SimpleViolins

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Contents

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
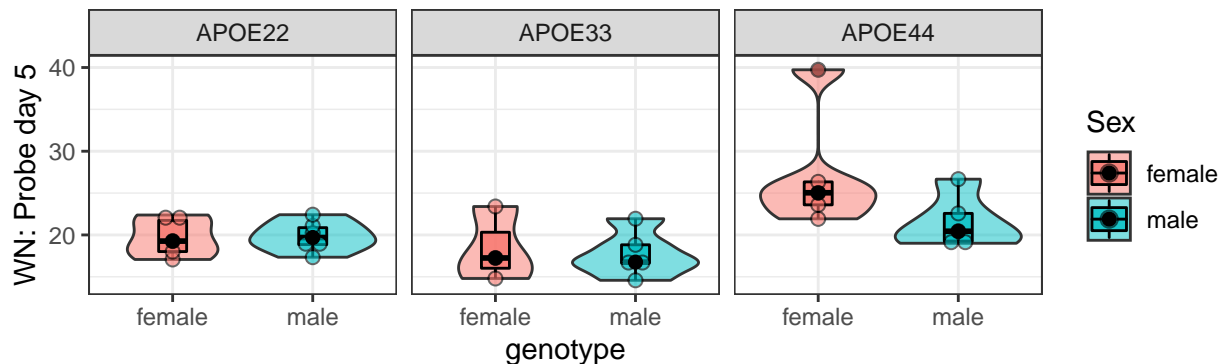
##Setup

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`.
```



```
## [1] "Probe day 5"
```

```
## [1] "probe day 5"
```

```
## [1] "omnibus testing"

##  model term    df1 df2 F.ratio p.value
##  Genotype       2  23   6.511  0.0057
##  Sex            1  23   2.021  0.1686
##  Genotype:Sex   2  23   1.643  0.2152

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  23   6.684  0.0051
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  23   1.211  0.3161

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  23   0.003  0.9549
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
##  Sex          1  23   0.066  0.8001
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
##  Sex          1  23   5.389  0.0295

## [1] "anova"

## 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

##  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"
```
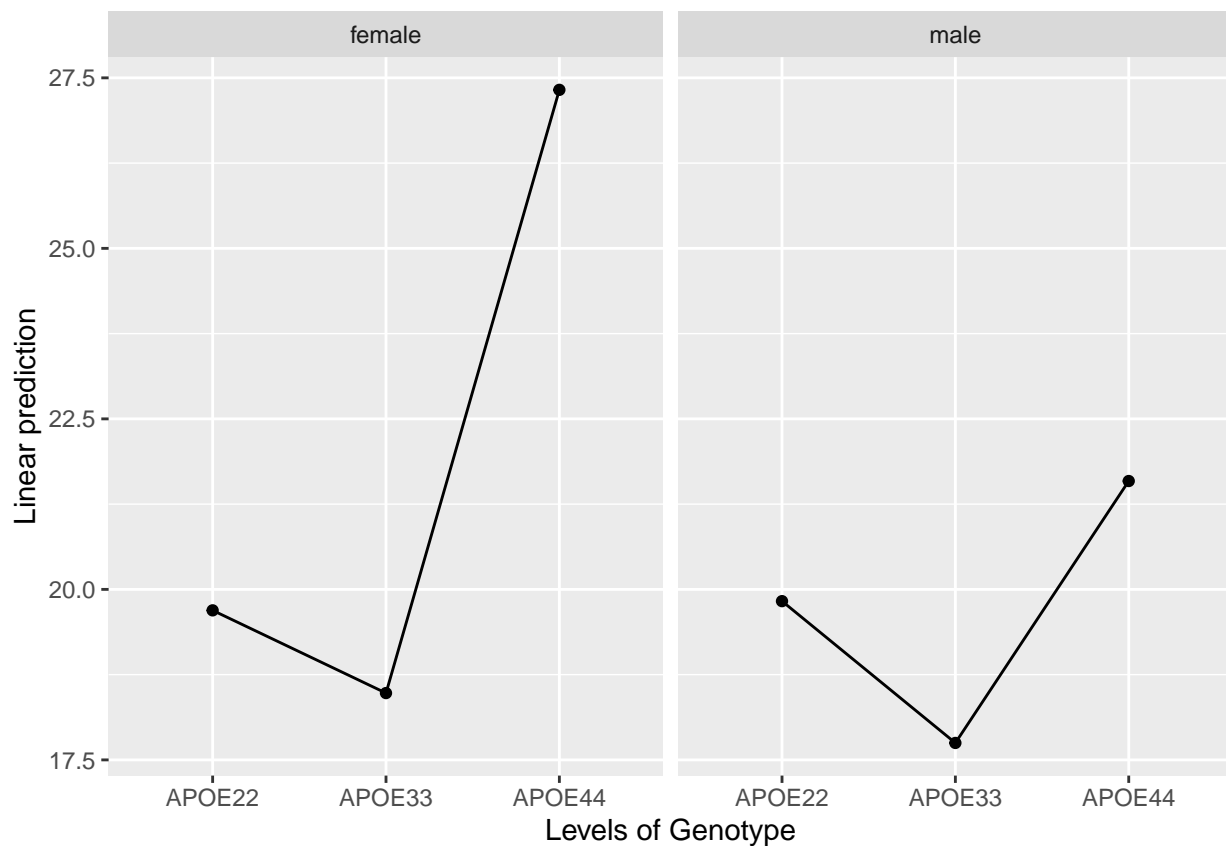
```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Fit: lm(formula = Probe_d5 ~ Genotype * Sex, data = geno_combined_FA)
##
## Linear Hypotheses:
##                                Estimate Std. Error t value Pr(>|t|)
## APOE22 female - APOE33 female == 0   1.2129     2.8527   0.425  0.99797
## APOE22 female - APOE44 female == 0  -7.6319     2.4705  -3.089  0.05101 .
## APOE22 female - APOE22 male == 0    -0.1352     2.3654  -0.057  1.00000
## APOE22 female - APOE33 male == 0     1.9439     2.4705   0.787  0.96673
## APOE22 female - APOE44 male == 0    -1.8965     2.4705  -0.768  0.97005
## APOE33 female - APOE44 female == 0  -8.8448     2.8527  -3.100  0.04994 *
## APOE33 female - APOE22 male == 0    -1.3481     2.7621  -0.488  0.99610
## APOE33 female - APOE33 male == 0     0.7309     2.8527   0.256  0.99983
## APOE33 female - APOE44 male == 0    -3.1094     2.8527  -1.090  0.87951
## APOE44 female - APOE22 male == 0     7.4967     2.3654   3.169  0.04296 *
## APOE44 female - APOE33 male == 0     9.5757     2.4705   3.876  0.00873 **
## APOE44 female - APOE44 male == 0     5.7354     2.4705   2.322  0.22447
## APOE22 male - APOE33 male == 0       2.0790     2.3654   0.879  0.94736
## APOE22 male - APOE44 male == 0      -1.7613     2.3654  -0.745  0.97371
## APOE33 male - APOE44 male == 0      -3.8403     2.4705  -1.554  0.63285
## ---
## 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   0.0138 *
## APOE33 - APOE44 == 0    -8.845      2.853  -3.100   0.0133 *
## ---
## 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)
```

```
## $`Genotype = APOE22`
##
##   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|)
## female - male == 0  -0.1352     2.3654  -0.057    0.955
## (Adjusted p values reported -- single-step method)
##
##
## $`Genotype = APOE33`
##
##   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|)
## female - male == 0   0.7309     2.8527   0.256      0.8
## (Adjusted p values reported -- single-step method)
##
##
## $`Genotype = APOE44`
##
##   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|)
## female - male == 0    5.735      2.471   2.322   0.0295 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)

## Genotype = APOE22:
##  contrast       estimate   SE df t.ratio p.value
##  female - male    -0.135 2.37 23  -0.057  0.9549
##
## Genotype = APOE33:
##  contrast       estimate   SE df t.ratio p.value
##  female - male     0.731 2.85 23   0.256  0.8001
##
## Genotype = APOE44:
##  contrast       estimate   SE df t.ratio p.value
##  female - male     5.735 2.47 23   2.322  0.0295

## 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
```