

Absolute Winding Number Differentiates Spatial Navigation Strategies with Genetic Risk for Alzheimer's disease

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Data sources

We evaluate genotype and sex differences in mouse models of Alzheimer's disease risk, based on APOE alleles: APOE2 is protective, APOE3 is control, and APOE4 represents genetic risk for AD. One allele increases risk by 3 times, and two APOE4 alleles increase risk by 10 times (ref) in relation to APOE3 . We use multiple data sources:

Morris Water Maze - testing spatial navigation memory

Segmentation: regional volumes

Microstructural properties: FA

Tractography Based Connectivity: Degree, and Clustering Coefficient

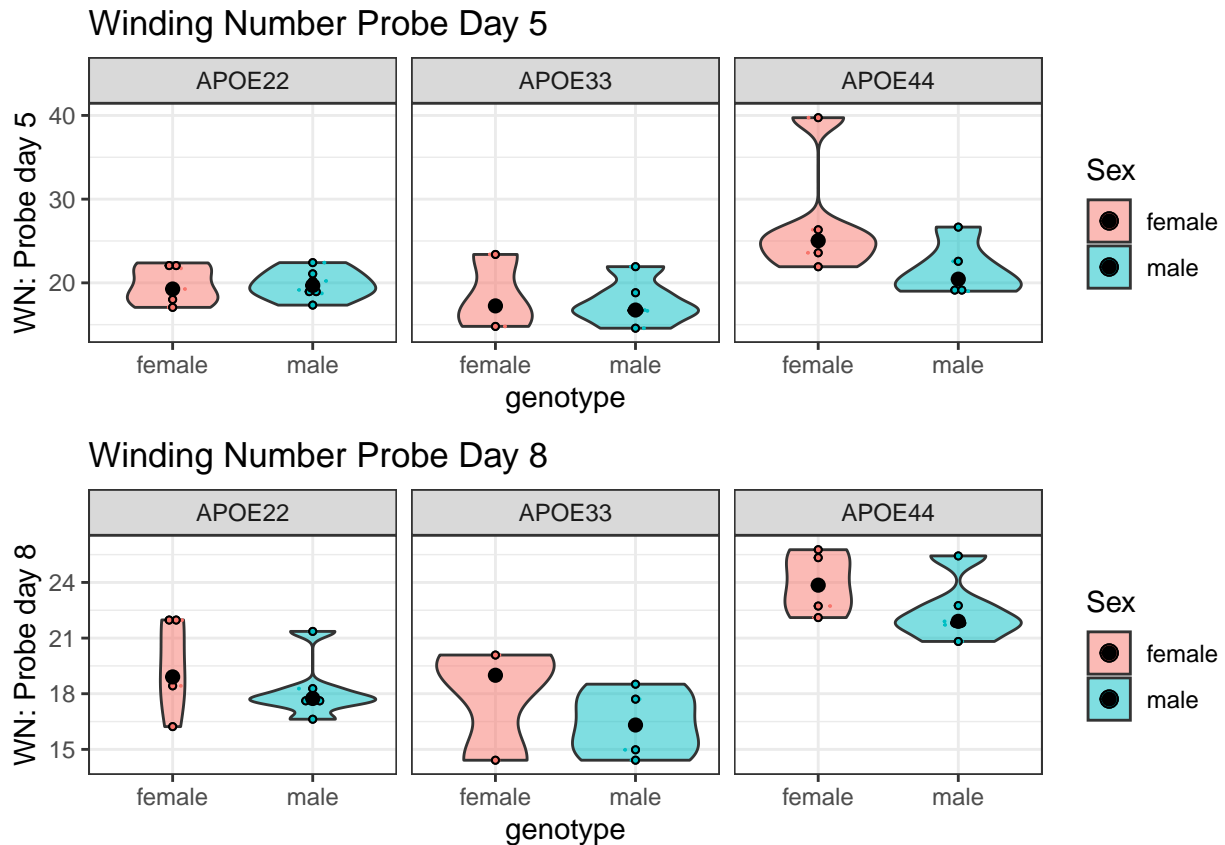
##Setup

We read the data and normalize volumes to the whole brain.

Plots for Winding Number

We embed plots for day 5 and day 8 probe trials:

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
```



```
## [1] "Probe day 5"
##
## Call:
## lm(formula = Probe_d5 ~ Genotype * Sex, data = geno_combined_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.4015 -2.3246 -0.9962  1.2548 12.4058
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    19.6924     1.7469   11.273 7.62e-11 ***
## GenotypeAPOE33    -1.2129     2.8527   -0.425  0.67466
## GenotypeAPOE44     7.6319     2.4705    3.089  0.00518 **
## Sexmale           0.1352     2.3654    0.057  0.95493
## GenotypeAPOE33:Sexmale -0.8661     3.7058   -0.234  0.81728
## GenotypeAPOE44:Sexmale -5.8705     3.4203   -1.716  0.09953 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.906 on 23 degrees of freedom
## Multiple R-squared:  0.4526, Adjusted R-squared:  0.3336
## F-statistic: 3.803 on 5 and 23 DF, p-value: 0.01174
##
## Call:
## lm(formula = Probe_d5 ~ Genotype, data = combo_f_FA)
```

```
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -5.402 -2.623 -1.232  2.046 12.406
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    19.692     2.297   8.574 6.38e-06 ***
## GenotypeAPOE33  -1.213     3.750  -0.323  0.7531
## GenotypeAPOE44   7.632     3.248   2.350  0.0407 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.136 on 10 degrees of freedom
## Multiple R-squared:  0.4361, Adjusted R-squared:  0.3233
## F-statistic: 3.867 on 2 and 10 DF,  p-value: 0.05701
##
## Call:
## lm(formula = Probe_d5 ~ Genotype, data = combo_m_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.1660 -1.4438 -0.8342  1.1177  5.0717
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    19.828     1.057  18.751 8.55e-11 ***
## GenotypeAPOE33  -2.079     1.568  -1.326  0.208
## GenotypeAPOE44   1.761     1.568   1.123  0.282
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.59 on 13 degrees of freedom
## Multiple R-squared:  0.2977, Adjusted R-squared:  0.1896
## F-statistic: 2.755 on 2 and 13 DF,  p-value: 0.1006
## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype      2  206.87  103.434   6.7786 0.004849 **
## Sex           1   33.13   33.134   2.1715 0.154148
## Genotype:Sex   2   50.15   25.077   1.6434 0.215215
## Residuals    23  350.95   15.259
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Analysis of Variance Table
##
## Response: Probe_d5
##              Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype      2  203.97  101.987   3.8669 0.05701 .
## Residuals    10  263.74   26.374
## ---
```

```

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

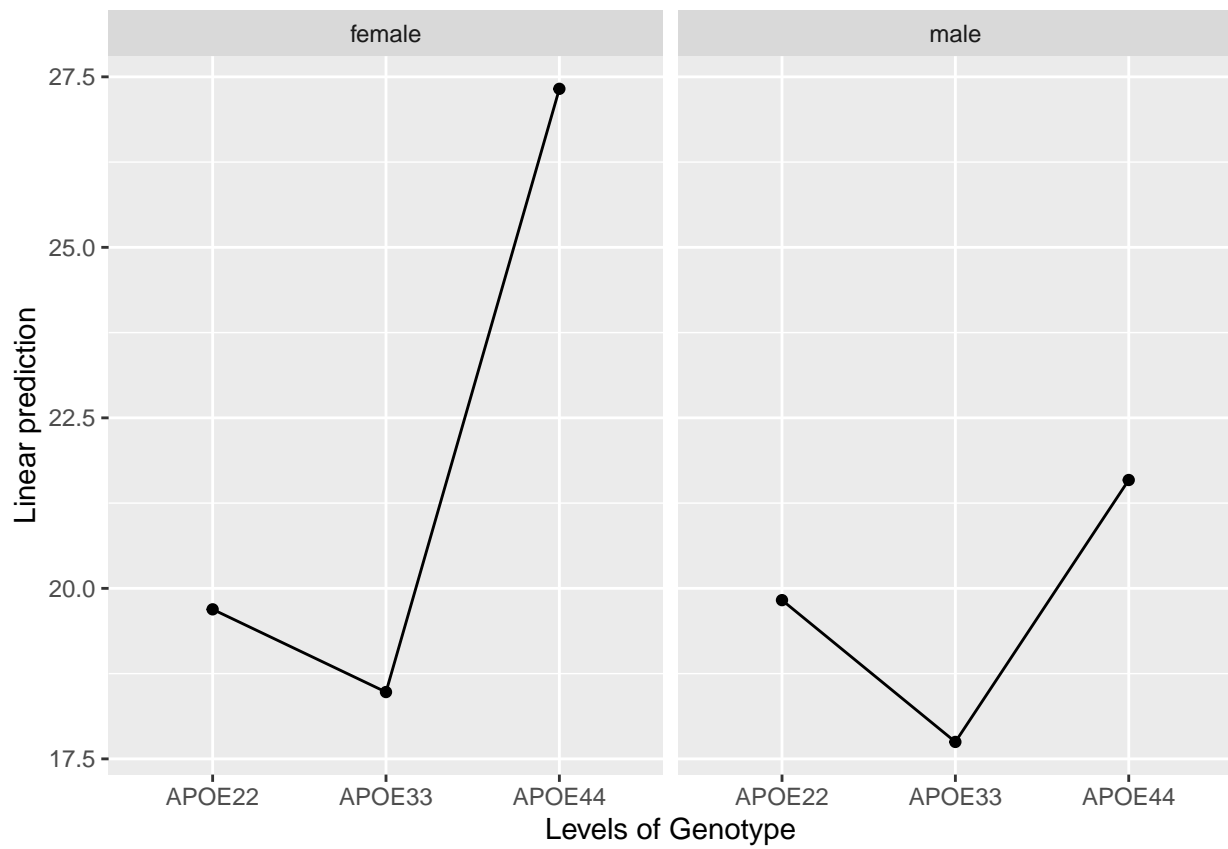
## Analysis of Variance Table
##
## Response: Probe_d5
##           Df Sum Sq Mean Sq F value Pr(>F)
## Genotype    2 36.965 18.4826  2.7551 0.1006
## Residuals   13 87.212  6.7086

## contrast      estimate    SE df t.ratio p.value
## APOE22 female effect  -1.084 1.61 23  -0.674  0.6184
## APOE33 female effect  -2.297 1.99 23  -1.157  0.5182
## APOE44 female effect   6.547 1.61 23   4.072  0.0028
## APOE22 male effect    -0.949 1.50 23  -0.633  0.6184
## APOE33 male effect    -3.028 1.61 23  -1.883  0.2171
## APOE44 male effect     0.812 1.61 23   0.505  0.6184
##
## P value adjustment: fdr method for 6 tests

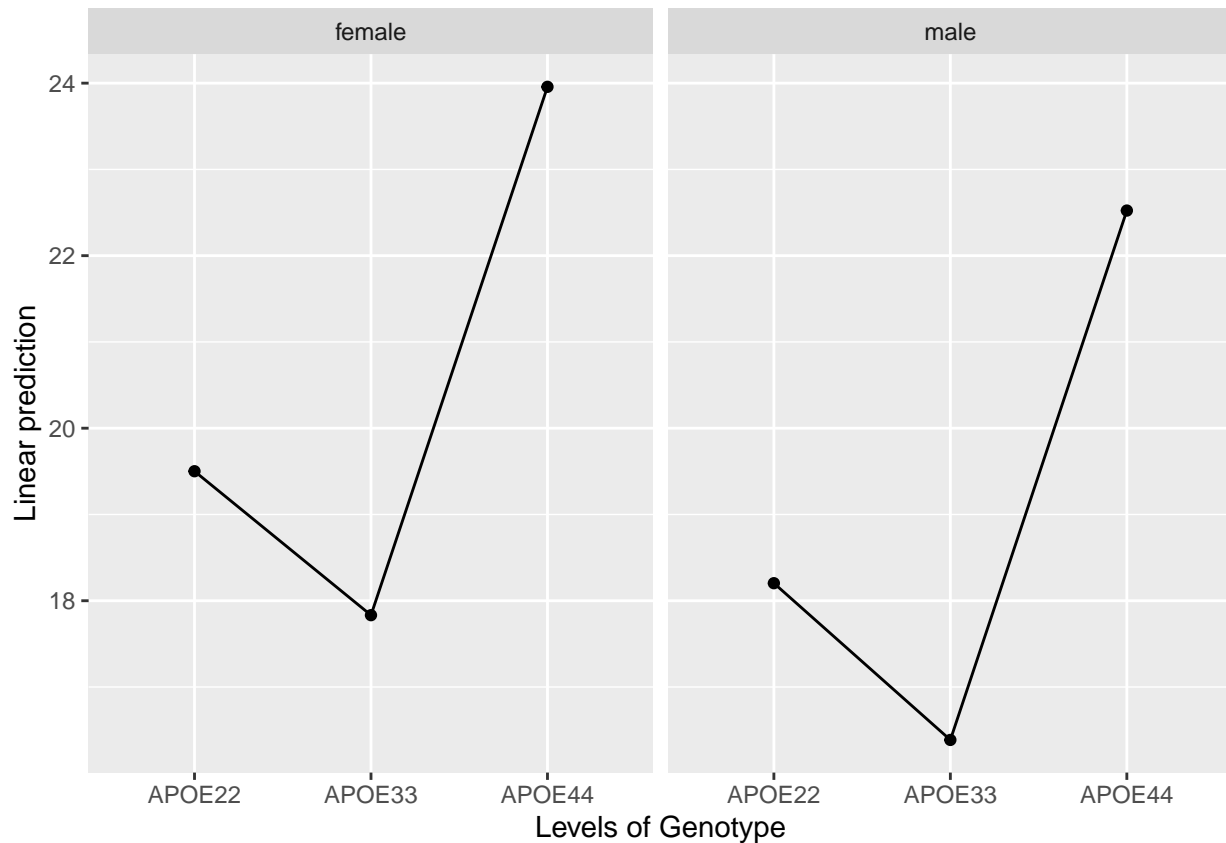
## $`simple contrasts for Genotype`
## Sex = female:
## contrast      estimate    SE df t.ratio p.value
## APOE22 effect  -2.140 1.50 23  -1.423  0.1681
## APOE33 effect  -3.353 1.71 23  -1.956  0.0941
## APOE44 effect   5.492 1.50 23   3.653  0.0040
##
## Sex = male:
## contrast      estimate    SE df t.ratio p.value
## APOE22 effect   0.106 1.34 23   0.079  0.9379
## APOE33 effect  -1.973 1.41 23  -1.403  0.2960
## APOE44 effect   1.867 1.41 23   1.328  0.2960
##
## P value adjustment: fdr method for 3 tests
##
## $`simple contrasts for Sex`
## Genotype = APOE22:
## contrast      estimate    SE df t.ratio p.value
## female effect  -0.0676 1.18 23  -0.057  0.9549
## male effect     0.0676 1.18 23   0.057  0.9549
##
## Genotype = APOE33:
## contrast      estimate    SE df t.ratio p.value
## female effect   0.3655 1.43 23   0.256  0.8001
## male effect    -0.3655 1.43 23  -0.256  0.8001
##
## Genotype = APOE44:
## contrast      estimate    SE df t.ratio p.value
## female effect   2.8677 1.24 23   2.322  0.0295
## male effect    -2.8677 1.24 23  -2.322  0.0295
##
## P value adjustment: fdr method for 2 tests

## [1] "Probe Day 5 Abs Winding Number"

```



[1] "Probe Day 8 Abs Winding Number"



```
## Genotype_poly Sex_consec estimate SE df t.ratio p.value
## linear male - female -5.87 3.42 23 -1.716 0.0995
## quadratic male - female -4.14 6.65 23 -0.622 0.5400

## Genotype Sex c.1 c.2
## 1 APOE22 female 1 -1
## 2 APOE33 female 0 2
## 3 APOE44 female -1 -1
## 4 APOE22 male -1 1
## 5 APOE33 male 0 -2
## 6 APOE44 male 1 1

##
## Simultaneous Tests for General Linear Hypotheses
##
## Fit: lm(formula = Probe_d5 ~ Genotype * Sex, data = geno_combined_FA)
##
## Linear Hypotheses:
##
## Estimate Std. Error t value Pr(>|t|)
## APOE22 female - APOE33 female == 0 1.2129 2.8527 0.425 0.9980
## APOE22 female - APOE44 female == 0 -7.6319 2.4705 -3.089 0.0511 .
## APOE22 female - APOE22 male == 0 -0.1352 2.3654 -0.057 1.0000
## APOE22 female - APOE33 male == 0 1.9439 2.4705 0.787 0.9667
## APOE22 female - APOE44 male == 0 -1.8965 2.4705 -0.768 0.9700
## APOE33 female - APOE44 female == 0 -8.8448 2.8527 -3.100 0.0498 *
## APOE33 female - APOE22 male == 0 -1.3481 2.7621 -0.488 0.9961
## APOE33 female - APOE33 male == 0 0.7309 2.8527 0.256 0.9998
## APOE33 female - APOE44 male == 0 -3.1094 2.8527 -1.090 0.8795
```

```

## APOE44 female - APOE22 male == 0      7.4967      2.3654      3.169      0.0430 *
## APOE44 female - APOE33 male == 0      9.5757      2.4705      3.876      0.0087 **
## APOE44 female - APOE44 male == 0      5.7354      2.4705      2.322      0.2244
## APOE22 male - APOE33 male == 0        2.0790      2.3654      0.879      0.9474
## APOE22 male - APOE44 male == 0       -1.7613      2.3654     -0.745      0.9737
## APOE33 male - APOE44 male == 0       -3.8403      2.4705     -1.554      0.6327
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)

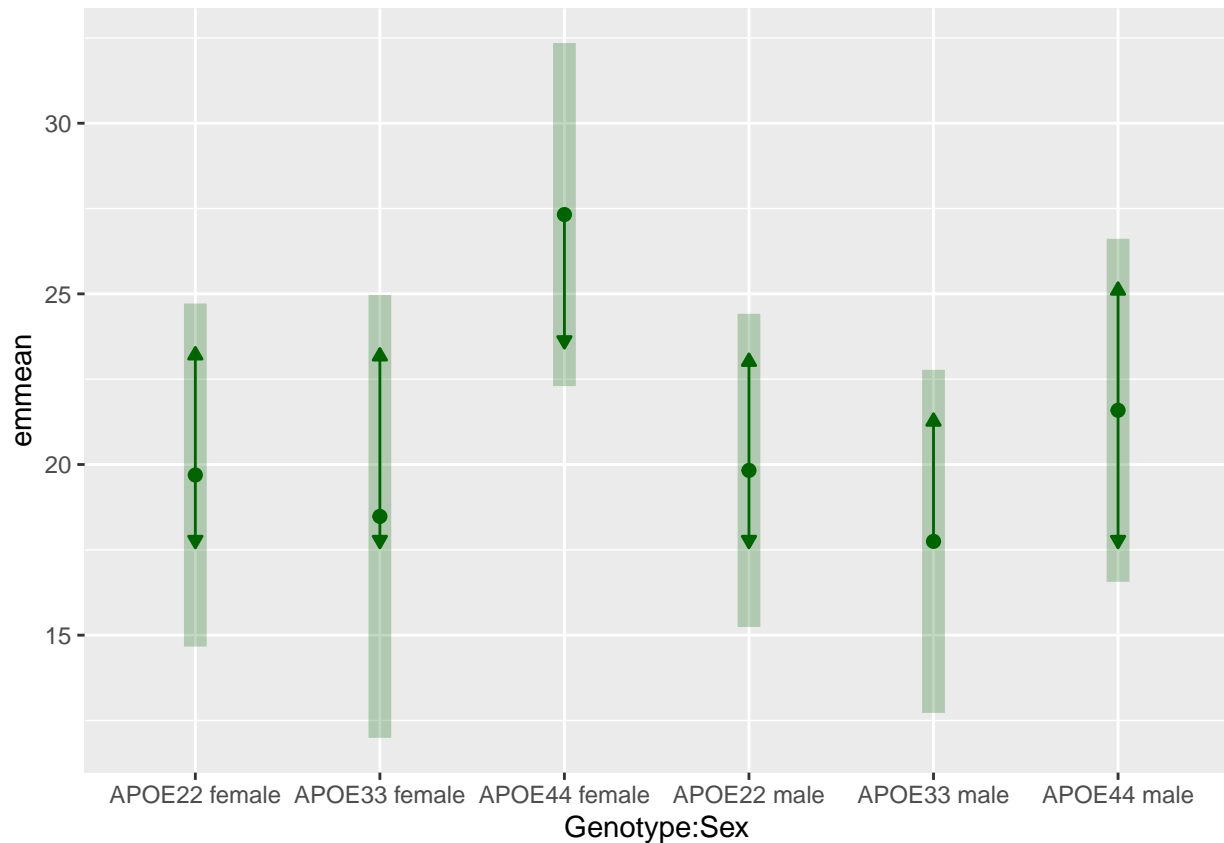
## $emmeans
##      Genotype Sex      emmean      SE df lower.CL upper.CL
## APOE22  female      19.7 1.75 23      16.1      23.3
## APOE33  female      18.5 2.26 23      13.8      23.1
## APOE44  female      27.3 1.75 23      23.7      30.9
## APOE22  male       19.8 1.59 23      16.5      23.1
## APOE33  male       17.7 1.75 23      14.1      21.4
## APOE44  male       21.6 1.75 23      18.0      25.2
##
## Confidence level used: 0.95
##
## $contrasts
##      contrast              estimate      SE df t.ratio p.value
## APOE22 female - APOE33 female      1.213 2.85 23      0.425 0.9980
## APOE22 female - APOE44 female     -7.632 2.47 23     -3.089 0.0515
## APOE22 female - APOE22 male      -0.135 2.37 23     -0.057 1.0000
## APOE22 female - APOE33 male       1.944 2.47 23      0.787 0.9670
## APOE22 female - APOE44 male     -1.896 2.47 23     -0.768 0.9703
## APOE33 female - APOE44 female     -8.845 2.85 23     -3.100 0.0503
## APOE33 female - APOE22 male     -1.348 2.76 23     -0.488 0.9961
## APOE33 female - APOE33 male       0.731 2.85 23      0.256 0.9998
## APOE33 female - APOE44 male     -3.109 2.85 23     -1.090 0.8804
## APOE44 female - APOE22 male       7.497 2.37 23      3.169 0.0434
## APOE44 female - APOE33 male       9.576 2.47 23      3.876 0.0088
## APOE44 female - APOE44 male       5.735 2.47 23      2.322 0.2259
## APOE22 male - APOE33 male         2.079 2.37 23      0.879 0.9478
## APOE22 male - APOE44 male     -1.761 2.37 23     -0.745 0.9739
## APOE33 male - APOE44 male     -3.840 2.47 23     -1.554 0.6346
##
## P value adjustment: tukey method for comparing a family of 6 estimates

## Sex = female:
##      contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33      1.21 2.85 23      0.425 0.9056
## APOE22 - APOE44     -7.63 2.47 23     -3.089 0.0138
## APOE33 - APOE44     -8.84 2.85 23     -3.100 0.0134
##
## Sex = male:
##      contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33      2.08 2.37 23      0.879 0.6587
## APOE22 - APOE44     -1.76 2.37 23     -0.745 0.7398
## APOE33 - APOE44     -3.84 2.47 23     -1.554 0.2851
##
## P value adjustment: tukey method for comparing a family of 3 estimates

```

```
##
## Simultaneous Tests for General Linear Hypotheses
##
## Linear Hypotheses:
##               Estimate Std. Error t value Pr(>|t|)
## APOE22 - APOE33, female == 0    1.213      2.853   0.425   0.9903
## APOE22 - APOE44, female == 0   -7.632      2.471  -3.089   0.0269 *
## APOE33 - APOE44, female == 0   -8.845      2.853  -3.100   0.0263 *
## APOE22 - APOE33, male == 0     2.079      2.365   0.879   0.8768
## APOE22 - APOE44, male == 0    -1.761      2.365  -0.745   0.9279
## APOE33 - APOE44, male == 0    -3.840      2.471  -1.554   0.4776
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)

## $`Sex = female`
##
## Simultaneous Tests for General Linear Hypotheses
##
## Fit: lm(formula = Probe_d5 ~ Genotype * Sex, data = geno_combined_FA)
##
## Linear Hypotheses:
##               Estimate Std. Error t value Pr(>|t|)
## APOE22 - APOE33 == 0    1.213      2.853   0.425   0.9052
## APOE22 - APOE44 == 0   -7.632      2.471  -3.089   0.0136 *
## APOE33 - APOE44 == 0   -8.845      2.853  -3.100   0.0132 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
##
## $`Sex = male`
##
## Simultaneous Tests for General Linear Hypotheses
##
## Fit: lm(formula = Probe_d5 ~ Genotype * Sex, data = geno_combined_FA)
##
## Linear Hypotheses:
##               Estimate Std. Error t value Pr(>|t|)
## APOE22 - APOE33 == 0     2.079      2.365   0.879   0.659
## APOE22 - APOE44 == 0    -1.761      2.365  -0.745   0.740
## APOE33 - APOE44 == 0    -3.840      2.471  -1.554   0.285
## (Adjusted p values reported -- single-step method)
```

##	Sex	Genotype	contrast	estimate	SE	df	t.ratio	p.value
##	female	.	APOE22 - APOE33	1.213	2.85	23	0.425	0.9968
##	female	.	APOE22 - APOE44	-7.632	2.47	23	-3.089	0.0365
##	female	.	APOE33 - APOE44	-8.845	2.85	23	-3.100	0.0356
##	male	.	APOE22 - APOE33	2.079	2.37	23	0.879	0.9256
##	male	.	APOE22 - APOE44	-1.761	2.37	23	-0.745	0.9615
##	male	.	APOE33 - APOE44	-3.840	2.47	23	-1.554	0.5602
##	.	APOE22	female - male	-0.135	2.37	23	-0.057	1.0000
##	.	APOE33	female - male	0.731	2.85	23	0.256	0.9997
##	.	APOE44	female - male	5.735	2.47	23	2.322	0.1754

P value adjustment: mvt method for 9 tests

##	Sex	contrast	estimate	SE	df	t.ratio	p.value
##	female	APOE22 - APOE33	1.21	2.85	23	0.425	0.6747
##	female	APOE22 - APOE44	-7.63	2.47	23	-3.089	0.0155
##	female	APOE33 - APOE44	-8.84	2.85	23	-3.100	0.0155
##	male	APOE22 - APOE33	2.08	2.37	23	0.879	0.5568
##	male	APOE22 - APOE44	-1.76	2.37	23	-0.745	0.5568
##	male	APOE33 - APOE44	-3.84	2.47	23	-1.554	0.2675
##	female	APOE22 - APOE33	1.21	2.85	23	0.425	0.6747
##	female	APOE22 - APOE44	-7.63	2.47	23	-3.089	0.0155
##	female	APOE33 - APOE44	-8.84	2.85	23	-3.100	0.0155
##	male	APOE22 - APOE33	2.08	2.37	23	0.879	0.5568
##	male	APOE22 - APOE44	-1.76	2.37	23	-0.745	0.5568
##	male	APOE33 - APOE44	-3.84	2.47	23	-1.554	0.2675

```

## P value adjustment: fdr method for 12 tests
## [1] "Probe day 8"
##
## Call:
## lm(formula = Probe_d8 ~ Genotype * Sex, data = geno_combined_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4167 -1.2288 -0.4318  1.3781  3.1566
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      19.5012      0.8881  21.959 < 2e-16 ***
## GenotypeAPOE33     -1.6686      1.4502  -1.151  0.26171
## GenotypeAPOE44       4.4562      1.2559   3.548  0.00171 **
## Sexmale           -1.2979      1.2024  -1.079  0.29161
## GenotypeAPOE33:Sexmale -0.1483      1.8839  -0.079  0.93796
## GenotypeAPOE44:Sexmale -0.1366      1.7387  -0.079  0.93808
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.986 on 23 degrees of freedom
## Multiple R-squared:  0.6975, Adjusted R-squared:  0.6317
## F-statistic: 10.61 on 5 and 23 DF,  p-value: 2.242e-05
##
## Call:
## lm(formula = Probe_d8 ~ Genotype, data = combo_f_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3.4167 -1.2288 -0.1041  1.8071  2.4777
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      19.501      1.026  19.000 3.54e-09 ***
## GenotypeAPOE33     -1.669      1.676  -0.996  0.3429
## GenotypeAPOE44       4.456      1.452   3.070  0.0118 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.295 on 10 degrees of freedom
## Multiple R-squared:  0.6165, Adjusted R-squared:  0.5398
## F-statistic: 8.039 on 2 and 10 DF,  p-value: 0.008292
##
## Call:
## lm(formula = Probe_d8 ~ Genotype, data = combo_m_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.9692 -0.9598 -0.4575  0.5022  3.1566
##
## Coefficients:

```

```

##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    18.2034     0.6982  26.072 1.31e-12 ***
## GenotypeAPOE33 -1.8169     1.0356  -1.754  0.1029
## GenotypeAPOE44  4.3196     1.0356   4.171  0.0011 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.71 on 13 degrees of freedom
## Multiple R-squared:  0.7246, Adjusted R-squared:  0.6822
## F-statistic: 17.1 on 2 and 13 DF,  p-value: 0.0002292

## Analysis of Variance Table
##
## Response: Probe_d8
##               Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype       2 195.444  97.722 24.7824 1.826e-06 ***
## Sex            1  13.625  13.625  3.4554  0.07589 .
## Genotype:Sex   2   0.034   0.017  0.0043  0.99572
## Residuals     23  90.694   3.943
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##               Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype       2  84.685  42.342  8.0389 0.008292 **
## Residuals     10  52.672   5.267
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Probe_d8
##               Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype       2 100.014  50.007 17.098 0.0002292 ***
## Residuals     13  38.022   2.925
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##
## Simultaneous Tests for General Linear Hypotheses
##
## Fit: lm(formula = Probe_d8 ~ Genotype * Sex, data = geno_combined_FA)
##
## Linear Hypotheses:
##               Estimate Std. Error t value Pr(>|t|)
## APOE22 female - APOE33 female == 0  1.6686     1.4502   1.151  0.85391
## APOE22 female - APOE44 female == 0 -4.4562     1.2559  -3.548  0.01859 *
## APOE22 female - APOE22 male == 0    1.2979     1.2024   1.079  0.88366
## APOE22 female - APOE33 male == 0    3.1148     1.2559   2.480  0.17016
## APOE22 female - APOE44 male == 0   -3.0217     1.2559  -2.406  0.19421
## APOE33 female - APOE44 female == 0 -6.1248     1.4502  -4.223  0.00382 **
## APOE33 female - APOE22 male == 0   -0.3707     1.4041  -0.264  0.99980
## APOE33 female - APOE33 male == 0    1.4461     1.4502   0.997  0.91346
## APOE33 female - APOE44 male == 0   -4.6904     1.4502  -3.234  0.03733 *

```

```

## APOE44 female - APOE22 male == 0      5.7541      1.2024      4.785 < 0.001 ***
## APOE44 female - APOE33 male == 0      7.5709      1.2559      6.028 < 0.001 ***
## APOE44 female - APOE44 male == 0      1.4344      1.2559      1.142 0.85762
## APOE22 male - APOE33 male == 0      1.8169      1.2024      1.511 0.65931
## APOE22 male - APOE44 male == 0     -4.3196      1.2024     -3.592 0.01679 *
## APOE33 male - APOE44 male == 0     -6.1365      1.2559     -4.886 < 0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)

## $emmeans
##      Genotype Sex      emmean      SE df lower.CL upper.CL
## APOE22  female      19.5 0.888 23      17.7      21.3
## APOE33  female      17.8 1.146 23      15.5      20.2
## APOE44  female      24.0 0.888 23      22.1      25.8
## APOE22  male       18.2 0.811 23      16.5      19.9
## APOE33  male       16.4 0.888 23      14.5      18.2
## APOE44  male       22.5 0.888 23      20.7      24.4
##
## Confidence level used: 0.95
##
## $contrasts
##      contrast              estimate      SE df t.ratio p.value
## APOE22 female - APOE33 female      1.669 1.45 23      1.151 0.8549
## APOE22 female - APOE44 female     -4.456 1.26 23     -3.548 0.0187
## APOE22 female - APOE22 male       1.298 1.20 23      1.079 0.8846
## APOE22 female - APOE33 male       3.115 1.26 23      2.480 0.1714
## APOE22 female - APOE44 male     -3.022 1.26 23     -2.406 0.1954
## APOE33 female - APOE44 female     -6.125 1.45 23     -4.223 0.0039
## APOE33 female - APOE22 male     -0.371 1.40 23     -0.264 0.9998
## APOE33 female - APOE33 male       1.446 1.45 23      0.997 0.9141
## APOE33 female - APOE44 male     -4.690 1.45 23     -3.234 0.0377
## APOE44 female - APOE22 male       5.754 1.20 23      4.785 0.0010
## APOE44 female - APOE33 male       7.571 1.26 23      6.028 0.0001
## APOE44 female - APOE44 male       1.434 1.26 23      1.142 0.8586
## APOE22 male - APOE33 male       1.817 1.20 23      1.511 0.6610
## APOE22 male - APOE44 male     -4.320 1.20 23     -3.592 0.0169
## APOE33 male - APOE44 male     -6.137 1.26 23     -4.886 0.0008
##
## P value adjustment: tukey method for comparing a family of 6 estimates

## Sex = female:
##      contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33      1.67 1.45 23      1.151 0.4937
## APOE22 - APOE44     -4.46 1.26 23     -3.548 0.0047
## APOE33 - APOE44     -6.12 1.45 23     -4.223 0.0009
##
## Sex = male:
##      contrast      estimate      SE df t.ratio p.value
## APOE22 - APOE33      1.82 1.20 23      1.511 0.3044
## APOE22 - APOE44     -4.32 1.20 23     -3.592 0.0042
## APOE33 - APOE44     -6.14 1.26 23     -4.886 0.0002
##
## P value adjustment: tukey method for comparing a family of 3 estimates

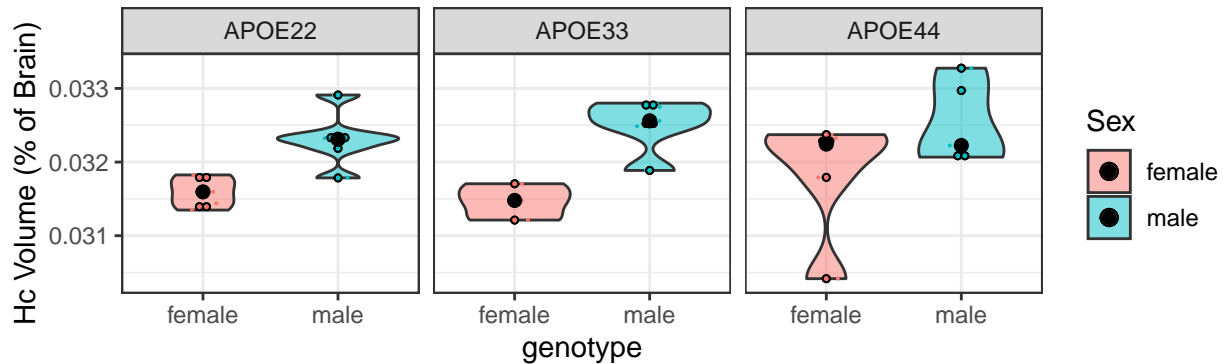
```

Plots for Volume

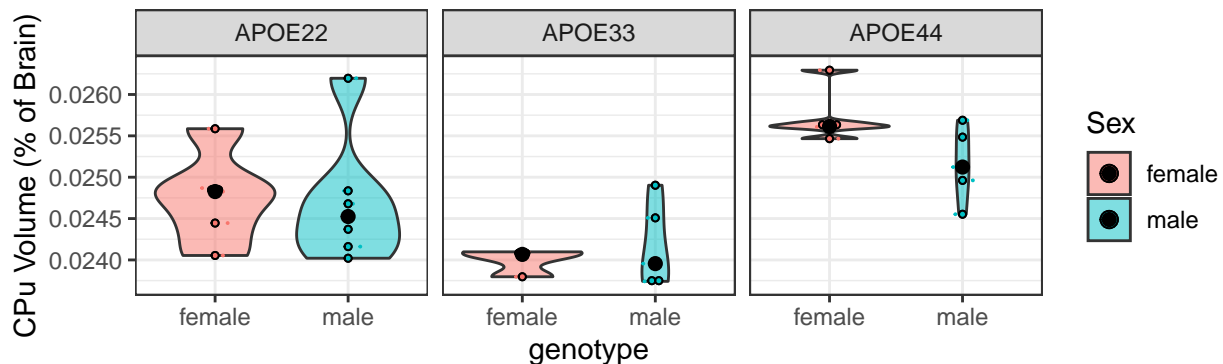
Hippocampus, Caudate Putamen, Brain

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
```

Hc Volume (% of Brain)

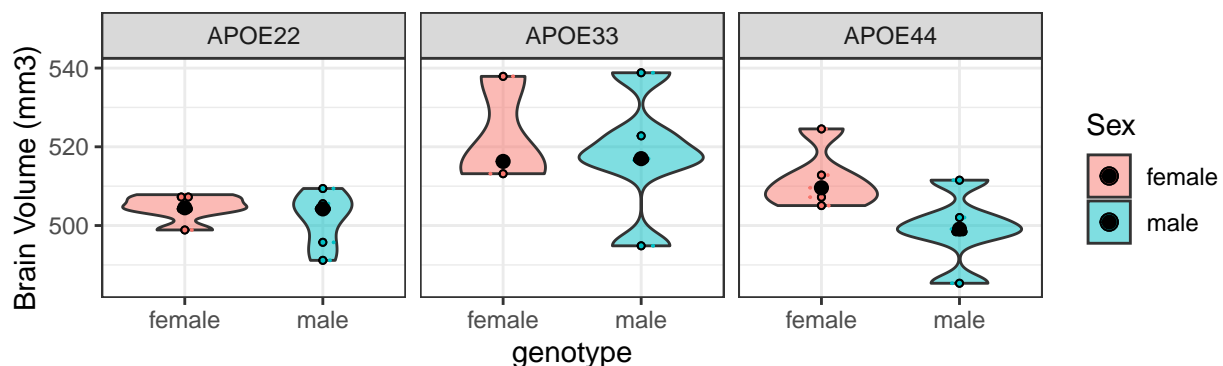


CPu Volume (% of Brain)



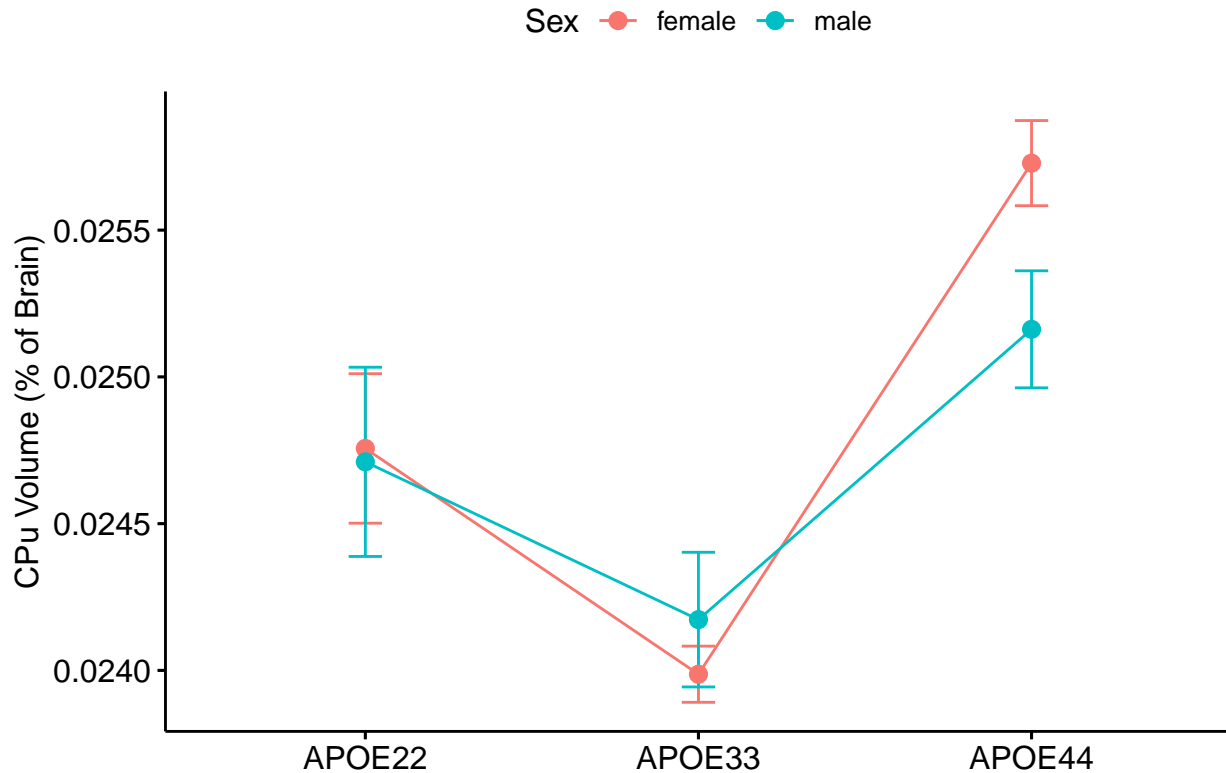
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
```

Brain Volume (mm3)

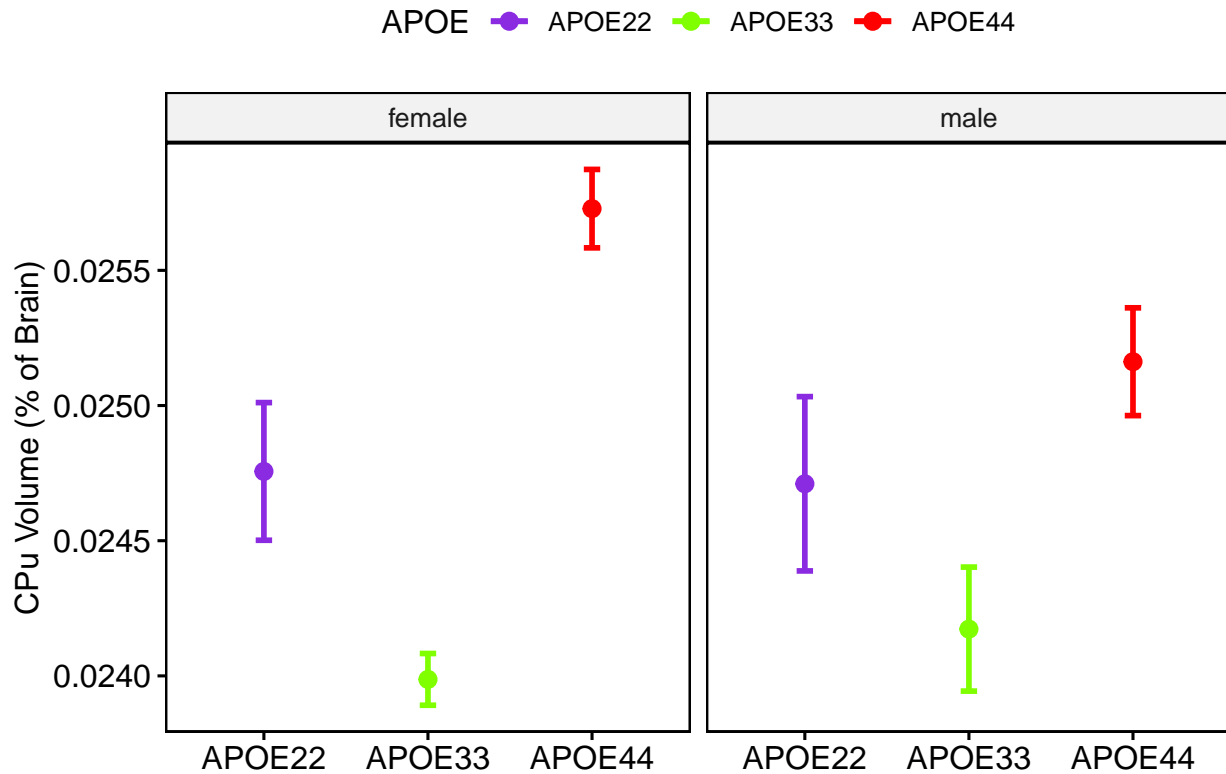


```
## geom_path: Each group consists of only one observation. Do you need to adjust
```

```
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## file saved to /Users/alex/AlexBadea_MyPapers/DavidDunson/Figures/Brain3Panels_Volume.pdf
```



```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```

```
## $emmeans
##   Genotype Sex    emmean      SE df lower.CL upper.CL
##   APOE22  female 0.0316 0.000217 23   0.0311   0.0320
##   APOE33  female 0.0315 0.000280 23   0.0309   0.0320
##   APOE44  female 0.0318 0.000217 23   0.0314   0.0323
##   APOE22  male   0.0323 0.000198 23   0.0319   0.0327
##   APOE33  male   0.0325 0.000217 23   0.0320   0.0329
##   APOE44  male   0.0325 0.000217 23   0.0321   0.0330
##
## Confidence level used: 0.95
##
## $contrasts
##   contrast                                estimate      SE df t.ratio p.value
##   APOE22 female - APOE33 female 0.000127 0.000355 23    0.359 0.9991
##   APOE22 female - APOE44 female -0.000237 0.000307 23   -0.772 0.9695
##   APOE22 female - APOE22 male  -0.000718 0.000294 23   -2.443 0.1830
##   APOE22 female - APOE33 male  -0.000903 0.000307 23   -2.942 0.0700
##   APOE22 female - APOE44 male  -0.000935 0.000307 23   -3.046 0.0564
##   APOE33 female - APOE44 female -0.000364 0.000355 23   -1.028 0.9037
##   APOE33 female - APOE22 male  -0.000846 0.000343 23   -2.463 0.1767
##   APOE33 female - APOE33 male  -0.001031 0.000355 23   -2.907 0.0753
##   APOE33 female - APOE44 male  -0.001063 0.000355 23   -2.997 0.0625
##   APOE44 female - APOE22 male  -0.000481 0.000294 23   -1.637 0.5842
##   APOE44 female - APOE33 male  -0.000666 0.000307 23   -2.170 0.2890
##   APOE44 female - APOE44 male  -0.000698 0.000307 23   -2.274 0.2445
```

```

## APOE22 male - APOE33 male      -0.000185 0.000294 23  -0.630  0.9875
## APOE22 male - APOE44 male      -0.000217 0.000294 23  -0.739  0.9748
## APOE33 male - APOE44 male      -0.000032 0.000307 23  -0.104  1.0000
##
## P value adjustment: tukey method for comparing a family of 6 estimates
##
## Simultaneous Tests for General Linear Hypotheses
##
## Fit: lm(formula = Hc ~ Genotype * Sex, data = geno_combined_VOL)
##
## Linear Hypotheses:
##
##              Estimate Std. Error t value Pr(>|t|)
## APOE22 female - APOE33 female == 0  1.273e-04  3.546e-04   0.359  0.9991
## APOE22 female - APOE44 female == 0 -2.371e-04  3.071e-04  -0.772  0.9693
## APOE22 female - APOE22 male == 0   -7.183e-04  2.940e-04  -2.443  0.1818
## APOE22 female - APOE33 male == 0   -9.035e-04  3.071e-04  -2.942  0.0693 .
## APOE22 female - APOE44 male == 0   -9.355e-04  3.071e-04  -3.046  0.0561 .
## APOE33 female - APOE44 female == 0 -3.644e-04  3.546e-04  -1.028  0.9029
## APOE33 female - APOE22 male == 0   -8.456e-04  3.433e-04  -2.463  0.1756
## APOE33 female - APOE33 male == 0   -1.031e-03  3.546e-04  -2.907  0.0746 .
## APOE33 female - APOE44 male == 0   -1.063e-03  3.546e-04  -2.997  0.0620 .
## APOE44 female - APOE22 male == 0   -4.812e-04  2.940e-04  -1.637  0.5824
## APOE44 female - APOE33 male == 0   -6.663e-04  3.071e-04  -2.170  0.2876
## APOE44 female - APOE44 male == 0   -6.983e-04  3.071e-04  -2.274  0.2431
## APOE22 male - APOE33 male == 0     -1.852e-04  2.940e-04  -0.630  0.9874
## APOE22 male - APOE44 male == 0     -2.172e-04  2.940e-04  -0.739  0.9746
## APOE33 male - APOE44 male == 0     -3.199e-05  3.071e-04  -0.104  1.0000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
##
## $emmeans
##   Genotype Sex   emmean      SE df lower.CL upper.CL
## APOE22  female 0.0248 0.000242 23   0.0243   0.0253
## APOE33  female 0.0240 0.000312 23   0.0233   0.0246
## APOE44  female 0.0257 0.000242 23   0.0252   0.0262
## APOE22  male   0.0247 0.000221 23   0.0243   0.0252
## APOE33  male   0.0242 0.000242 23   0.0237   0.0247
## APOE44  male   0.0252 0.000242 23   0.0247   0.0257
##
## Confidence level used: 0.95
##
## $contrasts
##   contrast      estimate      SE df t.ratio p.value
## APOE22 female - APOE33 female  7.69e-04 0.000395 23   1.946  0.4014
## APOE22 female - APOE44 female -9.72e-04 0.000342 23  -2.840  0.0862
## APOE22 female - APOE22 male    4.57e-05 0.000328 23   0.139  1.0000
## APOE22 female - APOE33 male    5.83e-04 0.000342 23   1.704  0.5430
## APOE22 female - APOE44 male   -4.06e-04 0.000342 23  -1.186  0.8391
## APOE33 female - APOE44 female -1.74e-03 0.000395 23  -4.406  0.0025
## APOE33 female - APOE22 male   -7.24e-04 0.000383 23  -1.891  0.4324
## APOE33 female - APOE33 male   -1.86e-04 0.000395 23  -0.471  0.9967
## APOE33 female - APOE44 male   -1.18e-03 0.000395 23  -2.973  0.0657
## APOE44 female - APOE22 male    1.02e-03 0.000328 23   3.105  0.0497

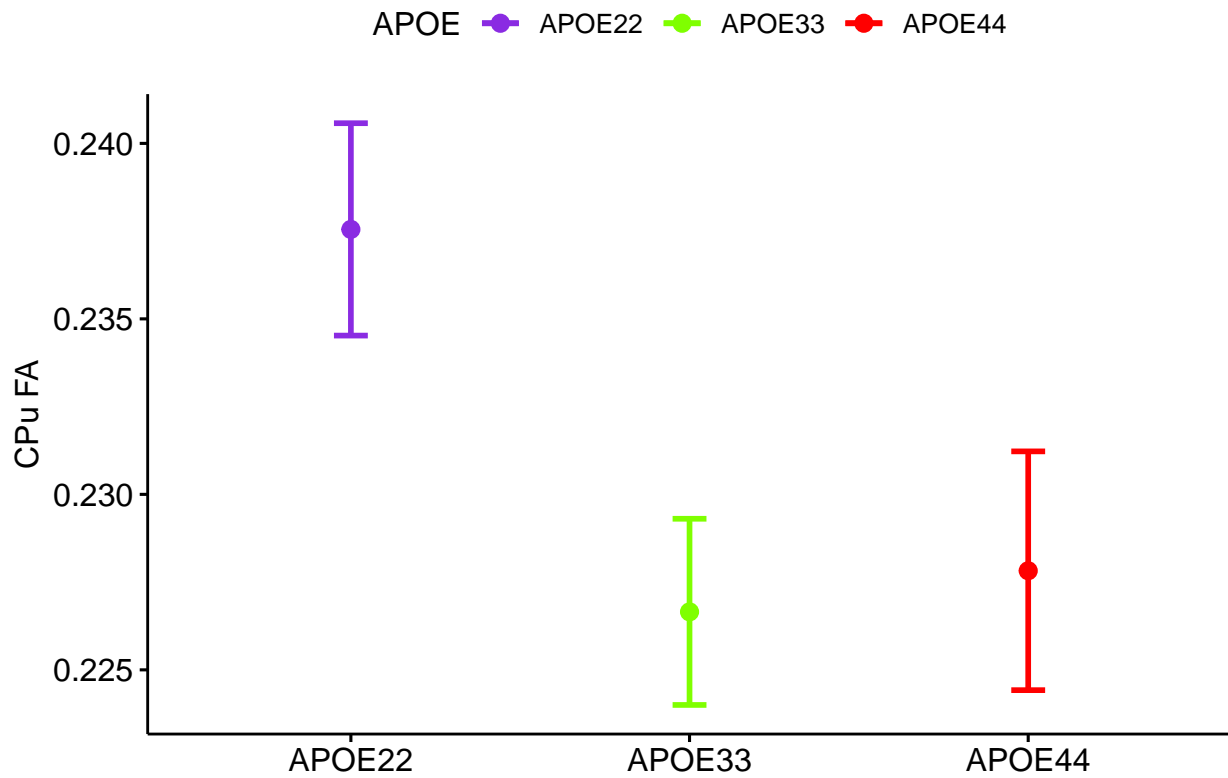
```



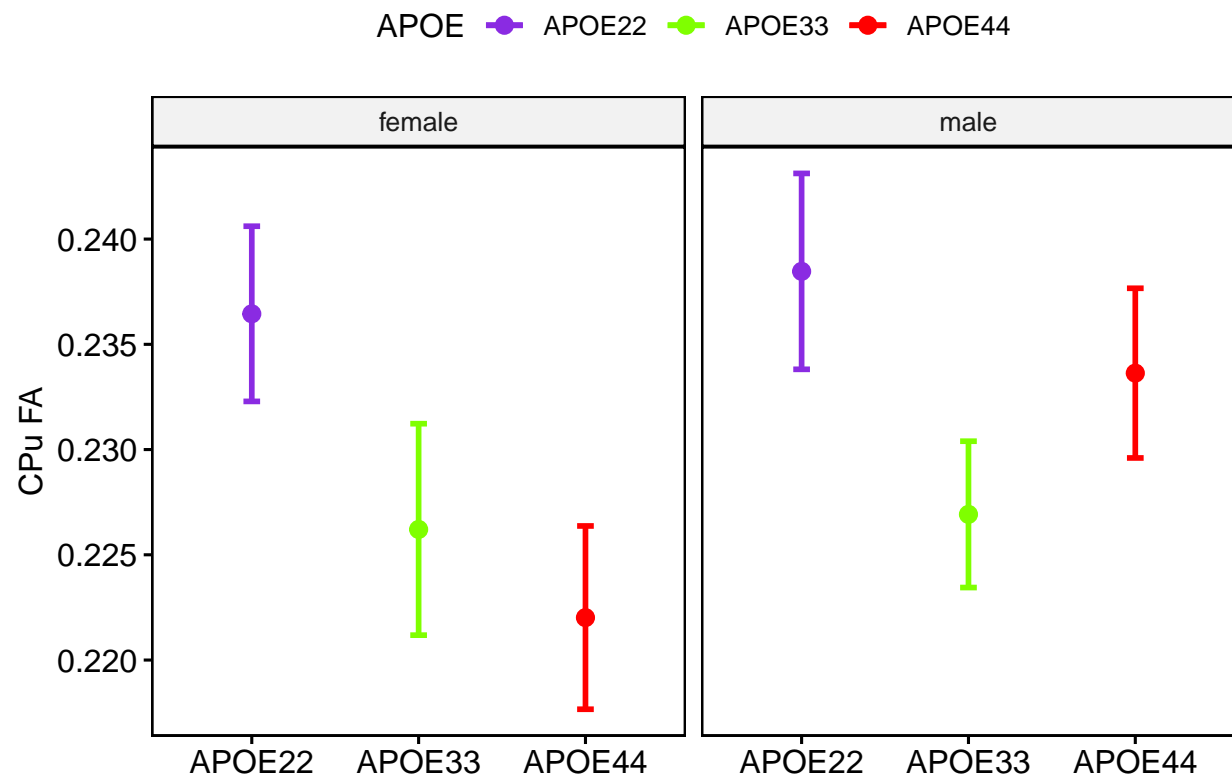
```

## APOE44 female - APOE33 male      1.56e-03 0.000342 23    4.544 0.0018
## APOE44 female - APOE44 male      5.66e-04 0.000342 23    1.654 0.5734
## APOE22 male - APOE33 male        5.38e-04 0.000328 23    1.640 0.5820
## APOE22 male - APOE44 male       -4.51e-04 0.000328 23   -1.378 0.7394
## APOE33 male - APOE44 male       -9.89e-04 0.000342 23   -2.889 0.0780
##
## P value adjustment: tukey method for comparing a family of 6 estimates
##
## Simultaneous Tests for General Linear Hypotheses
##
## Fit: lm(formula = CPu ~ Genotype * Sex, data = geno_combined_VOL)
##
## Linear Hypotheses:
##
##              Estimate Std. Error t value Pr(>|t|)
## APOE22 female - APOE33 female == 0  7.692e-04  3.952e-04   1.946 0.39953
## APOE22 female - APOE44 female == 0 -9.720e-04  3.423e-04  -2.840 0.08536 .
## APOE22 female - APOE22 male == 0    4.568e-05  3.277e-04   0.139 0.99999
## APOE22 female - APOE33 male == 0    5.832e-04  3.423e-04   1.704 0.54105
## APOE22 female - APOE44 male == 0   -4.058e-04  3.423e-04  -1.186 0.83802
## APOE33 female - APOE44 female == 0 -1.741e-03  3.952e-04  -4.406 0.00240 **
## APOE33 female - APOE22 male == 0   -7.235e-04  3.827e-04  -1.891 0.43047
## APOE33 female - APOE33 male == 0   -1.860e-04  3.952e-04  -0.471 0.99671
## APOE33 female - APOE44 male == 0   -1.175e-03  3.952e-04  -2.973 0.06524 .
## APOE44 female - APOE22 male == 0    1.018e-03  3.277e-04   3.105 0.04922 *
## APOE44 female - APOE33 male == 0    1.555e-03  3.423e-04   4.544 0.00177 **
## APOE44 female - APOE44 male == 0    5.662e-04  3.423e-04   1.654 0.57150
## APOE22 male - APOE33 male == 0     5.375e-04  3.277e-04   1.640 0.58025
## APOE22 male - APOE44 male == 0   -4.515e-04  3.277e-04  -1.378 0.73787
## APOE33 male - APOE44 male == 0   -9.890e-04  3.423e-04  -2.889 0.07737 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
##
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?

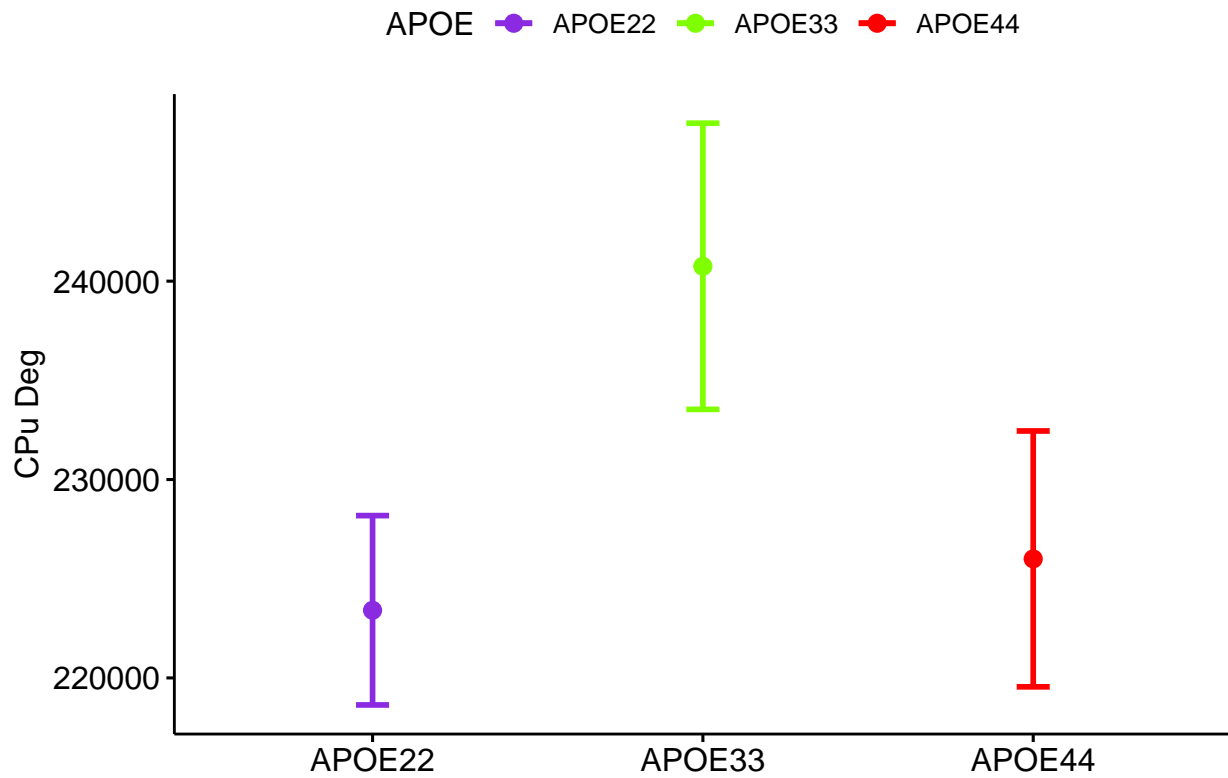
```



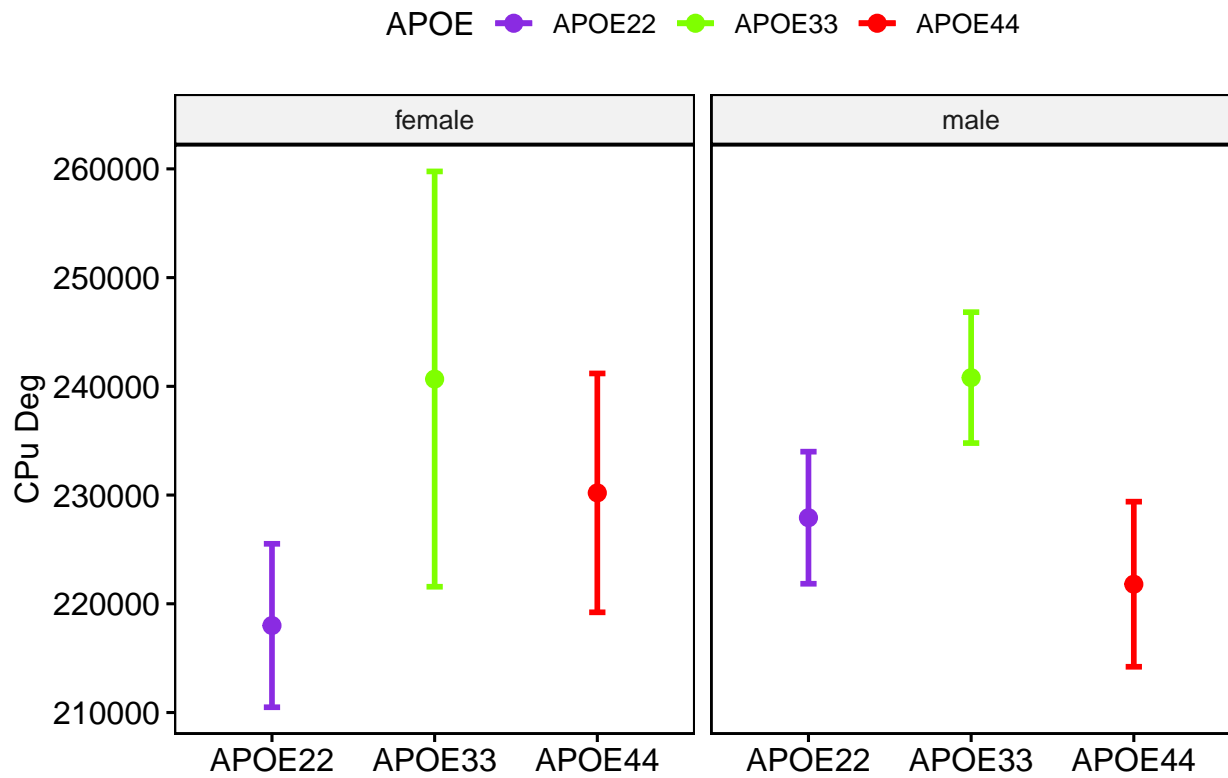
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



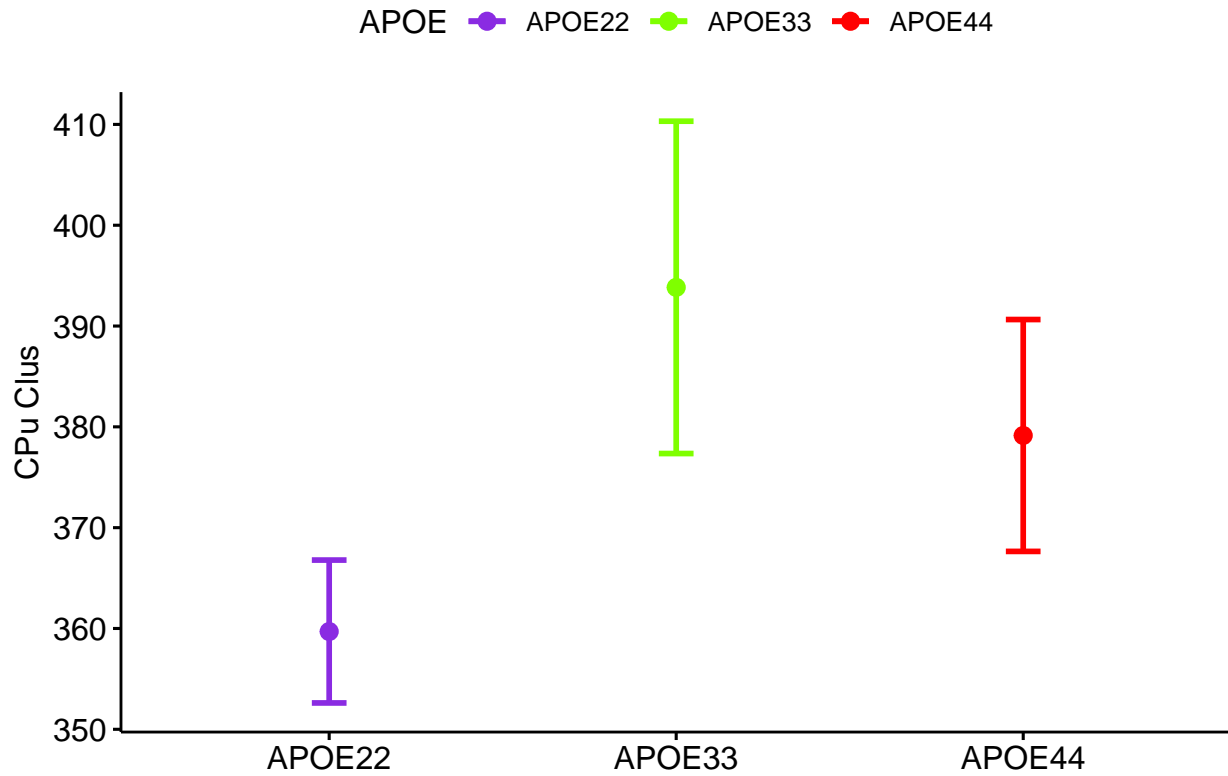
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



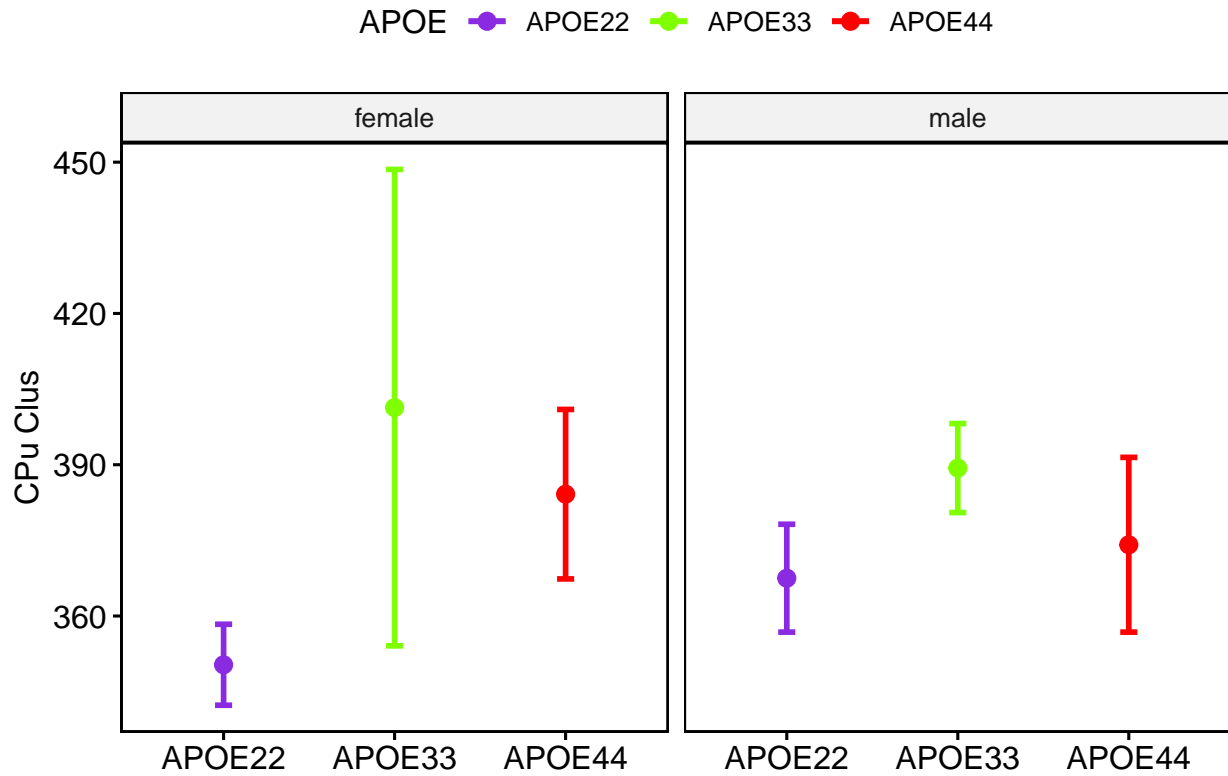
```
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?
```



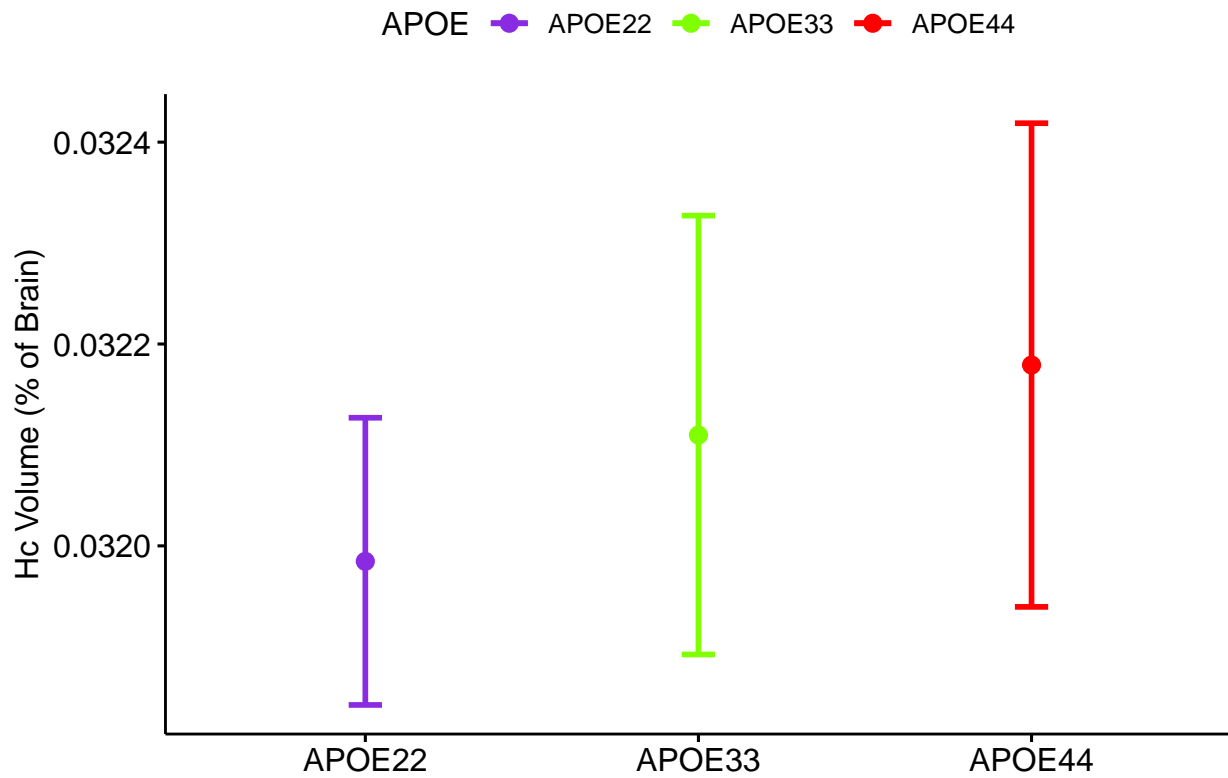
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



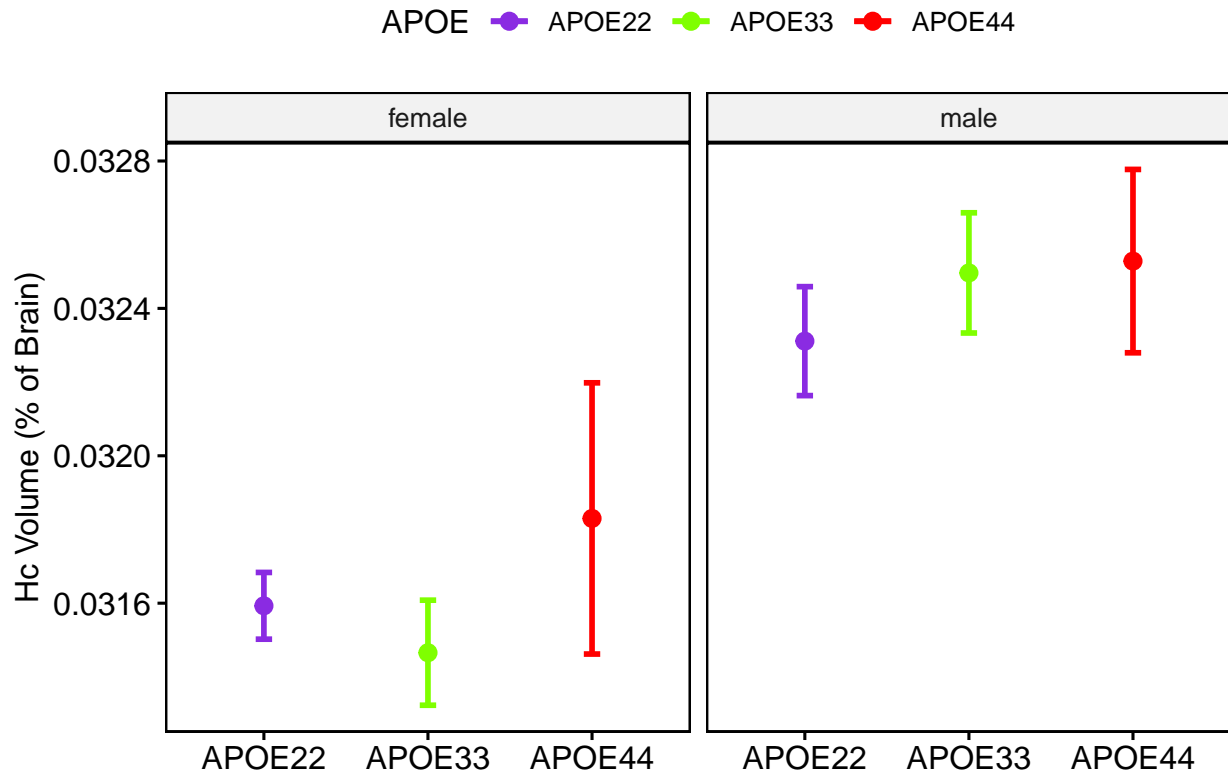
```
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?
```



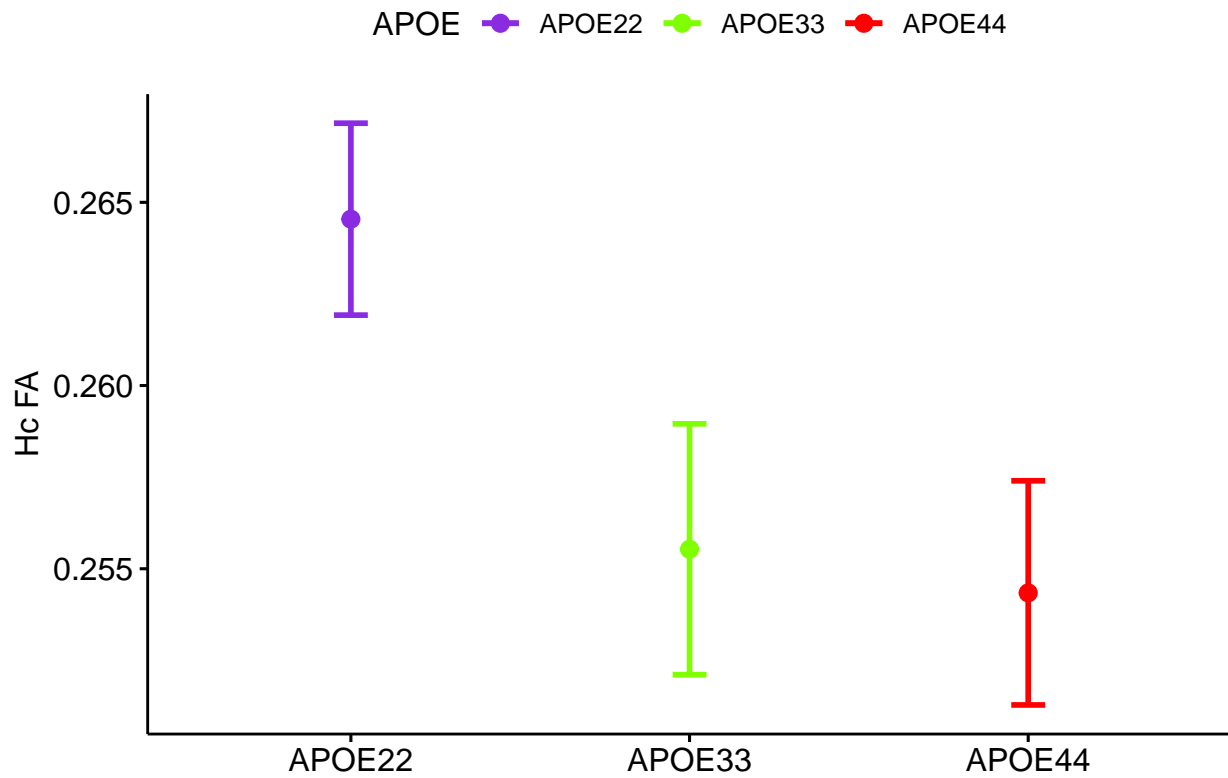
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## [1] "Hc Volume"
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



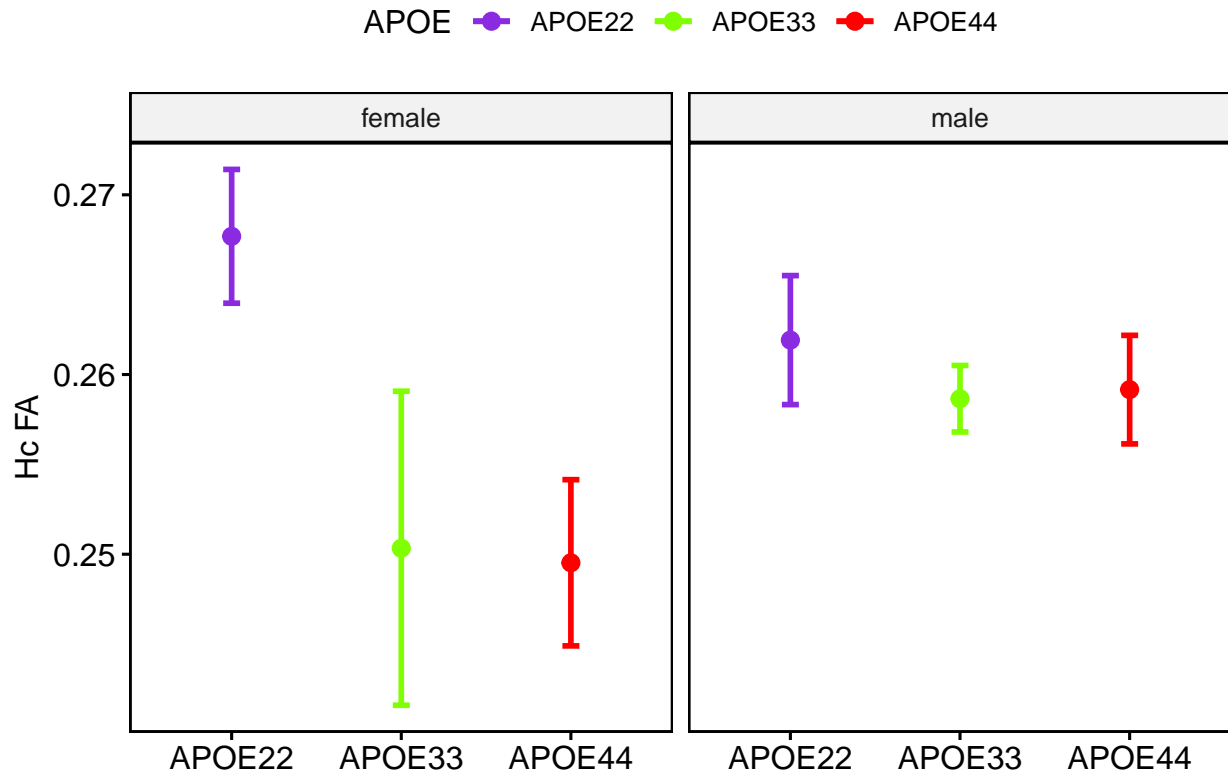
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```

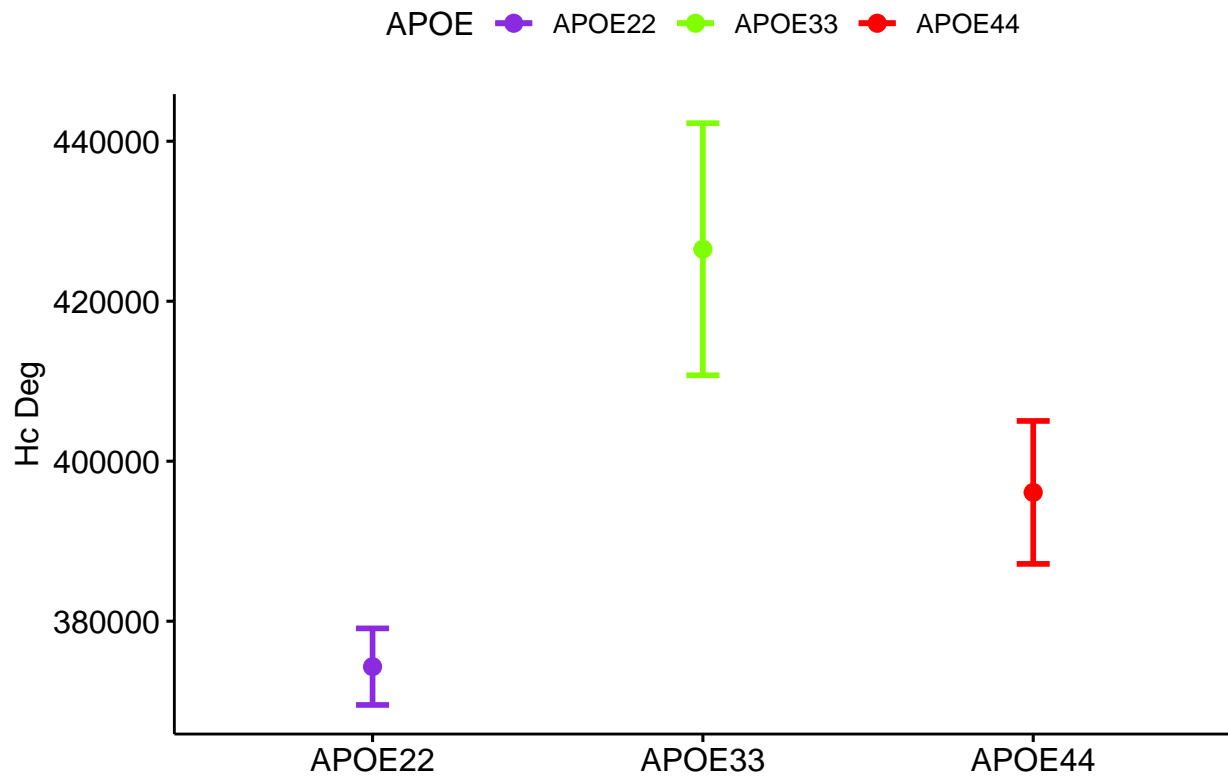
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



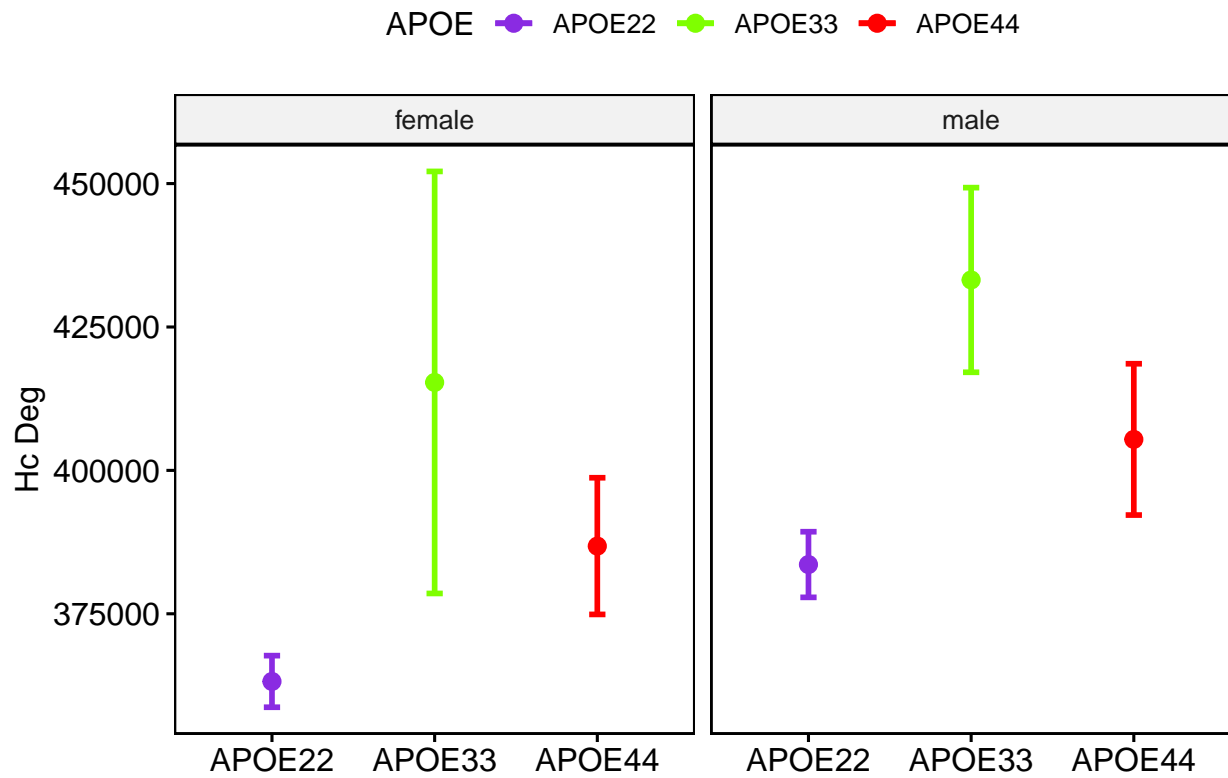
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



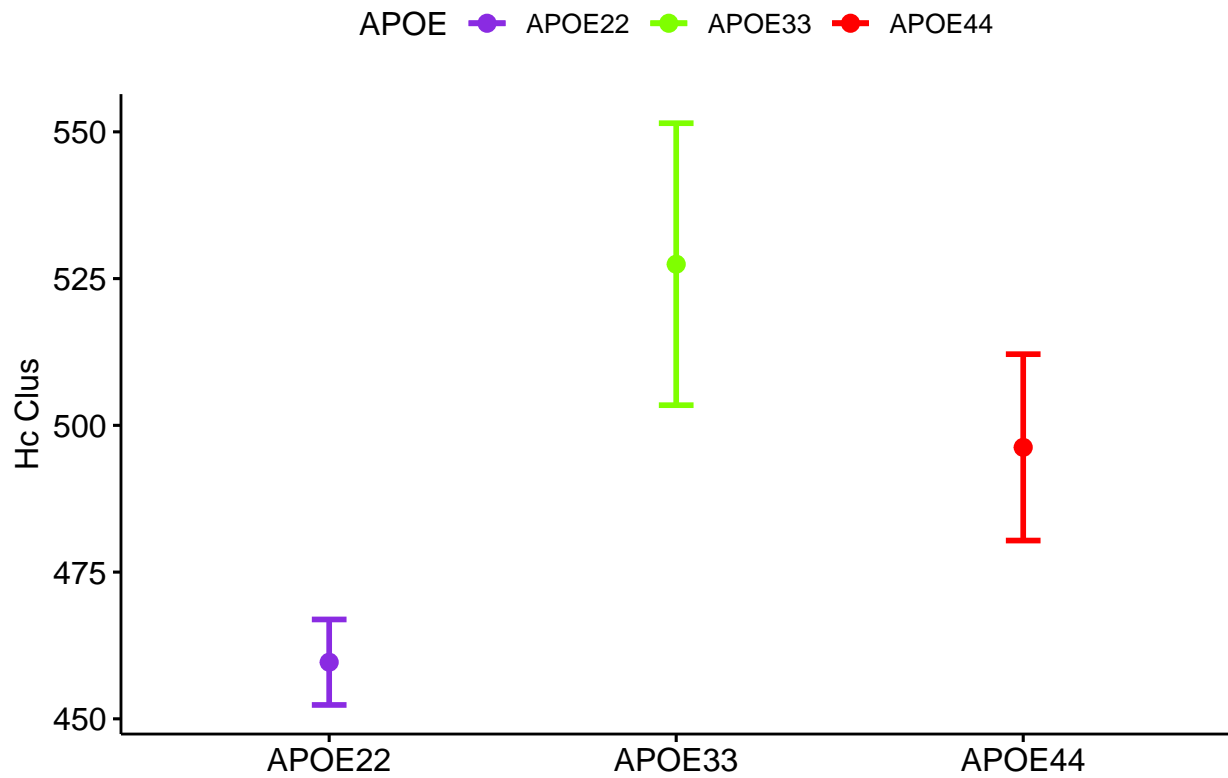
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



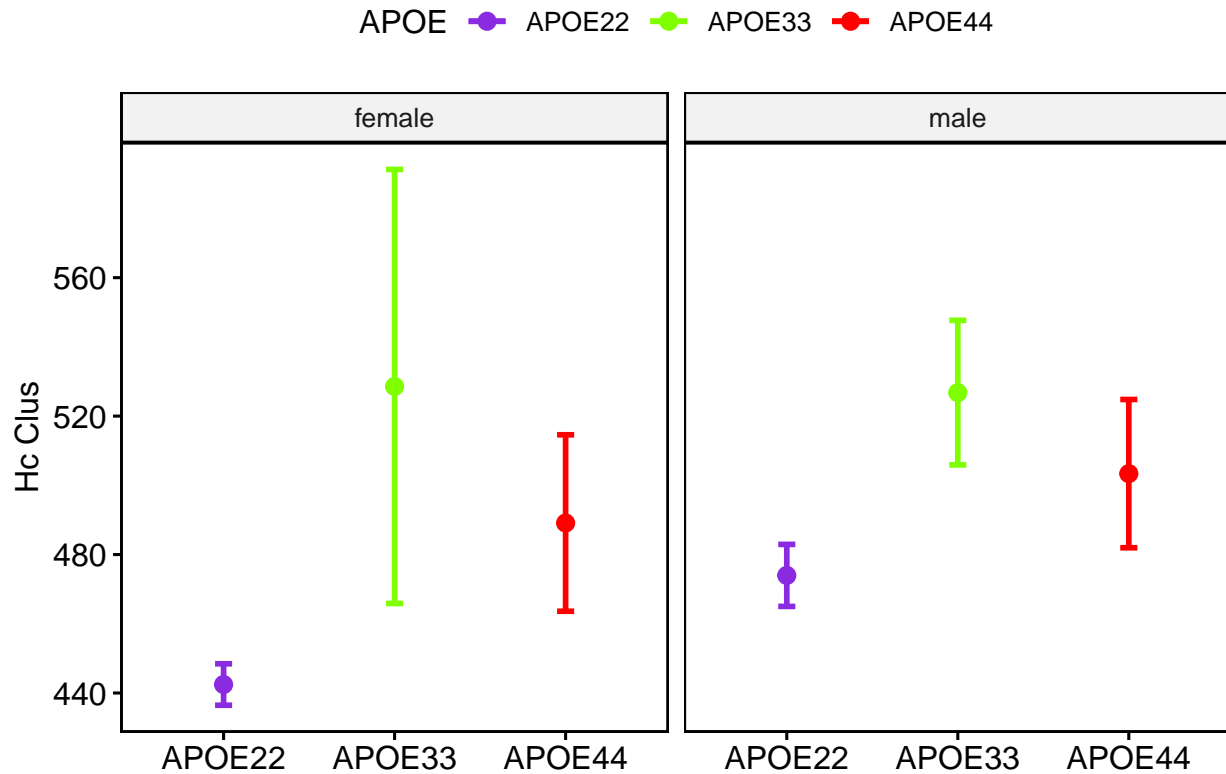
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```

```
##
```

```
## Call:
```

```
## lm(formula = Hc ~ Genotype * Sex, data = geno_combined_VOL)
```

```
##
```

```
## Residuals:
```

```
##      Min       1Q   Median       3Q      Max
## -1.413e-03 -2.449e-04  1.222e-05  2.522e-04  7.467e-04
```

```
##
```

```
## Coefficients:
```

```
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)      3.159e-02  2.171e-04 145.497  <2e-16 ***
```

```
## GenotypeAPOE33    -1.273e-04  3.546e-04  -0.359   0.7228
```

```
## GenotypeAPOE44     2.371e-04  3.071e-04   0.772   0.4478
```

```
## Sexmale           7.183e-04  2.940e-04   2.443   0.0227 *
```

```
## GenotypeAPOE33:Sexmale  3.125e-04  4.606e-04   0.678   0.5043
```

```
## GenotypeAPOE44:Sexmale -1.995e-05  4.251e-04  -0.047   0.9630
```

```
## ---
```

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

```
##
```

```
## Residual standard error: 0.0004855 on 23 degrees of freedom
```

```
## Multiple R-squared:  0.4708, Adjusted R-squared:  0.3557
```

```
## F-statistic: 4.092 on 5 and 23 DF,  p-value: 0.00837
```

```
##
```

```
## Call:
```

```

## lm(formula = Hc ~ Genotype, data = combo_f_VOL)
##
## Residuals:
##      Min        1Q      Median        3Q       Max
## -1.413e-03 -1.529e-04  1.321e-05  2.401e-04  5.422e-04
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.0315929  0.0002448 129.072  <2e-16 ***
## GenotypeAPOE33 -0.0001273  0.0003997  -0.319    0.757
## GenotypeAPOE44  0.0002371  0.0003462   0.685    0.509
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0005473 on 10 degrees of freedom
## Multiple R-squared:  0.08551, Adjusted R-squared:  -0.09739
## F-statistic: 0.4675 on 2 and 10 DF, p-value: 0.6396
##
## Call:
## lm(formula = Hc ~ Genotype, data = combo_m_VOL)
##
## Residuals:
##      Min        1Q      Median        3Q       Max
## -0.0006101 -0.0003333  0.0000013  0.0002651  0.0007467
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.0323112  0.0001764 183.195  <2e-16 ***
## GenotypeAPOE33 0.0001852  0.0002616   0.708    0.492
## GenotypeAPOE44 0.0002172  0.0002616   0.830    0.421
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.000432 on 13 degrees of freedom
## Multiple R-squared:  0.0598, Adjusted R-squared:  -0.08484
## F-statistic: 0.4134 on 2 and 13 DF, p-value: 0.6698
## Analysis of Variance Table
##
## Response: Hc
##           Df      Sum Sq    Mean Sq F value    Pr(>F)
## Genotype    2 2.0430e-07 1.0210e-07  0.4333 0.6535491
## Sex          1 4.4749e-06 4.4749e-06 18.9821 0.0002313 ***
## Genotype:Sex  2 1.4360e-07 7.1800e-08  0.3047 0.7402957
## Residuals   23 5.4221e-06 2.3570e-07
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Analysis of Variance Table
##
## Response: Hc
##           Df      Sum Sq    Mean Sq F value    Pr(>F)
## Genotype    2 2.8010e-07 1.4005e-07  0.4675 0.6396
## Residuals   10 2.9956e-06 2.9956e-07

```



```

## Analysis of Variance Table
##
## Response: Hc
##           Df      Sum Sq   Mean Sq F value Pr(>F)
## Genotype    2 1.5434e-07 7.7170e-08  0.4134 0.6698
## Residuals  13 2.4265e-06 1.8665e-07
## [1] "CPu Volume"
##
## Call:
## lm(formula = CPu ~ Genotype * Sex, data = geno_combined_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -7.026e-04 -3.106e-04 -6.856e-05  1.250e-04  1.486e-03
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.476e-02  2.420e-04 102.283 < 2e-16 ***
## GenotypeAPOE33 -7.692e-04  3.952e-04  -1.946  0.06395 .
## GenotypeAPOE44  9.720e-04  3.423e-04   2.840  0.00928 **
## Sexmale        -4.568e-05  3.277e-04  -0.139  0.89036
## GenotypeAPOE33:Sexmale 2.317e-04  5.134e-04   0.451  0.65601
## GenotypeAPOE44:Sexmale -5.205e-04  4.739e-04  -1.098  0.28336
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0005412 on 23 degrees of freedom
## Multiple R-squared:  0.5711, Adjusted R-squared:  0.4778
## F-statistic: 6.124 on 5 and 23 DF,  p-value: 0.0009559
##
## Call:
## lm(formula = CPu ~ Genotype, data = combo_f_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -7.026e-04 -1.906e-04 -6.856e-05  1.107e-04  8.300e-04
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.0247562  0.0001883 131.487 < 2e-16 ***
## GenotypeAPOE33 -0.0007692  0.0003075  -2.502  0.03135 *
## GenotypeAPOE44  0.0009720  0.0002663   3.651  0.00446 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.000421 on 10 degrees of freedom
## Multiple R-squared:  0.7719, Adjusted R-squared:  0.7263
## F-statistic: 16.92 on 2 and 10 DF,  p-value: 0.0006174
##
## Call:
## lm(formula = CPu ~ Genotype, data = combo_m_VOL)
##

```

```

## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.0006900 -0.0004200 -0.0001197  0.0003258  0.0014856
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.0247106  0.0002523  97.948  <2e-16 ***
## GenotypeAPOE33 -0.0005375  0.0003742  -1.436    0.175
## GenotypeAPOE44  0.0004515  0.0003742   1.207    0.249
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.000618 on 13 degrees of freedom
## Multiple R-squared:  0.3306, Adjusted R-squared:  0.2277
## F-statistic: 3.211 on 2 and 13 DF,  p-value: 0.07358

## Analysis of Variance Table
##
## Response: CPu
##      Df      Sum Sq    Mean Sq F value    Pr(>F)
## Genotype    2 8.0970e-06 4.0485e-06 13.8218 0.0001142 ***
## Sex          1 1.9980e-07 1.9980e-07  0.6822 0.4173028
## Genotype:Sex  2 6.7230e-07 3.3610e-07  1.1476 0.3349205
## Residuals    23 6.7368e-06 2.9290e-07
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: CPu
##      Df      Sum Sq    Mean Sq F value    Pr(>F)
## Genotype    2 5.9982e-06 2.9991e-06 16.921 0.0006174 ***
## Residuals   10 1.7724e-06 1.7724e-07
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: CPu
##      Df      Sum Sq    Mean Sq F value    Pr(>F)
## Genotype    2 2.4523e-06 1.2261e-06  3.2108 0.07358 .
## Residuals   13 4.9644e-06 3.8188e-07
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Brain Volume"

##
## Call:
## lm(formula = Brain ~ Genotype * Sex, data = geno_combined_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -23.1520  -5.4838  -0.0532   3.4798  20.8142
##
## Coefficients:

```

```

##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      504.359      4.403 114.561  <2e-16 ***
## GenotypeAPOE33      18.090      7.189   2.516   0.0193 *
## GenotypeAPOE44       7.488      6.226   1.203   0.2413
## Sexmale           -2.641      5.961  -0.443   0.6619
## GenotypeAPOE33:Sexmale -1.806      9.339  -0.193   0.8483
## GenotypeAPOE44:Sexmale -10.056      8.620  -1.167   0.2553
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.844 on 23 degrees of freedom
## Multiple R-squared:  0.4588, Adjusted R-squared:  0.3412
## F-statistic: 3.9 on 5 and 23 DF,  p-value: 0.01047
##
## Call:
## lm(formula = Brain ~ Genotype, data = combo_f_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -9.2858 -5.4838 -0.4342  2.2928 15.4434
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      504.359      3.592 140.421  <2e-16 ***
## GenotypeAPOE33      18.090      5.865   3.084   0.0116 *
## GenotypeAPOE44       7.488      5.080   1.474   0.1712
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 8.031 on 10 degrees of freedom
## Multiple R-squared:  0.4881, Adjusted R-squared:  0.3858
## F-statistic: 4.768 on 2 and 10 DF,  p-value: 0.03514
##
## Call:
## lm(formula = Brain ~ Genotype, data = combo_m_VOL)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -23.1520  -2.5670   0.8804   4.0770  20.8142
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      501.718      4.506 111.337  <2e-16 ***
## GenotypeAPOE33      16.284      6.684   2.436   0.030 *
## GenotypeAPOE44     -2.568      6.684  -0.384   0.707
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.04 on 13 degrees of freedom
## Multiple R-squared:  0.402, Adjusted R-squared:  0.31
## F-statistic: 4.37 on 2 and 13 DF,  p-value: 0.03535
## Analysis of Variance Table

```

```
##
## Response: Brain
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype    2 1430.77   715.38   7.3818 0.003338 **
## Sex          1   314.81   314.81   3.2485 0.084612 .
## Genotype:Sex  2   144.35    72.18   0.7448 0.485956
## Residuals   23 2228.96    96.91
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

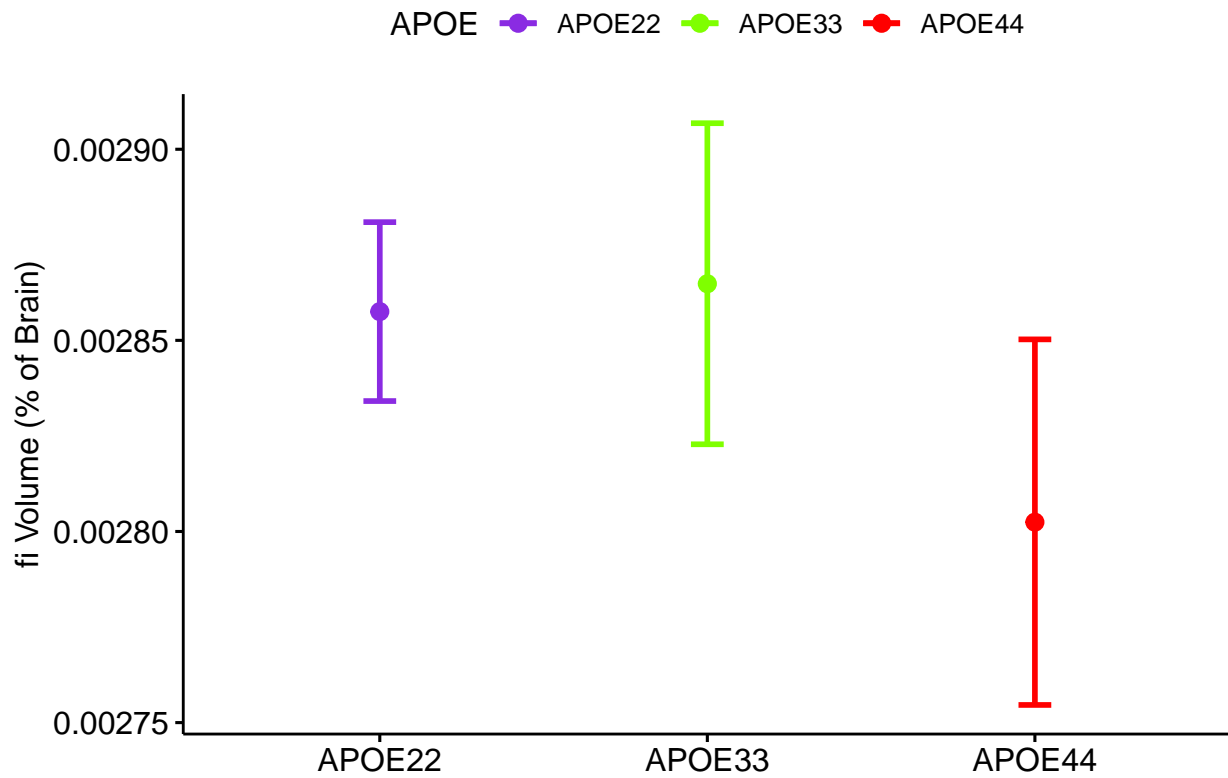
## Analysis of Variance Table
##
## Response: Brain
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype    2  615.15  307.574   4.7683 0.03514 *
## Residuals  10  645.04   64.504
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Brain
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype    2 1064.9   532.45    4.37 0.03535 *
## Residuals  13 1583.9   121.84
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

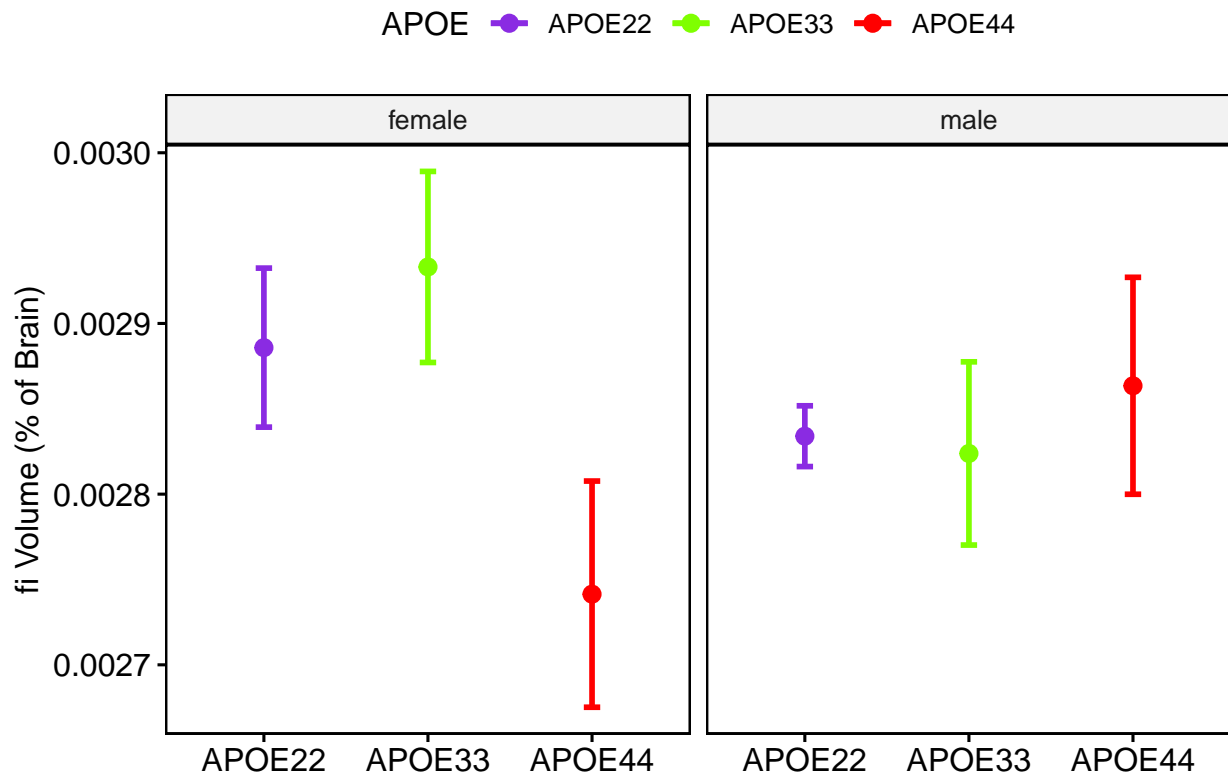
Plots for FA

Gray Matter of hippocampus and caudate putamen (Hc and CPu) ; white matter of fimbria (fi), fornix (fx) and internal capsule (ic)

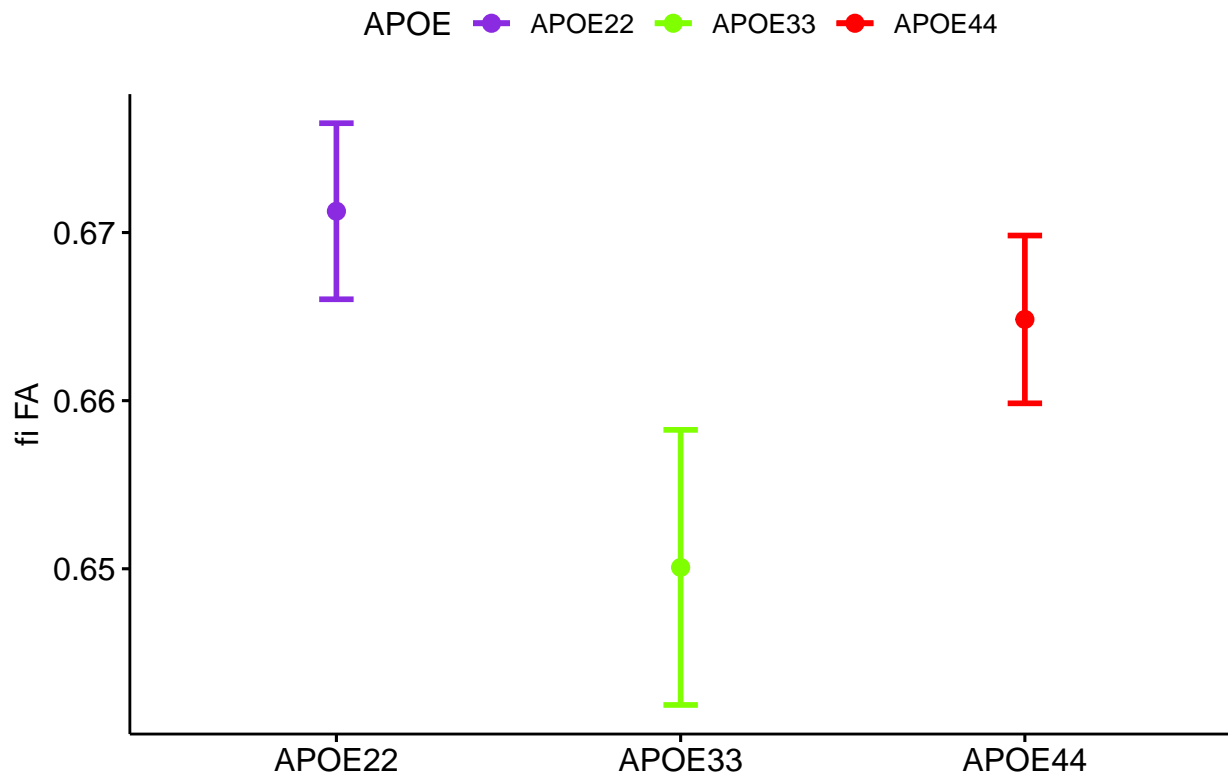
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



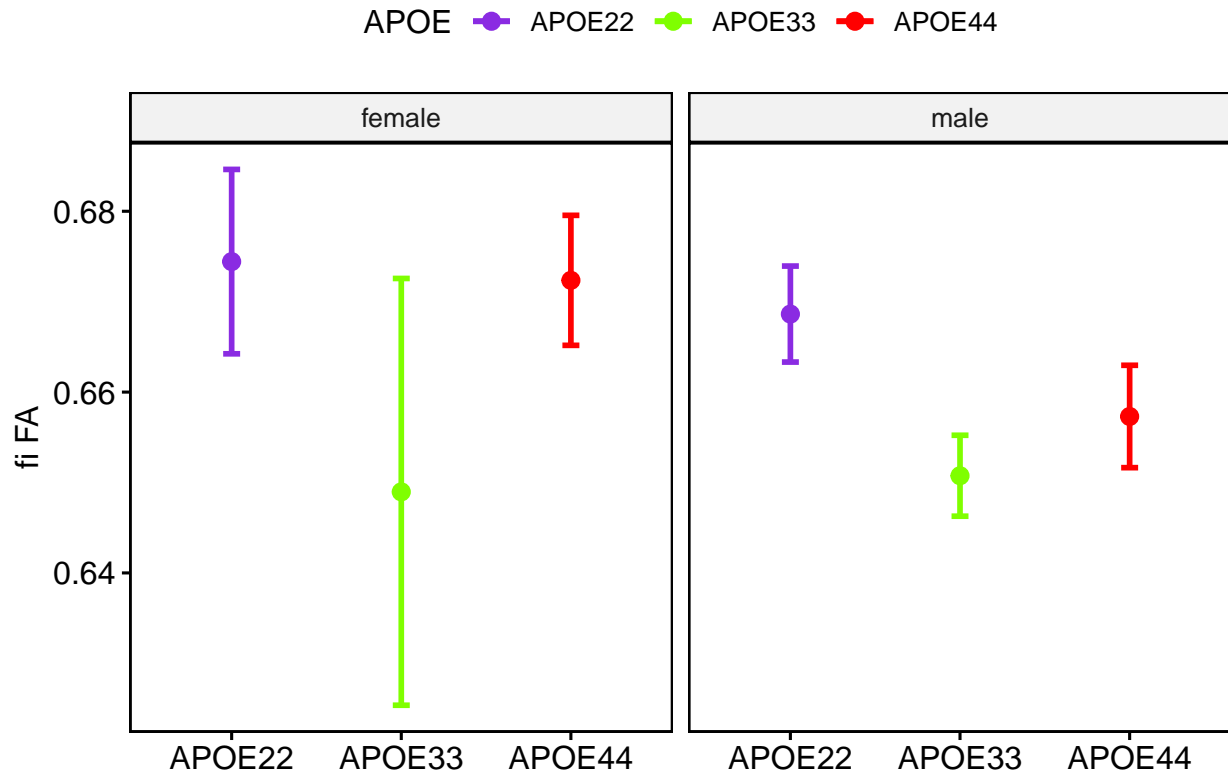
```
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?
```



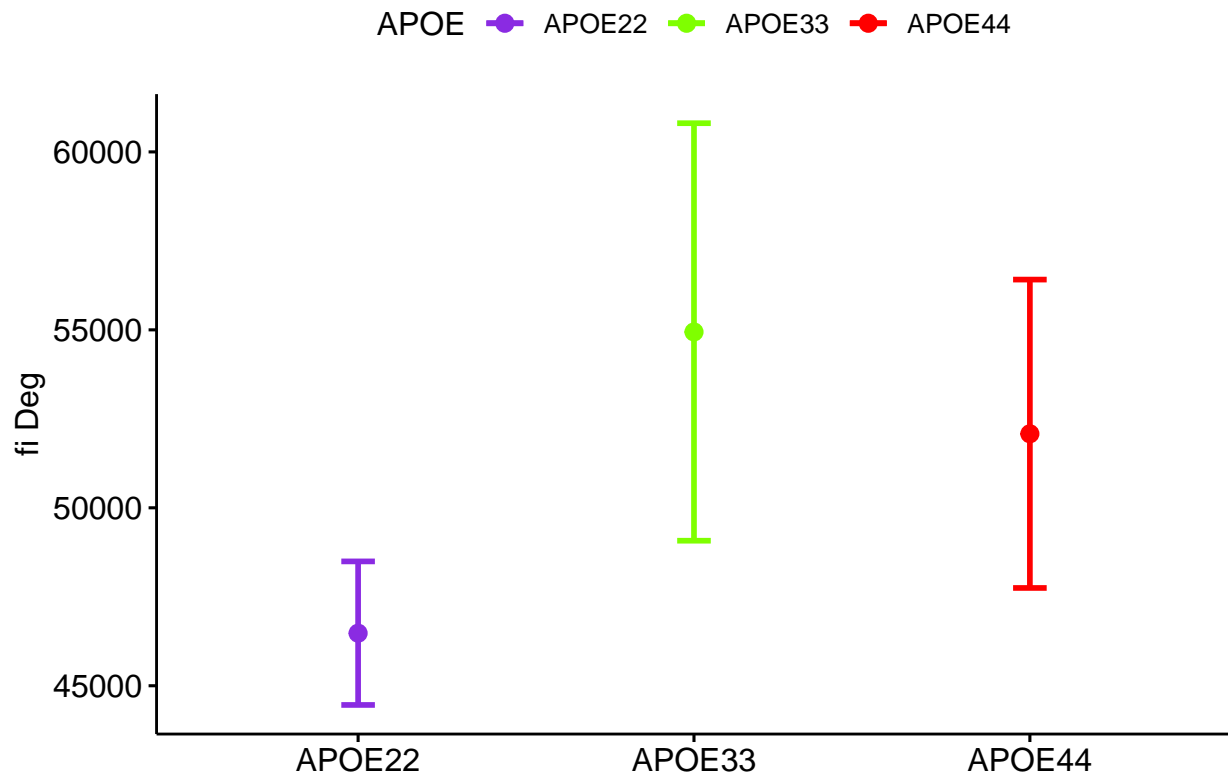
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



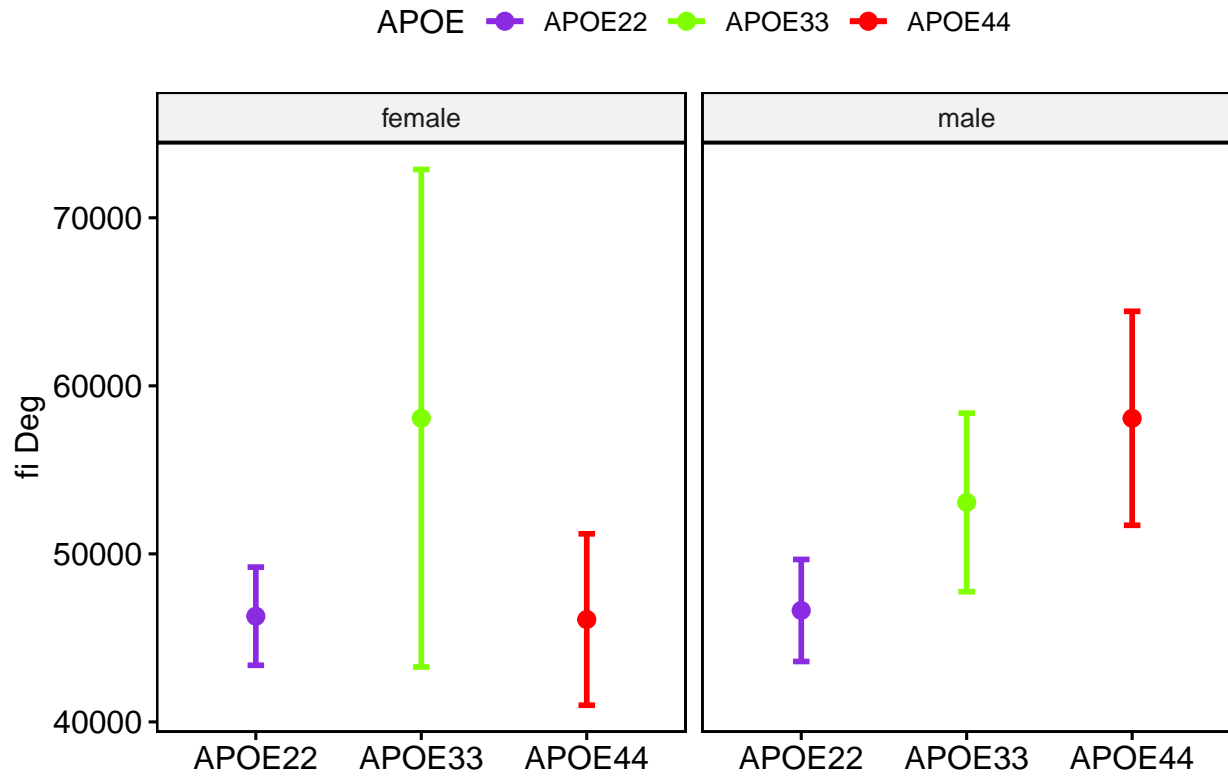
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



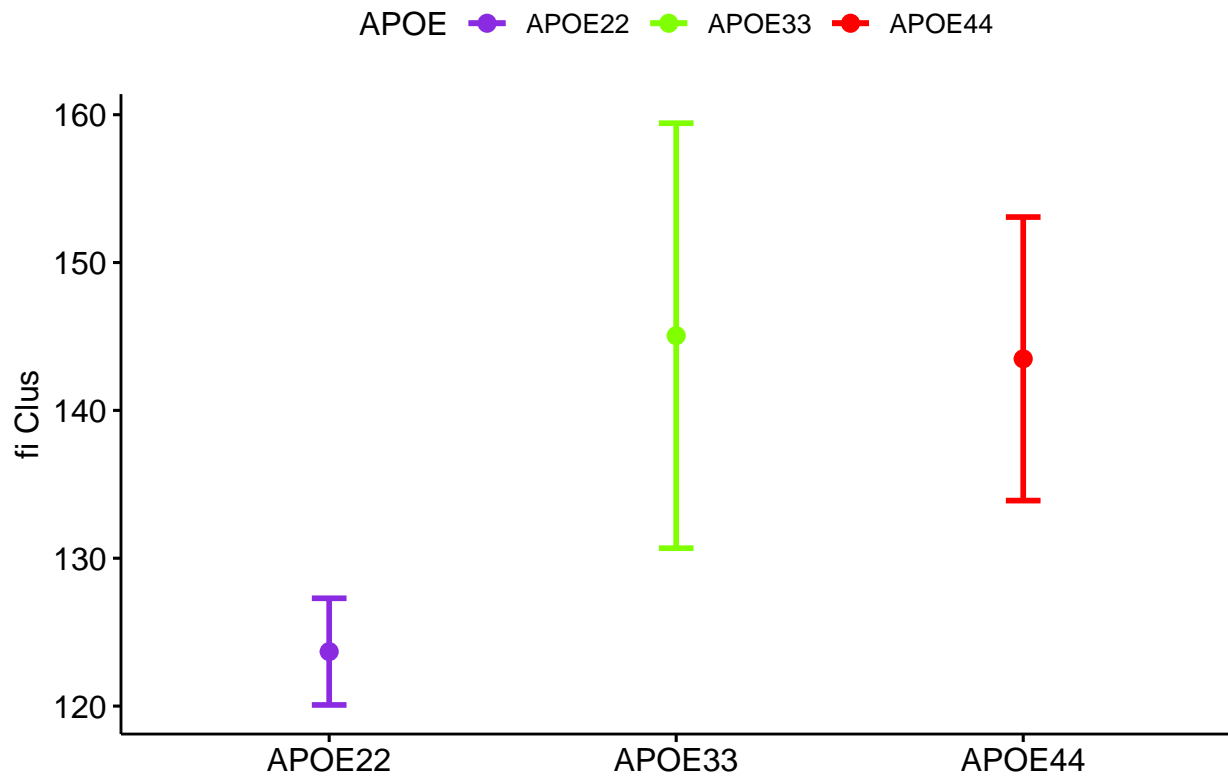
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```

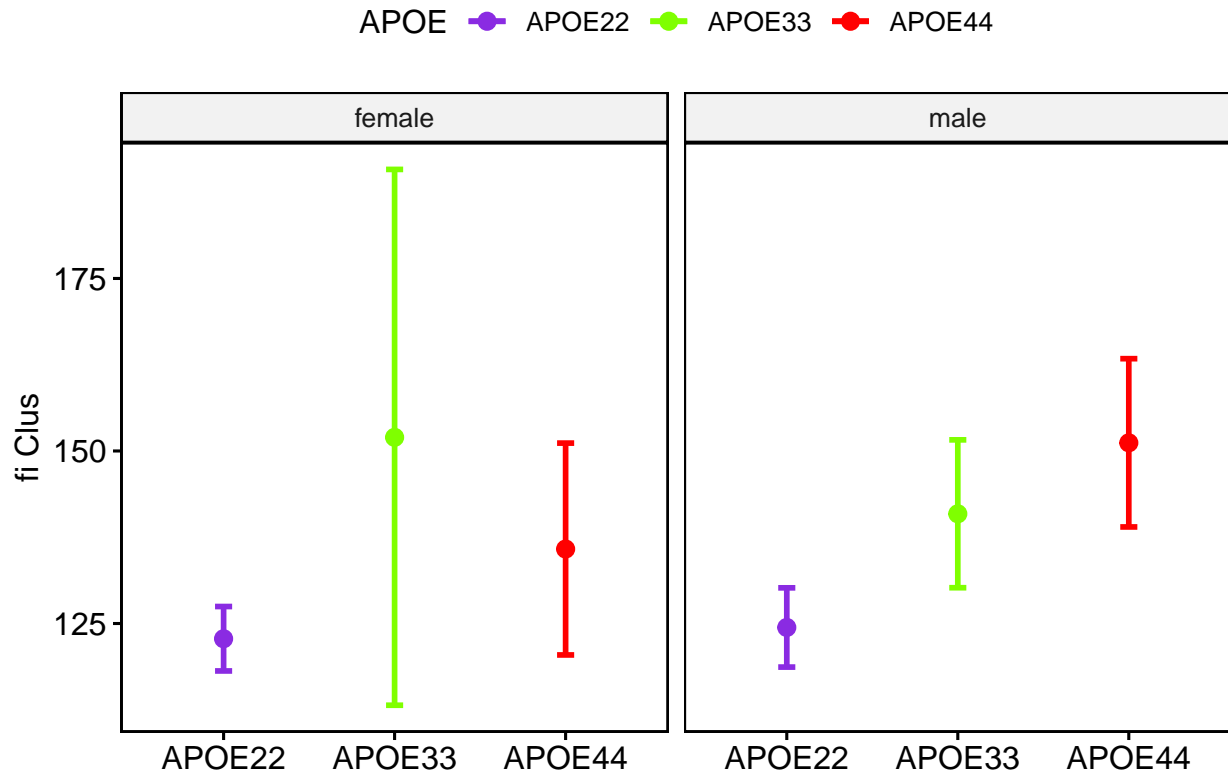
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



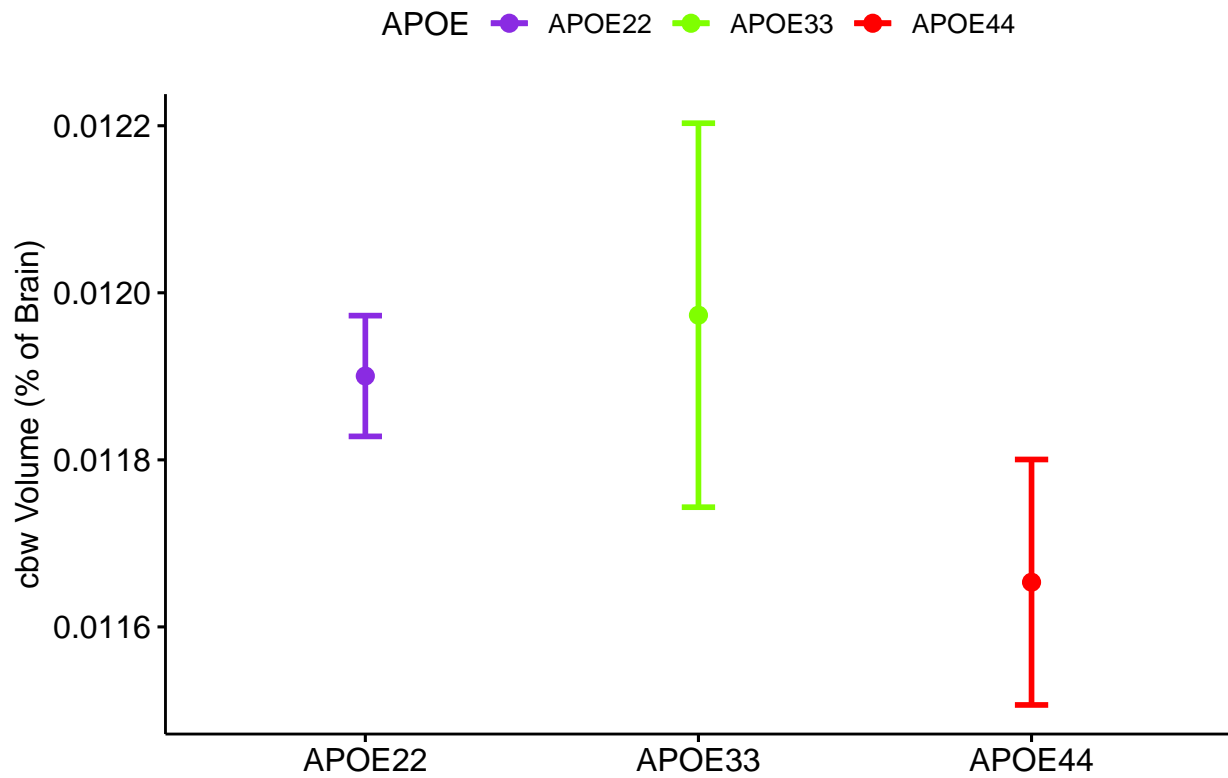
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



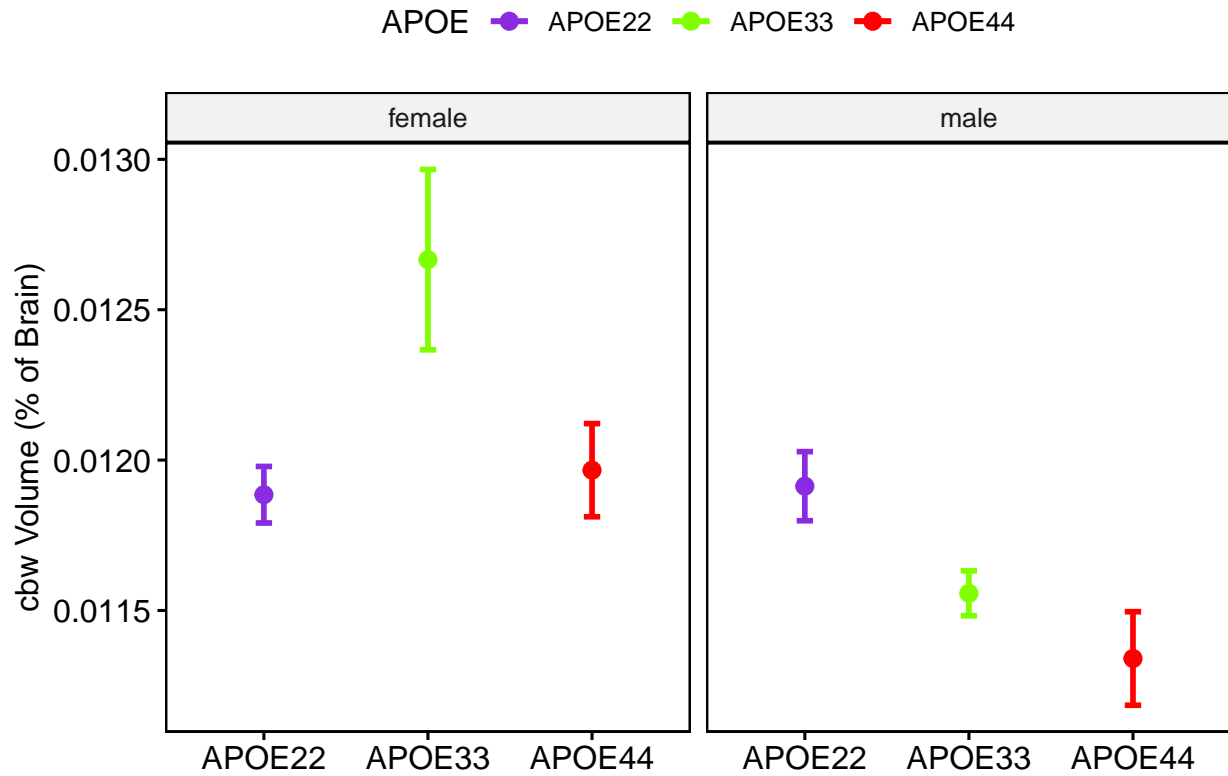
```
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?
```



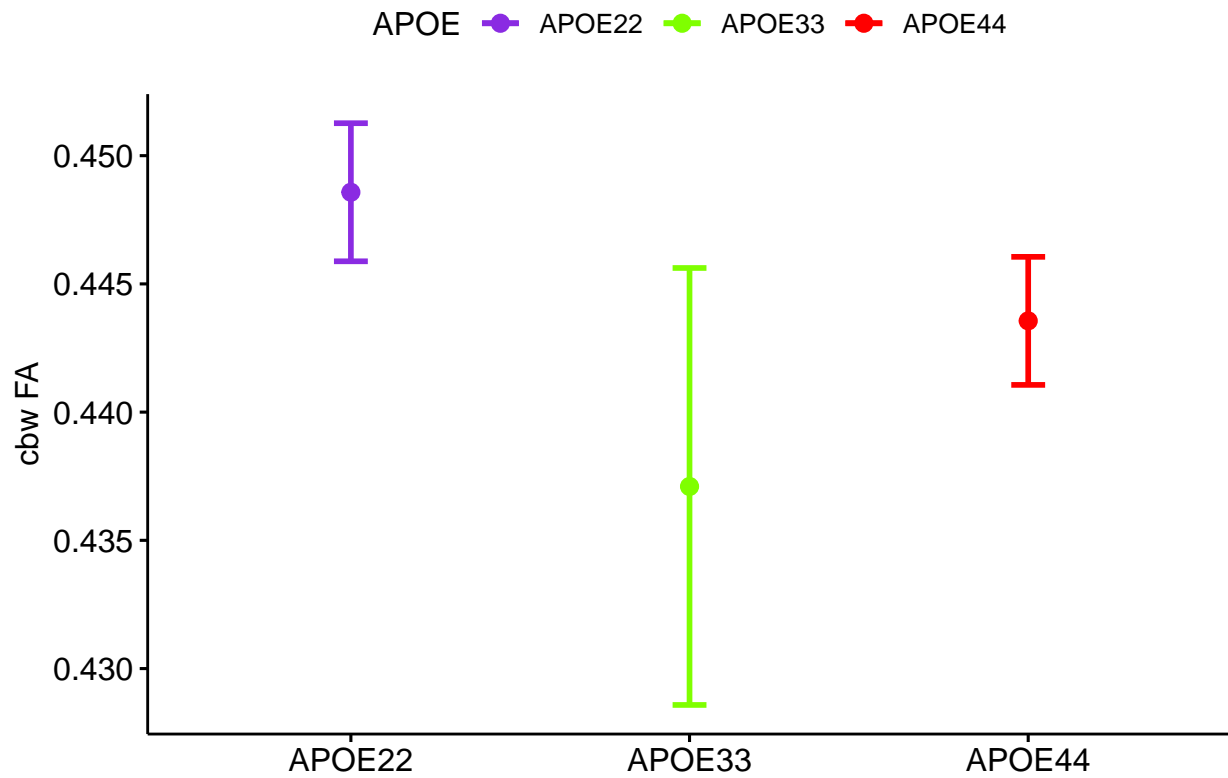
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



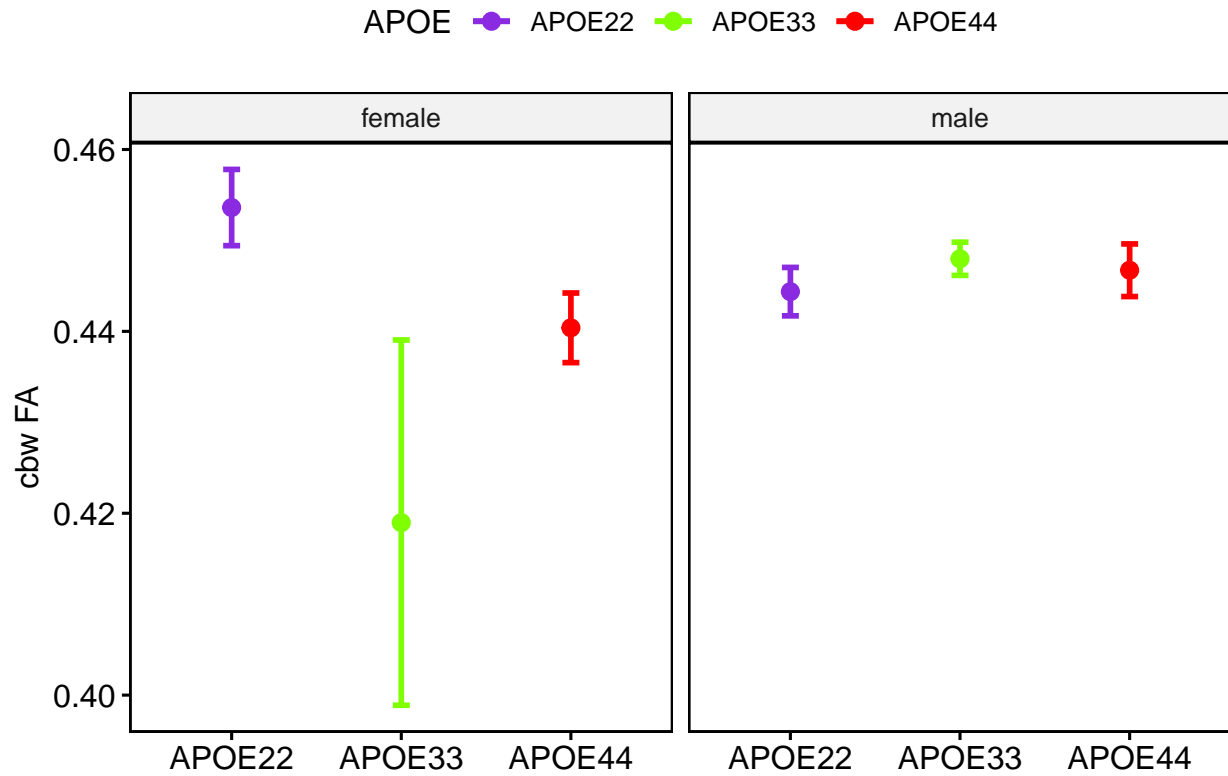
```
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?
```



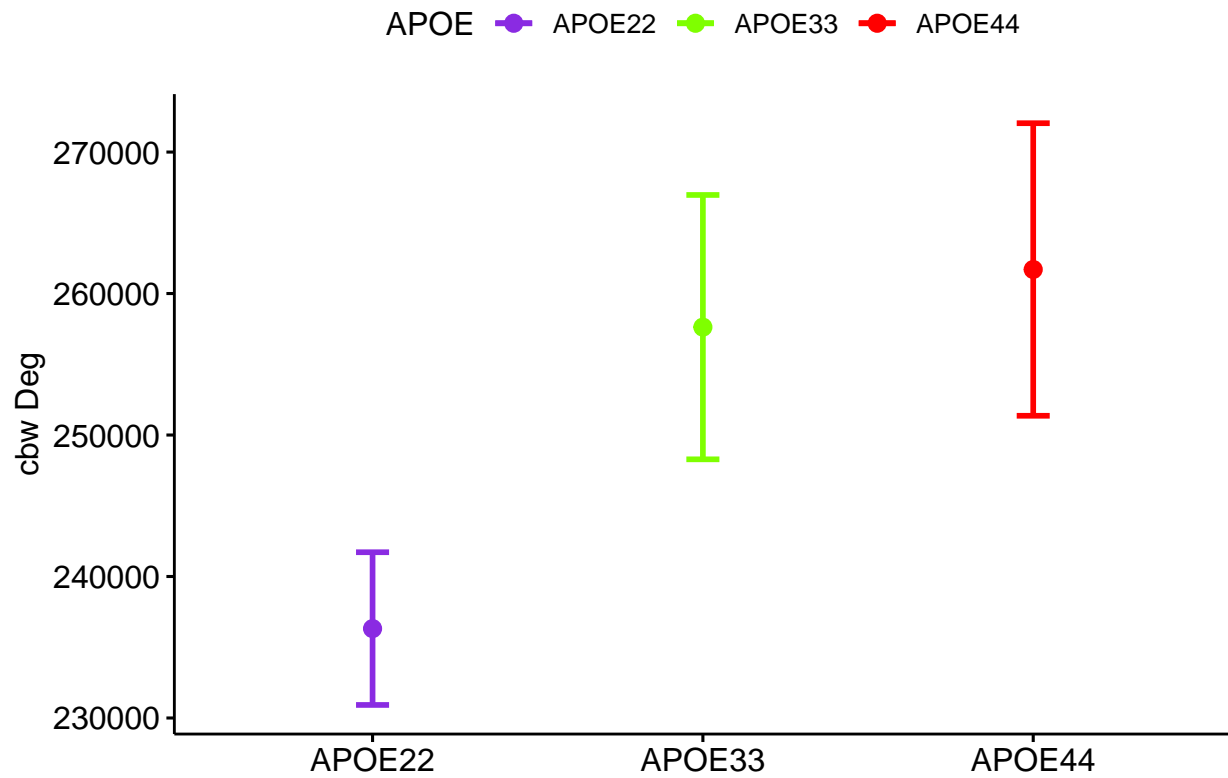
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



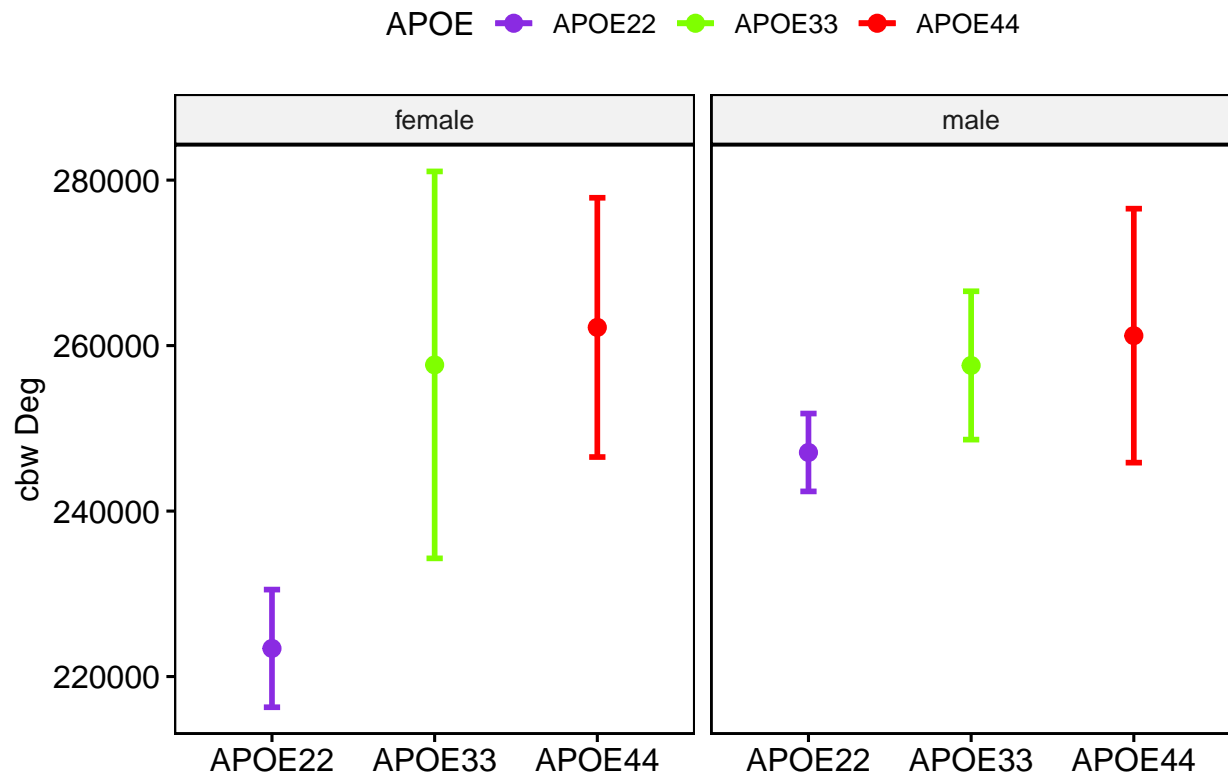
```
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?
```



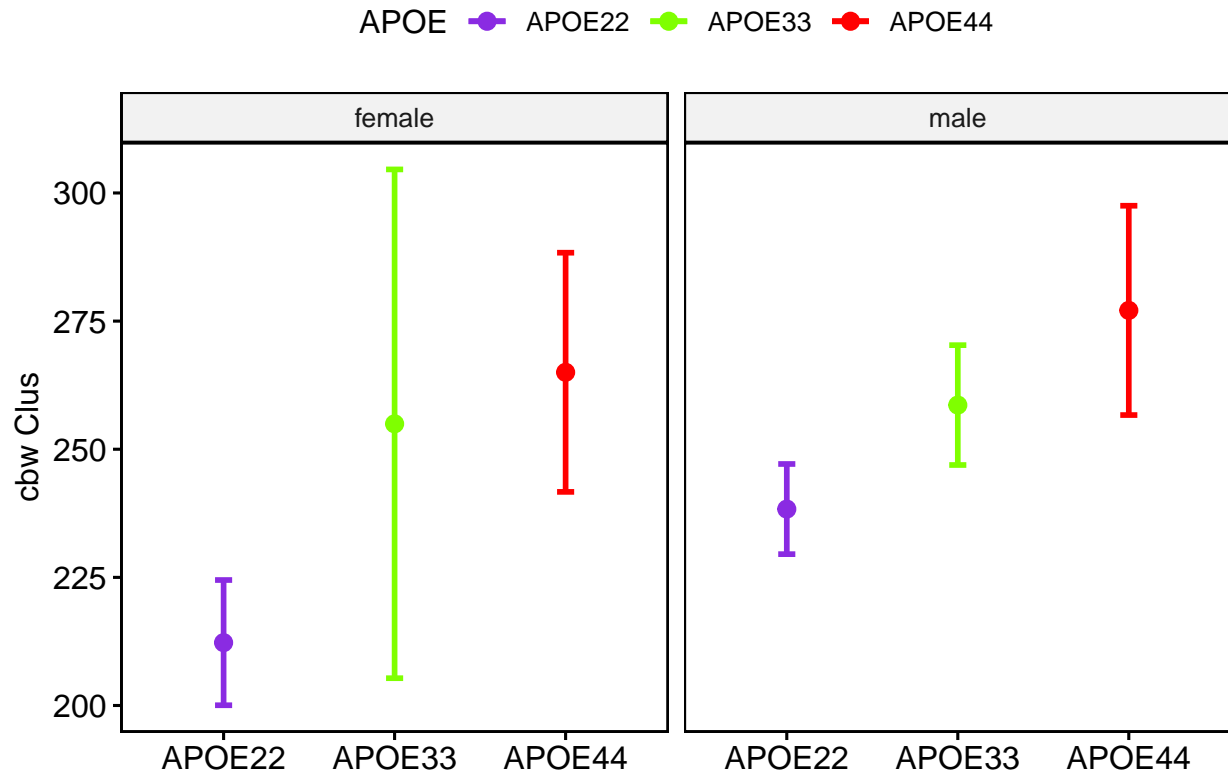
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```

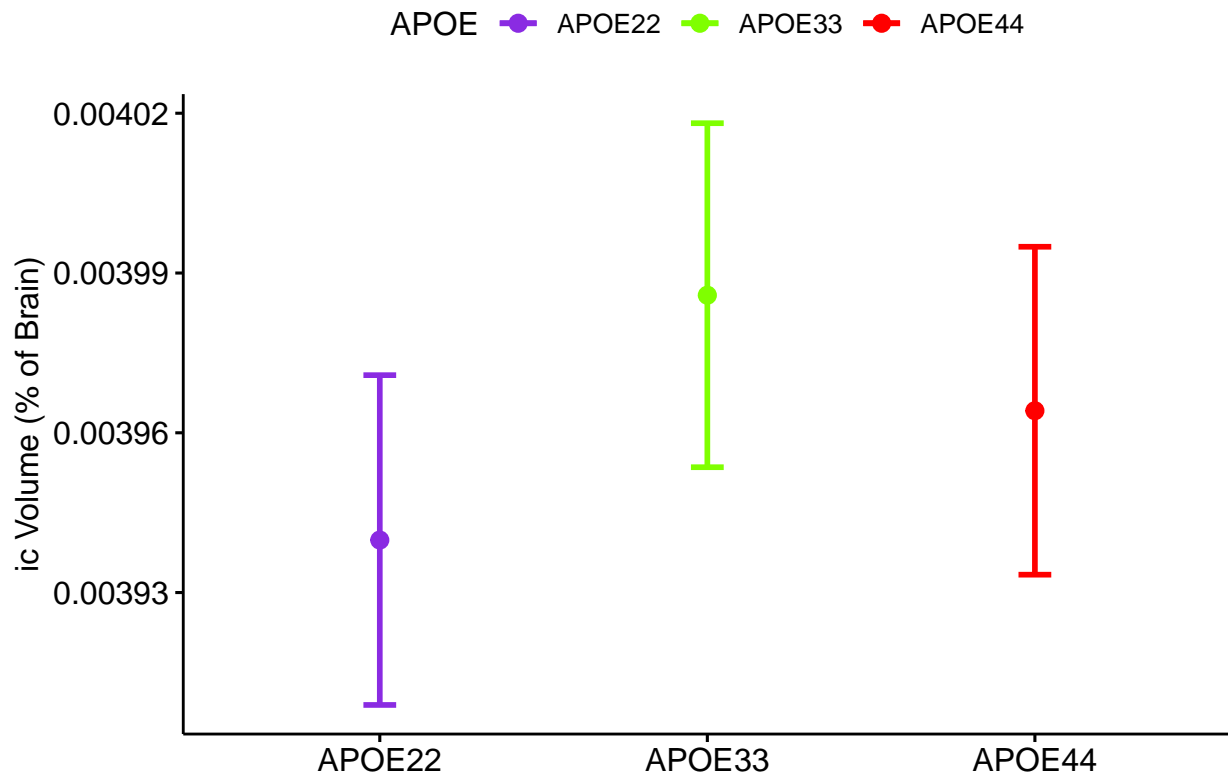
```
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?
```



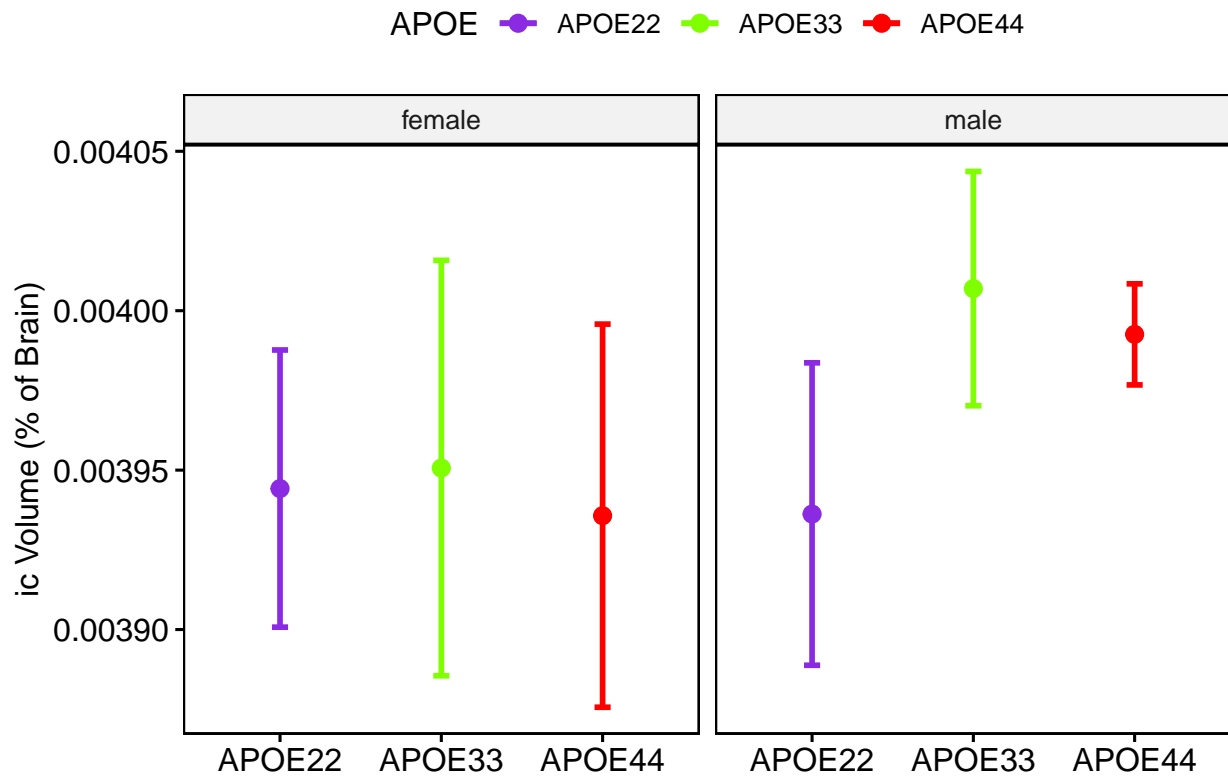
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



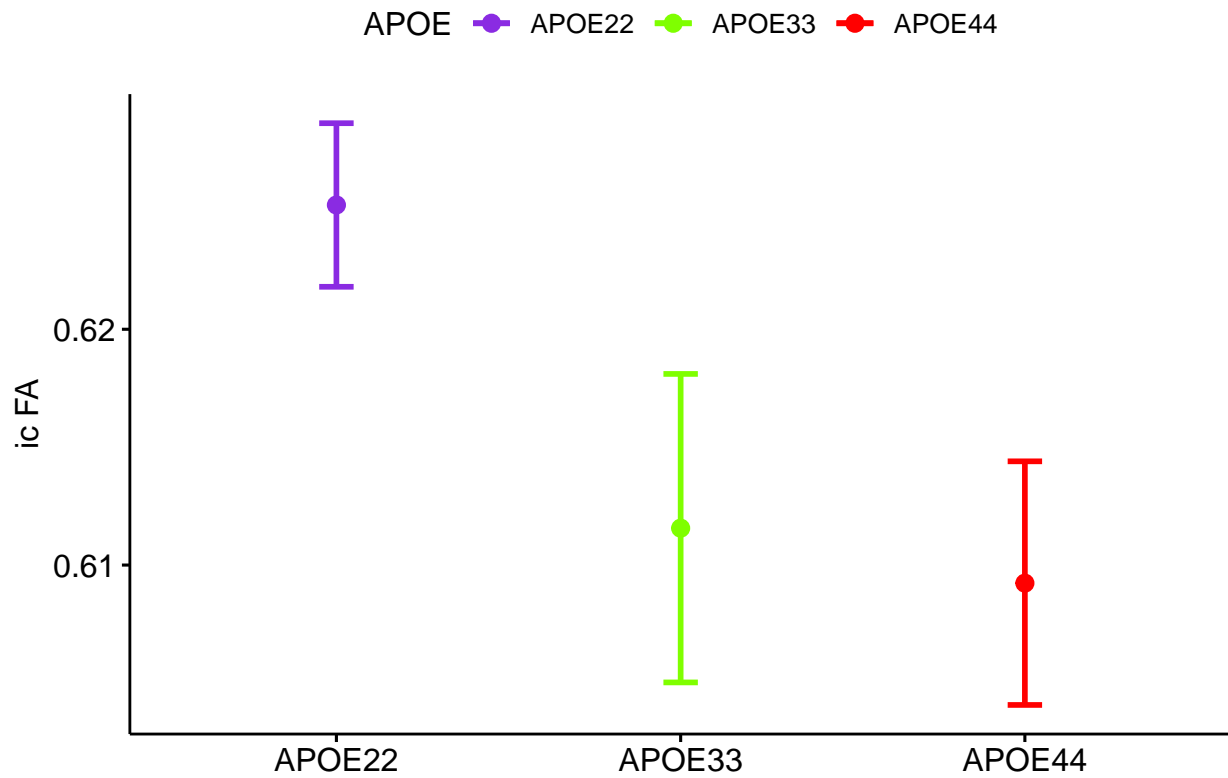
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



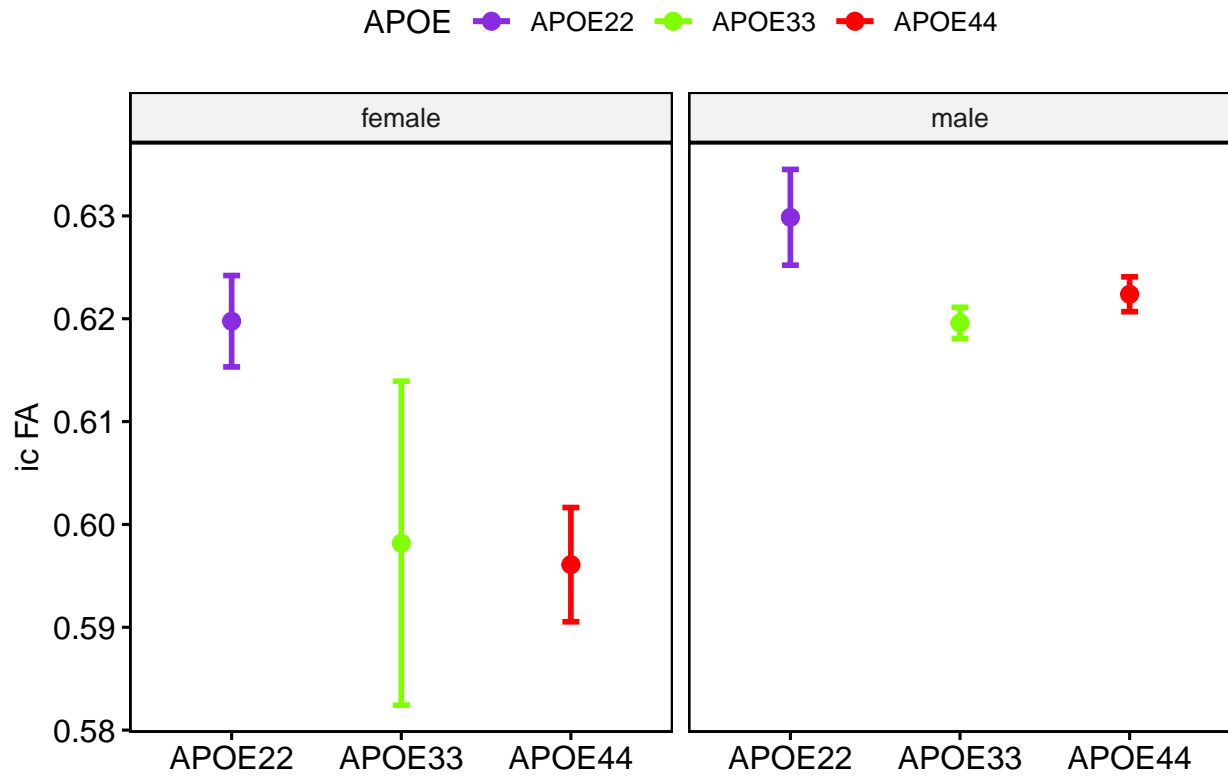
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



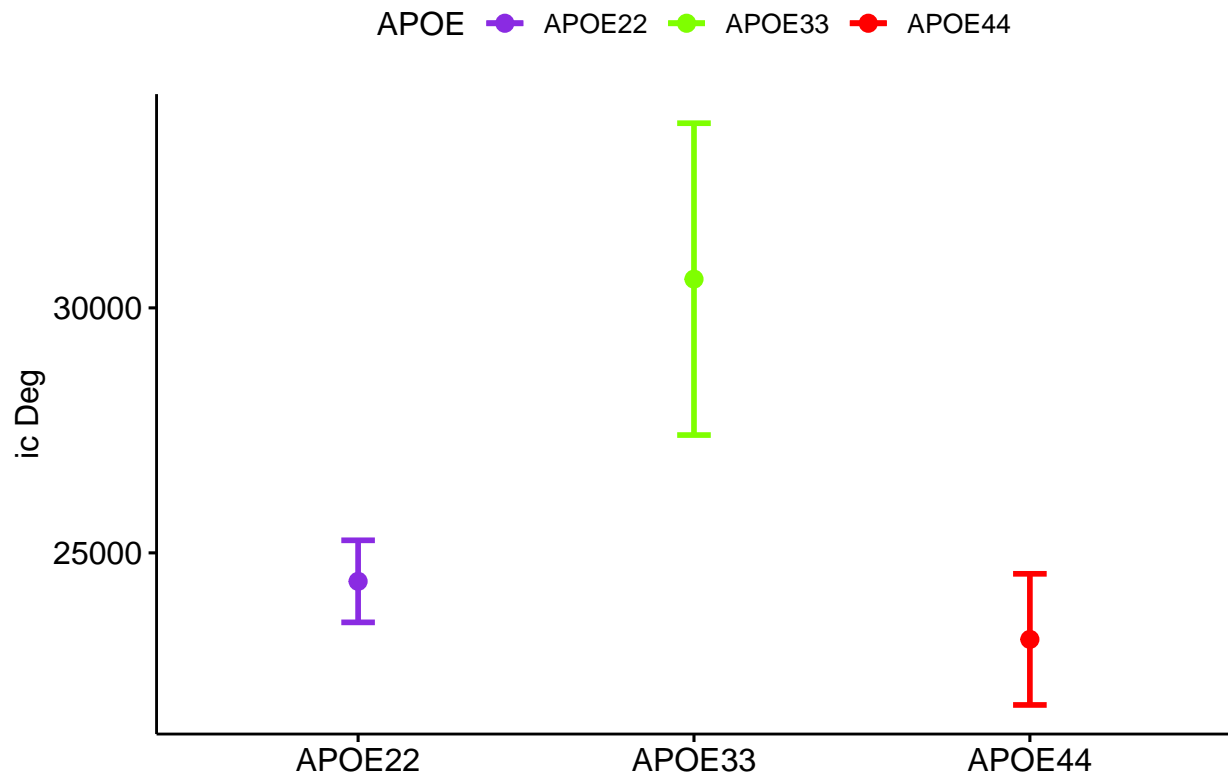
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



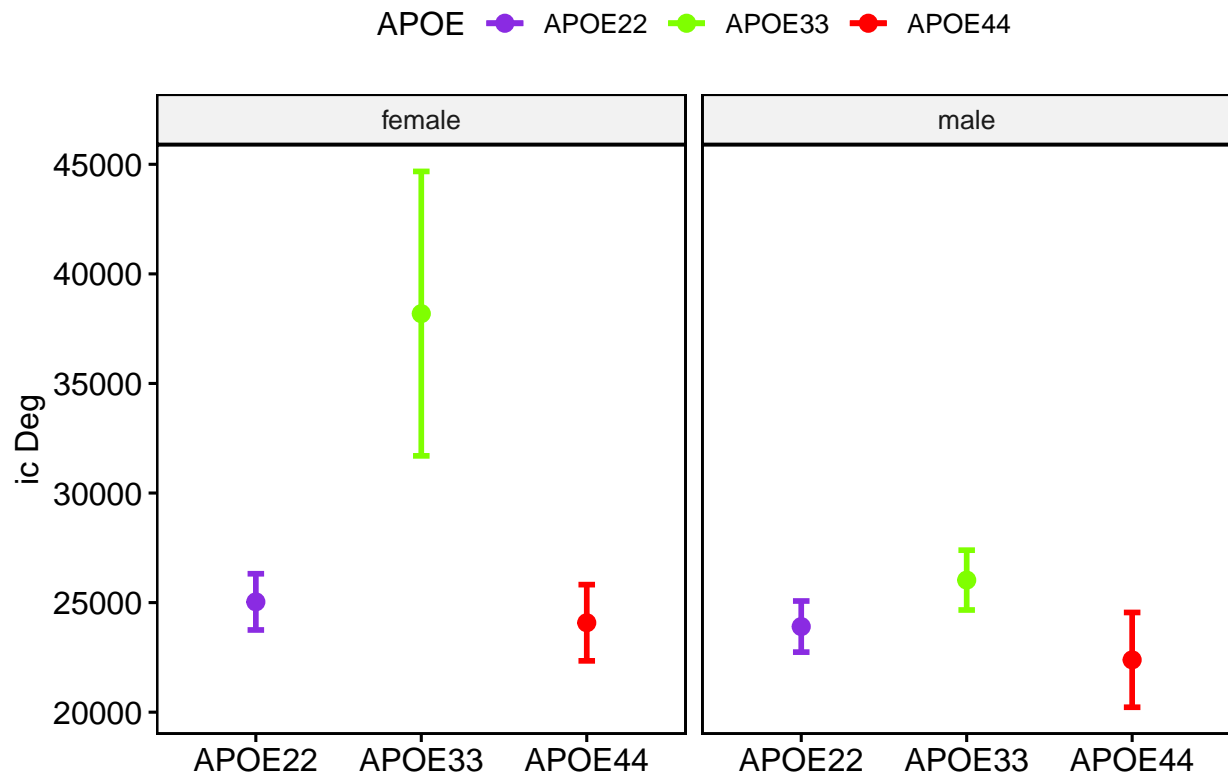
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



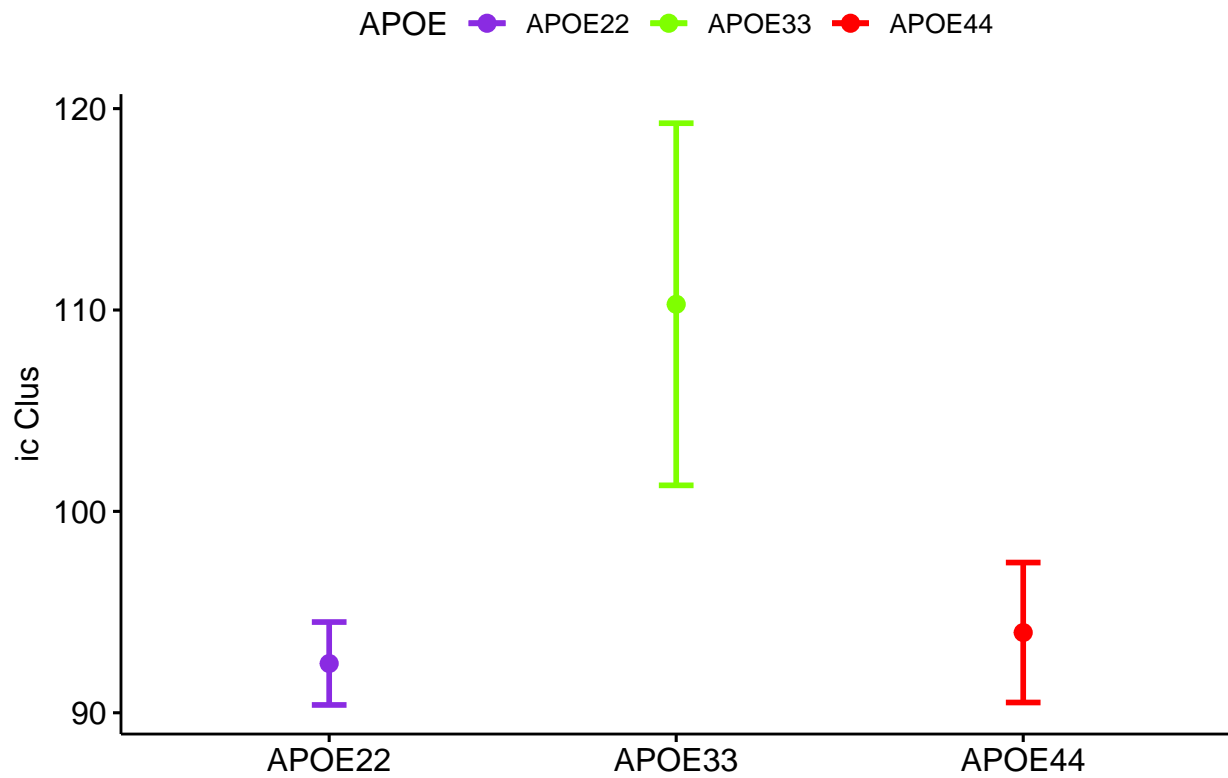
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



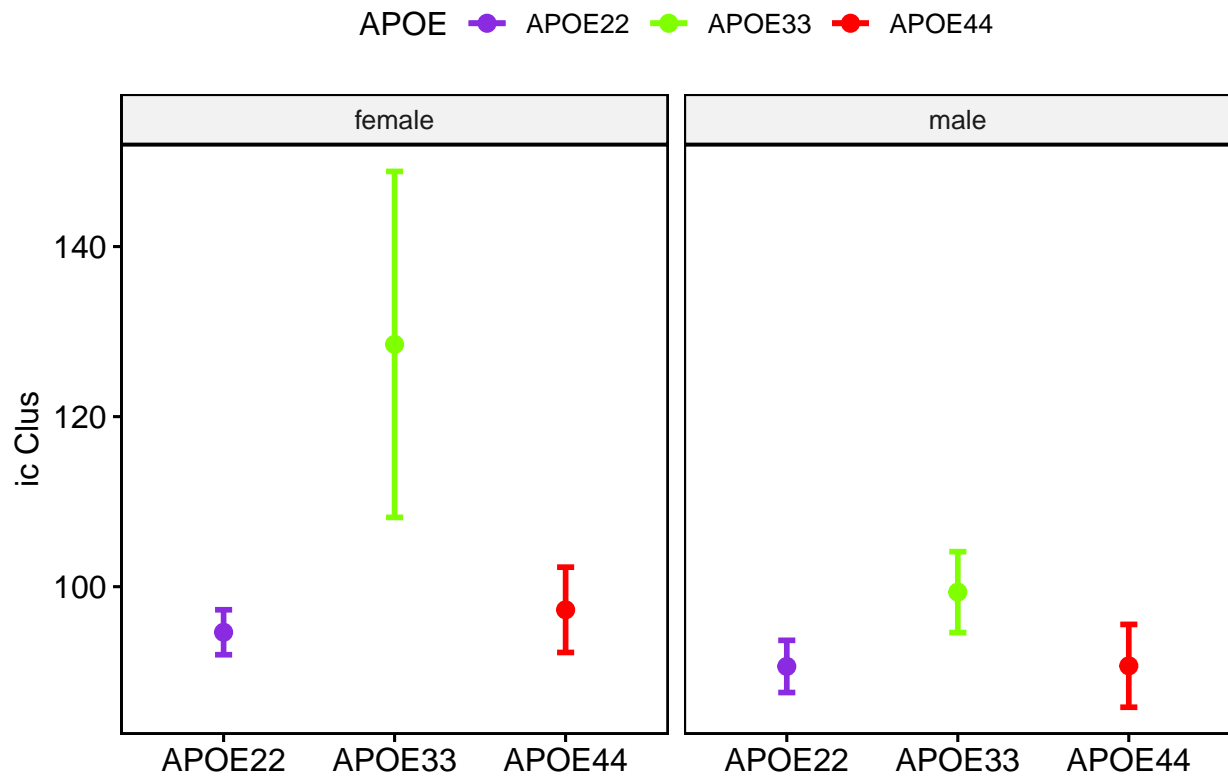
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```

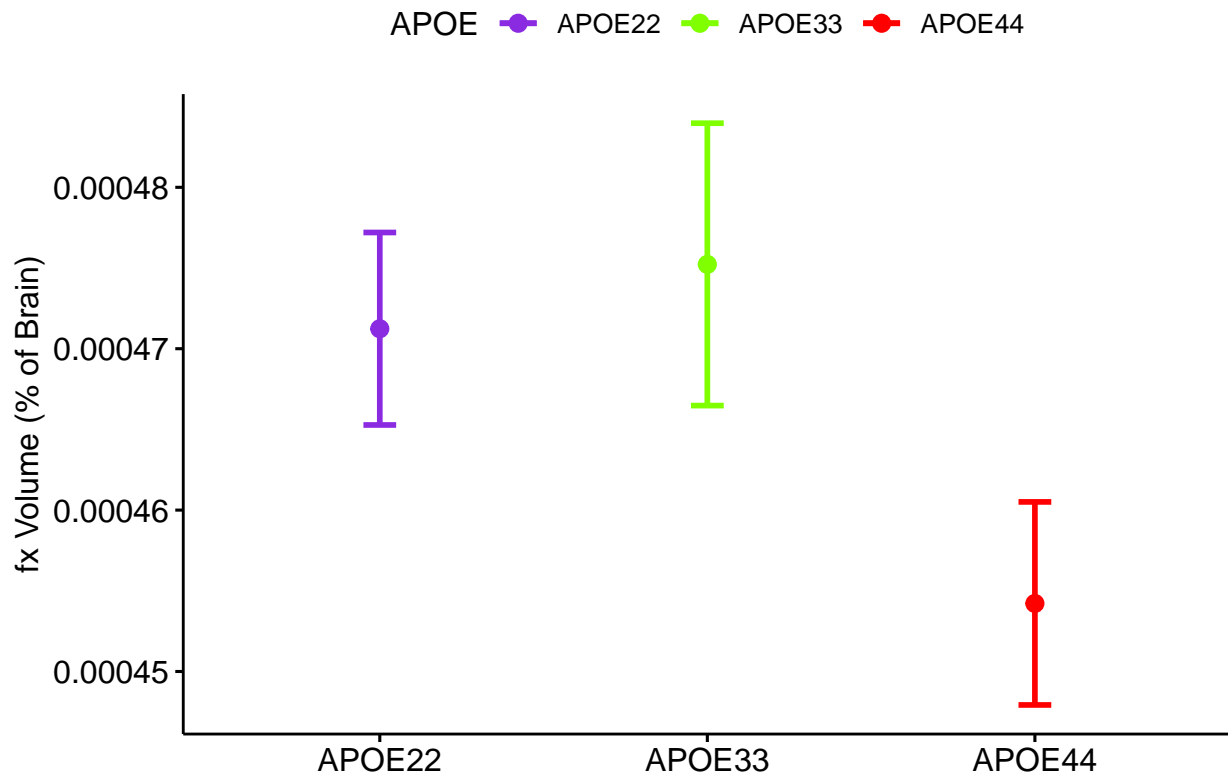
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



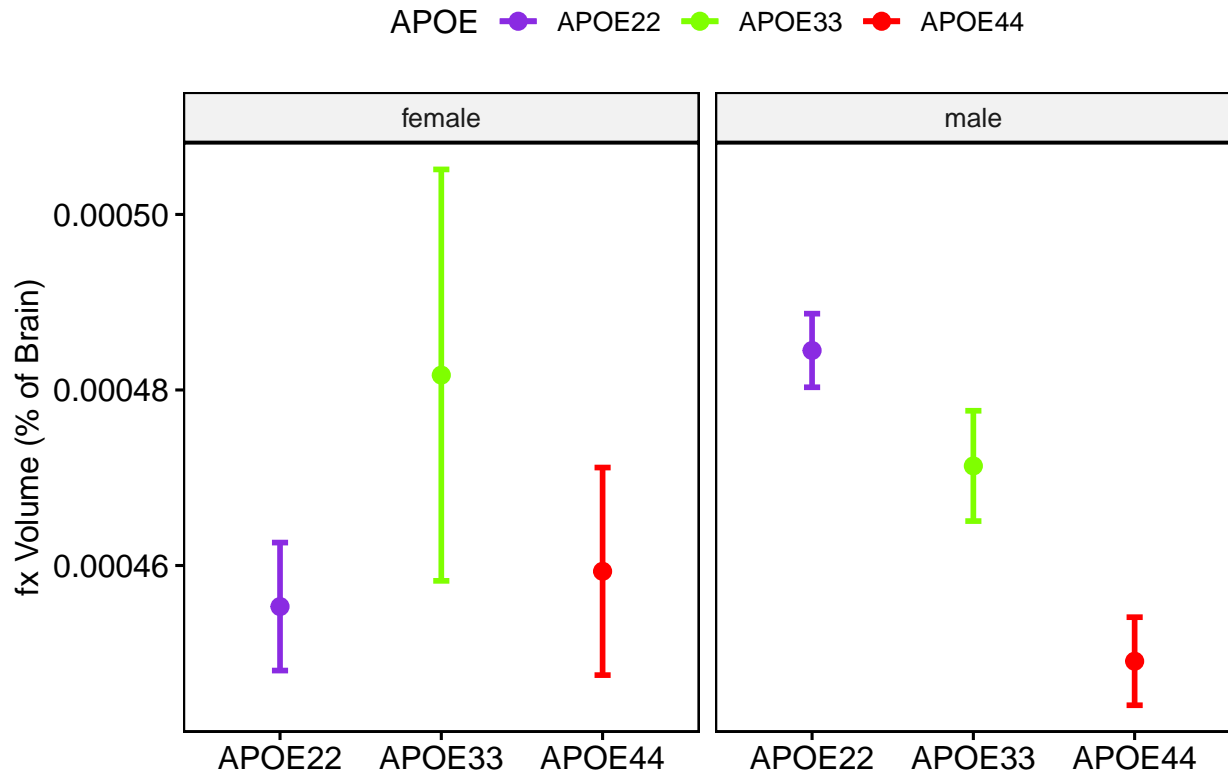
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



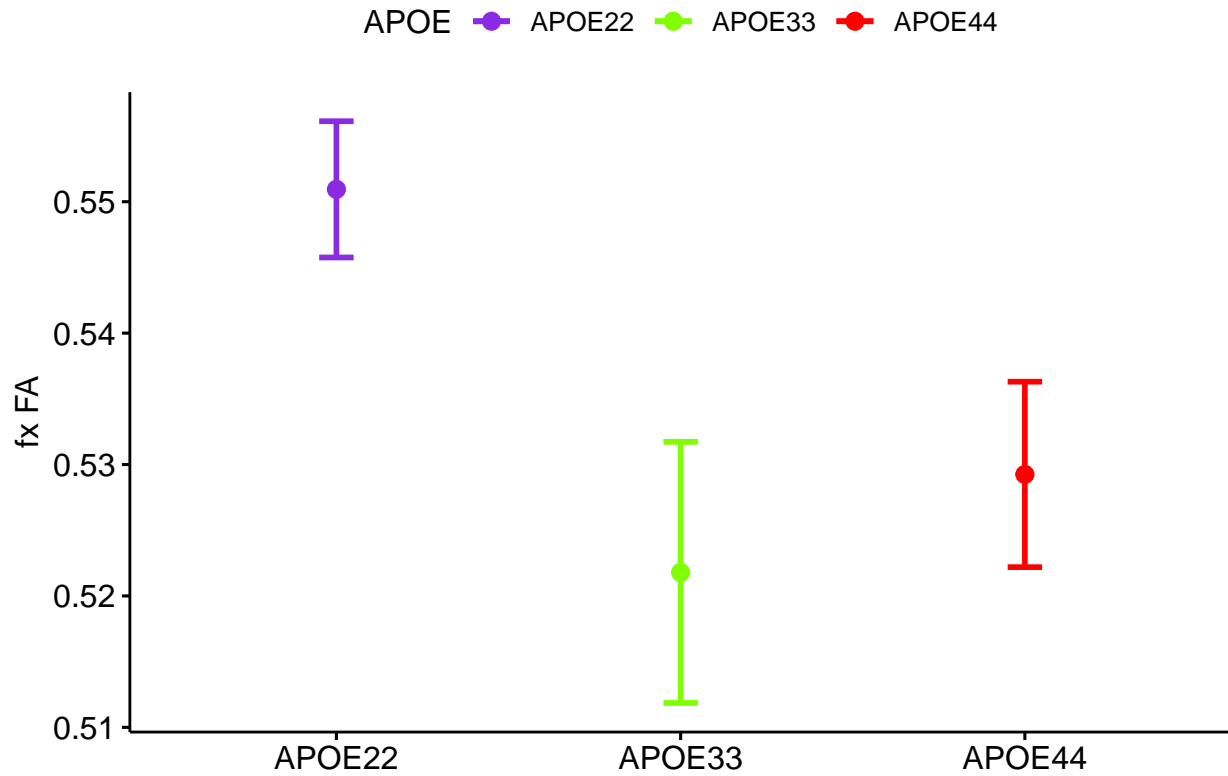
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



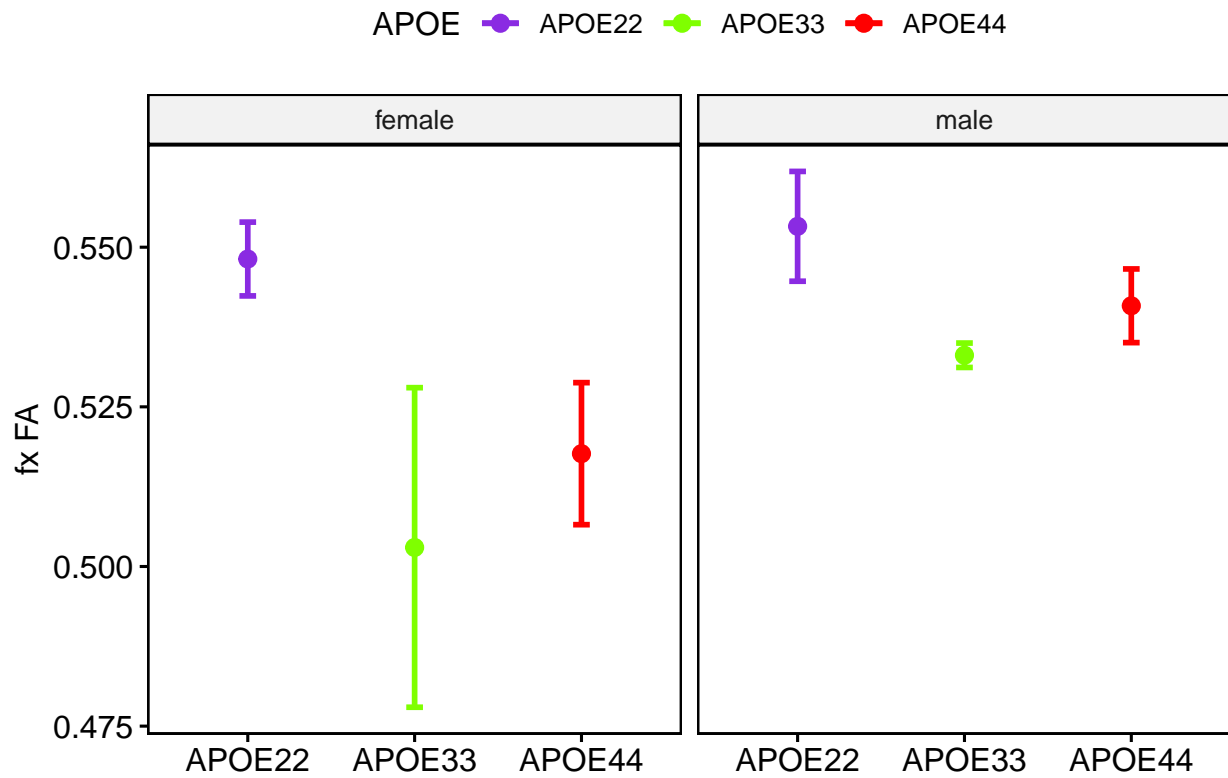
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



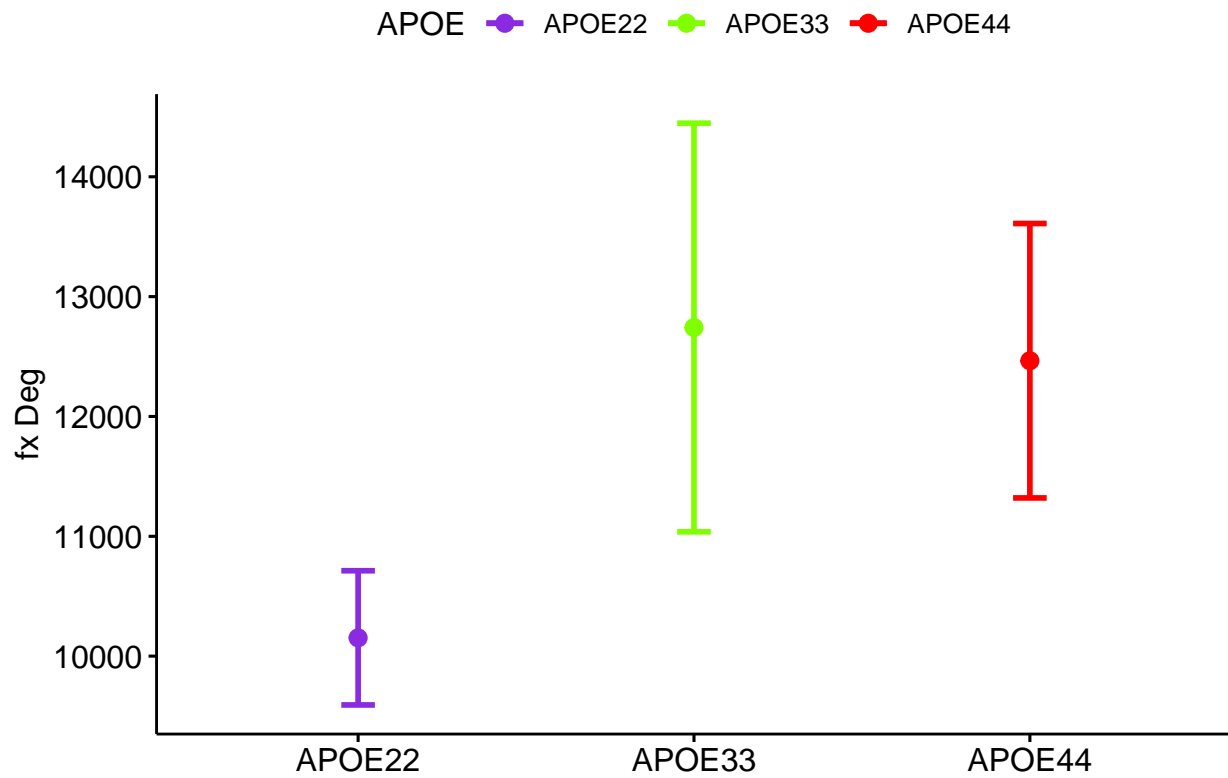
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



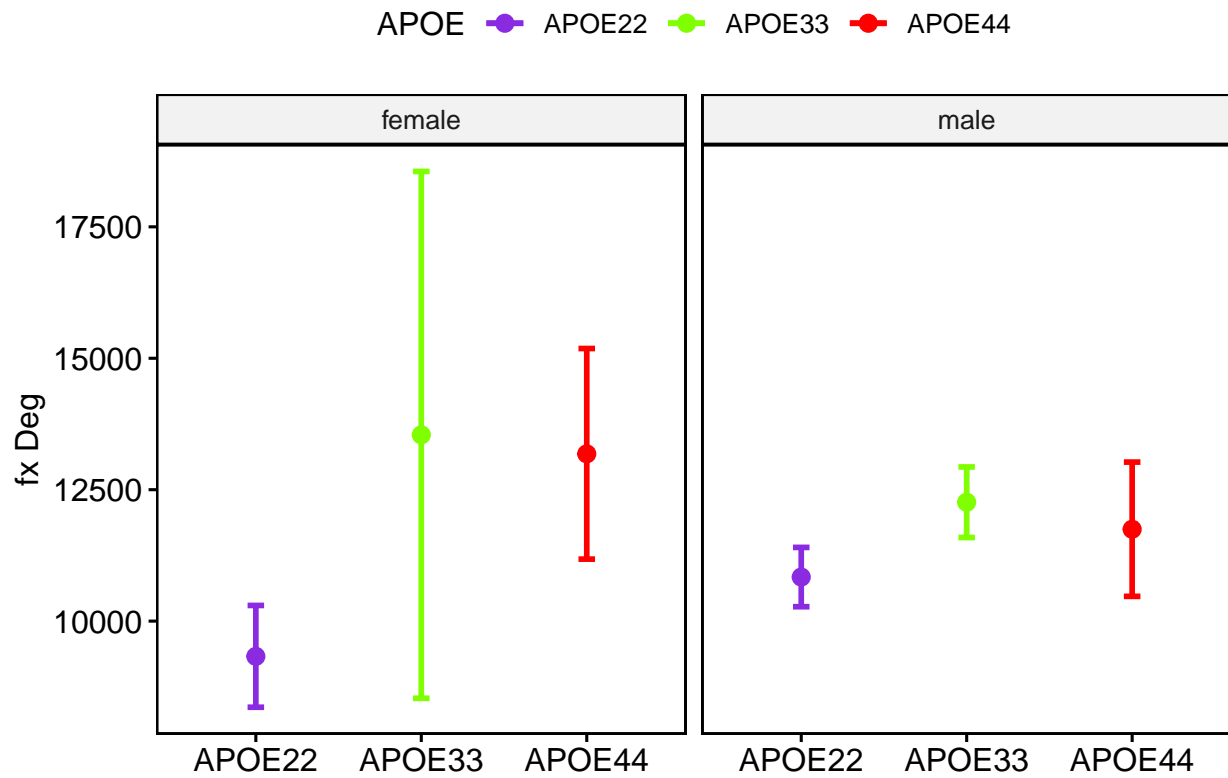
```
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?
```



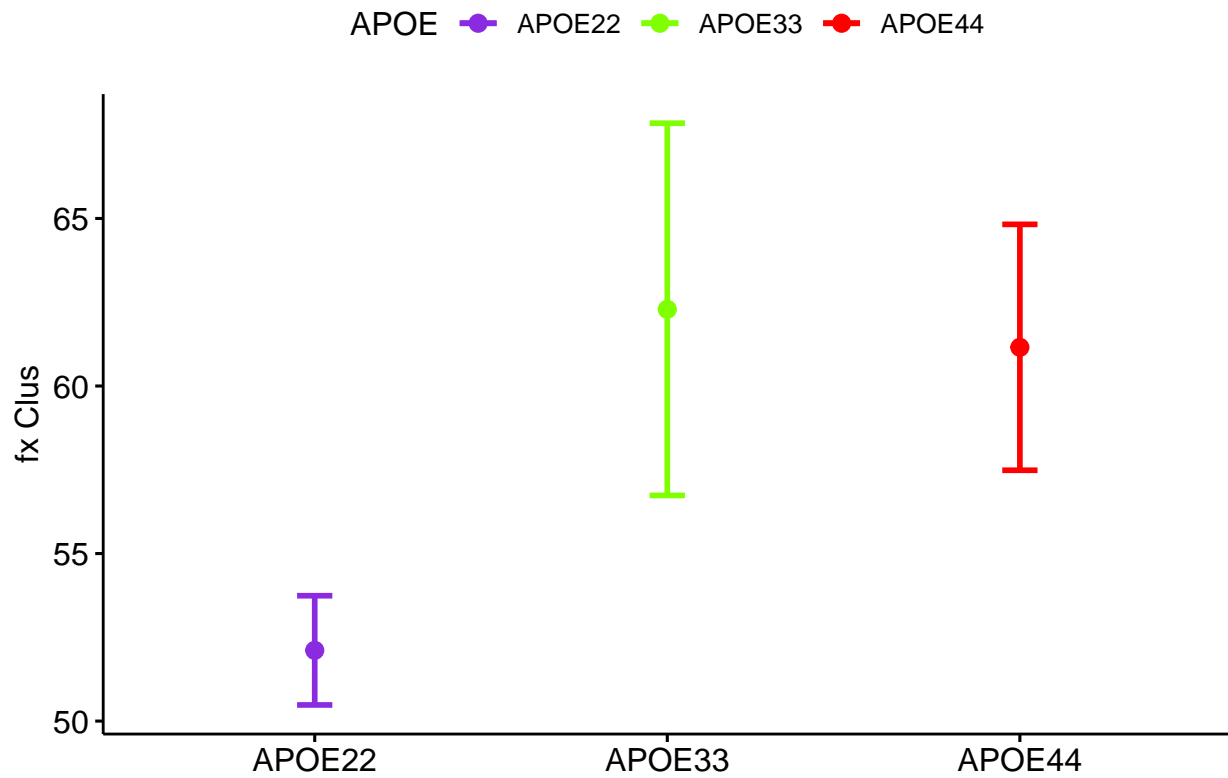
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



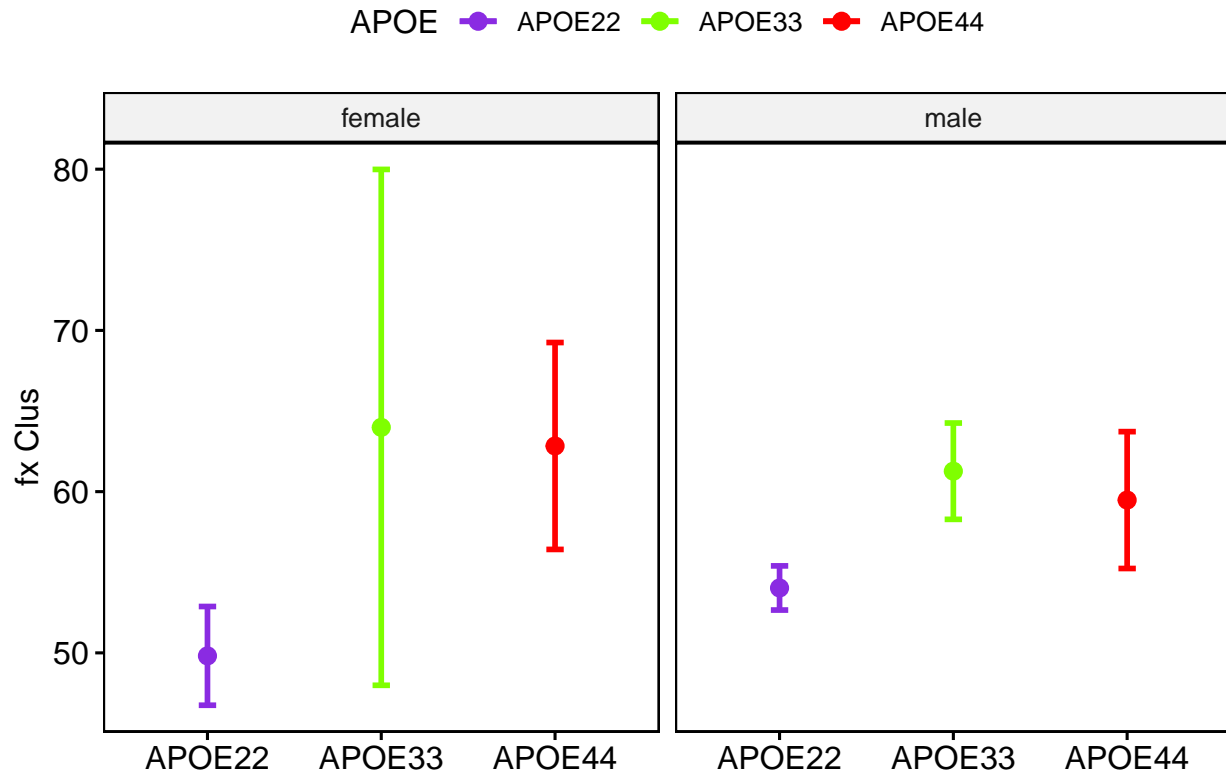
```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```

```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```

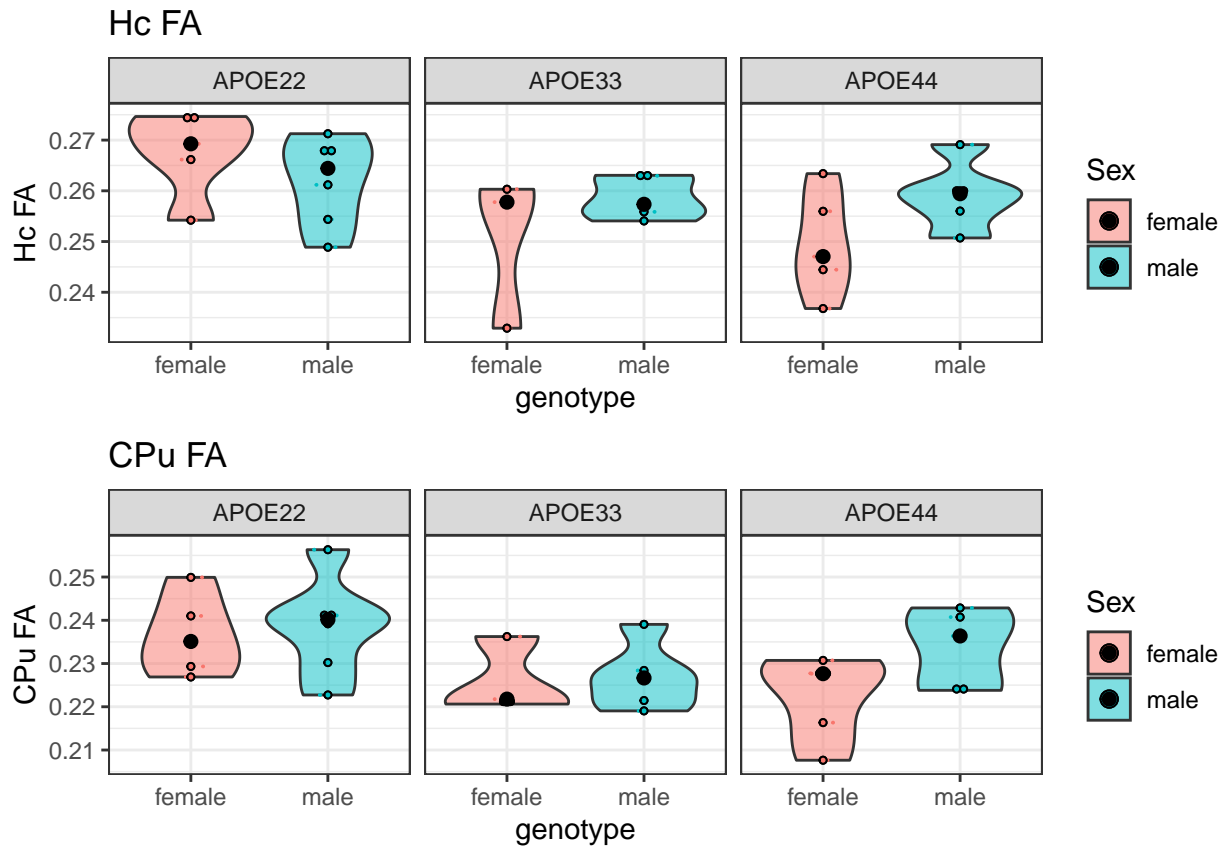


```
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?  
## geom_path: Each group consists of only one observation. Do you need to adjust  
## the group aesthetic?
```

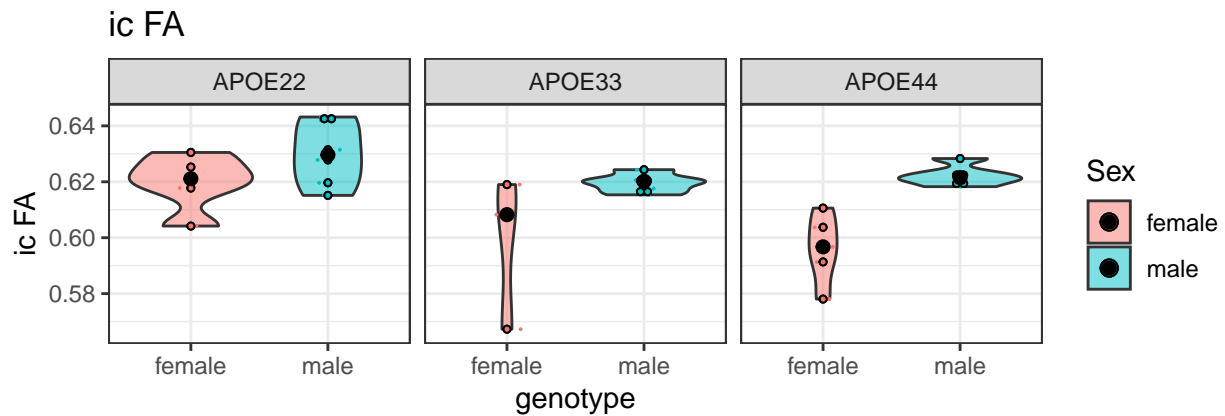
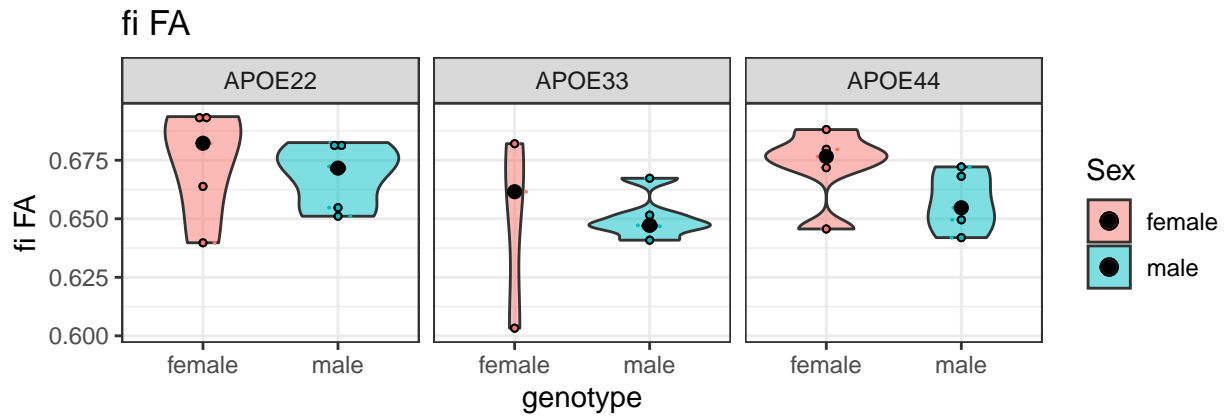


```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?

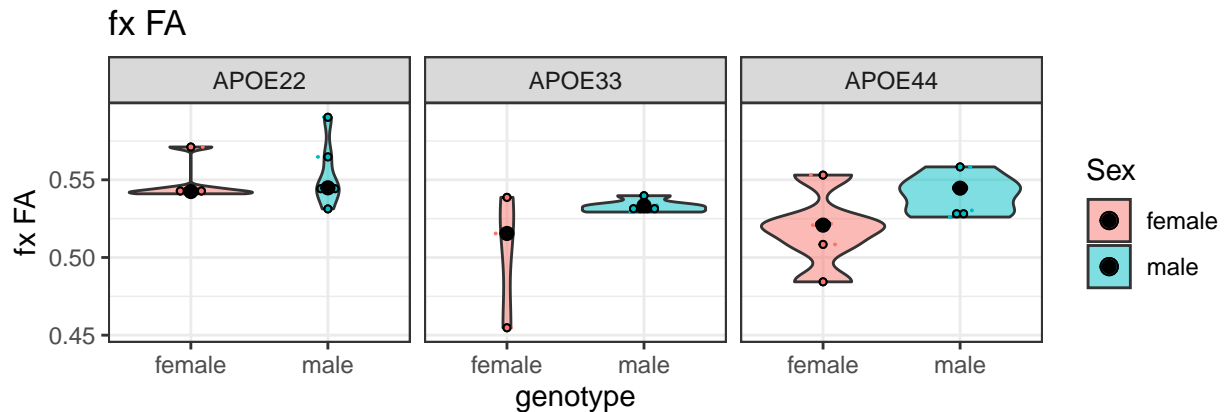
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
```



```
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
```



```
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
```



```
## [1] "Hc FA"
##
## Call:
## lm(formula = Hc ~ Genotype * Sex, data = geno_combined_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.0174129 -0.0045908  0.0002655  0.0064382  0.0138615
##
## Coefficients:
```

```

##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.267691   0.003956  67.663 < 2e-16 ***
## GenotypeAPOE33   -0.017357   0.006460  -2.687  0.01317 *
## GenotypeAPOE44   -0.018166   0.005595  -3.247  0.00356 **
## Sexmale          -0.005776   0.005357  -1.078  0.29211
## GenotypeAPOE33:Sexmale 0.014094   0.008392   1.679  0.10661
## GenotypeAPOE44:Sexmale 0.015411   0.007746   1.990  0.05866 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.008846 on 23 degrees of freedom
## Multiple R-squared:  0.3788, Adjusted R-squared:  0.2437
## F-statistic: 2.805 on 5 and 23 DF,  p-value: 0.04041

##
## Call:
## lm(formula = Hc ~ Genotype, data = combo_f_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.017413 -0.005077  0.001575  0.006957  0.013862
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.267691   0.004822  55.509 8.73e-14 ***
## GenotypeAPOE33 -0.017357   0.007875  -2.204   0.0521 .
## GenotypeAPOE44 -0.018166   0.006820  -2.664   0.0237 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01078 on 10 degrees of freedom
## Multiple R-squared:  0.4581, Adjusted R-squared:  0.3497
## F-statistic: 4.227 on 2 and 10 DF,  p-value: 0.04673

##
## Call:
## lm(formula = Hc ~ Genotype, data = combo_m_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.0130315 -0.0035130 -0.0002347  0.0047378  0.0099443
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.261915   0.002858  91.64 <2e-16 ***
## GenotypeAPOE33 -0.003263   0.004239  -0.77   0.455
## GenotypeAPOE44 -0.002755   0.004239  -0.65   0.527
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.007001 on 13 degrees of freedom
## Multiple R-squared:  0.0515, Adjusted R-squared: -0.09442
## F-statistic: 0.3529 on 2 and 13 DF,  p-value: 0.7091

## Analysis of Variance Table

```

```

##
## Response: Hc
##           Df      Sum Sq    Mean Sq F value  Pr(>F)
## Genotype    2 0.00064461 0.00032230  4.1185 0.02959 *
## Sex          1 0.00008065 0.00008065  1.0306 0.32059
## Genotype:Sex  2 0.00037217 0.00018609  2.3778 0.11517
## Residuals   23 0.00179995 0.00007826
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Hc
##           Df      Sum Sq    Mean Sq F value  Pr(>F)
## Genotype    2 0.00098301 0.00049151  4.2269 0.04673 *
## Residuals  10 0.00116280 0.00011628
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Hc
##           Df      Sum Sq    Mean Sq F value  Pr(>F)
## Genotype    2 0.00003460 1.7298e-05  0.3529 0.7091
## Residuals  13 0.00063715 4.9012e-05

## [1] "CPu FA"

##
## Call:
## lm(formula = CPu ~ Genotype * Sex, data = geno_combined_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.0157390 -0.0071250  0.0007236  0.0057157  0.0178542
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.236449   0.004266  55.423  <2e-16 ***
## GenotypeAPOE33 -0.010244   0.006967  -1.470   0.1550
## GenotypeAPOE44 -0.014434   0.006033  -2.392   0.0253 *
## Sexmale         0.002017   0.005777   0.349   0.7302
## GenotypeAPOE33:Sexmale -0.001301  0.009050  -0.144   0.8869
## GenotypeAPOE44:Sexmale  0.009600  0.008353   1.149   0.2623
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.00954 on 23 degrees of freedom
## Multiple R-squared:  0.3388, Adjusted R-squared:  0.195
## F-statistic: 2.357 on 5 and 23 DF,  p-value: 0.07251

##
## Call:
## lm(formula = CPu ~ Genotype, data = combo_f_FA)
##
## Residuals:

```

```

##           Min           1Q       Median           3Q           Max
## -0.014377 -0.005680 -0.001346  0.005716  0.013471
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.236449   0.004188  56.462 7.37e-14 ***
## GenotypeAPOE33 -0.010244   0.006839  -1.498   0.165
## GenotypeAPOE44 -0.014434   0.005922  -2.437   0.035 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.009364 on 10 degrees of freedom
## Multiple R-squared:  0.382, Adjusted R-squared:  0.2584
## F-statistic: 3.091 on 2 and 10 DF,  p-value: 0.09015
##
## Call:
## lm(formula = CPu ~ Genotype, data = combo_m_FA)
##
## Residuals:
##           Min           1Q       Median           3Q           Max
## -0.015739 -0.007968  0.001099  0.003847  0.017854
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.238466   0.003949  60.389 <2e-16 ***
## GenotypeAPOE33 -0.011545   0.005857  -1.971   0.0704 .
## GenotypeAPOE44 -0.004835   0.005857  -0.825   0.4240
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.009673 on 13 degrees of freedom
## Multiple R-squared:  0.2304, Adjusted R-squared:  0.112
## F-statistic: 1.946 on 2 and 13 DF,  p-value: 0.1823
## Analysis of Variance Table
##
## Response: CPu
##           Df      Sum Sq    Mean Sq F value Pr(>F)
## Genotype    2 0.00072293 0.00036146  3.9719 0.03298 *
## Sex          1 0.00018127 0.00018127  1.9919 0.17153
## Genotype:Sex  2 0.00016811 0.00008405  0.9236 0.41131
## Residuals   23 0.00209312 0.00009101
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Analysis of Variance Table
##
## Response: CPu
##           Df      Sum Sq    Mean Sq F value Pr(>F)
## Genotype    2 0.00054200 2.7100e-04  3.0906 0.09015 .
## Residuals  10 0.00087686 8.7686e-05
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Analysis of Variance Table

```



```

##
## Response: CPu
##           Df      Sum Sq    Mean Sq F value Pr(>F)
## Genotype   2 0.00036413 1.8206e-04   1.946 0.1823
## Residuals 13 0.00121626 9.3559e-05

## [1] "fi FA"

##
## Call:
## lm(formula = fi ~ Genotype * Sex, data = geno_combined_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.045696 -0.009889  0.002339  0.012594  0.033102
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.674432   0.008517   79.184 <2e-16 ***
## GenotypeAPOE33 -0.025466   0.013909  -1.831  0.0801 .
## GenotypeAPOE44 -0.002072   0.012045  -0.172  0.8649
## Sexmale        -0.005803   0.011532  -0.503  0.6196
## GenotypeAPOE33:Sexmale 0.007586   0.018068   0.420  0.6785
## GenotypeAPOE44:Sexmale -0.009255   0.016676  -0.555  0.5843
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01905 on 23 degrees of freedom
## Multiple R-squared:  0.2502, Adjusted R-squared:  0.08722
## F-statistic: 1.535 on 5 and 23 DF,  p-value: 0.2181

##
## Call:
## lm(formula = fi ~ Genotype, data = combo_f_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.045696 -0.010606  0.007315  0.015746  0.033102
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.674432   0.011362   59.357 4.47e-14 ***
## GenotypeAPOE33 -0.025466   0.018555  -1.373   0.2
## GenotypeAPOE44 -0.002072   0.016069  -0.129   0.9
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02541 on 10 degrees of freedom
## Multiple R-squared:  0.177, Adjusted R-squared:  0.01237
## F-statistic: 1.075 on 2 and 10 DF,  p-value: 0.3776

##
## Call:
## lm(formula = fi ~ Genotype, data = combo_m_FA)
##
## Residuals:

```

```

##           Min           1Q           Median           3Q           Max
## -0.0175431 -0.0082795 -0.0008975  0.0110151  0.0165586
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.668630   0.004919 135.923  <2e-16 ***
## GenotypeAPOE33 -0.017881   0.007296  -2.451   0.0292 *
## GenotypeAPOE44 -0.011327   0.007296  -1.552   0.1446
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01205 on 13 degrees of freedom
## Multiple R-squared:  0.3246, Adjusted R-squared:  0.2207
## F-statistic: 3.124 on 2 and 13 DF,  p-value: 0.078

## Analysis of Variance Table
##
## Response: fi
##           Df      Sum Sq    Mean Sq F value Pr(>F)
## Genotype    2  0.0021195  0.00105977   2.9217 0.07402 .
## Sex          1  0.0003538  0.00035376   0.9753 0.33364
## Genotype:Sex  2  0.0003108  0.00015541   0.4285 0.65660
## Residuals   23  0.0083426  0.00036272
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: fi
##           Df      Sum Sq    Mean Sq F value Pr(>F)
## Genotype    2  0.0013881  0.00069404   1.0752 0.3776
## Residuals   10  0.0064552  0.00064552

## Analysis of Variance Table
##
## Response: fi
##           Df      Sum Sq    Mean Sq F value Pr(>F)
## Genotype    2  0.00090716  0.00045358   3.124  0.078 .
## Residuals   13  0.00188746  0.00014519
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "ic FA"

##
## Call:
## lm(formula = ic ~ Genotype * Sex, data = geno_combined_FA)
##
## Residuals:
##           Min           1Q           Median           3Q           Max
## -0.0308930 -0.0041263  0.0006374  0.0059384  0.0208270
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.619760   0.005320 116.495  < 2e-16 ***
## GenotypeAPOE33 -0.021588   0.008688  -2.485  0.02067 *

```

```

## GenotypeAPOE44          -0.023672    0.007524   -3.146   0.00452 **
## Sexmale                  0.010103    0.007203    1.403   0.17412
## GenotypeAPOE33:Sexmale  0.011325    0.011286    1.004   0.32604
## GenotypeAPOE44:Sexmale  0.016188    0.010416    1.554   0.13380
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0119 on 23 degrees of freedom
## Multiple R-squared:  0.5763, Adjusted R-squared:  0.4842
## F-statistic: 6.258 on 5 and 23 DF,  p-value: 0.000839

##
## Call:
## lm(formula = ic ~ Genotype, data = combo_f_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.030893 -0.004746  0.001343  0.010066  0.020827
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.619760   0.007072   87.633 9.16e-16 ***
## GenotypeAPOE33 -0.021588   0.011549   -1.869   0.0911 .
## GenotypeAPOE44 -0.023672   0.010002   -2.367   0.0395 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01581 on 10 degrees of freedom
## Multiple R-squared:  0.3932, Adjusted R-squared:  0.2718
## F-statistic:  3.24 on 2 and 10 DF,  p-value: 0.08228

##
## Call:
## lm(formula = ic ~ Genotype, data = combo_m_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.014724 -0.002558 -0.000158  0.002379  0.013310
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.629862   0.003109  202.585 <2e-16 ***
## GenotypeAPOE33 -0.010262   0.004612   -2.225   0.0444 *
## GenotypeAPOE44 -0.007484   0.004612   -1.623   0.1286
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.007616 on 13 degrees of freedom
## Multiple R-squared:  0.2944, Adjusted R-squared:  0.1858
## F-statistic: 2.712 on 2 and 13 DF,  p-value: 0.1037

## Analysis of Variance Table
##
## Response: ic
##              Df    Sum Sq    Mean Sq F value    Pr(>F)

```

```

## Genotype      2 0.0015605 0.00078027 5.5137 0.0110621 *
## Sex           1 0.0025078 0.00250781 17.7213 0.0003339 ***
## Genotype:Sex  2 0.0003595 0.00017977 1.2703 0.2997152
## Residuals     23 0.0032548 0.00014151
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: ic
##           Df      Sum Sq    Mean Sq F value    Pr(>F)
## Genotype    2 0.0016204 0.00081017  3.2396 0.08228 .
## Residuals   10 0.0025008 0.00025008
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: ic
##           Df      Sum Sq    Mean Sq F value    Pr(>F)
## Genotype    2 0.00031453 0.00015727  2.7115 0.1037
## Residuals   13 0.00075400 0.00005800

## [1] "fx FA"

##
## Call:
## lm(formula = fx ~ Genotype * Sex, data = geno_combined_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.048213 -0.008483 -0.003539  0.006695  0.036991
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.548151   0.009258  59.211 < 2e-16 ***
## GenotypeAPOE33 -0.045172   0.015118  -2.988 0.00657 **
## GenotypeAPOE44 -0.030483   0.013092  -2.328 0.02905 *
## Sexmale         0.005117   0.012535   0.408 0.68688
## GenotypeAPOE33:Sexmale 0.024983   0.019638   1.272 0.21602
## GenotypeAPOE44:Sexmale 0.018041   0.018125   0.995 0.32993
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0207 on 23 degrees of freedom
## Multiple R-squared:  0.4363, Adjusted R-squared:  0.3138
## F-statistic:  3.56 on 5 and 23 DF,  p-value: 0.01572

##
## Call:
## lm(formula = fx ~ Genotype, data = combo_f_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.048213 -0.007154 -0.003539  0.012483  0.035729
##

```

```

## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.54815    0.01175  46.668 4.92e-13 ***
## GenotypeAPOE33 -0.04517    0.01918  -2.355  0.0403 *
## GenotypeAPOE44 -0.03048    0.01661  -1.835  0.0964 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02626 on 10 degrees of freedom
## Multiple R-squared:  0.3889, Adjusted R-squared:  0.2667
## F-statistic: 3.182 on 2 and 10 DF,  p-value: 0.08521

##
## Call:
## lm(formula = fx ~ Genotype, data = combo_m_FA)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.021995 -0.008767 -0.001684  0.004700  0.036991
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.553269    0.006158  89.851  <2e-16 ***
## GenotypeAPOE33 -0.020189    0.009133  -2.210  0.0456 *
## GenotypeAPOE44 -0.012442    0.009133  -1.362  0.1962
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01508 on 13 degrees of freedom
## Multiple R-squared:  0.2797, Adjusted R-squared:  0.1689
## F-statistic: 2.524 on 2 and 13 DF,  p-value: 0.1186

## Analysis of Variance Table
##
## Response: fx
##           Df    Sum Sq   Mean Sq F value   Pr(>F)
## Genotype    2  0.0045172  0.00225862   5.2709 0.01305 *
## Sex          1  0.0023173  0.00231728   5.4078 0.02923 *
## Genotype:Sex  2  0.0007937  0.00039683   0.9261 0.41038
## Residuals   23  0.0098557  0.00042851
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: fx
##           Df    Sum Sq   Mean Sq F value   Pr(>F)
## Genotype    2  0.0043904  0.00219518   3.1822 0.08521 .
## Residuals  10  0.0068983  0.00068983
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: fx
##           Df    Sum Sq   Mean Sq F value   Pr(>F)

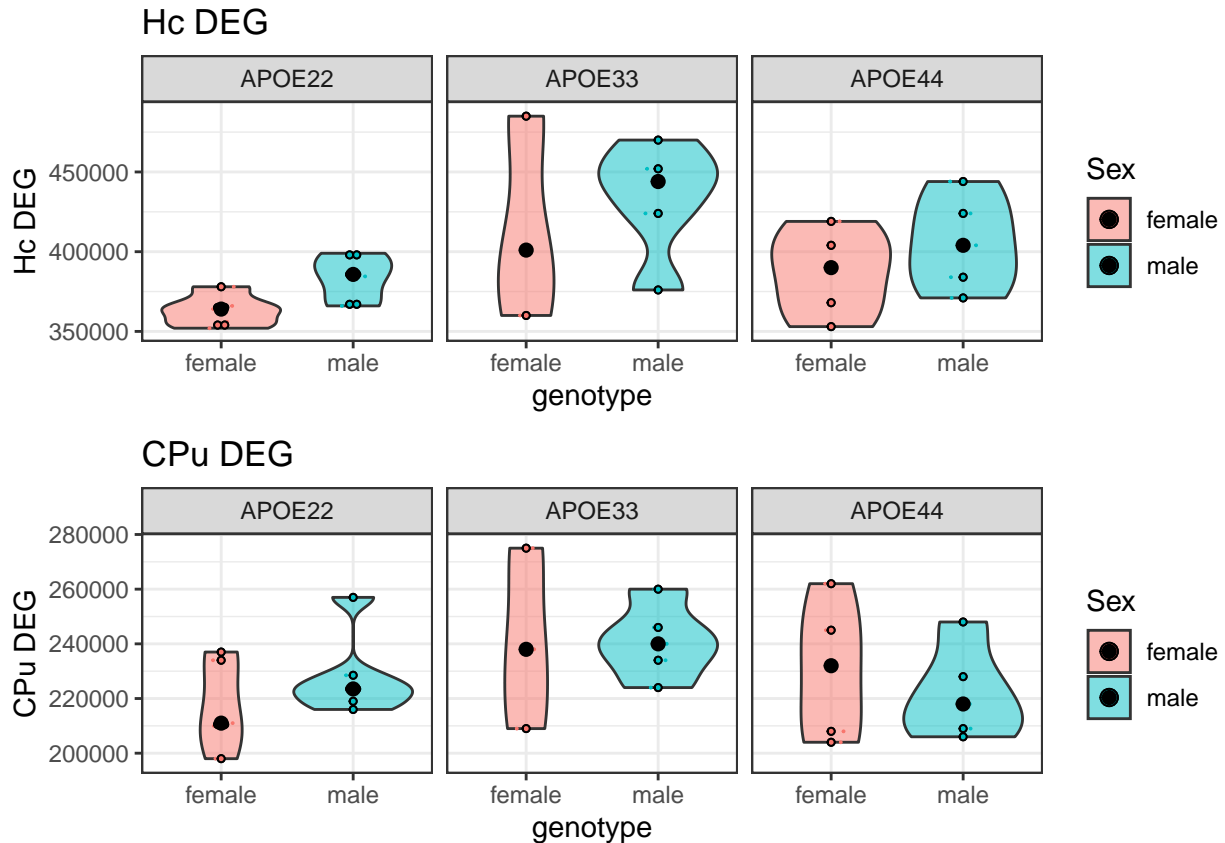
```

```
## Genotype    2 0.0011483 0.00057414 2.5237 0.1186
## Residuals  13 0.0029575 0.00022750
```

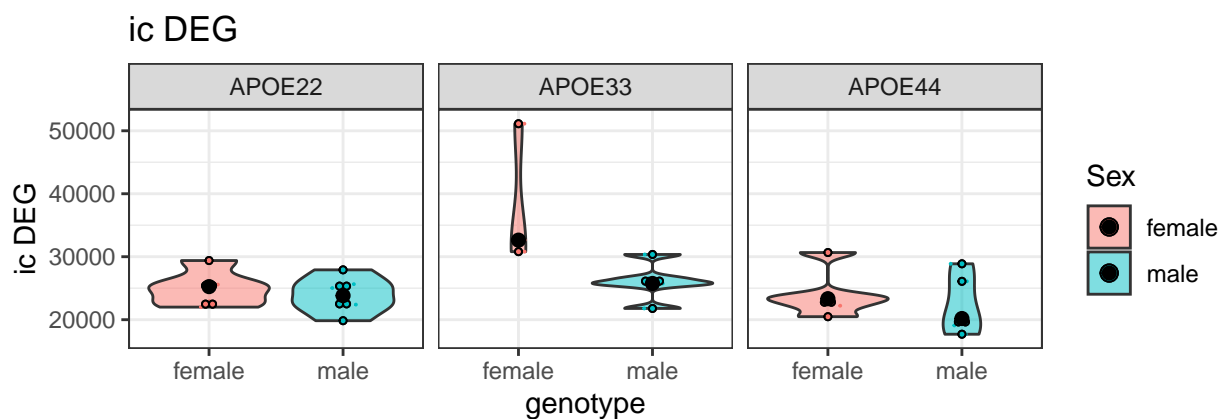
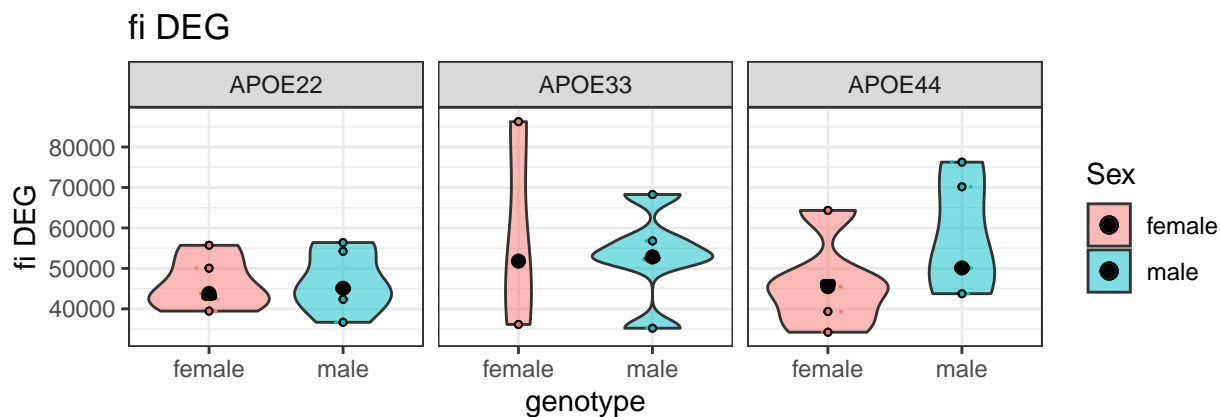
Plots for Connectivity Degree

Hc and CPu

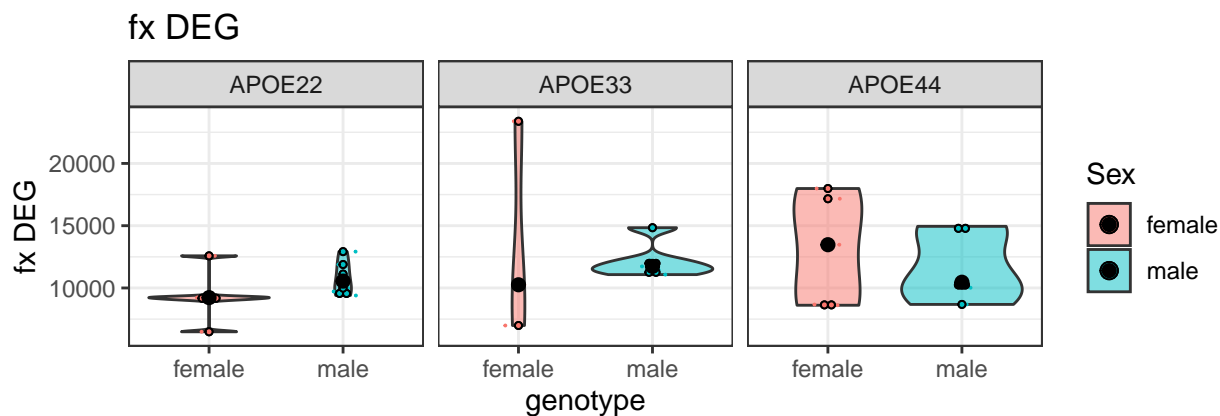
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
```



```
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
```



```
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
```



```
## [1] "Hc DEG"
##
## Call:
## lm(formula = Hc ~ Genotype * Sex, data = geno_combined_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -57200 -15583    917   15417  69667
##
## Coefficients:
```

```

##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      363200      13515  26.873  <2e-16 ***
## GenotypeAPOE33      52133      22070   2.362   0.027 *
## GenotypeAPOE44      23600      19114   1.235   0.229
## Sexmale           20383      18300   1.114   0.277
## GenotypeAPOE33:Sexmale -2517      28670  -0.088   0.931
## GenotypeAPOE44:Sexmale -1783      26462  -0.067   0.947
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 30220 on 23 degrees of freedom
## Multiple R-squared:  0.4199, Adjusted R-squared:  0.2938
## F-statistic:  3.33 on 5 and 23 DF,  p-value: 0.02083

##
## Call:
## lm(formula = Hc ~ Genotype, data = combo_f_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -55333 -14333      800  14800  69667
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      363200      15076  24.091 3.46e-10 ***
## GenotypeAPOE33      52133      24619   2.118   0.0603 .
## GenotypeAPOE44      23600      21321   1.107   0.2942
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 33710 on 10 degrees of freedom
## Multiple R-squared:  0.3117, Adjusted R-squared:  0.174
## F-statistic: 2.264 on 2 and 10 DF,  p-value: 0.1545

##
## Call:
## lm(formula = Hc ~ Genotype, data = combo_m_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -57200 -16083      2167  16212  38600
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      383583      11118  34.500 3.61e-14 ***
## GenotypeAPOE33      49617      16491   3.009   0.0101 *
## GenotypeAPOE44      21817      16491   1.323   0.2087
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 27230 on 13 degrees of freedom
## Multiple R-squared:  0.4106, Adjusted R-squared:  0.3199
## F-statistic: 4.527 on 2 and 13 DF,  p-value: 0.0322

## Analysis of Variance Table

```



```

##
## Response: Hc
##           Df      Sum Sq    Mean Sq F value    Pr(>F)
## Genotype    2 1.2612e+10 6305878370   6.9043 0.004482 **
## Sex          1 2.5886e+09 2588593164   2.8343 0.105800
## Genotype:Sex  2 7.9682e+06   3984100   0.0044 0.995648
## Residuals   23 2.1006e+10  913325000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Hc
##           Df      Sum Sq    Mean Sq F value    Pr(>F)
## Genotype    2 5.1465e+09 2573251282   2.2643 0.1545
## Residuals  10 1.1364e+10 1136426667

## Analysis of Variance Table
##
## Response: Hc
##           Df      Sum Sq    Mean Sq F value    Pr(>F)
## Genotype    2 6715901042 3357950521   4.5273 0.0322 *
## Residuals  13 9642208333  741708333
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "CPu DEG"

##
## Call:
## lm(formula = CPu ~ Genotype * Sex, data = geno_combined_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -31667 -11917  -3800   14800   34333
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      218000       8706  25.040  <2e-16 ***
## GenotypeAPOE33      22667      14217   1.594   0.125
## GenotypeAPOE44      12200      12312   0.991   0.332
## Sexmale           9917      11788   0.841   0.409
## GenotypeAPOE33:Sexmale -9783      18468  -0.530   0.601
## GenotypeAPOE44:Sexmale -18317     17045  -1.075   0.294
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 19470 on 23 degrees of freedom
## Multiple R-squared:  0.1853, Adjusted R-squared:  0.008217
## F-statistic: 1.046 on 5 and 23 DF,  p-value: 0.4148

##
## Call:
## lm(formula = CPu ~ Genotype, data = combo_f_DEG)
##
## Residuals:

```

```

##      Min      1Q Median      3Q      Max
## -31667 -20000 -2667  16000  34333
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    218000     10706   20.361  1.8e-09 ***
## GenotypeAPOE33    22667     17484    1.296    0.224
## GenotypeAPOE44    12200     15141    0.806    0.439
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 23940 on 10 degrees of freedom
## Multiple R-squared:  0.1492, Adjusted R-squared:  -0.02091
## F-statistic: 0.8771 on 2 and 10 DF,  p-value: 0.4457
##
## Call:
## lm(formula = CPu ~ Genotype, data = combo_m_DEG)
##
## Residuals:
##      Min      1Q Median      3Q      Max
## -16800 -9667 -3858  5450  29083
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    227917     6186   36.844 1.55e-14 ***
## GenotypeAPOE33    12883     9175    1.404    0.184
## GenotypeAPOE44   -6117     9175   -0.667    0.517
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 15150 on 13 degrees of freedom
## Multiple R-squared:  0.2406, Adjusted R-squared:  0.1237
## F-statistic: 2.059 on 2 and 13 DF,  p-value: 0.1672
## Analysis of Variance Table
##
## Response: CPu
##           Df      Sum Sq   Mean Sq F value Pr(>F)
## Genotype    2 1538125392 769062696  2.0294 0.1543
## Sex          1   5580291   5580291  0.0147 0.9045
## Genotype:Sex  2  439053800 219526900  0.5793 0.5683
## Residuals   23  8716275000 378968478
##
## Analysis of Variance Table
##
## Response: CPu
##           Df      Sum Sq   Mean Sq F value Pr(>F)
## Genotype    2 1005456410 502728205  0.8771 0.4457
## Residuals  10  5731466667 573146667
##
## Analysis of Variance Table
##
## Response: CPu
##           Df      Sum Sq   Mean Sq F value Pr(>F)
## Genotype    2  945426042 472713021  2.0588 0.1672

```

```

## Residuals 13 2984808333 229600641
## [1] "fi DEG"
##
## Call:
## lm(formula = fi ~ Genotype * Sex, data = geno_combined_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -21929.3  -6854.2   -855.8   7591.3  28195.7
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      46291.2      5639.7   8.208 2.75e-08 ***
## GenotypeAPOE33      11781.1      9209.5   1.279   0.214
## GenotypeAPOE44      -198.8      7975.7  -0.025   0.980
## Sexmale             340.5      7636.1   0.045   0.965
## GenotypeAPOE33:Sexmale -5351.0     11963.5  -0.447   0.659
## GenotypeAPOE44:Sexmale 11634.5     11041.8   1.054   0.303
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 12610 on 23 degrees of freedom
## Multiple R-squared:  0.173, Adjusted R-squared:  -0.006832
## F-statistic: 0.962 on 5 and 23 DF,  p-value: 0.4612
##
## Call:
## lm(formula = fi ~ Genotype, data = combo_f_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -21929  -6759  -2484   3752  28196
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      46291.2      6334.6   7.308 2.58e-05 ***
## GenotypeAPOE33      11781.1     10344.3   1.139   0.281
## GenotypeAPOE44      -198.8      8958.4  -0.022   0.983
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 14160 on 10 degrees of freedom
## Multiple R-squared:  0.1397, Adjusted R-squared:  -0.03235
## F-statistic: 0.812 on 2 and 10 DF,  p-value: 0.4712
##
## Call:
## lm(formula = fi ~ Genotype, data = combo_m_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -17851.8  -7967.4   -786.2   8132.3  18195.6
##
## Coefficients:

```

```

##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      46632      4601  10.135 1.54e-07 ***
## GenotypeAPOE33      6430      6825   0.942   0.363
## GenotypeAPOE44     11436      6825   1.676   0.118
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11270 on 13 degrees of freedom
## Multiple R-squared:  0.1798, Adjusted R-squared:  0.05356
## F-statistic: 1.424 on 2 and 13 DF,  p-value: 0.2758

## Analysis of Variance Table
##
## Response: fi
##           Df      Sum Sq   Mean Sq F value Pr(>F)
## Genotype    2  359036685 179518342  1.1288 0.3407
## Sex          1   64911127  64911127  0.4082 0.5292
## Genotype:Sex  2  340979282 170489641  1.0721 0.3588
## Residuals   23  3657650816 159028296

## Analysis of Variance Table
##
## Response: fi
##           Df      Sum Sq   Mean Sq F value Pr(>F)
## Genotype    2  325822817 162911408   0.812 0.4712
## Residuals  10 2006327623 200632762

## Analysis of Variance Table
##
## Response: fi
##           Df      Sum Sq   Mean Sq F value Pr(>F)
## Genotype    2  361879946 180939973  1.4244 0.2758
## Residuals  13 1651323193 127024861

## [1] "ic DEG"

##
## Call:
## lm(formula = ic ~ Genotype * Sex, data = geno_combined_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -7382.7 -3038.0  -364.2  1734.8 12936.3
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      25034.0      2121.7  11.799 3.09e-11 ***
## GenotypeAPOE33     13151.7      3464.7   3.796 0.000933 ***
## GenotypeAPOE44      -952.8      3000.5  -0.318 0.753693
## Sexmale           -1127.8      2872.8  -0.393 0.698232
## GenotypeAPOE33:Sexmale -11030.6      4500.7  -2.451 0.022274 *
## GenotypeAPOE44:Sexmale  -566.4      4154.0  -0.136 0.892737
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4744 on 23 degrees of freedom

```

```

## Multiple R-squared:  0.5186, Adjusted R-squared:  0.414
## F-statistic: 4.956 on 5 and 23 DF,  p-value: 0.003181

##
## Call:
## lm(formula = ic ~ Genotype, data = combo_f_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -7382.7 -3038.0  -749.2   545.0 12936.3
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    25034.0     2630.8   9.516 2.5e-06 ***
## GenotypeAPOE33  13151.7     4296.1   3.061  0.012 *
## GenotypeAPOE44   -952.8     3720.5  -0.256  0.803
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5883 on 10 degrees of freedom
## Multiple R-squared:  0.5546, Adjusted R-squared:  0.4655
## F-statistic: 6.225 on 2 and 10 DF,  p-value: 0.01753

##
## Call:
## lm(formula = ic ~ Genotype, data = combo_m_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -4695.0 -2475.2  -316.2  2227.1  6488.0
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)     23906       1483  16.117 5.67e-10 ***
## GenotypeAPOE33    2121       2200   0.964  0.353
## GenotypeAPOE44   -1519       2200  -0.691  0.502
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3633 on 13 degrees of freedom
## Multiple R-squared:  0.1632, Adjusted R-squared:  0.03445
## F-statistic: 1.268 on 2 and 13 DF,  p-value: 0.3141

## Analysis of Variance Table
##
## Response: ic
##           Df      Sum Sq   Mean Sq F value    Pr(>F)
## Genotype    2 269891145 134945572   5.9956 0.008023 **
## Sex          1 127638555 127638555   5.6710 0.025910 *
## Genotype:Sex  2 160184427  80092213   3.5585 0.045034 *
## Residuals   23 517669221  22507357
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##

```

```

## Response: ic
##           Df      Sum Sq   Mean Sq F value   Pr(>F)
## Genotype    2 430863880 215431940   6.2253 0.01753 *
## Residuals  10 346057481  34605748
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: ic
##           Df      Sum Sq   Mean Sq F value   Pr(>F)
## Genotype    2  33467243 16733622   1.2676 0.3141
## Residuals  13 171611740 13200903

## [1] "fx DEG"

##
## Call:
## lm(formula = fx ~ Genotype * Sex, data = geno_combined_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6556.3 -1442.3  -249.8   2080.7   9842.7
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)         9330         1617   5.768 7.09e-06 ***
## GenotypeAPOE33         4214         2641   1.595   0.124
## GenotypeAPOE44         3852         2287   1.684   0.106
## Sexmale              1508         2190   0.689   0.498
## GenotypeAPOE33:Sexmale -2790         3431  -0.813   0.424
## GenotypeAPOE44:Sexmale -2943         3167  -0.929   0.362
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3617 on 23 degrees of freedom
## Multiple R-squared:  0.1552, Adjusted R-squared:  -0.02843
## F-statistic: 0.8452 on 5 and 23 DF, p-value: 0.5318

##
## Call:
## lm(formula = fx ~ Genotype, data = combo_f_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -6556.3 -3286.3  -103.8   3252.2   9842.7
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)         9330         2235   4.175  0.0019 **
## GenotypeAPOE33         4214         3649   1.155  0.2751
## GenotypeAPOE44         3852         3160   1.219  0.2508
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4997 on 10 degrees of freedom

```

```
## Multiple R-squared:  0.1646, Adjusted R-squared:  -0.002534
## F-statistic: 0.9848 on 2 and 10 DF,  p-value: 0.407

##
## Call:
## lm(formula = fx ~ Genotype, data = combo_m_DEG)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -3069.0 -1212.6  -673.3   1305.2   3200.0
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    10838.3      809.9   13.382 5.59e-09 ***
## GenotypeAPOE33    1423.5      1201.3    1.185   0.257
## GenotypeAPOE44     909.7      1201.3    0.757   0.462
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1984 on 13 degrees of freedom
## Multiple R-squared:  0.1012, Adjusted R-squared:  -0.03703
## F-statistic: 0.7322 on 2 and 13 DF,  p-value: 0.4997

## Analysis of Variance Table
##
## Response: fx
##           Df      Sum Sq  Mean Sq F value Pr(>F)
## Genotype    2  40847168 20423584   1.5615 0.2313
## Sex          1   494574   494574   0.0378 0.8475
## Genotype:Sex  2  13933495  6966747   0.5326 0.5941
## Residuals   23 300830010 13079566

## Analysis of Variance Table
##
## Response: fx
##           Df      Sum Sq  Mean Sq F value Pr(>F)
## Genotype    2  49176065 24588033   0.9848 0.407
## Residuals  10 249666606 24966661

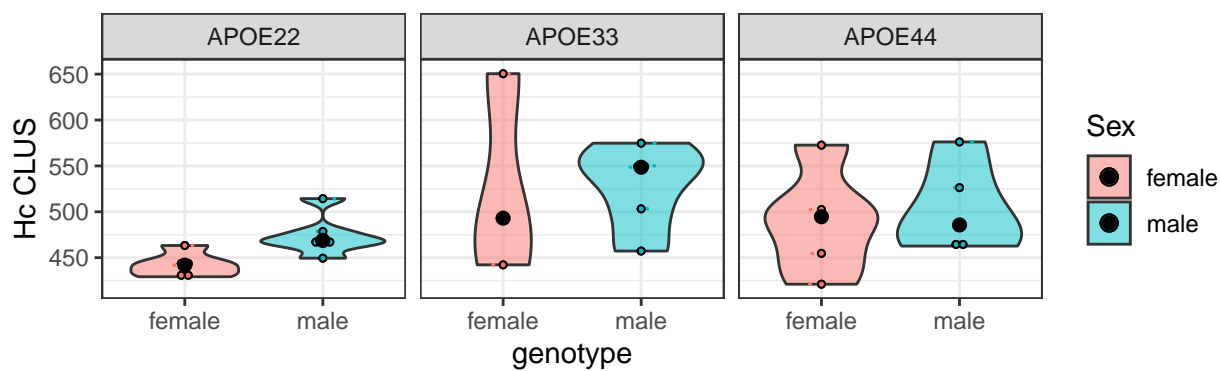
## Analysis of Variance Table
##
## Response: fx
##           Df      Sum Sq  Mean Sq F value Pr(>F)
## Genotype    2  5763268 2881634   0.7322 0.4997
## Residuals  13 51163404 3935646
```

Plots for Clustering Coefficient

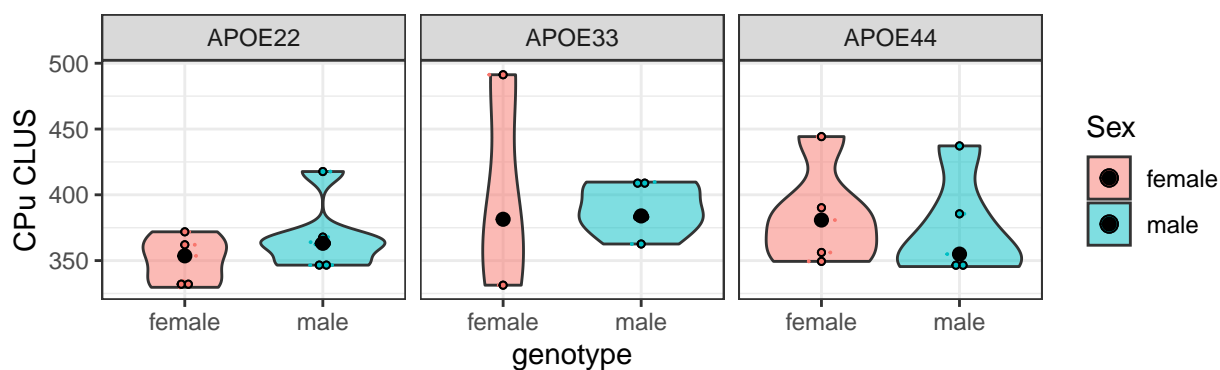
Hc and CPu, fi, fx, ic

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
```

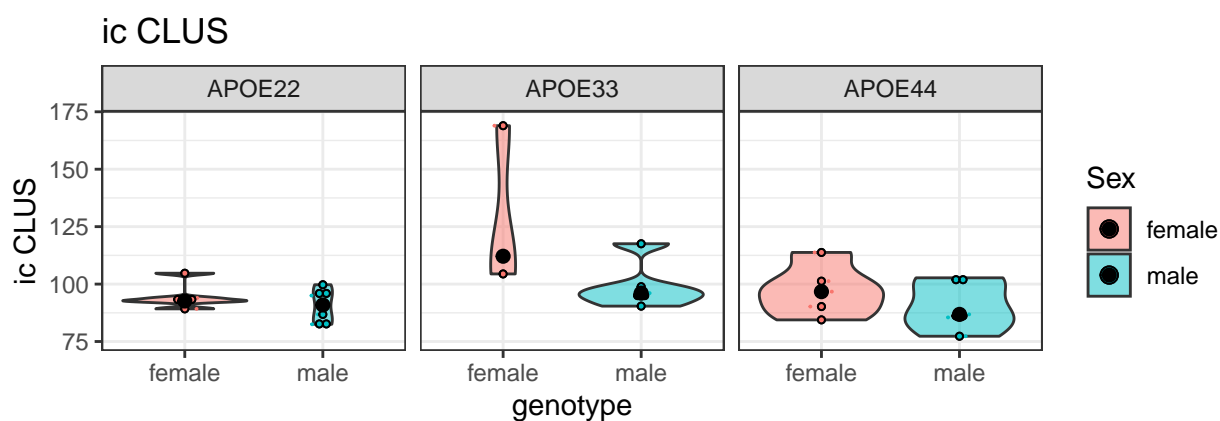
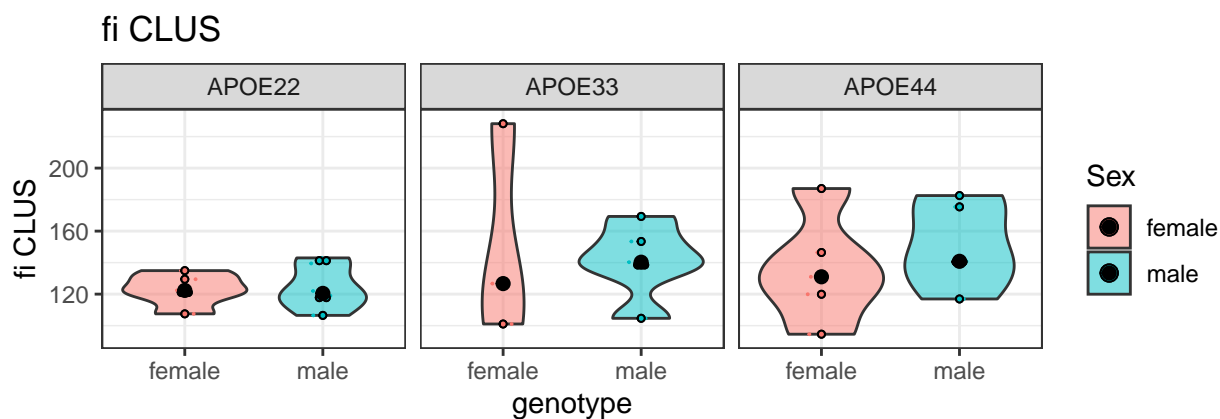
Hc CLUS



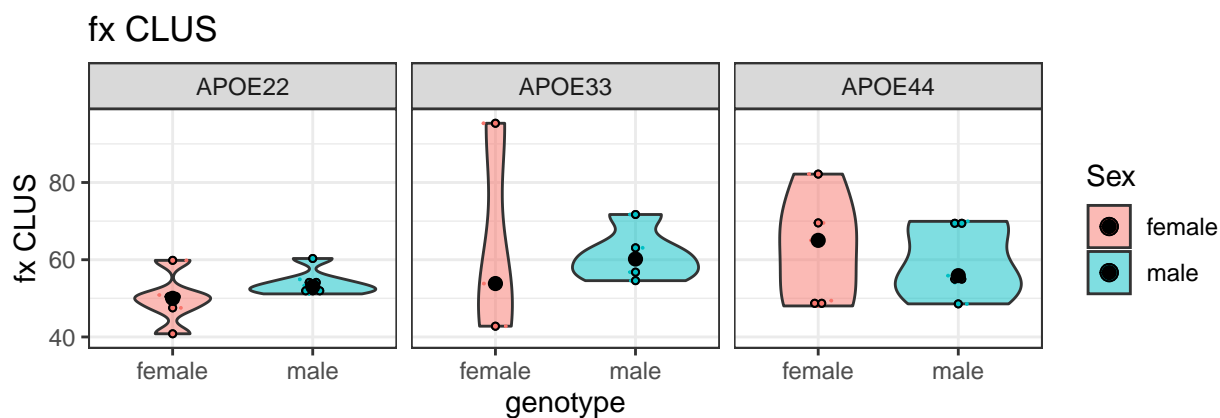
CPu CLUS



```
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
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```

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
```



```
## [1] "Hc CLUS"
##
## Call:
## lm(formula = Hc ~ Genotype * Sex, data = geno_combined_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -86.377 -24.544  -3.834  21.724 121.923
##
## Coefficients:
```

```

##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      442.45      22.38  19.769 6.23e-16 ***
## GenotypeAPOE33      86.11      36.55   2.356  0.0274 *
## GenotypeAPOE44      46.66      31.65   1.474  0.1540
## Sexmale           31.52      30.30   1.040  0.3091
## GenotypeAPOE33:Sexmale -33.30      47.48  -0.701  0.4901
## GenotypeAPOE44:Sexmale -17.24      43.82  -0.394  0.6976
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 50.05 on 23 degrees of freedom
## Multiple R-squared:  0.3022, Adjusted R-squared:  0.1505
## F-statistic: 1.992 on 5 and 23 DF,  p-value: 0.1179
##
## Call:
## lm(formula = Hc ~ Genotype, data = combo_f_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -86.377 -34.420  -0.572  13.380 121.923
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      442.45      27.31  16.199 1.67e-08 ***
## GenotypeAPOE33      86.11      44.60   1.931  0.0823 .
## GenotypeAPOE44      46.66      38.63   1.208  0.2549
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 61.08 on 10 degrees of freedom
## Multiple R-squared:  0.2805, Adjusted R-squared:  0.1365
## F-statistic: 1.949 on 2 and 10 DF,  p-value: 0.1929
##
## Call:
## lm(formula = Hc ~ Genotype, data = combo_m_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -69.586 -23.788  -5.164  23.035  72.752
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      473.97      16.13  29.378 2.84e-13 ***
## GenotypeAPOE33      52.81      23.93   2.207  0.0459 *
## GenotypeAPOE44      29.41      23.93   1.229  0.2408
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 39.52 on 13 degrees of freedom
## Multiple R-squared:  0.2752, Adjusted R-squared:  0.1636
## F-statistic: 2.468 on 2 and 13 DF,  p-value: 0.1235
## Analysis of Variance Table

```

```

##
## Response: Hc
##           Df Sum Sq Mean Sq F value Pr(>F)
## Genotype    2  21720  10860.2   4.3361 0.02524 *
## Sex          1   1971   1971.3   0.7871 0.38416
## Genotype:Sex  2   1254    627.1   0.2504 0.78060
## Residuals   23   57605   2504.6
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: Hc
##           Df Sum Sq Mean Sq F value Pr(>F)
## Genotype    2  14539   7269.7   1.9488 0.1929
## Residuals  10   37303   3730.3

## Analysis of Variance Table
##
## Response: Hc
##           Df Sum Sq Mean Sq F value Pr(>F)
## Genotype    2   7707.2   3853.6   2.4675 0.1235
## Residuals  13  20302.4   1561.7

## [1] "CPu CLUS"

##
## Call:
## lm(formula = CPu ~ Genotype * Sex, data = geno_combined_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -70.017 -20.873  -5.233   11.696   89.933
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      350.33      16.50   21.229  <2e-16 ***
## GenotypeAPOE33      50.99      26.95    1.892  0.0711 .
## GenotypeAPOE44      33.83      23.34    1.449  0.1607
## Sexmale           17.17      22.34    0.768  0.4501
## GenotypeAPOE33:Sexmale -29.15      35.01   -0.833  0.4135
## GenotypeAPOE44:Sexmale -27.20      32.31   -0.842  0.4086
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 36.9 on 23 degrees of freedom
## Multiple R-squared:  0.1803, Adjusted R-squared:  0.002162
## F-statistic: 1.012 on 5 and 23 DF,  p-value: 0.4332

##
## Call:
## lm(formula = CPu ~ Genotype, data = combo_f_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -70.02 -20.64  -3.34   11.70   89.93

```

```

##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)    350.33     20.16  17.377 8.44e-09 ***
## GenotypeAPOE33    50.99     32.92   1.549   0.152
## GenotypeAPOE44    33.83     28.51   1.186   0.263
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 45.08 on 10 degrees of freedom
## Multiple R-squared:  0.2142, Adjusted R-squared:  0.05707
## F-statistic: 1.363 on 2 and 10 DF,  p-value: 0.2996
##
## Call:
## lm(formula = CPu ~ Genotype, data = combo_m_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -28.662 -20.893  -5.313  13.261  63.048
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## (Intercept)    367.503     11.872  30.955 1.45e-13 ***
## GenotypeAPOE33    21.839     17.609   1.240   0.237
## GenotypeAPOE44     6.629     17.609   0.376   0.713
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 29.08 on 13 degrees of freedom
## Multiple R-squared:  0.1085, Adjusted R-squared: -0.02865
## F-statistic: 0.7911 on 2 and 13 DF,  p-value: 0.474
## Analysis of Variance Table
##
## Response: CPu
##           Df Sum Sq Mean Sq F value Pr(>F)
## Genotype    2  5566.0  2783.01   2.0439 0.1524
## Sex          1     0.1    0.07  0.0001 0.9943
## Genotype:Sex  2  1324.6   662.30   0.4864 0.6210
## Residuals   23 31317.3  1361.62
##
## Analysis of Variance Table
##
## Response: CPu
##           Df Sum Sq Mean Sq F value Pr(>F)
## Genotype    2  5540.7  2770.3   1.3631 0.2996
## Residuals  10 20323.4   2032.3
##
## Analysis of Variance Table
##
## Response: CPu
##           Df Sum Sq Mean Sq F value Pr(>F)
## Genotype    2  1338.1   669.05   0.7911 0.474
## Residuals   13 10993.9   845.69

```

```
## [1] "fi CLUS"

##
## Call:
## lm(formula = fi ~ Genotype * Sex, data = geno_combined_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -50.937 -15.302  -3.082  12.532  76.223
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      122.792      13.335   9.208 3.54e-09 ***
## GenotypeAPOE33       29.185      21.776   1.340   0.193
## GenotypeAPOE44       13.000      18.858   0.689   0.497
## Sexmale           1.635      18.055   0.091   0.929
## GenotypeAPOE33:Sexmale -12.713      28.287  -0.449   0.657
## GenotypeAPOE44:Sexmale  13.757      26.108   0.527   0.603
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 29.82 on 23 degrees of freedom
## Multiple R-squared:  0.1536, Adjusted R-squared:  -0.03045
## F-statistic: 0.8345 on 5 and 23 DF,  p-value: 0.5387
##
## Call:
## lm(formula = fi ~ Genotype, data = combo_f_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -50.937 -15.872  -3.082  10.638  76.223
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      122.79      16.85   7.288 2.64e-05 ***
## GenotypeAPOE33       29.18      27.51   1.061   0.314
## GenotypeAPOE44       13.00      23.83   0.546   0.597
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 37.67 on 10 degrees of freedom
## Multiple R-squared:  0.1019, Adjusted R-squared:  -0.07773
## F-statistic: 0.5672 on 2 and 10 DF,  p-value: 0.5843
##
## Call:
## lm(formula = fi ~ Genotype, data = combo_m_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -36.238 -10.512  -3.267  15.938  31.386
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```

```

## (Intercept)      124.427      8.956  13.892 3.54e-09 ***
## GenotypeAPOE33    16.471      13.285   1.240  0.2369
## GenotypeAPOE44    26.757      13.285   2.014  0.0652 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 21.94 on 13 degrees of freedom
## Multiple R-squared:  0.2437, Adjusted R-squared:  0.1274
## F-statistic: 2.095 on 2 and 13 DF,  p-value: 0.1627

## Analysis of Variance Table
##
## Response: fi
##           Df Sum Sq Mean Sq F value Pr(>F)
## Genotype    2  2880.1  1440.06   1.6197 0.2197
## Sex          1    69.2    69.17   0.0778 0.7828
## Genotype:Sex  2   760.5   380.25   0.4277 0.6571
## Residuals   23 20448.9   889.08

## Analysis of Variance Table
##
## Response: fi
##           Df Sum Sq Mean Sq F value Pr(>F)
## Genotype    2   1610   805.01   0.5672 0.5843
## Residuals   10 14192 1419.18

## Analysis of Variance Table
##
## Response: fi
##           Df Sum Sq Mean Sq F value Pr(>F)
## Genotype    2 2016.4  1008.21   2.0947 0.1627
## Residuals   13 6257.1   481.31

## [1] "ic CLUS"

##
## Call:
## lm(formula = ic ~ Genotype * Sex, data = geno_combined_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -24.073  -7.060  -2.001   6.264  40.447
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      94.638      6.141  15.412 1.3e-13 ***
## GenotypeAPOE33     33.855     10.028   3.376  0.0026 **
## GenotypeAPOE44      2.640      8.684   0.304  0.7639
## Sexmale           -4.018      8.314  -0.483  0.6334
## GenotypeAPOE33:Sexmale -25.115     13.026  -1.928  0.0663 .
## GenotypeAPOE44:Sexmale  -2.570     12.023  -0.214  0.8326
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 13.73 on 23 degrees of freedom
## Multiple R-squared:  0.4432, Adjusted R-squared:  0.3222

```

```

## F-statistic: 3.661 on 5 and 23 DF,  p-value: 0.01391
##
## Call:
## lm(formula = ic ~ Genotype, data = combo_f_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -24.073  -7.060  -1.994   3.992  40.447
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    94.638     7.908   11.968   3e-07 ***
## GenotypeAPOE33  33.855     12.913    2.622  0.0255 *
## GenotypeAPOE44   2.640     11.183    0.236  0.8181
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 17.68 on 10 degrees of freedom
## Multiple R-squared:  0.4404, Adjusted R-squared:  0.3284
## F-statistic: 3.934 on 2 and 10 DF,  p-value: 0.0549
##
## Call:
## lm(formula = ic ~ Genotype, data = combo_m_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -13.381  -6.051  -3.556   6.972  18.200
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  90.61975     3.93808   23.011 6.43e-12 ***
## GenotypeAPOE33  8.73985     5.84111    1.496   0.158
## GenotypeAPOE44  0.06985     5.84111    0.012   0.991
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.646 on 13 degrees of freedom
## Multiple R-squared:  0.1773, Adjusted R-squared:  0.05072
## F-statistic: 1.401 on 2 and 13 DF,  p-value: 0.2812
## Analysis of Variance Table
##
## Response: ic
##              Df Sum Sq Mean Sq F value  Pr(>F)
## Genotype      2 1707.6   853.79   4.5285 0.02197 *
## Sex           1   948.0   948.05   5.0285 0.03487 *
## Genotype:Sex  2   796.0   397.98   2.1109 0.14399
## Residuals    23 4336.3   188.54
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Analysis of Variance Table
##
## Response: ic

```

```

##           Df Sum Sq Mean Sq F value Pr(>F)
## Genotype   2 2460.2 1230.10  3.9342 0.0549 .
## Residuals 10 3126.7  312.67
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: ic
##           Df Sum Sq Mean Sq F value Pr(>F)
## Genotype   2  260.68 130.341  1.4008 0.2812
## Residuals 13 1209.66  93.051

## [1] "fx CLUS"

##
## Call:
## lm(formula = fx ~ Genotype * Sex, data = geno_combined_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -21.200  -5.411  -1.081   6.294  31.356
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      49.814      5.227   9.530 1.88e-09 ***
## GenotypeAPOE33     14.173      8.535   1.661  0.1104
## GenotypeAPOE44     13.019      7.392   1.761  0.0915 .
## Sexmale           4.212      7.077   0.595  0.5575
## GenotypeAPOE33:Sexmale -6.930     11.088  -0.625  0.5381
## GenotypeAPOE44:Sexmale -7.567     10.233  -0.739  0.4671
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 11.69 on 23 degrees of freedom
## Multiple R-squared:  0.1861, Adjusted R-squared:  0.009187
## F-statistic: 1.052 on 5 and 23 DF,  p-value: 0.4119

##
## Call:
## lm(formula = fx ~ Genotype, data = combo_f_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -21.2000 -10.1560   0.1914   6.7048  31.3560
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      49.814      7.137   6.980 3.81e-05 ***
## GenotypeAPOE33     14.173     11.655   1.216  0.252
## GenotypeAPOE44     13.019     10.093   1.290  0.226
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 15.96 on 10 degrees of freedom
## Multiple R-squared:  0.1801, Adjusted R-squared:  0.01606

```



```
## F-statistic: 1.098 on 2 and 10 DF, p-value: 0.3706
##
## Call:
## lm(formula = fx ~ Genotype, data = combo_m_CLUS)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -10.912  -3.820  -1.176   2.932  10.457
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    54.026     2.762   19.563 5.02e-11 ***
## GenotypeAPOE33    7.243     4.096    1.768   0.100
## GenotypeAPOE44    5.452     4.096    1.331   0.206
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.764 on 13 degrees of freedom
## Multiple R-squared:  0.211, Adjusted R-squared:  0.08966
## F-statistic: 1.739 on 2 and 13 DF, p-value: 0.2142
## Analysis of Variance Table
##
## Response: fx
##           Df Sum Sq Mean Sq F value Pr(>F)
## Genotype    2  628.07  314.035   2.2990 0.1230
## Sex          1    0.56   0.560   0.0041 0.9495
## Genotype:Sex  2   89.81  44.907   0.3288 0.7231
## Residuals   23 3141.70 136.596
##
## Analysis of Variance Table
##
## Response: fx
##           Df Sum Sq Mean Sq F value Pr(>F)
## Genotype    2  559.26  279.63   1.0979 0.3706
## Residuals  10 2546.85  254.69
##
## Analysis of Variance Table
##
## Response: fx
##           Df Sum Sq Mean Sq F value Pr(>F)
## Genotype    2 159.11  79.557   1.7386 0.2142
## Residuals   13  594.85  45.758
```

Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.