

SimpleViolins

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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

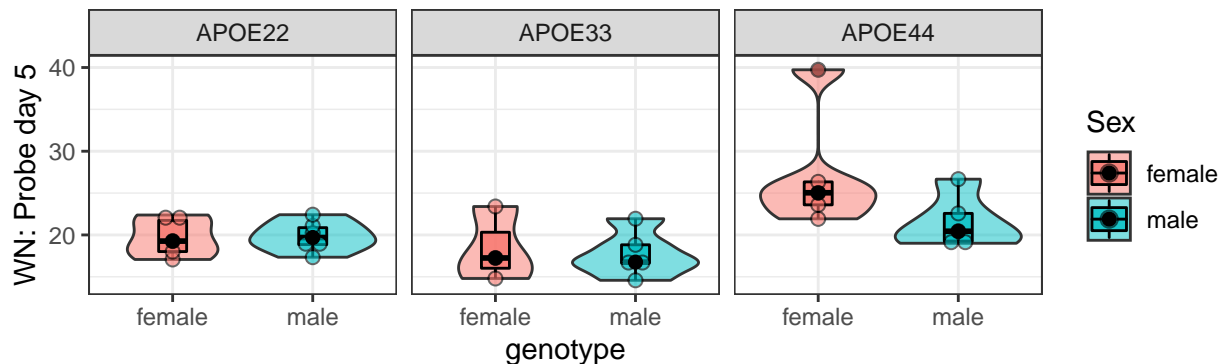
We read the data and normalize volumes to the whole brain.

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`.

Winding Number Probe Day 5



[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"

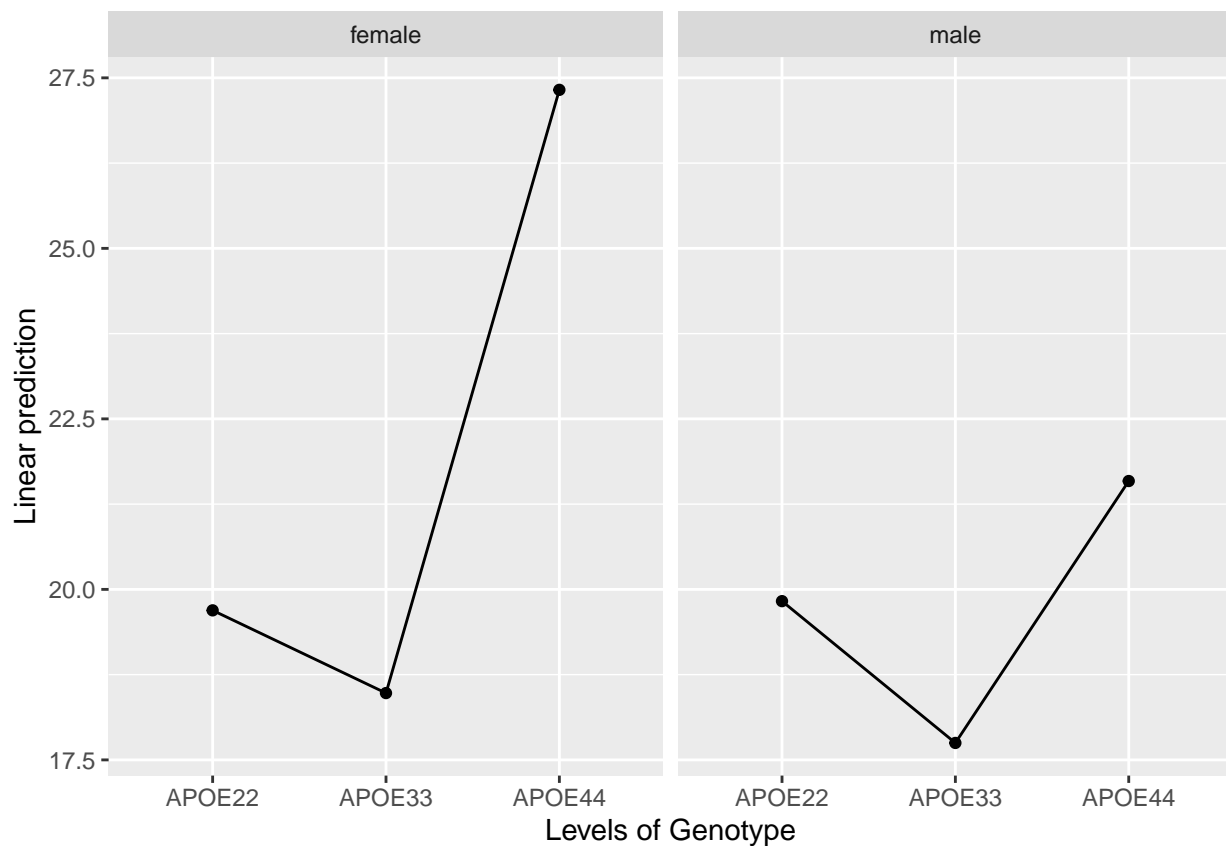
## Analysis of Variance Table
##
## Response: Probe_d5
##          Df Sum Sq Mean Sq F value    Pr(>F)
## Genotype   2 206.87  103.434   6.7786 0.004849 **
## Sex         1   33.13   33.134   2.1715 0.154148
## Genotype:Sex 2   50.15   25.077   1.6434 0.215215
## Residuals  23 350.95   15.259
## ---
## 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
##

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```
## 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 0.05112 .
## 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 0.97004
## APOE33 female - APOE44 female == 0 -8.8448 2.8527 -3.100 0.04985 *
## 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 0.87948
## APOE44 female - APOE22 male == 0 7.4967 2.3654 3.169 0.04301 *
## APOE44 female - APOE33 male == 0 9.5757 2.4705 3.876 0.00872 **
## APOE44 female - APOE44 male == 0 5.7354 2.4705 2.322 0.22431
## APOE22 male - APOE33 male == 0 2.0790 2.3654 0.879 0.94736
## APOE22 male - APOE44 male == 0 -1.7613 2.3654 -0.745 0.97369
## APOE33 male - APOE44 male == 0 -3.8403 2.4705 -1.554 0.63284
## ---
## 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 0.0137 *
## 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)

```

```

## $`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
```

