Lecture 21: ANOVA Examples, Introduction to Regression

STAT 324

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ANOVA Examples

Toy example. Completely made up. Just to show calculations.

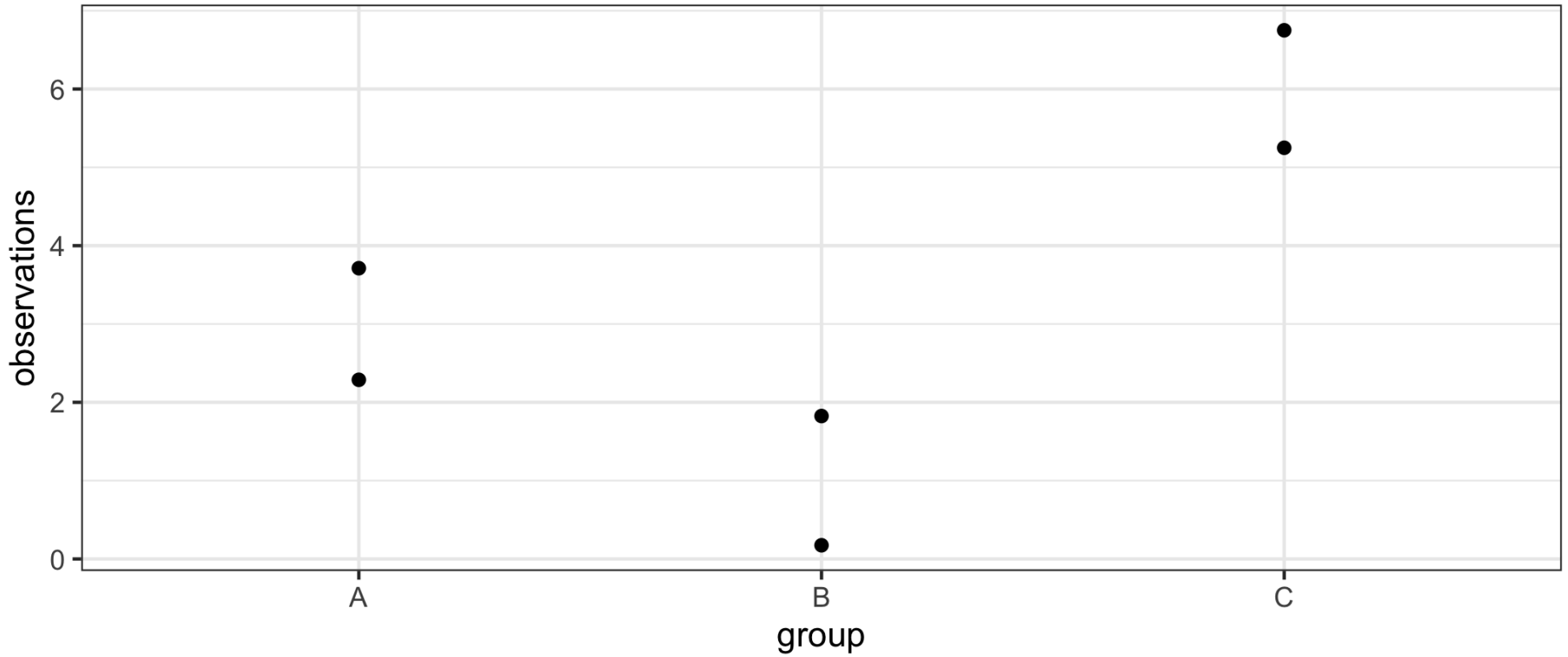
```
library(tidyverse); library(distributions3); theme_set(theme_bw())

toy_data <- tibble(group = rep(LETTERS[1:3], each = 2),
                   observations = rep(c(3,1,6), each = 2) + c(-0.75,0.75)*rep(c(0.95,

toy_data
```

```
# A tibble: 6 x 2
  group observations
  <chr>        <dbl>
1 A            2.29
2 A            3.71
3 B            0.175
4 B            1.83
5 C            5.25
6 C            6.75
```

ANOVA Examples

Plot:

```
ggplot(toy_data, aes(x = group, y = observations)) +
  geom_point()
```



ANOVA Examples

Want to test $H_0 : \mu_A = \mu_B = \mu_C$ against H_A : difference somewhere using $\alpha = 0.1$. First, need to check for equal variance in the three groups, and normality of data. (Note: latter is kind of pointless with this amount of data, but we will do so anyway.)

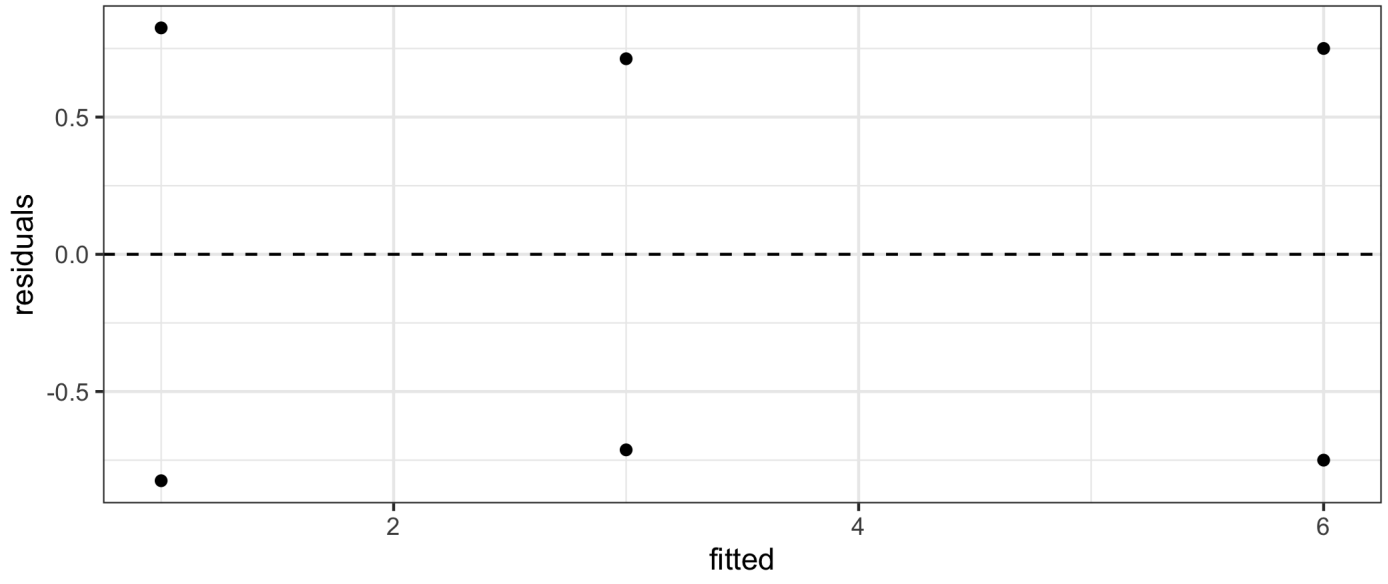
Remember, we check this using the residuals. Generally, residuals = observations - fitted. In particular for ANOVA, residuals = observations - group means.

```
residuals <- toy_data %>%
  group_by(group) %>%
  mutate(fitted = mean(observations),
         residuals = observations - fitted)
```

ANOVA Examples

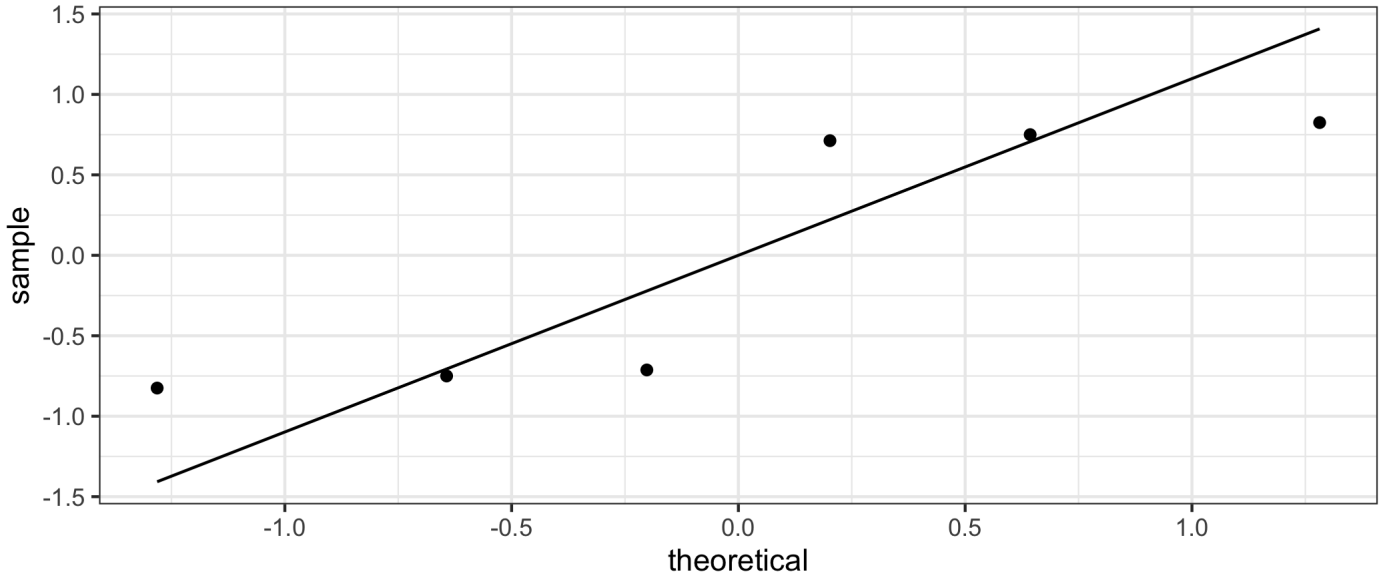
Equal variance: are residuals equally spread around 0 no matter the value of the fitted value?

```
ggplot(residuals,
       aes(x = fitted, y = residuals)) +
  geom_hline(yintercept = 0,
             linetype = "dashed") +
  geom_point()
```



ANOVA Examples

```
ggplot(residuals,
       aes(sample = residuals)) +
  geom_qq() + geom_qq_line()
```



ANOVA Examples

Observations:

```
toy_data
```

```
# A tibble: 6 x 2
  group observations
  <chr>        <dbl>
1 A             2.29
2 A             3.71
3 B             0.175
4 B             1.83
5 C             5.25
6 C             6.75
```

Overall mean:

```
toy_data %>%
  summarize(overall_mean = mean(observat
```

```
# A tibble: 1 x 1
  overall_mean
         <dbl>
1         3.33
```

Group means:

```
toy_data %>%
  group_by(group) %>%
  summarize(group_means = mean(observati
```

```
# A tibble: 3 x 2
  group group_means
  <chr>        <dbl>
1 A                3
2 B                1
3 C                6
```

ANOVA Examples

$$\begin{aligned}\text{SSTrt} &= \sum_{i=1}^{3}\sum_{j=1}^{n_i}(\bar{y}_{i\cdot} - \bar{y}_{\cdot\cdot})^2 \\ &= (3-3.33)^2 + (3-3.33)^2 + \\ &\quad (1-3.33)^2 + (1-3.33)^2 + \\ &\quad (6-3.33)^2 + (6-3.33)^2 \\ &= 25.33\end{aligned}$$

$$\begin{aligned}\text{SSTotal} &= \sum_{i=1}^{3}\sum_{j=1}^{n_i}(y_{ij} - \bar{y}_{i\cdot})^2 \\ &= (2.2875-3.33)^2 + (3.7125-3.33)^2 + \\ &\quad (0.175-3.33)^2 + (1.825-3.33)^2 + \\ &\quad (5.25-3.33)^2 + (6.75-3.33)^2 \\ &= 28.83\end{aligned}$$

$$\begin{aligned}\text{SSE} &= \sum_{i=1}^{3}\sum_{j=1}^{n_i}(y_{ij} - \bar{y}_{i\cdot})^2 \\ &= (2.2875-3)^2 + (3.7125-3)^2 + \\ &\quad (0.175-1)^2 + (1.825-1)^2 + \\ &\quad (5.25-6)^2 + (6.75-6)^2 \\ &= 3.5\end{aligned}$$

$$df_{\text{Trt}} = t - 1 = 3 - 1 = 2$$

$$df_{\text{E}} = N - t = 6 - 3 = 3$$

$$df_{\text{Total}} = N - 1 = 6 - 1 = 5$$

ANOVA Examples

$$MSTrt = \frac{SS_{\text{Trt}}}{df_{\text{Trt}}} = \frac{25.33}{2} \approx 12.66$$

$$MSE = \frac{SS_{\text{E}}}{df_{\text{E}}} = \frac{3.5}{3} \approx 1.17$$

$$F_{\text{obs}} = \frac{MSTrt}{MSE} = \frac{12.66}{1.17} \approx 10.82$$

$$\text{p-value} = P(F > F_{\text{obs}}) = P(F > 10.82), \text{ where } F \sim F_{2,3}$$

```
F_2_3 <- FisherF(2,3)
1 - cdf(F_2_3, 10.82)
```

```
[1] 0.04248355
```

Source	SS	df	MSE	F_obs	p-value
Treatment	25.33	2	12.66	10.82	0.04
Error	3.5	3	1.17		
Total	28.83	5			

Since the p-value is less than $\alpha = 0.01$, we reject the null hypothesis.

ANOVA Examples

Double check using built-in aov function:

```
toy_anova <- aov(data = toy_data,
                 observations ~ group)

summary(toy_anova)
```

```
            Df Sum Sq Mean Sq F value Pr(>F)
group        2 25.333  12.667   10.85 0.0423 *
Residuals    3  3.502   1.167
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Looks good ($\pm$ rounding error).

ANOVA Examples

Where is the difference? We do pairwise tests. Example: group A vs group B.

Using Fisher's LSD, we do pairwise t-tests using MSE "instead of" s_p^2. First, need quantile from t-distribution:

```
quantile(StudentsT(df = 2), 1-0.1/2)
```

```
[1] 2.919986
```

$$\bar{y}_{A\cdot} - \bar{y}_{B\cdot} \pm t_{0.1/2, df_E}\sqrt{MSE(1/n_A + 1/n_B)} = 3 - 1 \pm 2.92\sqrt{1.167(1/10 + 1/10)}$$
$$= 2 \pm 0.998$$

Using Bonferroni, we use $t_{(\alpha/2)/m, df_E}$ instead of $t_{\alpha/2, df_E}$:

```
quantile(StudentsT(df = 2), 1-(0.1/2)/3)
```

```
[1] 5.339333
```

$$\bar{y}_{A\cdot} - \bar{y}_{B\cdot} \pm t_{(0.1/2)/3, df_E}\sqrt{MSE(1/n_A + 1/n_B)} = 3 - 1 \pm 5.34\sqrt{1.167(1/10 + 1/10)}$$
$$= 2 \pm 1.824$$

ANOVA Examples

Using Tukey's HSD method, we use $\frac{Q_{\alpha,t,df_{\text{E}}}}{\sqrt{2}}$ instead of $t_{\alpha/2,df_{\text{E}}}$:

```
quantile(Tukey(3, 3, 1), 0.95)/sqrt(2) # or qtukey(0.95, 3, 3)/sqrt(2)
```

```
[1] 4.178763
```

$$\bar{y}_{A\cdot} - \bar{y}_{B\cdot} \pm \frac{Q_{\alpha,t,df_{\text{E}}}}{\sqrt{2}}\sqrt{MSE(1/n_A + 1/n_B)} = 3 - 1 \pm 4.18\sqrt{1.167(1/10 + 1/10)}$$
$$= 2 \pm 1.428$$

ANOVA Examples

A neat function for this is `PostHocTest` from the `DescTools` package. It can do any of the above mentioned methods:

```
# If not installed, use install.packages("DescTools") to install
library(DescTools)

(LSD <- PostHocTest(toy_anova, method = "lsd", conf.level = 0.9))
```

```
  Posthoc multiple comparisons of means : Fisher LSD
    90% family-wise confidence level

$group
    diff     lwr.ci    upr.ci   pval
B-A   -2 -4.5424904 0.5424904 0.1612
C-A    3  0.4575096 5.5424904 0.0692 .
C-B    5  2.4575096 7.5424904 0.0190 *

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

ANOVA Examples

```
(HSD <- PostHocTest(toy_anova, method = "hsd", conf.level = 0.9))
```

```
  Posthoc multiple comparisons of means : Tukey HSD
    90% family-wise confidence level

$group
    diff     lwr.ci   upr.ci   pval
B-A   -2 -5.4127784 1.412778 0.2957
C-A    3 -0.4127784 6.412778 0.1342
C-B    5  1.5872216 8.412778 0.0382 *

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

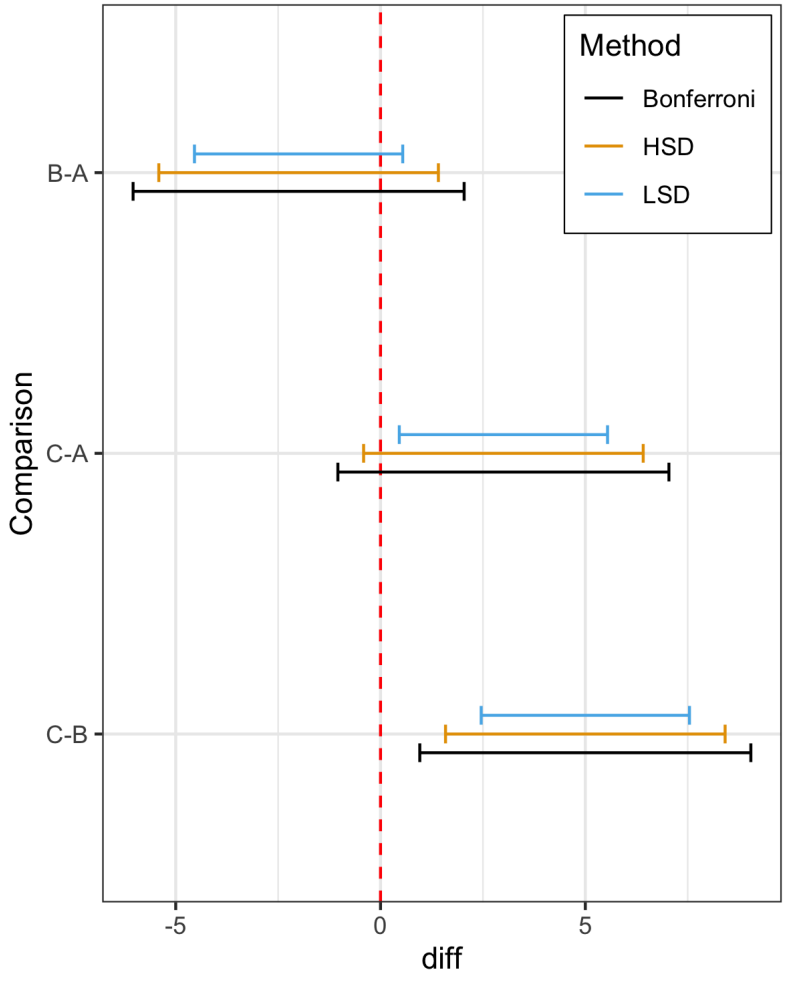
ANOVA Examples

```
(BONF <- PostHocTest(toy_anova, method = "bonferroni", conf.level = 0.9))
```

```
  Posthoc multiple comparisons of means : Bonferroni
    90% family-wise confidence level

$group
    diff     lwr.ci   upr.ci   pval
B-A   -2 -6.0410924 2.041092 0.4837
C-A    3 -1.0410924 7.041092 0.2075
C-B    5  0.9589076 9.041092 0.0570 .

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

ANOVA Examples

```
for_comparisons_plot <- bind_rows(
  LSD$group %>%
    as_tibble(rownames = "Comparison") %
    mutate(type = "LSD"),
  HSD$group %>%
    as_tibble(rownames = "Comparison") %
    mutate(type = "HSD"),
  BONF$group %>%
    as_tibble(rownames = "Comparison") %
    mutate(type = "Bonferroni")
) %>%
  mutate(Comparison = forcats::fct_reorc


ggplot(for_comparisons_plot,
       aes(x = diff, xmin = lwr.ci, xmax
  geom_vline(xintercept = 0, color = "re
  geom_errorbar(position = position_dodg
  ggthemes::scale_color_colorblind("Meth
  theme(legend.position = c(1,1), # move
        legend.justification = c(1.05,1.
        legend.background = element_rect
```



ANOVA Examples

Real data: Plant growth data.

```
data("PlantGrowth"); plant_growth <- as_

DT::datatable(plant_growth,
              options = list(paging = FA
              rownames = FALSE)
```

Yield from plants measured by dried weight.

Three groups: control (`ctrl`), treatment 1 (`trt1`), and treatment 2 (`trt2`).

Question: is the yield different between the groups? And if so, which give the largest yield?

weight	group
4.17	ctrl
5.58	ctrl
5.18	ctrl
6.11	ctrl
4.5	ctrl
4.61	ctrl
5.17	ctrl
4.53	ctrl
5.33	ctrl
5.14	ctrl
4.81	trt1

ANOVA Examples

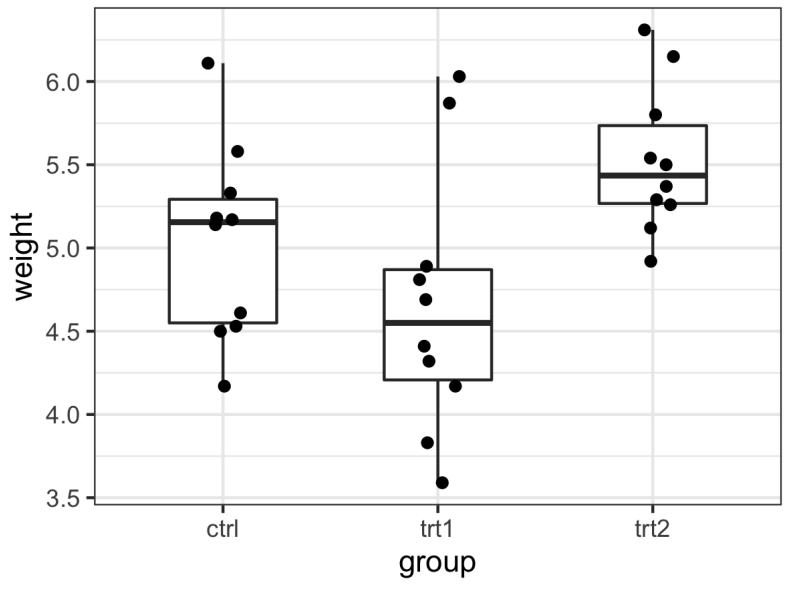
First, we aim at answering **if** there's a difference. I.e. we want to test $H_0 : \mu_{\text{ctrl}} = \mu_{\text{trt1}} = \mu_{\text{trt2}}$ against the alternative H_A : at least one is different. We will use $\alpha = 0.05$.

Summary statistics:

```
plant_growth %>%
  group_by(group) %>%
  summarize(n = n(),
            average = mean(weight),
            s = sd(weight))
```

```
# A tibble: 3 x 4
  group     n average     s
  <fct> <int>   <dbl> <dbl>
1 ctrl     10    5.03 0.583
2 trt1     10    4.66 0.794
3 trt2     10    5.53 0.443
```

```
ggplot(plant_growth, aes(x = group, y =
  geom_boxplot(width = 0.5, coef = Inf)
  geom_jitter(width = 0.1, height = 0)
```



ANOVA Examples

The question is: does it seem like the variation between the groups is small enough that it could be due to random chance? Or is it large enough that we reject the null?

Answer this question by looking at "variation between groups"/"variation within groups", i.e. the F statistic.

"variation within groups" = MSTrt = $\frac{SSTrt}{df_{\text{Trt}}} = \frac{1}{t-1}\sum_{i=1}^{t}\sum_{j=1}^{n_i}(\bar{y}_{i\cdot} - \bar{y}_{\cdot\cdot})^2$

"variation between groups" = MSE = $\frac{SSE}{df_{\text{E}}} = \frac{1}{N-t}\sum_{i=1}^{t}\sum_{j=1}^{n_i}(y_{ij} - \bar{y}_{i\cdot})^2$

	Treatment	Observation	Group Average	Overall Average	SSTrt contribution	SSE contribution
1	ctrl	4.17	5.032	5.07	0	0.74
2	ctrl	5.58	5.032	5.07	0	0.3
3	ctrl	5.18	5.032	5.07	0	0.02
4	ctrl	6.11	5.032	5.07	0	1.16
5	ctrl	4.5	5.032	5.07	0	0.28

ANOVA Examples

```
plant_growth_ANOVA <- aov(data = plant_growth,
                          weight ~ group)
```

Before we look at the results, we check the assumptions. The `broom` package has some great tools for working with models. Here, we use the `augment` function to attach fitted and residual values to the original data.

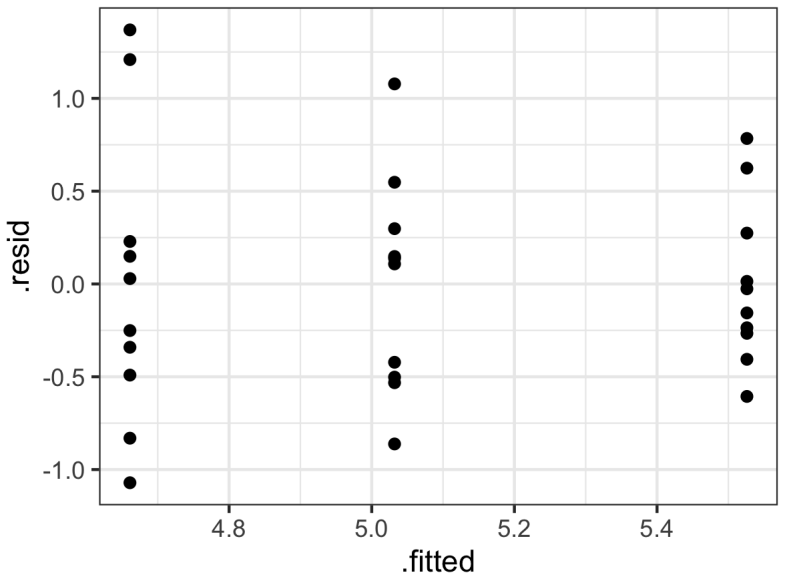
```
library(broom)

augment(plant_growth_ANOVA) %>%
  mutate_if(is.numeric, round, digits = 3) %>%
  DT::datatable(options = list(dom = "t", paging = F, scrollY = "25vh"),
                rownames = FALSE)
```

weight	group	.fitted	.se.fit	.resid	.hat	.sigma	.cooksd	.std.resid
4.17	ctrl	5.032	0.197	-0.862	0.1	0.61	0.079	-1.458
5.58	ctrl	5.032	0.197	0.548	0.1	0.625	0.032	0.927
5.18	ctrl	5.032	0.197	0.148	0.1	0.635	0.002	0.25
6.11	ctrl	5.032	0.197	1.078	0.1	0.595	0.123	1.823

ANOVA Examples

Equal variance:

```
ggplot(augment(plant_growth_ANOVA),
       aes(x = .fitted, y = .resid)) +
  geom_point()
```




```
plant_growth %>%
  group_by(group) %>%
  summarize(s = sd(weight))
```

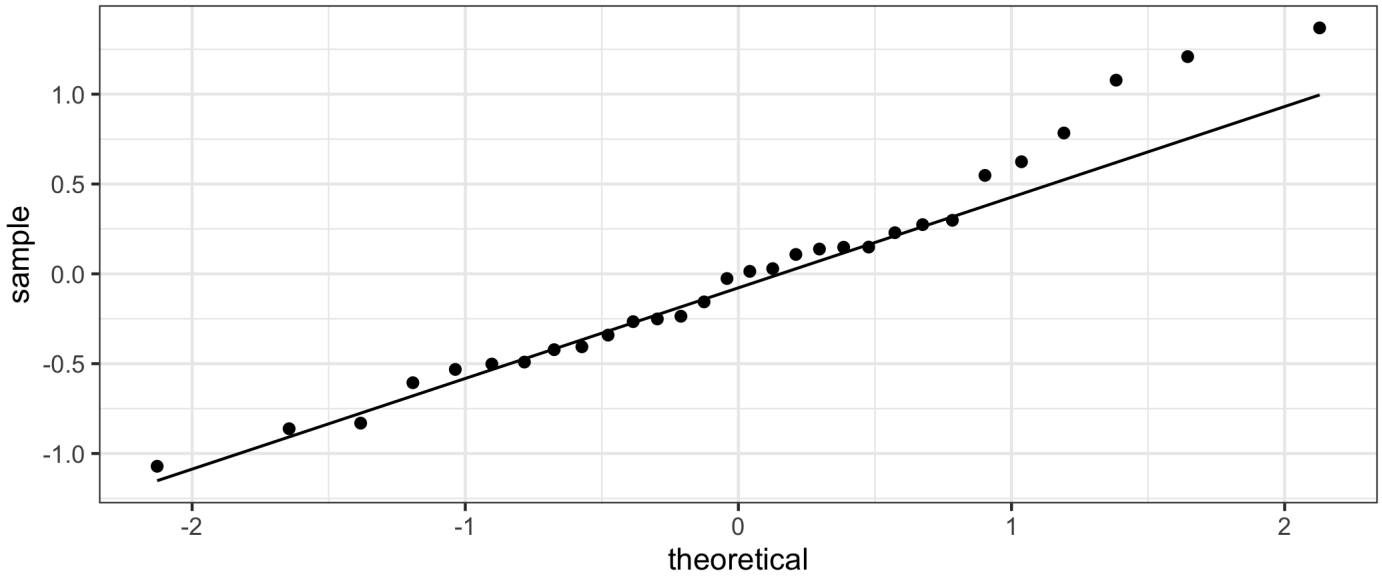
```
# A tibble: 3 x 2
  group     s
  <fct> <dbl>
1 ctrl  0.583
2 trt1  0.794
3 trt2  0.443
```

Not super happy about the figure above. For now, we will accept it.

ANOVA Examples

Normality?

```
ggplot(augment(plant_growth_ANOVA),
       aes(sample = .resid)) +
  geom_qq() +
  geom_qq_line()
```



Looks pretty good!

ANOVA Examples

Let's finally take a look at the ANOVA table:

```
summary(plant_growth_ANOVA)
```

```
            Df Sum Sq Mean Sq F value Pr(>F)
group        2  3.766  1.8832   4.846 0.0159 *
Residuals   27 10.492  0.3886
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Since the p-value is less than $\alpha = 0.05$, we reject the null hypothesis.

ANOVA Examples

Where is the difference? Using LSD:

```
PostHocTest(plant_growth_ANOVA, method = "lsd")
```

```
  Posthoc multiple comparisons of means : Fisher LSD
    95% family-wise confidence level

$group
             diff      lwr.ci    upr.ci   pval
trt1-ctrl -0.371 -0.94301261 0.2010126 0.1944
trt2-ctrl  0.494 -0.07801261 1.0660126 0.0877 .
trt2-trt1  0.865  0.29298739 1.4370126 0.0045 **

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

ANOVA Examples

Using Tukey's:

```
PostHocTest(plant_growth_ANOVA, method = "hsd")
```

```
  Posthoc multiple comparisons of means : Tukey HSD
    95% family-wise confidence level

$group
             diff     lwr.ci    upr.ci   pval
trt1-ctrl -0.371 -1.0622161 0.3202161 0.3909
trt2-ctrl  0.494 -0.1972161 1.1852161 0.1980
trt2-trt1  0.865  0.1737839 1.5562161 0.0120 *

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

ANOVA Examples

Using Bonferroni:

```
PostHocTest(plant_growth_ANOVA, method = "bonferroni")
```

```
  Posthoc multiple comparisons of means : Bonferroni
    95% family-wise confidence level

$group
             diff     lwr.ci    upr.ci   pval
trt1-ctrl -0.371 -1.0825786 0.3405786 0.5832
trt2-ctrl  0.494 -0.2175786 1.2055786 0.2630
trt2-trt1  0.865  0.1534214 1.5765786 0.0134 *

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

ANOVA Examples

What if the data is not normal? The Kruskal Wallis test is the Wilcoxon Rank Sum test equivalent for the multiple groups scenario. We will not go into details, since it's rather complicated, but the intuition is the same as for the Wilcoxon Rank Sum test: use ranks instead of the actual values, and see if the ranks are generally different between the groups.

```
kruskal.test(data = plant_growth, weight ~ group)
```

```
    Kruskal-Wallis rank sum test

data:  weight by group
Kruskal-Wallis chi-squared = 7.9882, df = 2, p-value = 0.01842
```

Since the p-value is less than $\alpha = 0.05$, we would reject the null hypothesis of no difference. To find out where the difference is, one would do pairwise Wilcoxon Rank Sum tests, and use the Bonferroni correction on the resulting p-values.

ANOVA Examples

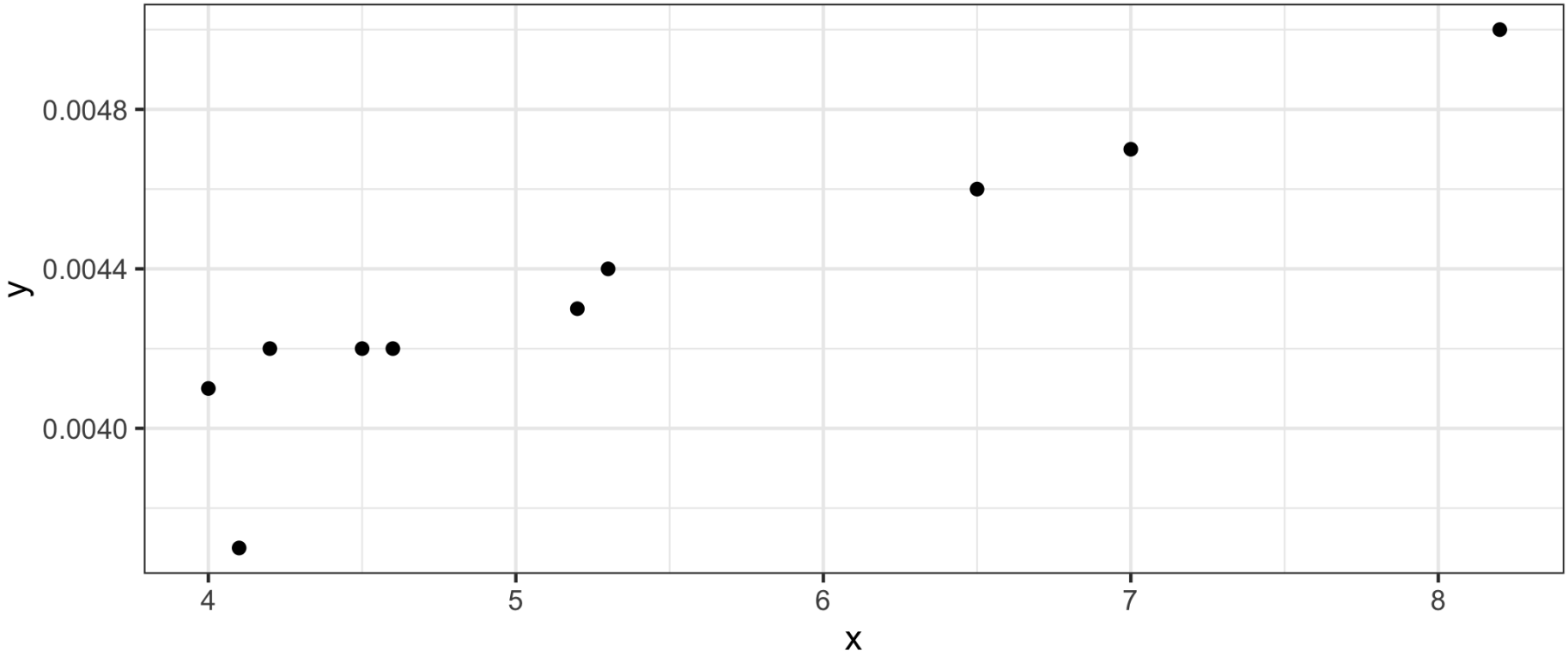
Pairwise Wilcoxon Rank Sum tests indicate a difference between treatments.

```
ctrl_vs_trt1 <- wilcox.test(data = filter(plant_growth, group != "trt2"),
                            weight ~ group)
ctrl_vs_trt2 <- wilcox.test(data = filter(plant_growth, group != "trt1"),
                            weight ~ group)
trt1_vs_trt2 <- wilcox.test(data = filter(plant_growth, group != "ctrl"),
                            weight ~ group)

tibble(comparison = c("ctrl_vs_trt1", "ctrl_vs_trt2", "trt1_vs_trt2"),
       p_values = c(ctrl_vs_trt1$p.value, ctrl_vs_trt2$p.value, trt1_vs_trt2$p.value)
  mutate(bonferroni_adjusted = p.adjust(p_values, method = "bonferroni"),
         BH_adjust = p.adjust(p_values, method = "BH"))
```

```
# A tibble: 3 x 4
  comparison   p_values bonferroni_adjusted BH_adjust
  <chr>           <dbl>                <dbl>     <dbl>
1 ctrl_vs_trt1  0.199                0.596     0.199
2 ctrl_vs_trt2  0.0630               0.189     0.0945
3 trt1_vs_trt2  0.00893              0.0268    0.0268
```

Introduction to Regression

So far, we have only talked about "differences in groups", but what if we are instead interested in the relationship between the mean, and a numeric value?



Introduction to Regression

Regression comes in many shapes and forms. The simplest is called (Simple) Linear Regression.

Idea: the *outcome variable* (y) is build from the *explanatory variable* (x) in a linear way plus some noise.

$$Y_i = \beta_0 + \beta_1 x_i + \epsilon_i, \quad \epsilon_i \sim N(0, \sigma^2).$$

In other words: there's a straight line that describes the data, but the actual observations are spread randomly around that line. The randomness is in the shape of a normal distribution with mean 0.

I.e. the average outcome is exactly given by the line:

$$E(Y_i) = \beta_0 + \beta_1 x_i + E(\epsilon_i) = \beta_0 + \beta_1 x_i.$$

Introduction to Regression

Fundamentally, we have this belief that there exist "true values" β_0, β_1 that we could find if we could measure all the x's and y's.

As always, we can't, so the question is, how do we estimate them? I.e. how do we come up with best guesses based on the data we have?

We use $\hat{\beta}_0$ and $\hat{\beta}_1$ to denote our "best guesses" for β_0 and β_1.

Given a set of best guess, we can use this model to find a suggestion as to what the outcome should be. We call this the *fitted value*. This is

$$\hat{y}_i = \hat{\beta}_0 + \hat{\beta}_1 x_i.$$

We want to find $\hat{\beta}_0, \hat{\beta}_1$ such that $\hat{y}_i = \hat{\beta}_0 + \hat{\beta}_1 x_i$ is as close to y_i as possible. I.e. we want to minimize $y_i - \hat{y}_i$ for all observations $i = 1, 2, \ldots, n$.

Problem: as we have seen before, differences can cancel out when we sum them up. So, instead we square the terms.

In the end, we aim at minimizing

$$\sum_{i=1}^{n}(y_i - \hat{y}_i)^2 = \sum_{i=1}^{n}(y_i - [\hat{\beta}_0 + \hat{\beta}_1 x_i])^2$$

This is actually the SSE! The sum of the squared differences from the observations to the fitted values.

How do we actually minimize this? For the math minded among you, differentiate with respect to the unknowns, set to zero, and solve. In the end, we get that the values of $\hat{\beta}_0$ and $\hat{\beta}_1$ that minimize SSE are

$$\hat{\beta}_1 = \frac{\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y})}{\sum_{i=1}^{n}(x_i - \bar{x})^2}$$
$$\hat{\beta}_0 = \bar{y} - \hat{\beta}_1 \bar{x},$$

where $\bar{x}$ and $\bar{y}$ are the averages of the x and y values, respectively.

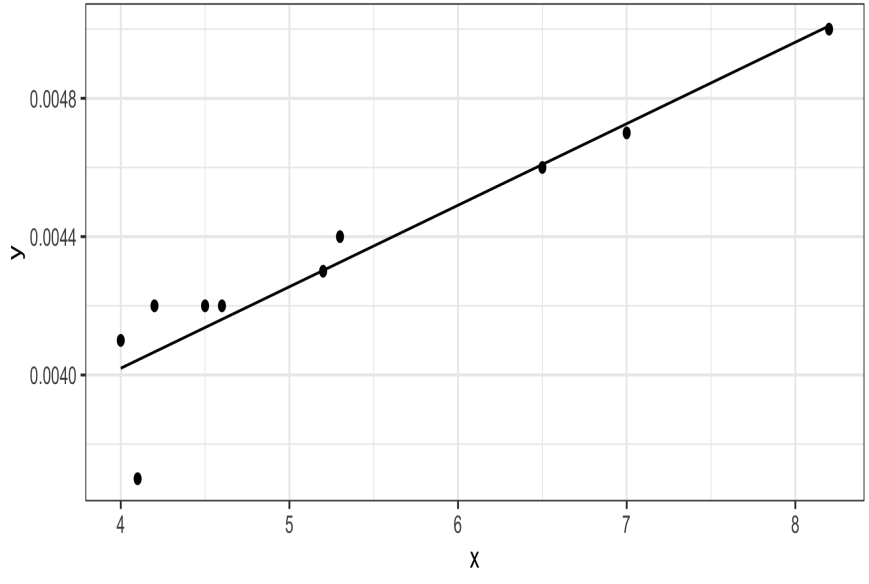
Introduction to Regression

This is obviously tedious to do by hand, but fortunately very easy to do in R:

```
lin_mod <- lm(data = regression_data, y

summary(lin_mod)
```

```
Call:
lm(formula = y ~ x, data = regression_dat

Residuals:
       Min          1Q      Median
-3.430e-04 -9.220e-06  1.842e-05  7.128e-

Coefficients:
             Estimate Std. Error t value
(Intercept) 3.077e-03  1.797e-04  17.121
x           2.357e-04  3.251e-05   7.249
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '

Residual standard error: 0.0001386 on 8 d
Multiple R-squared:  0.8679,    Adjusted
F-statistic: 52.55 on 1 and 8 DF,  p-valu
```

```
ggplot(augment(lin_mod),
       aes(x = x, y = y)) +
  geom_point() +
  geom_line(aes(y = .fitted))
```



Introduction to Regression

Interpretations:

- β_0 is the value of y_i suggested by the model if $x_i = 0$
    - rarely care much about this value
- β_1 is the increase of y_i if x_i is increased by 1 unit.
    - this is where it's at: if x and y are not associated, $\beta_1 = 0$.
    - i.e. the interesting *test* is whether $H_0 : \beta_1 = 0$ or $H_A : \beta_1 \neq 0$.
    - positive β_1: increased x increases y
    - negative β_1: increased x decreases y

For our example data:

$\hat{\beta}_0 = 0.0030766$, $\hat{\beta}_1 = 2.3570172 \times 10^{-4}$.

We would reject $H_0 : \beta_1 = 0$ in favor of $H_A : \beta_1 \neq 0$ since the p-value is 0.0000881.

Since $\hat{\beta}_1 > 0$, this seems to indicate that increased x increases y.

Introduction to Regression

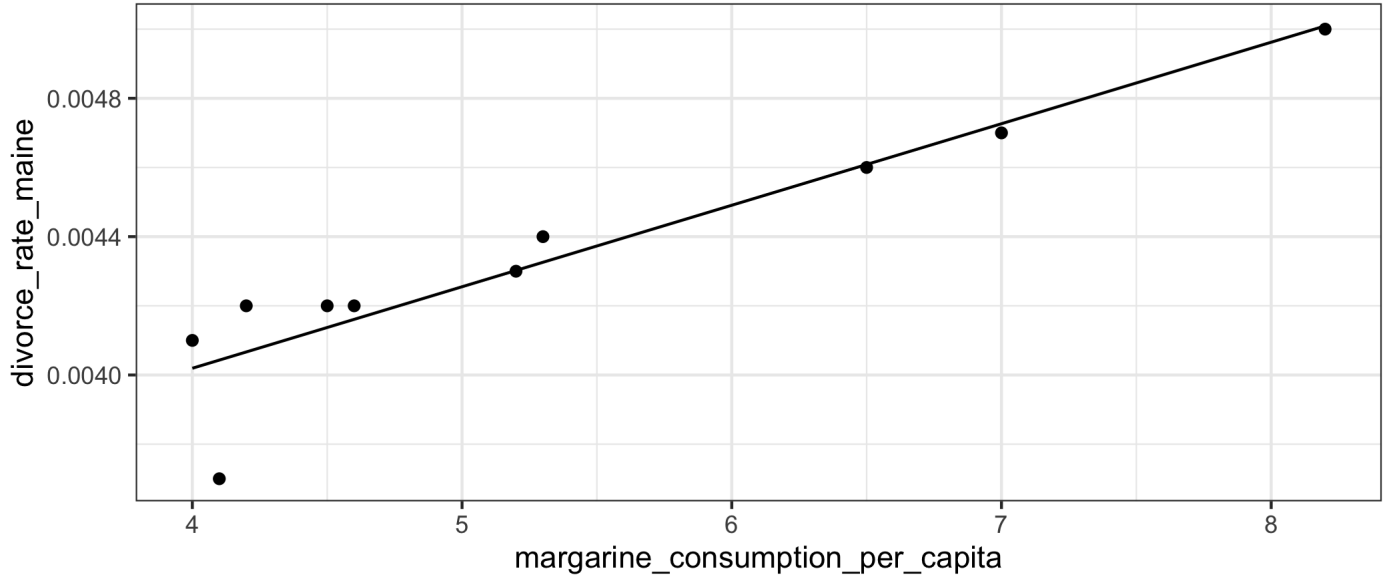
So, does this mean that if we could take a value of x and increase it by 1 unit, then y would increase by 2.3570172×10^{-4}?

No. This sort of conclusion is trying to say that x *causes* y. I.e. we start to move into assessing causality, which is notoriously hard, and we have to be super careful.

To illustrate this, let's reveal the labels of our regression data:

Introduction to Regression

```
divorce_margarine_lin_mod <- lm(data = divorce_margarine,
                                divorce_rate_maine ~ margarine_consumption_per_capita

ggplot(augment(divorce_margarine_lin_mod),
       aes(x = margarine_consumption_per_capita, y = divorce_rate_maine)) +
  geom_point() +
  geom_line(aes(y = .fitted))
```



If we take the leap to causality: decreasing margarine consumption decreases the divorce rate in Maine...???

Introduction to Regression

We see that the two variables (margarine consumption per capita and divorce rate in Maine) are *correlated*, but that does **NOT** imply any sort of causal relationship.

This doesn't mean we cannot get to causality, it is simply much more complicated.

More examples of spurious correlation can be found here.