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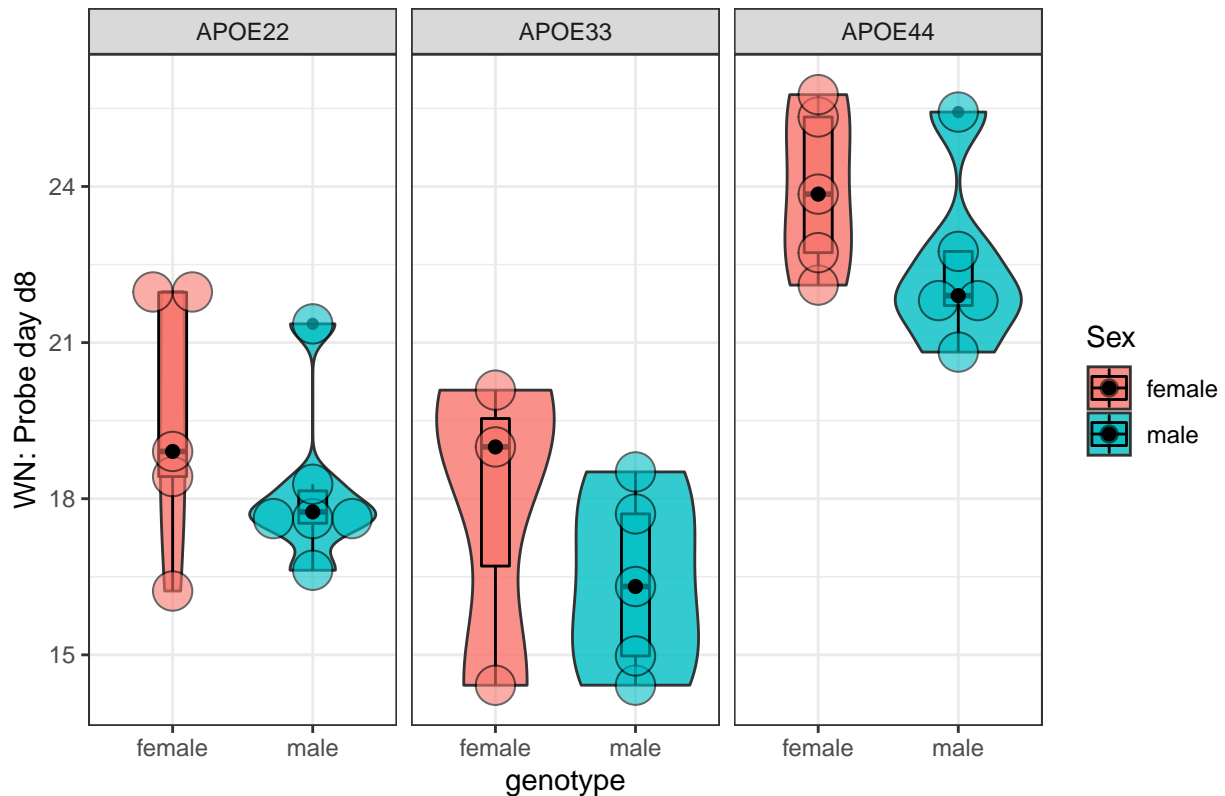
We read the data and normalize volumes to the whole brain.

Plots for Winding Number

We embed plots for day d8 probe trials:

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

Winding Number Probe Day d8


```
## [1] "Probe day d8"

## [1] "probe day d8"

## [1] "omnibus testing"

##  model term    df1 df2 F.ratio p.value
##  Genotype        2  23  23.066  <.0001
##  Sex             1  23   3.406  0.0779
##  Genotype:Sex    2  23   0.004  0.9957

## Sex = female:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  23  10.738  0.0005
##
## Sex = male:
##  model term df1 df2 F.ratio p.value
##  Genotype     2  23  12.682  0.0002

## Genotype = APOE22:
##  model term df1 df2 F.ratio p.value
##  Sex          1  23   1.165  0.2916
##
## Genotype = APOE33:
##  model term df1 df2 F.ratio p.value
##  Sex          1  23   0.994  0.3290
##
## Genotype = APOE44:
##  model term df1 df2 F.ratio p.value
```

```
## Sex           1  23   1.305  0.2651
## [1] "anova"
## 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

##  contrast               estimate    SE df t.ratio p.value
##  APOE22 female effect    -0.233 0.817 23  -0.285  0.7784
##  APOE33 female effect    -1.901 1.009 23  -1.884  0.0867
##  APOE44 female effect     4.223 0.817 23   5.167  0.0002
##  APOE22 male effect      -1.531 0.762 23  -2.009  0.0846
##  APOE33 male effect      -3.348 0.817 23  -4.095  0.0013
##  APOE44 male effect       2.789 0.817 23   3.412  0.0048
##
## P value adjustment: fdr method for 6 tests

## $`simple contrasts for Genotype`
## Sex = female:
##  contrast      estimate    SE df t.ratio p.value
##  APOE22 effect   -0.929 0.764 23  -1.216  0.2364
##  APOE33 effect   -2.598 0.871 23  -2.981  0.0100
##  APOE44 effect    3.527 0.764 23   4.615  0.0004
##
## Sex = male:
##  contrast      estimate    SE df t.ratio p.value
##  APOE22 effect   -0.834 0.684 23  -1.220  0.2347
##  APOE33 effect   -2.651 0.715 23  -3.708  0.0017
##  APOE44 effect    3.485 0.715 23   4.875  0.0002
##
## P value adjustment: fdr method for 3 tests
##
## $`simple contrasts for Sex`
## Genotype = APOE22:
##  contrast      estimate    SE df t.ratio p.value
##  female effect    0.649 0.601 23   1.079  0.2916
##  male effect     -0.649 0.601 23  -1.079  0.2916
##
## Genotype = APOE33:
##  contrast      estimate    SE df t.ratio p.value
##  female effect    0.723 0.725 23   0.997  0.3290
##  male effect     -0.723 0.725 23  -0.997  0.3290
##
## Genotype = APOE44:
##  contrast      estimate    SE df t.ratio p.value
##  female effect    0.717 0.628 23   1.142  0.2651
##  male effect     -0.717 0.628 23  -1.142  0.2651
##
```

P value adjustment: fdr method for 2 tests

[1] "Probe Day d8 Abs Winding Number"
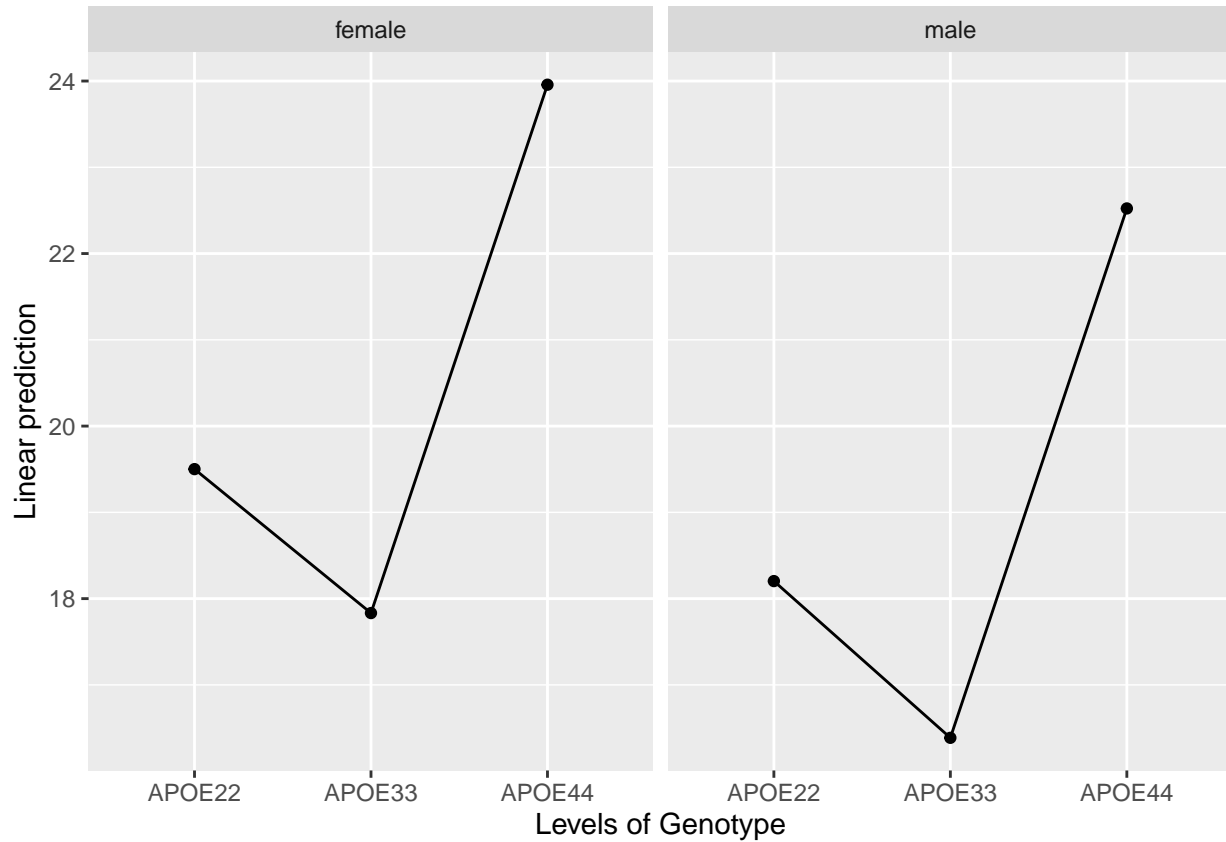

```
##
##    Simultaneous Tests for General Linear Hypotheses
##
## Fit: lm(formula = Probe_d8 ~ Genotype * Sex, data = geno_combined_FA)
##
## Linear Hypotheses:
##                               Estimate Std. Error t value Pr(>|t|)
## APOE22 female - APOE33 female == 0   1.6686     1.4502   1.151   0.8539
## APOE22 female - APOE44 female == 0  -4.4562     1.2559  -3.548   0.0186 *
## APOE22 female - APOE22 male == 0     1.2979     1.2024   1.079   0.8837
## APOE22 female - APOE33 male == 0     3.1148     1.2559   2.480   0.1700
## APOE22 female - APOE44 male == 0    -3.0217     1.2559  -2.406   0.1943
## APOE33 female - APOE44 female == 0  -6.1248     1.4502  -4.223   0.0038 **
## APOE33 female - APOE22 male == 0    -0.3707     1.4041  -0.264   0.9998
## APOE33 female - APOE33 male == 0     1.4461     1.4502   0.997   0.9135
## APOE33 female - APOE44 male == 0    -4.6904     1.4502  -3.234   0.0374 *
## 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   0.8577
## APOE22 male - APOE33 male == 0       1.8169     1.2024   1.511   0.6593
## APOE22 male - APOE44 male == 0      -4.3196     1.2024  -3.592   0.0168 *
## 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)

## $`Sex = female`
##
##   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 - APOE33 == 0    1.669      1.450   1.151  0.49269
## APOE22 - APOE44 == 0   -4.456      1.256  -3.548  0.00464 **
## APOE33 - APOE44 == 0   -6.125      1.450  -4.223  < 0.001 ***
## ---
## 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_d8 ~ Genotype * Sex, data = geno_combined_FA)
##
## Linear Hypotheses:
##                     Estimate Std. Error t value Pr(>|t|)
## APOE22 - APOE33 == 0    1.817      1.202   1.511  0.30426
## APOE22 - APOE44 == 0   -4.320      1.202  -3.592  0.00434 **
## APOE33 - APOE44 == 0   -6.137      1.256  -4.886  < 0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
## $`Genotype = APOE22`
##
##   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|)
## female - male == 0    1.298      1.202   1.079    0.292
## (Adjusted p values reported -- single-step method)
##
##
## $`Genotype = APOE33`
##
##   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|)
## female - male == 0    1.446      1.450   0.997    0.329
## (Adjusted p values reported -- single-step method)
```

```
##
##
## $`Genotype = APOE44`
##
##   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|)
## female - male == 0   1.434      1.256   1.142    0.265
## (Adjusted p values reported -- single-step method)

## Genotype = APOE22:
##  contrast       estimate   SE df t.ratio p.value
##  female - male      1.30 1.20 23   1.079  0.2916
##
## Genotype = APOE33:
##  contrast       estimate   SE df t.ratio p.value
##  female - male      1.45 1.45 23   0.997  0.3290
##
## Genotype = APOE44:
##  contrast       estimate   SE df t.ratio p.value
##  female - male      1.43 1.26 23   1.142  0.2651

## 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
```