Introduction to Statistics in R Presented by:

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Introduction to Statistics in R

Day 3 - ANOVA

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What is ANOVA?

Recap on our progress:

Enter ANOVA

Enter ANOVA

Enter ANOVA

$$H_0 : \mu_1 = \mu_2 = \cdots = \mu_k$$

At least one group is different

What is our test then?

K t

$$k = \frac{\text{Measure of Between-Group Variability}}{\text{Measure of Within-Group Variability}}$$

The math

$$SS_B = \sum_{i=1}^{k} n_i(\bar(y)_i - \bar(y))^2$$

$$SS_W = \sum_{i=1}^{k}\sum_{j=1}^{n_i}(y_{ij} - \bar(y)_i)^2$$

$$SS = SS_B + SS_W$$

i k j n_i

ANOVA Variances

ANOVA Table

	DF	SUM SQ.	MEAN SQ	F VALUE	PR(>F)
Between (treatment)	$k-1$	SS_B	$MS_B = \frac{SS_B}{k-1}$	$\frac{MS_{trt}}{MS_{err}}$	p-value
Within (error)	$N-k$	SS_W	$MS_W = \frac{SS_W}{N-k}$		
Total	$N-1$	SS_T			

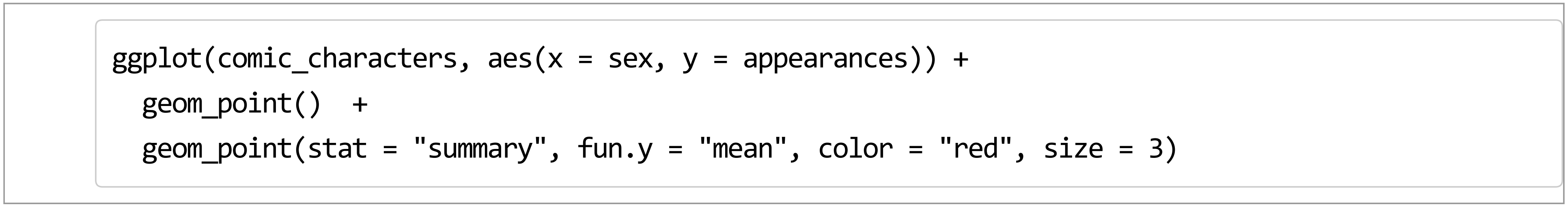
Calculating ANOVA

The Data for Class

`fivethirtyeight`

```
library(fivethirtyeight)
?comic_characters
```

Difference in Appearances by Gender



```
ggplot(comic_characters, aes(x = sex, y = appearances)) +
  geom_point()  +
  geom_point(stat = "summary", fun.y = "mean", color = "red", size = 3)
```

Difference in Appearances by Gender

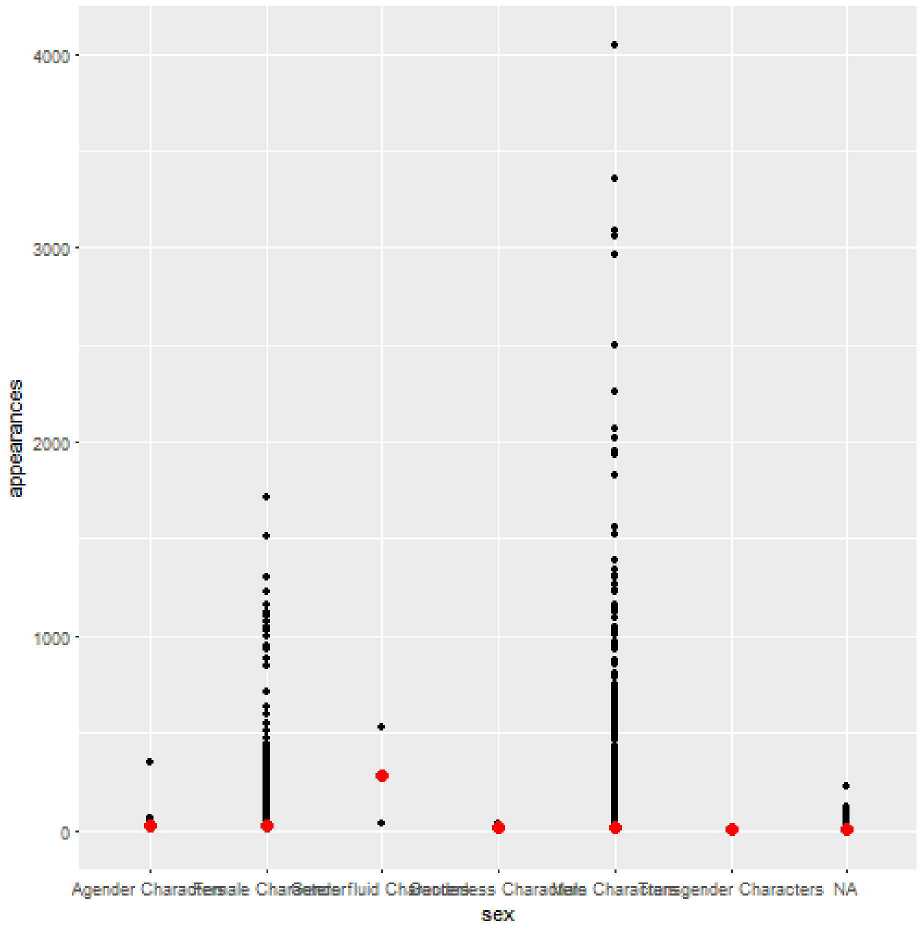
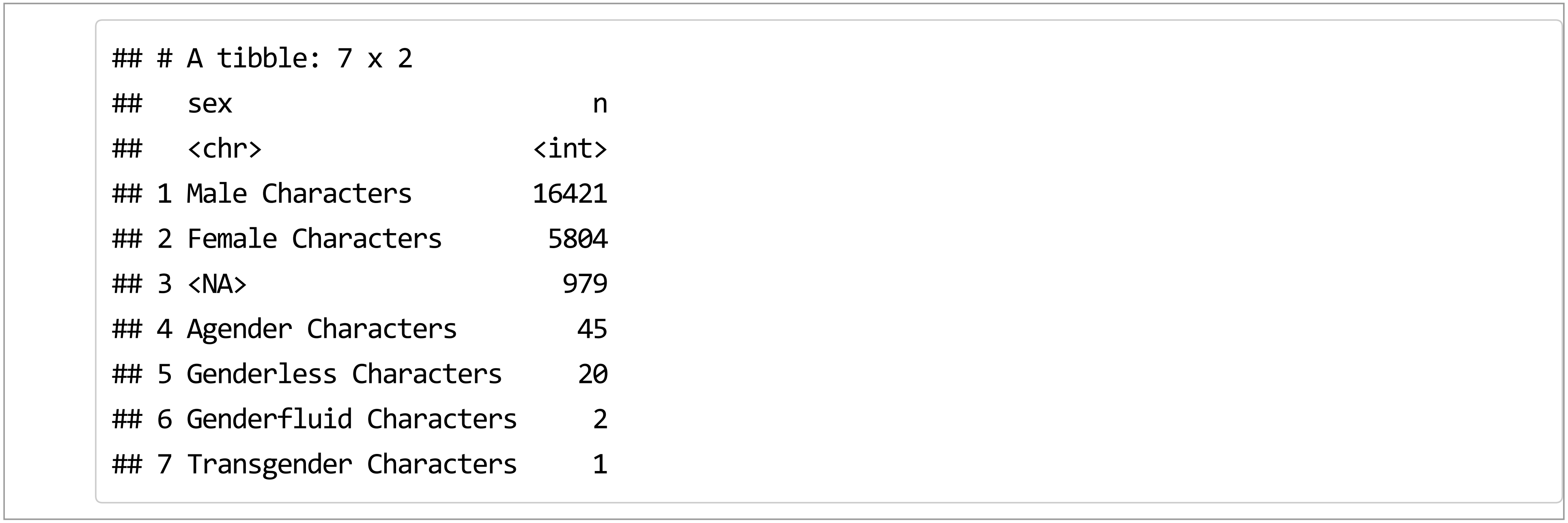


Table of Gender

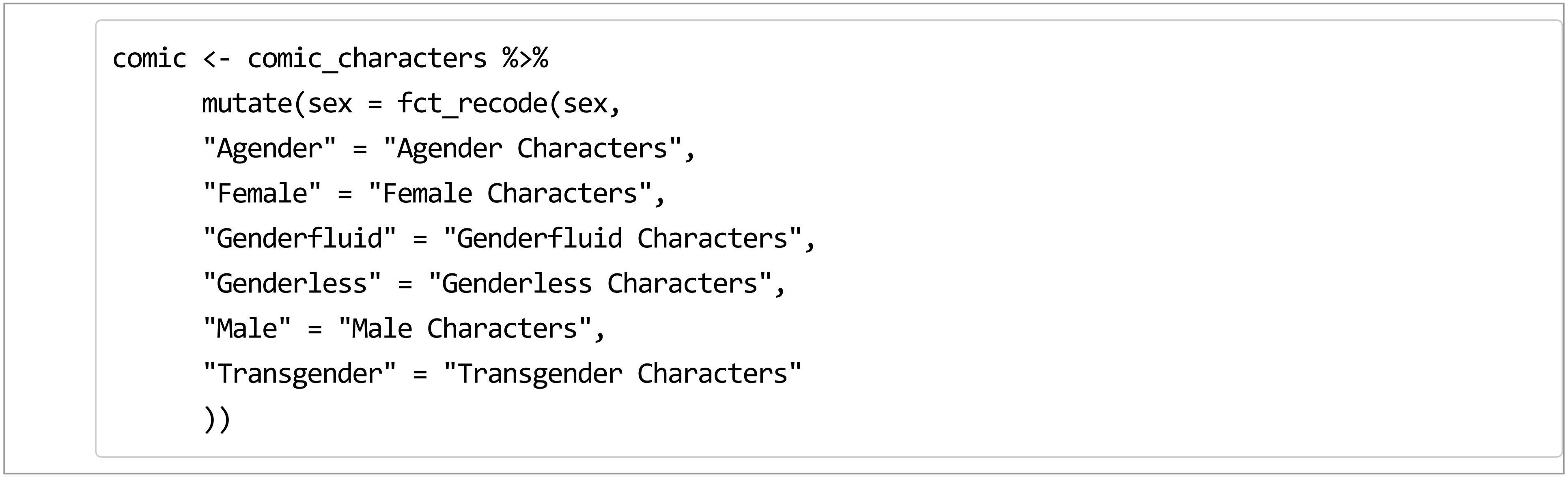
```
comic_characters %>%
    group_by(sex) %>%
    tally(sort = TRUE)
```

Table of Gender



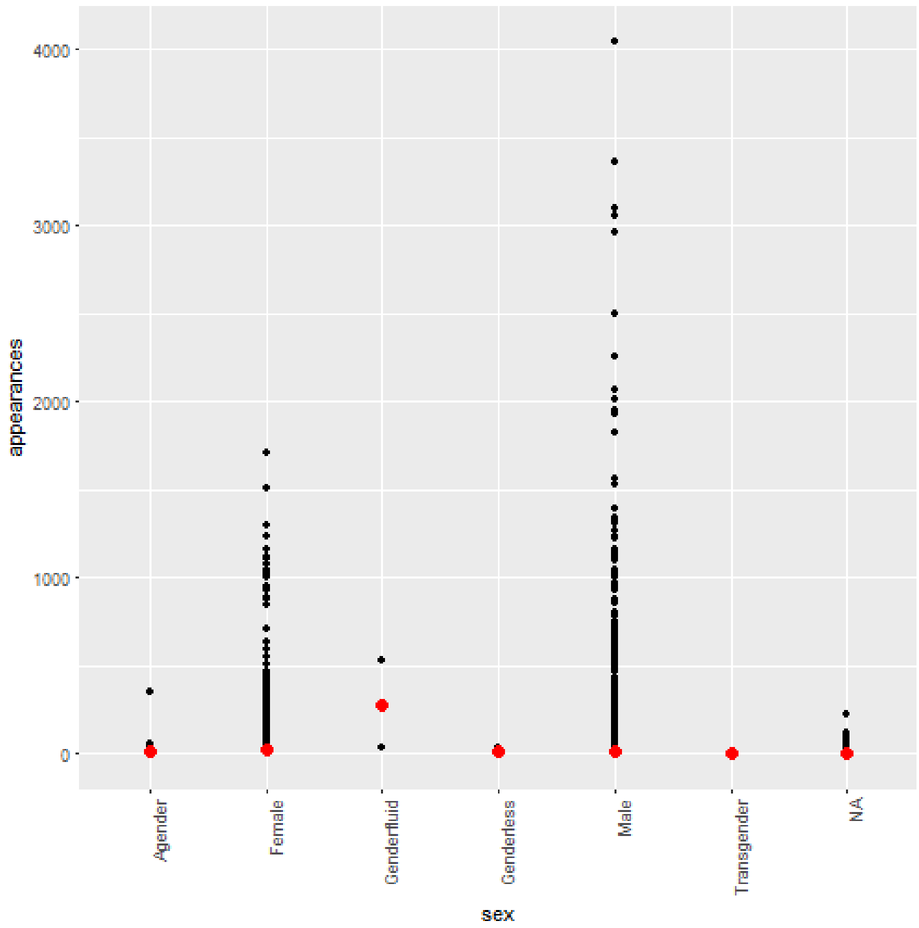
```
## # A tibble: 7 x 2
##   sex                        n
##   <chr>                  <int>
## 1 Male Characters        16421
## 2 Female Characters       5804
## 3 <NA>                     979
## 4 Agender Characters        45
## 5 Genderless Characters     20
## 6 Genderfluid Characters     2
## 7 Transgender Characters     1
```

Data Cleaning

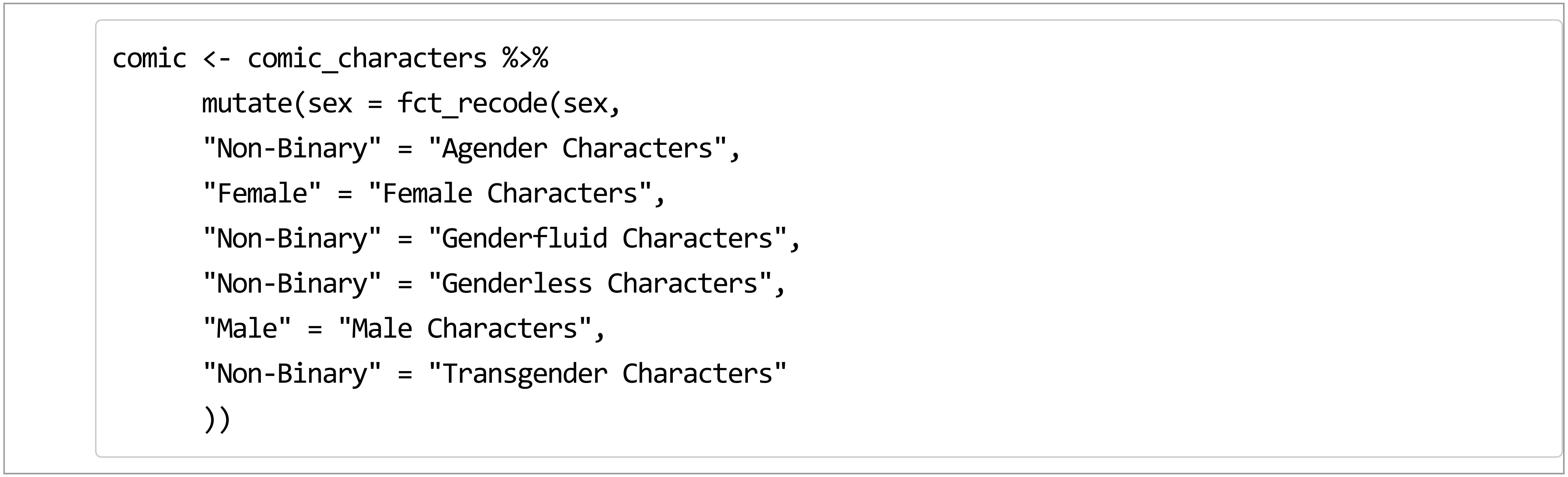


```r
comic <- comic_characters %>%
      mutate(sex = fct_recode(sex,
      "Agender" = "Agender Characters",
      "Female" = "Female Characters",
      "Genderfluid" = "Genderfluid Characters",
      "Genderless" = "Genderless Characters",
      "Male" = "Male Characters",
      "Transgender" = "Transgender Characters"
      ))
```

Data Cleaning

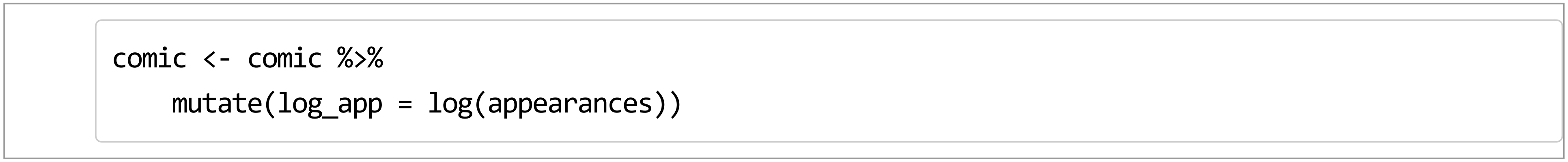


Cleaning Data



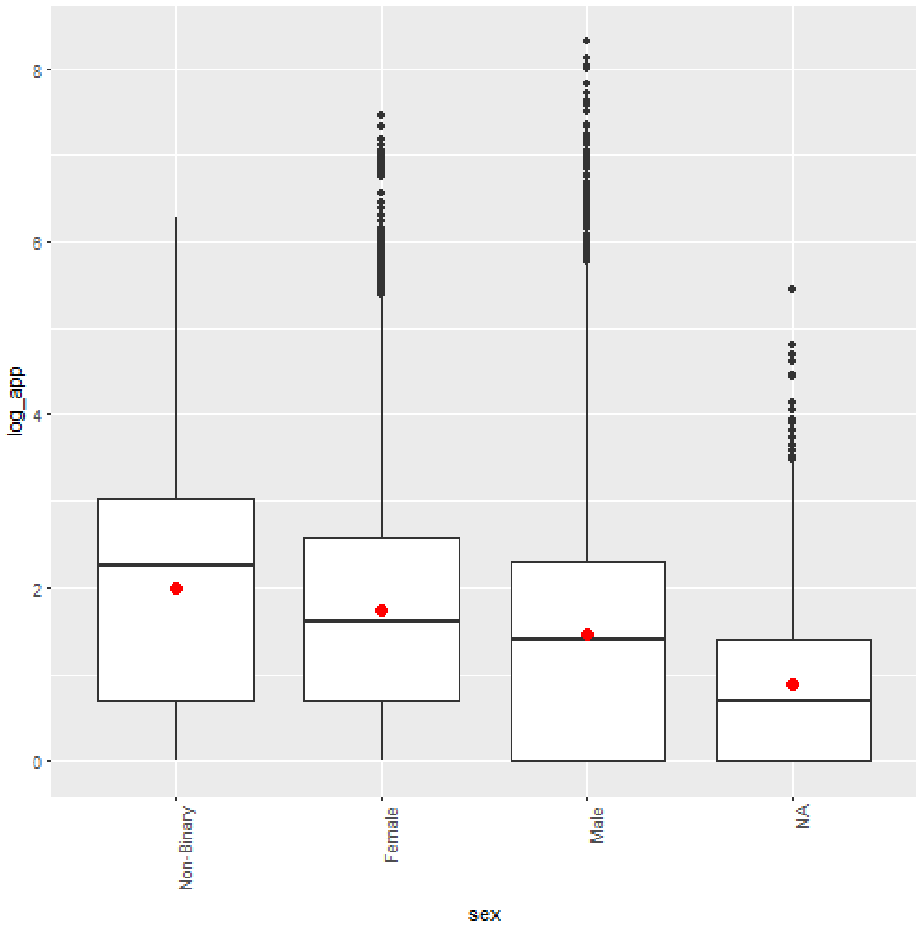
```
comic <- comic_characters %>%
      mutate(sex = fct_recode(sex,
      "Non-Binary" = "Agender Characters",
      "Female" = "Female Characters",
      "Non-Binary" = "Genderfluid Characters",
      "Non-Binary" = "Genderless Characters",
      "Male" = "Male Characters",
      "Non-Binary" = "Transgender Characters"
      ))
```

Cleaning Data



```
comic <- comic %>%
    mutate(log_app = log(appearances))
```

Boxplots

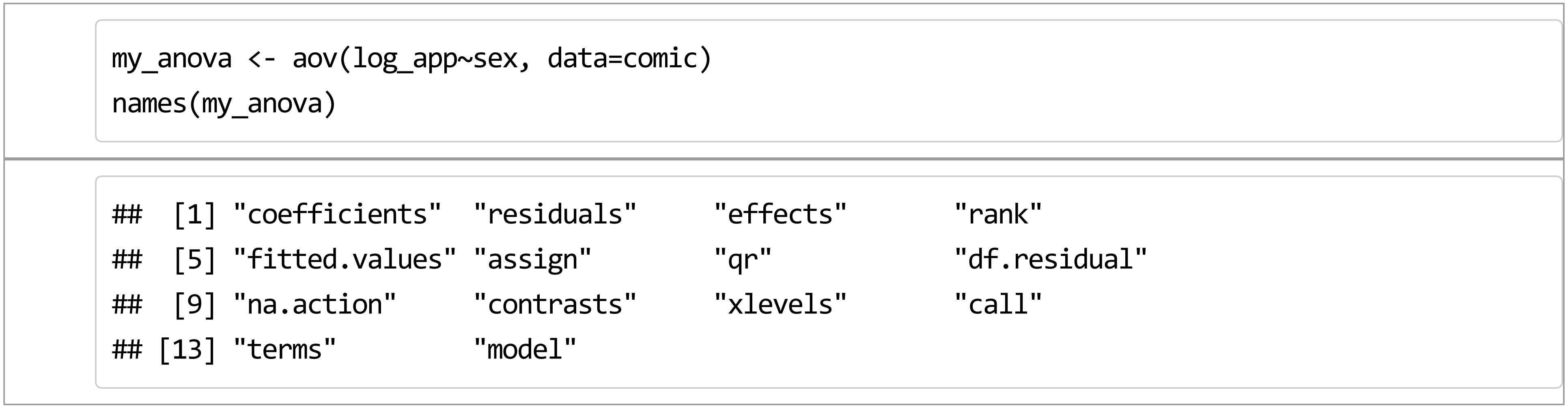


Finally ANOVA

```
aov(log_app~sex, data=comic)
```

```
## Call:
##    aov(formula = log_app ~ sex, data = comic)
##
## Terms:
##                      sex Residuals
## Sum of Squares    296.09  40225.14
## Deg. of Freedom        2     20966
##
## Residual standard error: 1.385132
## Estimated effects may be unbalanced
## 2303 observations deleted due to missingness
```

What can we do to get more information



```
my_anova <- aov(log_app~sex, data=comic)
names(my_anova)
```

```
##  [1] "coefficients"  "residuals"     "effects"       "rank"
##  [5] "fitted.values" "assign"        "qr"            "df.residual"
##  [9] "na.action"     "contrasts"     "xlevels"       "call"
## [13] "terms"         "model"
```

Summary

```
summary(my_anova)
```

```
##                 Df Sum Sq Mean Sq F value Pr(>F)    
## sex              2    296  148.05   77.16 <2e-16 ***
## Residuals    20966  40225    1.92                   
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 2303 observations deleted due to missingness
```

What were we testing again?

$$H_0 : \mu_1 = \mu_2 = \cdots = \mu_k$$

At least one group is different

What is Next?

What about Multiple Testing

$$\begin{aligned}
\Pr(\text{At least 1 Significant Result}) &= 1 - \Pr(\text{No Significant Results}) \\
&= 1 - (1 - 0.05)^{20} \\
&= 0.6415141
\end{aligned}$$

What Type of Multiple Tests for ANOVA

$$\text{FWER} \leq 0.05$$

The Bonferroni Correction

n

$$\alpha^* = \frac{\alpha}{n}$$

$$\min\left[2 \times \binom{k}{2} \times \Pr(\mid t \mid < t_{n-k}), 1\right]$$

The Bonferroni Correction

$n = 20$ $\alpha = 0.05$

$$\alpha^* = \frac{\alpha}{n} = \frac{0.05}{20} = 0.0025$$

$$\begin{aligned}\Pr(\text{At least 1 Significant Result}) &= 1 - \Pr(\text{No Significant Results}) \\ &= 1 - (1 - 0.0025)^{20} \\ &= 0.04883012\end{aligned}$$

Bonferonni in R

```
pairwise.t.test(x,g,p.adjust.method,...)
```

```
x

g

p.adjust.method

...
```

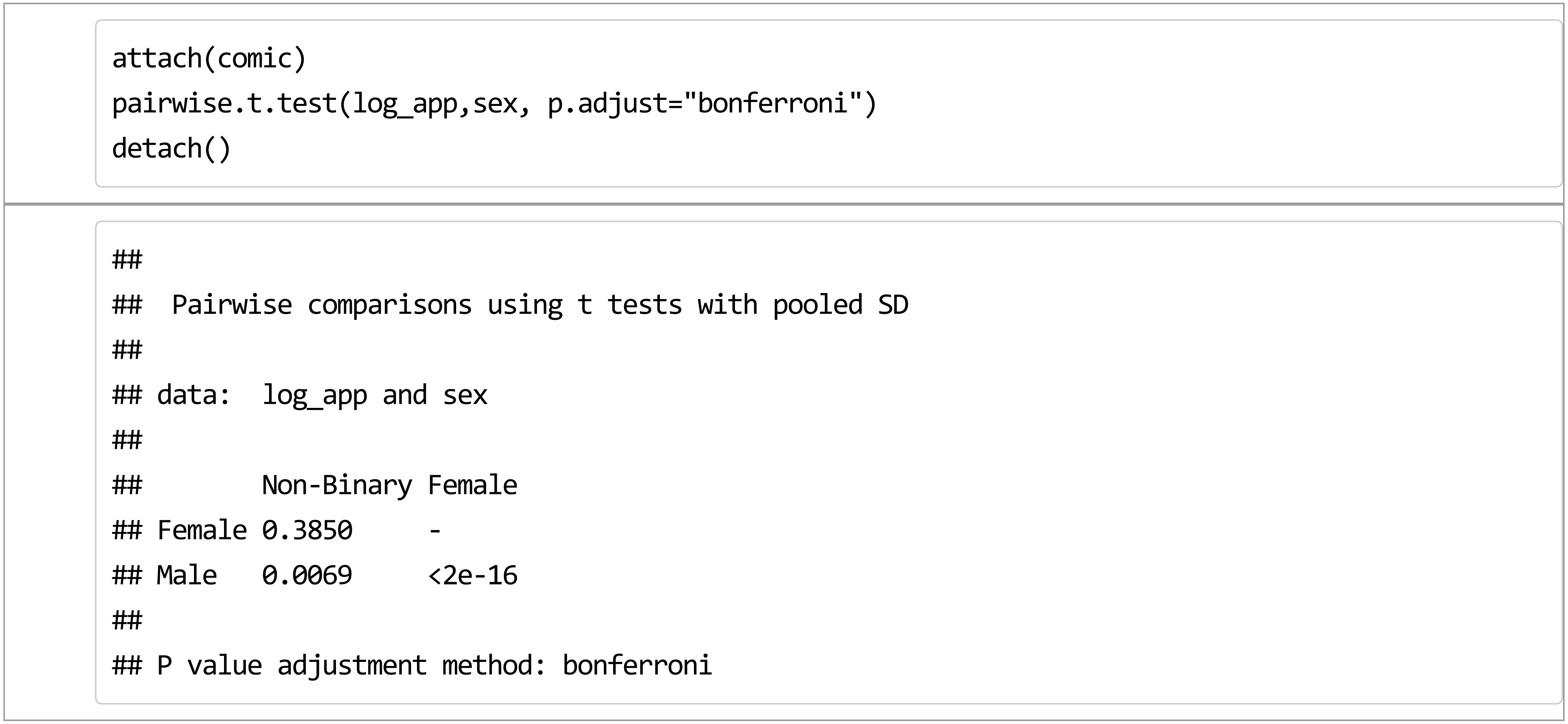
Bonferonni in R

```
attach(comic)
pairwise.t.test(log_app,sex, p.adjust="none")
detach()
```

```
##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  log_app and sex
##
##        Non-Binary Female
## Female 0.1283     -
## Male   0.0023     <2e-16
##
## P value adjustment method: none
```

$$\alpha = 0.0025$$

Bonferonni in R



```
attach(comic)
pairwise.t.test(log_app,sex, p.adjust="bonferroni")
detach()
```

```
##
##  Pairwise comparisons using t tests with pooled SD
##
## data:  log_app and sex
##
##        Non-Binary Female
## Female 0.3850     -
## Male   0.0069     <2e-16
##
## P value adjustment method: bonferroni
```

Tukey HSD Test

Tukey HSD in R

```
TukeyHSD(my_anova, conf.level=0.95)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = log_app ~ sex, data = comic)
##
## $sex
##                          diff        lwr        upr     p adj
## Female-Non-Binary -0.2648371 -0.6730209  0.1433466 0.2811377
## Male-Non-Binary   -0.5292183 -0.9358797 -0.1225569 0.0064760
## Male-Female       -0.2643812 -0.3154401 -0.2133222 0.0000000
```

Results

Assumptions of ANOVA

Testing Assumptions of ANOVA

Testing Assumptions of ANOVA

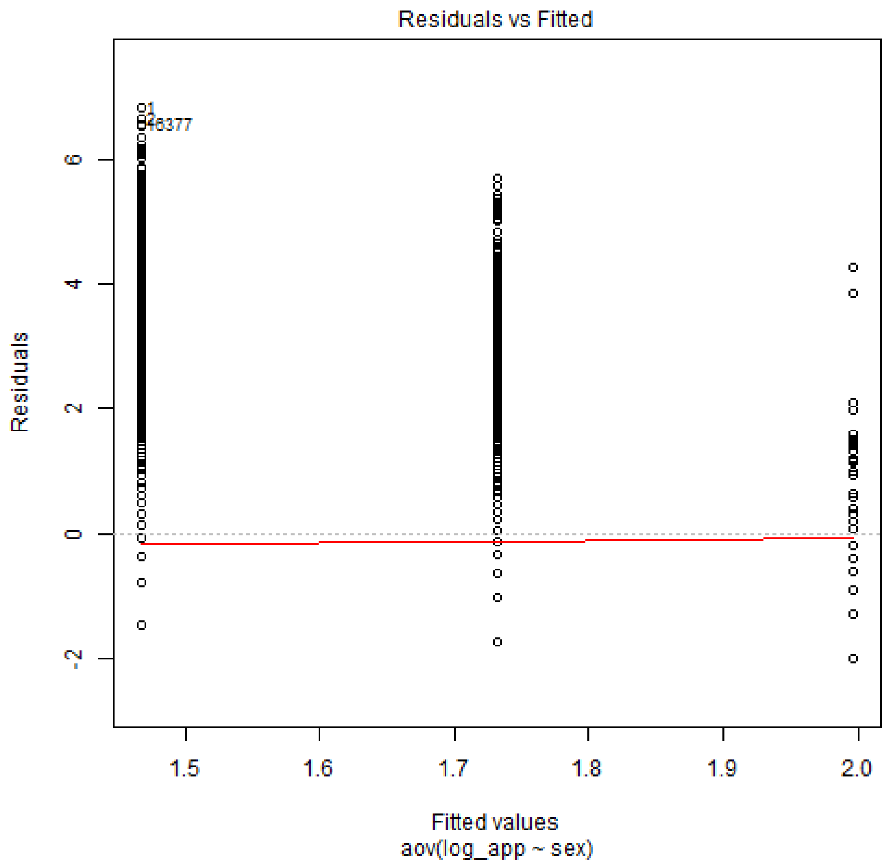
$$\sigma_1^2 = \sigma_2^2 = \cdots = \sigma_k^2$$

at least one variance is different

```
plot(my_anova, 1)

library(car)
leveneTest(log_app~sex, data = comic)
```

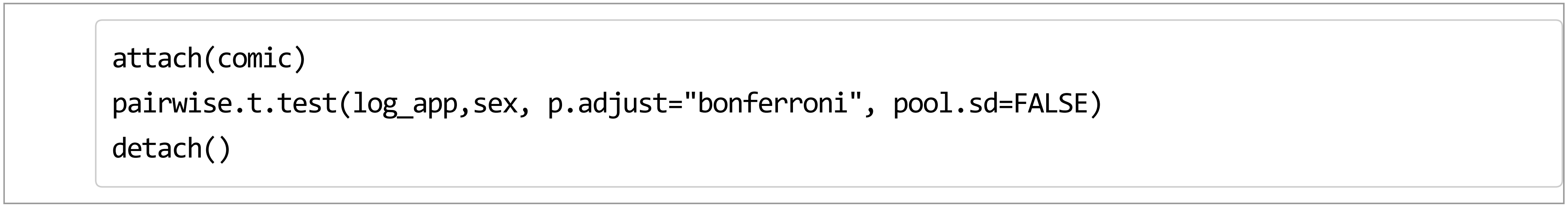
Testing Assumptions of ANOVA



Testing Assumptions of ANOVA

```
## Levene's Test for Homogeneity of Variance (center = median)
##          Df F value Pr(>F)
## group     2  0.1827 0.8331
##       20966
```

What if we do not have Homoscedastic Variances?

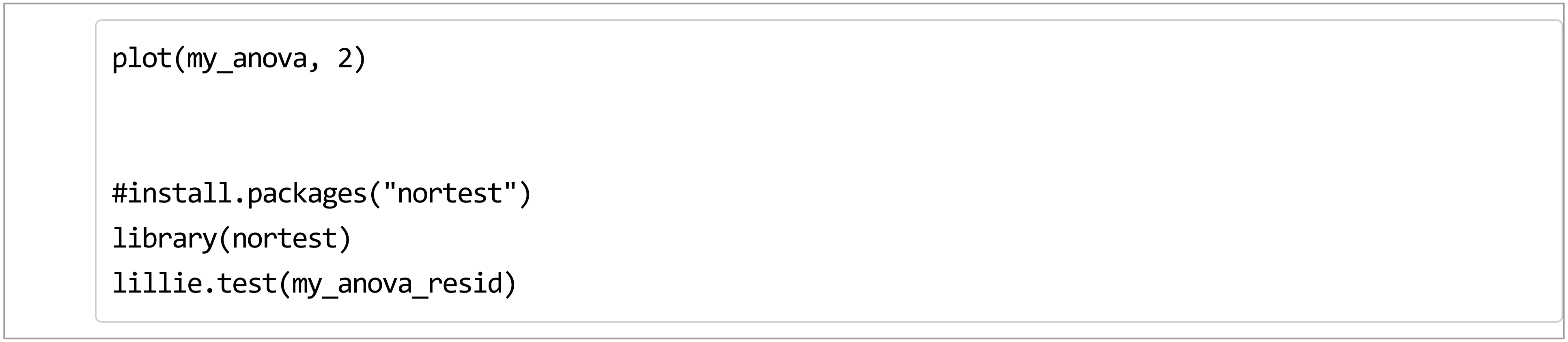


```
attach(comic)
pairwise.t.test(log_app,sex, p.adjust="bonferroni", pool.sd=FALSE)
detach()
```

Testing Assumptions of ANOVA

Population is Normally Distributed

Population is not Normally Distributed

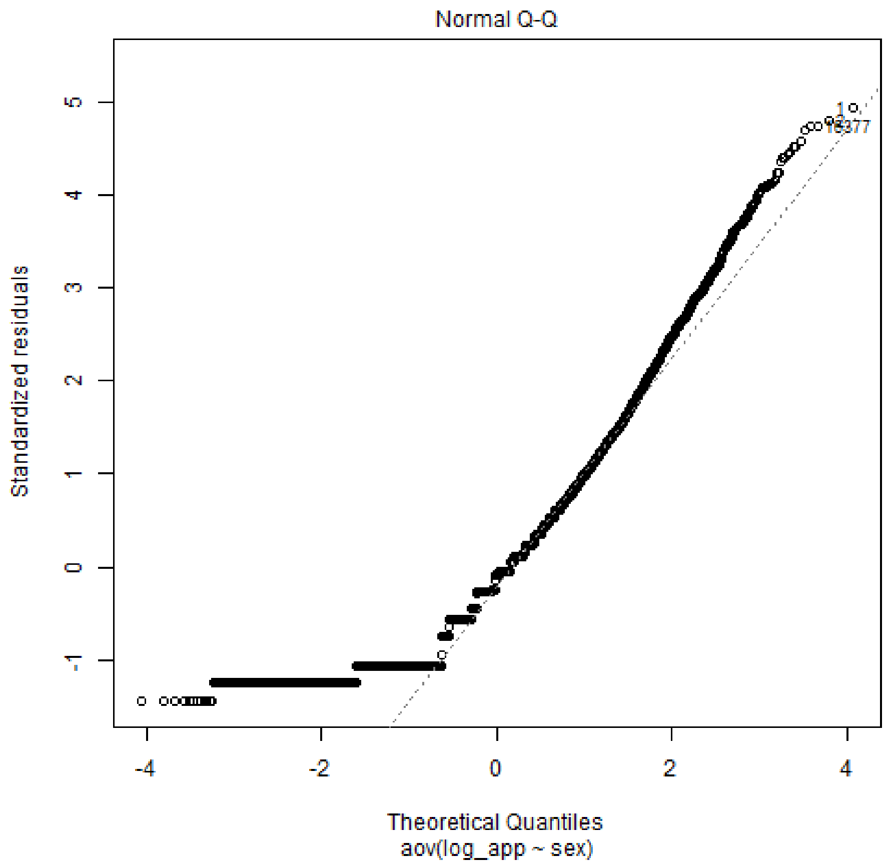


```
plot(my_anova, 2)



#install.packages("nortest")
library(nortest)
lillie.test(my_anova_resid)
```

Testing Assumptions of ANOVA



Testing Assumptions of ANOVA

```
## Error in sort(x[complete.cases(x)]): object 'my_anova_resid' not found
```

What if Normality is not met?

Questions

Lab Time