

# SimpleViolins

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10/29/2021

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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:

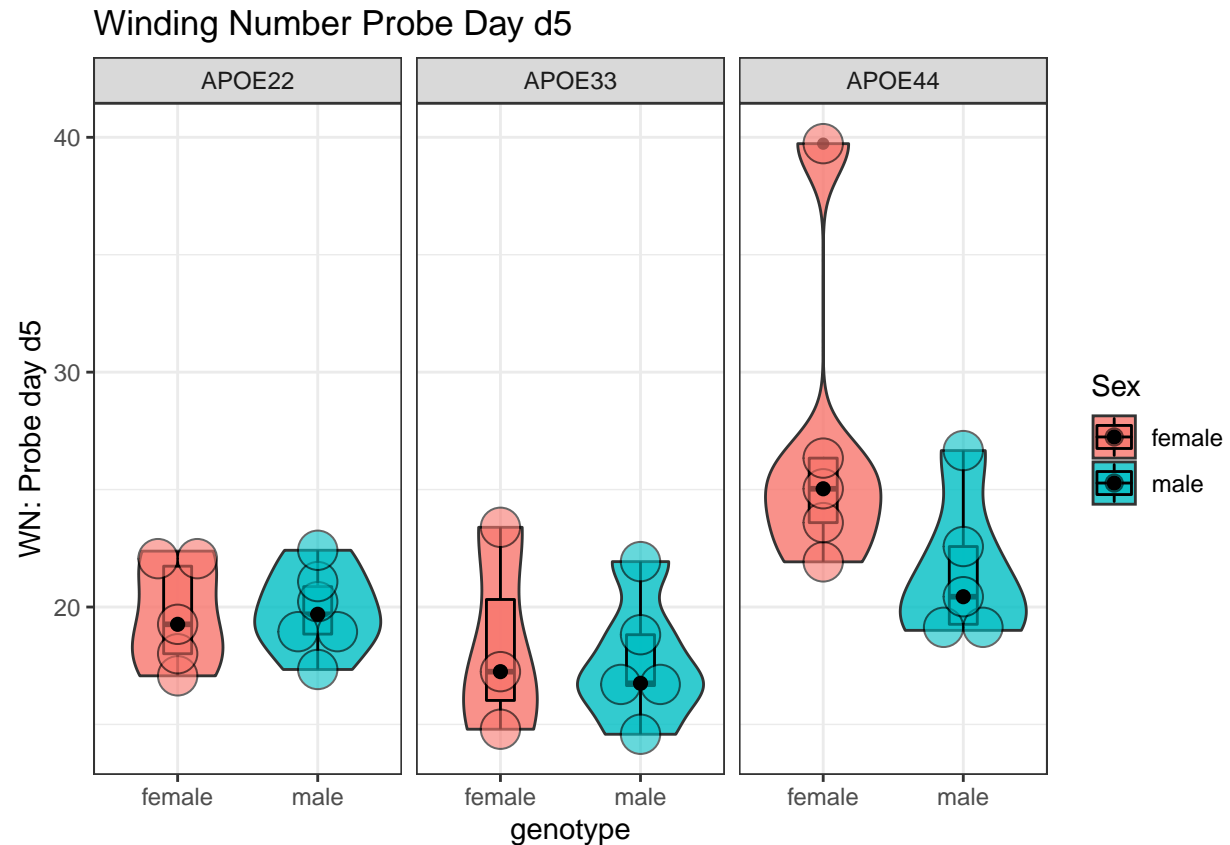
Morris Water Maze - testing spatial navigation memory Segmentation: regional volumes Microstructural properties: FA Tractography Based Connectivity: Degree, and Clustering Coefficient

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

## Plots for Winding Number

We embed plots for day d5 probe trials:

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



```
## [1] "Probe day d5"
## [1] "probe day d5"
## [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

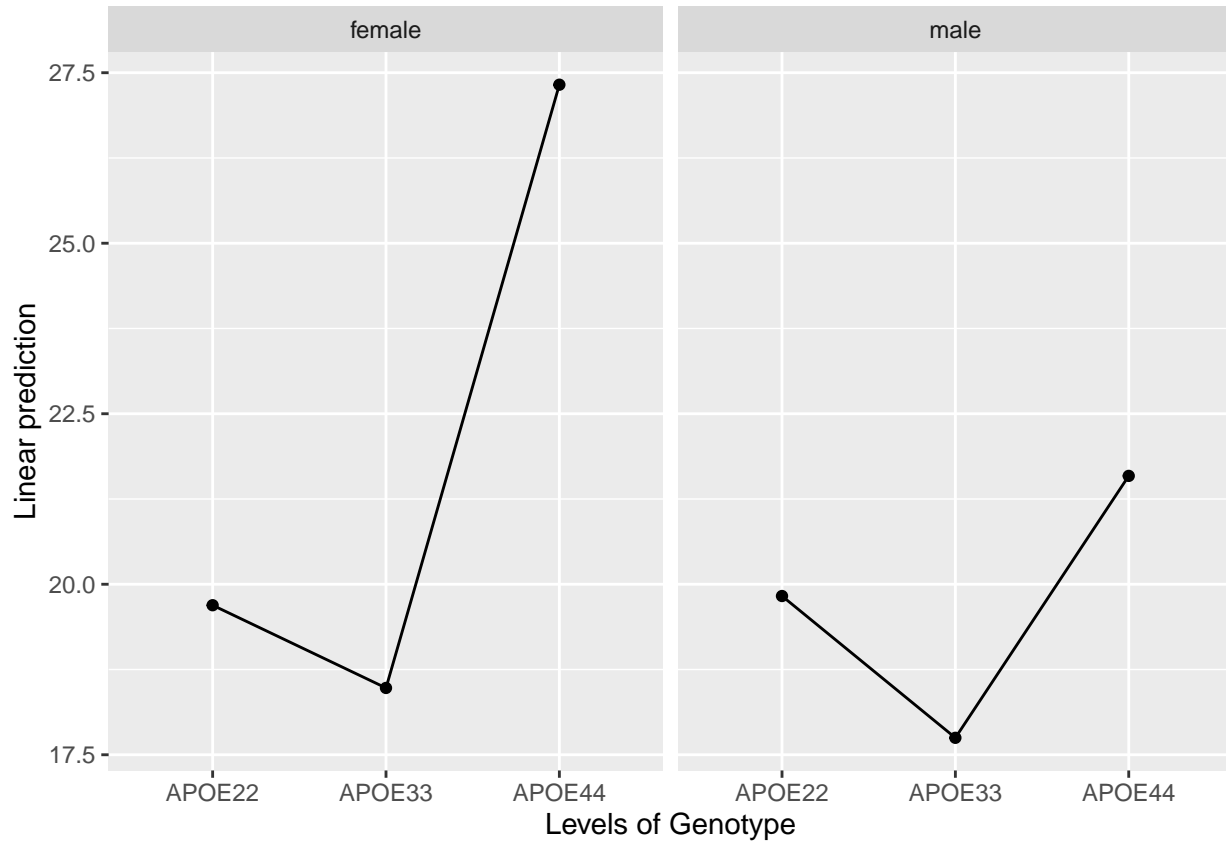
## contrast          estimate    SE df t.ratio p.value
## APOE22 female effect  -1.084 1.61 23  -0.674 0.6184
## APOE33 female effect  -2.297 1.99 23  -1.157 0.5182
## APOE44 female effect   6.547 1.61 23   4.072 0.0028
## APOE22 male effect    -0.949 1.50 23  -0.633 0.6184
## APOE33 male effect    -3.028 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 d5 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  0.05099 .
## 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  0.04990 *
## 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  0.87946
## APOE44 female - APOE22 male == 0   7.4967    2.3654   3.169  0.04308 *
## APOE44 female - APOE33 male == 0   9.5757    2.4705   3.876  0.00877 **
## APOE44 female - APOE44 male == 0   5.7354    2.4705   2.322  0.22444
## APOE22 male - APOE33 male == 0    2.0790    2.3654   0.879  0.94737
## APOE22 male - APOE44 male == 0   -1.7613    2.3654  -0.745  0.97369
## APOE33 male - APOE44 male == 0   -3.8403    2.4705  -1.554  0.63271
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```

## (Adjusted p values reported -- single-step method)
## `$Sex = female`
##
## Simultaneous Tests for General Linear Hypotheses
##
## Fit: lm(formula = Probe_d5 ~ Genotype * Sex, data = geno_combined_FA)
##
## Linear Hypotheses:
##              Estimate Std. Error t value Pr(>|t|)
## APOE22 - APOE33 == 0    1.213      2.853   0.425  0.9053
## APOE22 - APOE44 == 0   -7.632      2.471  -3.089  0.0137 *
## APOE33 - APOE44 == 0   -8.845      2.853  -3.100  0.0134 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
##
##
## `$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

```

