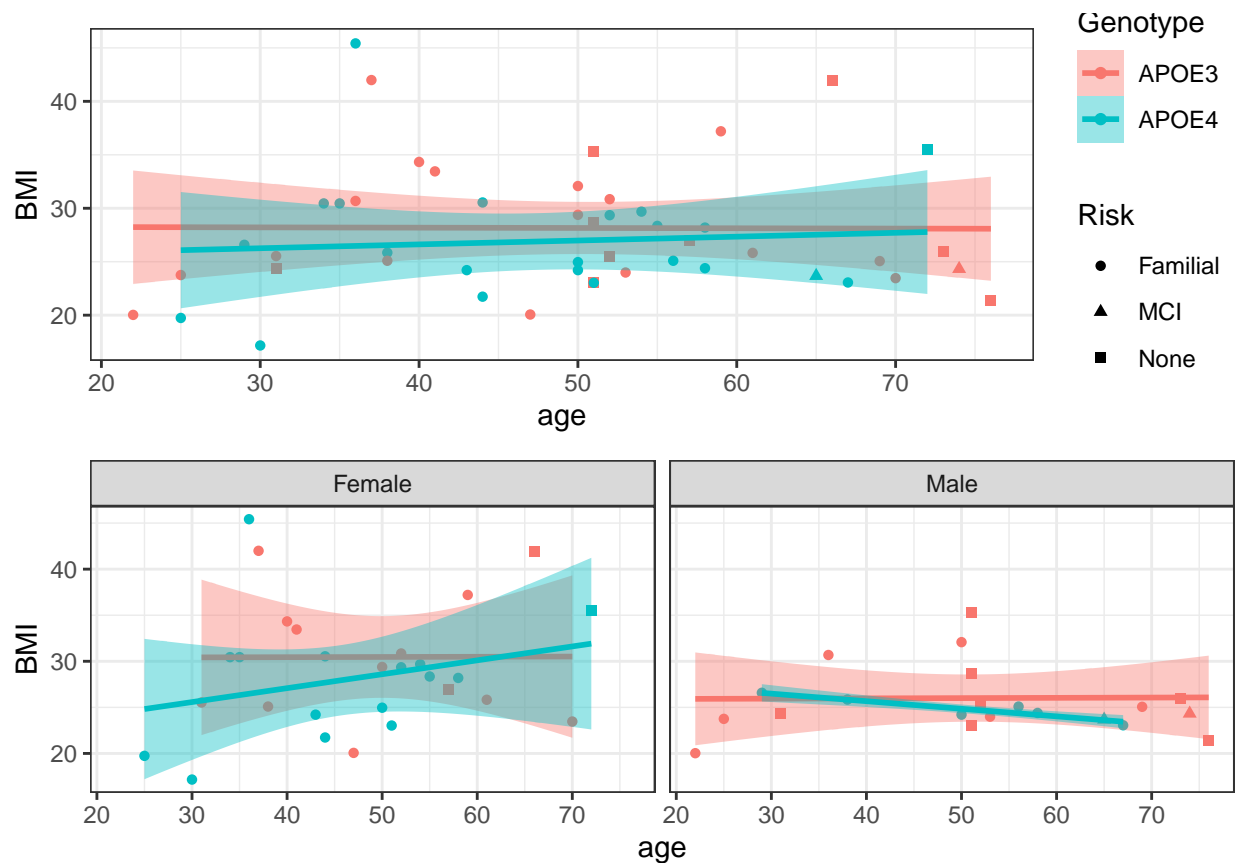


Physiological Visualizatiions

```
## 'geom_smooth()' using formula 'y ~ x'
```



```
##
## Call:
## lm(formula = BMI ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -10.4015  -3.5326  -0.5133   2.8534  18.9403
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  30.3585686   7.166487   4.236 0.000125 ***
## age           0.0021935   0.1397763   0.016 0.987556
## GenotypeAPOE4 -9.3144056   9.3606755  -0.995 0.325545
## sexMale      -4.5007164   8.7053601  -0.517 0.607930
## age:GenotypeAPOE4  0.1487938   0.1895051   0.785 0.436867
```

```

## age:sexMale          0.0007414  0.1672565   0.004 0.996485
## GenotypeAPOE4:sexMale 12.4152868 14.0133038   0.886 0.380804
## age:GenotypeAPOE4:sexMale -0.2339838  0.2717826  -0.861 0.394288
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.889 on 41 degrees of freedom
## Multiple R-squared:  0.1543, Adjusted R-squared:  0.009895
## F-statistic: 1.069 on 7 and 41 DF,  p-value: 0.4007

##
## Call:
## lm(formula = BMI ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -10.402  -4.943  -1.040   3.666  18.940
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    30.358569    8.562542   3.546  0.00165 **
## age              0.002193    0.167001   0.013  0.98963
## GenotypeAPOE4   -9.314406   11.183913  -0.833  0.41315
## age:GenotypeAPOE4  0.148794    0.226416   0.657  0.51733
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 7.036 on 24 degrees of freedom
## Multiple R-squared:  0.07298, Adjusted R-squared: -0.04289
## F-statistic: 0.6298 on 3 and 24 DF,  p-value: 0.6029

##
## Call:
## lm(formula = BMI ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.8956 -1.7474 -0.3917  0.2064  9.2544
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    25.857852    3.111770   8.310 2.17e-07 ***
## age              0.002935    0.057838   0.051  0.960
## GenotypeAPOE4    3.100881    6.566417   0.472  0.643
## age:GenotypeAPOE4 -0.085190    0.122670  -0.694  0.497
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.708 on 17 degrees of freedom
## Multiple R-squared:  0.06424, Adjusted R-squared: -0.1009
## F-statistic: 0.389 on 3 and 17 DF,  p-value: 0.7624

## Analysis of Variance Table

```

```
##
## Response: BMI
##           Df Sum Sq Mean Sq F value Pr(>F)
## age       1    2.51   2.510   0.0724 0.78925
## Genotype  1   18.09  18.087   0.5216 0.47427
## sex       1  185.40 185.396   5.3463 0.02586 *
## age:Genotype 1   10.51  10.507   0.3030 0.58500
## age:sex     1   15.65  15.648   0.4512 0.50552
## Genotype:sex 1    1.53   1.527   0.0440 0.83481
## age:Genotype:sex 1  25.70  25.702   0.7412 0.39429
## Residuals   41 1421.77  34.677
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

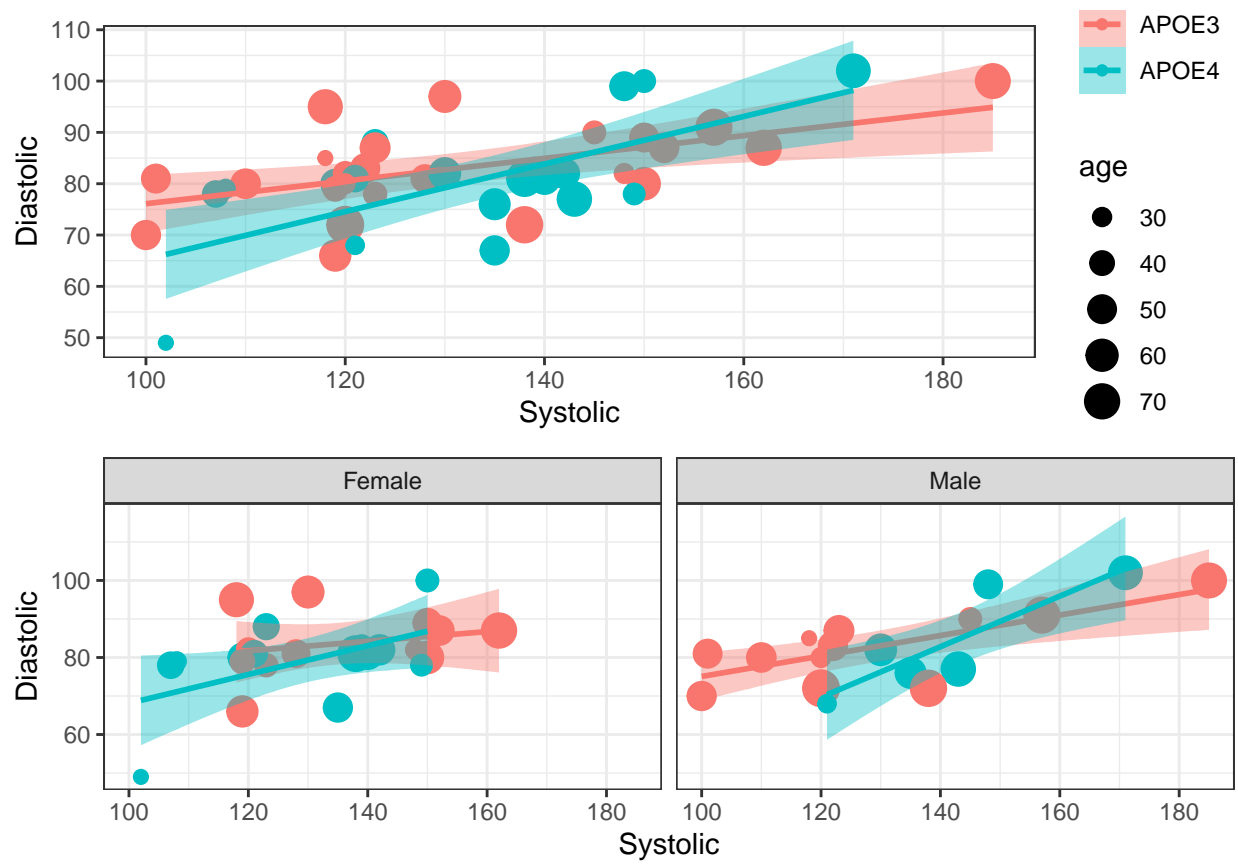
```
## Analysis of Variance Table
##
```

```
## Response: BMI
##           Df Sum Sq Mean Sq F value Pr(>F)
## age       1   40.05  40.046   0.8090 0.3774
## Genotype  1   32.11  32.111   0.6487 0.4285
## age:Genotype 1   21.38  21.378   0.4319 0.5173
## Residuals  24 1188.04  49.502
```

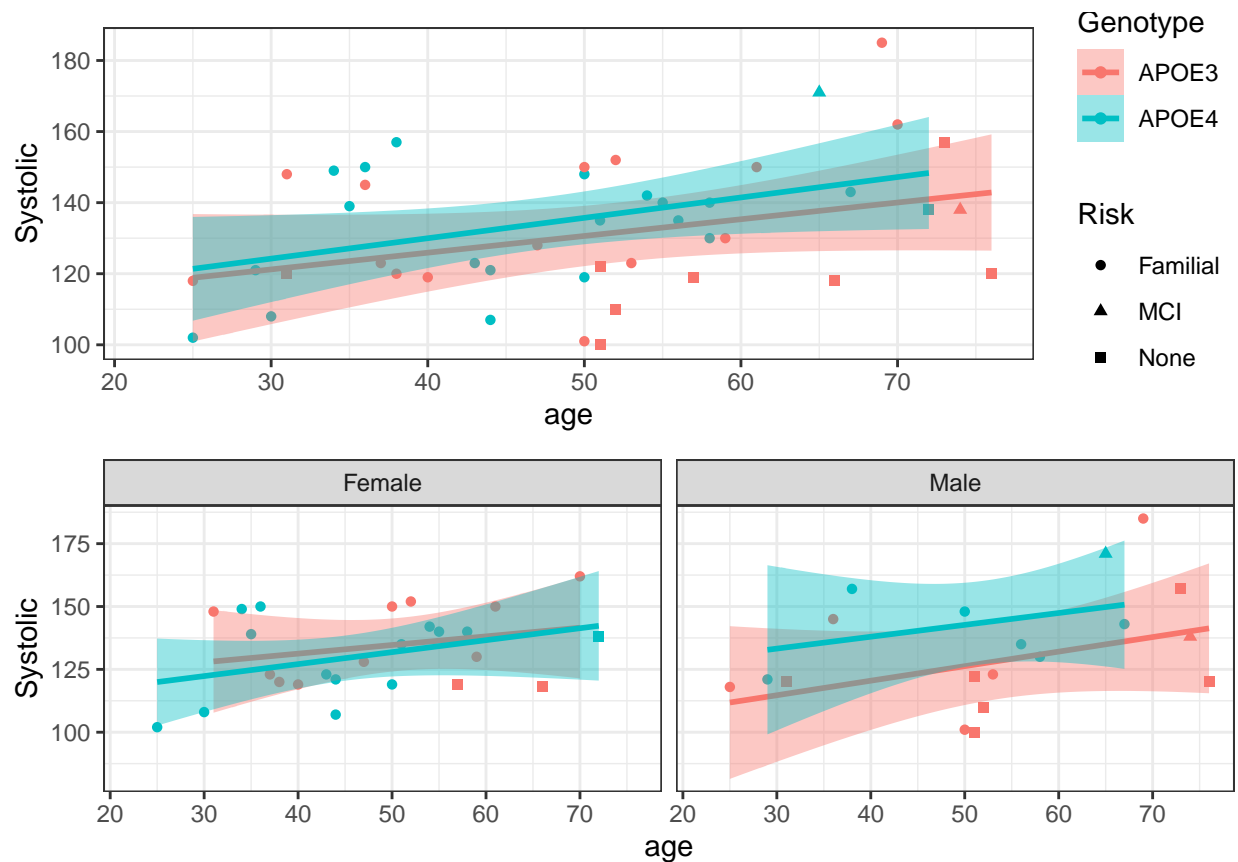
```
## Analysis of Variance Table
##
```

```
## Response: BMI
##           Df Sum Sq Mean Sq F value Pr(>F)
## age       1   1.526   1.5260   0.1110 0.7431
## Genotype  1   7.889   7.8888   0.5738 0.4591
## age:Genotype 1   6.631   6.6309   0.4823 0.4968
## Residuals  17 233.734  13.7490
```

```
## 'geom_smooth()' using formula 'y ~ x'
```



```
## 'geom_smooth()' using formula 'y ~ x'
```



```
##
## Call:
## lm(formula = Systolic ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -26.852 -12.249  -4.852  14.293  47.734
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    117.4944    23.2963   5.043 1.23e-05 ***
## age              0.3439     0.4477   0.768  0.447
## GenotypeAPOE4   -9.4437    29.9762  -0.315  0.755
## sexMale        -20.1489    29.5434  -0.682  0.499
## age:GenotypeAPOE4  0.1320     0.6031   0.219  0.828
## age:sexMale       0.2347     0.5534   0.424  0.674
## GenotypeAPOE4:sexMale 31.1914    45.2957   0.689  0.495
## age:GenotypeAPOE4:sexMale -0.2386     0.8704  -0.274  0.786
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 18.4 on 37 degrees of freedom
## (4 observations deleted due to missingness)
## Multiple R-squared:  0.207, Adjusted R-squared:  0.05695
## F-statistic:  1.38 on 7 and 37 DF, p-value: 0.2429
```

```
##
## Call:
## lm(formula = Systolic ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -22.189 -11.827  -4.915  13.602  24.817
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    117.4944     20.0789   5.852 6.9e-06 ***
## age              0.3439      0.3859   0.891  0.382
## GenotypeAPOE4   -9.4437     25.8362  -0.366  0.718
## age:GenotypeAPOE4  0.1320      0.5198   0.254  0.802
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 15.86 on 22 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.1344, Adjusted R-squared:  0.01635
## F-statistic: 1.138 on 3 and 22 DF,  p-value: 0.3554
```

```
##
## Call:
## lm(formula = Systolic ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -26.852 -14.127  -4.852  11.805  47.734
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)     97.3455     21.3210   4.566 0.000371 ***
## age              0.5786      0.3817   1.516 0.150387
## GenotypeAPOE4    21.7476     39.8501   0.546 0.593271
## age:GenotypeAPOE4 -0.1065      0.7365  -0.145 0.886926
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 21.59 on 15 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.2532, Adjusted R-squared:  0.1038
## F-statistic: 1.695 on 3 and 15 DF,  p-value: 0.2107
```

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

```
##
```

```
## Response: Systolic
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
age	1	2012.3	2012.27	5.9455	0.01968 *
Genotype	1	274.5	274.48	0.8110	0.37365
sex	1	0.1	0.09	0.0003	0.98730
age:Genotype	1	21.6	21.57	0.0637	0.80211
age:sex	1	12.2	12.22	0.0361	0.85033
Genotype:sex	1	922.4	922.45	2.7255	0.10722

```
## age:Genotype:sex 1    25.4    25.42  0.0751 0.78555
## Residuals        37 12522.7   338.45
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
##
```

```
## Response: Systolic
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## age         1   784.1   784.12   3.1188 0.09127 .
## Genotype    1    58.4    58.38   0.2322 0.63466
## age:Genotype 1    16.2    16.22   0.0645 0.80184
## Residuals   22  5531.3   251.42
```

```
## ---
```

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

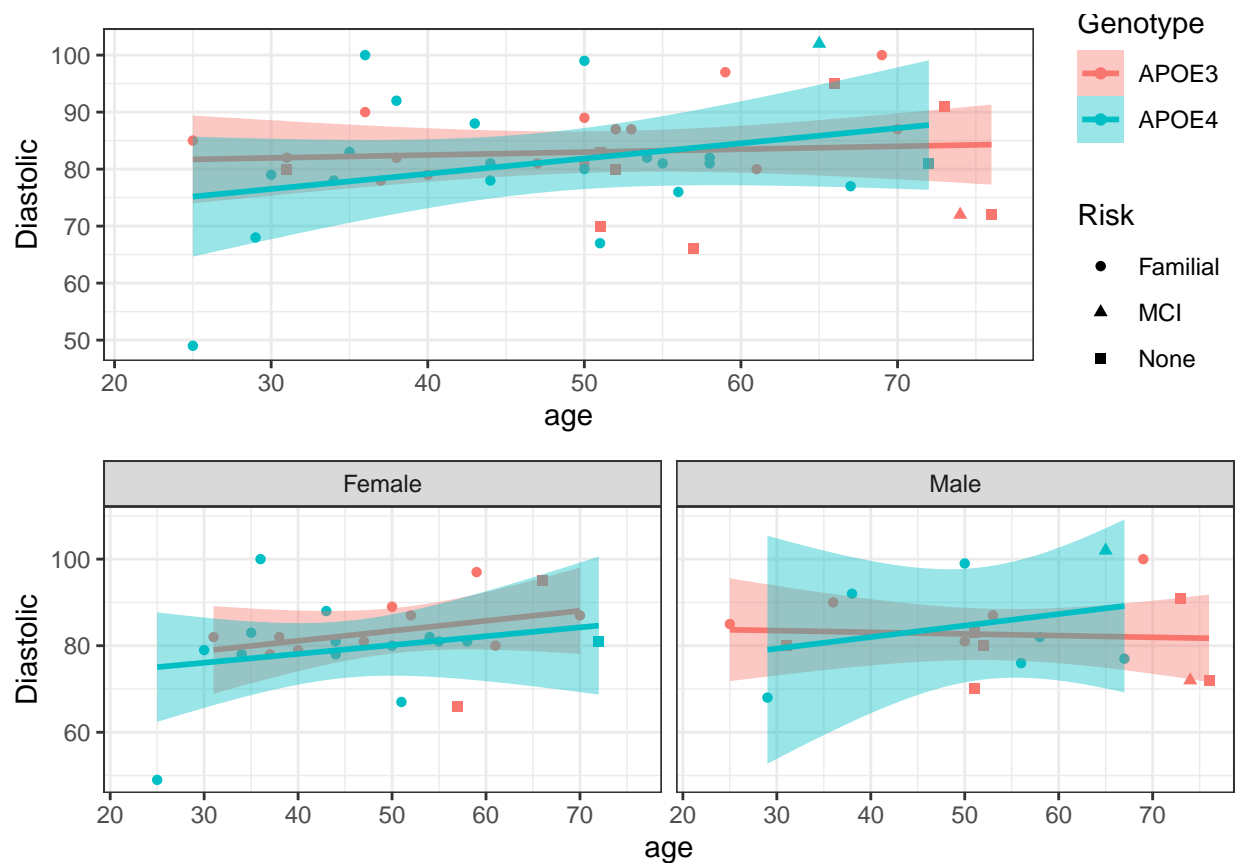
```
## Analysis of Variance Table
```

```
##
```

```
## Response: Systolic
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)
## age         1  1206.2  1206.18   2.5879 0.1285
## Genotype    1  1154.4  1154.43   2.4768 0.1364
## age:Genotype 1     9.8     9.75   0.0209 0.8869
## Residuals   15  6991.4   466.10
```

```
## 'geom_smooth()' using formula 'y ~ x'
```



```
##
## Call:
## lm(formula = Diastolic ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -26.0485  -3.6360  -0.1482   5.5712  22.7076
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    71.84179    13.04030     5.509 2.9e-06 ***
## age             0.23174     0.25060     0.925  0.361
## GenotypeAPOE4   -1.89306    16.77939    -0.113  0.911
## sexMale         12.81075    16.53714     0.775  0.443
## age:GenotypeAPOE4 -0.02775     0.33758    -0.082  0.935
## age:sexMale      -0.27048     0.30976    -0.873  0.388
## GenotypeAPOE4:sexMale -11.39433    25.35465    -0.449  0.656
## age:GenotypeAPOE4:sexMale 0.33217     0.48721     0.682  0.500
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.3 on 37 degrees of freedom
## (4 observations deleted due to missingness)
## Multiple R-squared:  0.1092, Adjusted R-squared:  -0.05936
## F-statistic: 0.6478 on 7 and 37 DF,  p-value: 0.7137

##
## Call:
## lm(formula = Diastolic ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -26.0485  -2.0170   0.4438   3.0743  22.7076
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    71.84179    12.61025     5.697 9.92e-06 ***
## age             0.23174     0.24233     0.956  0.349
## GenotypeAPOE4   -1.89306    16.22603    -0.117  0.908
## age:GenotypeAPOE4 -0.02775     0.32644    -0.085  0.933
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.958 on 22 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.1224, Adjusted R-squared:  0.002756
## F-statistic: 1.023 on 3 and 22 DF,  p-value: 0.4015

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



```
## -12.677 -9.747 -1.716 7.959 18.020
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    84.65254    10.64275   7.954 9.24e-07 ***
## age            -0.03874     0.19054  -0.203   0.842
## GenotypeAPOE4  -13.28739    19.89186  -0.668   0.514
## age:GenotypeAPOE4 0.30442     0.36764   0.828   0.421
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.78 on 15 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.06278,    Adjusted R-squared:  -0.1247
## F-statistic: 0.3349 on 3 and 15 DF,  p-value: 0.8003
```

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

```
##
```

```
## Response: Diastolic
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1  189.0  189.024   1.7825 0.1900
## Genotype      1   17.9   17.851   0.1683 0.6840
## sex           1   22.4   22.393   0.2112 0.6485
## age:Genotype  1   88.4   88.397   0.8336 0.3672
## age:sex       1   43.2   43.196   0.4073 0.5273
## Genotype:sex  1   70.7   70.695   0.6666 0.4195
## age:Genotype:sex 1   49.3   49.295   0.4648 0.4996
## Residuals     37 3923.7  106.047
```

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

```
##
```

```
## Response: Diastolic
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1  239.69  239.689   2.4170 0.1343
## Genotype      1   63.95   63.948   0.6449 0.4305
## age:Genotype  1    0.72    0.717   0.0072 0.9330
## Residuals     22 2181.68   99.167
```

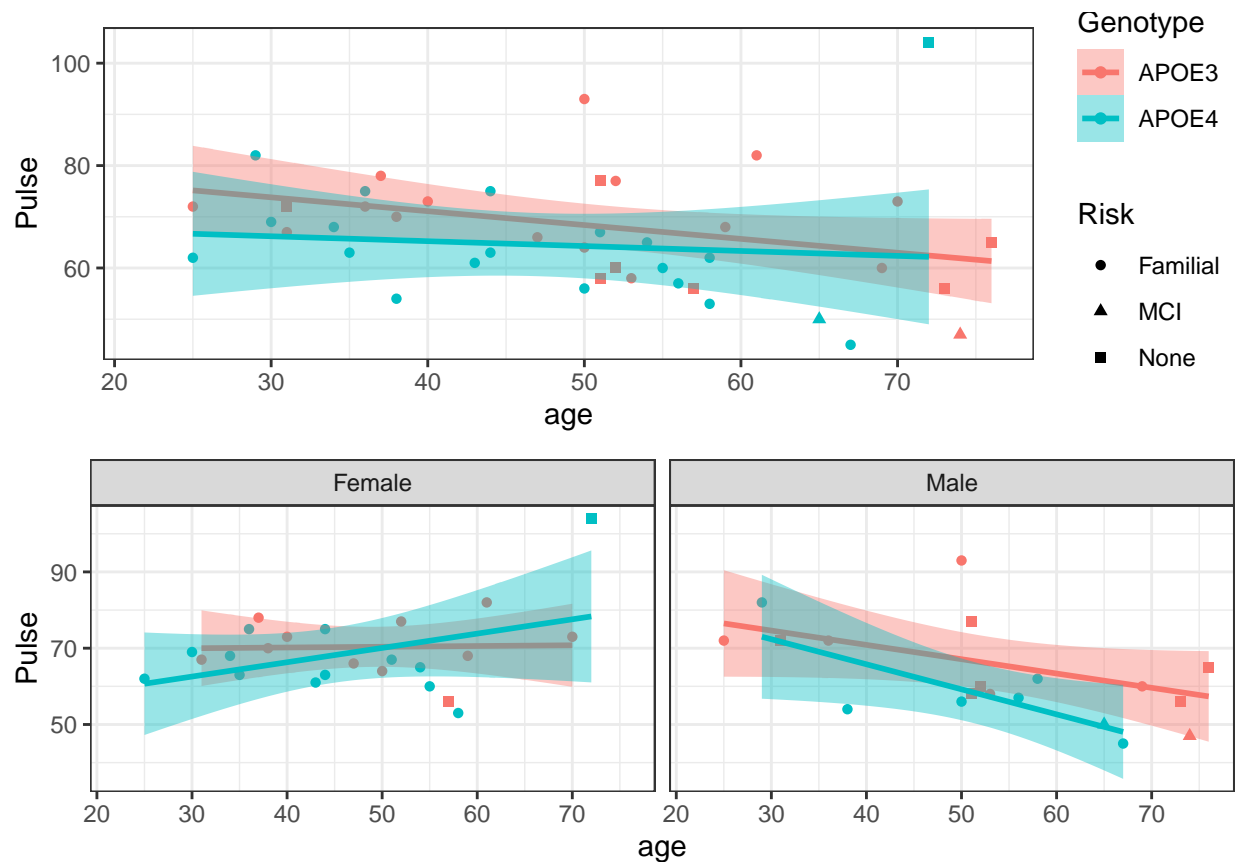
```
## Analysis of Variance Table
```

```
##
```

```
## Response: Diastolic
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## age           1    6.64    6.636   0.0571 0.8143
## Genotype      1   30.43   30.427   0.2620 0.6162
## age:Genotype  1   79.63   79.632   0.6857 0.4206
## Residuals     15 1742.04  116.136
```

```
## 'geom_smooth()' using formula 'y ~ x'
```



```
##
## Call:
## lm(formula = Pulse ~ age * Genotype * sex, data = geno_combined)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -20.072  -5.591  -1.439   6.511  25.885
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    69.40345    13.52376   5.132 1.08e-05 ***
## age              0.01949     0.26739   0.073   0.942
## GenotypeAPOE4   -18.10294    17.04985  -1.062   0.296
## sexMale         16.47070    16.81552   0.979   0.334
## age:GenotypeAPOE4  0.35589     0.34861   1.021   0.314
## age:sexMale     -0.39467     0.32173  -1.227   0.228
## GenotypeAPOE4:sexMale 24.26004    25.28987   0.959   0.344
## age:GenotypeAPOE4:sexMale -0.63696     0.49061  -1.298   0.203
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.12 on 35 degrees of freedom
## (6 observations deleted due to missingness)
## Multiple R-squared:  0.3526, Adjusted R-squared:  0.2232
## F-statistic: 2.724 on 7 and 35 DF, p-value: 0.02296
```

```
##
## Call:
## lm(formula = Pulse ~ age * Genotype, data = combo_f)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -20.0723  -5.2072  -0.7913   6.4745  25.6724
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    69.40345    13.61116     5.099 5.48e-05 ***
## age             0.01949     0.26912     0.072  0.943
## GenotypeAPOE4  -18.10294    17.16003    -1.055  0.304
## age:GenotypeAPOE4  0.35589     0.35086     1.014  0.323
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.18 on 20 degrees of freedom
## (4 observations deleted due to missingness)
## Multiple R-squared:  0.1337, Adjusted R-squared:  0.003728
## F-statistic: 1.029 on 3 and 20 DF,  p-value: 0.4011

##
## Call:
## lm(formula = Pulse ~ age * Genotype, data = combo_m)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -13.094  -5.430  -2.244   4.679  25.885
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    85.8742     9.9067     8.668 3.16e-07 ***
## age            -0.3752     0.1774    -2.115  0.0515 .
## GenotypeAPOE4     6.1571    18.5162     0.333  0.7441
## age:GenotypeAPOE4 -0.2811     0.3422    -0.821  0.4243
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 10.03 on 15 degrees of freedom
## (2 observations deleted due to missingness)
## Multiple R-squared:  0.4485, Adjusted R-squared:  0.3382
## F-statistic: 4.066 on 3 and 15 DF,  p-value: 0.02673

## Analysis of Variance Table
##
## Response: Pulse
##              Df Sum Sq Mean Sq F value  Pr(>F)
## age             1  252.7   252.70   2.4678 0.12520
## Genotype        1  191.8   191.80   1.8731 0.17984
## sex             1  372.8   372.77   3.6404 0.06462 .
## age:Genotype    1   81.6    81.64   0.7973 0.37800
## age:sex         1  746.4   746.42   7.2894 0.01061 *
## Genotype:sex    1  134.4   134.41   1.3126 0.25970
```

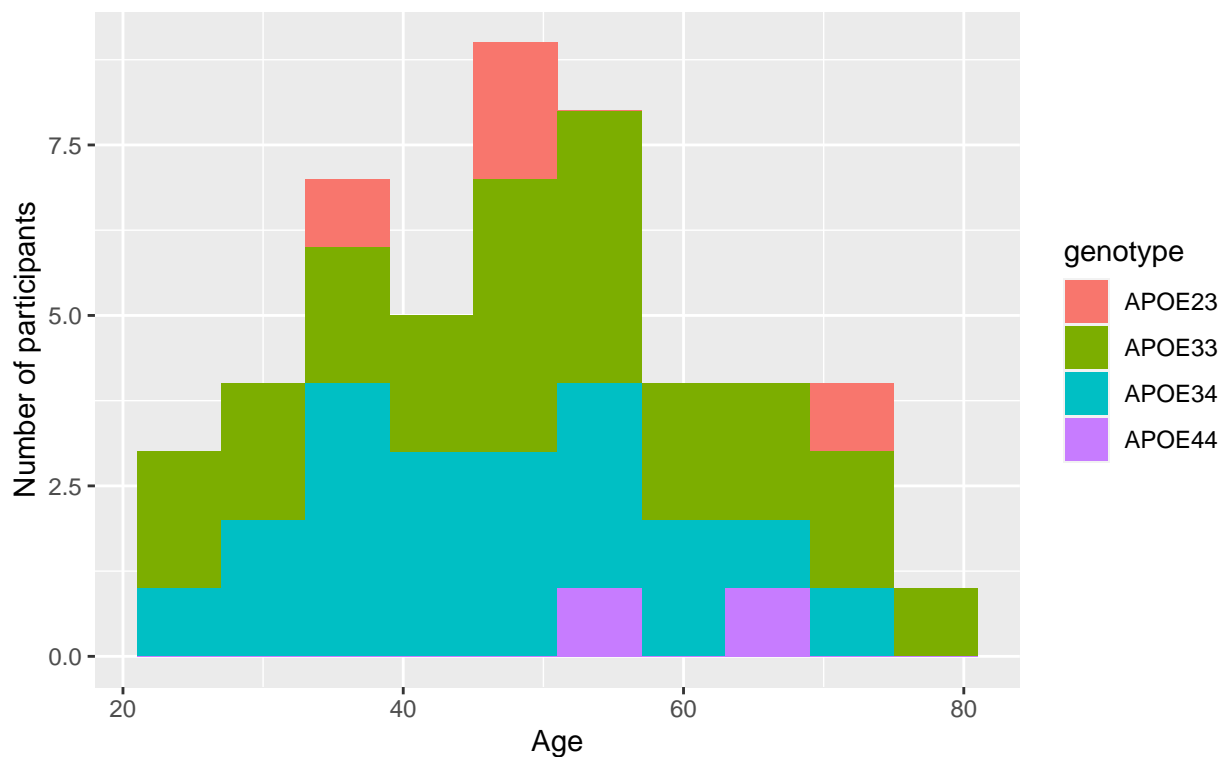
```
## age:Genotype:sex 1 172.6 172.60 1.6856 0.20267
## Residuals      35 3583.9 102.40
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## Analysis of Variance Table
##
## Response: Pulse
##           Df Sum Sq Mean Sq F value Pr(>F)
## age        1  204.56  204.563   1.9721 0.1756
## Genotype    1    8.82    8.821   0.0850 0.7736
## age:Genotype 1  106.72  106.720   1.0289 0.3225
## Residuals   20 2074.52  103.726
```

```
## Analysis of Variance Table
##
## Response: Pulse
##           Df Sum Sq Mean Sq F value Pr(>F)
## age        1  838.29  838.29   8.3306 0.01130 *
## Genotype    1  321.36  321.36   3.1935 0.09415 .
## age:Genotype 1   67.88   67.88   0.6746 0.42432
## Residuals   15 1509.42   100.63
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Cohort physiological distribution

Age by genotype



Cohort physiological distribution

Age by sex

