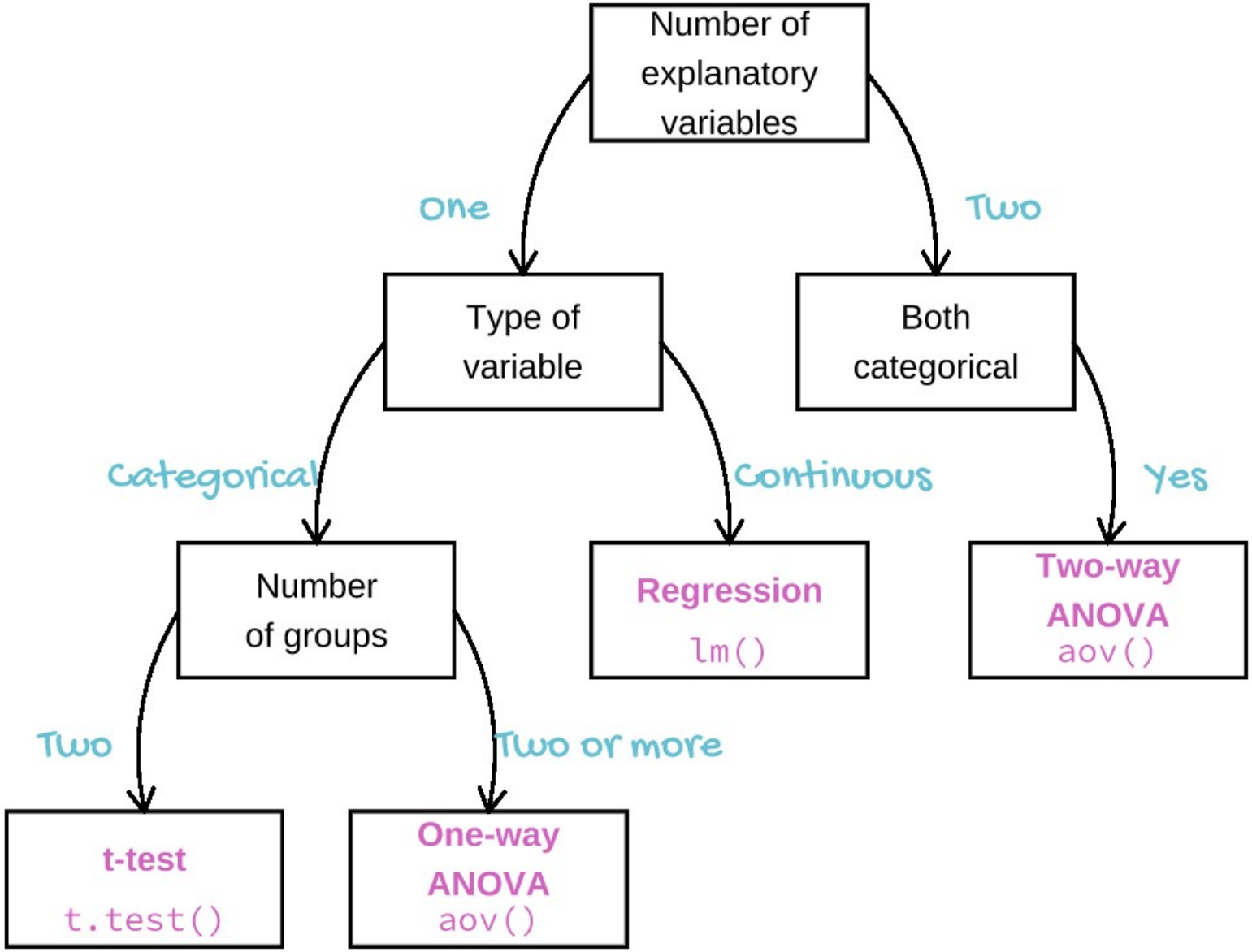

Laboratory & Professional Skills:
Data Analysis

# Emma Rand
# Data Analysis in R

## Correlation and Regression

# Previous weeks

- We have considered data with categorical explanatory variables


Number of explanatory variables
One
Two
Type of variable
Both categorical
Categorical
Continuous
Yes
Number of groups
Regression
lm()
Two-way ANOVA
aov()
Two
Two or more
t-test
t.test()
One-way ANOVA
aov()

# Summary of this week

- Situations where our explanatory variable is ‘continuous’ rather than categorical.
- Parametric and non-parametric correlation
  - Meaning
  - Assumptions
  - Carrying out, interpreting and Reporting
  - Tests of correlation coefficients
- Regression
  - Meaning and terminology
  - Carrying out, interpreting and Reporting
  - Assumptions
  - Assessment of fit (explanatory power)

# Learning objectives for the week

By the end of this week the successful student should be able to :

- Explain the principles of correlation and of regression and know when each can be applied (MLO 1)
- Select, appropriately correlation and regression (MLO 2)
- Apply and interpret a correlation in R (MLO 3 and 4)
- Appreciate the difference between statistical significance and biological significance (MLO 1 and 4)
- Apply and interpret a simple linear regression in R (MLO 3 and 4)
- Evaluate whether the assumptions of regression are met (MLO 2)
- Summarise and illustrate with appropriate R figures test results scientifically (MLO 3 and 4)

# Introduction

Correlation and Regression

# Similar but different

## Correlation

- Linear
- Association
- Axes can be switched
- two randomly sampled continuous or ordered discrete variables
- Scatter plot, no line

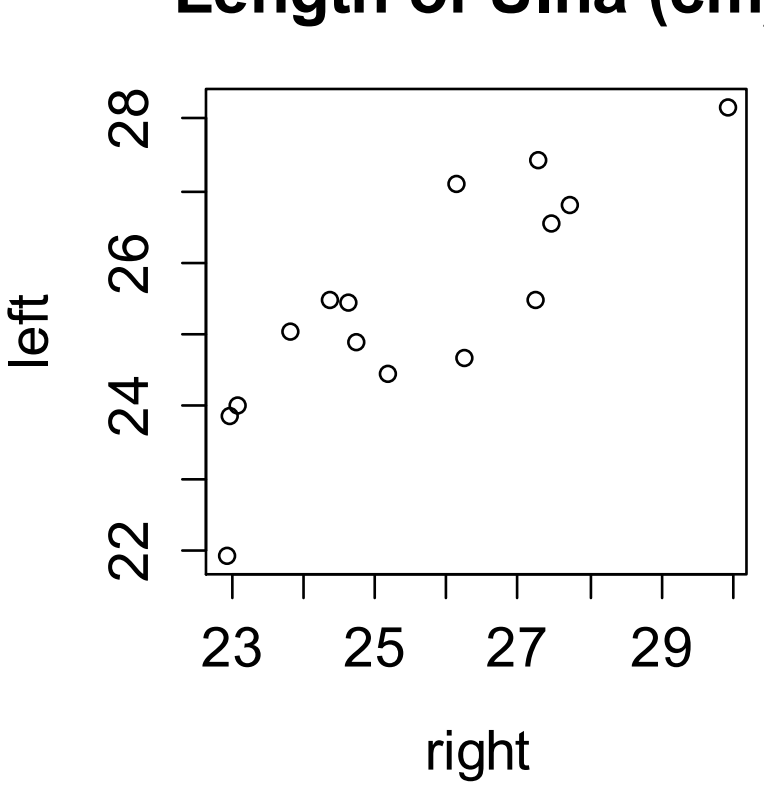
## Regression

- Linear
- Prediction
- Axes cannot be switched
- X is “sampled without error”; y randomly sampled for each x
- Scatter plot, must have the regression line

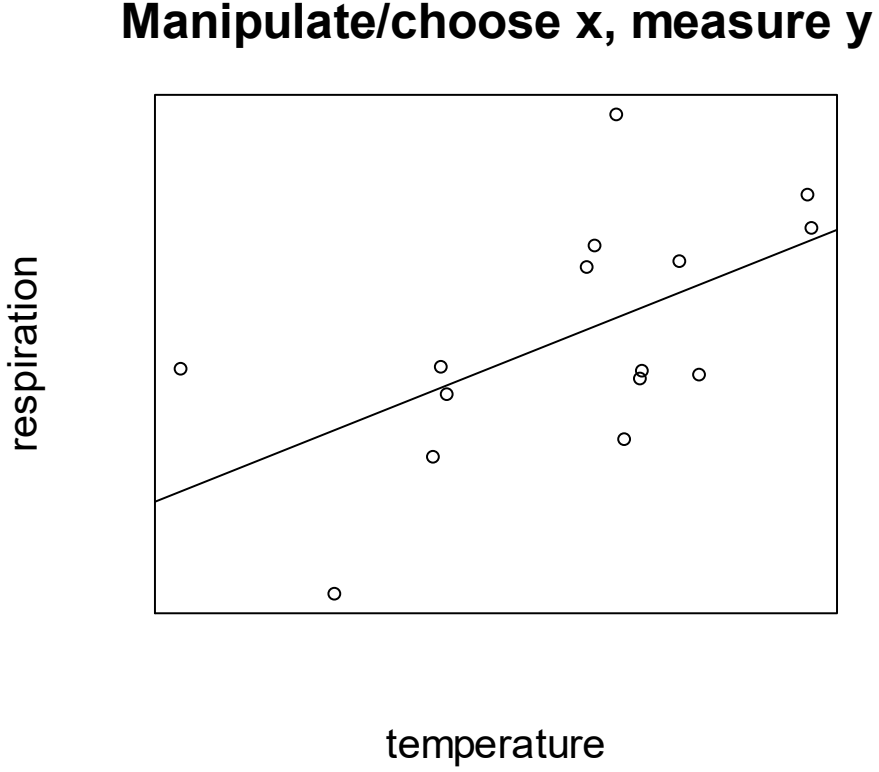
Correlation and Regression

# Similar but different

Correlation




Regression



# Correlation

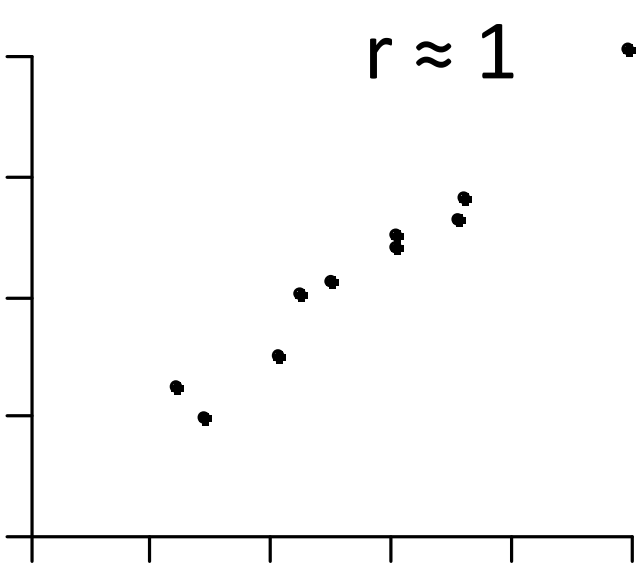
Correlation

# Basics

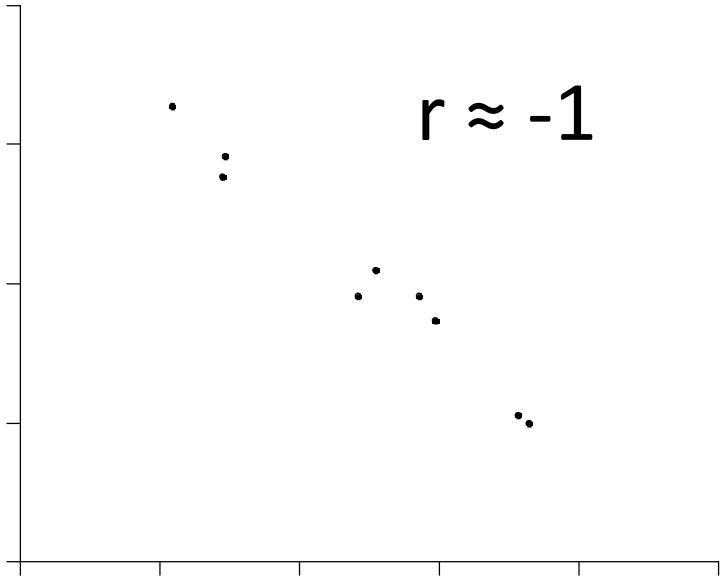
- Sample correlation: *r*
- Reflects degree of linear association between two sampled variables: -1 to +1
- Several types but same principles
- Here: Pearson's (Pearson's Product Moment Correlation Coefficient)
- Parametric

Correlation

# Example of correlations




Positive: Highest scores on one axis associated with highest scores on other

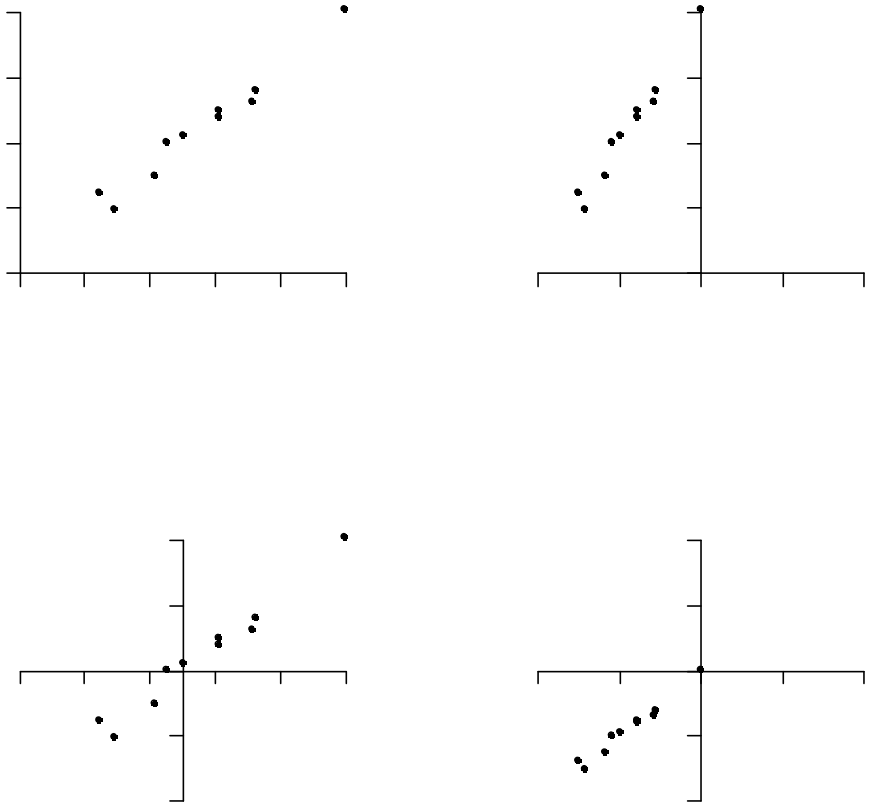



Negative: Highest scores on one axis associated with lowest scores on other

Correlation

# Example of positive correlations

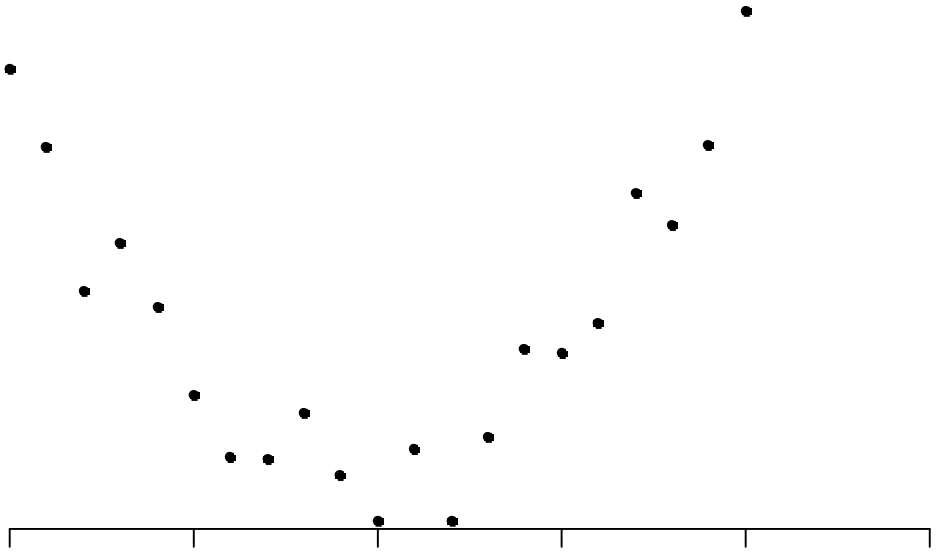
$r \approx 1$



Highest scores on one axis associated with highest scores on other

# Correlation but not linear

$r \approx 0$



Cannot use Pearson's PMMC

Correlation

# Example

Wheat seeds: High quality visualization of the internal kernel structure by a soft X-ray technique and 7 measurements taken:

- Area
- Perimeter
- Compactness
- Kernel length
- Kernel width
- Asymmetry coefficient
- Length of kernel groove

We will examine the correlation between compactness and kernel width

Two-way ANOVA example

# Reading in and examining the structure of the data

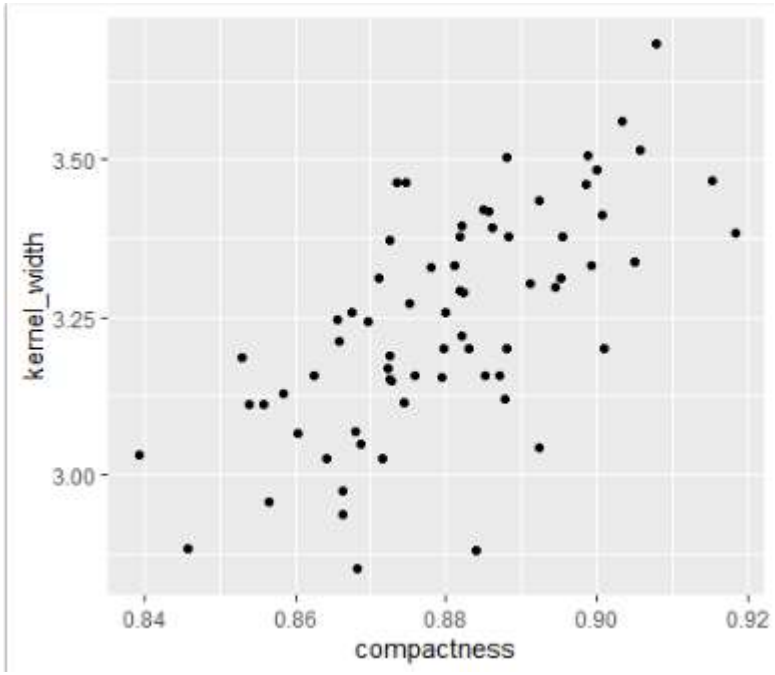
```
file <- "data-raw/seeds_dataset.xlsx"
seeds <- read_excel(file, sheet = "seeds_dataset")
glimpse(seeds)
Observations: 70
Variables: 7
$ area           <dbl> 15.26, 14.88, 14.29, 13.84, 16.14, 14.38, 14.69, 14.11, 1...
$ perimeter      <dbl> 14.84, 14.57, 14.09, 13.94, 14.99, 14.21, 14.49, 14.10, 1...
$ compactness    <dbl> 0.8710, 0.8811, 0.9050, 0.8955, 0.9034, 0.8951, 0.8799, 0...
$ kernal_length  <dbl> 5.763, 5.554, 5.291, 5.324, 5.658, 5.386, 5.563, 5.420, 6...
$ kernel_width   <dbl> 3.312, 3.333, 3.337, 3.379, 3.562, 3.312, 3.259, 3.302, 3...
$ asymmetry_coef <dbl> 2.2210, 1.0180, 2.6990, 2.2590, 1.3550, 2.4620, 3.5860, 2...
$ groove_length  <dbl> 5.220, 4.956, 4.825, 4.805, 5.175, 4.956, 5.219, 5.000, 5...
```

Correlation

# Plot your data

## Plot your data: roughly

```
ggplot(data = seeds, aes(x = compactness, y = kernel_width)) +
  geom_point()
```

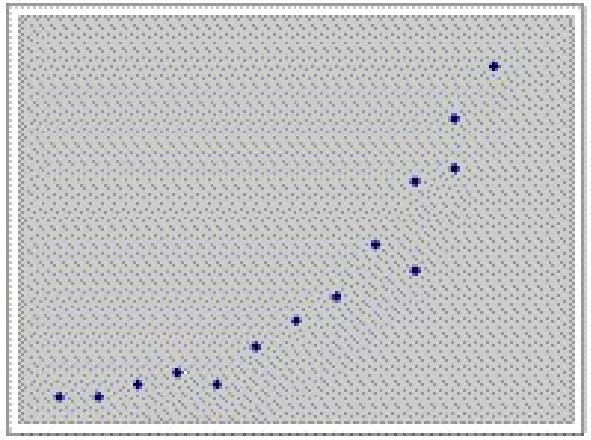



Check roughly linear

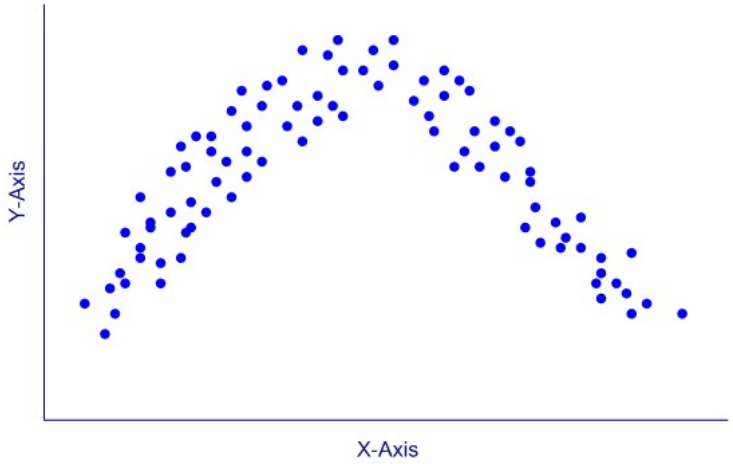
This looks ok

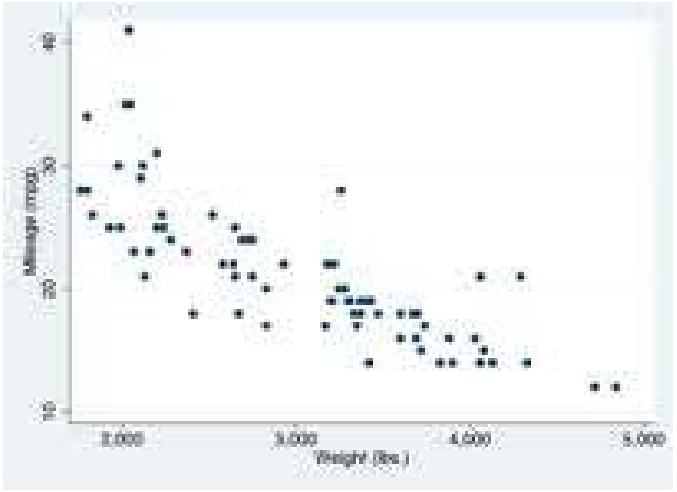
Correlation

# Plot your data



Not suitable for linear correlation



Correlation

# Running the test

```
cor.test(data = seeds, ~ compactness + kernel_width)

        Pearson's product-moment correlation

data:  compactness and kernel_width
t = 7.3738, df = 68, p-value = 2.998e-10
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.5117537 0.7794620
sample estimates:
      cor
0.6665731
```

A variable is not being explained:
~ compactness + kernel_width

Correlation

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Gives type of correlation done. Pearson's in the default

Correlation

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The correlation coefficient, *r*

Correlation

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sample estimates:
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0.6665731
```

Confidence interval on, *r*

Correlation

# Running the test

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cor.test(data = seeds, ~ compactness + kernel_width)

        Pearson's product-moment correlation

data:  compactness and kernel_width
t = 7.3738, df = 68, p-value = 2.998e-10
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95 percent confidence interval:
 0.5117537 0.7794620
sample estimates:
      cor
0.6665731
```

Test of whether *r* is significantly from zero

Correlation

# Reporting the result

```
data:  compactness and kernel_width
t = 7.3738, df = 68, p-value = 2.998e-10
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.5117537 0.7794620
sample estimates:
      cor
0.6665731
```

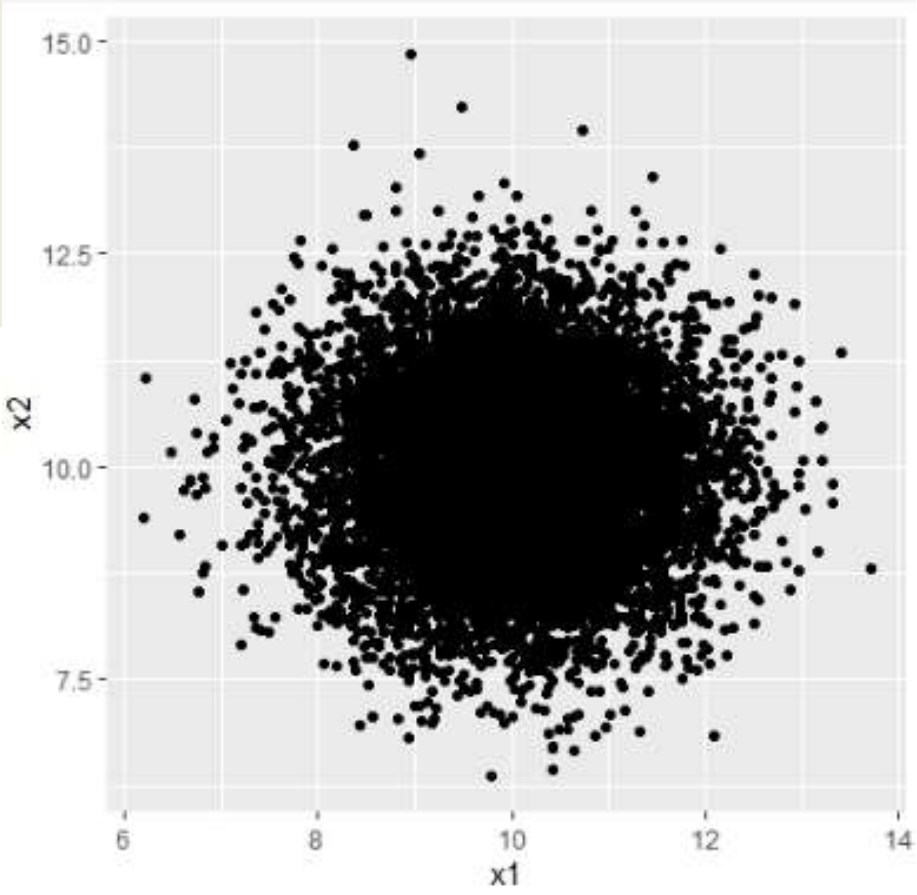
- There is a significant positive correlation ($r$ = 0.67) between compactness and kernel width ($t$ = 7.37; $d.f.$ = 68, $p < 0.001$).

# Understanding the test of significance

- The R output contains a test of whether *r* = 0
- uses *t* $$t = \frac{\text{statistic - hypothesised value}}{\text{estimated SE of the statistic}}$$
- For correlation: $t_{[d.f.]} = \frac{r}{s.e.}$
- Where standard error of r is $\sqrt{\frac{1-r^2}{N-2}}$
  - d.f. are N-2
- Sensitivity to sample size

# Statistical significance ≠Biological significance

```
data:  x1 and x2
t = -2.2154, df = 9998, p-value = 0.02675
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.041733016 -0.002552103
sample estimates:
        cor
-0.02215107
```



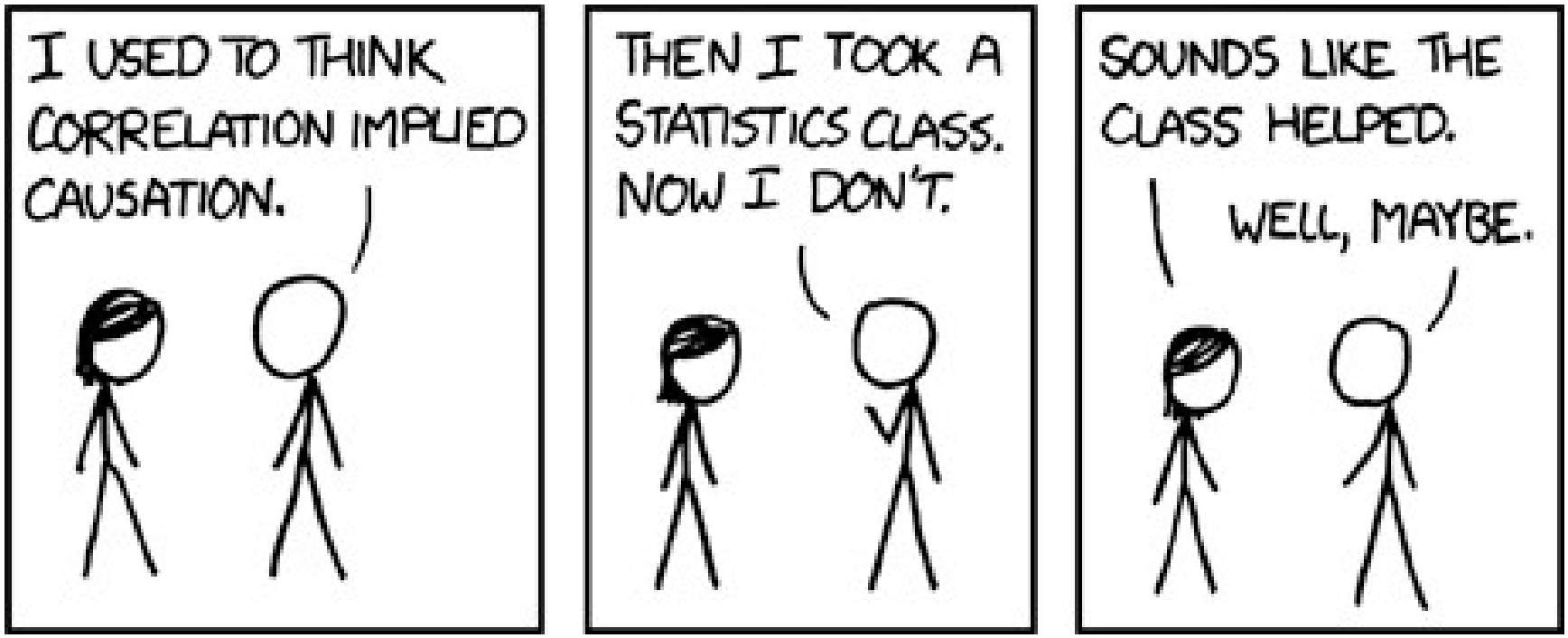

Large samples mean small probability

But *r* is tiny!

Our knowledge determines biological significance

# Correlation summary

- Association
- Pearson's is Parametric; Spearman's is non-parametric
- Two randomly sampled continuous/ordered variables
- Function in R:
  `cor.test(data = df, ~ x1 + x2)`
- quote r, its significance and n
- if scatterplot included do NOT show a fitted line


I USED TO THINK CORRELATION IMPLIED CAUSATION.
THEN I TOOK A STATISTICS CLASS. NOW I DON'T.
SOUNDS LIKE THE CLASS HELPED.
WELL, MAYBE.

# Regression

# Regression

- Linear
- Prediction: One variable causes the other
- Axes cannot be switched
- X is “sampled without error”; y randomly sampled for each x
- We will consider linear regression only best fitting straight line:

$$y = b_1 x + b_0$$

# Null hypothesis

Can be expressed as:

- $b_1 = 0$
- x cannot predict *y*
- Regression line doesn't explain variance in *y*

Assumptions

- Normality and homoscedascity of residuals
- X is "sampled without error";
- y randomly sampled for each x and normally distributed

Regression

# Example

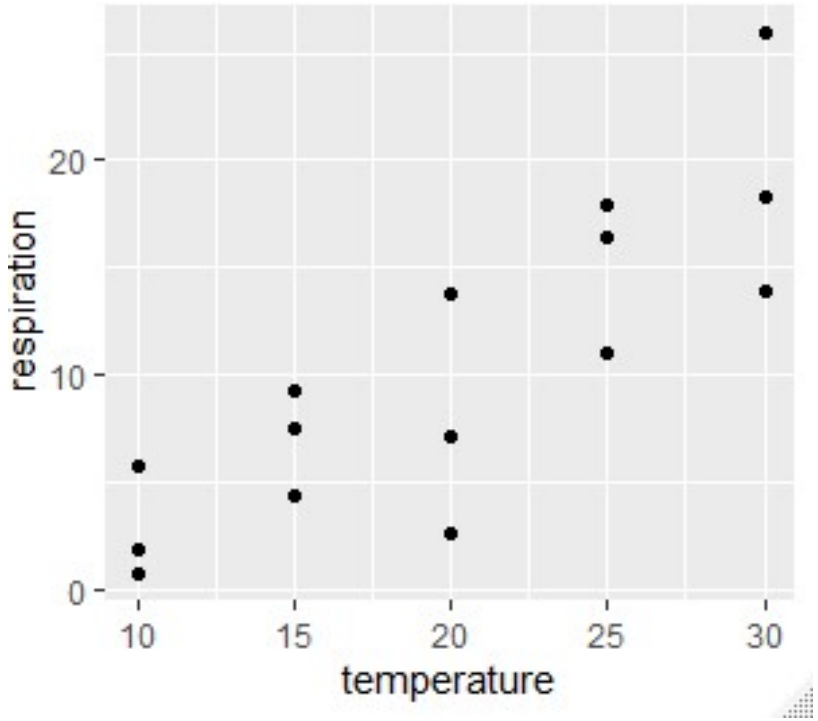
Brine Shrimp (*Artemia salina*) were put in water baths at 10C, 15C, 20C, 25C, 30C and their respiration rate measured (units)

| | temperature | respiration |
|---|---|---|
| 1 | 10 | 0.785 |
| 2 | 10 | 5.784 |
| 3 | 10 | 1.879 |
| 4 | 15 | 9.331 |
| 5 | 15 | 4.412 |
| 6 | 15 | 7.515 |
| 7 | 20 | 13.852 |
| 8 | 20 | 2.633 |
| 9 | 20 | 7.157 |
| 10 | 25 | 17.983 |
| 11 | 25 | 16.426 |
| 12 | 25 | 11.029 |
| 13 | 30 | 18.353 |
| 14 | 30 | 13.934 |
| 15 | 30 | 25.965 |

# Plot your data

## Plot your data: roughly

```
ggplot(data = shrimp, aes(x = temperature, y = respiration)) +
  geom_point()
```




Check roughly linear

This looks ok

# Running the test

```
mod <- lm(data = shrimp,
          respiration ~ temperature)
summary(mod)
```

Regression

# Understanding the output

Core statistical ideas – very extendable. You will see again next year

```
Call:
lm(formula = respiration ~ temperature, data = shrimp)

Residuals:
    Min      1Q  Median      3Q     Max
-7.8362 -2.6216 -0.3377  3.1854  7.2433

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -6.0359     3.1560  -1.912   0.0781 .
temperature   0.8253     0.1488   5.547 9.43e-05 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.074 on 13 degrees of freedom
Multiple R-squared:  0.703,       Adjusted R-squared:  0.6801
F-statistic: 30.77 on 1 and 13 DF,  p-value: 9.433e-05
```

Regression

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```

$b_0$ and $b_1$

$$y = 0.83x - 6.03$$

# Understanding the output

```
Call:
lm(formula = respiration ~ temperature, data =

Residuals:
    Min      1Q  Median      3Q     Max
-7.8362 -2.6216 -0.3377  3.1854  7.2433

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Multiple R-squared:  0.703,       Adjusted R-squared:  0.6801
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```

Test: $b_0 = 0$
Often not impt

Test: $b_1 = 0$
Always of interest

Regression

# Understanding the output

```
Call:
lm(formula = respiration ~ temperature, data = shrimp)

Residuals:
    Min      1Q  Median      3Q     Max
-7.8362 -2.6216 -0.3377  3.1854  7.2433

Coefficients:
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temperature   0.8253     0.1488   5.547 9.43e-05 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.074 on 13 degrees of freedom
Multiple R-squared:  0.703,       Adjusted R-squared:  0.680
F-statistic: 30.77 on 1 and 13 DF,  p-value: 9.433e-05
```

Test: $b_1 = 0$
Always of interest

Test of ‘model’
Same as $b_1 = 0$
in single
regression

Regression

# Understanding the output

```
Call:
lm(formula = respiration ~ temperature, data = shrimp)

Residuals:
    Min      1Q  Median      3Q     Max
-7.8362 -2.6216 -0.3377  3.1854  7.2433

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  -6.0359     3.1560  -1.912   0.0781 .
temperature   0.8253     0.1488   5.547 9.43e-05 ***
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Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.074 on 13 degrees of freedom
Multiple R-squared:  0.703,       Adjusted R-squared:  0.6801
F-statistic: 30.77 on 1 and 13 DF,  p-value: 9.433e-05
```

Multiple R-squared: Proportion of y explained by x

Regression

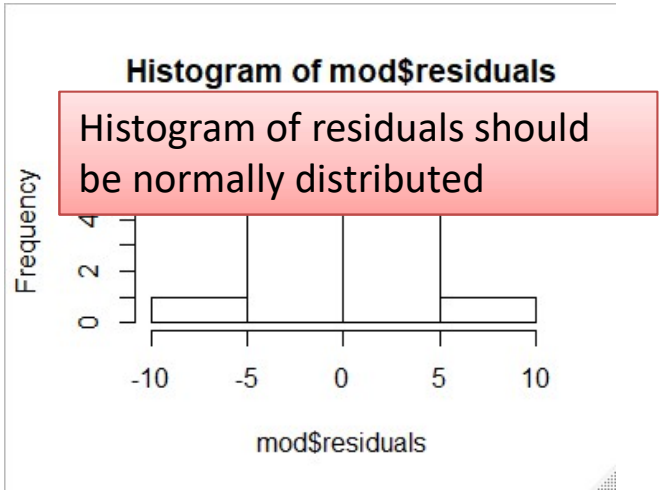
# Checking Assumptions

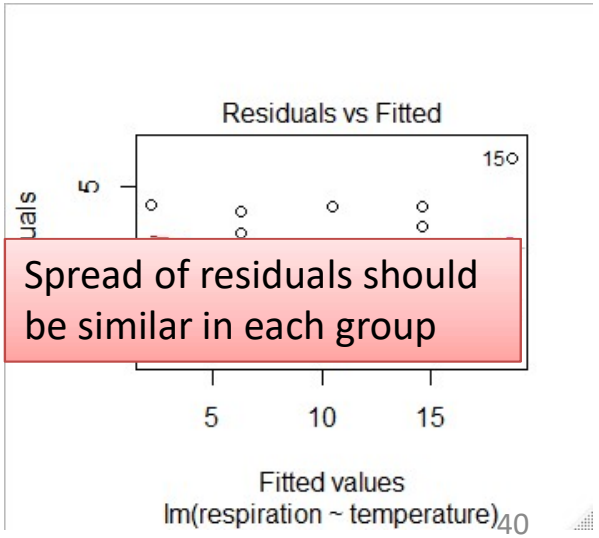
Residuals are calculated for you already!

```
hist(mod$residuals)
shapiro.test(mod$residuals)

        Shapiro-Wilk normality test

data:  (mod$residuals)
W = 0.97969, p-value = 0.9673
plot(mod, which = 1)
```



Regression

# Reporting the results

```
Coefficients:
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(Intercept)  -6.0359     3.1560  -1.912   0.0781 .
temperature   0.8253     0.1488   5.547 9.43e-05 ***
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Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’
    1

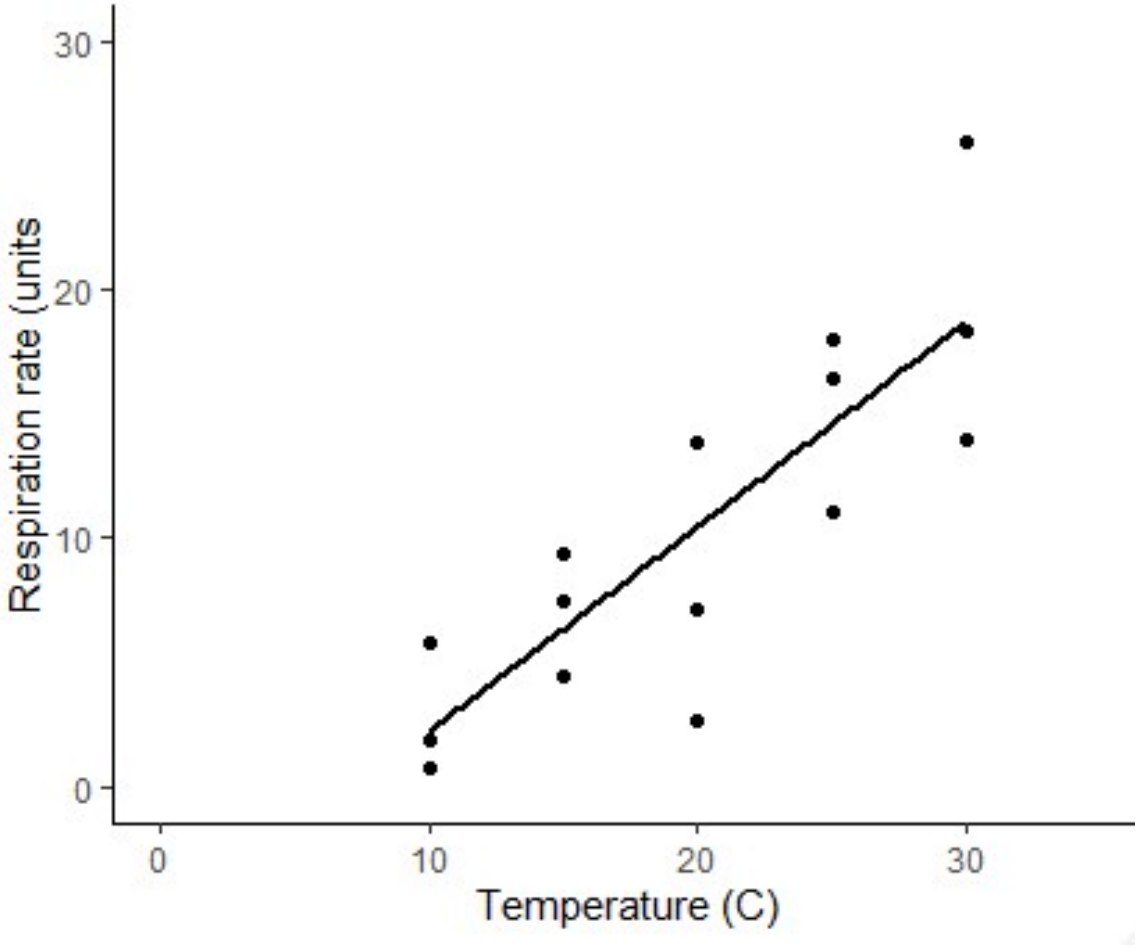
Residual standard error: 4.074 on 13 degrees of freedom
Multiple R-squared:  0.703,   Adjusted R-squared:  0.6801
F-statistic: 30.77 on 1 and 13 DF,  p-value: 9.433e-05
```

Reporting the result: “significance, direction, magnitude”

The temperature explained a significant amount of the variation in respiration rate (ANOVA: $F = 30.8$; $d.f. = 1, 13$; $p < 0.001$). The regression line is: Respiration rate= 0.83 * temperature - 6.04

Regression

# Reporting the results: figure



# Regression summary

- Linear
- Prediction: One variable causes the other
- Axes cannot be switched
- X is “sampled without error”; y randomly sampled for each x
- linear regression: $y = b_1 x + b_0$

  Function in R:

```
mod <- lm(data = df, y ~ x)
Summary(mod)
```

- quote regression equation and test result (either ANOVA or *t*
- Scatterplot with fitted line (data and the model)