -15.813  -5.578   18.009   40.349
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      23.2602   19.3095   1.205   0.2431
## age              0.8921    0.3657   2.440   0.0247 *
## GenotypeAPOE4     1.4653   37.3859   0.039   0.9691
## age:GenotypeAPOE4  0.1210    0.7229   0.167   0.8688
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Residual standard error: 24.04 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared: 0.3223, Adjusted R-squared: 0.2153
## F-statistic: 3.012 on 3 and 19 DF, p-value: 0.05566
```

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

```
##
```

```
## Response: trailB
```

```
##          Df Sum Sq Mean Sq F value Pr(>F)
## age          1    1559    1558.5   0.2066 0.6517
## Genotype      1     390     390.1   0.0517 0.8212
## sex           1    11836   11836.2   1.5692 0.2171
## age:Genotype  1    18073   18072.6   2.3960 0.1290
## age:sex       1    12501   12501.0   1.6573 0.2049
## Genotype:sex  1     1770    1770.2   0.2347 0.6305
## age:Genotype:sex 1    12127   12127.1   1.6077 0.2116
## Residuals    43   324346    7542.9
```

```
## 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
```

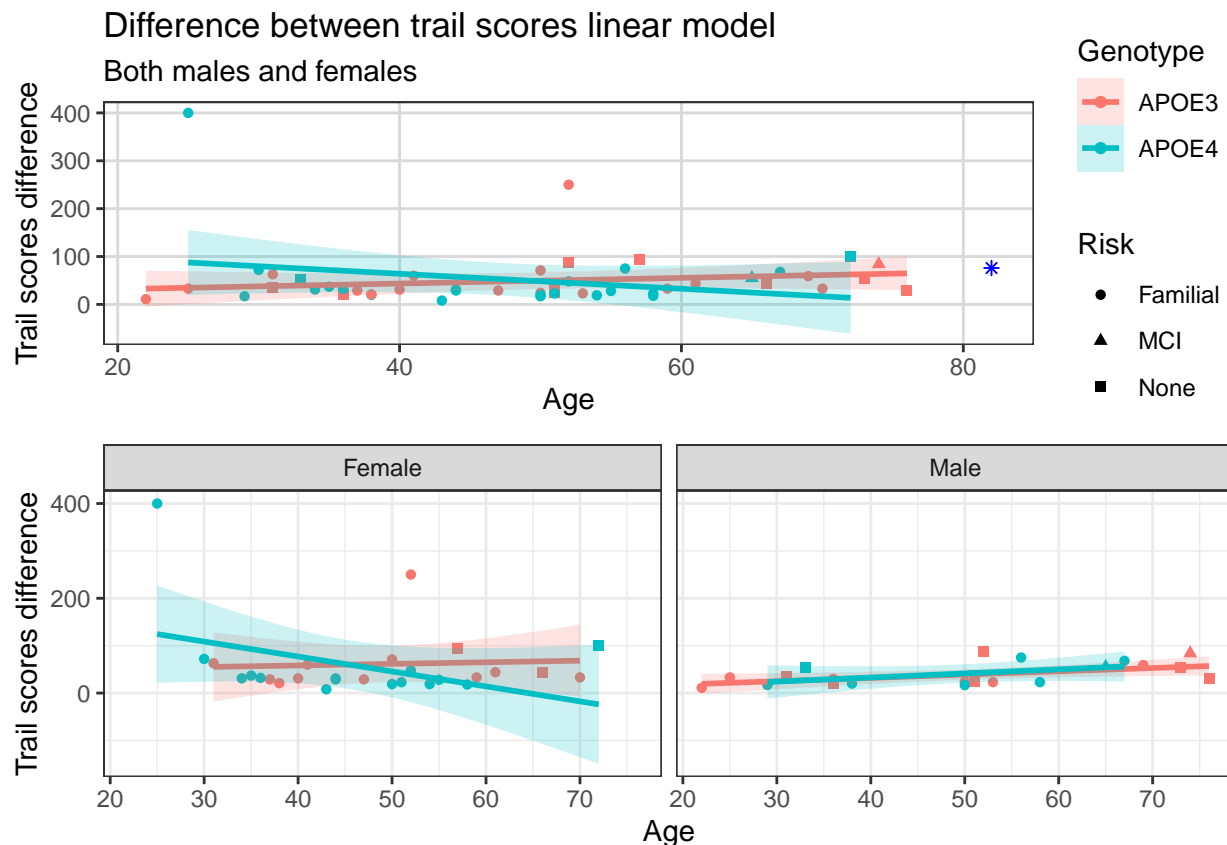
```
##
```

```
## Response: trailB
```

```
##          Df Sum Sq Mean Sq F value Pr(>F)
## age          1   4912.5   4912.5   8.5030 0.008862 **
## Genotype      1    291.1    291.1   0.5038 0.486460
## age:Genotype  1     16.2     16.2   0.0280 0.868839
## Residuals    19  10977.1    577.7
```

```
## ---
```

```
## 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  -27.188   -9.664    8.225   275.581
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      44.8907    74.6955   0.601  0.5510
## age              0.3350     1.4568   0.230  0.8192
## GenotypeAPOE4    158.3667    97.5631   1.623  0.1119
## sexMale          -40.7678    89.5018  -0.455  0.6510
## age:GenotypeAPOE4 -3.4885     1.9751  -1.766  0.0845 .
## age:sexMale       0.3619     1.7304   0.209  0.8353
## GenotypeAPOE4:sexMale -164.1608   136.4994  -1.203  0.2357
## age:GenotypeAPOE4:sexMale  3.6537     2.7034   1.352  0.1836
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 61.38 on 43 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.1564, Adjusted R-squared:  0.01903
## F-statistic: 1.139 on 7 and 43 DF, p-value: 0.3576
```



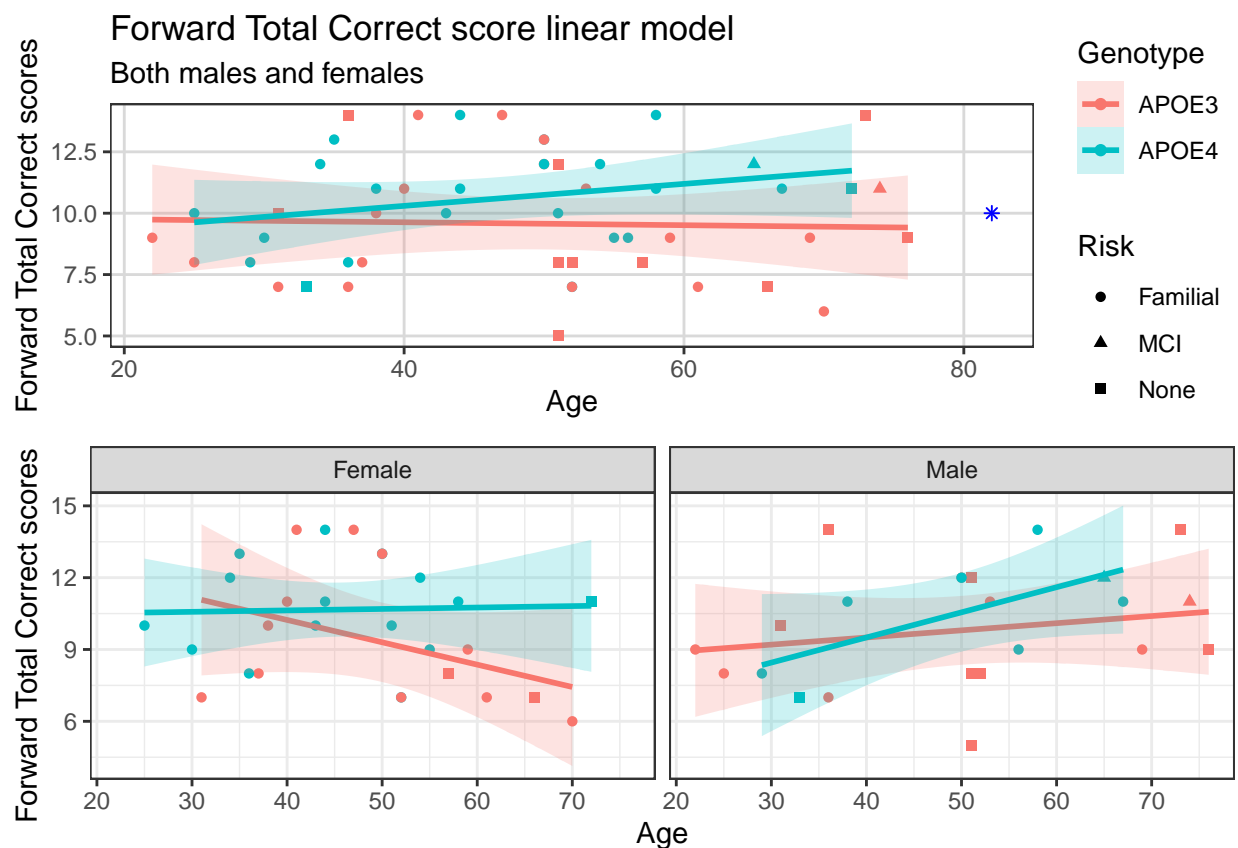
```
##
## Call:
## lm(formula = trailDiff ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -65.037 -35.382 -24.791   2.961 275.581
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      44.891      97.470   0.461   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
## -27.085 -12.875  -1.664   10.615   46.640
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      4.1229     16.5245   0.250   0.8056
## age              0.6969      0.3130   2.227   0.0383 *
## GenotypeAPOE4    -5.7942     31.9938  -0.181   0.8582
## age:GenotypeAPOE4  0.1652      0.6186   0.267   0.7923
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 20.57 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.2862, Adjusted R-squared:  0.1735
## F-statistic: 2.54 on 3 and 19 DF,  p-value: 0.08705

## Analysis of Variance Table
##
## Response: trailDiff
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1    550   549.8    0.1460 0.7043
## Genotype      1    113   112.9    0.0300 0.8634
## sex           1   5165  5165.3    1.3712 0.2481
## age:Genotype  1   9658  9657.9    2.5638 0.1167
## age:sex       1   7097  7096.8    1.8839 0.1770
## Genotype:sex  1    560   560.4    0.1488 0.7016
## age:Genotype:sex 1   6881  6881.1    1.8266 0.1836
## Residuals    43 161984  3767.1
```

```
## 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 3163.5   3163.5   7.4769 0.01317 *
## Genotype     1   30.1    30.1   0.0712 0.79250
## age:Genotype  1   30.2    30.2   0.0713 0.79234
## Residuals   19 8039.0    423.1
## ---
## 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
## -4.8299 -1.5751 -0.3479  1.4249  4.6181
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      13.96810    2.89148   4.831 1.76e-05 ***
## age              -0.09335    0.05639  -1.655  0.1051
## GenotypeAPOE4     -3.57378    3.77669  -0.946  0.3493
## sexMale           -5.66116    3.46464  -1.634  0.1096
## age:GenotypeAPOE4  0.09933    0.07646   1.299  0.2008
## age:sexMale        0.12321    0.06699   1.839  0.0728 .
## GenotypeAPOE4:sexMale 0.57034    5.28392   0.108  0.9145
## age:GenotypeAPOE4:sexMale -0.02421    0.10465  -0.231  0.8181
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.376 on 43 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.1742, Adjusted R-squared:  0.03973
## F-statistic: 1.296 on 7 and 43 DF,  p-value: 0.2756

##
## 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
## -4.8299 -1.6721 -0.1272  1.5774  4.6181
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      8.30694    1.91683   4.334 0.000358 ***
## age              0.02986    0.03630   0.823 0.420961

```

```
## GenotypeAPOE4      -3.00345      3.71125  -0.809 0.428372
## age:GenotypeAPOE4  0.07512      0.07176   1.047 0.308307
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.386 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.174, Adjusted R-squared:  0.04357
## F-statistic: 1.334 on 3 and 19 DF,  p-value: 0.2929
```

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

```
##
```

```
## Response: fwd_total_correct
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	0.797	0.7971	0.1412	0.70894
Genotype	1	14.485	14.4849	2.5660	0.11650
sex	1	0.428	0.4282	0.0758	0.78432
age:Genotype	1	5.721	5.7211	1.0135	0.31970
age:sex	1	28.371	28.3713	5.0260	0.03018 *
Genotype:sex	1	1.087	1.0867	0.1925	0.66304
age:Genotype:sex	1	0.302	0.3022	0.0535	0.81811
Residuals	43	242.730	5.6449		

```
## ---
```

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

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

```
##
```

```
## Response: fwd_total_correct
```

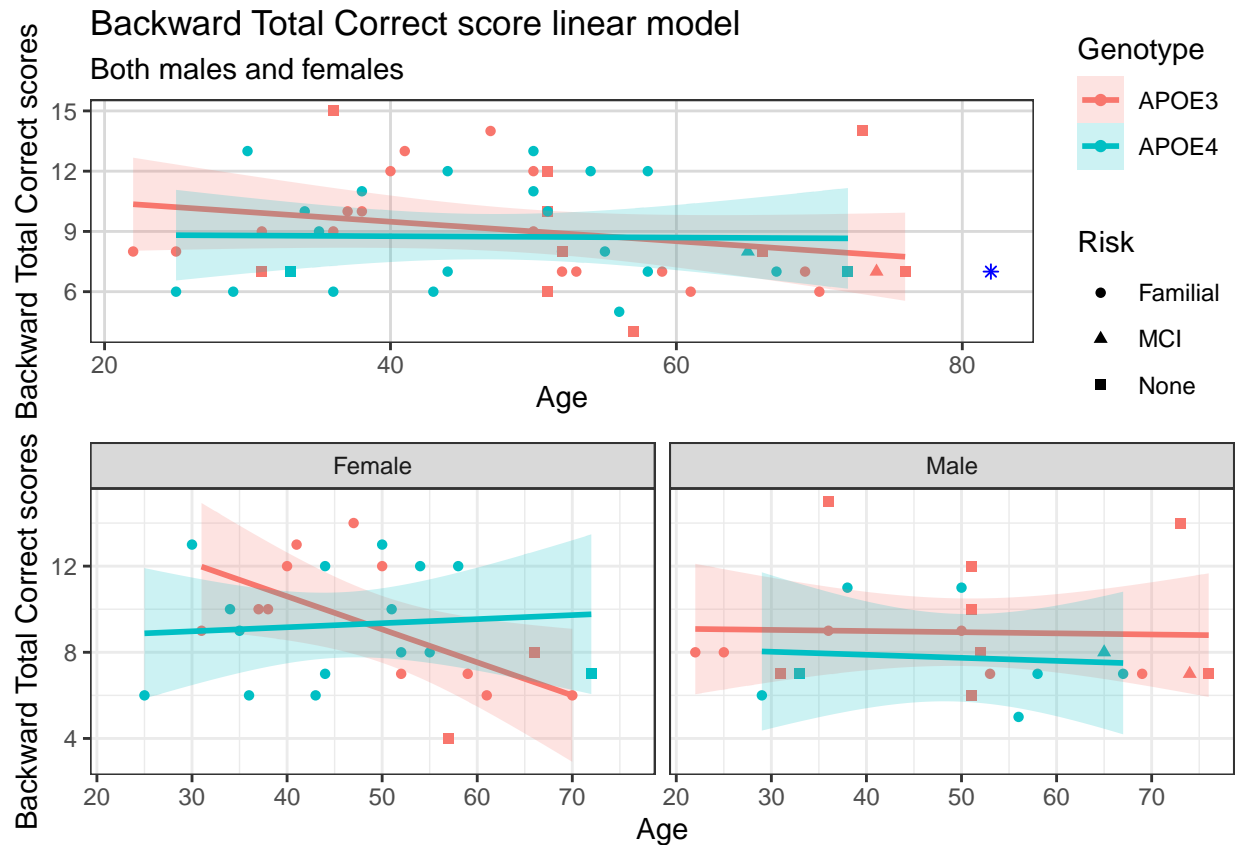
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	9.401	9.4014	1.6768	0.2077
Genotype	1	9.476	9.4760	1.6901	0.2059
age:Genotype	1	9.528	9.5278	1.6994	0.2047
Residuals	24	134.559	5.6066		

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

```
##
```

```
## Response: fwd_total_correct
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	13.808	13.8080	2.4253	0.1359
Genotype	1	2.738	2.7383	0.4810	0.4964
age:Genotype	1	6.239	6.2391	1.0959	0.3083
Residuals	19	108.171	5.6932		



```
##
## Call:
## lm(formula = bckwds_total_correct ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.9927 -1.8189 -0.6863  1.9507  5.9921
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    16.72528     3.23303   5.173 5.73e-06 ***
## age             -0.15320     0.06306  -2.430  0.0194 *
## GenotypeAPOE4   -8.31578     4.22280  -1.969  0.0554 .
## sexMale         -7.52574     3.87389  -1.943  0.0586 .
## age:GenotypeAPOE4  0.17203     0.08549   2.012  0.0505 .
## age:sexMale      0.14788     0.07490   1.974  0.0548 .
## GenotypeAPOE4:sexMale  7.56577     5.90807   1.281  0.2072
## age:GenotypeAPOE4:sexMale -0.18084     0.11701  -1.545  0.1296
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.657 on 43 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.1554, Adjusted R-squared:  0.0179
## F-statistic:  1.13 on 7 and 43 DF,  p-value: 0.3624
```

```
##
## 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
## -2.9280 -1.8189 -0.9227  0.7705  5.9921
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    9.199537     2.149412   4.280 0.000404 ***
## age           -0.005324     0.040707  -0.131 0.897317
## GenotypeAPOE4  -0.750008     4.161563  -0.180 0.858886
## age:GenotypeAPOE4 -0.008808     0.080464  -0.109 0.913983
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.676 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.05374, Adjusted R-squared: -0.09567
## F-statistic: 0.3597 on 3 and 19 DF, p-value: 0.7828

## Analysis of Variance Table
##
## Response: bckwds_total_correct
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1   8.940   8.9397   1.2668 0.2666
## Genotype      1   1.589   1.5885   0.2251 0.6376
## sex           1   5.602   5.6024   0.7939 0.3779
## age:Genotype  1   5.492   5.4923   0.7783 0.3826
## age:sex       1  12.825  12.8248   1.8173 0.1847
## Genotype:sex  1   4.530   4.5296   0.6418 0.4275
## age:Genotype:sex 1  16.856  16.8562   2.3885 0.1296
```

```
## Residuals      43 303.461  7.0572
```

```
## 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
```

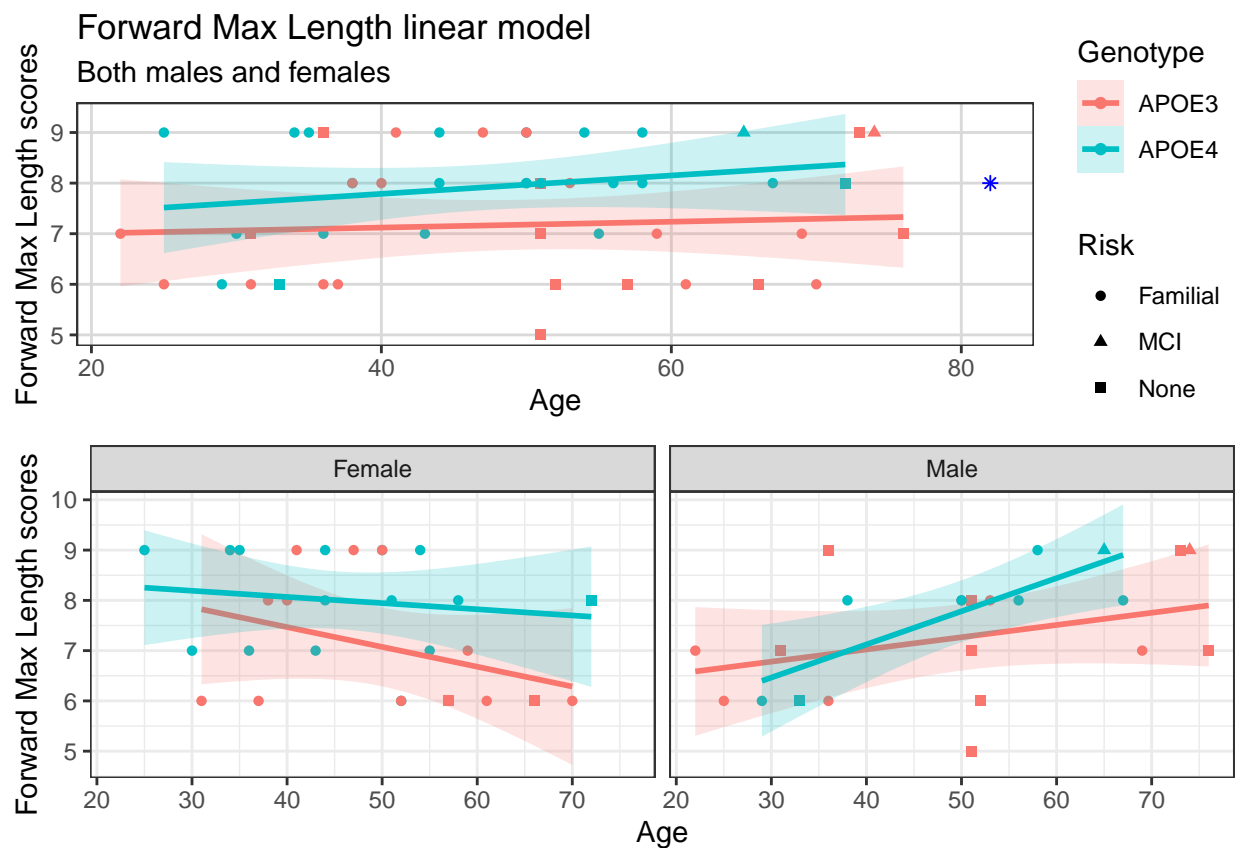
```
##           Df Sum Sq Mean Sq F value Pr(>F)
```

```
## age        1   0.288   0.2882   0.0403 0.8431
```

```
## Genotype    1   7.351   7.3510   1.0269 0.3236
```

```
## age:Genotype 1   0.086   0.0858   0.0120 0.9140
```

```
## Residuals   19 136.014   7.1586
```



```
##
```

```
## Call:
```

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

```
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.2910 -0.8409  0.1531  0.7406  2.0736
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      9.04364    1.35453   6.677 3.79e-08 ***
## age             -0.03939    0.02642  -1.491  0.1432
## GenotypeAPOE4    -0.48462    1.76922  -0.274  0.7855
## sexMale          -2.99225    1.62303  -1.844  0.0721 .
## age:GenotypeAPOE4  0.02712    0.03582   0.757  0.4531
## age:sexMale       0.06370    0.03138   2.030  0.0486 *
## GenotypeAPOE4:sexMale -1.08124    2.47529  -0.437  0.6644
## age:GenotypeAPOE4:sexMale 0.01453    0.04902   0.296  0.7684
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.113 on 43 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.2678, Adjusted R-squared:  0.1485
## F-statistic: 2.246 on 7 and 43 DF,  p-value: 0.04864

##
## 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
## -2.2910 -0.6952  0.1951  0.6992  2.0736
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```



```
## (Intercept)      6.05139    0.85294    7.095 9.51e-07 ***
## age              0.02431    0.01615    1.505    0.149
## GenotypeAPOE4    -1.56586    1.65142   -0.948    0.355
## age:GenotypeAPOE4 0.04164    0.03193    1.304    0.208
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.062 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.3233, Adjusted R-squared:  0.2165
## F-statistic: 3.026 on 3 and 19 DF,  p-value: 0.05491
```

Analysis of Variance Table

##

Response: fwd_max_length

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## age         1  0.549   0.5488   0.4430 0.509212
## Genotype     1  7.327   7.3268   5.9146 0.019254 *
## sex          1  0.003   0.0034   0.0028 0.958213
## age:Genotype  1  0.358   0.3582   0.2892 0.593537
## age:sex       1 10.723  10.7230   8.6561 0.005234 **
## Genotype:sex  1  0.409   0.4085   0.3298 0.568781
## age:Genotype:sex 1  0.109   0.1088   0.0878 0.768427
## Residuals    43 53.268   1.2388
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Analysis of Variance Table

##

Response: fwd_max_length

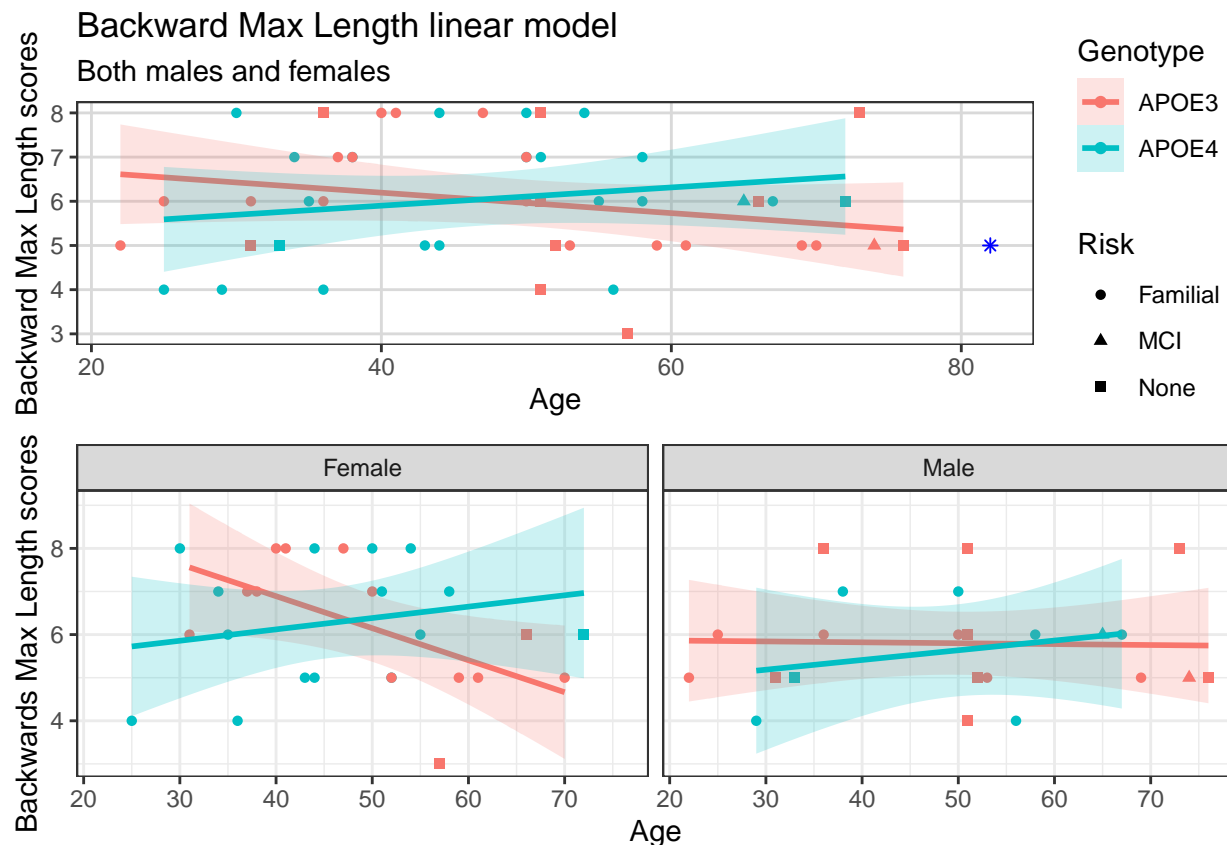
```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## age         1  3.827   3.8272   2.8840 0.10240
## Genotype     1  4.471   4.4706   3.3689 0.07886 .
## age:Genotype  1  0.710   0.7101   0.5351 0.47156
## Residuals    24 31.849   1.3271
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05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

Analysis of Variance Table

##

Response: fwd_max_length

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## age         1  7.0082   7.0082   6.2169 0.02205 *
## Genotype     1  1.3083   1.3083   1.1606 0.29483
## age:Genotype  1  1.9174   1.9174   1.7009 0.20775
## Residuals    19 21.4183   1.1273
## ---
## 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 -0.84896 -0.01952  1.03899  2.24792
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      9.86227    1.62707   6.061 2.98e-07 ***
## age             -0.07428    0.03173  -2.341  0.0239 *
## GenotypeAPOE4    -4.79679    2.12519  -2.257  0.0291 *
## sexMale          -3.95810    1.94959  -2.030  0.0485 *
## age:GenotypeAPOE4  0.10066    0.04302   2.340  0.0240 *
## age:sexMale       0.07220    0.03769   1.915  0.0621 .
## GenotypeAPOE4:sexMale 3.40171    2.97332   1.144  0.2589
## age:GenotypeAPOE4:sexMale -0.07604    0.05889  -1.291  0.2035
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.337 on 43 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.1646, Adjusted R-squared:  0.02858
## F-statistic:  1.21 on 7 and 43 DF,  p-value: 0.3181
```

```
##
## 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
## -1.79792 -0.79479 -0.01952  0.20104  2.24792
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    5.904167    1.034404   5.708 1.68e-05 ***
## age           -0.002083    0.019590  -0.106  0.916
## GenotypeAPOE4  -1.395082    2.002751  -0.697  0.494
## age:GenotypeAPOE4 0.024627    0.038723   0.636  0.532
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.288 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.02879, Adjusted R-squared: -0.1246
## F-statistic: 0.1877 on 3 and 19 DF,  p-value: 0.9034

## Analysis of Variance Table
##
## Response: bckwds_max_length
##              Df Sum Sq Mean Sq F value Pr(>F)
## age              1  0.467   0.4671   0.2614 0.6118
## Genotype          1  0.043   0.0433   0.0242 0.8770
## sex              1  2.650   2.6502   1.4827 0.2300
## age:Genotype      1  4.966   4.9664   2.7785 0.1028
## age:sex           1  3.766   3.7659   2.1069 0.1539
## Genotype:sex      1  0.268   0.2679   0.1499 0.7006
## age:Genotype:sex  1  2.980   2.9801   1.6673 0.2035
```

```
## Residuals      43 76.859  1.7874
```

```
## 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
```

```
## ---
```

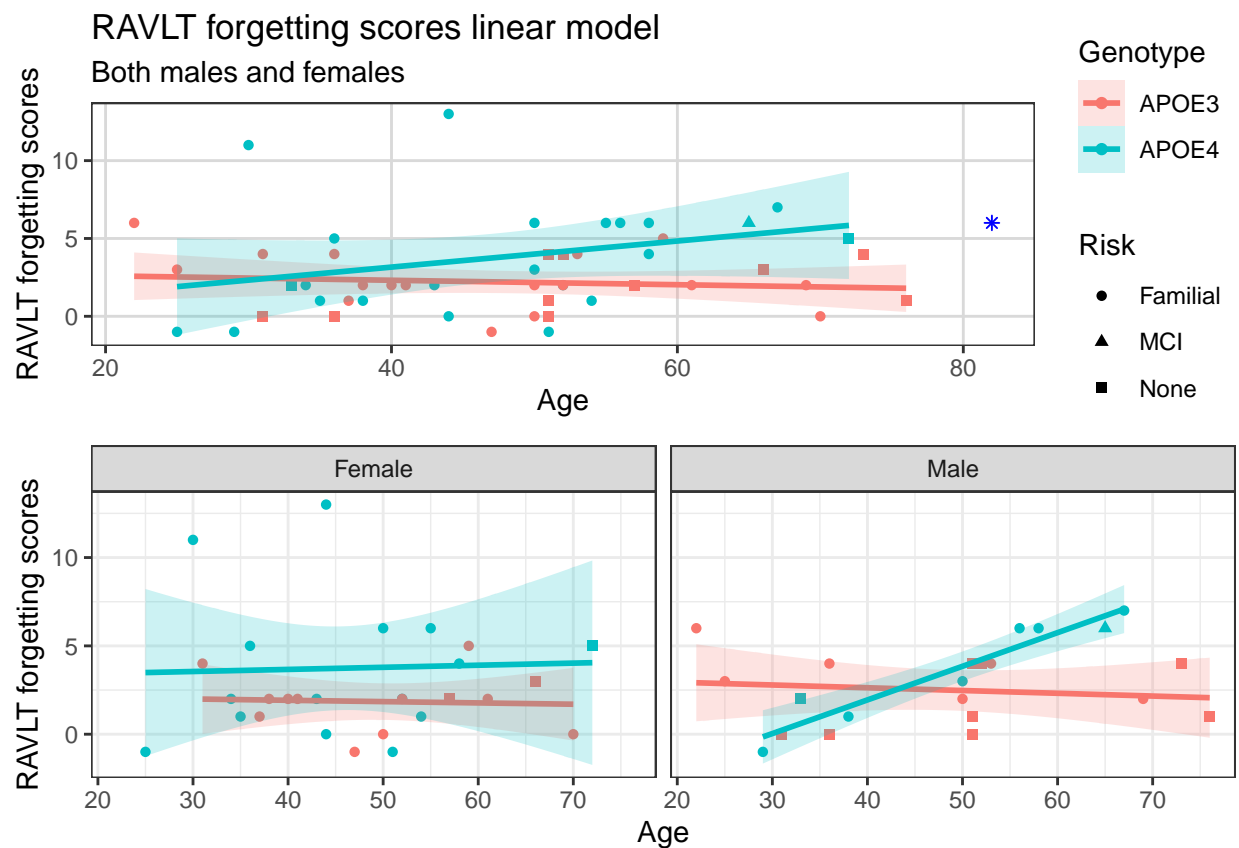
```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
##
```

```
## Response: bckwds_max_length
```

```
##          Df Sum Sq Mean Sq F value Pr(>F)
## age       1  0.1072  0.10725   0.0647 0.8020
## Genotype   1  0.1559  0.15592   0.0940 0.7624
## age:Genotype 1  0.6706  0.67058   0.4045 0.5324
## Residuals 19 31.5010  1.65795
```



```
##
```

```
## Call:
```

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

```
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4.7982 -1.6721  0.0729  1.3617  9.2849
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.216131   3.350983   0.661   0.512
## age             -0.007411   0.065357  -0.113   0.910
## GenotypeAPOE4     0.976811   4.376866   0.223   0.824
## sexMale          1.040196   4.067477   0.256   0.799
## age:GenotypeAPOE4  0.019279   0.088609   0.218   0.829
## age:sexMale       -0.008253   0.079492  -0.104   0.918
## GenotypeAPOE4:sexMale -9.910124   6.158011  -1.609   0.115
## age:GenotypeAPOE4:sexMale 0.186829   0.122479   1.525   0.135
##
## Residual standard error: 2.753 on 42 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.2167, Adjusted R-squared:  0.08611
## F-statistic:  1.66 on 7 and 42 DF,  p-value: 0.1456

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

##
## Call:
## lm(formula = RAVLT_FORGETTING ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.7708 -0.8457 -0.1292  1.3711  3.0883
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      3.25633    1.42582   2.284 0.034746 *
## age             -0.01566    0.02798  -0.560 0.582563
## GenotypeAPOE4    -8.93331    2.67896  -3.335 0.003688 **
## age:GenotypeAPOE4  0.20611    0.05229   3.941 0.000957 ***
```

```

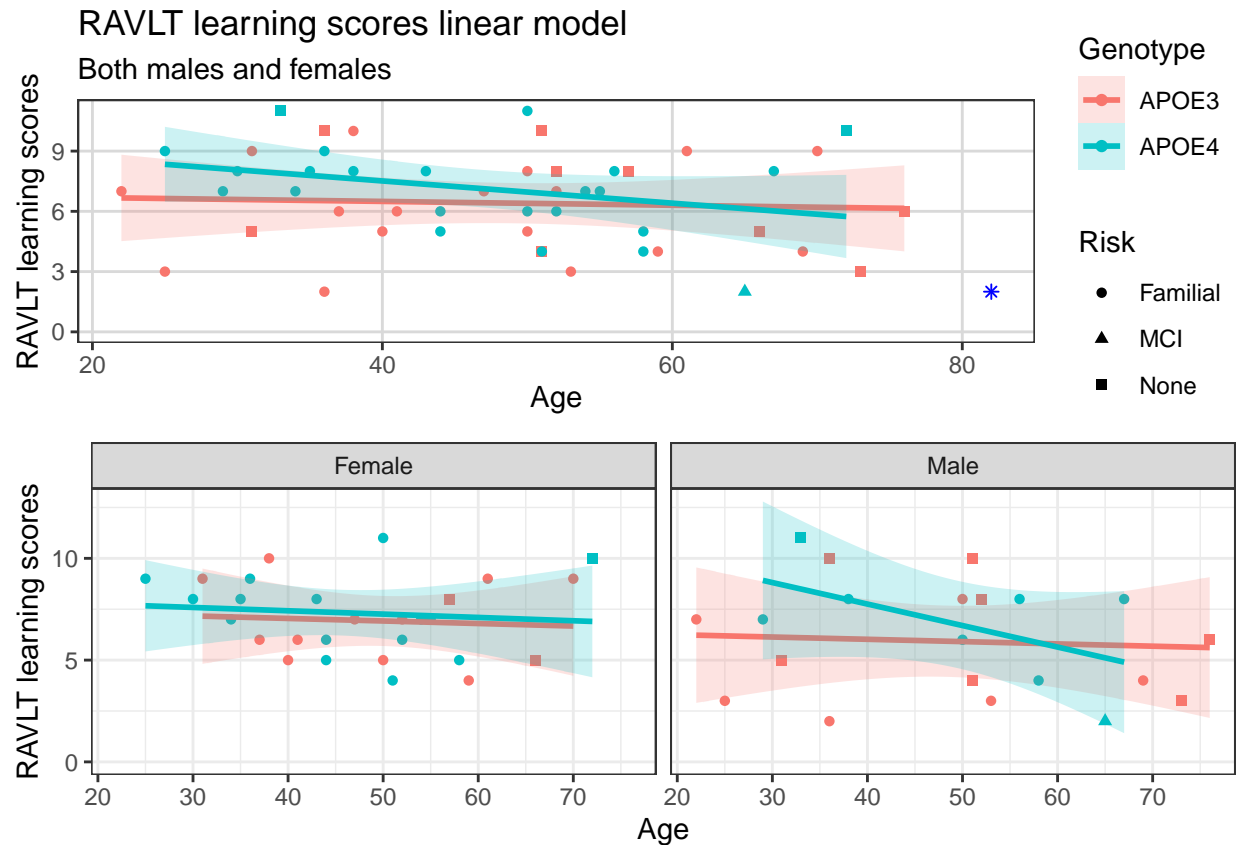
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.703 on 18 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.5459, Adjusted R-squared:  0.4703
## F-statistic: 7.214 on 3 and 18 DF,  p-value: 0.002222

## Analysis of Variance Table
##
## Response: RAVLT_FORGETTING
##              Df Sum Sq Mean Sq F value    Pr(>F)
## age           1   3.84   3.842   0.5067 0.48051
## Genotype      1  31.92  31.916   4.2097 0.04646 *
## sex           1   1.51   1.513   0.1996 0.65733
## age:Genotype  1  20.23  20.229   2.6682 0.10985
## age:sex       1  10.86  10.857   1.4321 0.23814
## Genotype:sex  1   2.08   2.075   0.2738 0.60357
## age:Genotype:sex 1  17.64  17.641   2.3268 0.13466
## Residuals    42 318.43   7.582
## ---
## 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 10.423   10.423   3.5944 0.0741443 .
## Genotype      1   7.288    7.288   2.5133 0.1303007
## age:Genotype  1 45.048   45.048  15.5349 0.0009569 ***
## Residuals    18 52.196    2.900
## ---
## 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
## -4.0670 -1.8865 -0.0717  1.9129  4.1020
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    7.544032   2.926035   2.578  0.0135 *
## age           -0.012438   0.057069  -0.218  0.8285
## GenotypeAPOE4    0.534668   3.821823   0.140  0.8894
## sexMale        -1.071501   3.551669  -0.302  0.7644
## age:GenotypeAPOE4 -0.003931   0.077372  -0.051  0.9597
## age:sexMale      0.001173   0.069411   0.017  0.9866
## GenotypeAPOE4:sexMale  4.972612   5.377096   0.925  0.3604
## age:GenotypeAPOE4:sexMale -0.090456   0.106947  -0.846  0.4025
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.404 on 42 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.1191, Adjusted R-squared:  -0.02768
## F-statistic: 0.8114 on 7 and 42 DF, p-value: 0.5828
```

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

##
## Call:
## lm(formula = RAVLT_FORGETTING ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.7708 -0.8457 -0.1292  1.3711  3.0883
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    3.25633   1.42582   2.284 0.034746 *
## age           -0.01566   0.02798  -0.560 0.582563
## GenotypeAPOE4  -8.93331   2.67896  -3.335 0.003688 **
## age:GenotypeAPOE4  0.20611   0.05229   3.941 0.000957 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.703 on 18 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.5459, Adjusted R-squared:  0.4703
## F-statistic: 7.214 on 3 and 18 DF, p-value: 0.002222

## Analysis of Variance Table
##
## Response: RAVLT_LEARNING
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1   8.242   8.2421   1.4258 0.2391
## Genotype       1   5.419   5.4194   0.9375 0.3385
## sex           1   7.518   7.5175   1.3005 0.2606
## age:Genotype   1   3.501   3.5007   0.6056 0.4408
## age:sex        1   3.031   3.0312   0.5244 0.4730
## Genotype:sex   1   0.988   0.9883   0.1710 0.6814
## age:Genotype:sex 1   4.135   4.1353   0.7154 0.4025
```



```
## Residuals      42 242.785  5.7806
```

```
## 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
```

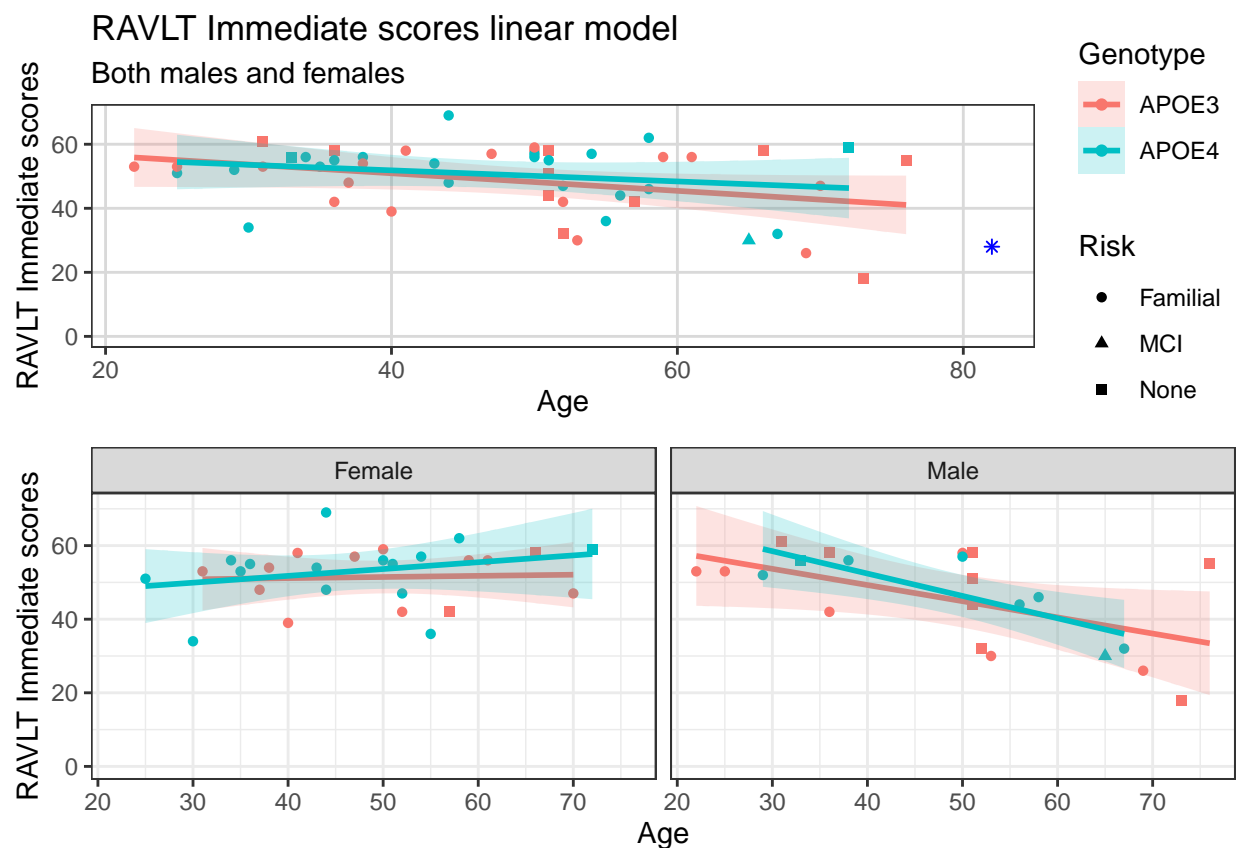
```
##
```

```
## Response: RAVLT_FORGETTING
```

```
##          Df Sum Sq Mean Sq F value    Pr(>F)
## age       1 10.423   10.423   3.5944 0.0741443 .
## Genotype   1  7.288    7.288   2.5133 0.1303007
## age:Genotype 1 45.048   45.048 15.5349 0.0009569 ***
## Residuals 18 52.196    2.900
```

```
## ---
```

```
## 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  -6.521   1.838   5.557  21.539
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    49.90158    11.43116     4.365 8.11e-05 ***
## age              0.03125     0.22295     0.140  0.8892
## GenotypeAPOE4   -5.54286    14.93074    -0.371  0.7123
## sexMale         16.96501    13.87533     1.223  0.2283
## age:GenotypeAPOE4  0.15414     0.30227     0.510  0.6128
## age:sexMale     -0.47079     0.27117    -1.736  0.0899 .
## GenotypeAPOE4:sexMale 15.39767    21.00674     0.733  0.4676
## age:GenotypeAPOE4:sexMale -0.32260     0.41781    -0.772  0.4444
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.393 on 42 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.3302, Adjusted R-squared:  0.2186
## F-statistic: 2.958 on 7 and 42 DF,  p-value: 0.01297

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

##
## Call:
## lm(formula = RAVLT_FORGETTING ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.7708 -0.8457 -0.1292  1.3711  3.0883
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)

```

```
## (Intercept)      3.25633      1.42582      2.284 0.034746 *
## age              -0.01566      0.02798     -0.560 0.582563
## GenotypeAPOE4    -8.93331      2.67896     -3.335 0.003688 **
## age:GenotypeAPOE4 0.20611      0.05229      3.941 0.000957 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.703 on 18 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.5459, Adjusted R-squared:  0.4703
## F-statistic: 7.214 on 3 and 18 DF,  p-value: 0.002222
```

Analysis of Variance Table

##

Response: RAVLT_IMMEDIATE

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	526.6	526.61	5.9689	0.018845 *
## Genotype	1	35.8	35.77	0.4055	0.527729
## sex	1	400.6	400.58	4.5404	0.039003 *
## age:Genotype	1	47.0	47.03	0.5331	0.469356
## age:sex	1	764.2	764.16	8.6615	0.005274 **
## Genotype:sex	1	0.2	0.18	0.0021	0.963955
## age:Genotype:sex	1	52.6	52.60	0.5962	0.444361
## Residuals	42	3705.5	88.23		

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		

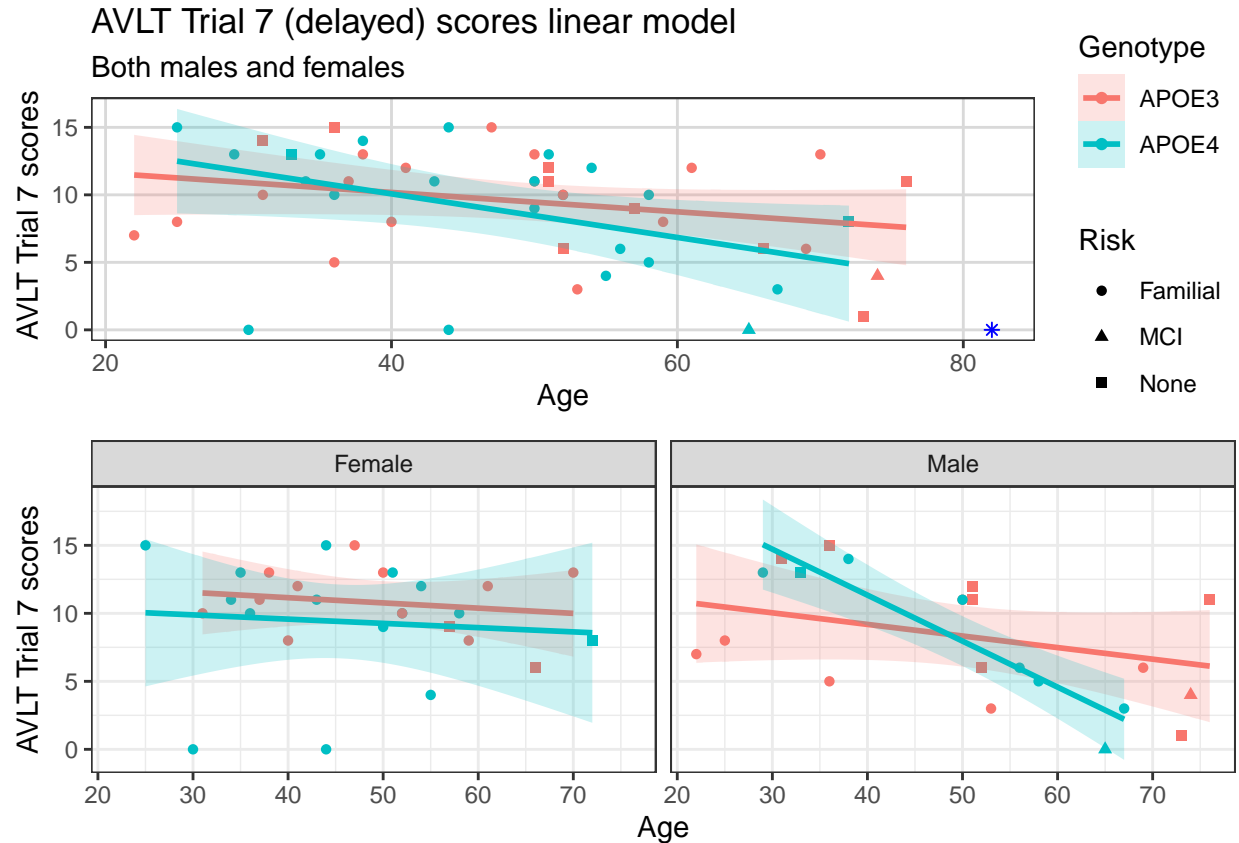
Analysis of Variance Table

##

Response: RAVLT_FORGETTING

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	10.423	10.423	3.5944	0.0741443 .
## Genotype	1	7.288	7.288	2.5133	0.1303007
## age:Genotype	1	45.048	45.048	15.5349	0.0009569 ***
## Residuals	18	52.196	2.900		

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
## -9.886  -2.226   0.302   2.752   5.552
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    12.688351    4.629210   2.741  0.00889 **
## age             -0.038442    0.090287  -0.426  0.67240
## GenotypeAPOE4   -1.864986    6.046415  -0.308  0.75923
## sexMale         -0.095758    5.546821  -0.017  0.98631
## age:GenotypeAPOE4  0.007182    0.122409   0.059  0.95349
## age:sexMale     -0.046744    0.107242  -0.436  0.66511
## GenotypeAPOE4:sexMale 14.136121    8.459466   1.671  0.10198
## age:GenotypeAPOE4:sexMale -0.260153    0.167540  -1.553  0.12781
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.804 on 43 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.294, Adjusted R-squared:  0.179
## F-statistic: 2.557 on 7 and 43 DF, p-value: 0.02703
```

```
##
## 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
	-5.3741	-2.3759	-0.2507	2.7519	5.4741

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

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	12.59259	2.84885	4.420	0.000294 ***
age	-0.08519	0.05395	-1.579	0.130874
GenotypeAPOE4	12.27114	5.51577	2.225	0.038412 *
age:GenotypeAPOE4	-0.25297	0.10665	-2.372	0.028408 *

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.546 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.4575, Adjusted R-squared:  0.3718
## F-statistic: 5.341 on 3 and 19 DF,  p-value: 0.007721

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

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	103.68	103.683	7.1660	0.01047 *
Genotype	1	8.59	8.594	0.5940	0.44511
sex	1	37.65	37.649	2.6021	0.11404
age:Genotype	1	14.76	14.760	1.0201	0.31814
age:sex	1	53.20	53.195	3.6766	0.06184 .
Genotype:sex	1	6.26	6.258	0.4325	0.51425
age:Genotype:sex	1	34.89	34.886	2.4111	0.12781

```
## Residuals      43 622.15  14.469
## ---
## 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
```

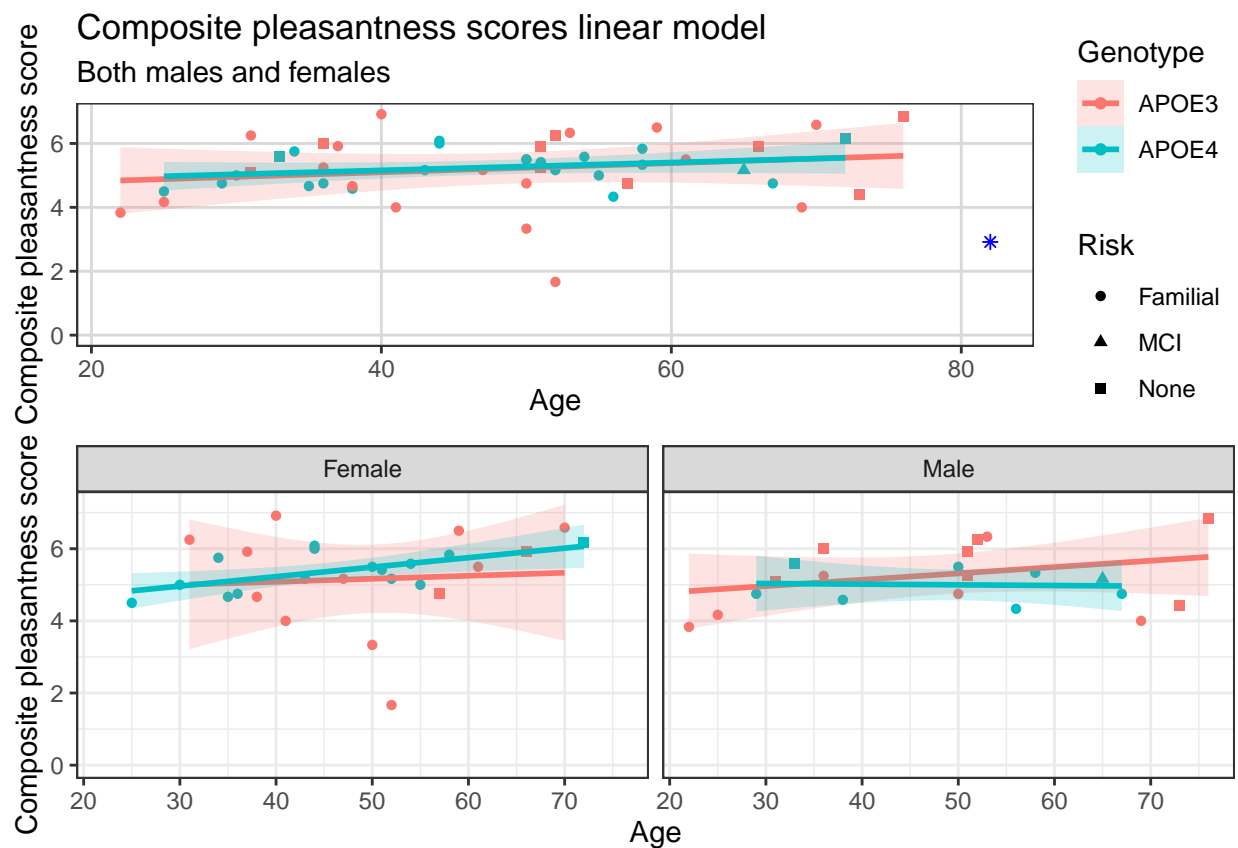
```
##
```

```
## Response: AVL_Trial7
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## age         1 130.323  130.323  10.3631 0.004516 **
## Genotype     1   0.419    0.419   0.0333 0.857158
## age:Genotype 1  70.757   70.757   5.6265 0.028408 *
## Residuals    19 238.937   12.576
```

```
## ---
```

```
## 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 -0.4217  0.0303  0.6081  1.8325
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      4.751795    1.204979   3.943 0.000299 ***
## age              0.008310    0.023502   0.354 0.725406
## GenotypeAPOE4     -0.576938    1.573877  -0.367 0.715779
## sexMale           -0.315086    1.462623  -0.215 0.830479
## age:GenotypeAPOE4  0.017986    0.031863   0.564 0.575424
## age:sexMale        0.009273    0.028585   0.324 0.747248
## GenotypeAPOE4:sexMale 1.231834    2.214358   0.556 0.580962
## age:GenotypeAPOE4:sexMale -0.037420    0.044042  -0.850 0.400344
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9901 on 42 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.07954,    Adjusted R-squared:  -0.07387
## F-statistic: 0.5185 on 7 and 42 DF,  p-value: 0.8155

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

##
## Call:
## lm(formula = Composite_Pleasantness ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.6499 -0.5339  0.1409  0.5756  1.0603
##

```

```
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    4.43671    0.68797   6.449 4.55e-06 ***
## age            0.01758    0.01350   1.302   0.209
## GenotypeAPOE4  0.65490    1.29261   0.507   0.619
## age:GenotypeAPOE4 -0.01943    0.02523  -0.770   0.451
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8216 on 18 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.1141, Adjusted R-squared:  -0.03352
## F-statistic: 0.773 on 3 and 18 DF,  p-value: 0.5241
```

Analysis of Variance Table

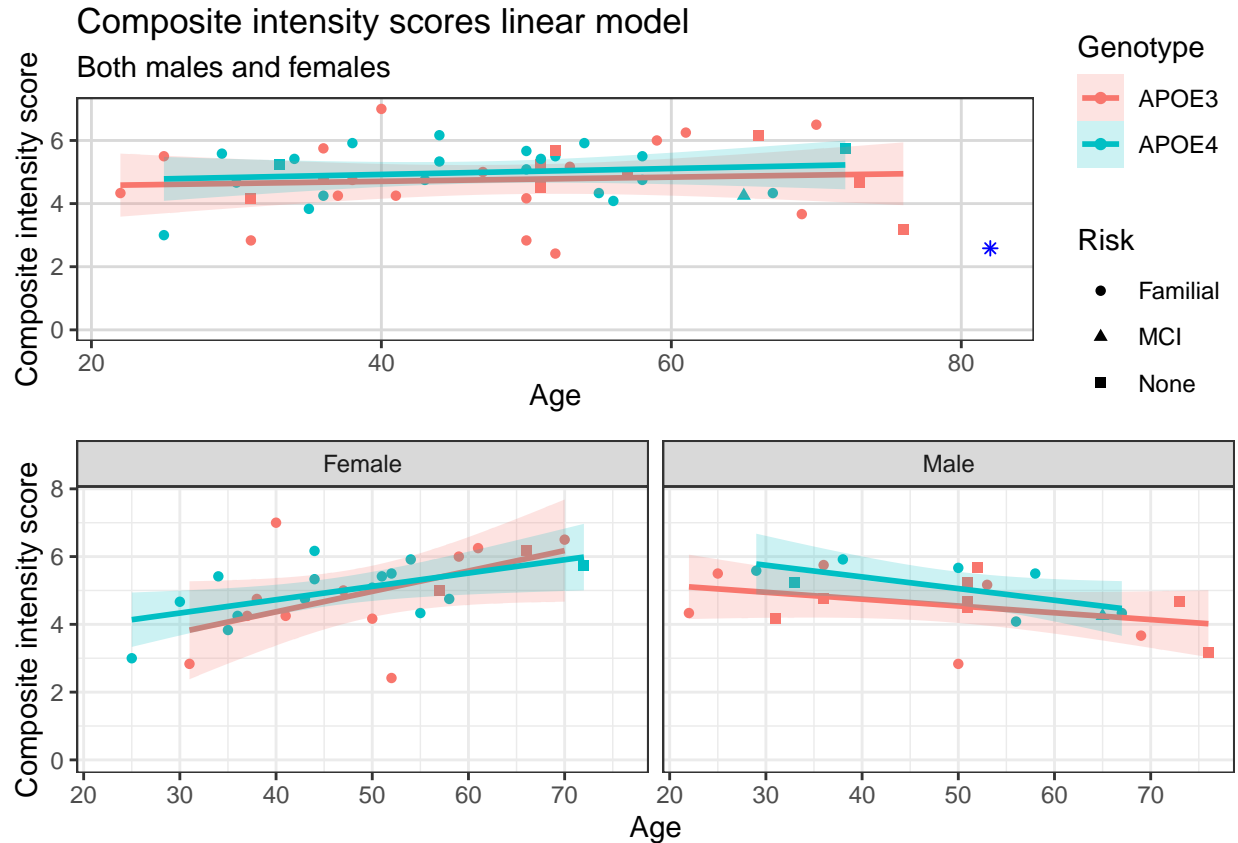
```
##
## Response: Composite_Pleasantness
##               Df Sum Sq Mean Sq F value Pr(>F)
## age            1  1.648  1.64788   1.6809 0.2019
## Genotype        1  0.023  0.02335   0.0238 0.8781
## sex            1  0.135  0.13494   0.1377 0.7125
## age:Genotype    1  0.003  0.00326   0.0033 0.9543
## age:sex         1  0.057  0.05726   0.0584 0.8102
## Genotype:sex    1  0.983  0.98344   1.0032 0.3223
## age:Genotype:sex 1  0.708  0.70769   0.7219 0.4003
## Residuals      42 41.174  0.98033
```

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  0.7065  0.70651   1.0465 0.3199
## Genotype        1  0.4585  0.45846   0.6791 0.4207
## age:Genotype    1  0.4005  0.40049   0.5932 0.4512
## Residuals      18 12.1517  0.67510
```

```
##
## Call:
## lm(formula = Composite_Intensity ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.67635 -0.46874  0.01877  0.49640  2.62961
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.961616   1.103966   1.777  0.08283 .
## age             0.060219   0.021531   2.797  0.00775 **
## GenotypeAPOE4    1.192275   1.441938   0.827  0.41299
## sexMale         3.588030   1.340012   2.678  0.01053 *
## age:GenotypeAPOE4 -0.020895  0.029192  -0.716  0.47808
## age:sexMale      -0.080355  0.026188  -3.068  0.00376 **
## GenotypeAPOE4:sexMale 0.039567  2.028728   0.020  0.98453
## age:GenotypeAPOE4:sexMale 0.006514  0.040350   0.161  0.87252
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9071 on 42 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.2987, Adjusted R-squared:  0.1818
## F-statistic: 2.555 on 7 and 42 DF, p-value: 0.02753
```

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

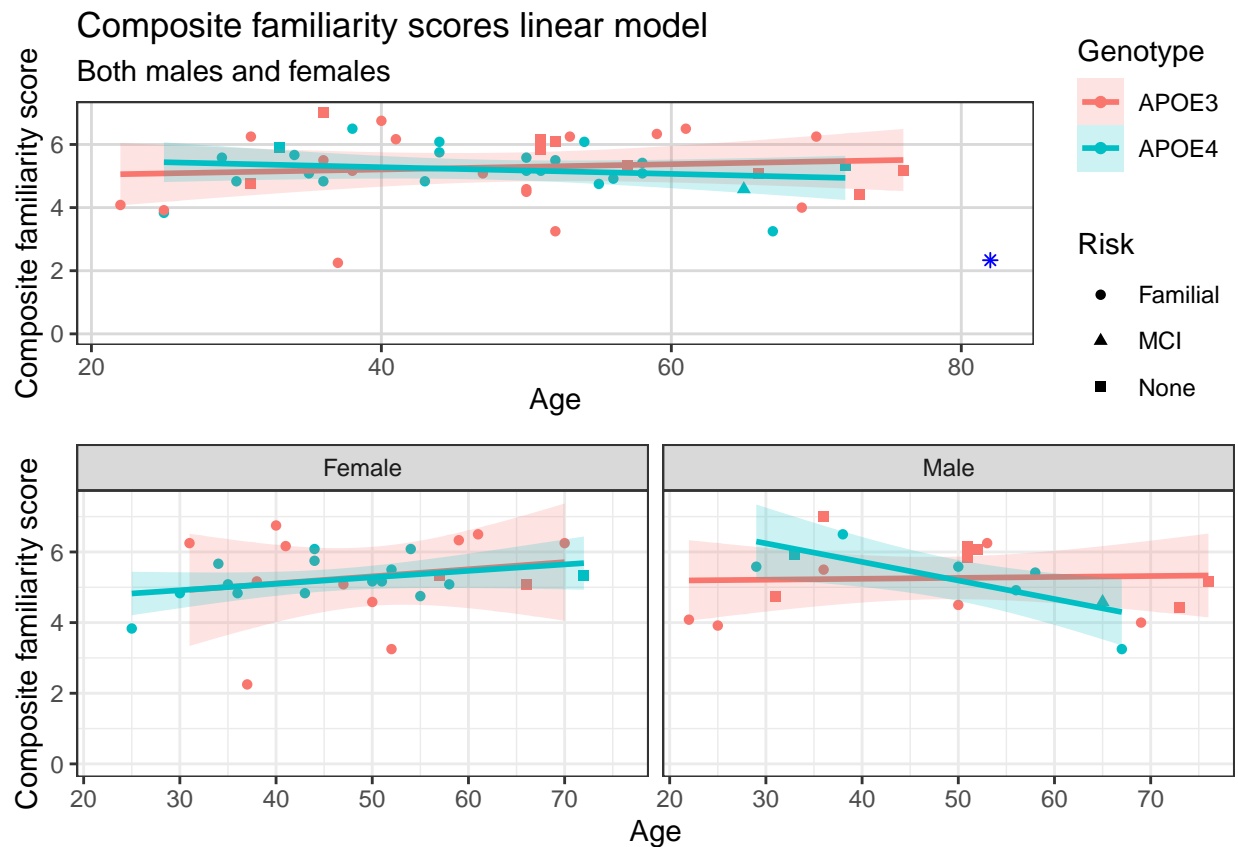
##
## Call:
## lm(formula = Composite_Intensity ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.70953 -0.46832 -0.04874  0.60499  1.16408
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    5.54965    0.64930   8.547 9.43e-08 ***
## age           -0.02014    0.01274  -1.580   0.132
## GenotypeAPOE4    1.23184    1.21996   1.010   0.326
## age:GenotypeAPOE4 -0.01438    0.02381  -0.604   0.553
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.7755 on 18 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.2947, Adjusted R-squared:  0.1771
## F-statistic: 2.507 on 3 and 18 DF,  p-value: 0.0917

## Analysis of Variance Table
##
## Response: Composite_Intensity
##              Df Sum Sq Mean Sq F value    Pr(>F)
## age            1  0.461  0.4612   0.5604 0.458253
## Genotype        1  0.714  0.7137   0.8674 0.357009
## sex            1  0.347  0.3474   0.4222 0.519371
## age:Genotype    1  0.036  0.0363   0.0441 0.834702
## age:sex         1 12.773 12.7735 15.5233 0.000302 ***
## Genotype:sex    1  0.365  0.3654   0.4441 0.508815
## age:Genotype:sex 1  0.021  0.0214   0.0261 0.872516
```

```
## Residuals      42 34.560  0.8229
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## Analysis of Variance Table
##
## Response: Composite_Intensity
##           Df Sum Sq Mean Sq F value    Pr(>F)
## age        1  2.9014   2.9014    4.8249 0.04139 *
## Genotype    1  1.4011   1.4010    2.3299 0.14429
## age:Genotype 1  0.2193   0.2193    0.3647 0.55344
## Residuals   18 10.8241   0.60134
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
##
## Call:
## lm(formula = Composite_Familiarity ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.79759 -0.52771 -0.02146  0.67737  1.77001
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      4.302877    1.187815   3.623  0.00078 ***
## age              0.020127    0.023167   0.869  0.38990
## GenotypeAPOE4     0.064319    1.551458   0.041  0.96713
## sexMale           0.833594    1.441790   0.578  0.56624
## age:GenotypeAPOE4 -0.001837    0.031409  -0.058  0.95363
## age:sexMale       -0.017530    0.028177  -0.622  0.53723
## GenotypeAPOE4:sexMale  2.620374    2.182816   1.200  0.23669
## age:GenotypeAPOE4:sexMale -0.053334    0.043415  -1.228  0.22610
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.976 on 42 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.1237, Adjusted R-squared:  -0.0223
## F-statistic: 0.8473 on 7 and 42 DF,  p-value: 0.5551

##
## 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

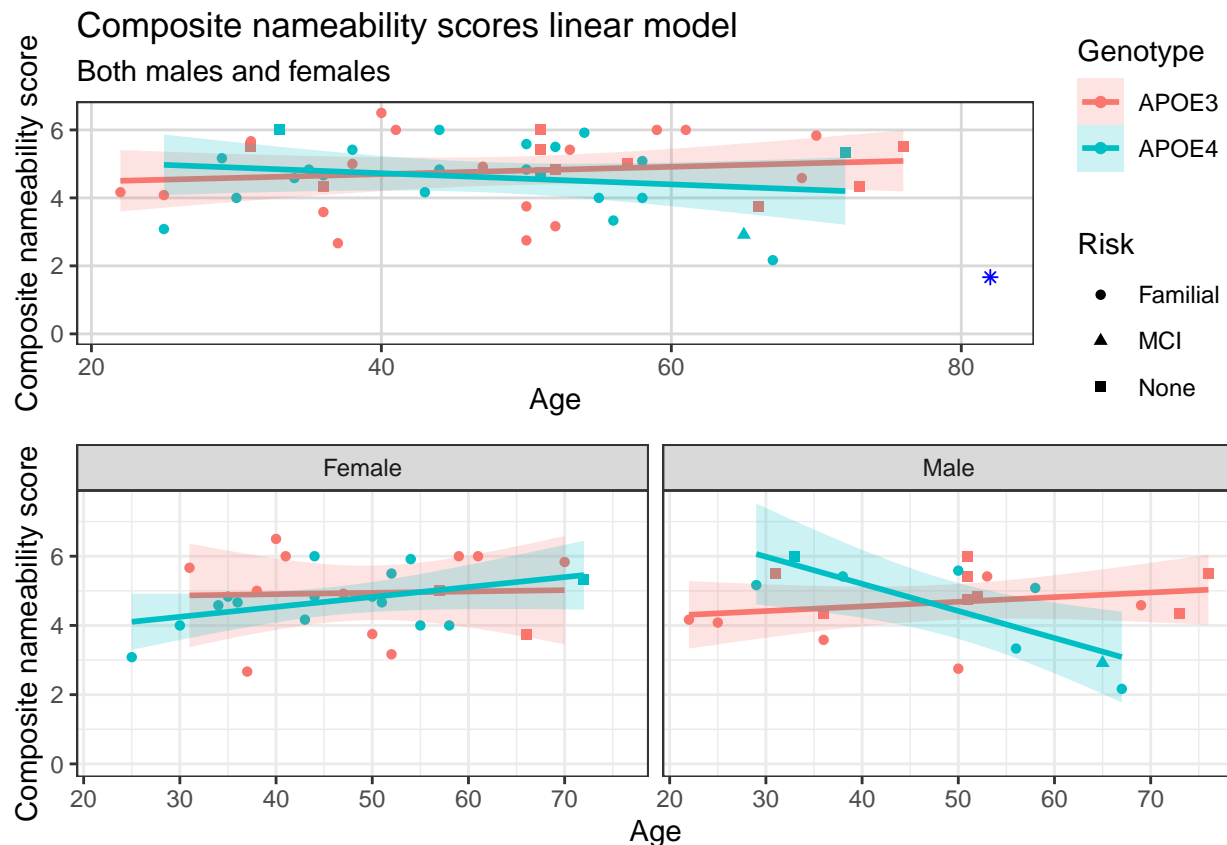
##
## Call:
## lm(formula = Composite_Familiarity ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.3157 -0.7531  0.1096  0.6687  1.7700
```

```
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    5.136471   0.775686   6.622 3.24e-06 ***
## age            0.002598   0.015224   0.171  0.8664
## GenotypeAPOE4   2.684693   1.457427   1.842  0.0820 .
## age:GenotypeAPOE4 -0.055172  0.028449  -1.939  0.0683 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9264 on 18 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.2114, Adjusted R-squared:  0.08
## F-statistic: 1.609 on 3 and 18 DF,  p-value: 0.2224
```

```
## Analysis of Variance Table
##
## Response: Composite_Familiarity
##               Df Sum Sq Mean Sq F value  Pr(>F)
## age            1  0.009  0.0086  0.0090 0.92468
## Genotype       1  0.071  0.0709  0.0745 0.78627
## sex            1  0.004  0.0040  0.0042 0.94878
## age:Genotype   1  0.787  0.7870  0.8262 0.36857
## age:sex        1  3.339  3.3388  3.5050 0.06816 .
## Genotype:sex   1  0.003  0.0032  0.0033 0.95413
## age:Genotype:sex 1  1.438  1.4377  1.5092 0.22610
## Residuals     42 40.009  0.9526
## ---
## 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  0.9102  0.9102  1.0605 0.3167
## Genotype       1  0.0037  0.0037  0.0044 0.9481
## age:Genotype   1  3.2279  3.2279  3.7611 0.0683 .
## Residuals     18 15.4481  0.8582
## ---
## 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 -0.57560  0.04163  0.71289  1.59604
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    4.749386   1.183443   4.013 0.000242 ***
## age             0.003864   0.023082   0.167 0.867841
## GenotypeAPOE4   -1.361723   1.545746  -0.881 0.383359
## sexMale         -0.735555   1.436482  -0.512 0.611296
## age:GenotypeAPOE4  0.024835   0.031293   0.794 0.431877
## age:sexMale       0.009533   0.028074   0.340 0.735882
## GenotypeAPOE4:sexMale  5.684170   2.174781   2.614 0.012381 *
## age:GenotypeAPOE4:sexMale -0.116574   0.043255  -2.695 0.010077 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9724 on 42 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.2438, Adjusted R-squared:  0.1177
## F-statistic: 1.934 on 7 and 42 DF,  p-value: 0.088
```

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

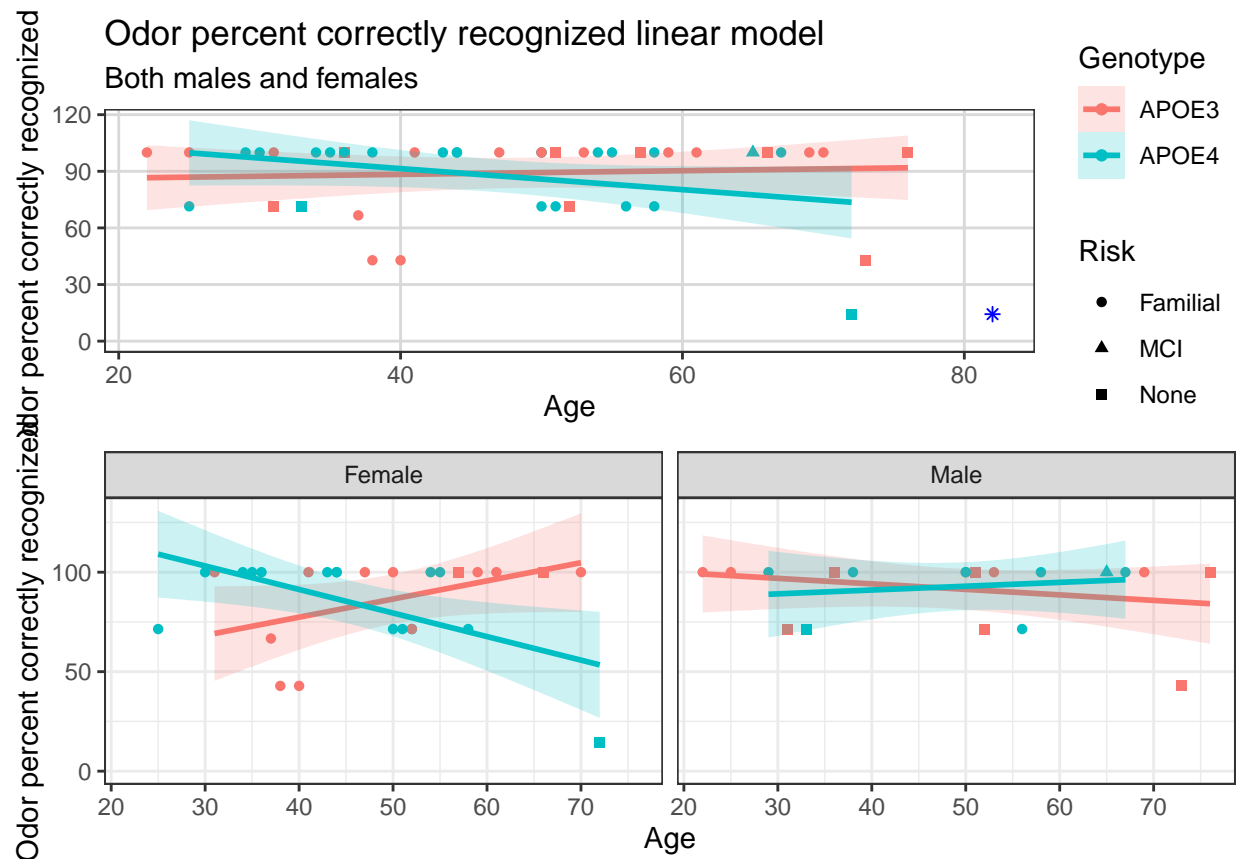
##
## Call:
## lm(formula = Composite_Nameability ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.93368 -0.55055 -0.04449  0.63660  1.30292
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    4.01383    0.75292   5.331 4.56e-05 ***
## age             0.01340    0.01478   0.907  0.37660
## GenotypeAPOE4   4.32245    1.41466   3.055  0.00681 **
## age:GenotypeAPOE4 -0.09174    0.02761  -3.322  0.00379 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8992 on 18 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.4071, Adjusted R-squared:  0.3083
## F-statistic: 4.12 on 3 and 18 DF, p-value: 0.02176

## Analysis of Variance Table
##
## Response: Composite_Nameability
##              Df Sum Sq Mean Sq F value  Pr(>F)
## age             1  0.002   0.0017  0.0018 0.96618
## Genotype        1  0.419   0.4188  0.4429 0.50939
## sex             1  0.819   0.8195  0.8666 0.35722
## age:Genotype    1  1.423   1.4235  1.5054 0.22668
## age:sex         1  3.267   3.2673  3.4553 0.07007 .
## Genotype:sex    1  0.002   0.0025  0.0026 0.95929
## age:Genotype:sex 1  6.868   6.8682  7.2633 0.01008 *
```

```
## Residuals      42 39.715  0.9456
## ---
## 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  0.8914  0.8914   1.1024 0.307624
## Genotype    1  0.1773  0.1773   0.2192 0.645233
## age:Genotype 1  8.9247  8.9247  11.0372 0.003791 **
## Residuals   18 14.5548  0.8086
## ---
## 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
## -42.142  -6.567   4.058   9.439  30.822
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      40.8875     22.5515   1.813  0.07697 .
## age              0.9126      0.4398   2.075  0.04417 *
## GenotypeAPOE4     97.7702     29.4555   3.319  0.00187 **
## sexMale          64.3087     27.3733   2.349  0.02359 *
## age:GenotypeAPOE4 -2.0962      0.5963  -3.515  0.00107 **
## age:sexMale       -1.1893      0.5350  -2.223  0.03165 *
## GenotypeAPOE4:sexMale -119.6267    41.4422  -2.887  0.00613 **
## age:GenotypeAPOE4:sexMale  2.5652      0.8243   3.112  0.00334 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 18.53 on 42 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.2708, Adjusted R-squared:  0.1493
## F-statistic: 2.228 on 7 and 42 DF,  p-value: 0.05084

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

##
## Call:
## lm(formula = Recognized ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -42.142   1.098   5.136   8.914  15.831
##

```

```
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    105.1962    13.7458   7.653 4.58e-07 ***
## age            -0.2767     0.2698  -1.026   0.319
## GenotypeAPOE4  -21.8565    25.8267  -0.846   0.409
## age:GenotypeAPOE4  0.4689     0.5041   0.930   0.365
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.42 on 18 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.06616,    Adjusted R-squared:  -0.08948
## F-statistic: 0.4251 on 3 and 18 DF,  p-value: 0.7374
```

Analysis of Variance Table

##

Response: Recognized

```
##               Df Sum Sq Mean Sq F value    Pr(>F)
## age            1  234.8   234.8   0.6838 0.412940
## Genotype       1   50.4    50.4   0.1468 0.703511
## sex            1  537.9   537.9   1.5664 0.217657
## age:Genotype   1 1110.8  1110.8   3.2350 0.079270 .
## age:sex        1   29.4    29.4   0.0857 0.771151
## Genotype:sex   1   66.8    66.8   0.1944 0.661533
## age:Genotype:sex 1 3325.7  3325.7   9.6853 0.003336 **
## Residuals     42 14421.6   343.4
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Analysis of Variance Table

##

Response: Recognized

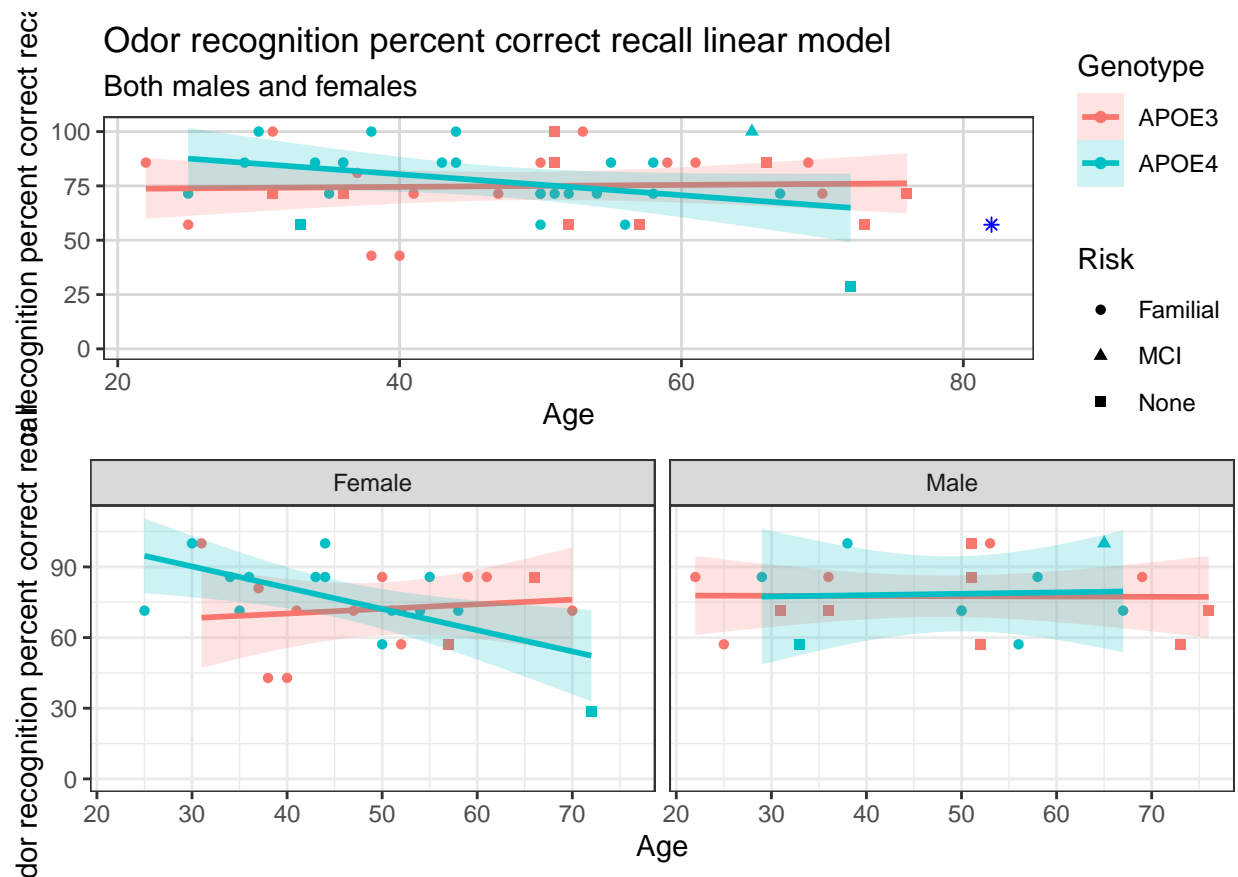
```
##               Df Sum Sq Mean Sq F value    Pr(>F)
## age            1  173.3   173.3   0.4346 0.516024
## Genotype       1   48.5    48.5   0.1217 0.730219
## age:Genotype   1 4243.2  4243.2  10.6406 0.003304 **
## Residuals     24 9570.5   398.8
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01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

Analysis of Variance Table

##

Response: Recognized

```
##               Df Sum Sq Mean Sq F value    Pr(>F)
## age            1  103.2  103.247   0.3831 0.5437
## Genotype       1    7.2    7.239   0.0269 0.8716
## age:Genotype   1  233.2  233.201   0.8653 0.3646
## Residuals     18 4851.1  269.507
```



```
##
## Call:
## lm(formula = PercentCorrectRecall ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -27.357 -12.733   1.044   9.448  31.553
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    62.3631    19.7818   3.153  0.00298 **
## age              0.1963     0.3858   0.509  0.61363
## GenotypeAPOE4    54.8840    25.8379   2.124  0.03959 *
## sexMale          15.6935    24.0115   0.654  0.51694
## age:GenotypeAPOE4 -1.0979     0.5231  -2.099  0.04187 *
## age:sexMale      -0.2067     0.4693  -0.441  0.66180
## GenotypeAPOE4:sexMale -57.2244    36.3525  -1.574  0.12296
## age:GenotypeAPOE4:sexMale  1.1661     0.7230   1.613  0.11428
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.25 on 42 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.1575, Adjusted R-squared:  0.01703
## F-statistic: 1.121 on 7 and 42 DF, p-value: 0.3682
```

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

##
## Call:
## lm(formula = PrecentCorrectRecall ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -21.8035  -7.9071   0.4102   8.2919  22.4983
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    78.05666    13.63890   5.723   2e-05 ***
## age            -0.01047     0.26769  -0.039   0.969
## GenotypeAPOE4  -2.34045    25.62598  -0.091   0.928
## age:GenotypeAPOE4  0.06815     0.50021   0.136   0.893
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.29 on 18 degrees of freedom
## (3 observations deleted due to missingness)
## Multiple R-squared:  0.002225, Adjusted R-squared:  -0.1641
## F-statistic: 0.01338 on 3 and 18 DF,  p-value: 0.9978

## Analysis of Variance Table
##
## Response: PrecentCorrectRecall
##              Df Sum Sq Mean Sq F value Pr(>F)
## age             1   270.1   270.12   1.0224  0.3177
## Genotype         1    35.8    35.83   0.1356  0.7145
## sex              1   212.2   212.24   0.8033  0.3752
## age:Genotype     1   697.1   697.08   2.6384  0.1118
## age:sex          1   170.0   169.97   0.6433  0.4270
## Genotype:sex     1     1.3     1.26   0.0048  0.9454
## age:Genotype:sex 1   687.2   687.24   2.6011  0.1143
```

```
## Residuals      42 11096.8  264.21
```

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

```
##
```

```
## Response: PrecentCorrectRecall
```

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

```
## age         1   704.5   704.53   2.6751 0.1150
```

```
## Genotype    1    34.7    34.65   0.1316 0.7200
```

```
## age:Genotype 1  1164.0  1164.04   4.4198 0.0462 *
```

```
## Residuals   24  6320.8   263.37
```

```
## ---
```

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

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

```
##
```

```
## Response: PrecentCorrectRecall
```

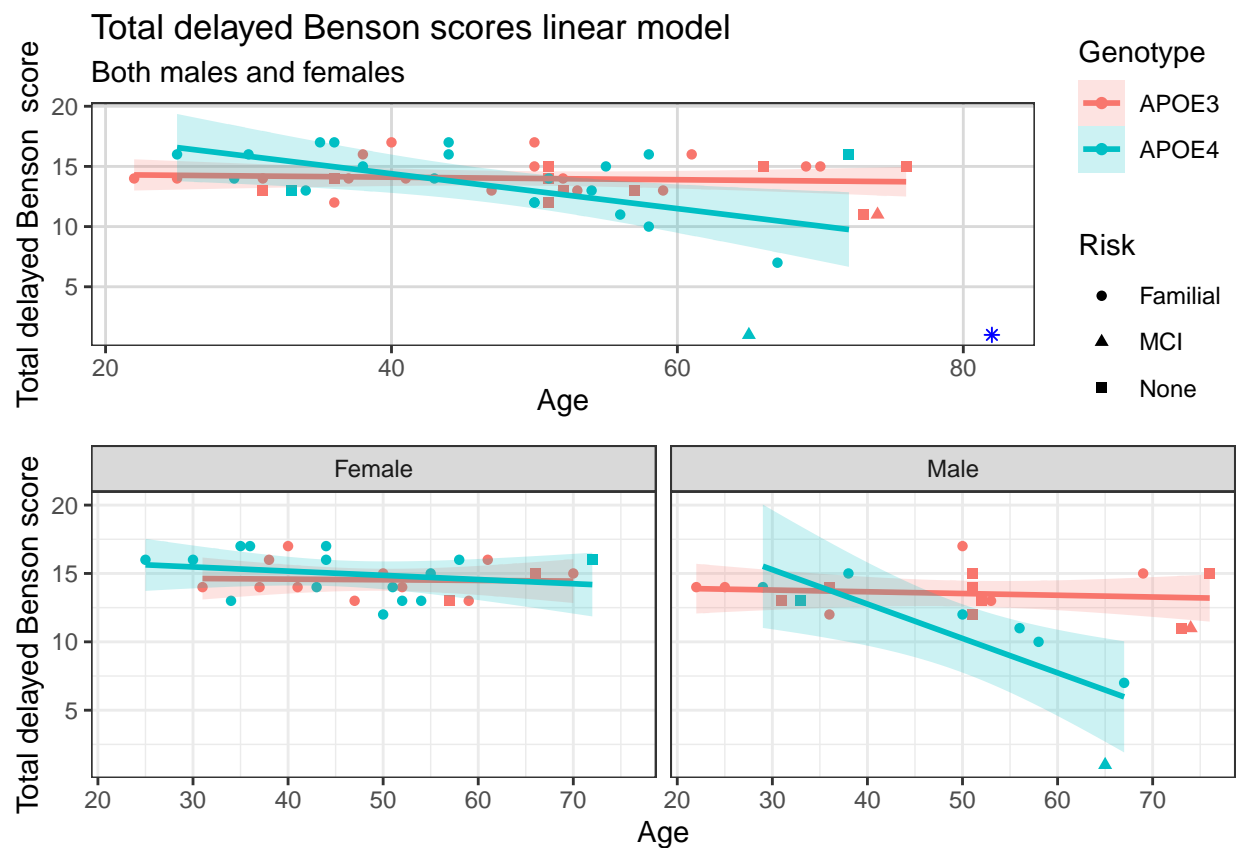
```
##           Df Sum Sq Mean Sq F value Pr(>F)
```

```
## age         1     0.5    0.546   0.0021 0.9643
```

```
## Genotype    1     5.2    5.180   0.0195 0.8904
```

```
## age:Genotype 1     4.9    4.926   0.0186 0.8931
```

```
## Residuals   18 4776.0   265.333
```



```
##
```

```
## Call:
```

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

```
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.4791 -1.5000  0.2884  1.4969  3.4667
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    14.776458   2.228846   6.630 4.43e-08 ***
## age           -0.004767   0.043471  -0.110  0.9132
## GenotypeAPOE4    1.621105   2.911194   0.557  0.5805
## sexMale        -0.606551   2.670652  -0.227  0.8214
## age:GenotypeAPOE4 -0.025926   0.058937  -0.440  0.6622
## age:sexMale     -0.007964   0.051634  -0.154  0.8781
## GenotypeAPOE4:sexMale  7.025609   4.073016   1.725  0.0917 .
## age:GenotypeAPOE4:sexMale -0.212688   0.080666  -2.637  0.0116 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.831 on 43 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.6039, Adjusted R-squared:  0.5395
## F-statistic: 9.367 on 7 and 43 DF,  p-value: 5.371e-07

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

##
## Call:
## lm(formula = Delay_BensonTotal ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.4791 -1.5214  0.1484  1.7215  3.4667
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)      14.16991      1.71935      8.241 1.07e-07 ***
## age              -0.01273      0.03256     -0.391 0.70016
## GenotypeAPOE4      8.64671      3.32889      2.597 0.01768 *
## age:GenotypeAPOE4 -0.23861      0.06436     -3.707 0.00149 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.14 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.6275, Adjusted R-squared:  0.5687
## F-statistic: 10.67 on 3 and 19 DF,  p-value: 0.0002477
```

Analysis of Variance Table

##

Response: Delay_BensonTotal

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	33.375	33.375	9.9505	0.002932 **
## Genotype	1	7.892	7.892	2.3531	0.132363
## sex	1	73.333	73.333	21.8638	2.904e-05 ***
## age:Genotype	1	33.741	33.741	10.0595	0.002795 **
## age:sex	1	15.701	15.701	4.6811	0.036098 *
## Genotype:sex	1	32.572	32.572	9.7112	0.003259 **
## age:Genotype:sex	1	23.317	23.317	6.9519	0.011604 *
## Residuals	43	144.226	3.354		

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		

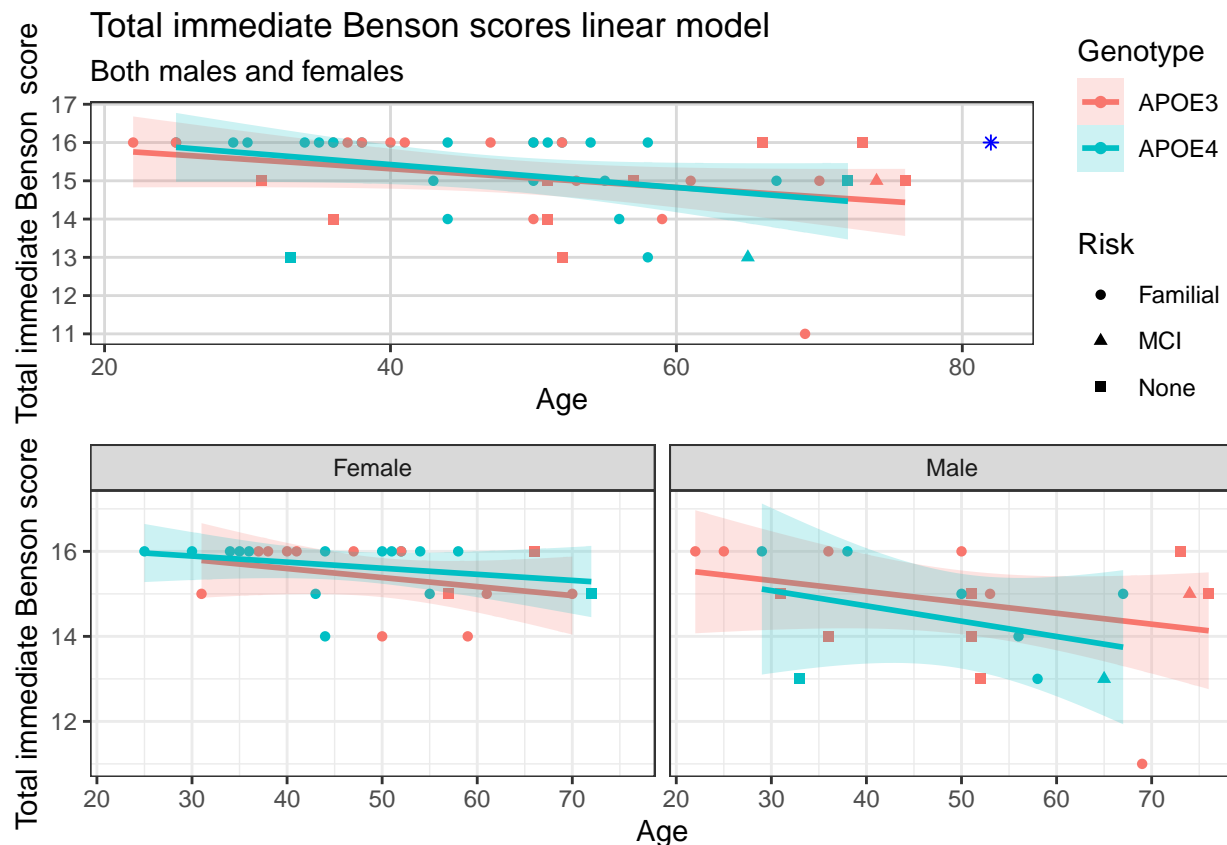
Analysis of Variance Table

##

Response: Delay_BensonTotal

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
## age	1	30.413	30.413	6.6397	0.018478 *
## Genotype	1	53.255	53.255	11.6264	0.002939 **
## age:Genotype	1	62.953	62.953	13.7436	0.001495 **
## Residuals	19	87.030	4.581		

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
## -3.3118 -0.4096  0.2257  0.5327  1.7910
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    16.442619   1.240488  13.255  <2e-16 ***
## age            -0.021193   0.024194  -0.876   0.386
## GenotypeAPOE4  -0.123756   1.620257  -0.076   0.939
## sexMale        -0.357897   1.486380  -0.241   0.811
## age:GenotypeAPOE4  0.006869   0.032802   0.209   0.835
## age:sexMale     -0.004502   0.028738  -0.157   0.876
## GenotypeAPOE4:sexMale  0.196167   2.266881   0.087   0.931
## age:GenotypeAPOE4:sexMale -0.017177   0.044896  -0.383   0.704
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.019 on 43 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.2799, Adjusted R-squared:  0.1627
## F-statistic: 2.388 on 7 and 43 DF,  p-value: 0.03725
```



```
##
## 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
## -3.3118 -0.7956  0.2771  0.8542  1.7910
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   16.08472   1.06667  15.079 5.02e-12 ***
## age           -0.02569   0.02020  -1.272   0.219
## GenotypeAPOE4  0.07241   2.06522   0.035   0.972
## age:GenotypeAPOE4 -0.01031   0.03993  -0.258   0.799
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.328 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.1459, Adjusted R-squared:  0.01101
## F-statistic: 1.082 on 3 and 19 DF,  p-value: 0.3807

## Analysis of Variance Table
##
## Response: Im_BensonTotal
##              Df Sum Sq Mean Sq F value    Pr(>F)
## age              1  7.101   7.1009   6.8346 0.012276 *
## Genotype          1  0.053   0.0527   0.0508 0.822819
## sex              1  8.653   8.6528   8.3283 0.006081 **
## age:Genotype      1  0.002   0.0019   0.0018 0.966506
## age:sex           1  0.202   0.2021   0.1945 0.661391
## Genotype:sex      1  1.201   1.2014   1.1563 0.288228
## age:Genotype:sex  1  0.152   0.1521   0.1464 0.703895
```

```
## Residuals      43 44.675  1.0390
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
##
```

```
## Response: Im_BensonTotal
```

```
##          Df Sum Sq Mean Sq F value Pr(>F)
## age       1  1.4560  1.45602   3.1260 0.08976 .
## Genotype   1  0.2841  0.28410   0.6099 0.44245
## age:Genotype 1  0.0456  0.04556   0.0978 0.75716
## Residuals 24 11.1786  0.46578
```

```
## ---
```

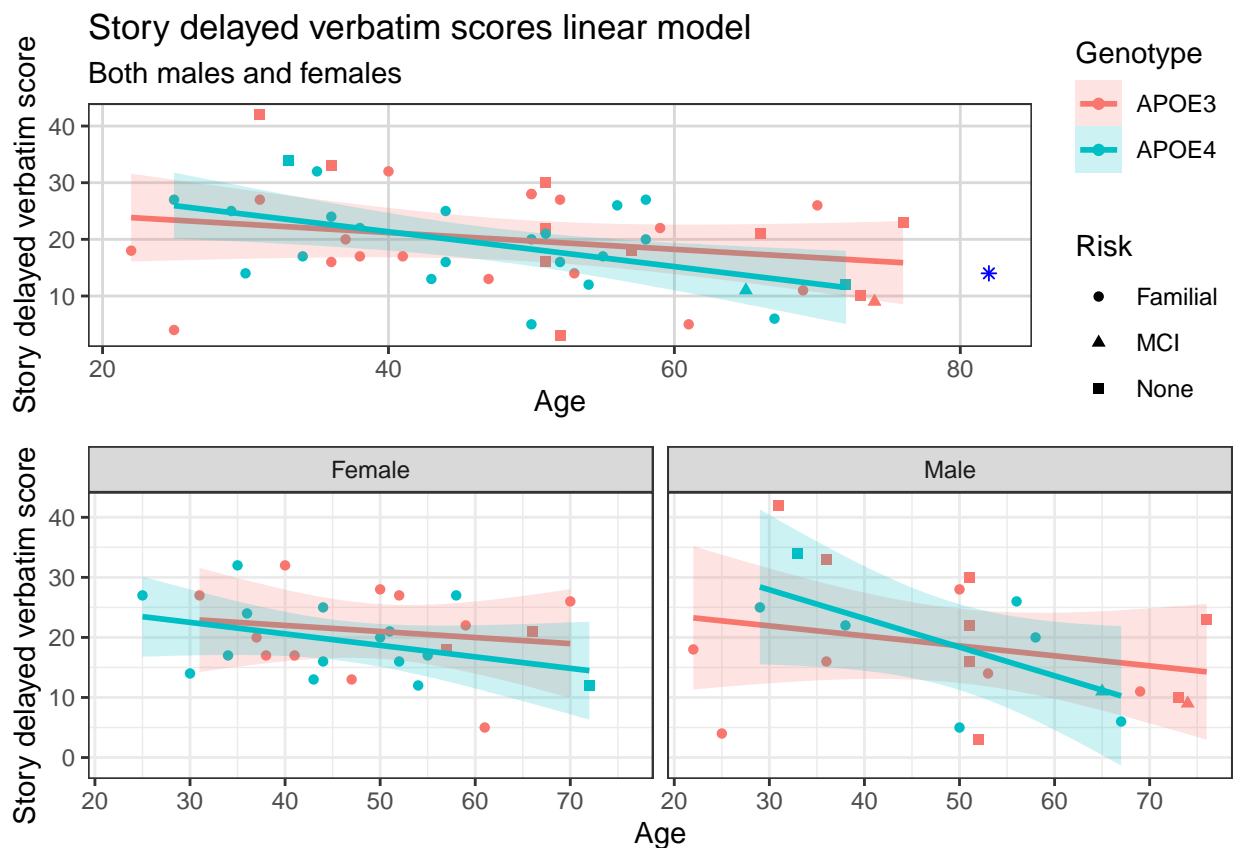
```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
##
```

```
## Response: Im_BensonTotal
```

```
##          Df Sum Sq Mean Sq F value Pr(>F)
## age       1  4.597   4.5971   2.6076 0.1228
## Genotype   1  1.006   1.0060   0.5706 0.4593
## age:Genotype 1  0.117   0.1175   0.0666 0.7991
## Residuals 19 33.497   1.7630
```



```
##
```

```
## Call:
## lm(formula = Delayed_verbatim ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -18.761  -4.836  -2.116   5.821  20.238
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    26.03471    10.31192   2.525  0.0153 *
## age           -0.10085     0.20112  -0.501  0.6186
## GenotypeAPOE4    2.21225    13.46885   0.164  0.8703
## sexMale         0.88704    12.35597   0.072  0.9431
## age:GenotypeAPOE4 -0.09052     0.27267  -0.332  0.7415
## age:sexMale     -0.06559     0.23889  -0.275  0.7850
## GenotypeAPOE4:sexMale 13.12508    18.84411   0.697  0.4899
## age:GenotypeAPOE4:sexMale -0.22050     0.37321  -0.591  0.5577
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.473 on 43 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.1631, Adjusted R-squared:  0.02684
## F-statistic: 1.197 on 7 and 43 DF,  p-value: 0.325

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

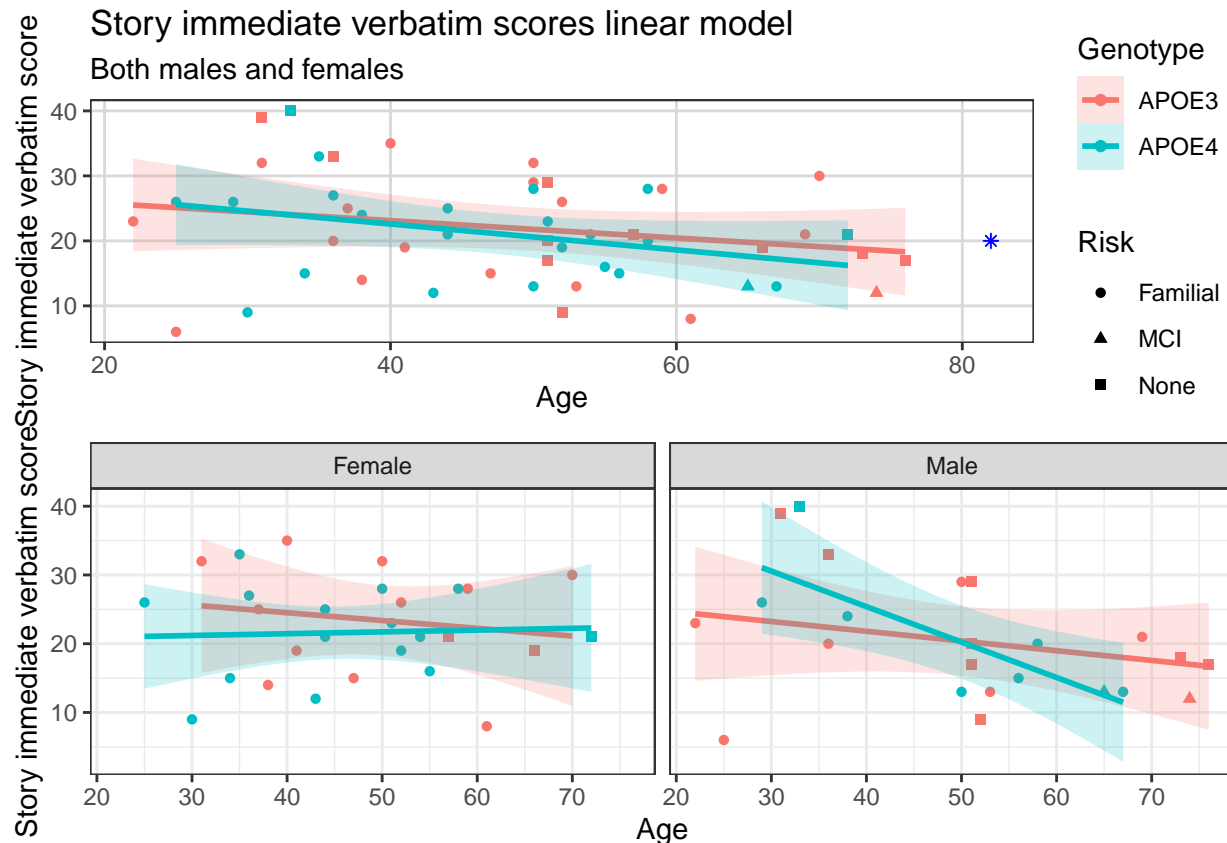
##
## Call:
## lm(formula = Delayed_verbatim ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -18.761  -4.851  -2.434   8.112  20.238
##
```

```
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    26.9218     8.2608   3.259  0.00413 **
## age           -0.1664     0.1565  -1.064  0.30074
## GenotypeAPOE4  15.3373    15.9941   0.959  0.34964
## age:GenotypeAPOE4 -0.3110     0.3092  -1.006  0.32718
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.28 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.1858, Adjusted R-squared:  0.05723
## F-statistic: 1.445 on 3 and 19 DF,  p-value: 0.261
```

```
## Analysis of Variance Table
##
## Response: Delayed_verbatim
##               Df Sum Sq Mean Sq F value Pr(>F)
## age            1  409.67  409.67   5.7061 0.02137 *
## Genotype       1   15.96   15.96   0.2223 0.63965
## sex            1   23.93   23.93   0.3333 0.56674
## age:Genotype   1   53.54   53.54   0.7458 0.39260
## age:sex        1   56.78   56.78   0.7909 0.37877
## Genotype:sex   1   16.62   16.62   0.2315 0.63287
## age:Genotype:sex 1    25.06   25.06   0.3491 0.55773
## Residuals     43 3087.18   71.79
## ---
## 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   72.26   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  351.42  351.42   3.3234 0.08407 .
## Genotype       1    0.05    0.05  0.0005 0.98286
## age:Genotype   1  106.96  106.96   1.0115 0.32718
## Residuals     19 2009.05  105.74
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



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

	Min	1Q	Median	3Q	Max
	-17.9359	-5.0364	-0.2586	5.6449	15.9127

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

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	29.02730	9.59509	3.025	0.00418 **
age	-0.11303	0.18714	-0.604	0.54903
GenotypeAPOE4	-8.61416	12.53257	-0.687	0.49556
sexMale	-1.55554	11.49705	-0.135	0.89301
age:GenotypeAPOE4	0.13909	0.25372	0.548	0.58638
age:sexMale	-0.02841	0.22228	-0.128	0.89890
GenotypeAPOE4:sexMale	27.15855	17.53417	1.549	0.12874
age:GenotypeAPOE4:sexMale	-0.51314	0.34727	-1.478	0.14679

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.884 on 43 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.1778, Adjusted R-squared:  0.0439
## F-statistic: 1.328 on 7 and 43 DF,  p-value: 0.2607
```

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

	Min	1Q	Median	3Q	Max
	-14.1326	-5.5066	-0.2027	5.7551	11.6746

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

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	29.0273	9.2303	3.145	0.00439 **
age	-0.1130	0.1800	-0.628	0.53603
GenotypeAPOE4	-8.6142	12.0561	-0.715	0.48181
age:GenotypeAPOE4	0.1391	0.2441	0.570	0.57405

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.584 on 24 degrees of freedom
## Multiple R-squared:  0.03244, Adjusted R-squared:  -0.0885
## F-statistic: 0.2683 on 3 and 24 DF, p-value: 0.8476

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

	Min	1Q	Median	3Q	Max
	-17.9359	-4.1321	-0.2586	3.5844	15.9127

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

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	27.4718	6.6254	4.146	0.000548 ***
age	-0.1414	0.1255	-1.127	0.273705
GenotypeAPOE4	18.5444	12.8278	1.446	0.164570
age:GenotypeAPOE4	-0.3740	0.2480	-1.508	0.147983

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.247 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.2714, Adjusted R-squared:  0.1563
## F-statistic: 2.359 on 3 and 19 DF, p-value: 0.1038

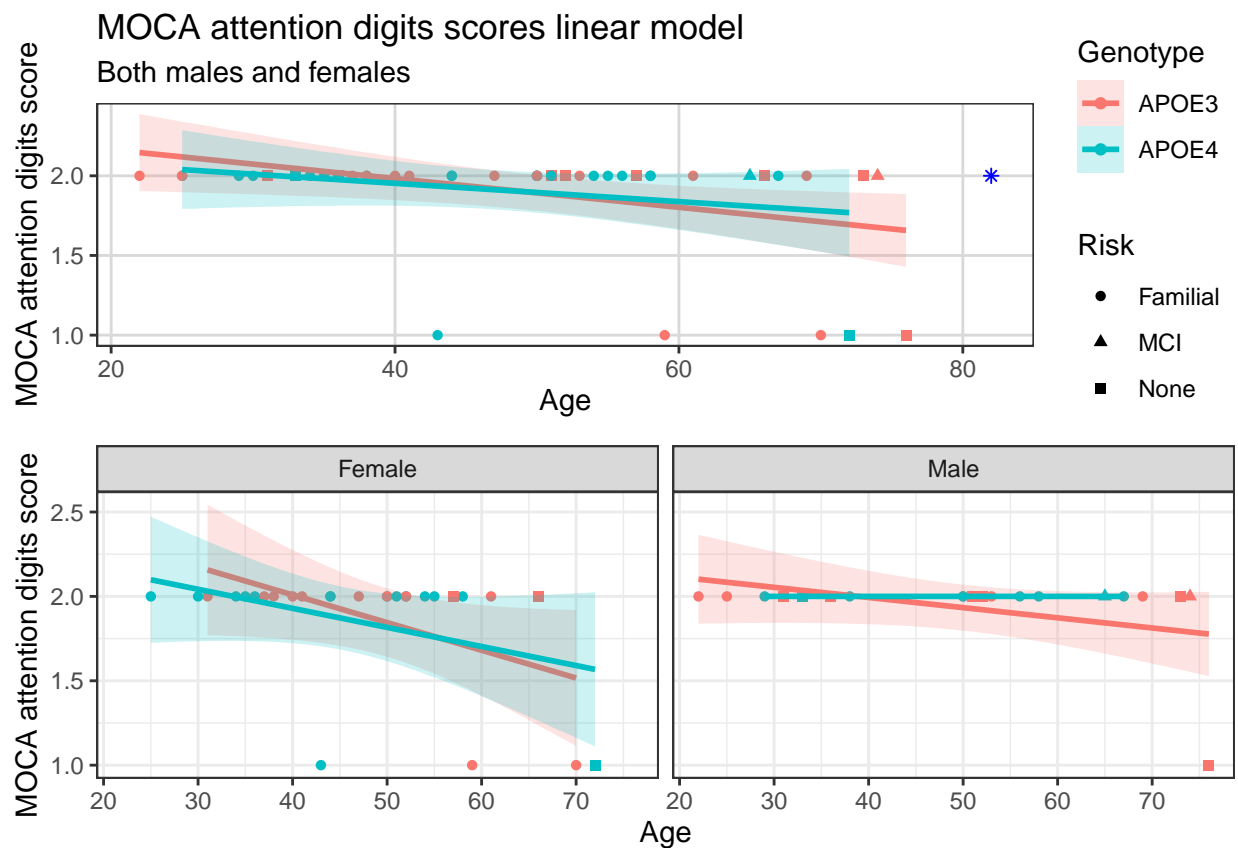
## Analysis of Variance Table
##
## Response: Immediate_verbatim
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	234.91	234.914	3.7792	0.05846 .
Genotype	1	13.78	13.779	0.2217	0.64015
sex	1	44.23	44.227	0.7115	0.40361
age:Genotype	1	7.00	7.001	0.1126	0.73881
age:sex	1	128.51	128.514	2.0675	0.15771
Genotype:sex	1	13.66	13.657	0.2197	0.64163
age:Genotype:sex	1	135.72	135.723	2.1834	0.14679

```
## Residuals      43 2672.89  62.160
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
## Analysis of Variance Table
##
## Response: Immediate_verbatim
##           Df Sum Sq Mean Sq F value Pr(>F)
## age        1  326.63   326.63   4.8022 0.04109 *
## Genotype    1    0.00    0.00   0.0000 0.99595
## age:Genotype 1  154.69   154.69   2.2743 0.14798
## Residuals  19 1292.33    68.02
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
##
```

```
## Call:
## lm(formula = MOCA_Attention_Digits ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.89530 -0.02979  0.00728  0.16806  0.41792
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.6661610   0.3448786    7.731 1.14e-09 ***
## age             -0.0164254   0.0067264   -2.442  0.0188 *
## GenotypeAPOE4    -0.2849044   0.4504611   -0.632  0.5304
## sexMale          -0.4319018   0.4132411   -1.045  0.3018
## age:GenotypeAPOE4  0.0051240   0.0091195    0.562  0.5771
## age:sexMale       0.0104069   0.0079896    1.303  0.1997
## GenotypeAPOE4:sexMale 0.0506451   0.6302347    0.080  0.9363
## age:GenotypeAPOE4:sexMale 0.0008945   0.0124818    0.072  0.9432
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2834 on 43 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.2343, Adjusted R-squared:  0.1097
## F-statistic:  1.88 on 7 and 43 DF,  p-value: 0.09664

##
## 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
## -0.77685 -0.00880  0.00000  0.07269  0.21111
##
```

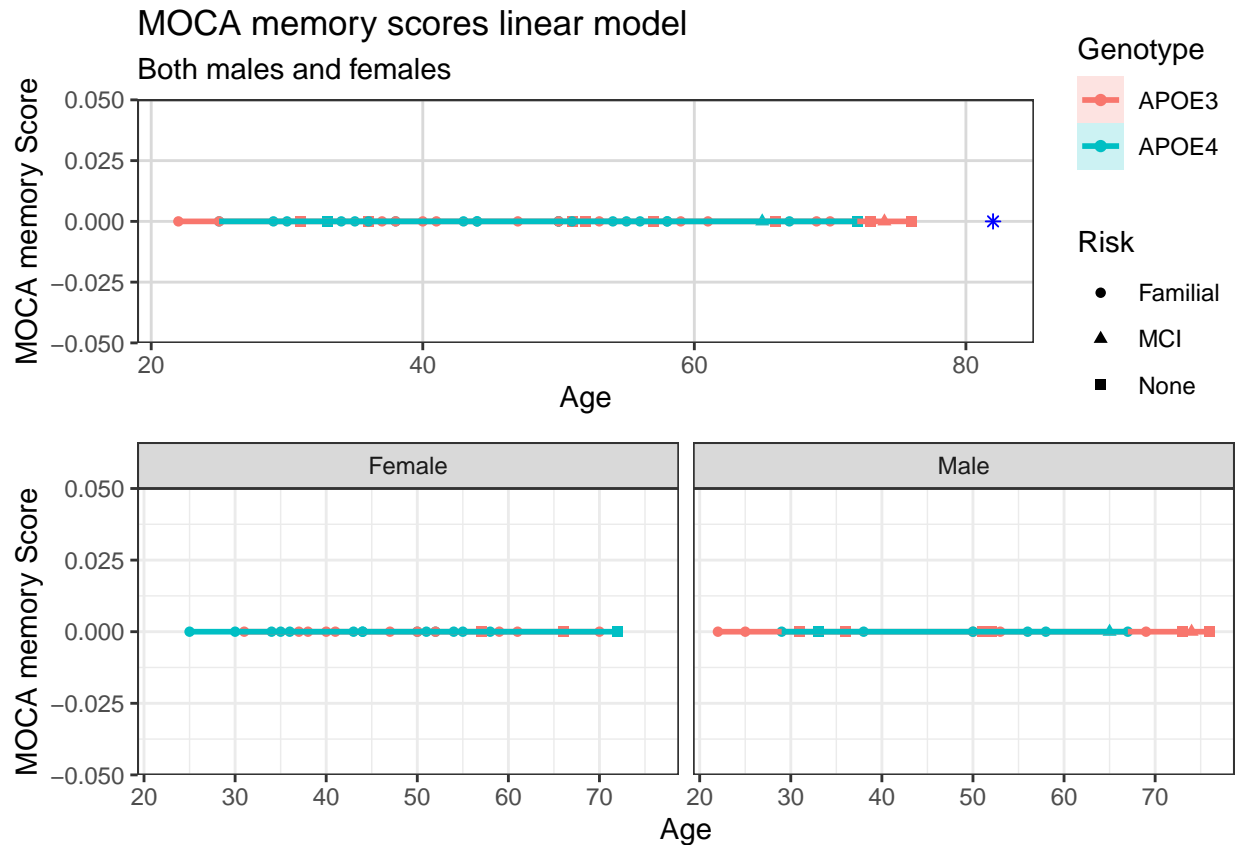


```
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.234259   0.162441  13.754 2.5e-11 ***
## age           -0.006019   0.003076  -1.956  0.0653 .
## GenotypeAPOE4  -0.234259   0.314509  -0.745  0.4655
## age:GenotypeAPOE4 0.006019   0.006081   0.990  0.3348
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2022 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.1878, Adjusted R-squared:  0.0596
## F-statistic: 1.465 on 3 and 19 DF,  p-value: 0.2558
```

```
## Analysis of Variance Table
##
## Response: MOCA_Attention_Digits
##               Df Sum Sq Mean Sq F value    Pr(>F)
## age             1 0.5999 0.59990    7.4702 0.009068 **
## Genotype         1 0.0002 0.00016    0.0020 0.964312
## sex             1 0.1777 0.17767    2.2124 0.144200
## age:Genotype     1 0.0160 0.01595    0.1987 0.658028
## age:sex          1 0.2366 0.23657    2.9458 0.093298 .
## Genotype:sex     1 0.0260 0.02598    0.3236 0.572428
## age:Genotype:sex 1 0.0004 0.00041    0.0051 0.943202
## Residuals       43 3.4531 0.08031
## ---
## 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 0.11797 0.117968    2.8852 0.1057
## Genotype         1 0.02165 0.021652    0.5296 0.4757
## age:Genotype     1 0.04005 0.040050    0.9795 0.3348
## Residuals       19 0.77685 0.040887
```



```
##
## 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 43 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  NaN, Adjusted R-squared:  NaN
## F-statistic:  NaN on 7 and 43 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 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  NaN, Adjusted R-squared:  NaN
## F-statistic:  NaN on 3 and 19 DF, p-value: NA
```

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

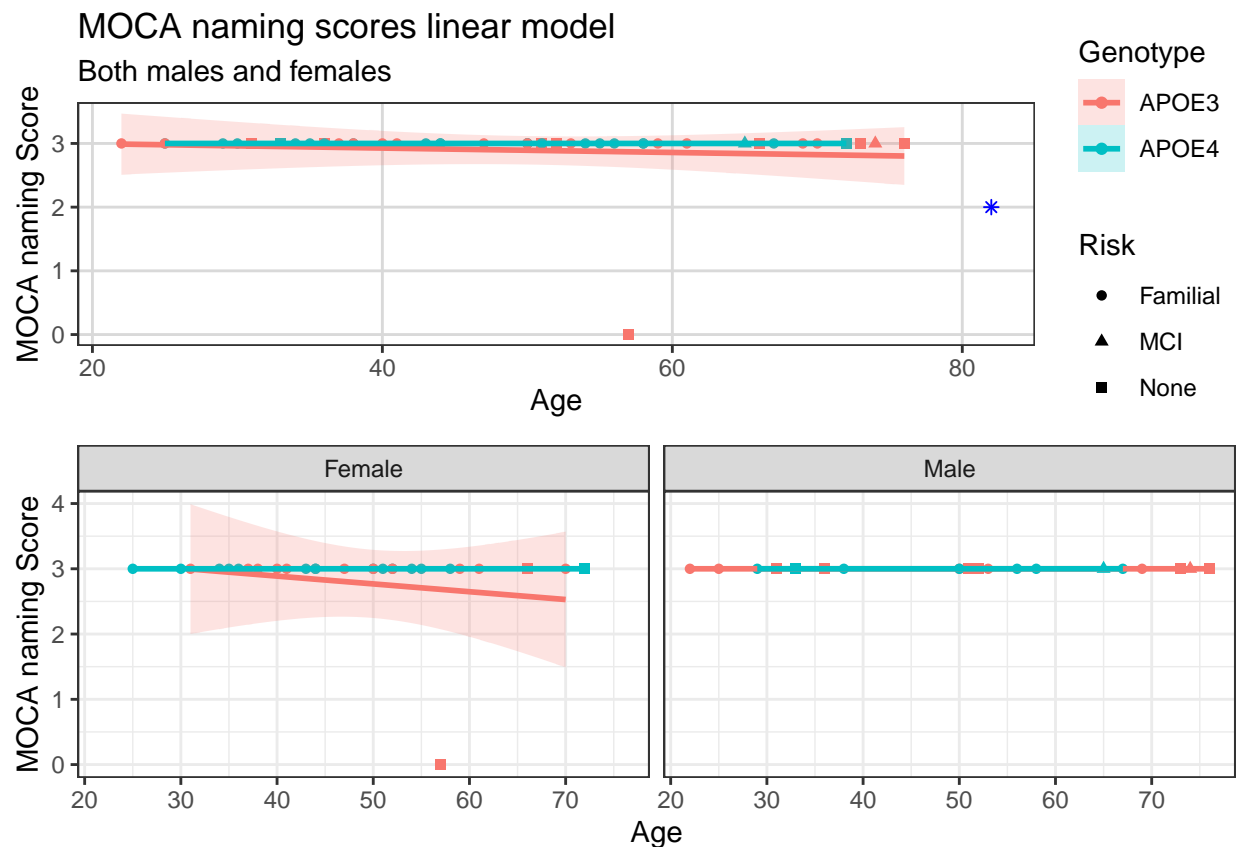
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	0	0	NaN	NaN
Genotype	1	0	0	NaN	NaN
sex	1	0	0	NaN	NaN
age:Genotype	1	0	0	NaN	NaN
age:sex	1	0	0	NaN	NaN
Genotype:sex	1	0	0	NaN	NaN
age:Genotype:sex	1	0	0	NaN	NaN
Residuals	43	0	0		

```
## 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   19      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    0.52669   6.392 9.85e-08 ***
## age             -0.01196    0.01027  -1.164   0.251
## GenotypeAPOE4    -0.36639    0.68794  -0.533   0.597
## sexMale          -0.36639    0.63109  -0.581   0.565
## age:GenotypeAPOE4  0.01196    0.01393   0.859   0.395
## age:sexMale       0.01196    0.01220   0.980   0.332
## GenotypeAPOE4:sexMale 0.36639    0.96248   0.381   0.705
## age:GenotypeAPOE4:sexMale -0.01196    0.01906  -0.628   0.534
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4328 on 43 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.08724, Adjusted R-squared:  -0.06135
## F-statistic: 0.5871 on 7 and 43 DF, p-value: 0.7626

##
## 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
##      0         0         0         0         0
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)           3           0      Inf <2e-16 ***
## age                   0           0      NaN    NaN
## GenotypeAPOE4         0           0      NaN    NaN
## age:GenotypeAPOE4     0           0      NaN    NaN
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
##
## Residual standard error: 0 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:   NaN, Adjusted R-squared:   NaN
## F-statistic:   NaN on 3 and 19 DF, p-value: NA
```

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

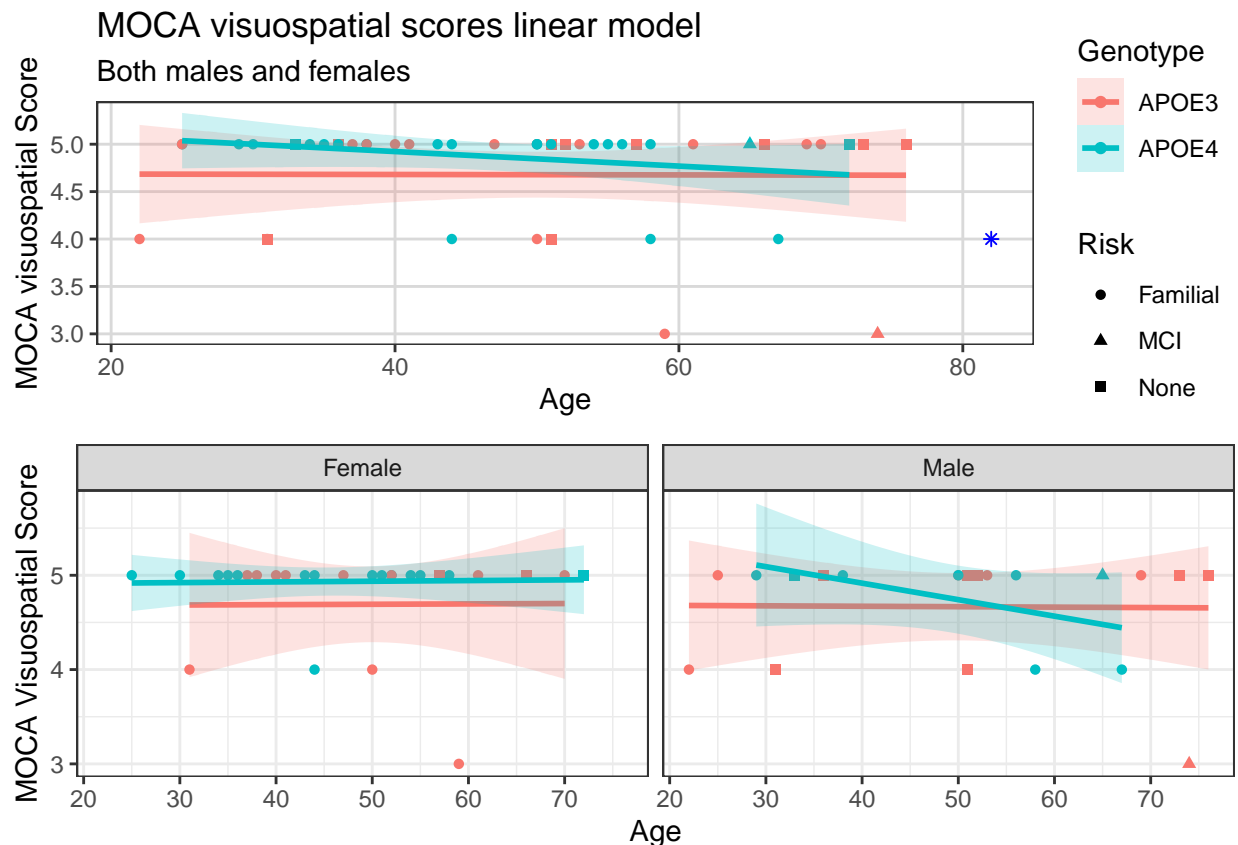
```
##
## Response: MOCA_Naming
##           Df Sum Sq Mean Sq F value Pr(>F)
## age           1 0.0643  0.064336   0.3435 0.5609
## Genotype       1 0.1262  0.126172   0.6736 0.4163
## sex           1 0.2251  0.225146   1.2021 0.2790
## age:Genotype   1 0.0170  0.016969   0.0906 0.7649
## age:sex        1 0.1264  0.126424   0.6750 0.4158
## Genotype:sex   1 0.1370  0.136993   0.7314 0.3972
## age:Genotype:sex 1 0.0738  0.073750   0.3938 0.5336
## Residuals     43 8.0537  0.187296
```

```
## 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      0      0      NaN    NaN
## Genotype       1      0      0      NaN    NaN
## age:Genotype   1      0      0      NaN    NaN
## Residuals     19      0      0
```



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

	Min	1Q	Median	3Q	Max
	-1.69585	0.04815	0.07791	0.31725	0.52120

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

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	4.672835	0.645013	7.245	5.7e-09 ***
age	0.000390	0.012580	0.031	0.975
GenotypeAPOE4	0.227530	0.842480	0.270	0.788
sexMale	0.016980	0.772868	0.022	0.983
age:GenotypeAPOE4	0.000334	0.017056	0.020	0.984
age:sexMale	-0.000853	0.014943	-0.057	0.955
GenotypeAPOE4:sexMale	0.698739	1.178703	0.593	0.556
age:GenotypeAPOE4:sexMale	-0.017368	0.023344	-0.744	0.461

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.53 on 43 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.08331,    Adjusted R-squared:  -0.06591
## F-statistic: 0.5583 on 7 and 43 DF,  p-value: 0.7852
```

```
##
## 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
	-1.6556	-0.2762	0.3268	0.3345	0.5212

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

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	4.689815	0.465428	10.076	4.66e-09 ***
age	-0.000463	0.008815	-0.053	0.959
GenotypeAPOE4	0.926269	0.901134	1.028	0.317
age:GenotypeAPOE4	-0.017034	0.017424	-0.978	0.341

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5794 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.07163,    Adjusted R-squared:  -0.07495
## F-statistic: 0.4887 on 3 and 19 DF,  p-value: 0.6942

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

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	0.1379	0.13787	0.4908	0.4873
Genotype	1	0.4122	0.41224	1.4676	0.2323
sex	1	0.0945	0.09450	0.3364	0.5649
age:Genotype	1	0.1120	0.11200	0.3987	0.5311
age:sex	1	0.1221	0.12215	0.4348	0.5131
Genotype:sex	1	0.0636	0.06356	0.2263	0.6367
age:Genotype:sex	1	0.1555	0.15548	0.5535	0.4609


```
## Residuals      43 12.0787 0.28090
```

```
## 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
```

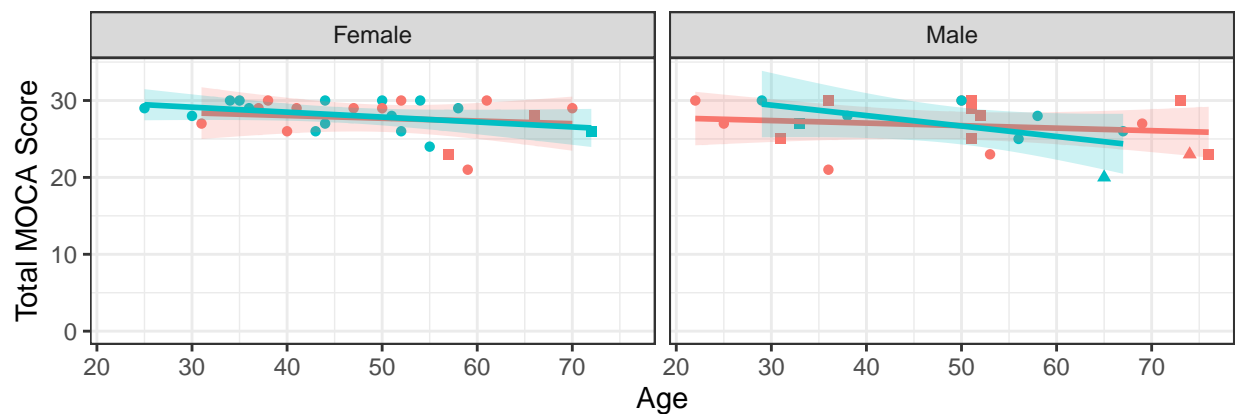
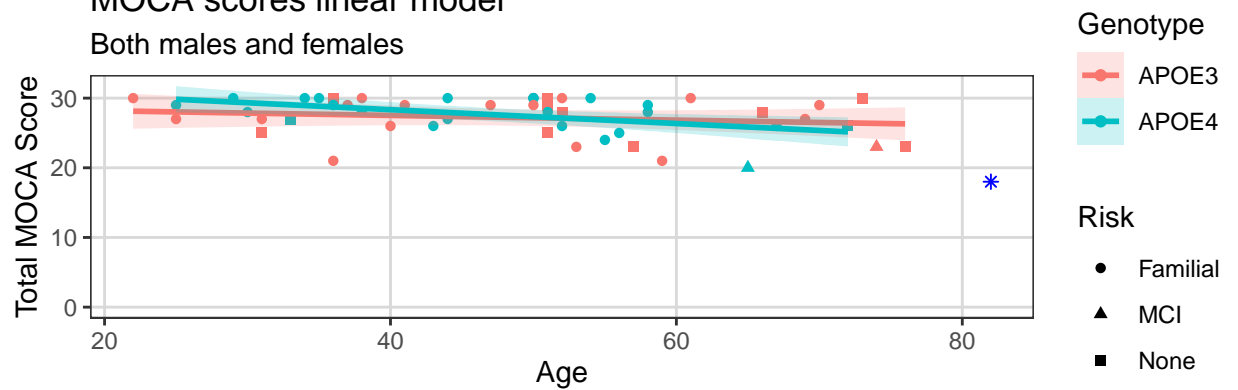
```
##
```

```
## Response: MOCA_Visuospatial
```

```
##          Df Sum Sq Mean Sq F value Pr(>F)
## age       1  0.1371  0.13711   0.4085 0.5304
## Genotype   1  0.0342  0.03416   0.1018 0.7532
## age:Genotype 1  0.3208  0.32081   0.9558 0.3405
## Residuals 19  6.3775  0.33566
```

MOCA scores linear model

Both males and females



```
##
```

```
## Call:
```

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

```
##
```

```
## Residuals:
```

```

##      Min      1Q Median      3Q      Max
## -6.374 -1.709  0.854  1.951  4.023
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    29.444830   3.308948   8.899 2.63e-11 ***
## age           -0.035104   0.064537  -0.544   0.589
## GenotypeAPOE4    1.614070   4.321963   0.373   0.711
## sexMale        -1.067978   3.964854  -0.269   0.789
## age:GenotypeAPOE4 -0.029147   0.087497  -0.333   0.741
## age:sexMale      0.002234   0.076657   0.029   0.977
## GenotypeAPOE4:sexMale  3.487881   6.046806   0.577   0.567
## age:GenotypeAPOE4:sexMale -0.073918   0.119757  -0.617   0.540
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.719 on 43 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.1638, Adjusted R-squared:  0.0277
## F-statistic: 1.203 on 7 and 43 DF,  p-value: 0.3216

##
## 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
## -6.1935 -2.1754  0.4633  2.3759  4.0227
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    28.37685    2.48845  11.403 6.1e-10 ***
## age           -0.03287    0.04713  -0.697   0.494

```

```
## GenotypeAPOE4      5.10195    4.81799    1.059    0.303
## age:GenotypeAPOE4 -0.10307    0.09316   -1.106    0.282
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.098 on 19 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.1498, Adjusted R-squared:  0.01559
## F-statistic: 1.116 on 3 and 19 DF,  p-value: 0.3673
```

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

```
##
```

```
## Response: MOCA_TOTAL
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	35.14	35.139	4.7534	0.03476 *
Genotype	1	1.09	1.088	0.1472	0.70312
sex	1	13.20	13.197	1.7852	0.18854
age:Genotype	1	8.35	8.350	1.1295	0.29382
age:sex	1	1.65	1.649	0.2230	0.63915
Genotype:sex	1	0.04	0.038	0.0051	0.94354
age:Genotype:sex	1	2.82	2.816	0.3810	0.54033
Residuals	43	317.88	7.393		

```
## ---
```

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

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

```
##
```

```
## Response: MOCA_TOTAL
```

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

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

```
##
```

```
## Response: MOCA_TOTAL
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	20.382	20.3822	2.1242	0.1613
Genotype	1	0.001	0.0009	0.0001	0.9925
age:Genotype	1	11.745	11.7449	1.2240	0.2824
Residuals	19	182.307	9.5951		