Lesson 8: Data visualization of two variables

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Learning Objectives

1. Visualize relationships between two numeric variables using scatterplots and determine their correlation
2. Visualize relationships between two categorical variables using contingency tables and segmented barplots
3. Visualize relationships between a categorical variable and a numeric variable using side-by-side boxplots, density plots, and ridgeline plots

Where are we?

Data
- Collecting data
- Categorical vs. Numeric
- Summary statistics
- Data visualization

Probability
- Probability rules
- Independence, conditional
- Random variables and probability distributions
- Linear combinations
- Binomial, Normal, and Poisson

Sampling Variability, and Statistical Inference
- Sampling distributions
- Central Limit Theorem
- Confidence Intervals
- Hypothesis tests

Inference for continuous data/outcomes
- One sample t-test
- 3+ independent samples
- Simple linear regression / correlation
- 2 sample tests: paired and independent
- Power and sample size
- Non-parametric tests

Inference for categorical data/outcomes
- One proportion test
- Fisher's exact test
- Non-parametric tests
- Chi-squared test
- 2 proportion test
- Power and sample size

R
- Basics
- Reproducibility
- Quarto
- Packages
- Data visualization
- Data wrangling
- R Projects
- …

Relationships between two variables

- Many studies are motivated by a researcher examining how two or more variables are related

- Example questions about relationships:
  - Do the values of one variable increase as the values of another decrease?
  - Do the values of one variable tend to differ by the levels of another variable?

categorial

- Today we are introducing **summarization and data visualization methods** for exploring and summarizing **relationships between two variables**

- Approaches vary depending on whether the two variables are:
  - Both numerical
  - Both categorical
  - One numerical and one categorical

We often identify a response variable from our research question

Response Variable

A **response variable** is defined by the particular research question a study seeks to address

- It **measures the outcome of interest** in the study

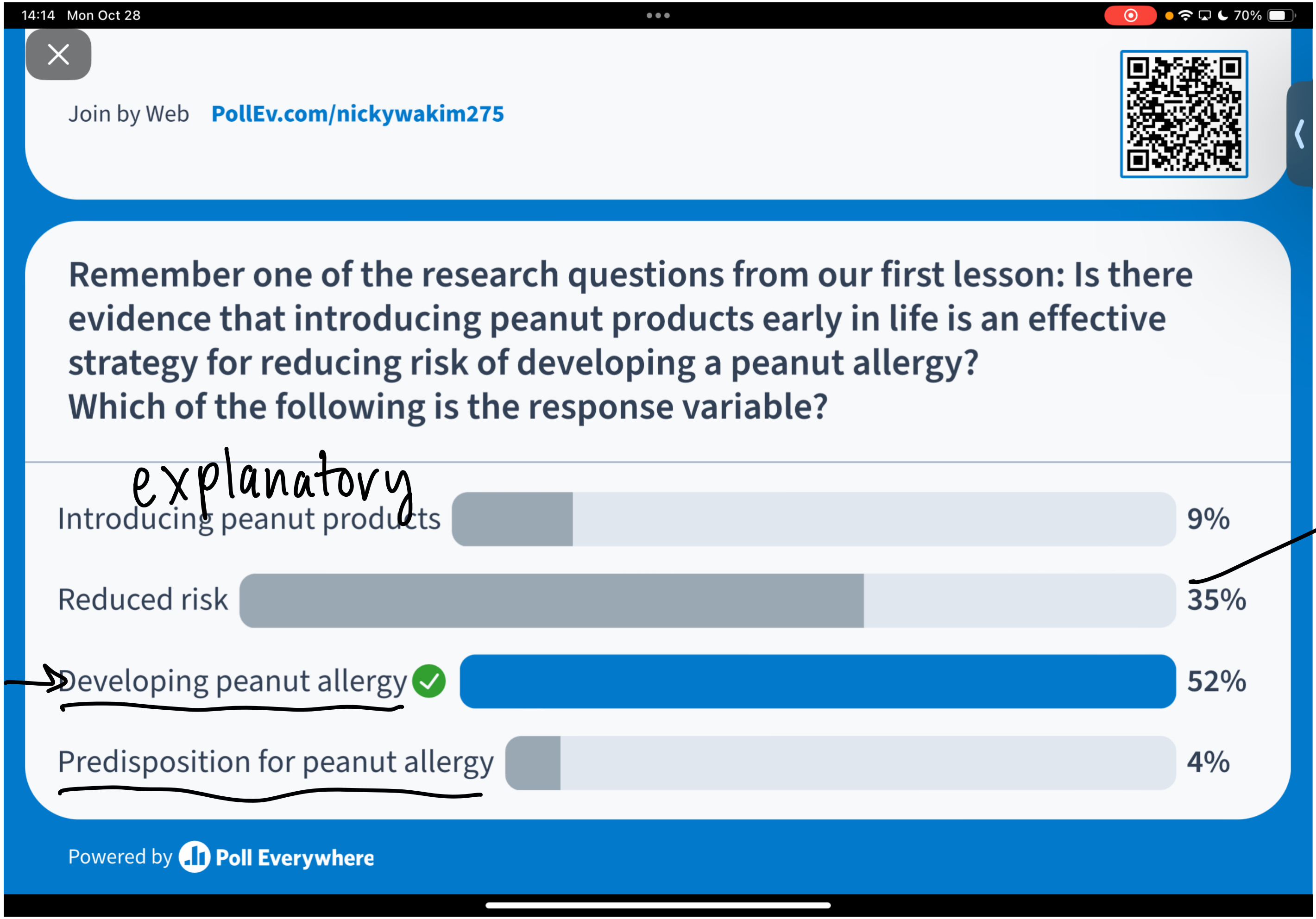
Explanatory Variable

A study will typically examine whether the values of a response variable differ as values of an **explanatory variable** change, and if so, how the two variables are related.

- A given study may examine several explanatory variables for a single response variable

- Sometimes we're interested in viewing the relationship between our **response variable** and **explanatory variable(s)**
- Sometimes we're just interested in viewing the relationship **between explanatory variables**

Poll Everywhere Question 1



Reduced risk is more of statistic the resp var

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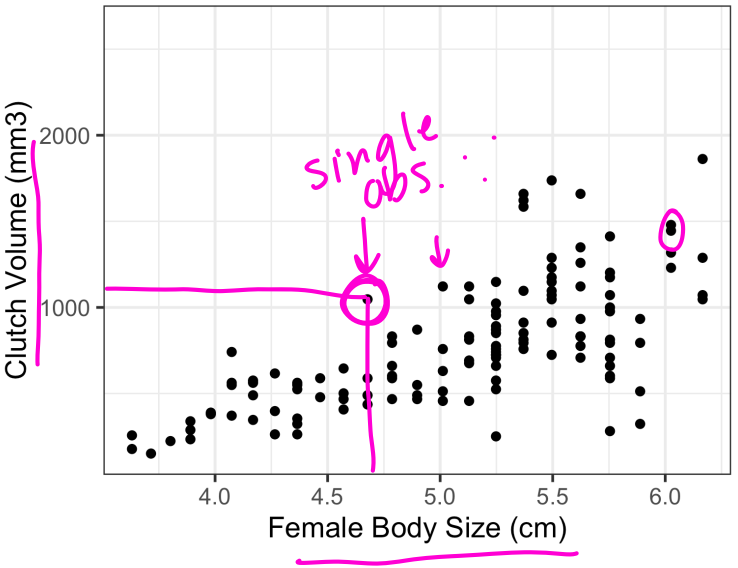
Scatterplots

- Scatterplots provide case-by-case view of the **relationship between two numerical variables**

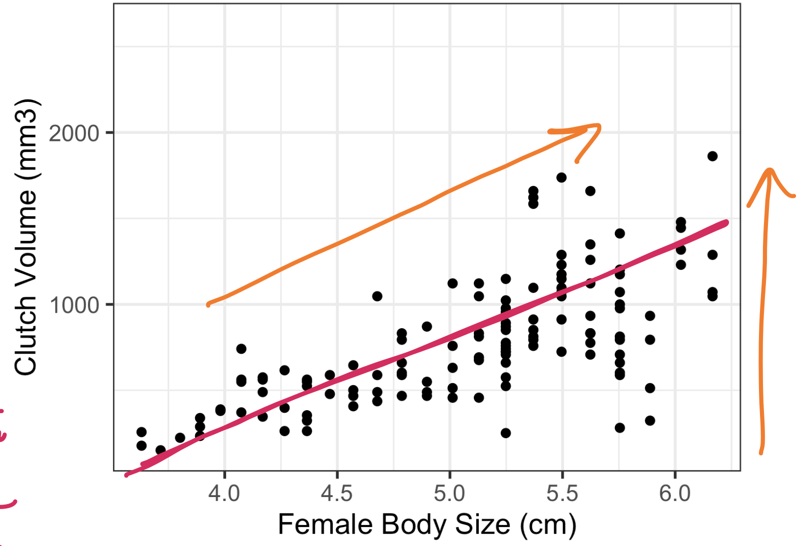
- We can make a scatterplot of clutch volume vs. body size, with clutch volume on the y-axis and body size on the x-axis
- Each point represents an observation (egg clutch) with its measurement for clutch volumn and body size of parent

```
ggplot(data = frog,
       aes(x = body.size,
           y = clutch.volume)) +
  geom_point(size = 3) +
  labs(x = "Female Body Size (cm)",
       y = "Clutch Volume (mm3)")
```



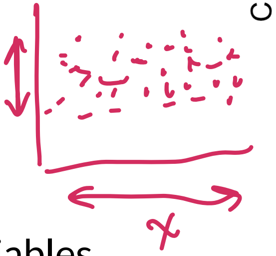
Describing associations between 2 numerical variables

- Two variables x and y are
  - **Positively associated** if y increases as x increases
  - **Negatively associated** if y decreases as x increases



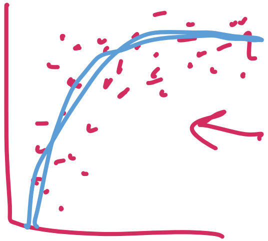
- If there is no association between the variables, then we say they are **uncorrelated** or **independent**

regardless of x, y generally stays same



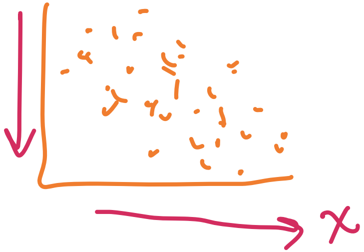
- The term "association" is a very general term
  - Can be used for numerical or categorical variables
  - Not specifically referring to linear associations

Female body size and clutch volume are positively associated with each other



← pos. association

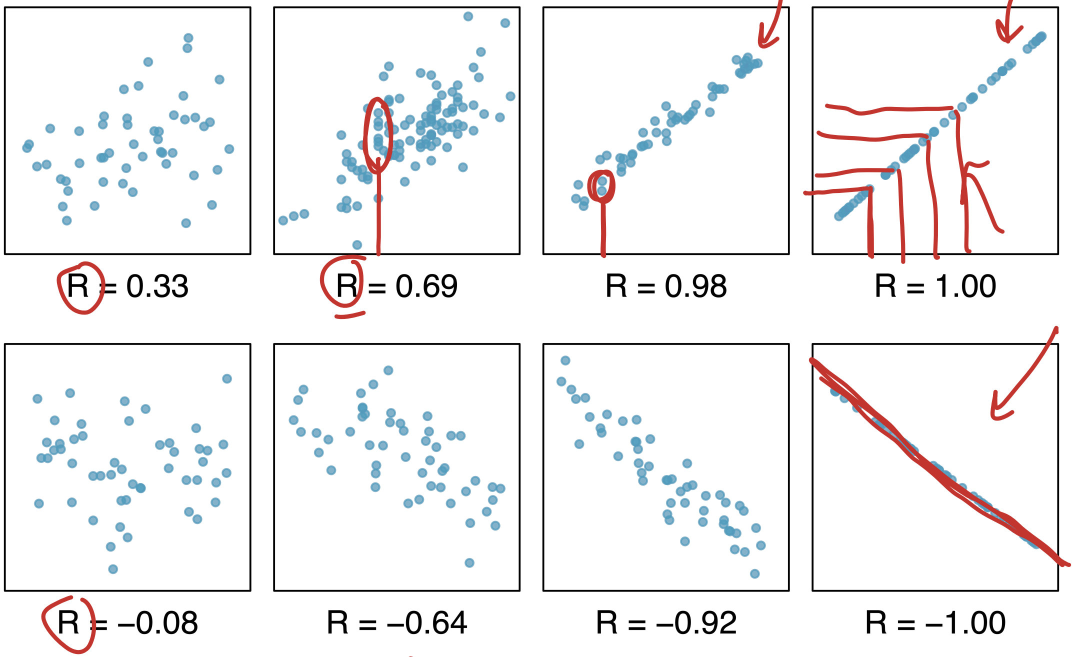
Neg assoc:



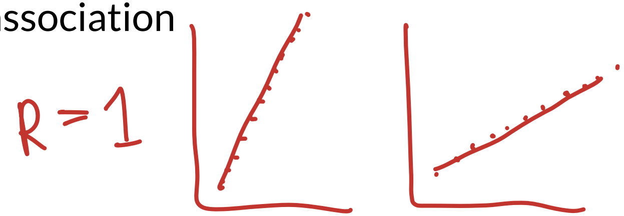
(Pearson) Correlation coefficient (r)

$-1 \le r \le 1$

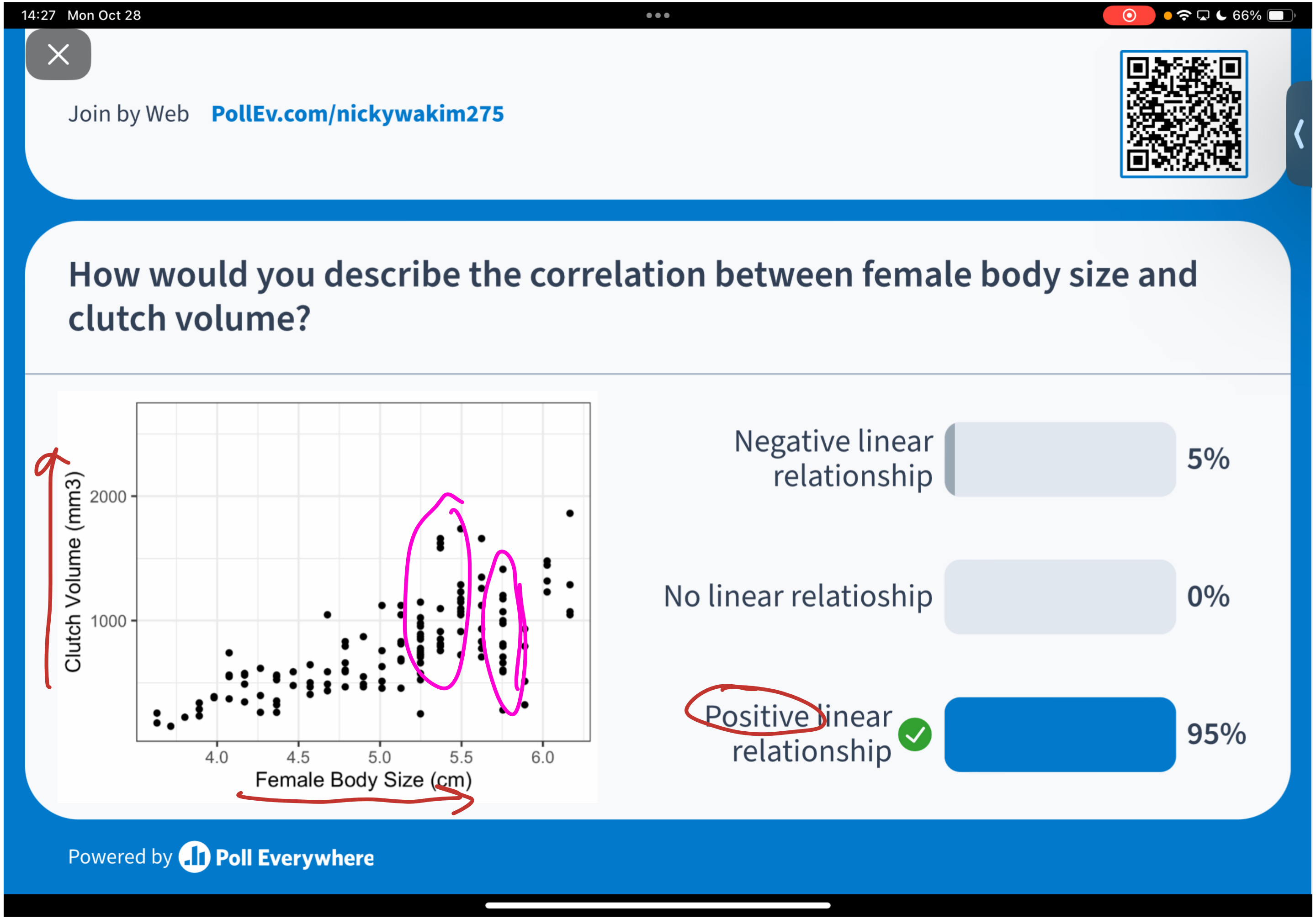
- $r = -1$ indicates a **perfect negative linear relationship**: As one variable increases, the value of the other variable tends to go down, following a *straight line*
- $r = 0$ indicates **no linear relationship**: The values of both variables go up/down independently of each other
- $r = 1$ indicates a **perfect positive linear relationship**: As the value of one variable goes up, the value of the other variable tends to go up as well in a linear fashion



- The closer r is to ±1, the stronger the linear association



Poll Everywhere Question 2

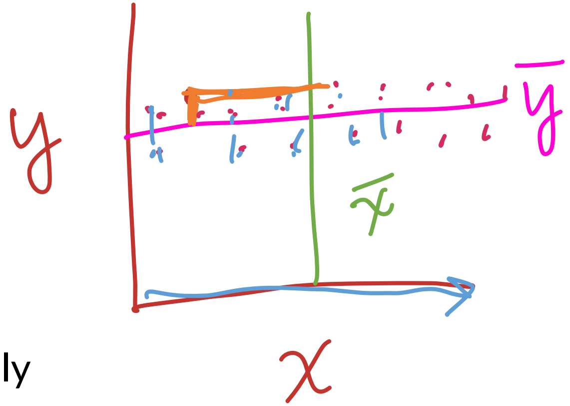


(Pearson) Correlation coefficient (r): formula

The (Pearson) correlation coefficient of variables x and y can be computed using the formula

$$r = \frac{1}{n-1} \sum_{i=1}^{n} \left(\frac{x_i - \bar{x}}{s_x} \right) \left(\frac{y_i - \bar{y}}{s_y} \right)$$

avg are 0.



where

- $(x_1, y_1), (x_2, y_2), \ldots, (x_n, y_n)$ are the n paired values of the variables x and y
- s_x and s_y are the sample standard deviations of the variables x and y, respectively

- We can use `cor()` in R to calculate this! two numeric variables!

```
cor(frog$body.size, frog$clutch.volume, use = "pairwise.complete.obs")
```

```
[1] 0.6755435
```

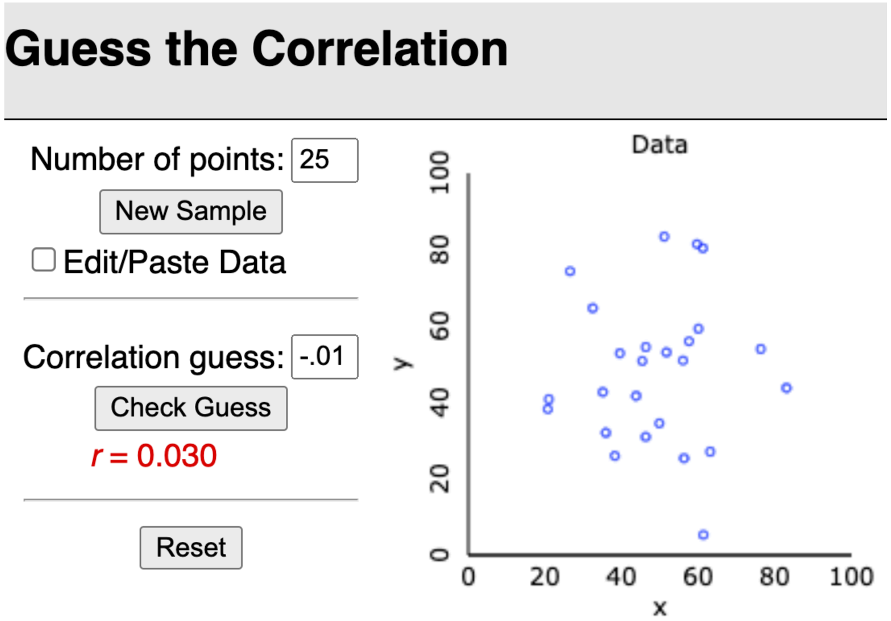
obs has one missing

?cor

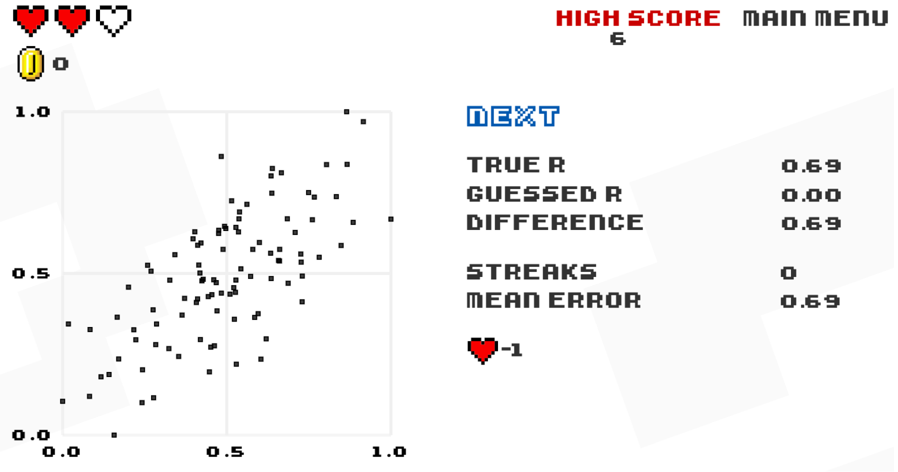
if no missing data, don't need to use "use"

Guess the correlation game!

Rossman & Chance's applet



Or, for the Atari-like experience



http://guessthecorrelation.com/

Tracks performance of guess vs. actual, error vs. actual, and error vs. trial

http://www.rossmanchance.com/applets/GuessCorrelation.html

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From Lesson 4: Contingency tables

- We can start looking at the **contingency table** for hypertension for different age groups
  - **Contingency table:** type of data table that displays the frequency distribution of two or more categorical variables

Table: Contingency table showing hypertension status and age group, in thousands.

Age Group	Hypertension	No Hypertension	Total
18-39 years	8836	112206	121042
40-59 years	42109	88663	130772
60+ years	39917	21589	61506
Total	90862	222458	313320

8,836,000 people are both 18-39 yo & have hyp

From Lesson 4: Probability tables

Table: Probability table summarizing hypertension status and age group.

Age Group	Hypertension	No Hypertension	Total
18-39 years	0.0282	0.3581	0.3863
40-59 years	0.1344	0.2830	0.4174
60+ years	0.1274	0.0689	0.1963
Total	0.2900	0.7100	1.0000

marginal for age grp

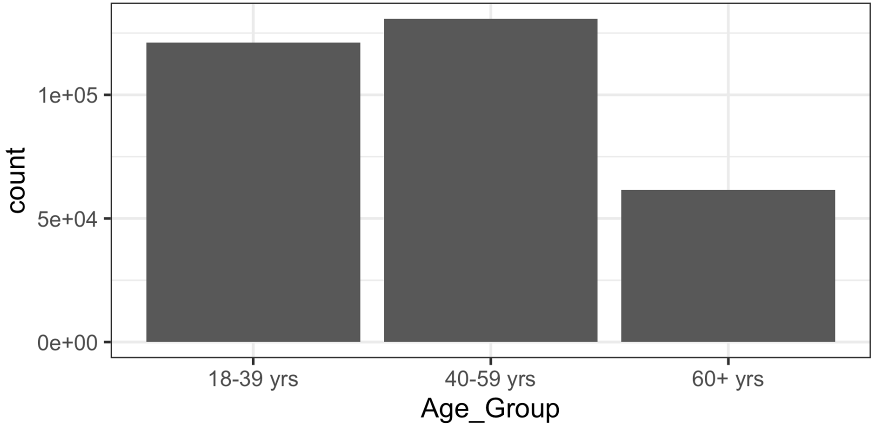
- **Joint probability**: intersection of row and column
- **Marginal probability**: row or column total

We can work towards visualizing the data in contingency and probability tables

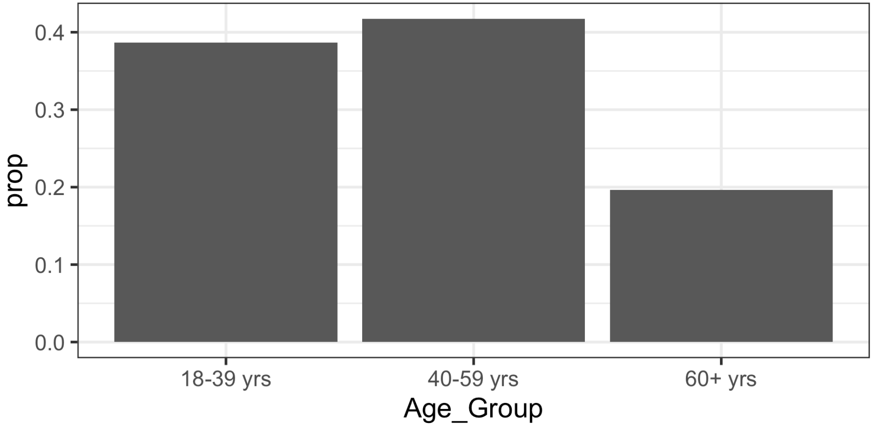
Last time: Barplots

Counts (below) vs. percentages (right)

```
ggplot(data = hyp_data,
       aes(x = Age_Group)) +
  geom_bar()
```




```
ggplot(data = hyp_data,
       aes(x = Age_Group)) +
  geom_bar(aes(y = stat(prop),
               group = 1))
```

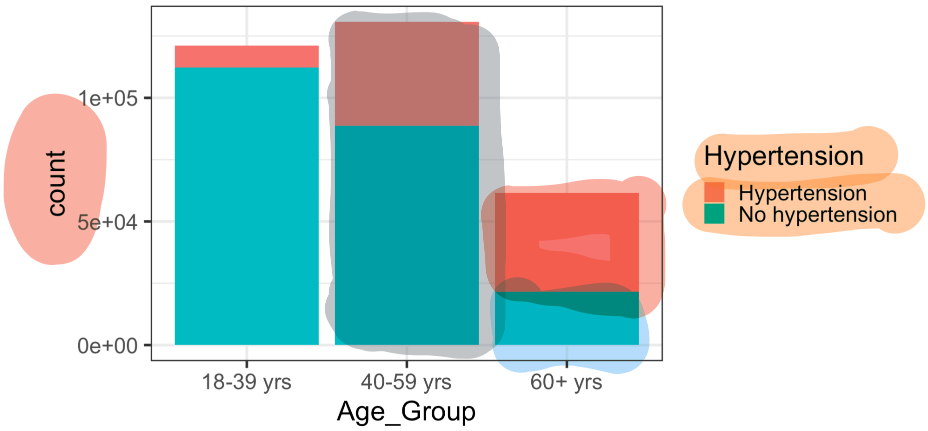


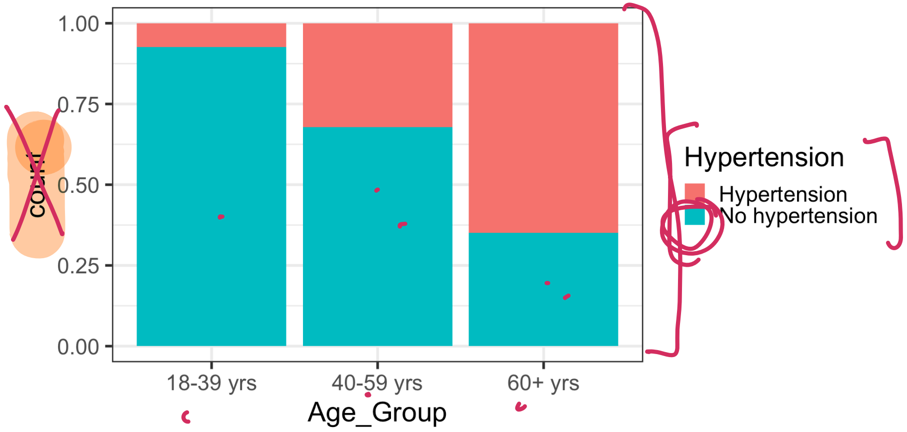
Barplots with 2 variables: segmented bar plots

- Way of visualizing the information from a contingency table

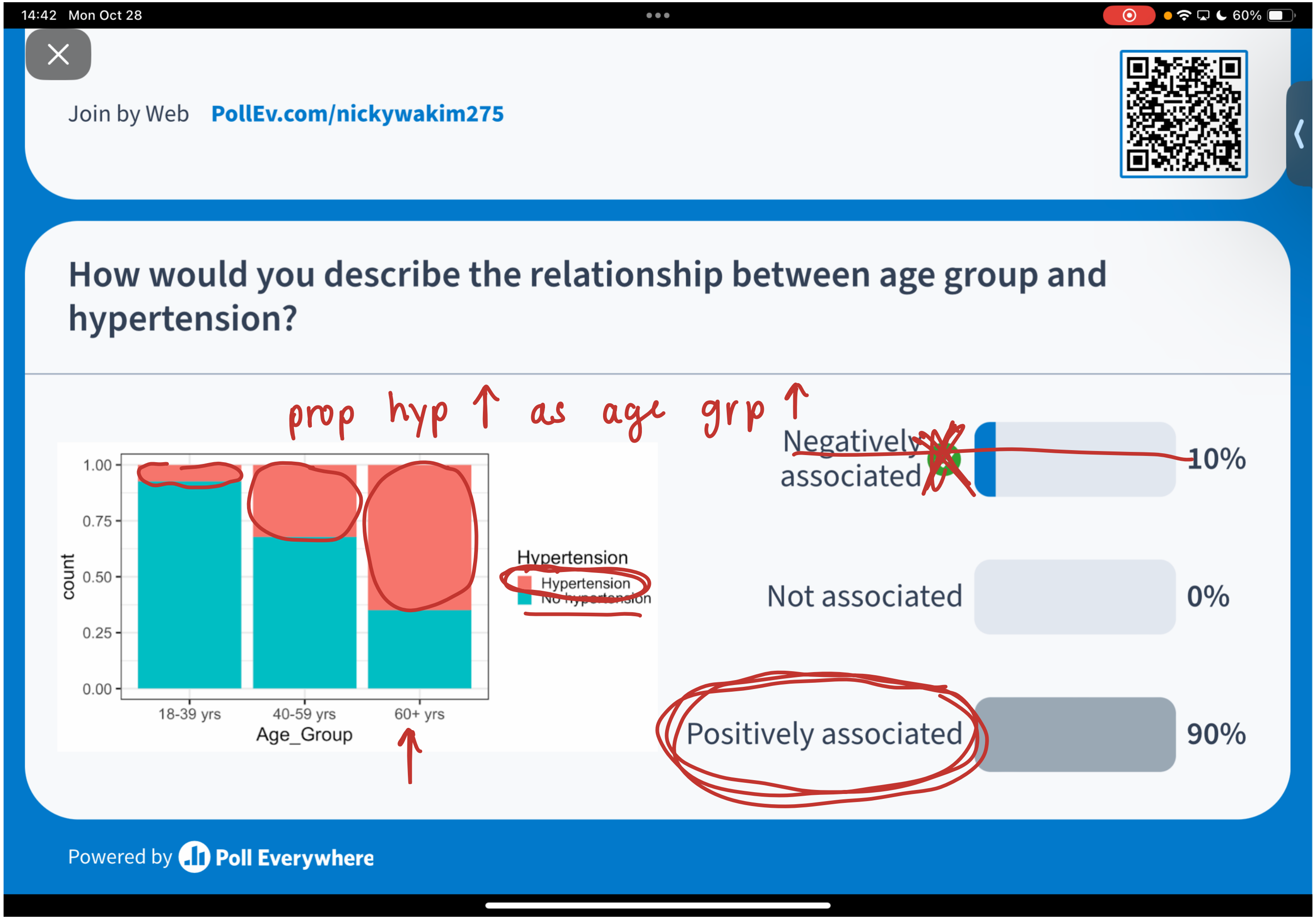
```
ggplot(data = hyp_data,
         aes(x = Age_Group,
         fill = Hypertension)) +
  geom_bar()
```

```
ggplot(data = hyp_data,
         aes(x = Age_Group,
         fill = Hypertension)) +
  geom_bar(position = "fill")
```



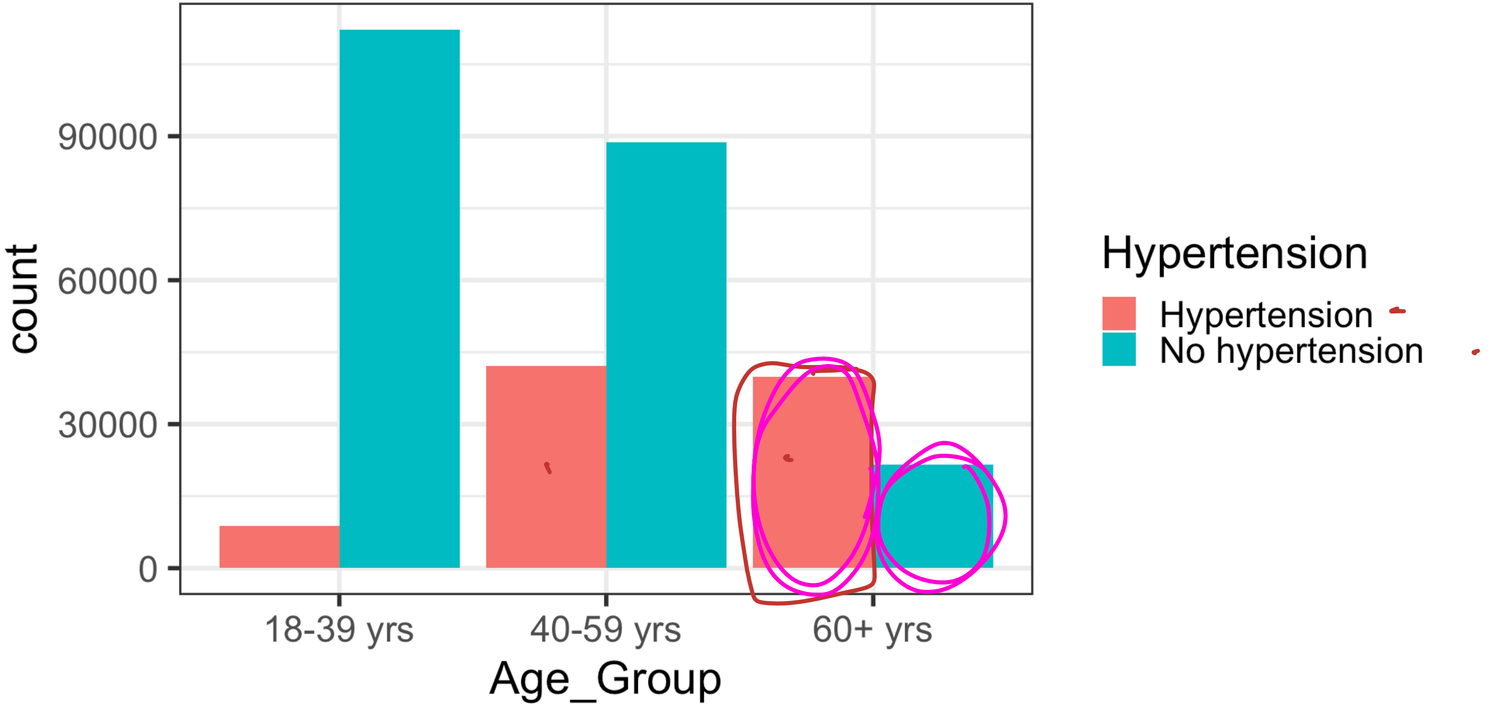


Poll Everywhere Question 3



Barplots with 2 variables: side-by-side bar plots

```
ggplot(data = hyp_data,
       aes(x = Age_Group,
       fill = Hypertension)) +
  geom_bar(position = "dodge")
```



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Visualizing relationships between numerical and categorical variables

- Useful visualizations for directly comparing how the distribution of a numerical variable differs by category:
  - Side-by-side boxplots
  - Side-by-side boxplots with data points
  - Density plots by group
  - Ridgeline plot

We need to introduce a new dataset for this

- Study investigating whether ACTN3 genotype at a particular location (residue 577) is associated with change in muscle function

- **Categorical variable:** genotypes (CC, TT, CT)

- **Numeric variable:** Muscle function, measured as percent change in non-dominant arm strength

- We can start the investigation by plotting the relationship

Side-by-side boxplots

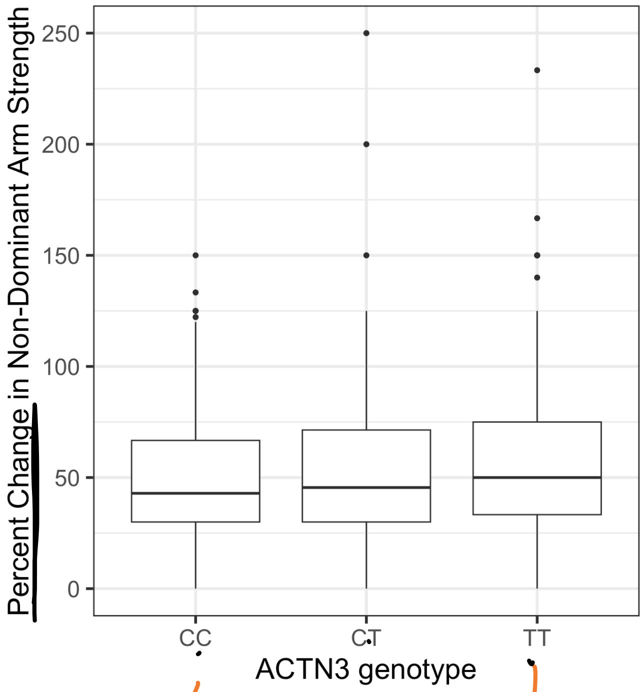
dataset using is 'famuss'

- We can look at the boxplot of percent change for each genotype

```
ggplot(data = famuss,
       aes(x = actn3.r577x,
           y = ndrm.ch)) +
  geom_boxplot() +
  labs(x = "ACTN3 genotype",
       y = "Percent Change in Non-Dominan
```

genotype

muscle fn



Side-by-side boxplots with data points

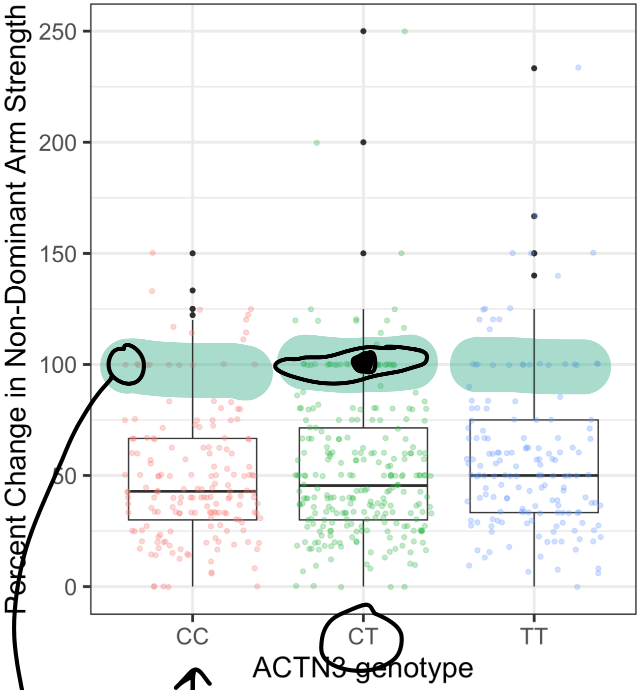
least likely to use

- We can look at the boxplot of percent change for each genotype **with points shown so we can see the distribution of observations better**

```
ggplot(data = famuss,
       aes(x = actn3.r577x,
           y = ndrm.ch)) +
  geom_boxplot() +
  labs(x = "ACTN3 genotype",
       y = "Percent Change in Non-Dominan
  geom_jitter(aes(color = actn3.r577x),
    alpha = 0.3,
    show.legend = FALSE,
    position = position_jitter(
      height = 0.4))
```

transparency

aes(x, y, color)



person w/ CC&100% change

Density plots by group

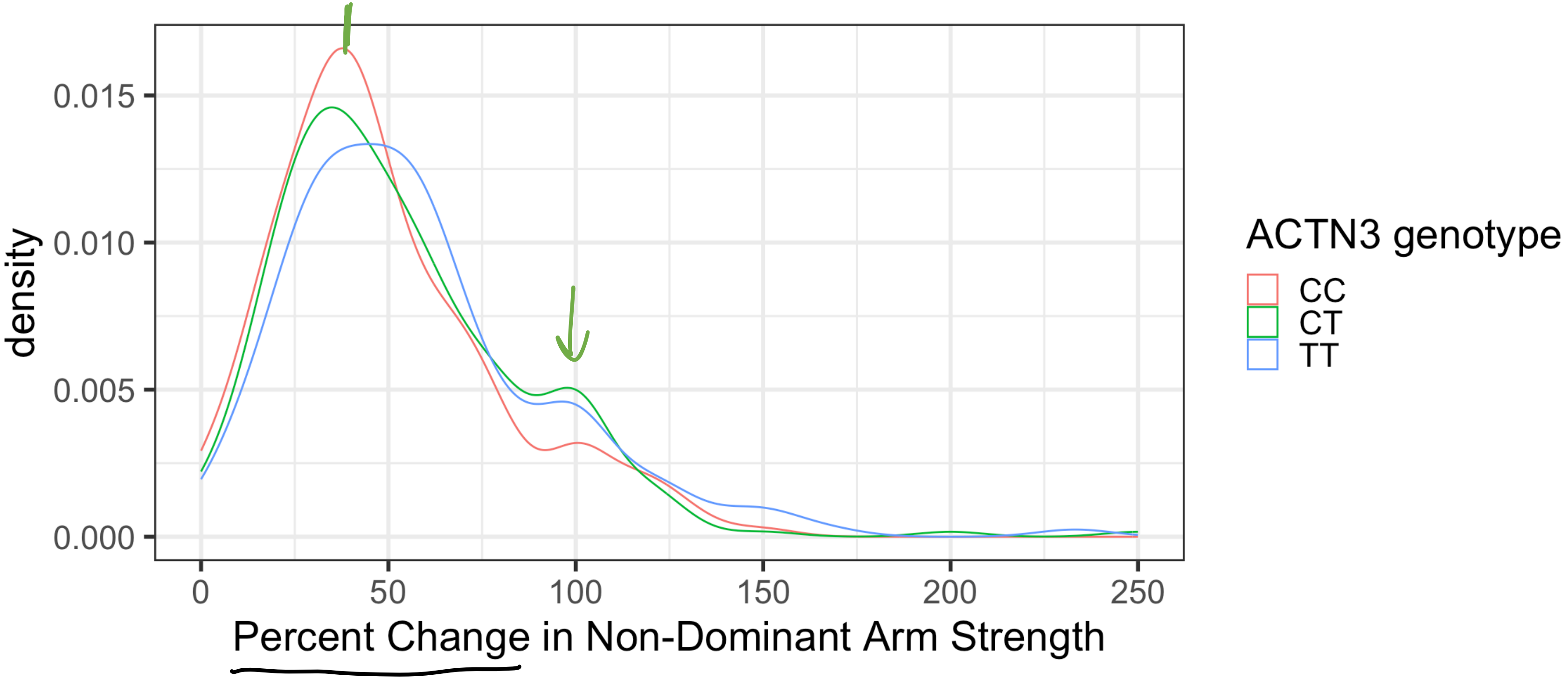
- Allows us to see the densities of percent change for each genotype

```
ggplot(data = famuss, aes(color = actn3.r577x, x = ndrm.ch)) +
  geom_density() +
  labs(x = "Percent Change in Non-Dominant Arm Strength", color = "ACTN3 genotype")
```

color by genotype

% change

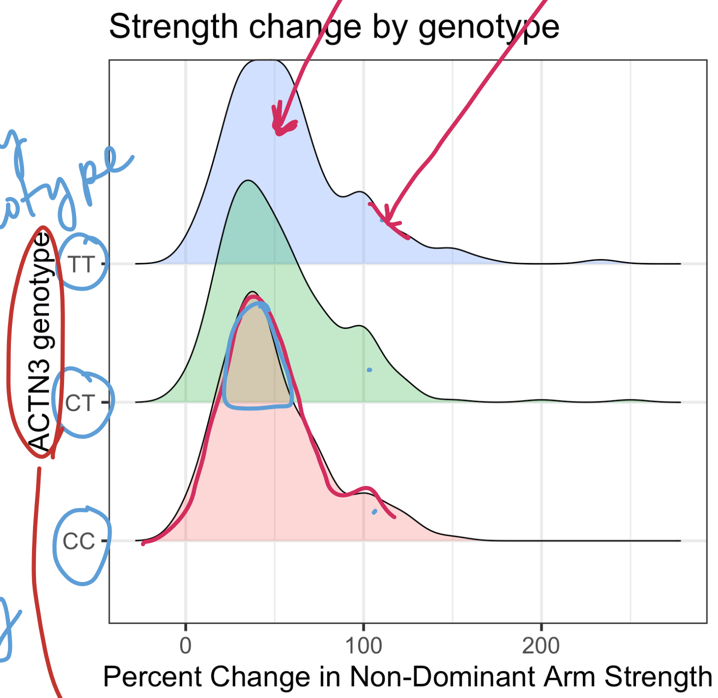
or geom_histogram()



Ridgeline plot

- Overlapped densities were easy enough to see with 3 genotypes
- If you have **many categories**, a ridgeline plot might make it easier to see

```
library(ggridges)
ggplot(data = famuss,
       aes(y = actn3.r577x,
           x = ndrm.ch,
           fill = actn3.r577x)) +
  geom_density_ridges(alpha = 0.3,
                      show.legend = FALSE) +
  labs(x = "Percent Change in Non-Dominan
       y = "ACTN3 genotype",
       title = "Strength change by genoty
```



Poll Everywhere Question 4