Chi-Squared Tests

Prof. Wells

STA 209, 5/3/23

Outline

In this lecture, we will. . .

- Determine whether data follows a certain distribution
- Investigate the chi-squared distribution.
- Use the chi-squared statistic to determine whether two variables are independent

Section 1

The Chi-Squared Test for Goodness of Fit

Inference for Categorical Variables

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What can we do if one or both the variables are categorical with more than 2 levels?

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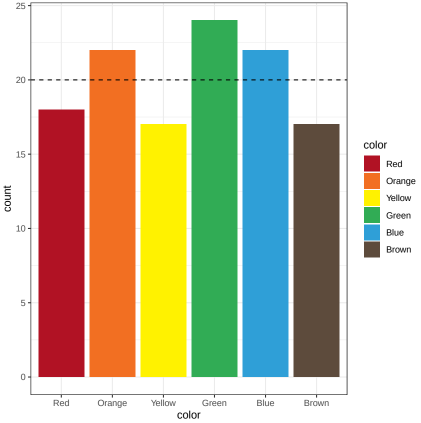

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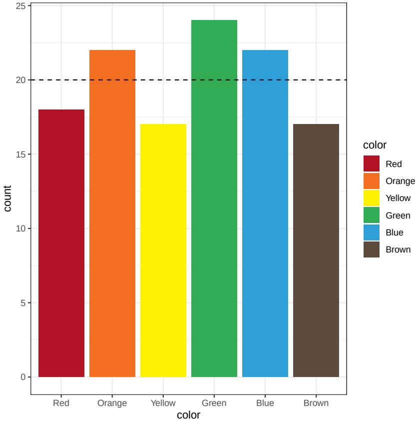

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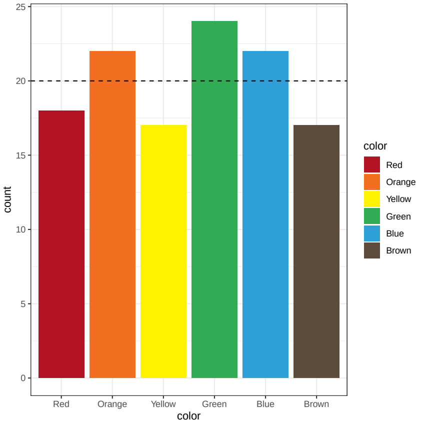

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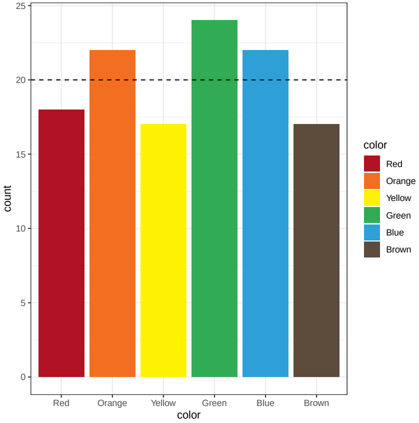

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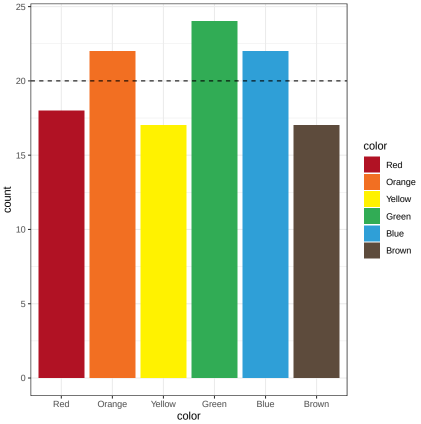

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- Does this give good evidence that M&M colors appear at different rates?
  - Suppose we had 20 colors instead of 6. . .
  - Would it really be unusual for 1 color to be over- or under-represented?

Data

- Let's consider some numeric data:

Color	Red	Orange	Yellow	Green	Blue	Brown
Frequency	.15	.183	.142	.2	.183	.142
Counts	18	22	17	24	22	17
Expected Counts	20	20	20	20	20	20
Difference (Obs - Exp)	-2	2	-3	4	2	-3

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  - We can represent this as a statement about the theoretical proportion of each each color, $p_r, p_o, p_y, p_g, p_b, p_{br}$
- We want to test the following hypotheses:

$$H_0: p_r = \frac{1}{6},\ p_o = \frac{1}{6},\ p_y = \frac{1}{6},\ p_g = \frac{1}{6},\ p_b = \frac{1}{6},\ p_{br} = \frac{1}{6}$$
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##   color  Sample_1 Sample_2 Sample_3 Sample_4 Sample_5 expected observed
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## 1 Blue   22       10       22       13       18       20       22
## 2 Brown  15       25       17       17       24       20       17
## 3 Green  28       17       24       23       18       20       24
## 4 Orange 19       21       23       29       26       20       22
## 5 Red    19       20       23       19       13       20       18
## 6 Yellow 17       27       11       19       21       20       17
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- How does the observed data compare?

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  - For example, if the categorical variable has 6 levels, this sum has 6 terms.

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  - But is this a fluke?

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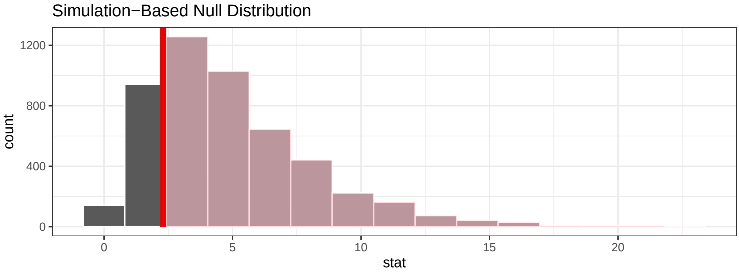

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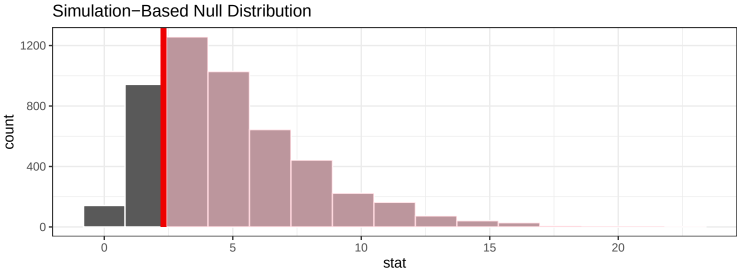

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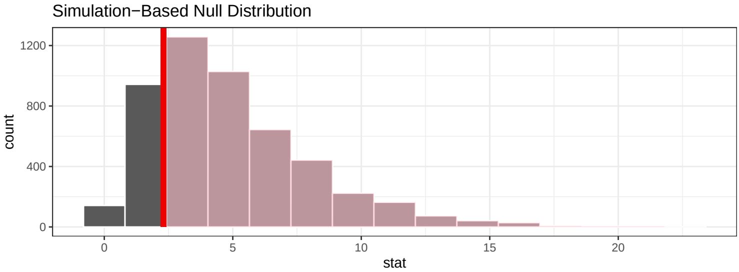

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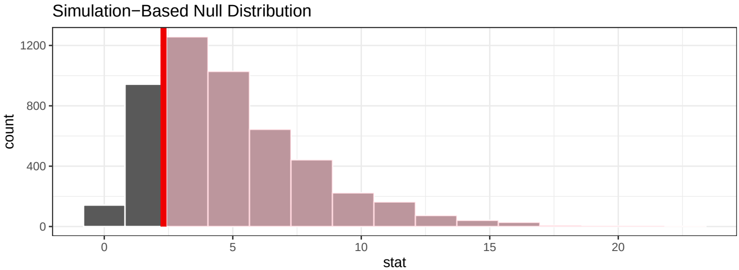

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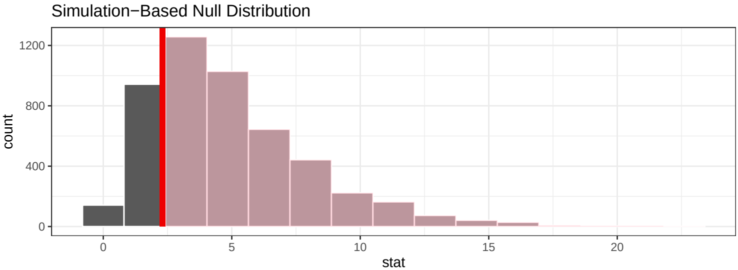

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  - A statistic more extreme would occur about 80% of the time!

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```
set.seed(1)
MMs %>% specify(response = color) %>%
  hypothesize(null = "point",
              p = c("Red" = 1/6, "Orange" = 1/6, "Yellow" = 1/6,
                    "Green" = 1/6, "Blue" = 1/6, "Brown" = 1/6))  %>%
  generate(reps = 5000, type = "simulate") %>%
  calculate(stat = "Chisq") %>%
  get_p_value(obs_stat = 2.3, direction = "right")
```

```
## # A tibble: 1 x 1
##   p_value
##     <dbl>
## 1   0.813
```

Conclusions

- We tested the following hypotheses:

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- The test provides inconclusive evidence that frequency differs among colors.
  - Importantly, it does not verify that colors ARE equally distributed.

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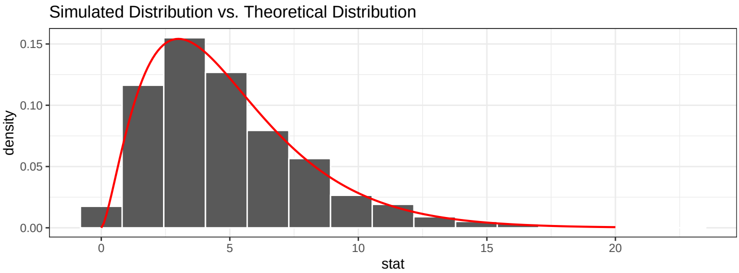

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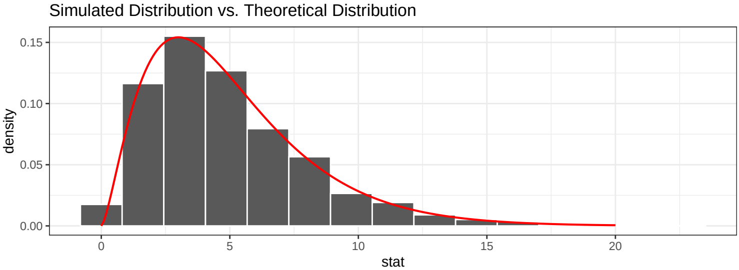

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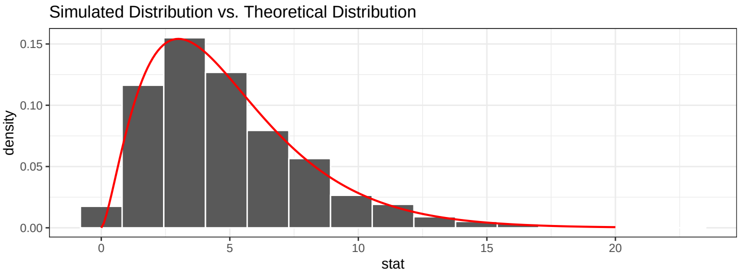

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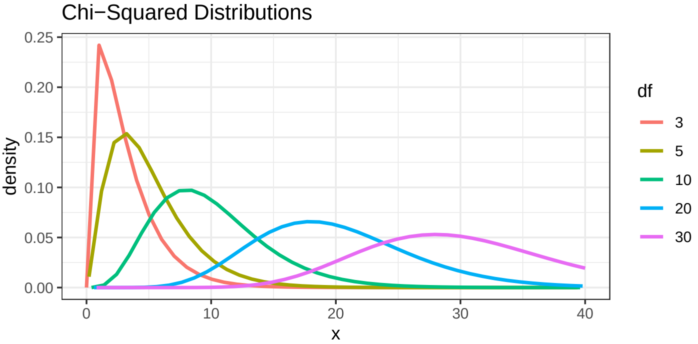
```
pchisq(q = 2.3, df = 5, lower.tail = F)
```

```
## [1] 0.8062669
```

The Chi-Squared Distribution

Just Normal distributions are described by their mean μ and standard deviation σ, the Chi-Square distribution is described by its degrees of freedom *df*.



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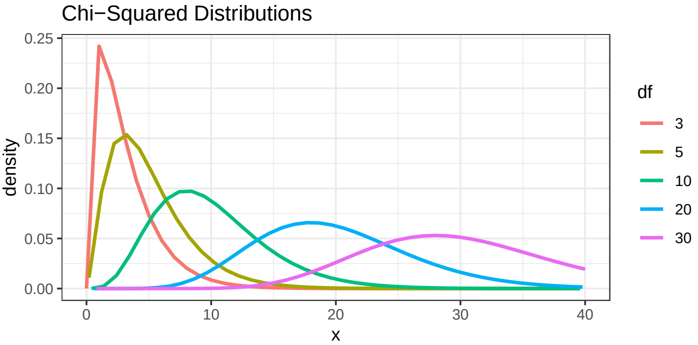

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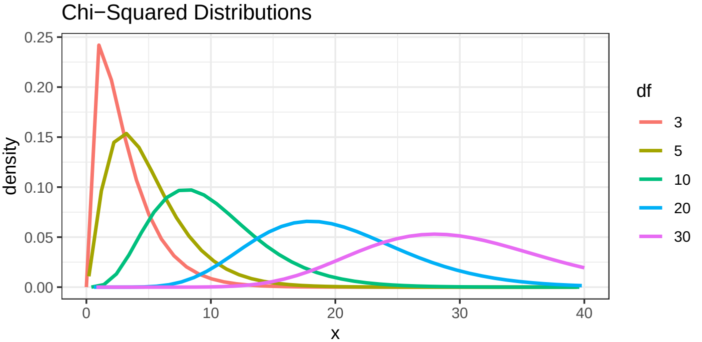

- The mean of a chi-square distribution is df, while the standard deviation is $\sqrt{2 \cdot df}$
- For Chi-Squared tests, larger degrees of freedom require larger χ^2 statistics to reject H_0.

Section 2

Chi-Square Test for Independence

Genetic Basis for Fast Twitch Muscles

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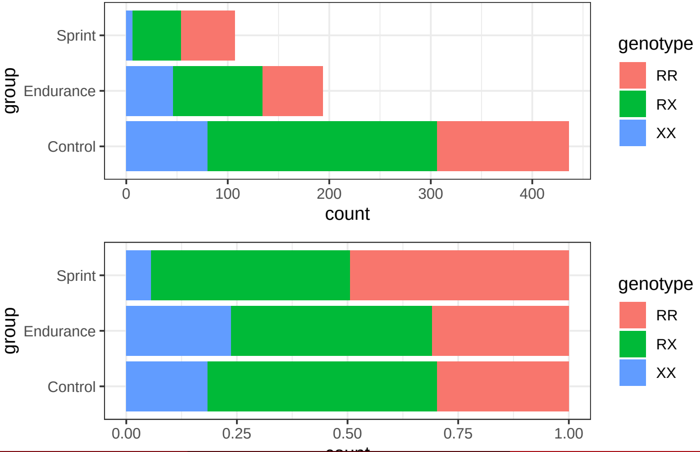
Genetic Basis for Fast Twitch Muscles

A study on genetics and fast-twitch muscles includes a sample of sprinters, endurance athletes, and a control group of non-athletes.

- Is there an association between a genotype classification (RR, RX, or XX) and group?



Contingency Table

Consider the contingency table for group and genotype

```
table(twitch$group, twitch$genotype) %>%
  addmargins()
```

```
##
##              RR  RX  XX Sum
##   Control   130 226  80 436
##   Endurance  60  88  46 194
##   Sprint     53  48   6 107
##   Sum       243 362 132 737
```

```
table(twitch$group, twitch$genotype) %>%
  prop.table( 1)
```

```
##
##                RR    RX    XX
##   Control   0.298 0.518 0.183
##   Endurance 0.309 0.454 0.237
##   Sprint    0.495 0.449 0.056
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- If group and genotype were independent, we would expect proportions to all be equal to the marginal proportions for genotype:

```
table(twitch$genotype) %>% prop.table()
```

```
##
##   RR   RX   XX
## 0.33 0.49 0.18
```

Expected Counts

If the null hypothesis is true, we can multiply the marginal proportions of `genotype` by the observed counts for `group` to get expected counts for each `genotype`-`group` pair:

	RR	RX	XX
Control	(0.33)(436)	(0.49)(436)	(0.18)(436)
Endurance	(0.33)(194)	(0.49)(194)	(0.18)(194)
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- We can compare to the observed data:

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- As before, we compute the chi-square statistic

$$\chi^2 = \sum \frac{(\text{Observed} - \text{Expected})^2}{\text{Expected}} = 25$$

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```
##   ID     group genotype
## 1  1 Endurance       RX
## 2  2    Sprint       XX
## 3  3   Control       XX
## 4  4    Sprint       RX
## 5  5   Control       RX
## 6  6    Sprint       RR
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```

Chi-Square Statistic in `infer`

Using `infer`...

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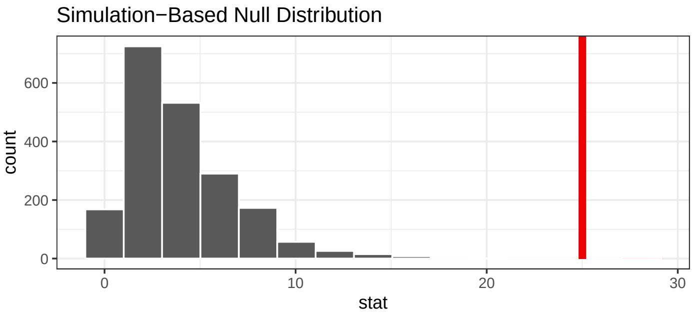
```
set.seed(49)
twitch_null <- twitch %>%
  specify(genotype ~ group) %>%
  hypothesize(null = "independence") %>%
  generate(reps = 2000, type = "permute") %>%
  calculate(stat="Chisq")
twitch_null %>% visualize()+shade_p_value(obs_stat = 25, direction = "right")
```



P-value and conclusions

Using `infer`, the approximate p-value is

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- What association is there?
  - We'll need to further study and experiment to find out.