Chi-Squared Tests

Nate Wells

Math 141, 4/7/21

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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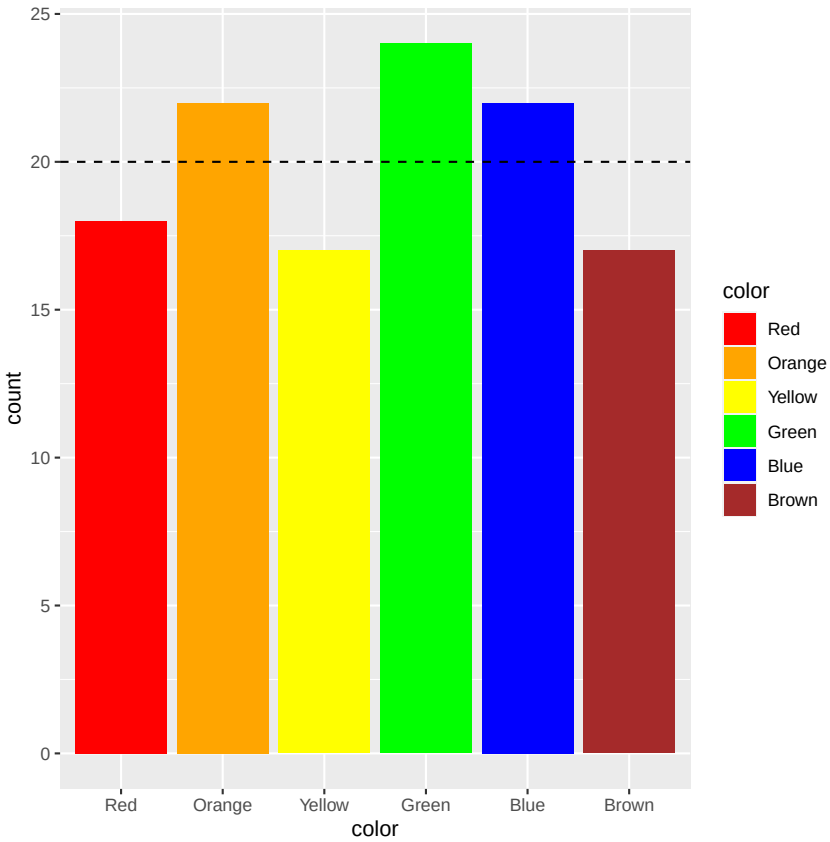

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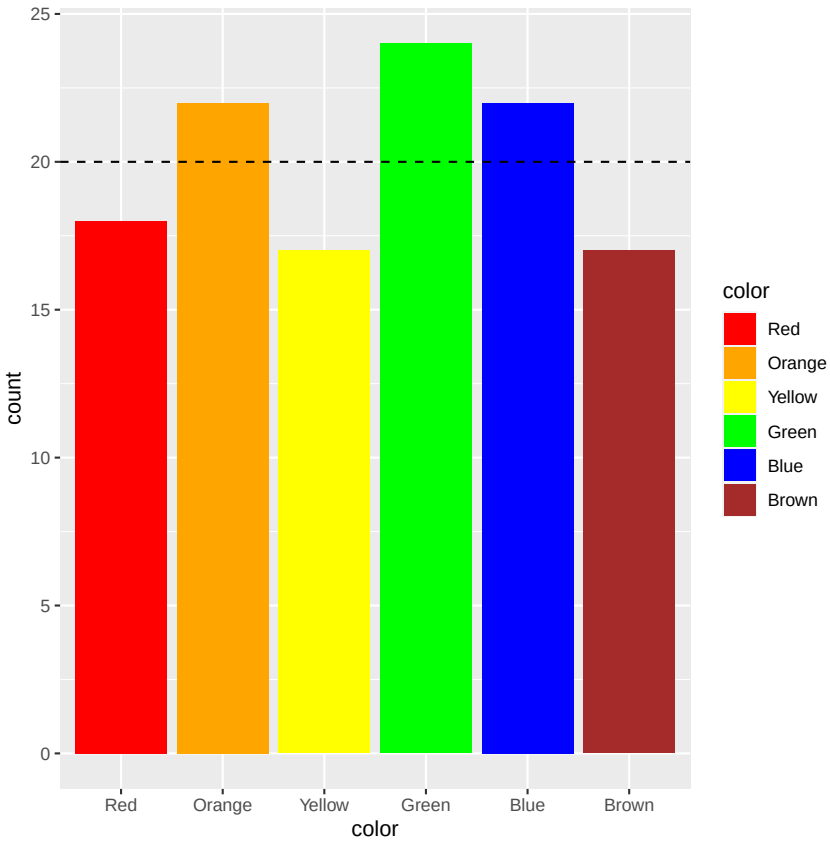

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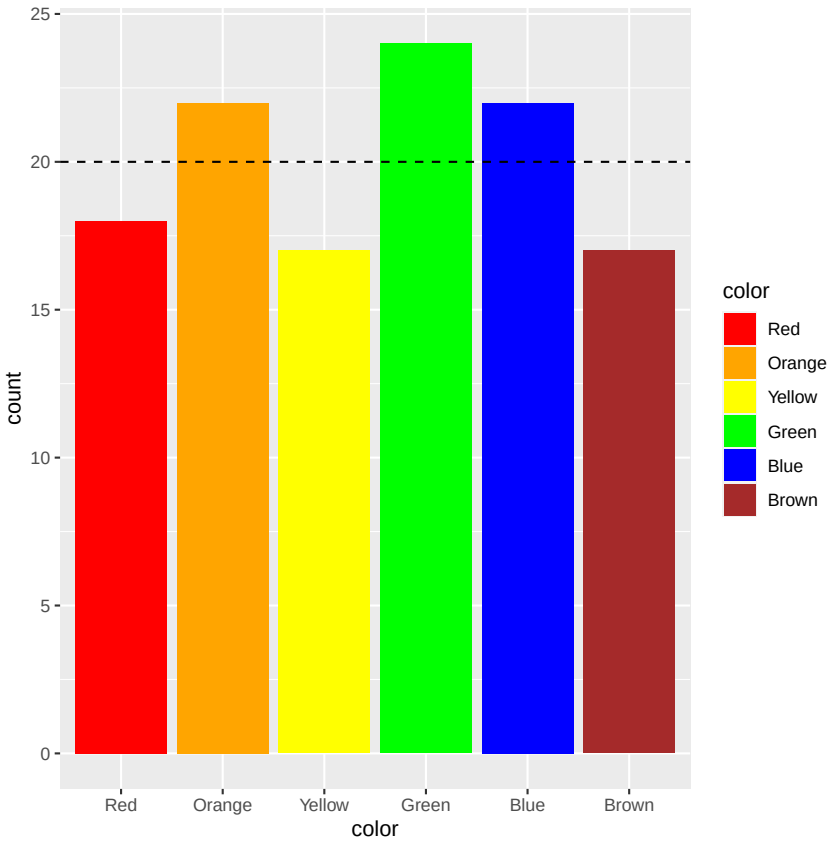

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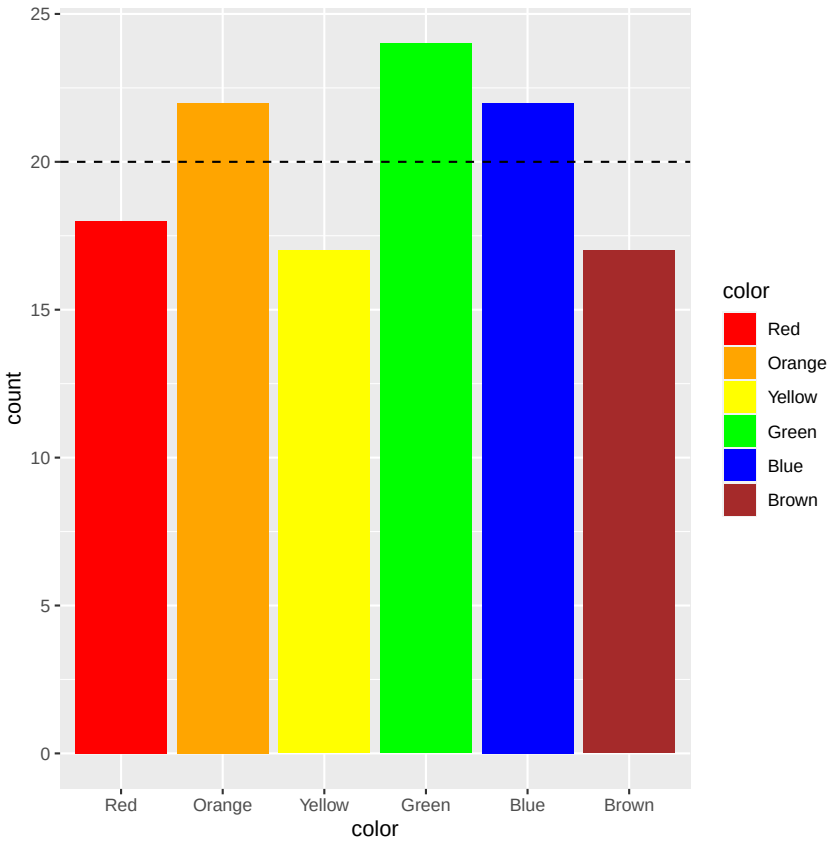

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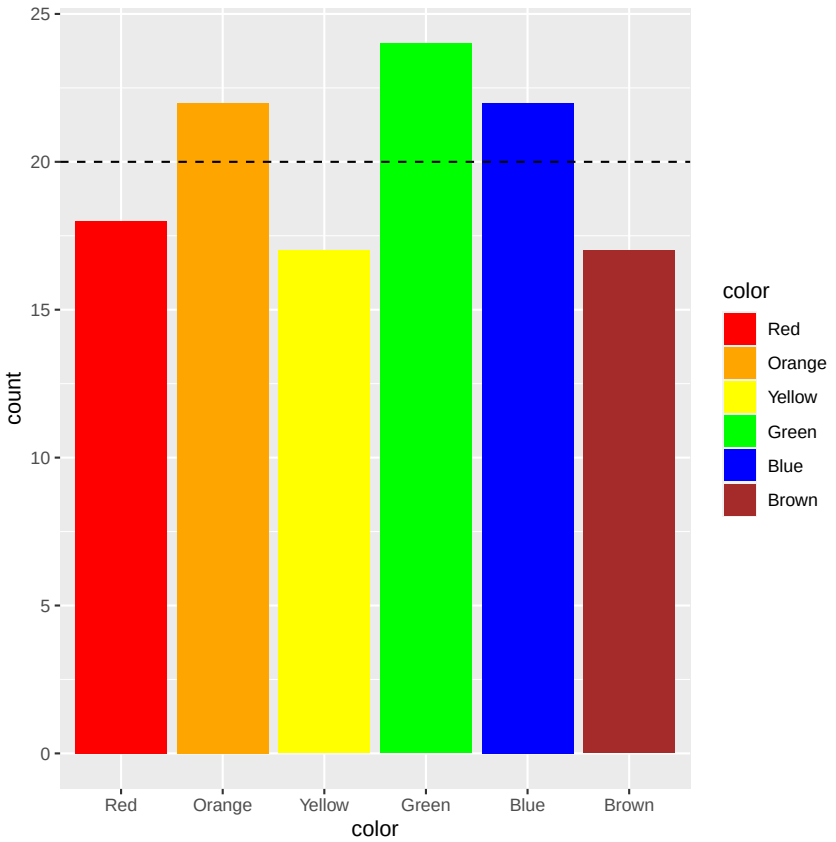

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- Does this give good evidence that M&M colors appear at different rates?
  - Suppose we had 20 colors instead of 6...
  - Would it really be unusual for 1 color to be over- or under-represented?

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 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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```
## # A tibble: 6 x 8
##   color  `1`   `2`   `3`   `4`   `5`   expected observed
##   <chr>  <chr> <chr> <chr> <chr> <chr> <chr>    <chr>
## 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
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- How does the observed data compare?

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- Then large values of χ^2 should correspond to extreme samples

Observed Statistic

- What is the χ^2 statistic for our observed sample?

$$\chi^2 = \frac{(22-20)^2}{20} + \frac{(17-20)^2}{20} + \frac{(24-20)^2}{20} + \frac{(22-20)^2}{20} + \frac{(18-20)^2}{20} + \frac{(17-20)^2}{20} = 2.3$$

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  - But is this a fluke?

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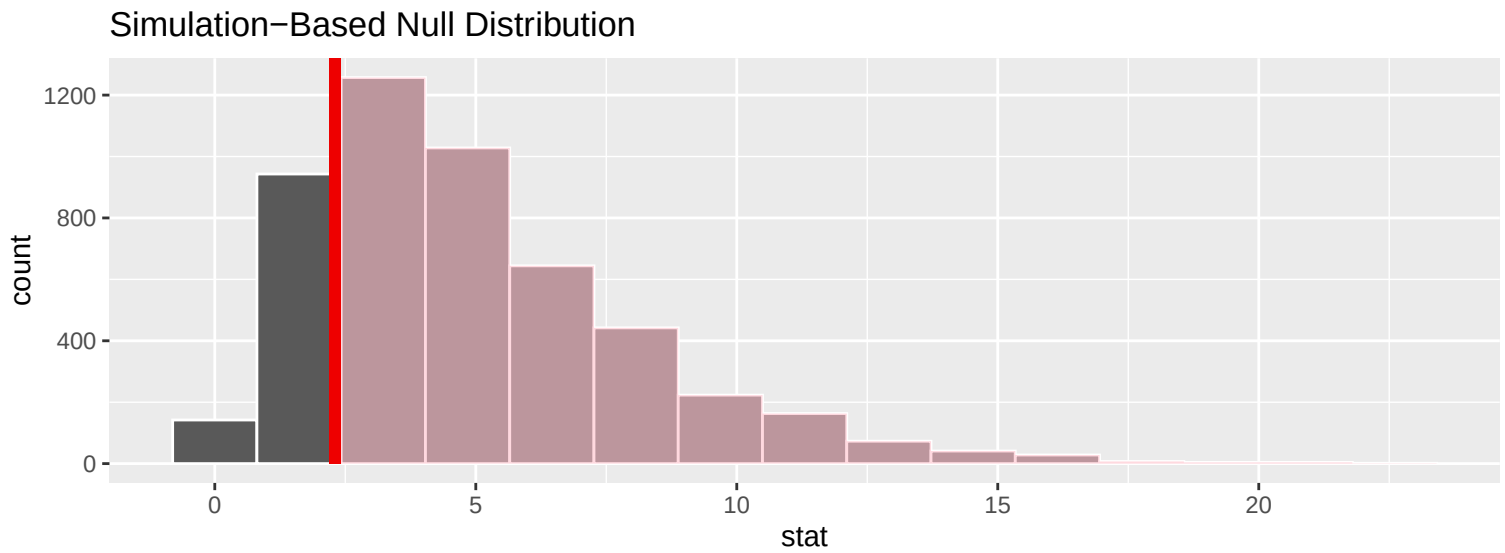

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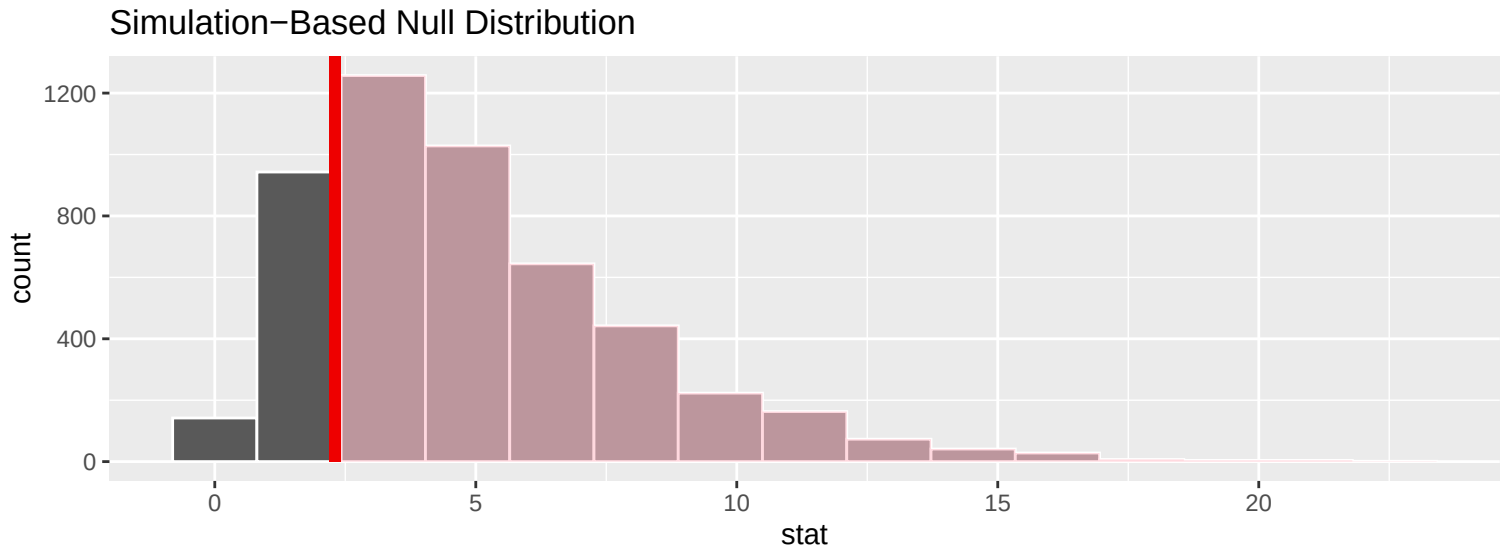

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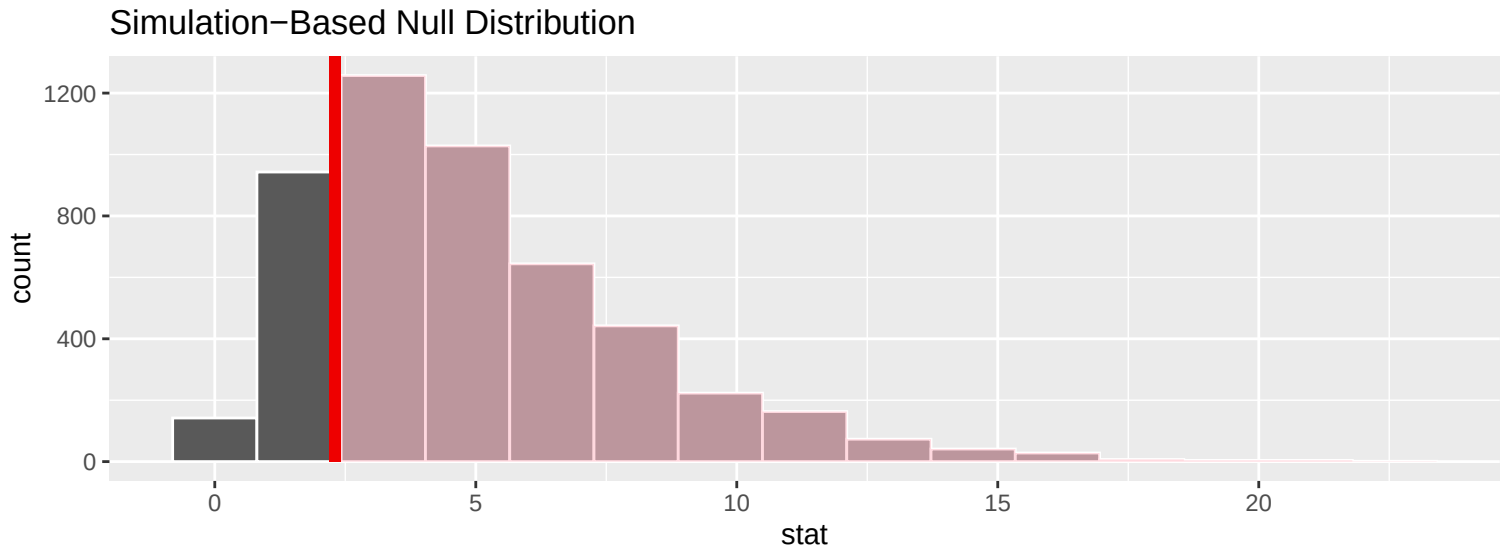

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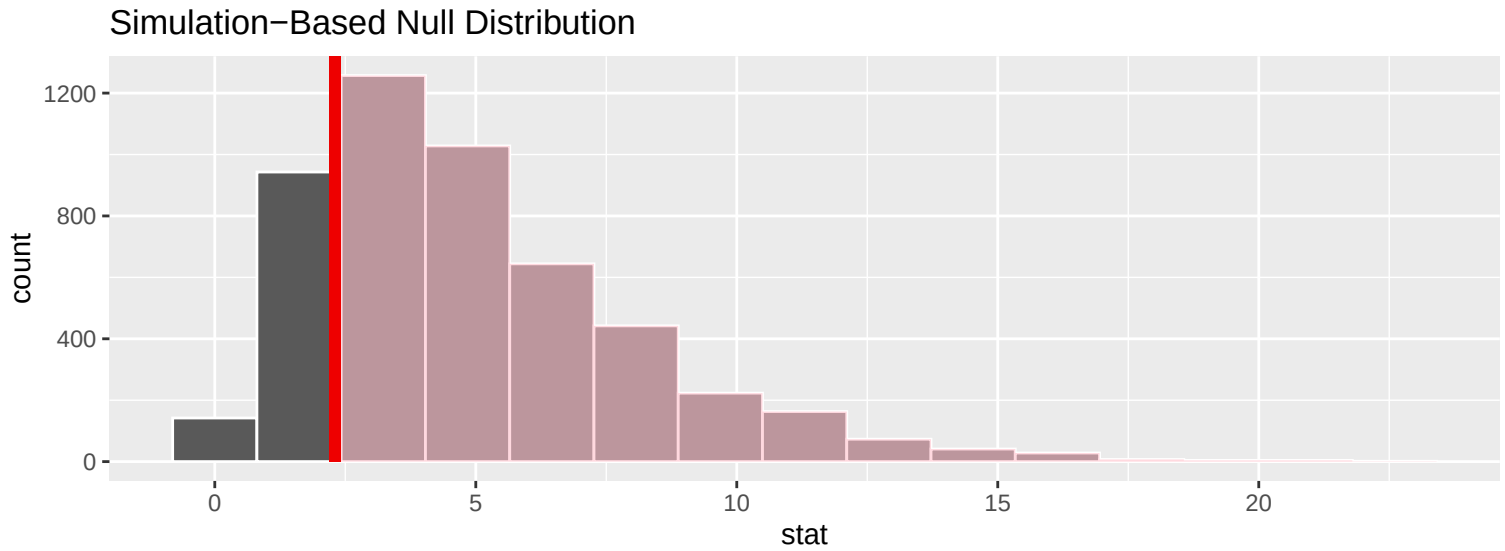

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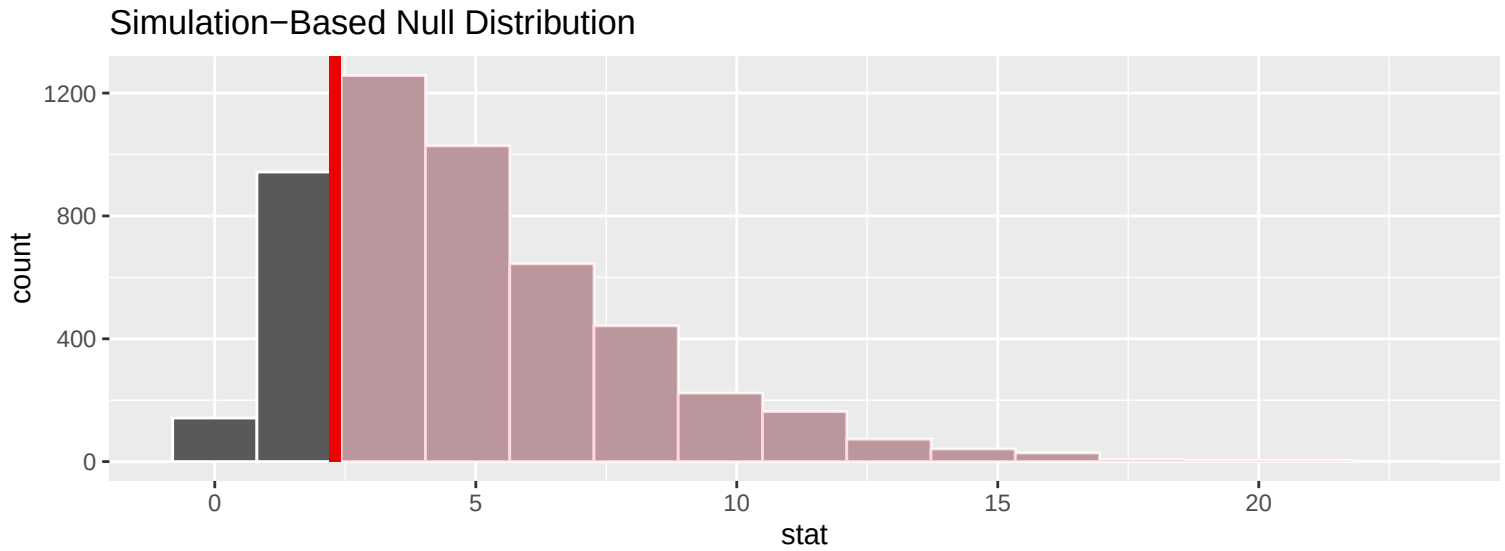

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  - A statistic more extreme would occur about 80% of the time!

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```
set.seed(1)
  chisq_null <- 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")

chisq_null %>% get_p_value(obs_stat =2.3, direction = "right")
```

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

Conclusions

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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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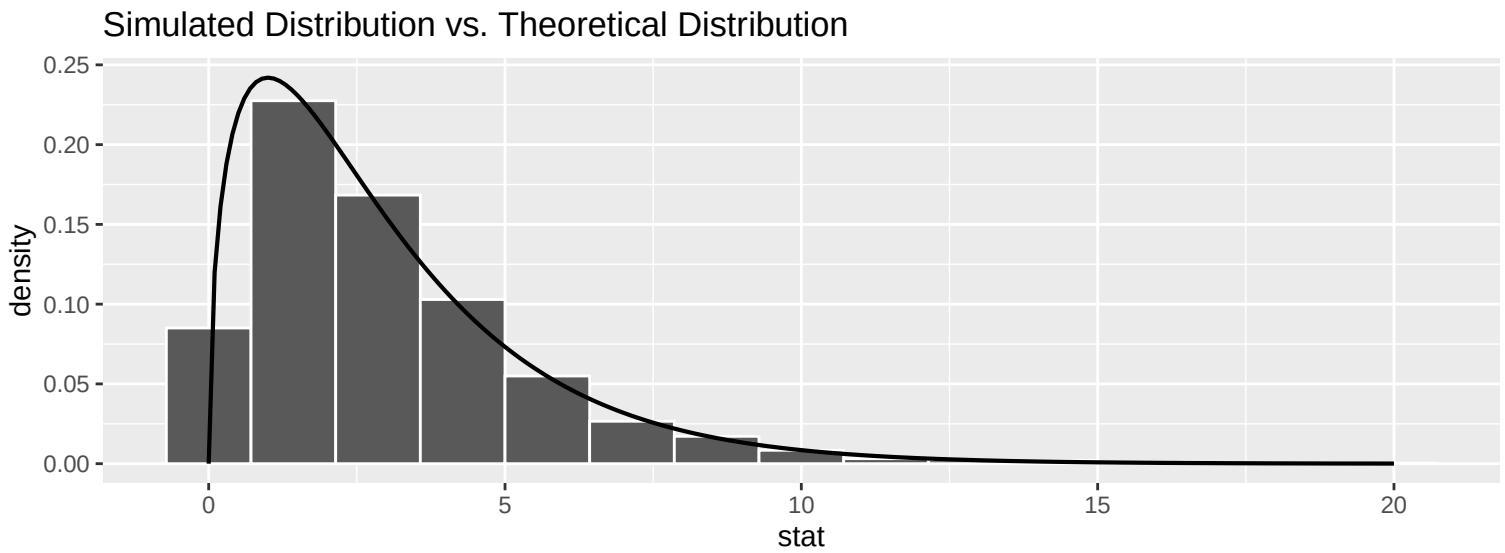

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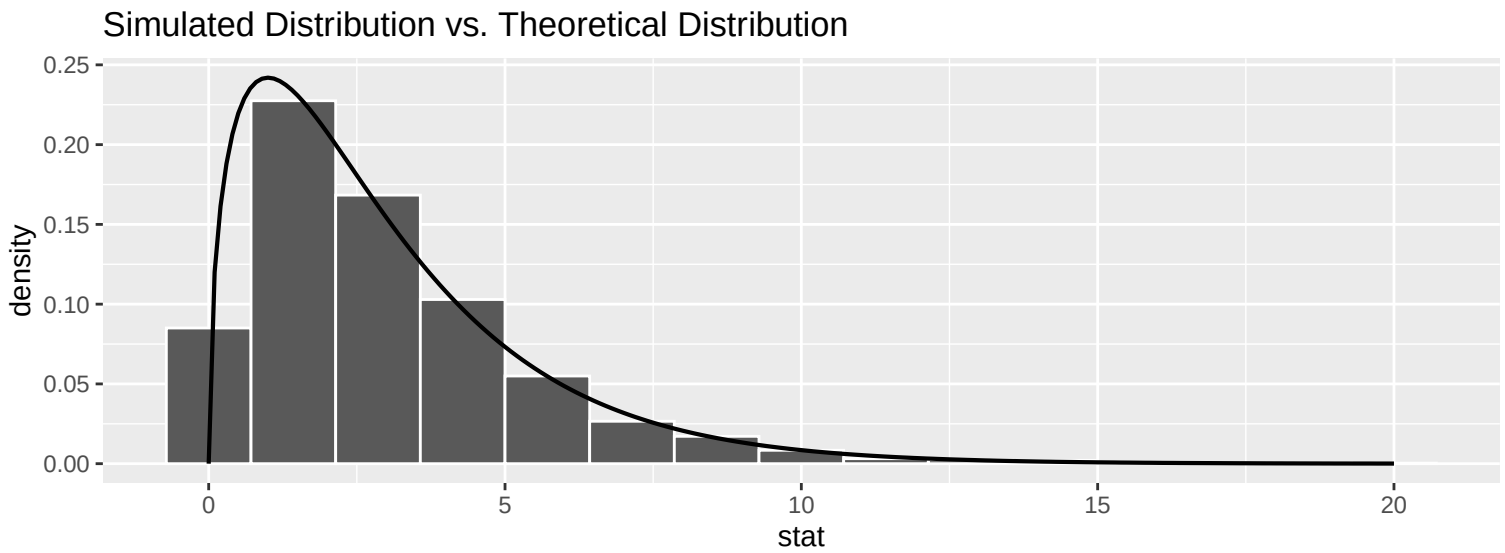

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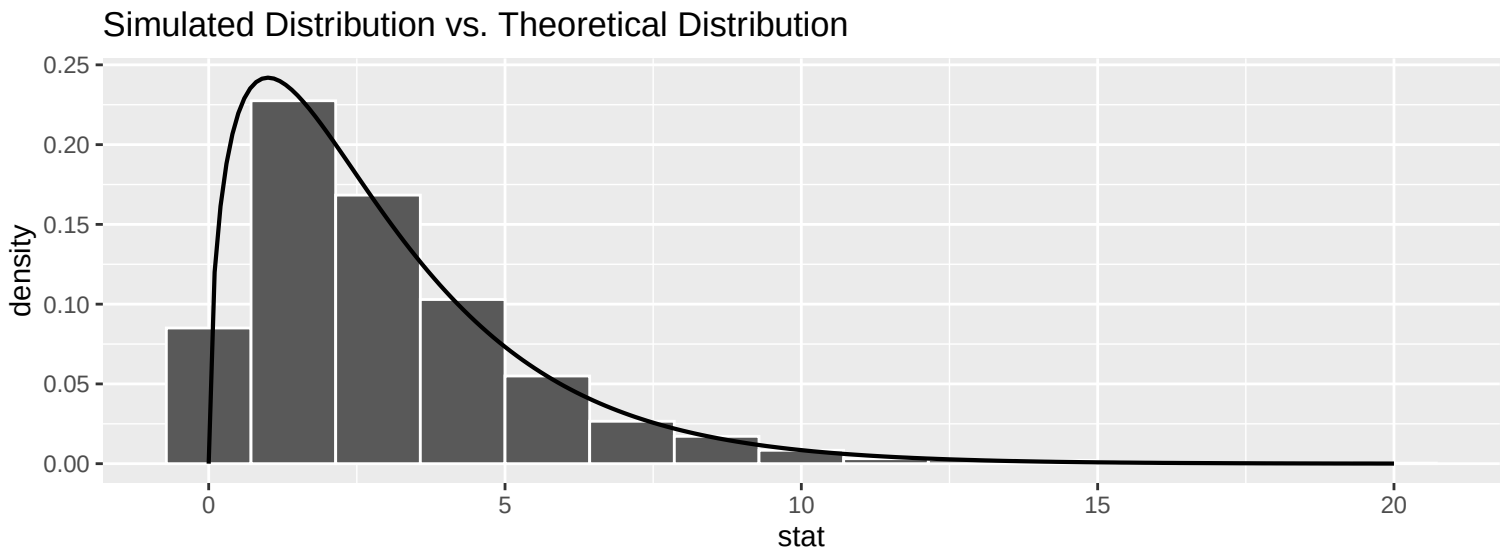

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```
pchisq(q = 2.3, df = 5, lower.tail = F)
```

```
## [1] 0.81
```

The Chi-Squared Distribution

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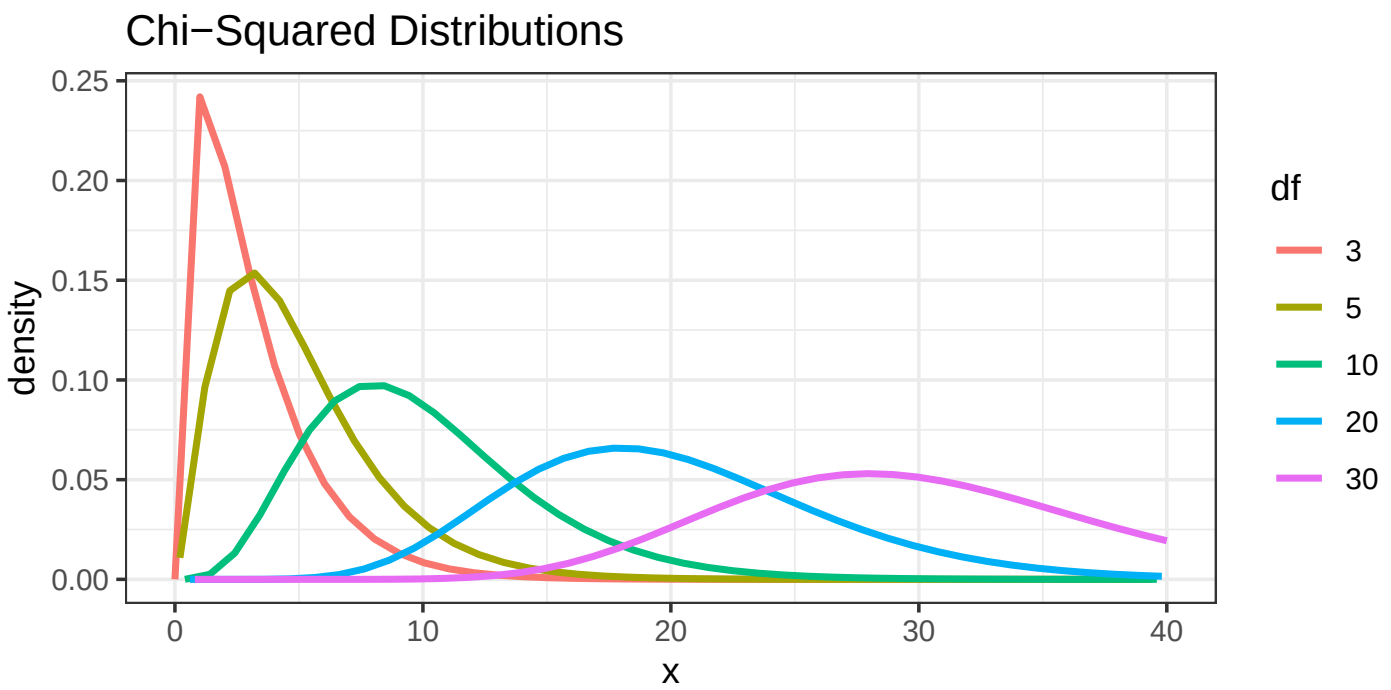

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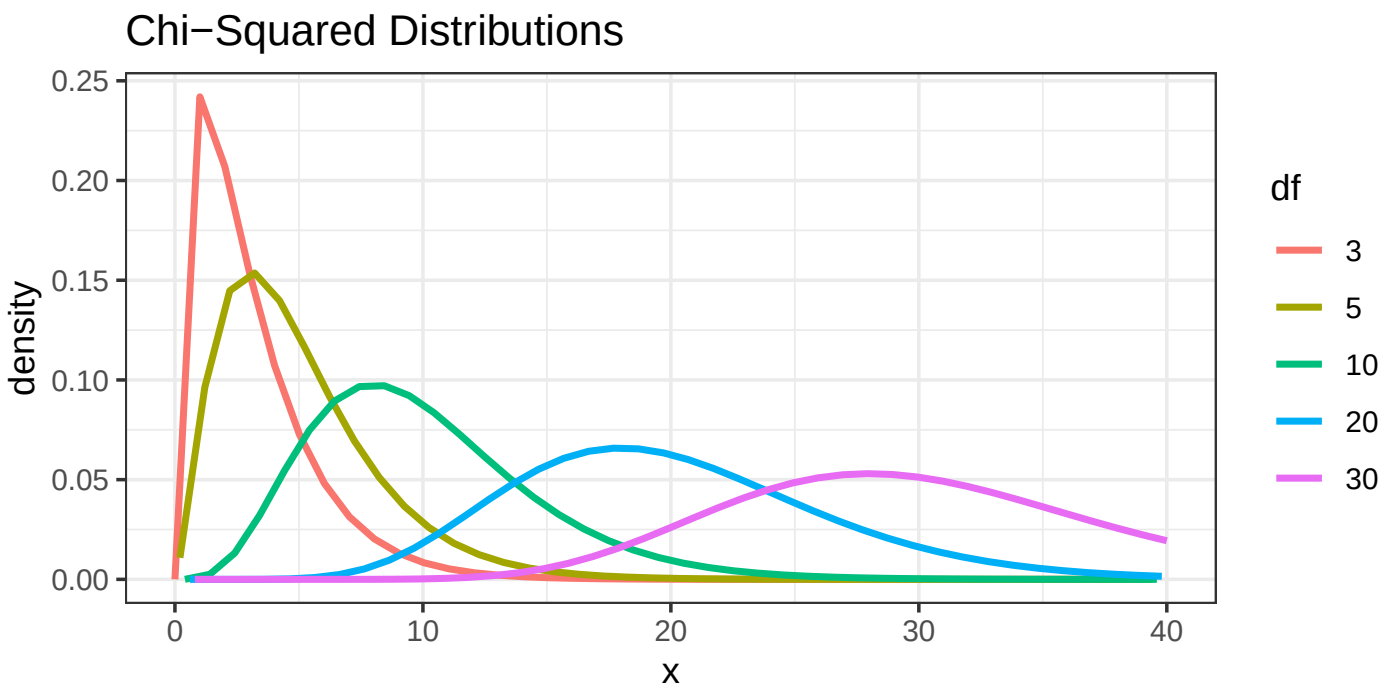

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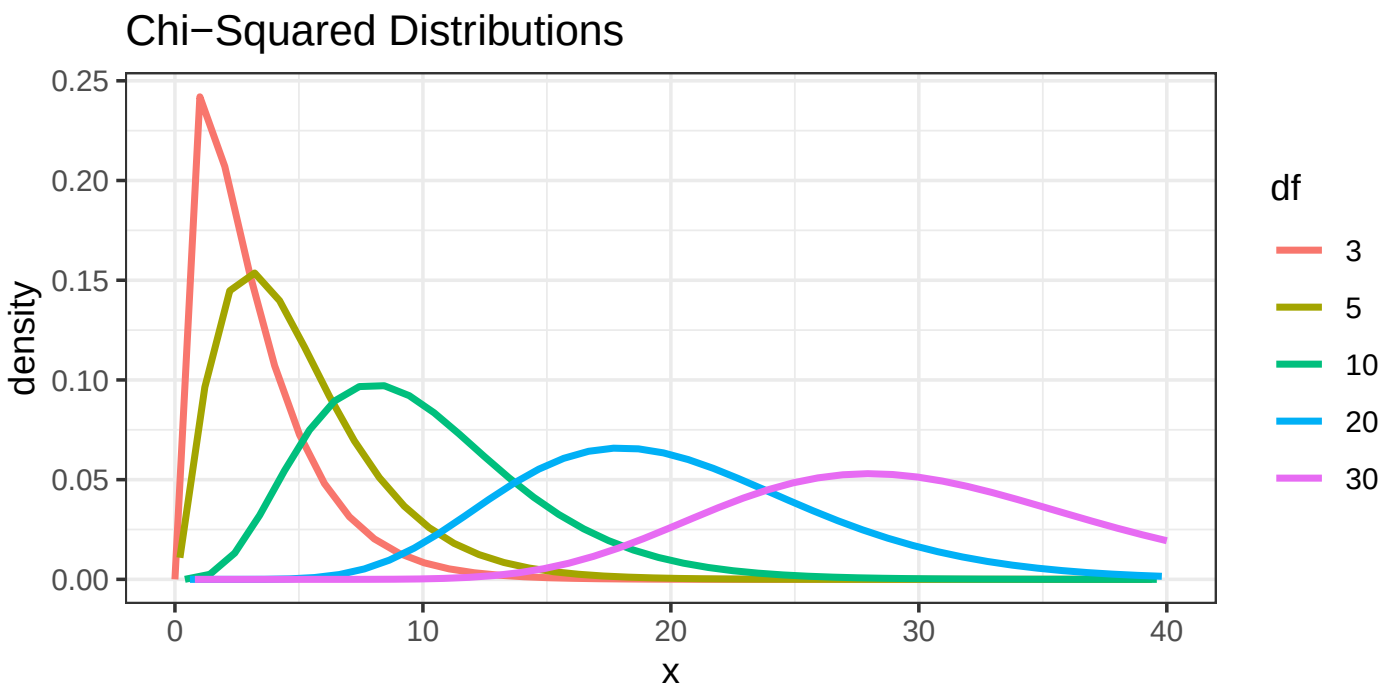


- Larger degrees of freedom correspond to larger means and larger standard deviations.
- For Chi-Squared tests, larger degrees of freedom require larger χ^2 statistic to reject H_0.

Section 2

Chi-Square Test for Independence

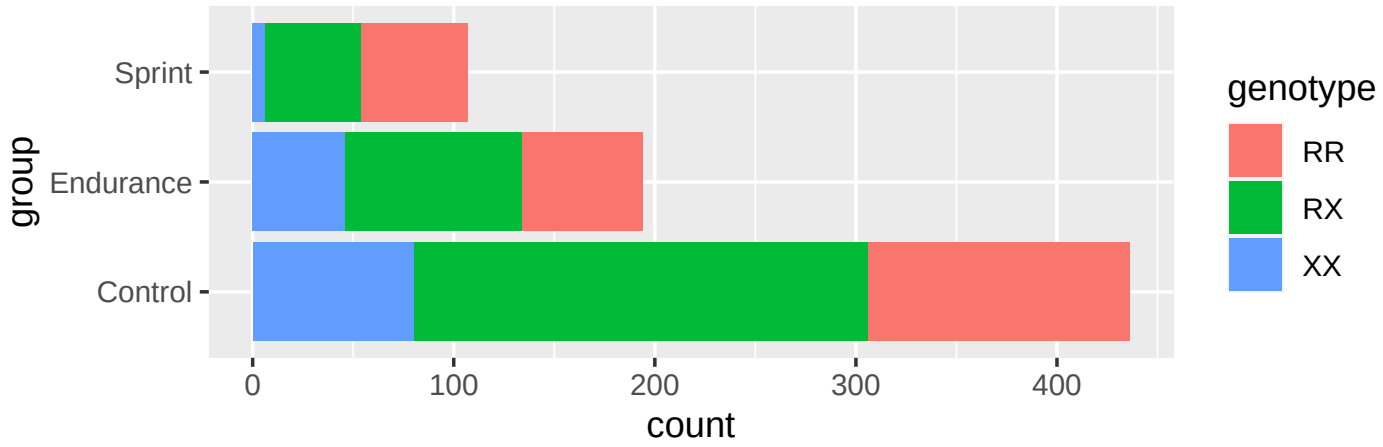
Genetic Basis for Fast Twitch Muscles

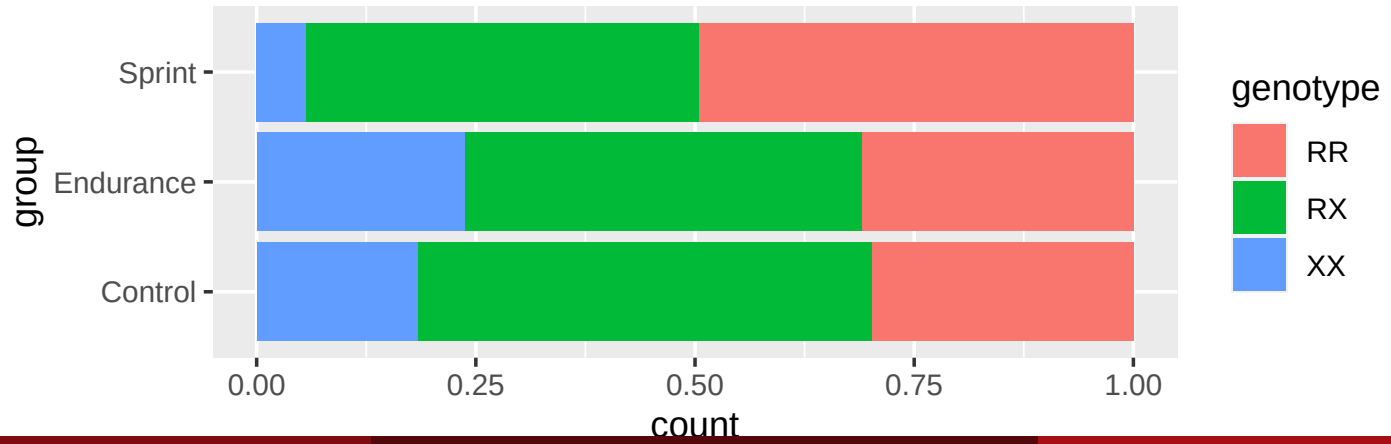
A study on genetics and fast-twitch muscles includes a sample of sprinters, endurance athletes, and a control group of non-athletes.

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)
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- We can compare to the observed data:

	RR	RX	XX	Sum
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- As before, we compute the chi-square statistic

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

The Null Distribution

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- We can simulate data under H_0 by permuting the `group` labels among individuals. (Just like we did for hypothesis tests for 2 proportions)
  - After each permutation, we compute a new χ^2 statistic.
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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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##   ID     group genotype
## 1  1 Endurance       RX
## 2  2    Sprint       RX
## 3  3   Control       XX
## 4  4    Sprint       RR
## 5  5   Control       XX
## 6  6    Sprint       RX
```

Chi-Square Statistic in `infer`

Using `infer`...

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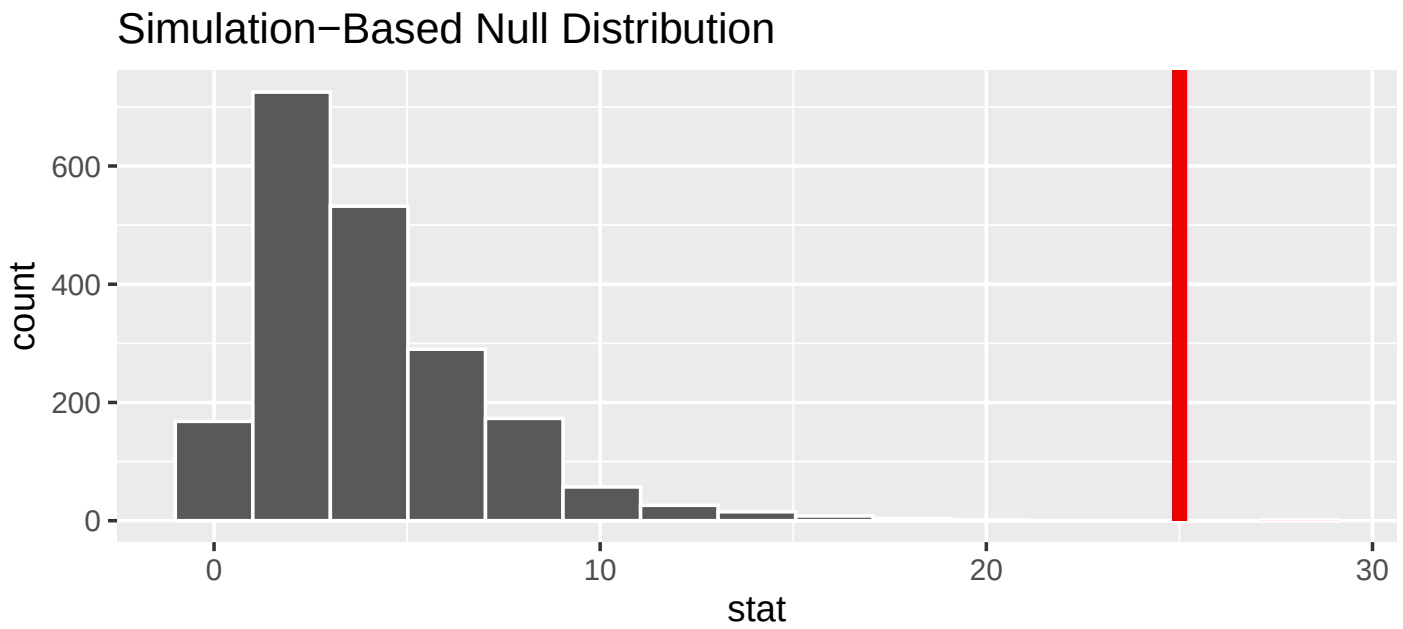
```
set.seed(49)
twitch_null <- twitch %>%
  specify(genotype ~ group) %>%
  hypothesize(null = "independence") %>%
  generate(reps = 2000, type = "permute") %>%
  calculate(stat="Chisq")
twitch_null %>% visualize()+shade_p_value(obs_stat = 25, direction = "right")
```



P-value and conclusions

Using `infer`, the approximate p-value is

```
twitch_null %>% get_p_value(obs_stat = 25, direction = "right")
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## # A tibble: 1 x 1
##   p_value
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  - This sample gives good evidence that `group` and `genotype` are associated.
- What association is there?
  - We'll need to further study and experiment to find out.