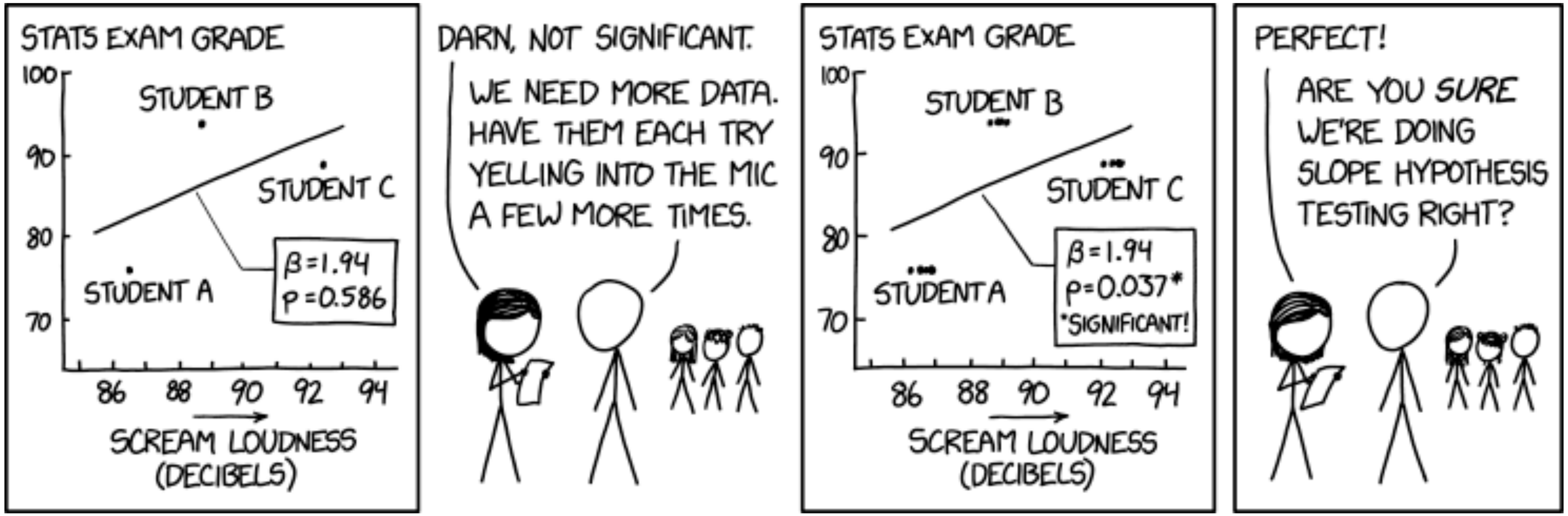
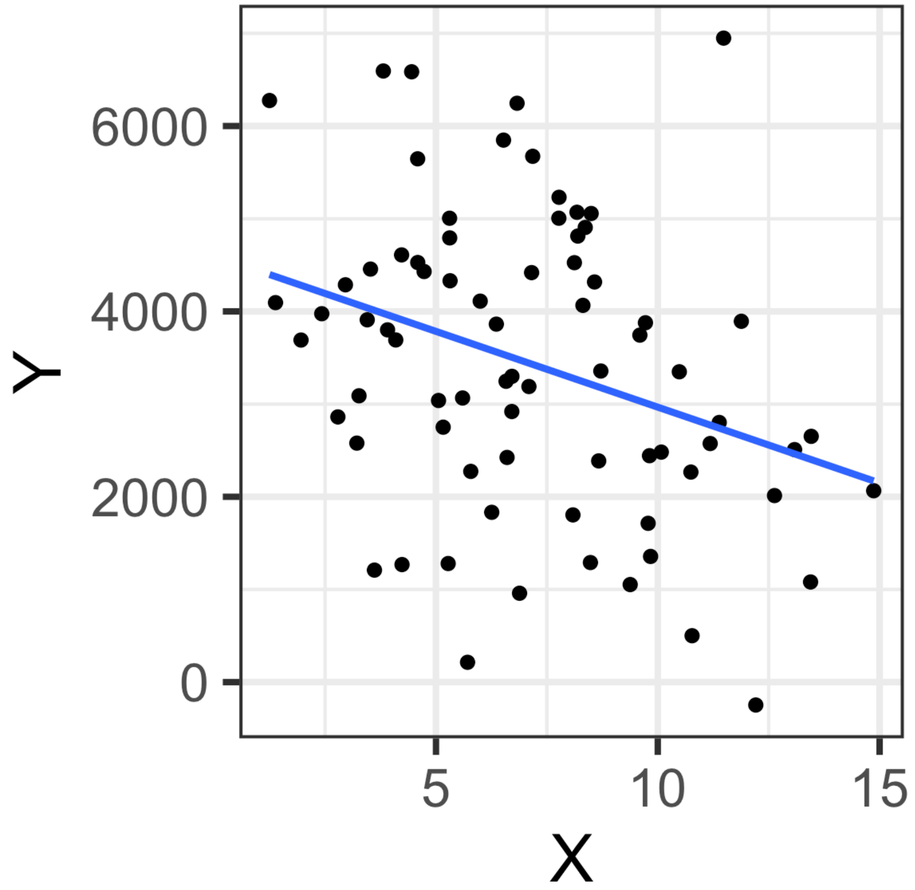


Lecture 14

11.18.21

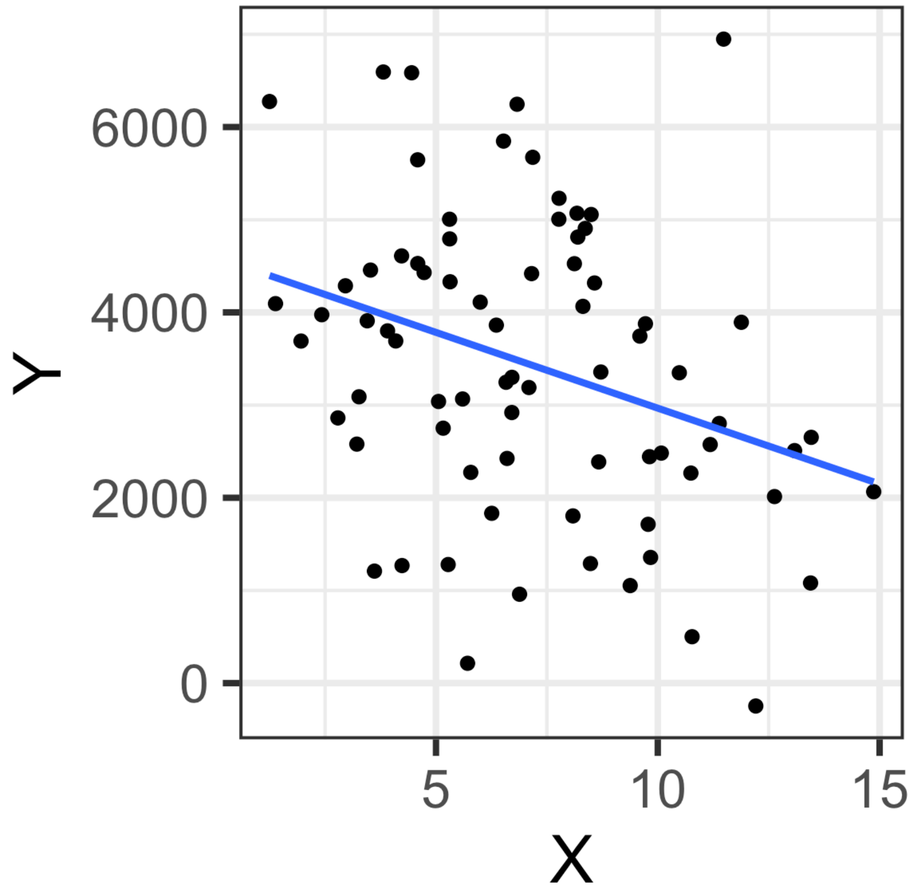
Refresher Quiz




```
> summary(lm(Y ~ X))

Residuals:
    Min      1Q  Median      3Q     Max
-3453.9  -992.9  -128.6  1022.9  4224.6

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  4601.95     442.18  10.407 4.52e-16 ***
X            -163.51      56.52  -2.893  0.00503 **
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 1536 on 73 degrees of freedom
Multiple R-squared:  0.1028,    Adjusted R-squared:  0.09055
F-statistic: 8.368 on 1 and 73 DF,  p-value: 0.00503
```

Given these data, what can you tell me about the relationship between X and Y? Be sure to be as specific as possible.

Refresher Quiz

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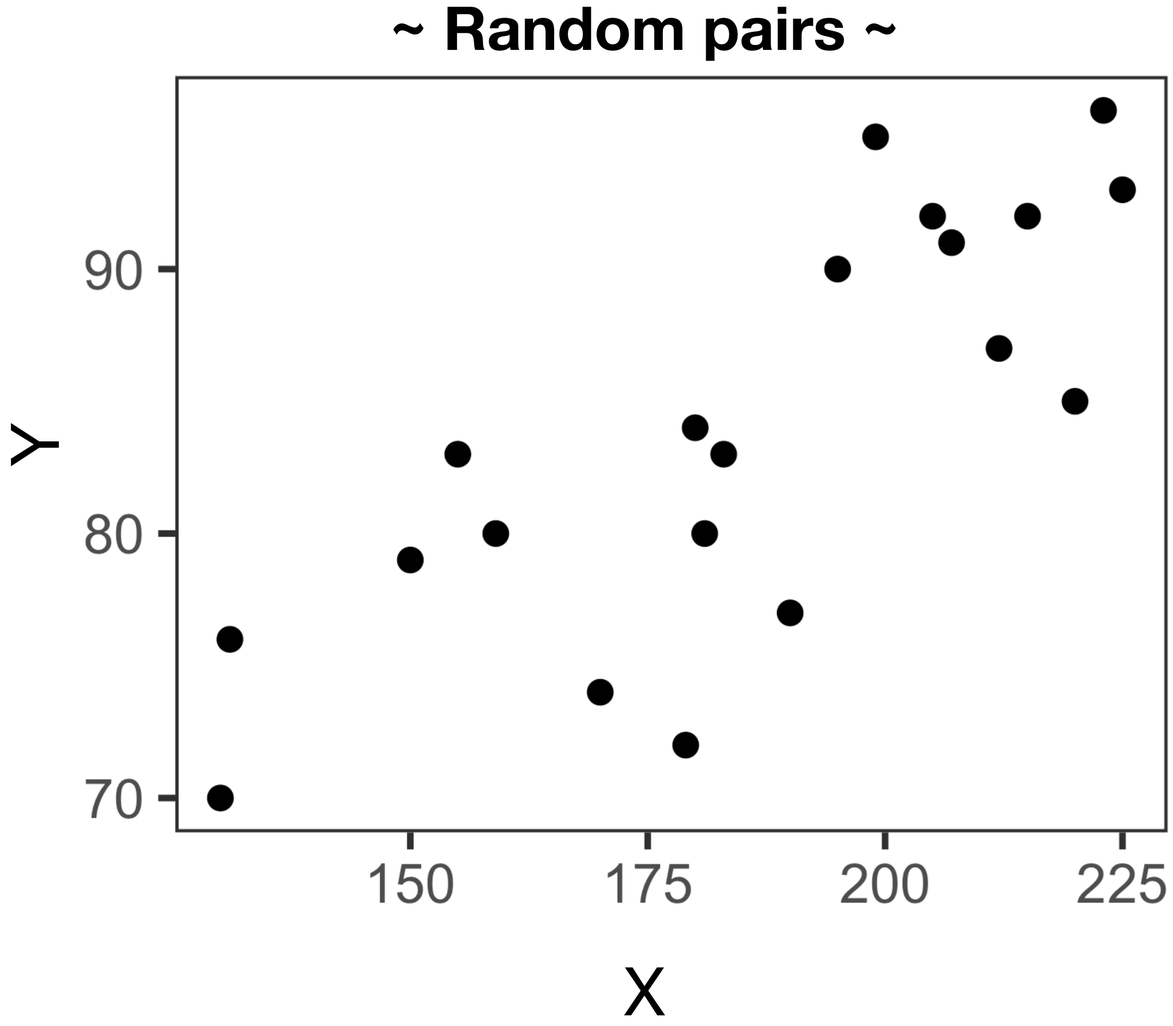
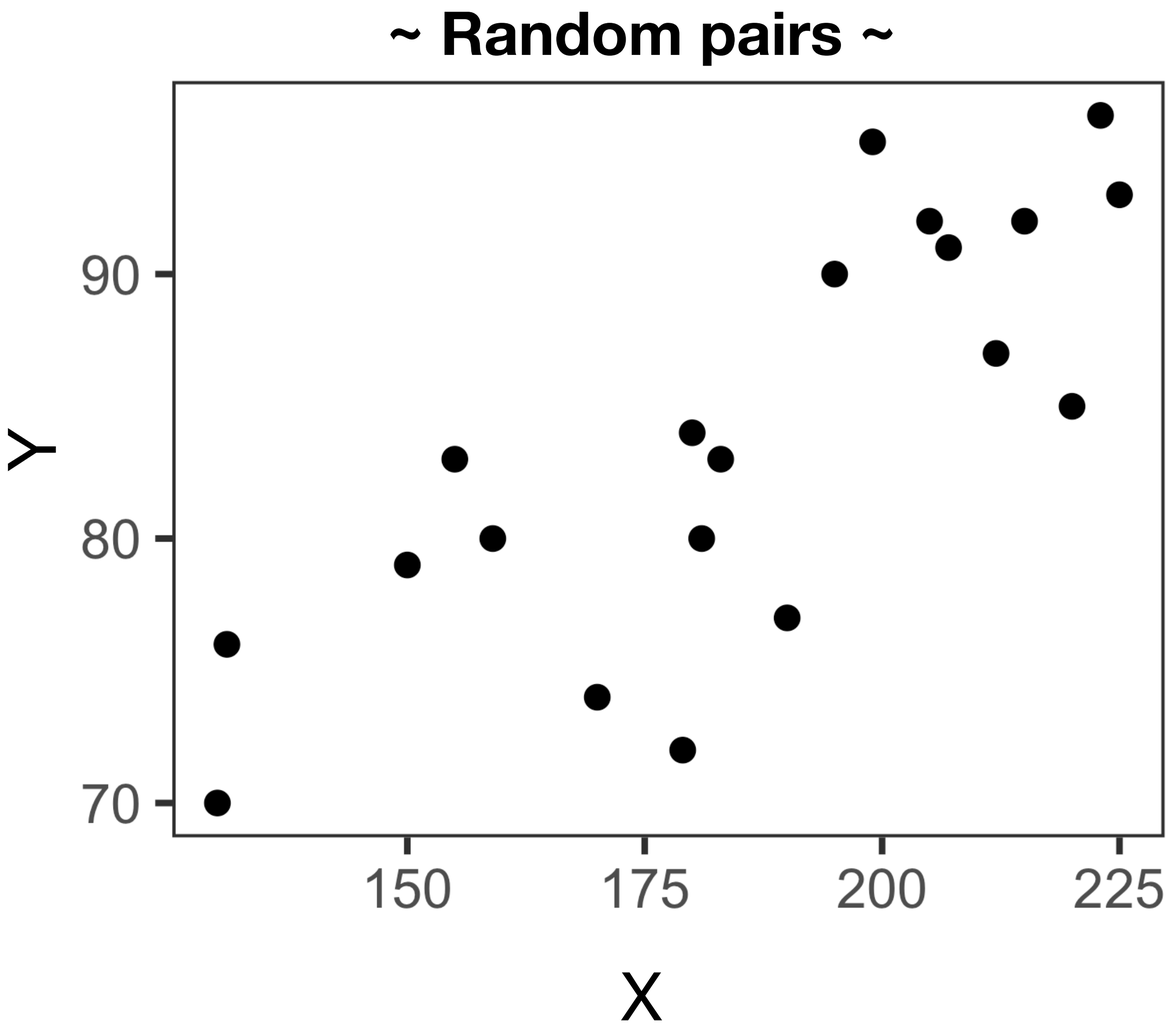
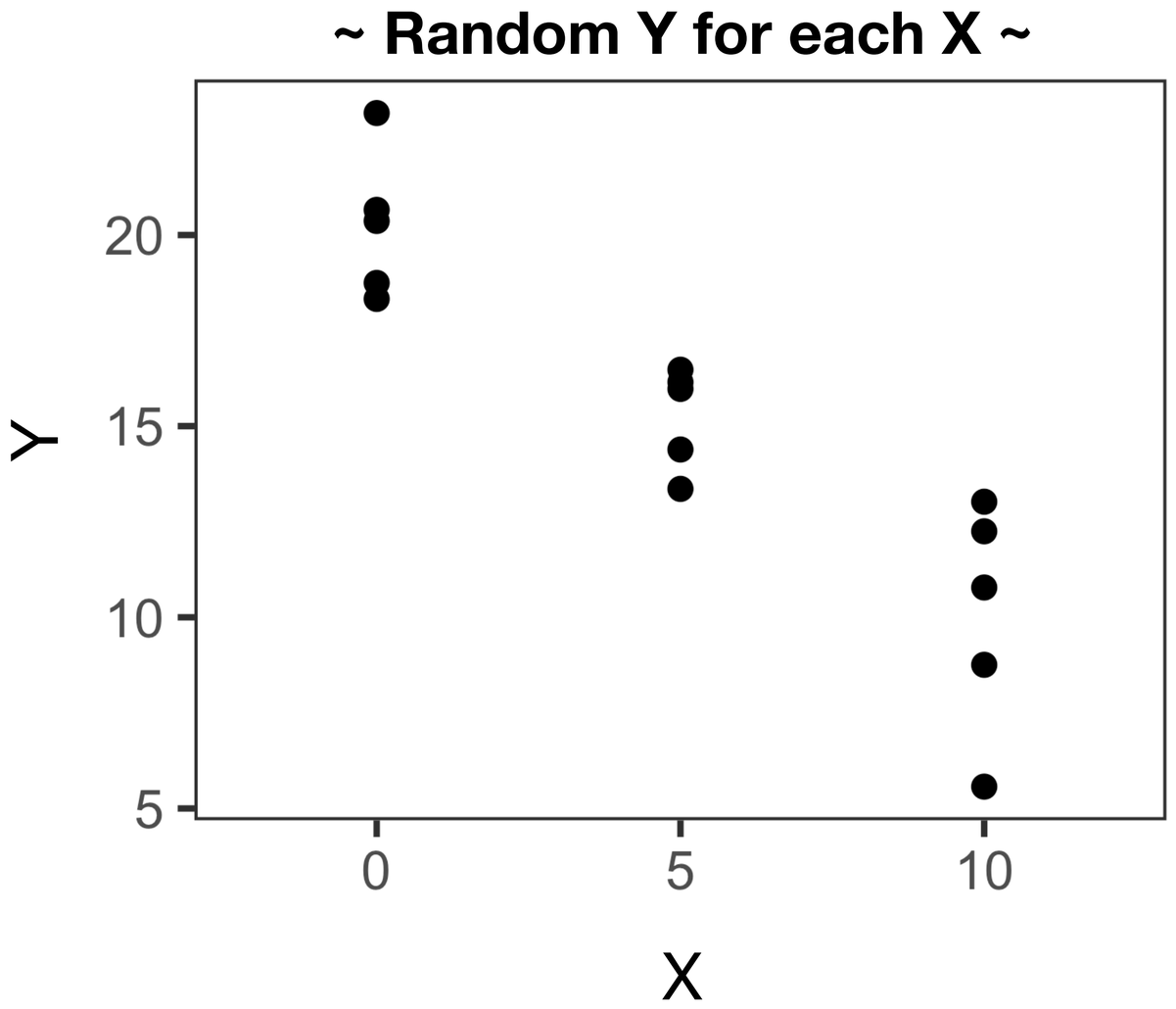
Assume: **random**, independent samples

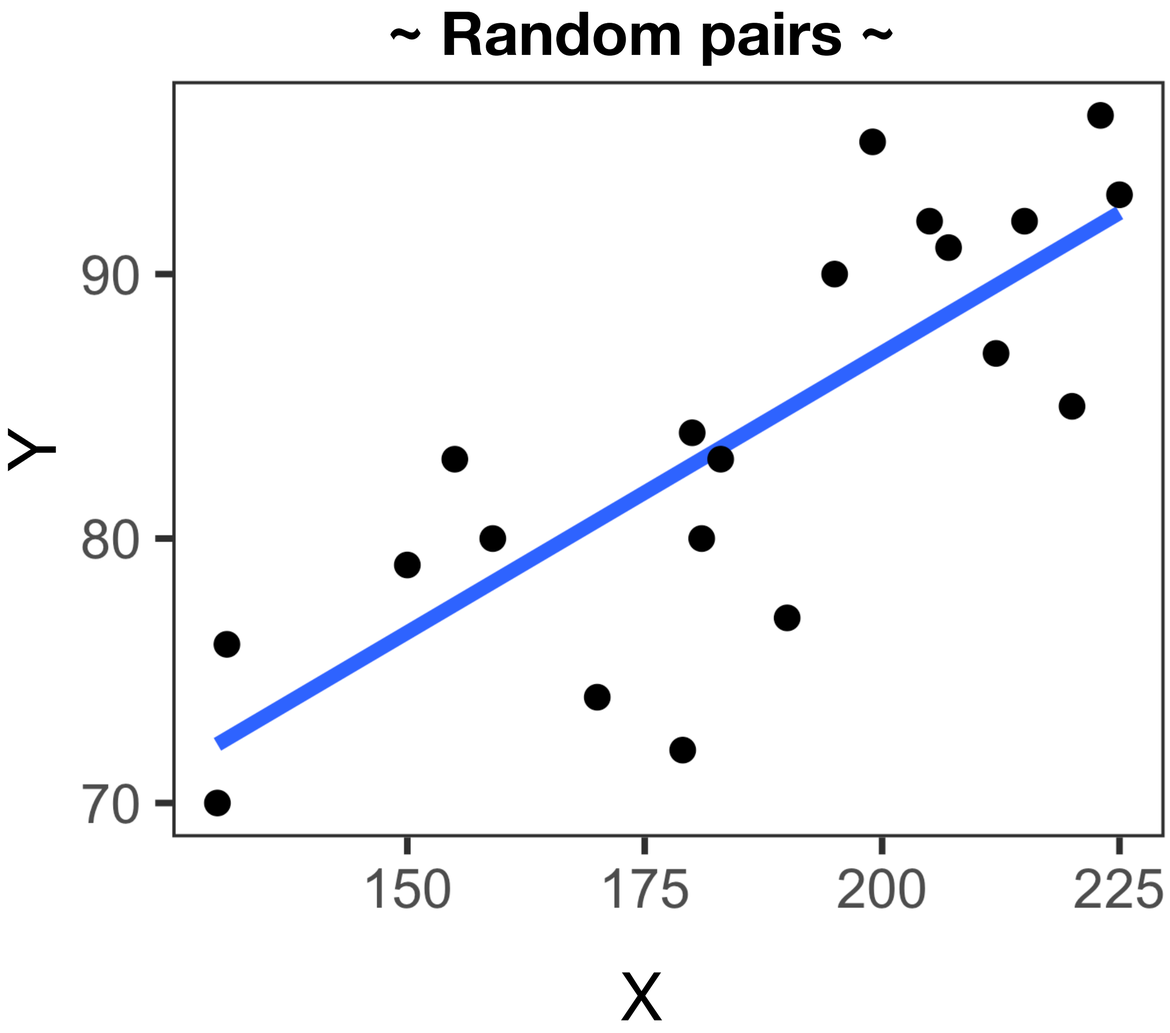


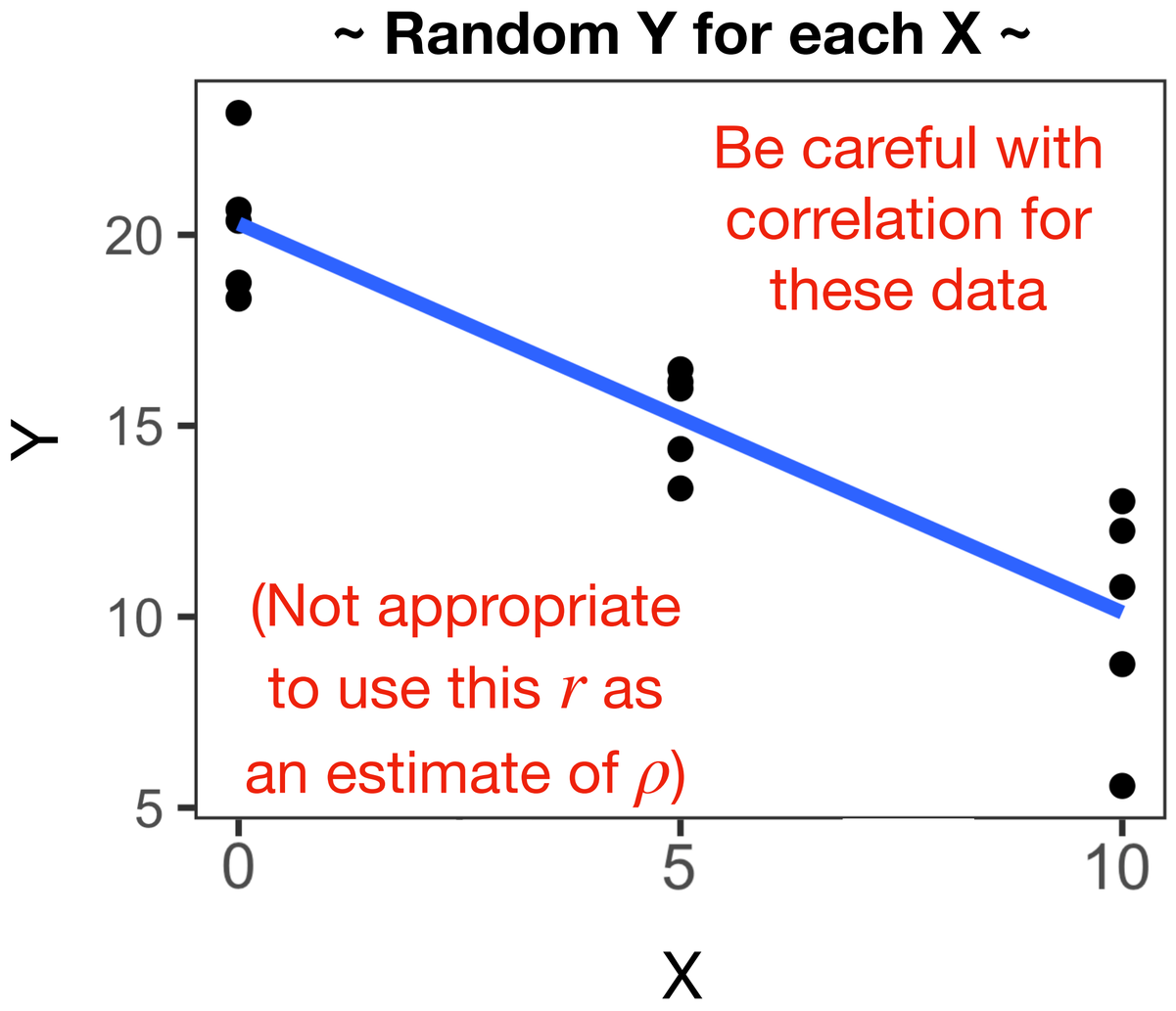
Assume: **random**, independent samples



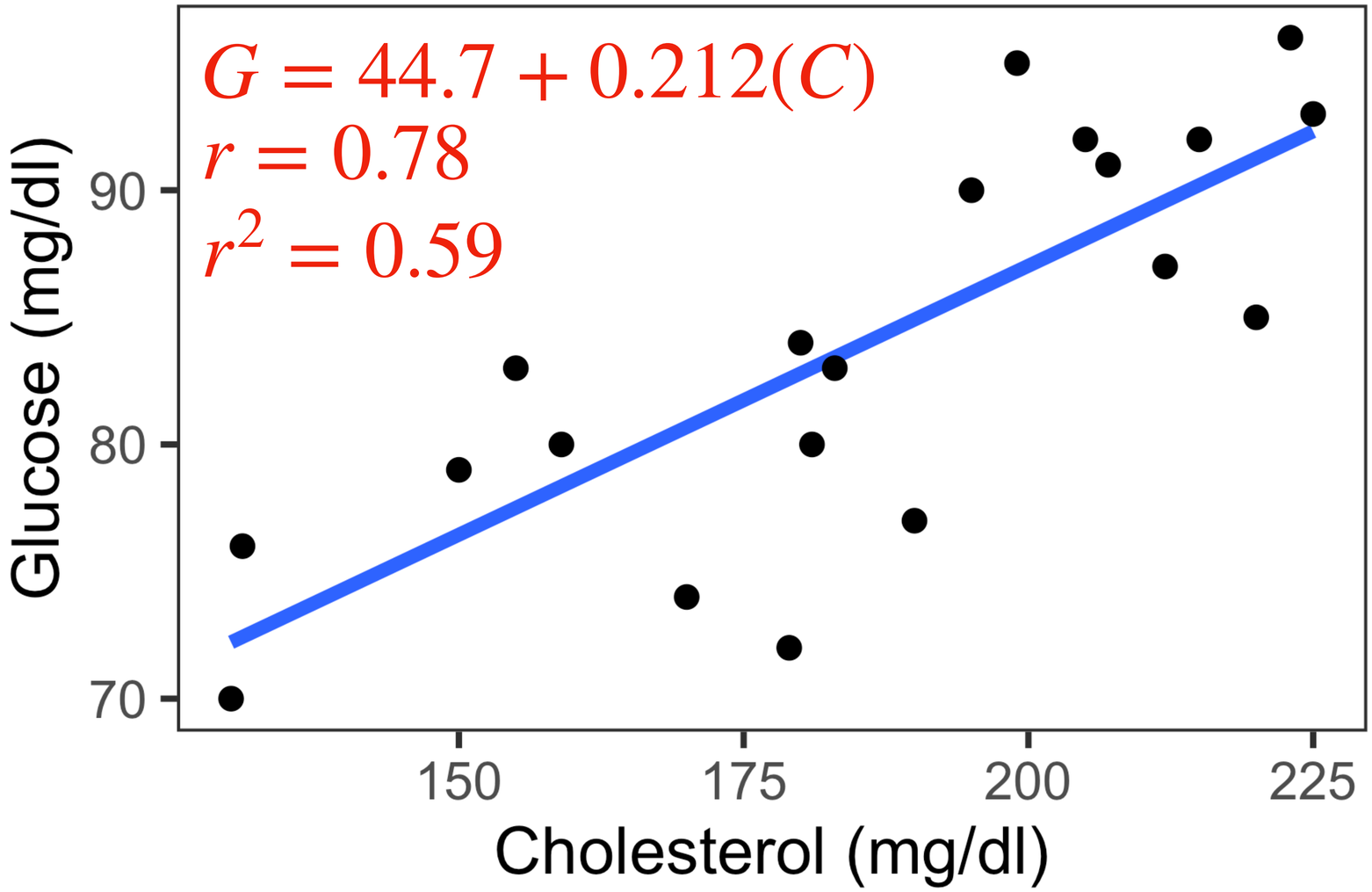


Assume: **random**, independent samples





Assume: random, **independent** samples



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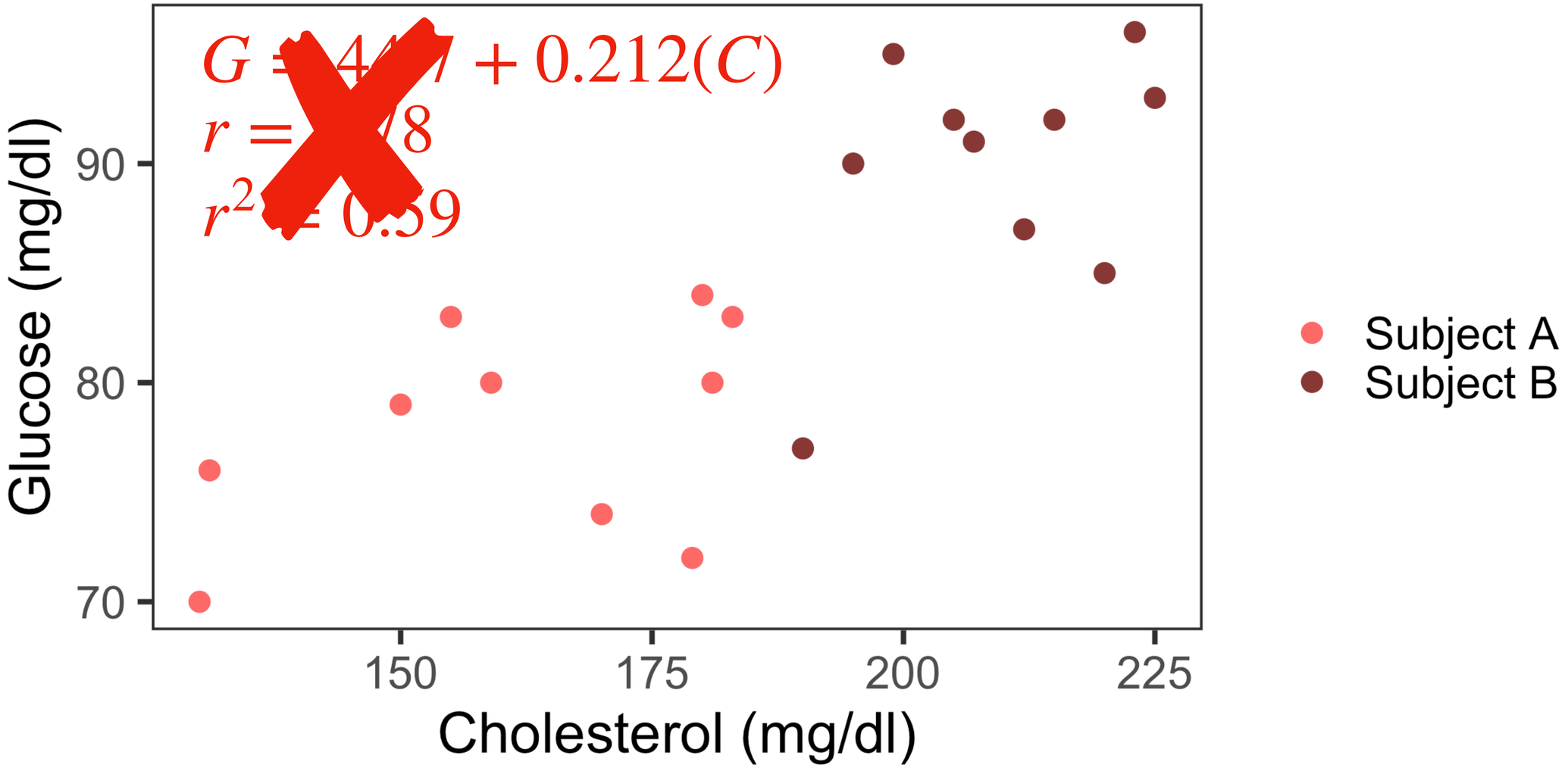
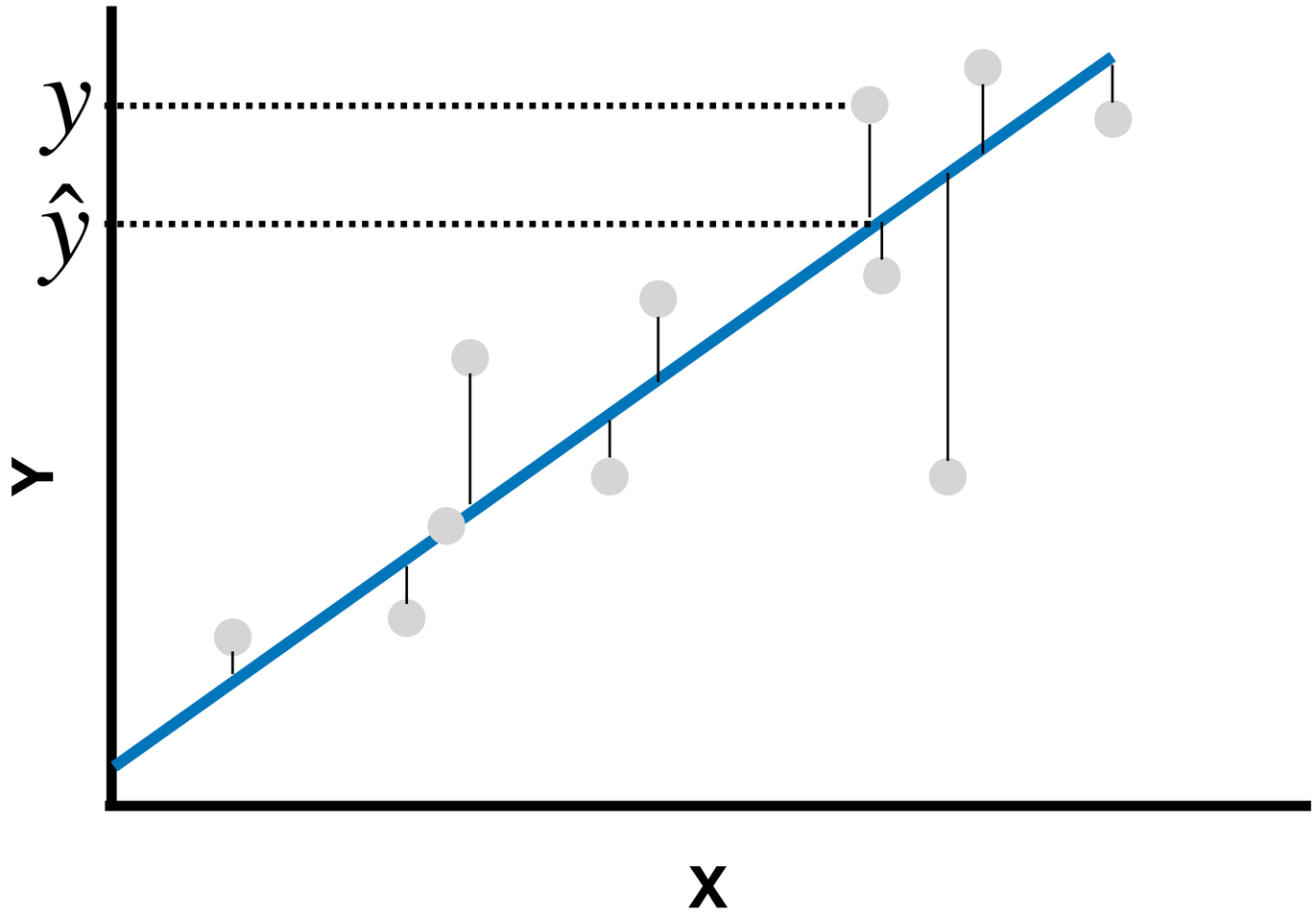


Conditions for inference with regression

- **Random sampling**: avoid pairing, blocking, or hierarchical structure
    - Each (X,Y) is a random pair from the large population **OR** for a set X value, each Y value is a random observation from its population
    - **Independence:** each observed pair (X,Y) must be considered independent of the others
- **Linearity:** there must be a linear relationship between X and Y
- **Normality:** The residuals must have a normal distribution

Residual plots to identify non-linearity



residual = observed - fitted

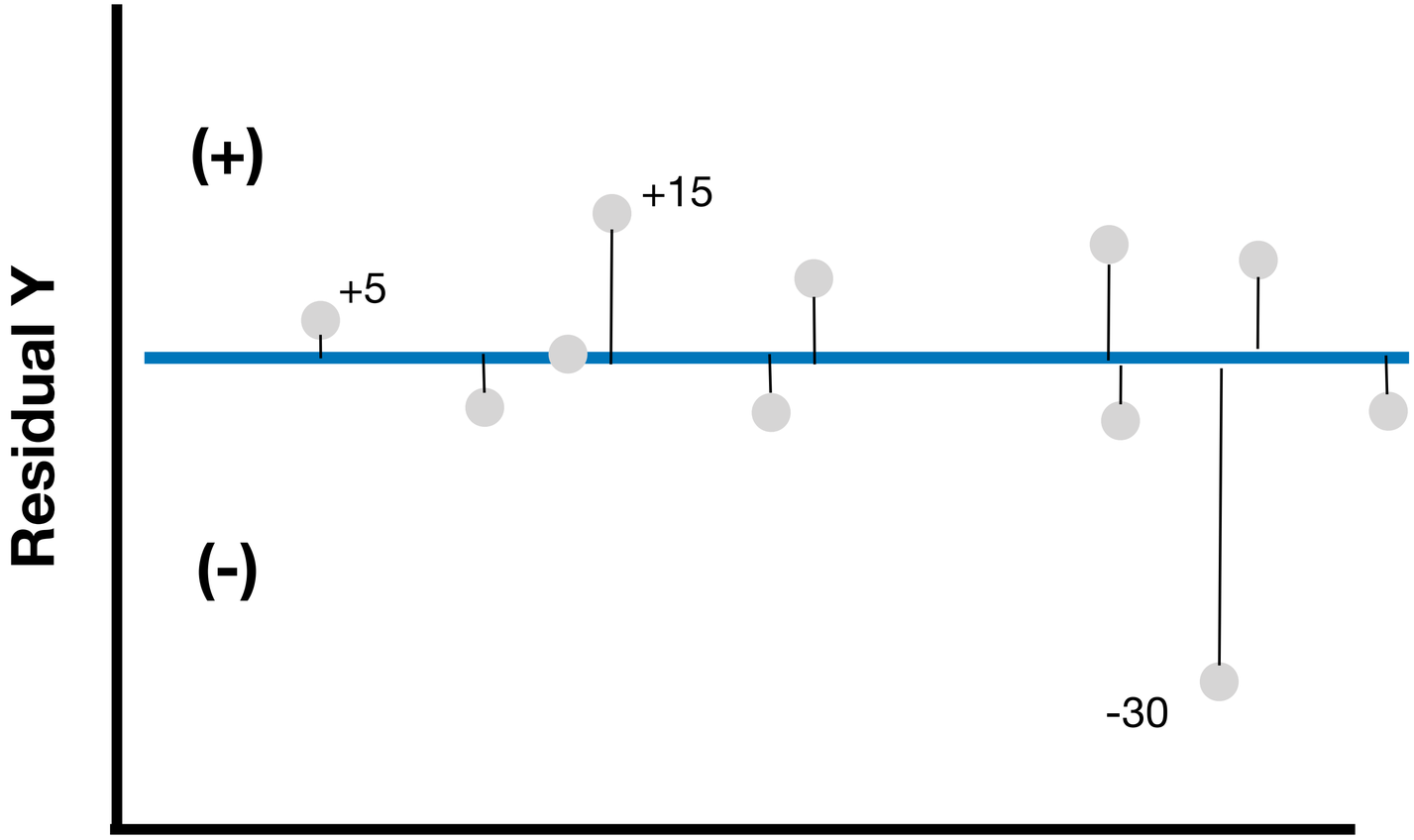
$$e_i = y_i - \hat{y}_i$$

```
> resid(lm(Y ~ X))
```

```
> fitted(lm(Y ~ X))
```

Residual plots to identify non-linearity

```
> plot(fitted(model), resid(model))
```



residual = observed - fitted

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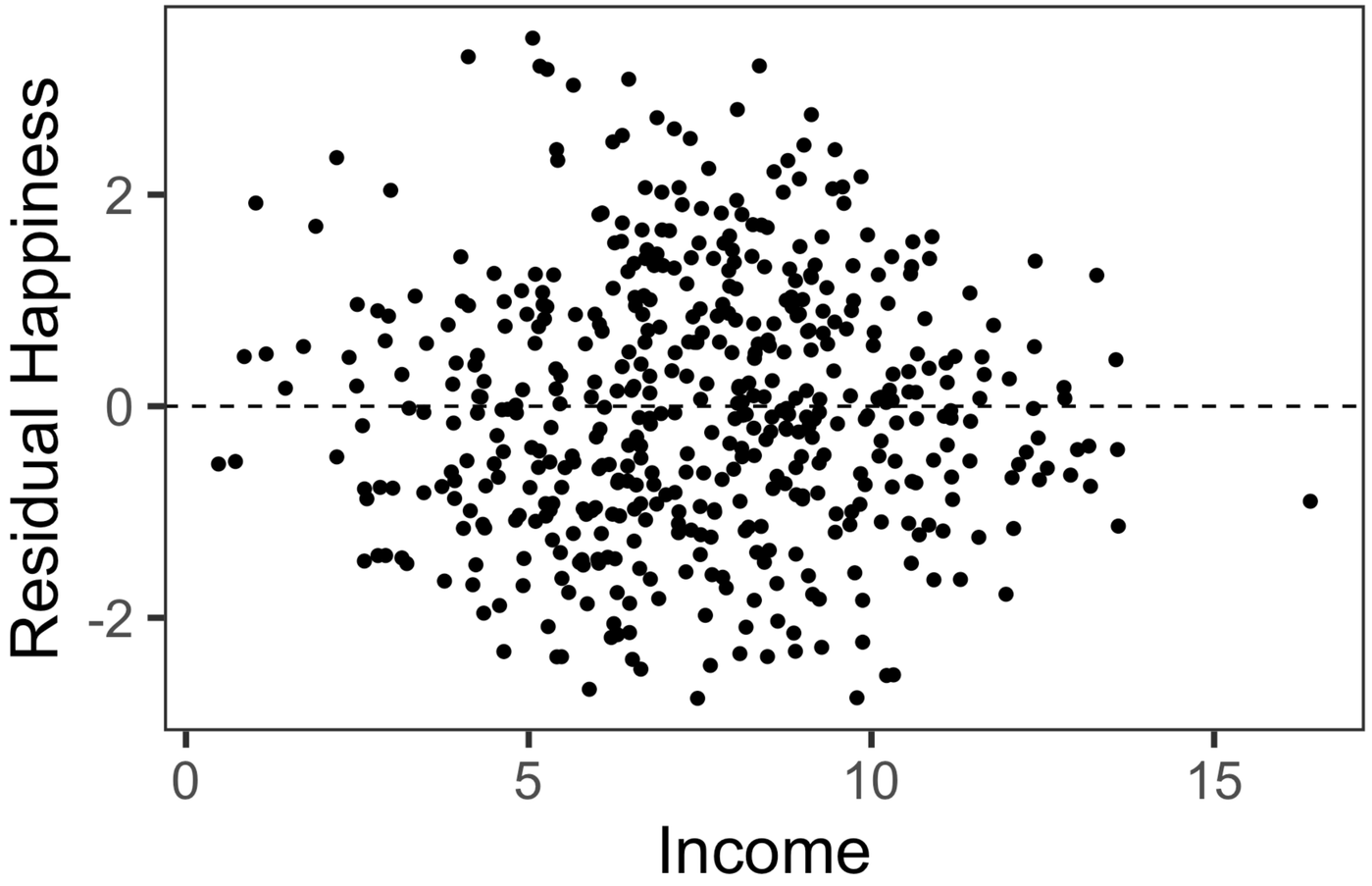
- Mean of zero
- Equally positive as negative
- No remaining shape
- Low residual values

Residual plots to identify non-linearity

```
> plot(fitted(model), resid(model))
```



residual = observed - fitted

$$e_i = y_i - \hat{y}_i$$

- Mean of zero
- Equally positive as negative
- No remaining shape
- Low residual values

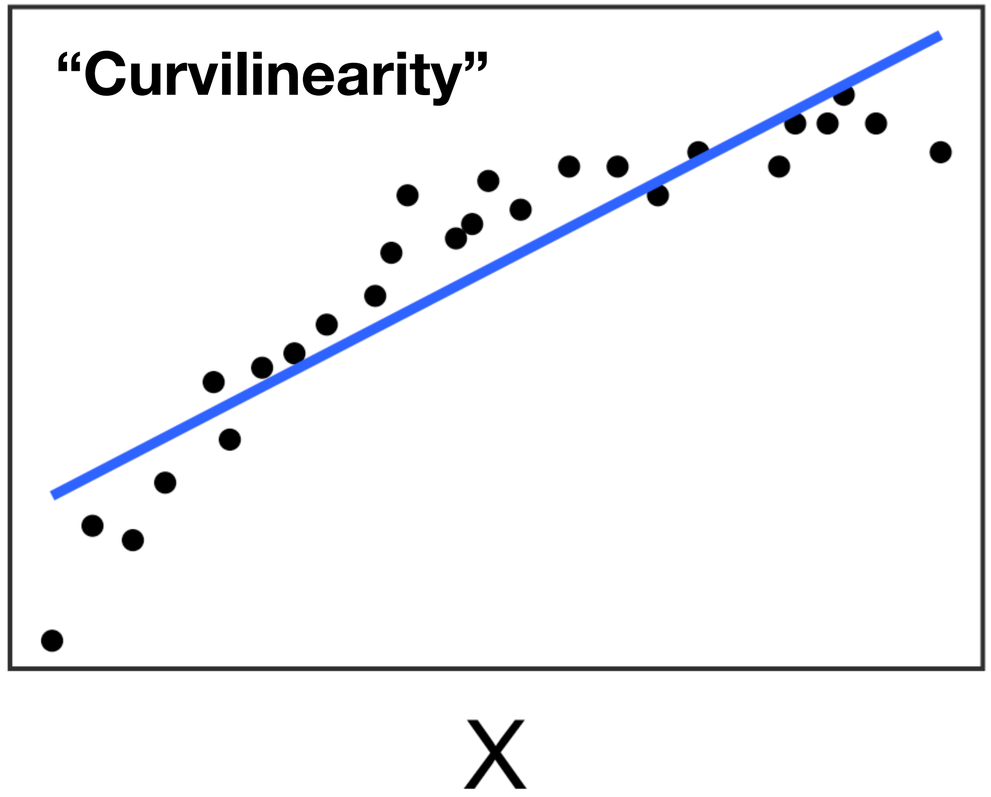
Residual plots to identify non-linearity

```
> summary(lm(happiness ~ income, data = income_data))

Call:
lm(formula = happiness ~ income, data = income_data)

Residuals:
    Min      1Q  Median      3Q     Max
-3.5033 -0.8873  0.0459  0.9218  3.1279

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.34291    0.16505   8.136  3.3e-15 ***
income       0.22765    0.01727  13.182  < 2e-16 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 1.234 on 496 degrees of freedom
Multiple R-squared:  0.2595,    Adjusted R-squared:  0.258
F-statistic: 173.8 on 1 and 496 DF,  p-value: < 2.2e-16
```

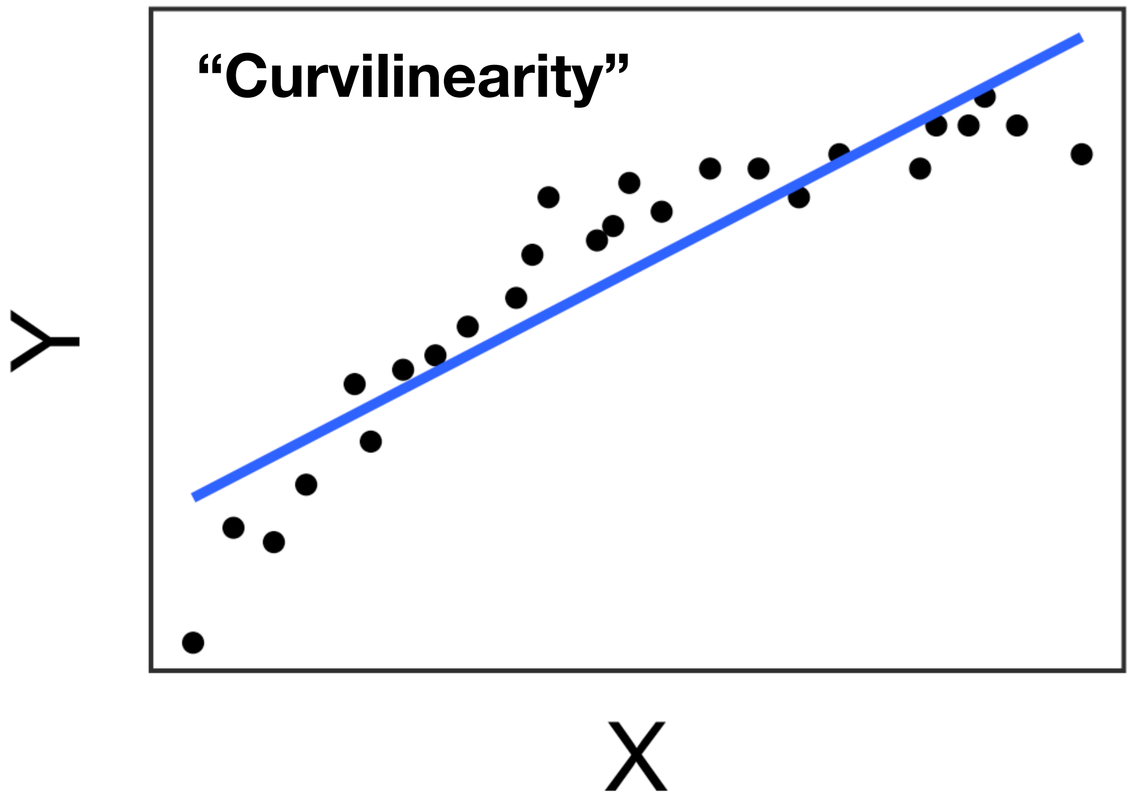
Residuals

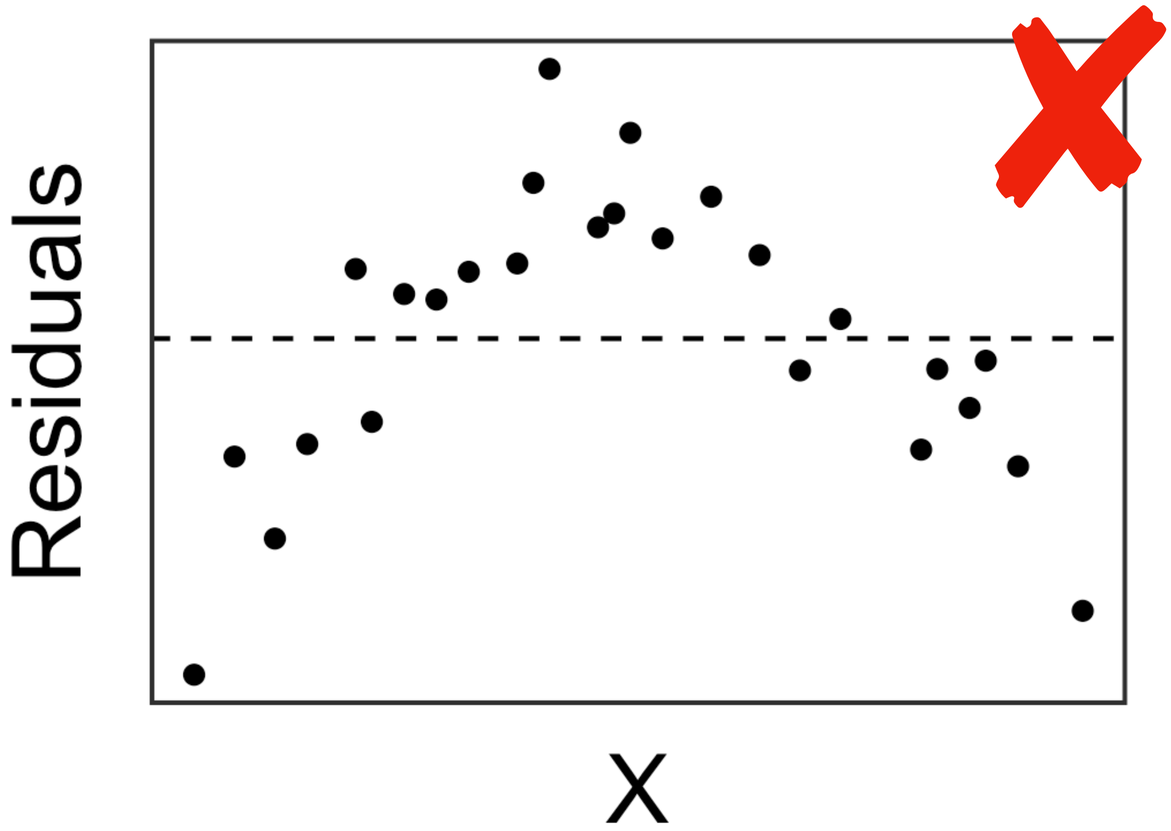
Can also see summary of residuals with `summary(lm(Y~X))`

Residual plots to identify non-linearity



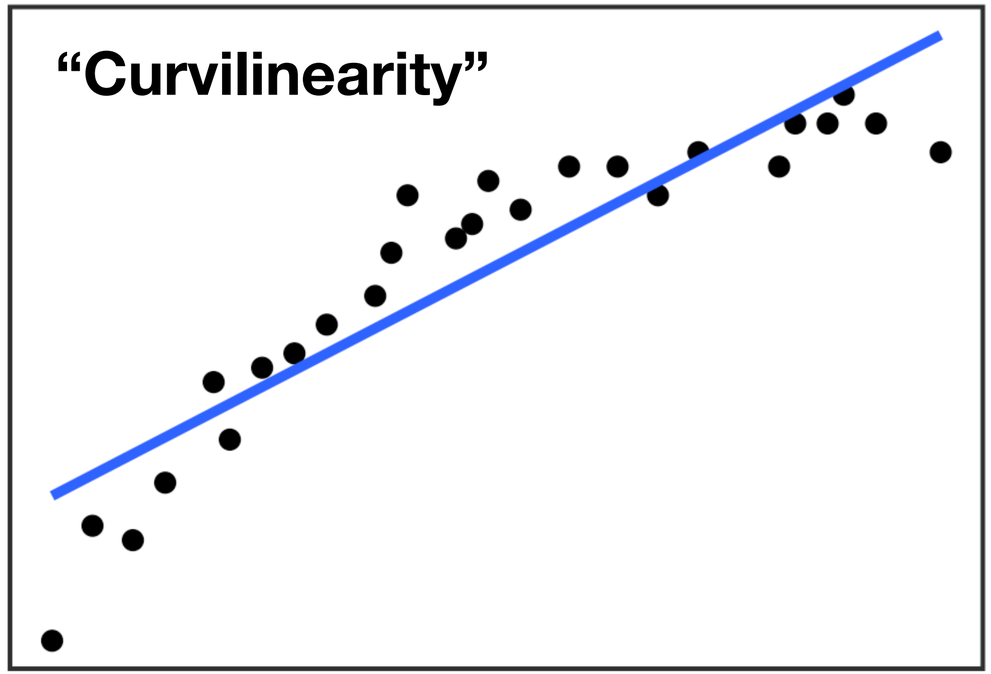
Residual plots to identify non-linearity

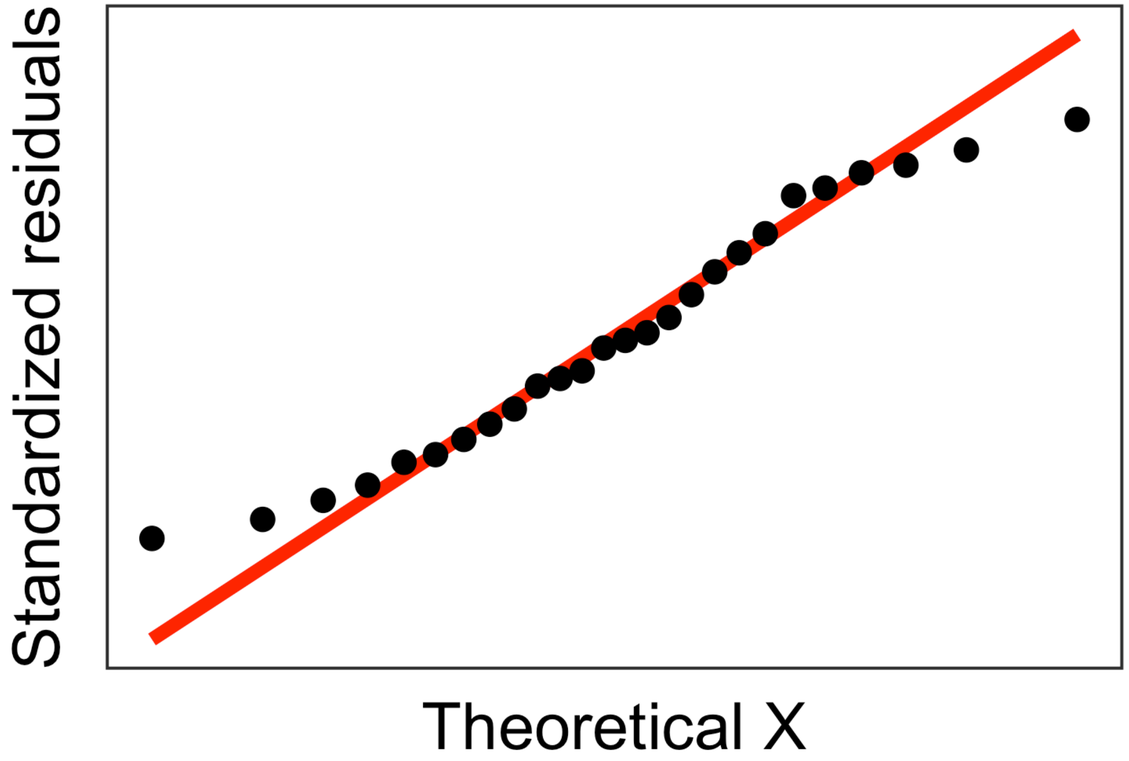




Data does not follow a linear model

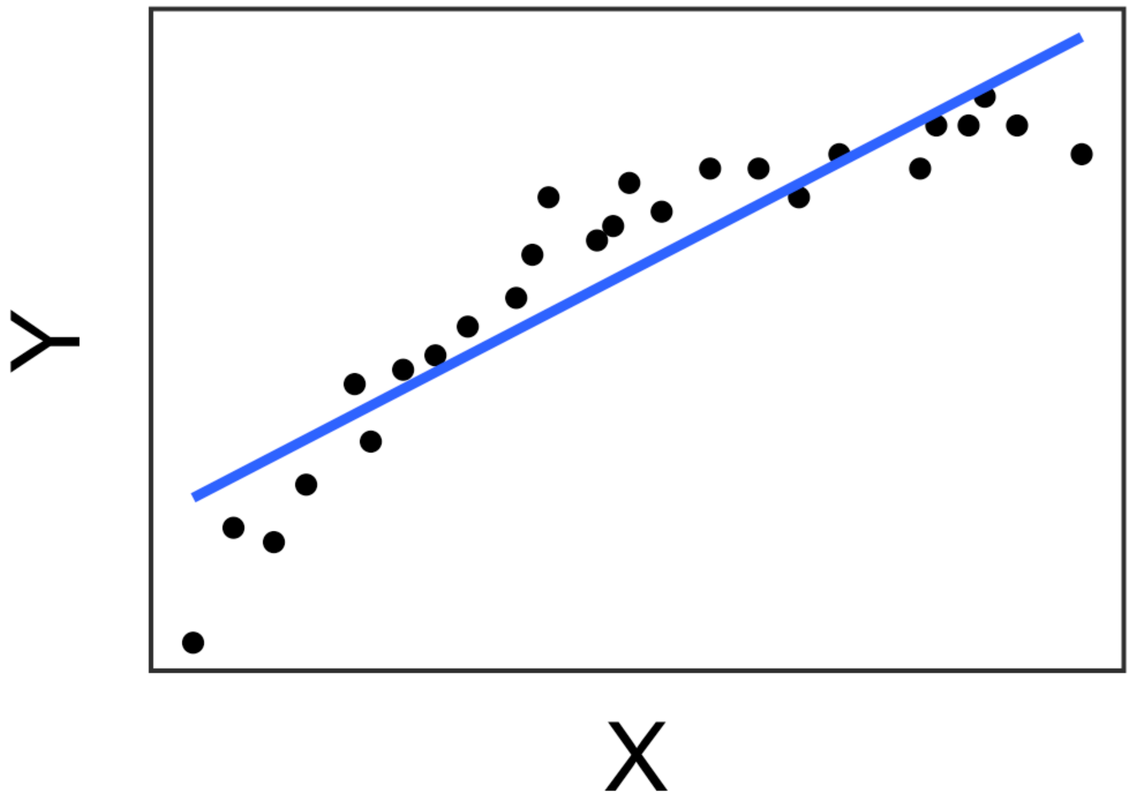
Q-Q plots to identify normality

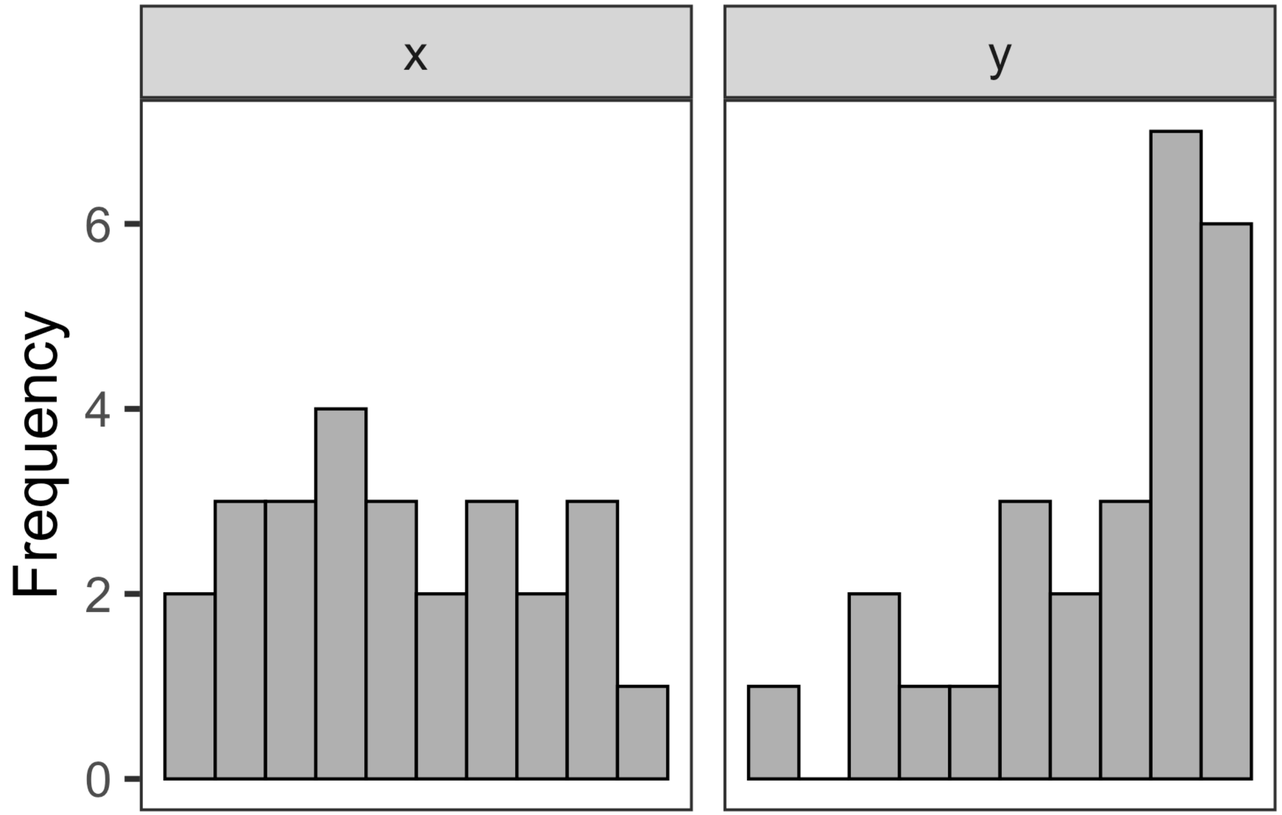




Residuals look normally distributed

Residual plots to identify non-linearity

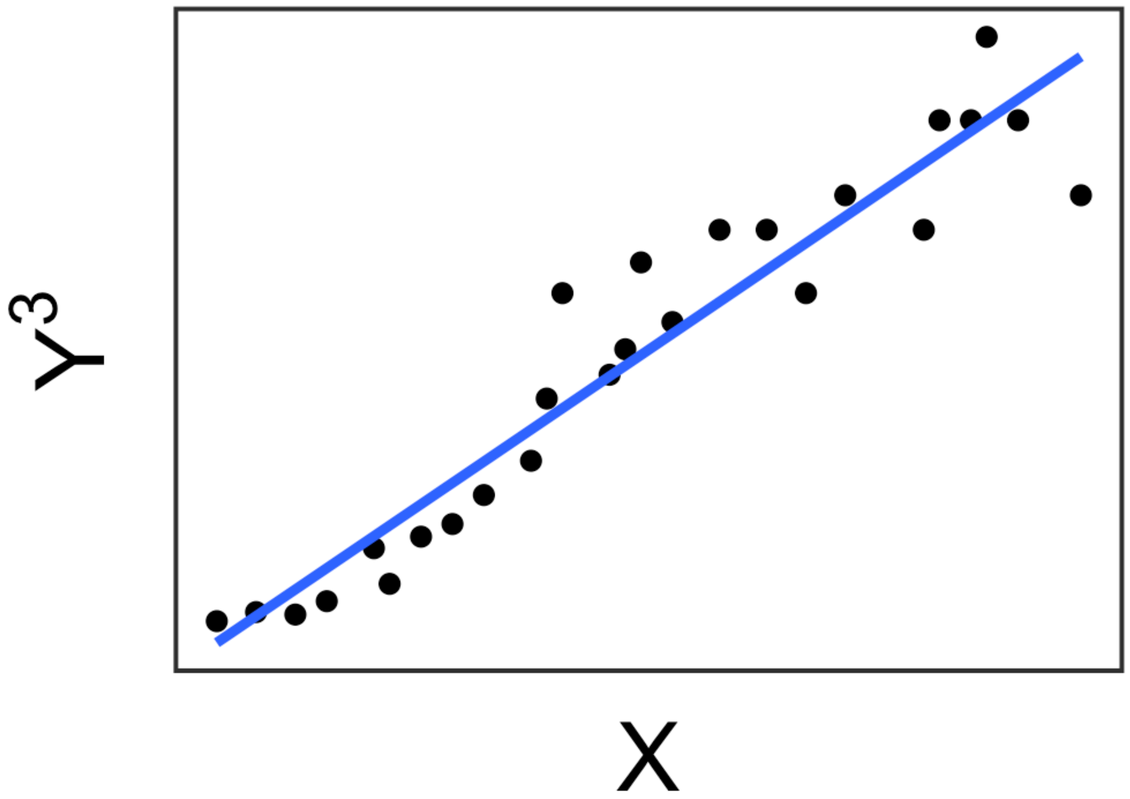


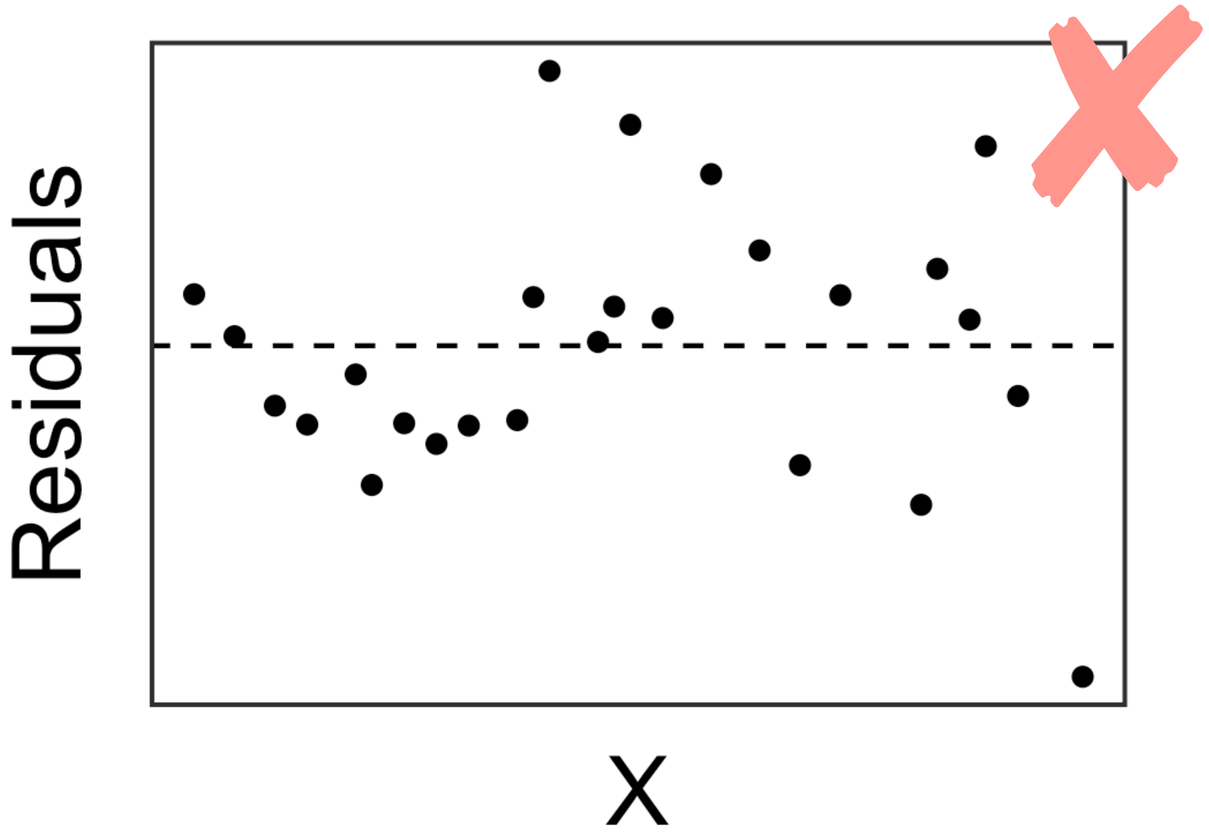


Y is left skewed

Could try Y^2

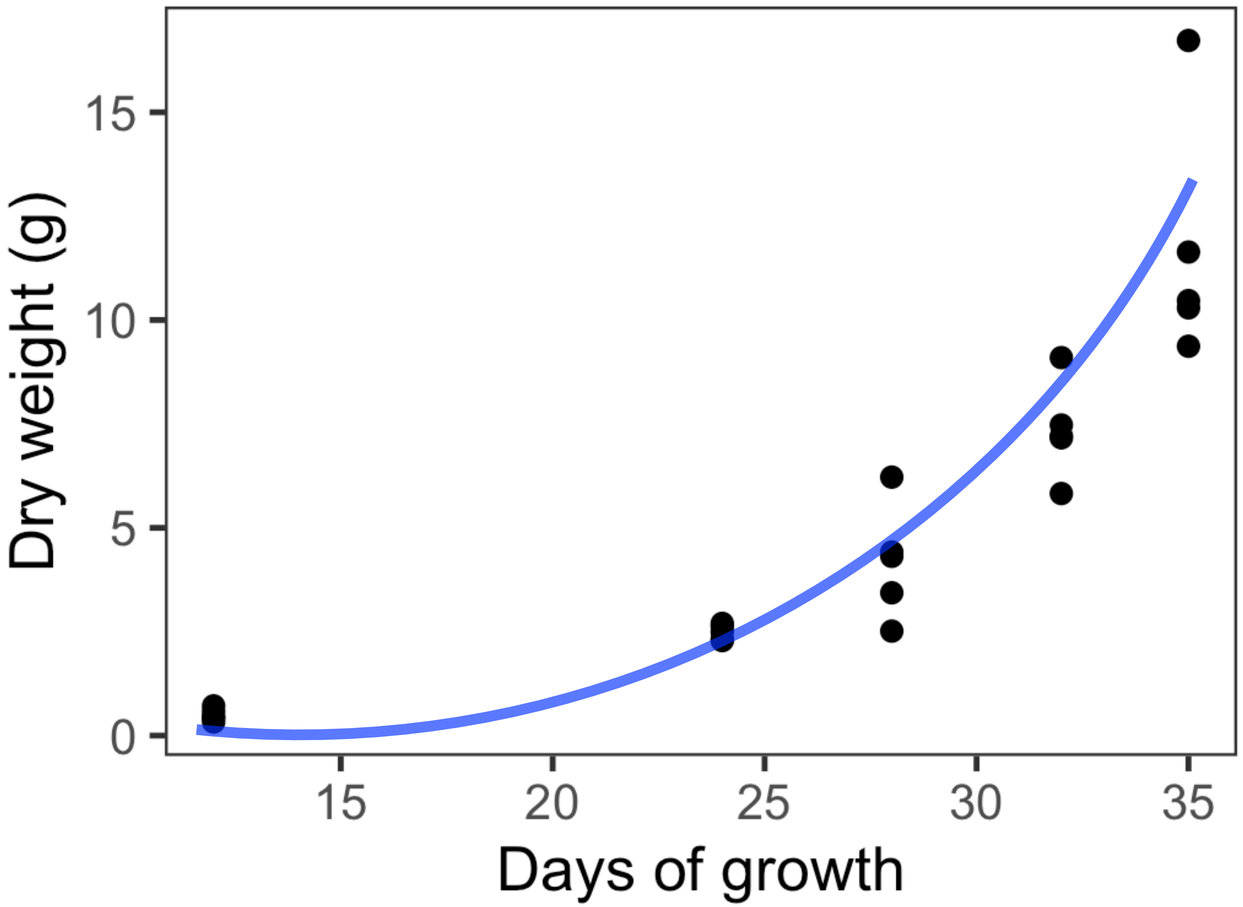
Residual plots to identify non-linearity





Not great, but much better!

Transformations to obtain linearity



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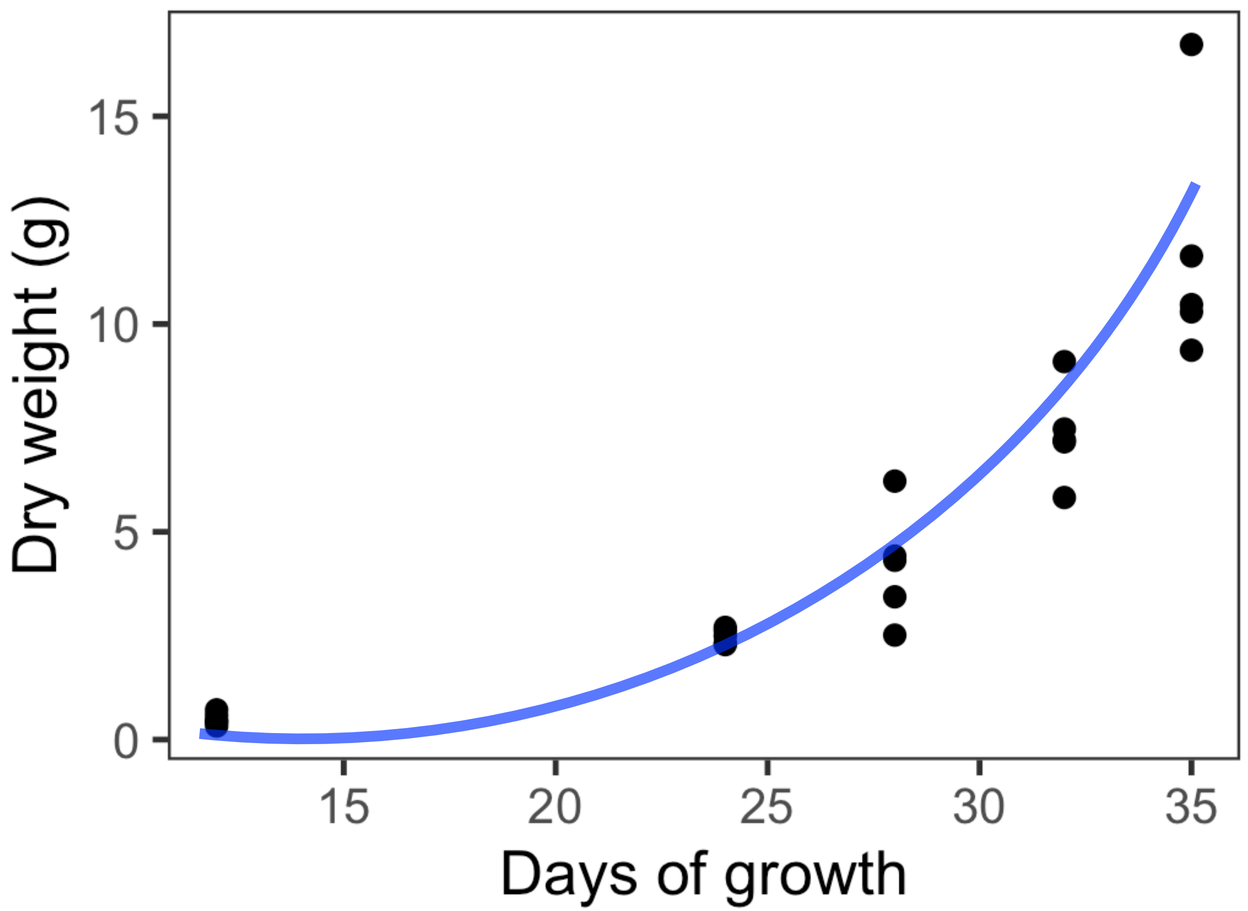

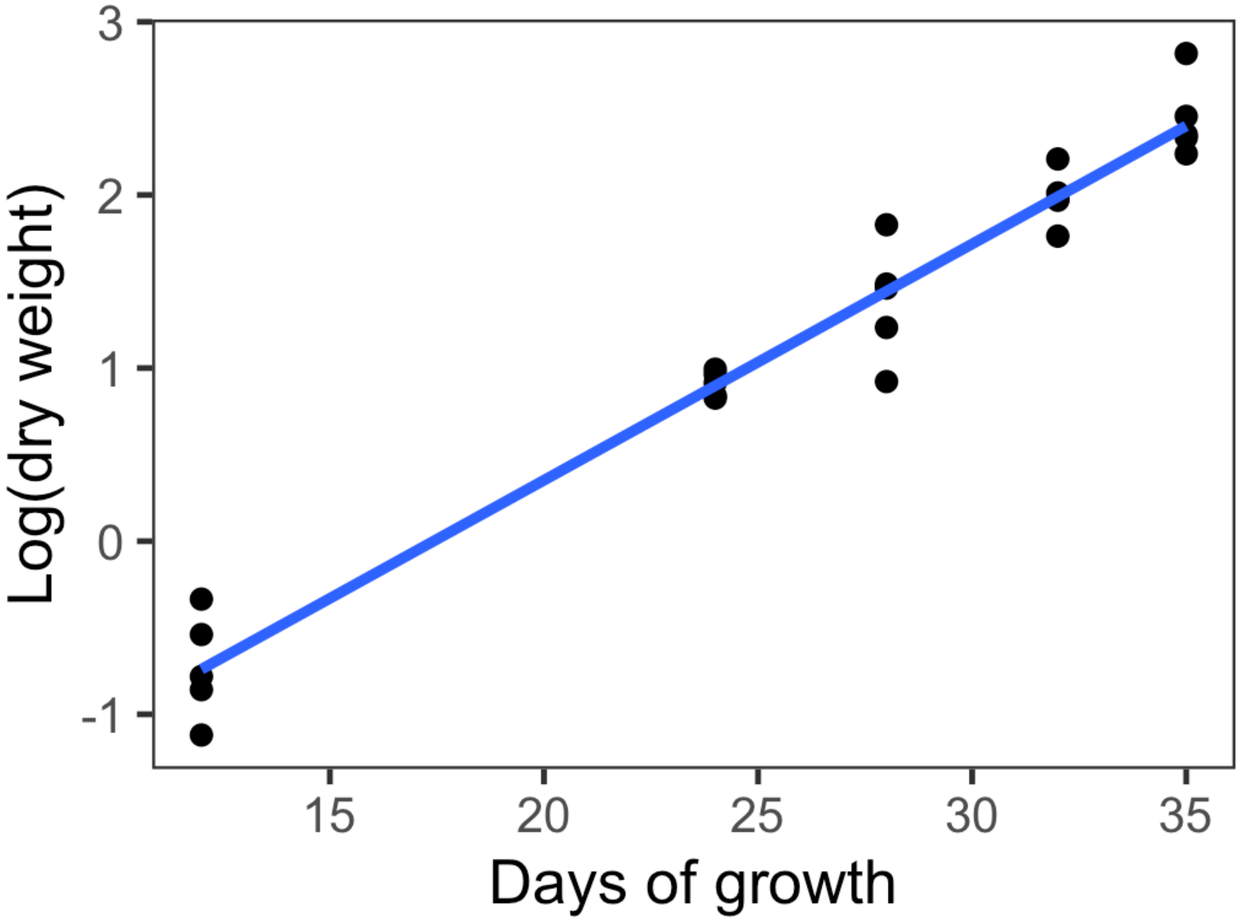

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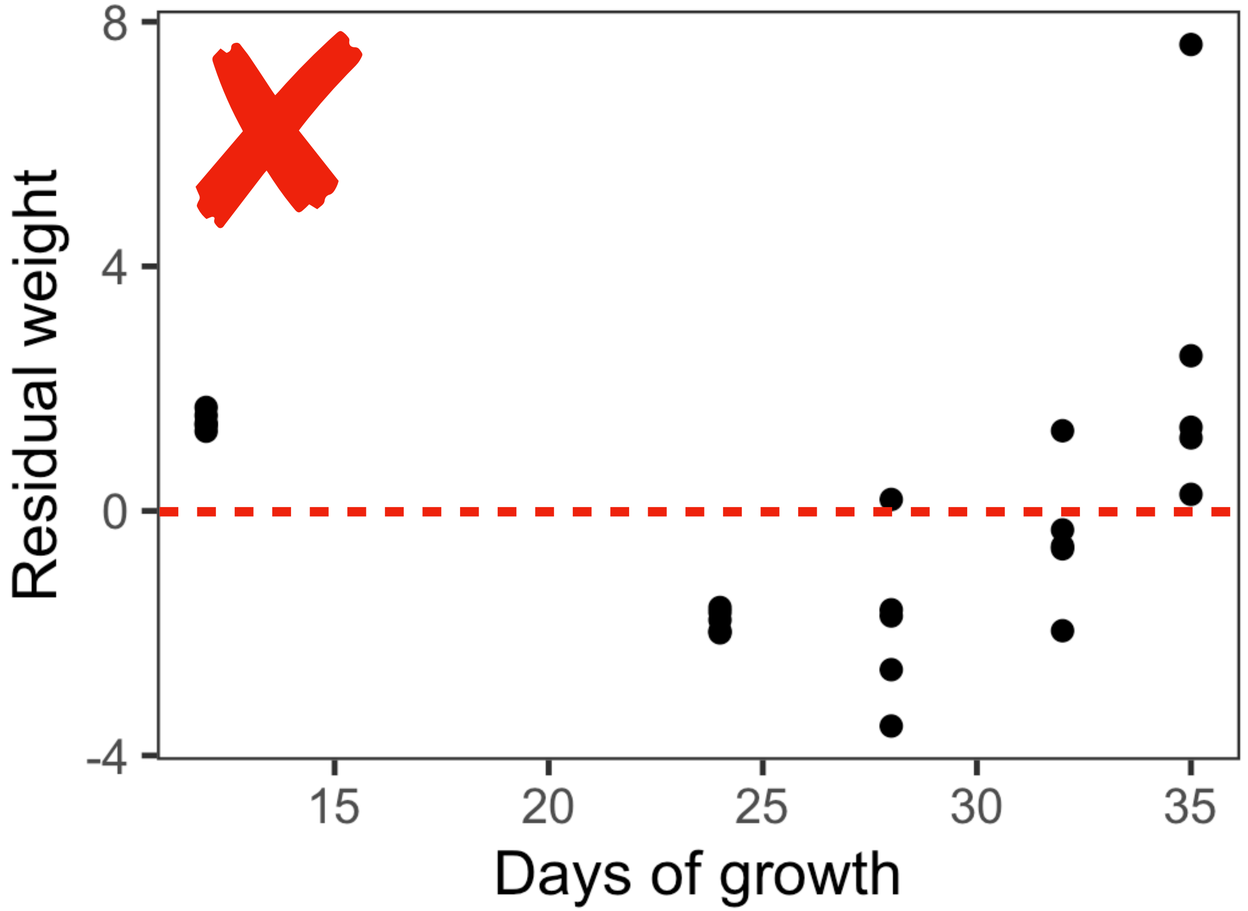

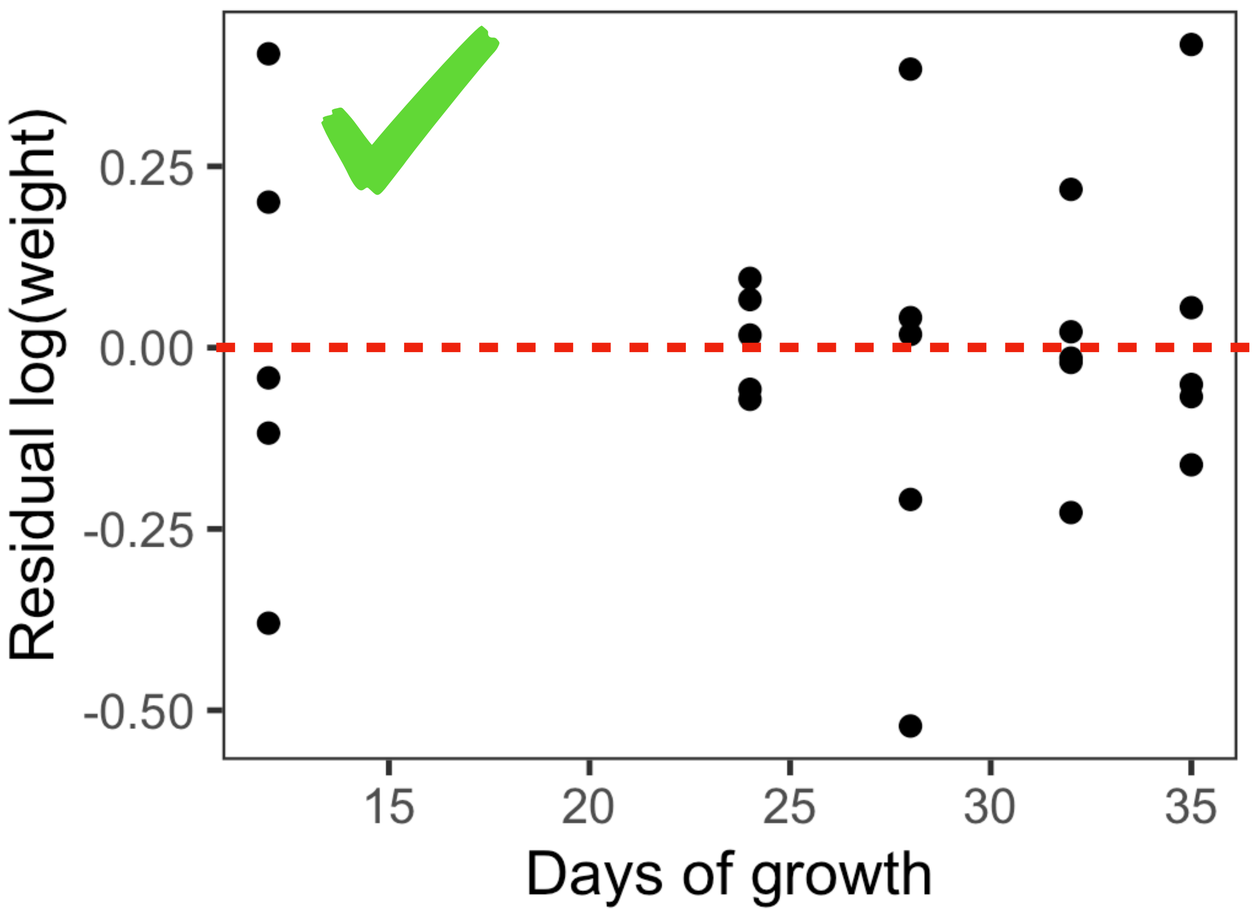

Transformations to obtain linearity

Great package for tidy statistics!

```
broom::augment(model)
```

happiness	income	.fitted	.resid	.std.resid	.hat	.sigma	.cooksd
2.3144890	3.862647	2.961527	-0.64703769	-0.90205658	0.002251376	0.7182356	9.180461e-04
3.4334898	4.979381	3.758680	-0.32519010	-0.45334273	0.002183070	0.7186765	2.248227e-04
4.5993734	4.923957	3.719116	0.88025693	1.22713119	0.002147257	0.7177335	1.620203e-03
2.7911138	3.214372	2.498771	0.29234235	0.40772807	0.003053610	0.7187050	2.545969e-04
5.5963983	7.196409	5.341251	0.25514736	0.35655407	0.006973369	0.7187334	4.463777e-04
2.4585559	3.729643	2.866585	-0.40802919	-0.56888086	0.002370292	0.7185909	3.844547e-04
3.1929918	4.674517	3.541060	-0.34806836	-0.48520140	0.002036760	0.7186549	2.402367e-04
1.9071368	4.498104	3.415132	-1.50799483	-2.10208970	0.002008681	0.7156164	4.446893e-03
2.9424499	3.121631	2.432570	0.50987997	0.71118370	0.003214180	0.7184589	8.154585e-04
3.7379416	4.639914	3.516360	0.22158191	0.30888007	0.002027982	0.7187563	9.693831e-05
3.1754061	4.632840	3.511309	-0.33590329	-0.46824107	0.002026383	0.7186666	2.225930e-04
2.0090465	2.773179	2.183836	-0.17478978	-0.24388421	0.003919933	0.7187824	1.170366e-04
5.9518141	7.119479	5.286336	0.66547825	0.92983921	0.006697419	0.7181987	2.914819e-03
5.9605473	7.466653	5.534158	0.42638937	0.59616497	0.008005262	0.7185679	1.434066e-03

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5.5963983	7.196409	5.341251	0.25514736	0.35655407	0.006973369	0.7187334	4.463777e-04
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1.9071368	4.498104	3.415132	-1.50799483	-2.10208970	0.002008681	0.7156164	4.446893e-03
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3.1754061	4.632840	3.511309	-0.33590329	-0.46824107	0.002026383	0.7186666	2.225930e-04
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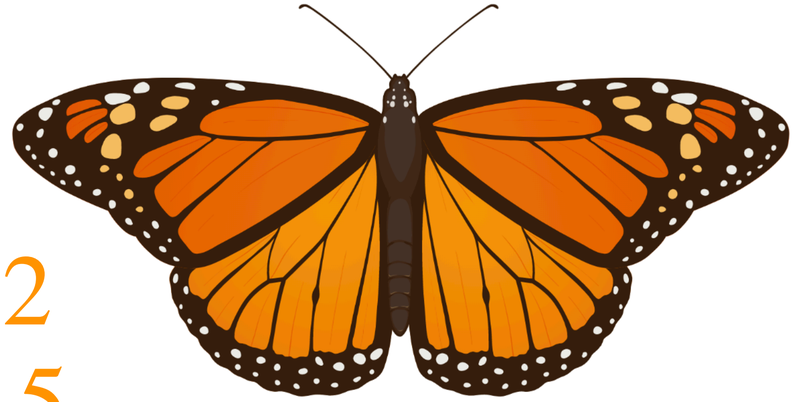
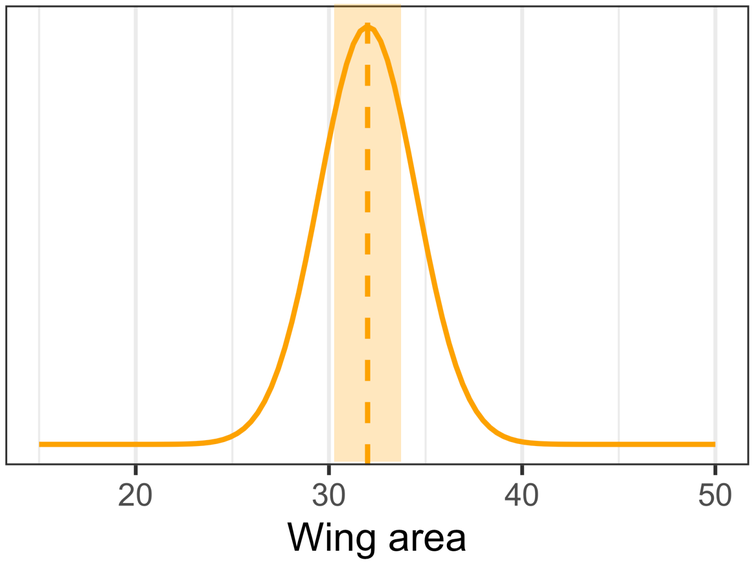
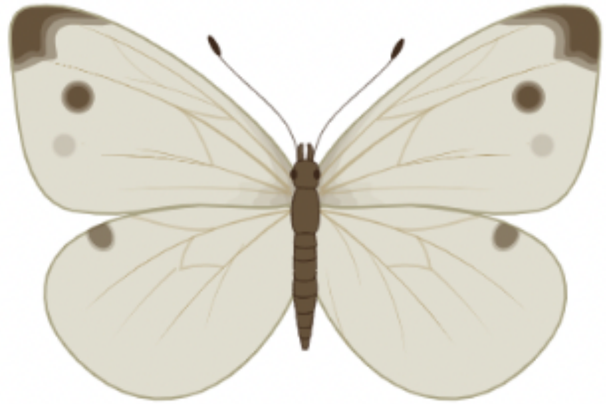
Regression and the *t*-test

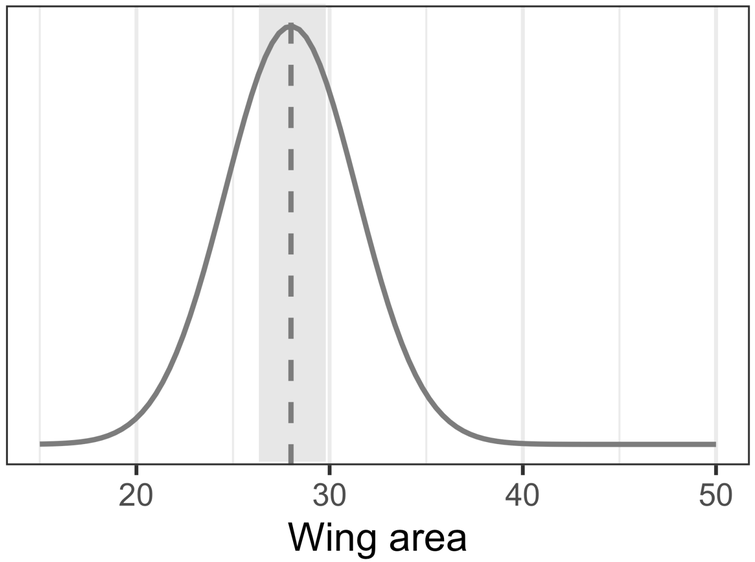
$\bar{y}_1 = 32$
$s_1 = 2.5$





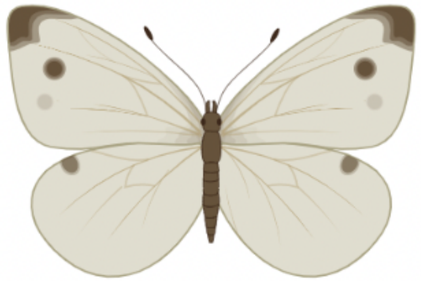


$\bar{y}_2 = 28$
$s_2 = 3.4$



Regression and the ***t*-test**

$\bar{y}_1 = 32$
$s_1 = 2.5$



$\bar{y}_2 = 28$
$s_2 = 3.4$

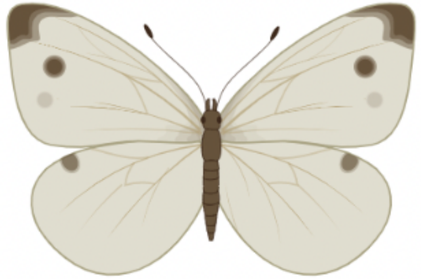
```
# make populations for butterfly
y1 <- rnorm(14, 32, 2.5)
y2 <- rnorm(12, 28, 3.4)

# calculate t test with t.test
t.test(y1, y2)
```

$$H_0 : \mu_1 = \mu_2$$
$$H_A : \mu_1 \neq \mu_2$$

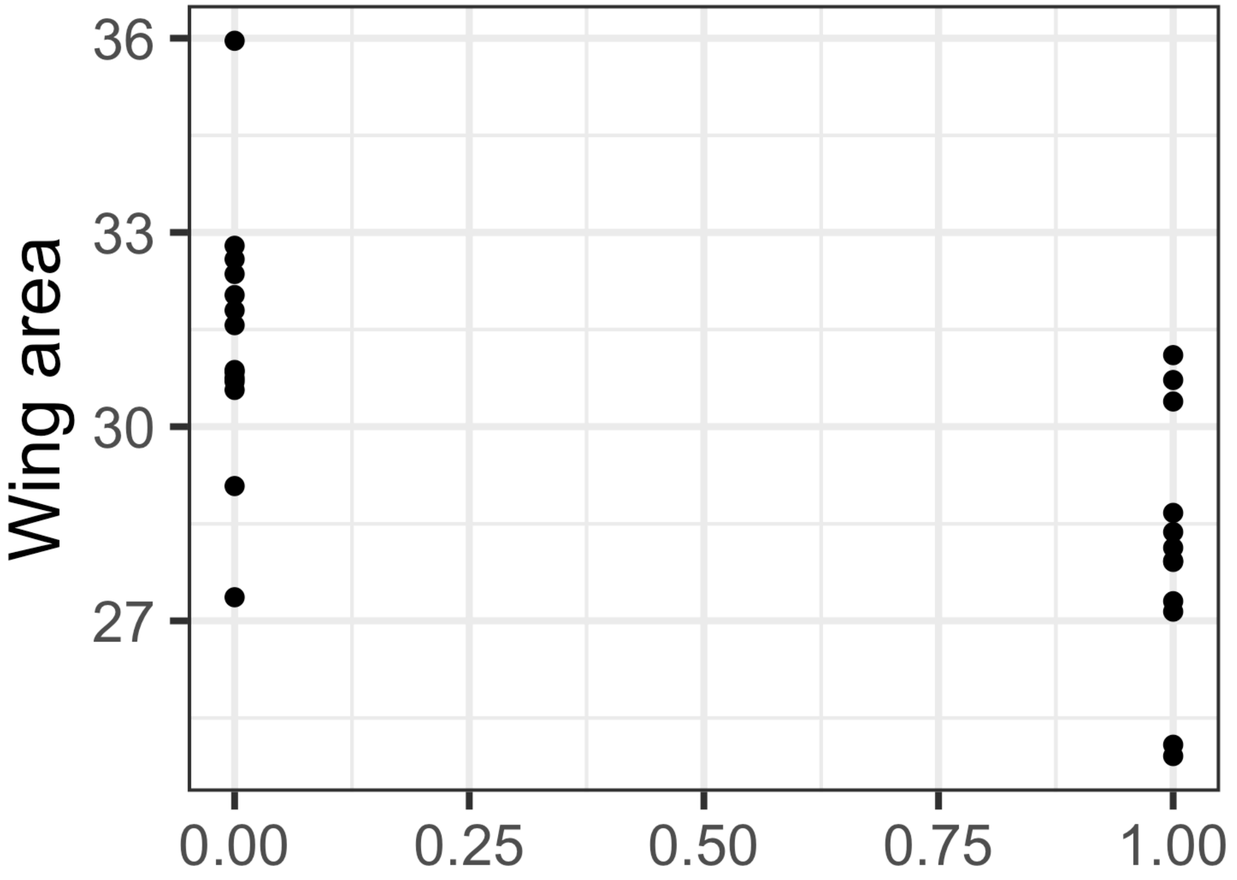
```
        Welch Two Sample t-test

data:  y1 and y2
t = 4.2051, df = 23.351, p-value = 0.0003288
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 1.646552 4.829972
sample estimates:
mean of x mean of y
 31.37680  28.13854
```

Regression and the *t*-test

$\bar{y}_1 = 32$
$s_1 = 2.5$



$\bar{y}_2 = 28$
$s_2 = 3.4$

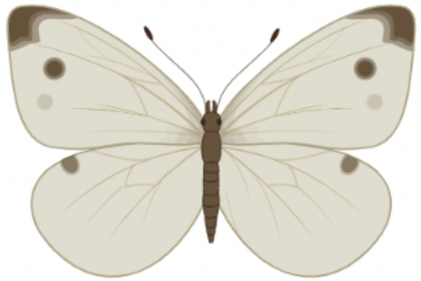


"Indicator variable"

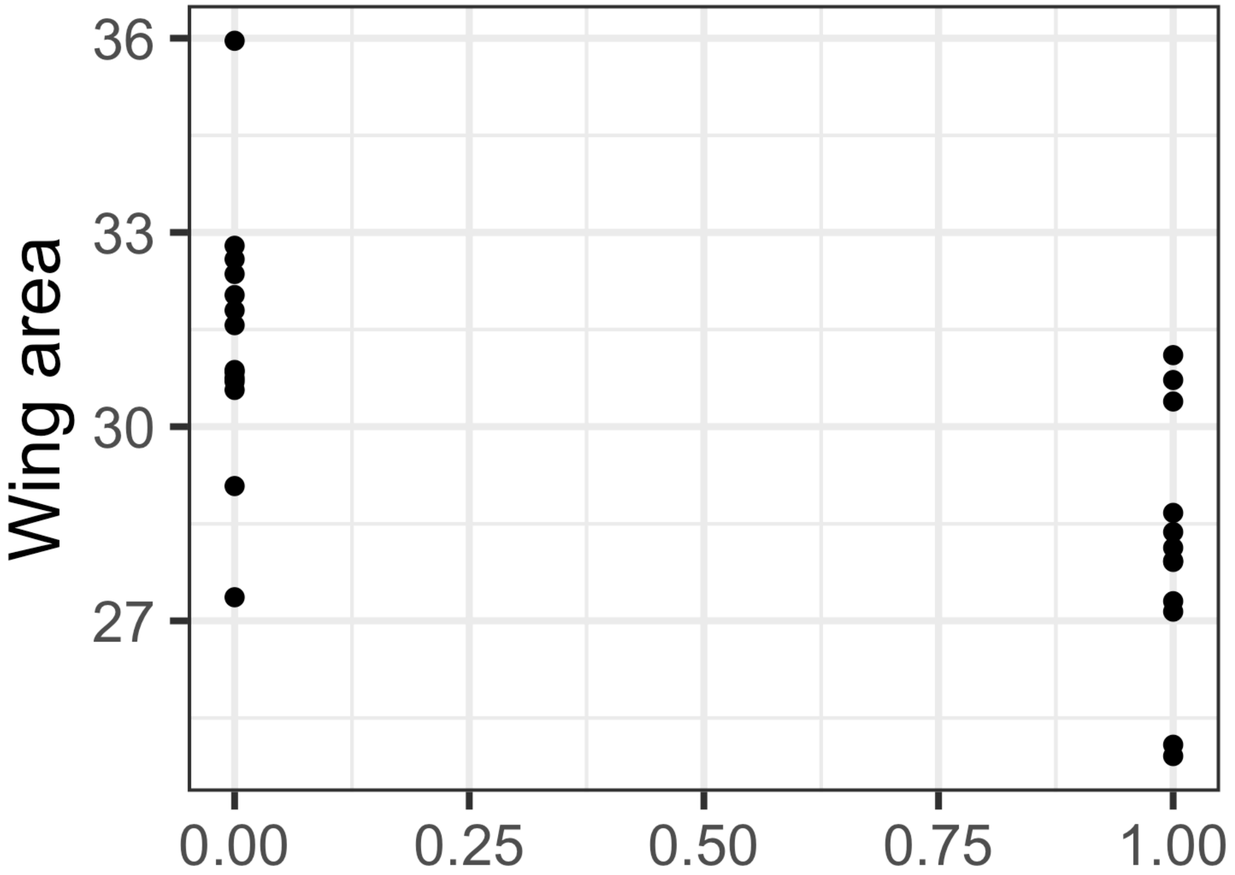
butterfly	area
0	32.79386
1	27.14261
0	31.56760
1	24.91155
0	31.79648
1	30.38884
0	30.69628
1	27.91059

Regression and the *t*-test

$\bar{y}_1 = 32$
$s_1 = 2.5$



$\bar{y}_2 = 28$
$s_2 = 3.4$

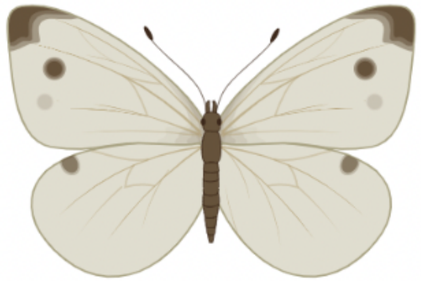


"Indicator variable"

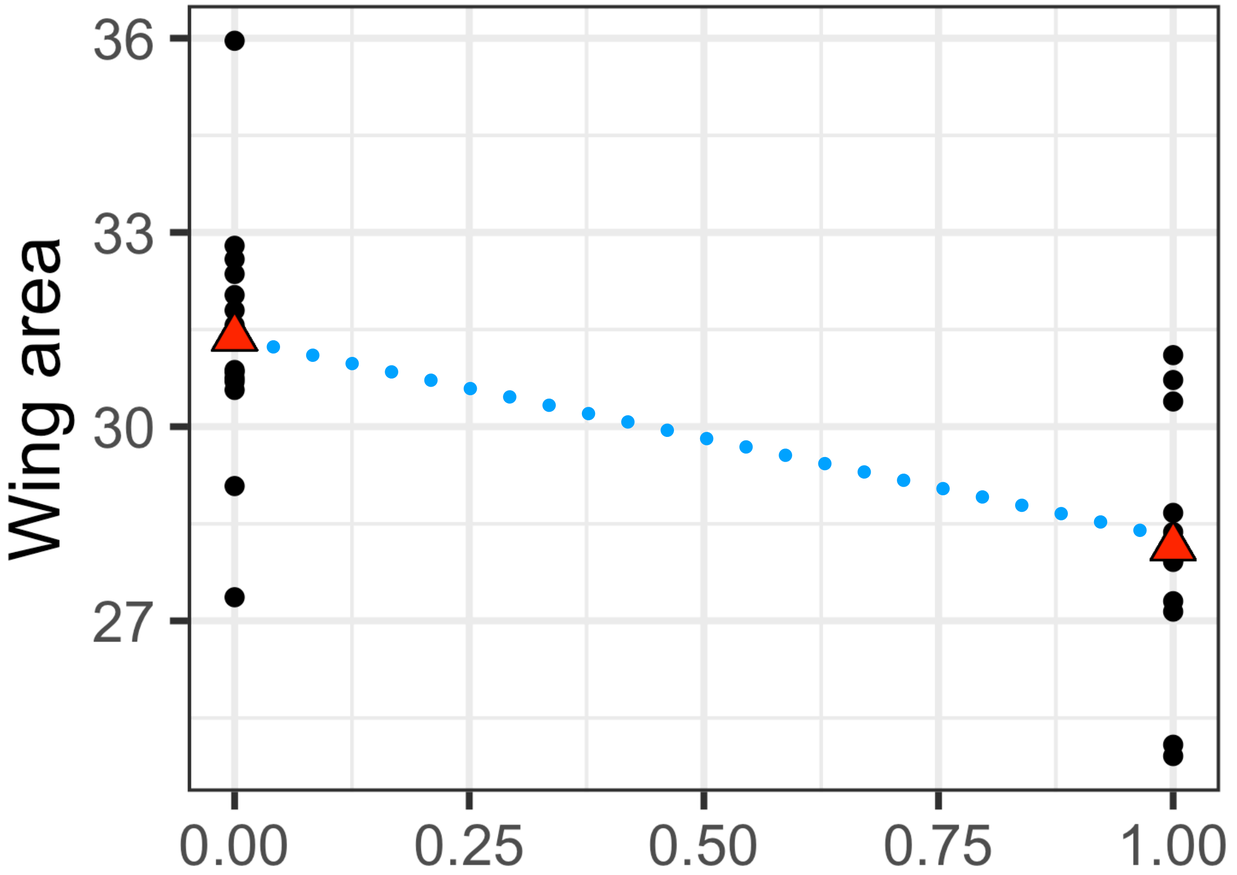
$$H_0 : \beta_1 = 0$$
$$H_A : \beta_1 \neq 0$$

Regression and the *t*-test

$\bar{y}_1 = 32$
$s_1 = 2.5$



$\bar{y}_2 = 28$
$s_2 = 3.4$



"Indicator variable"

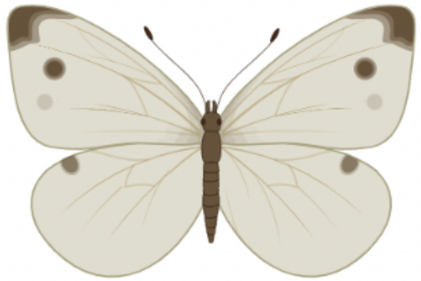
$$H_0 : \beta_1 = 0$$
$$H_A : \beta_1 \neq 0$$

Difference between group means = β_1!

$(H_0 : \mu_1 - \mu_2 = 0)$

Regression and the *t*-test

$\bar{y}_1 = 32$
$s_1 = 2.5$



$\bar{y}_2 = 28$
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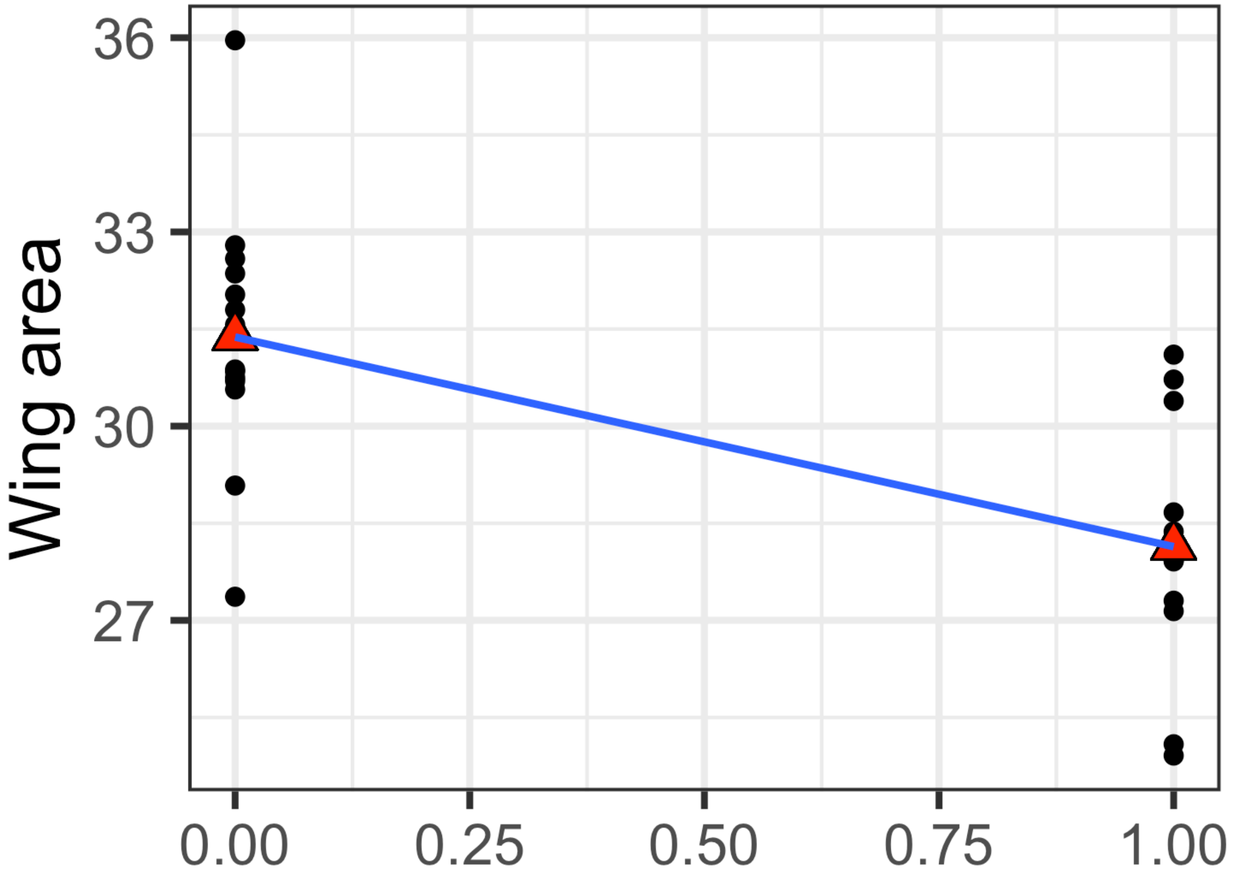
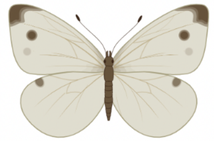


"Indicator variable"



$$H_0 : \beta_1 = 0$$
$$H_A : \beta_1 \neq 0$$

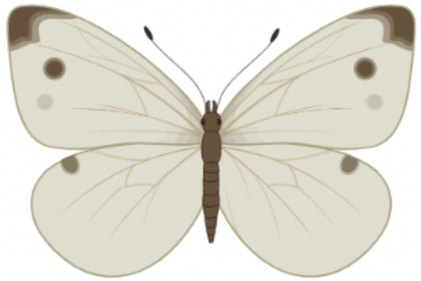
Difference between group means = β_1!

$(H_0 : \mu_1 - \mu_2 = 0)$

Regression and the *t*-test

$\bar{y}_1 = 32$

$s_1 = 2.5$



$\bar{y}_2 = 28$

$s_2 = 3.4$

```
Call:
lm(formula = area ~ butterfly, data = butterfly)

Residuals:
    Min      1Q  Median      3Q     Max
-4.0121 -0.7773 -0.1108  0.9000  4.5842

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  31.3768     0.5229  60.003  < 2e-16 ***
butterfly    -3.2383     0.7697  -4.207 0.000312 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 1.957 on 24 degrees of freedom
Multiple R-squared:  0.4245,    Adjusted R-squared:  0.4005
F-statistic:  17.7 on 1 and 24 DF,  p-value: 0.0003119
```

***t*-test: $t_s = 4.2051$**

$$H_0 : \beta_1 = 0$$

$$H_A : \beta_1 \neq 0$$

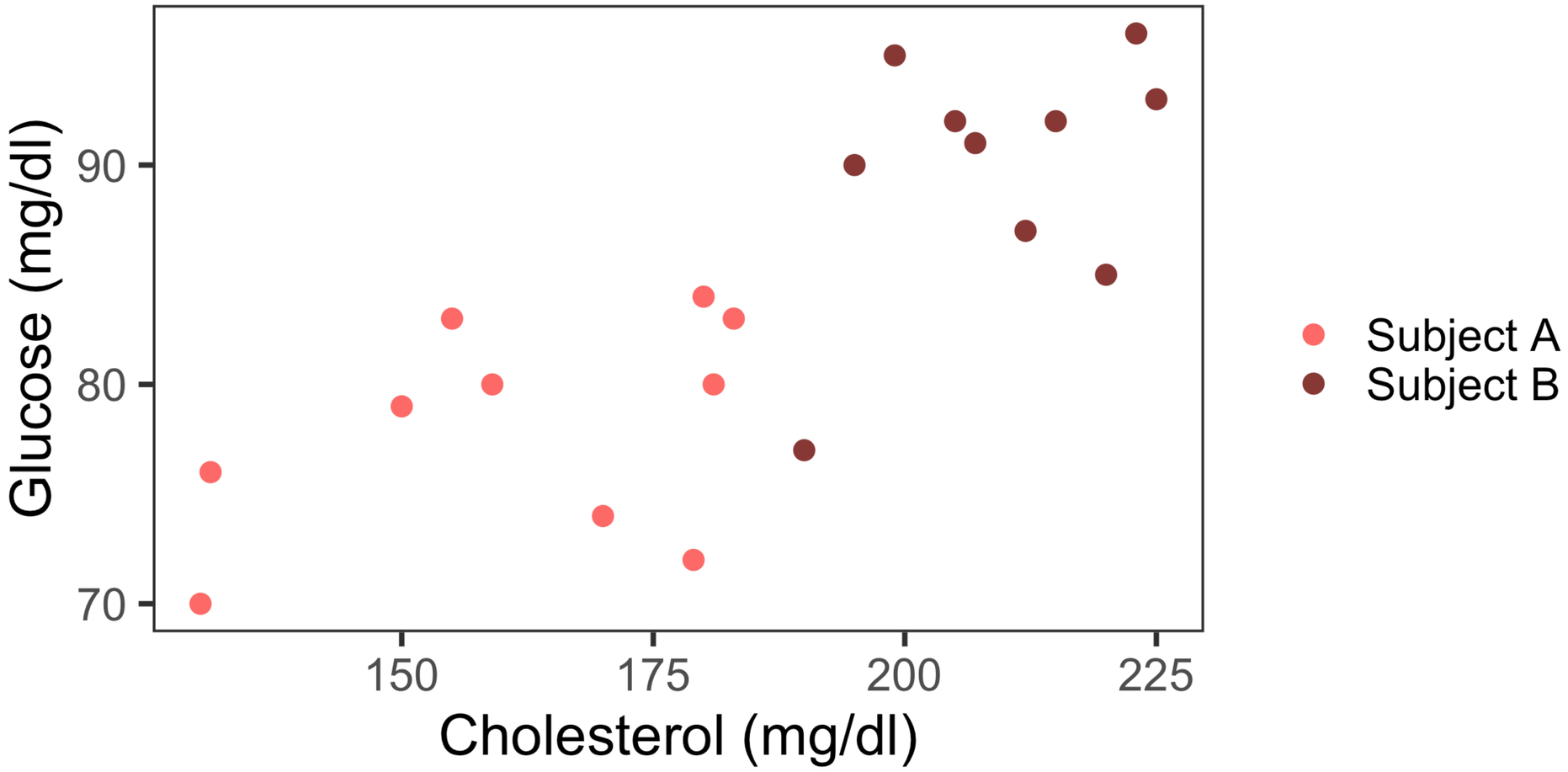
Difference between group means = β_1!

$(H_0 : \mu_1 - \mu_2 = 0)$

Variance explained

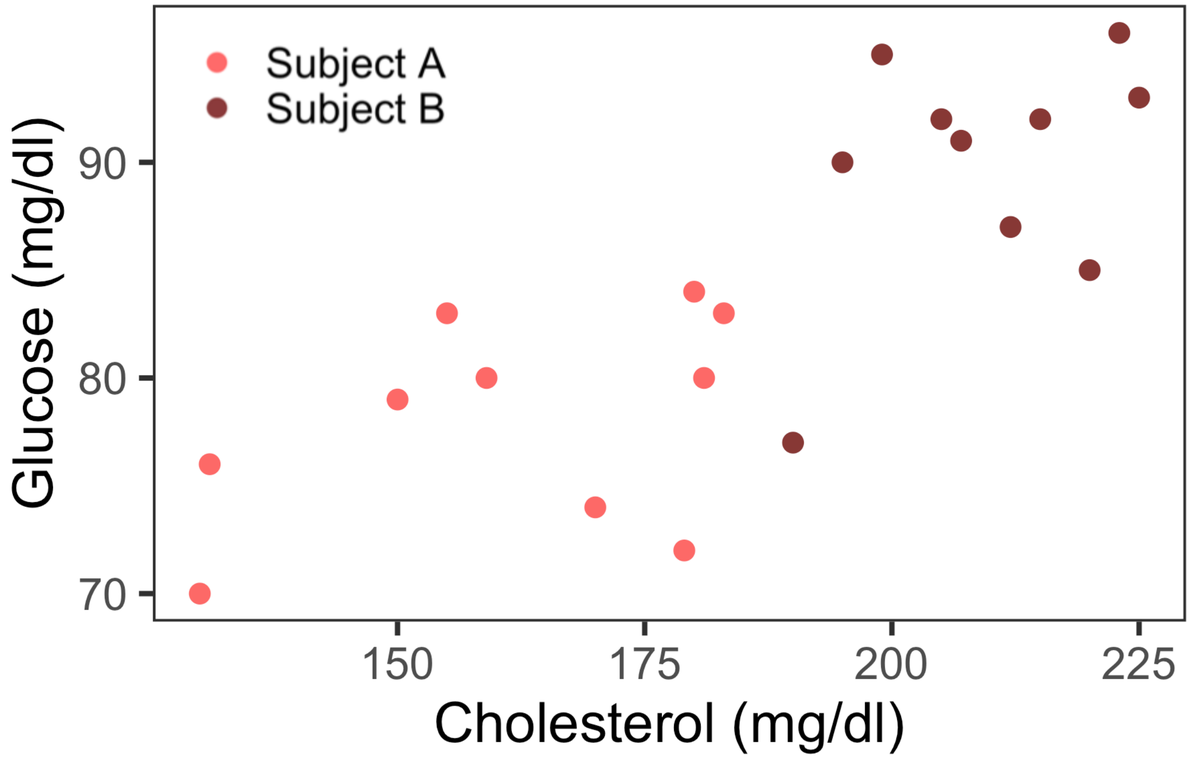
Regression and the ***t*-test**

Is there a relationship between cholesterol and glucose?



Regression and the ***t*-test**

Is there a relationship between cholesterol and glucose?



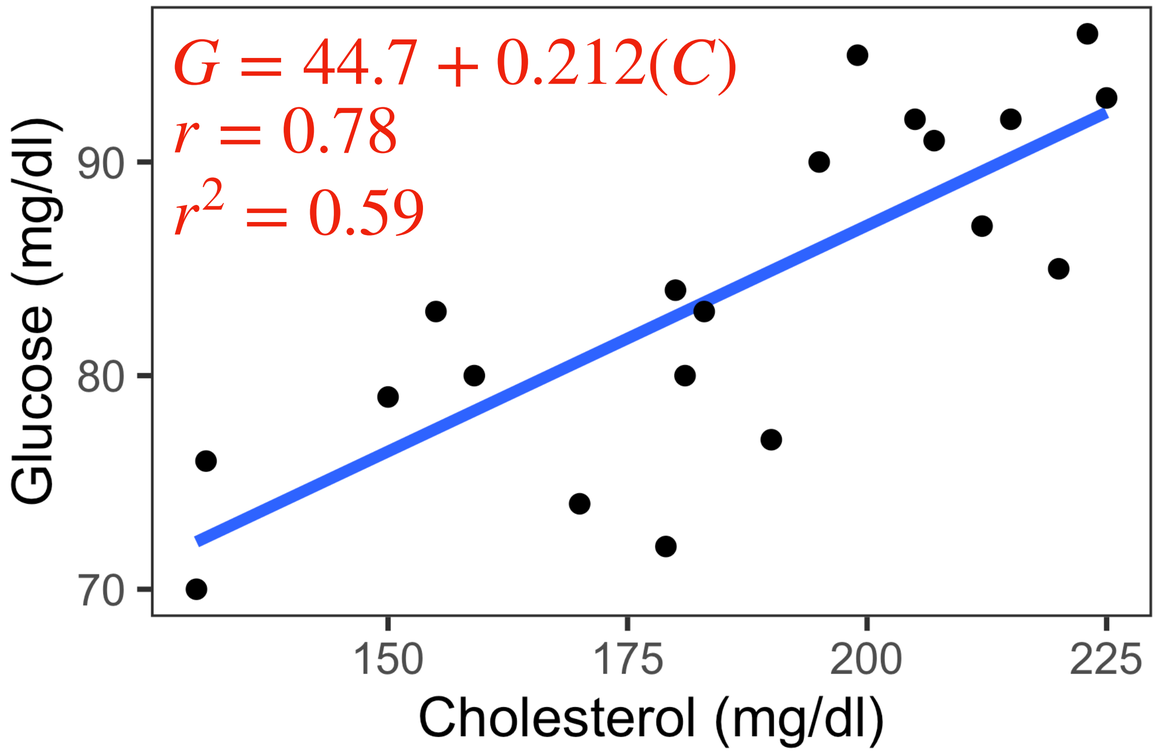
	Glucose (mg/dl)	
	Subject A	**Subject B**
Mean	78.1	89.8
SD	4.89	5.59
n	10	10

```
> t.test(subjectA$G, subjectB$G)

        t = -4.9814,
        df = 17.681,
        p-value = 0.0001018
```

Regression and the ***t*-test**

Is there a relationship between cholesterol and glucose?

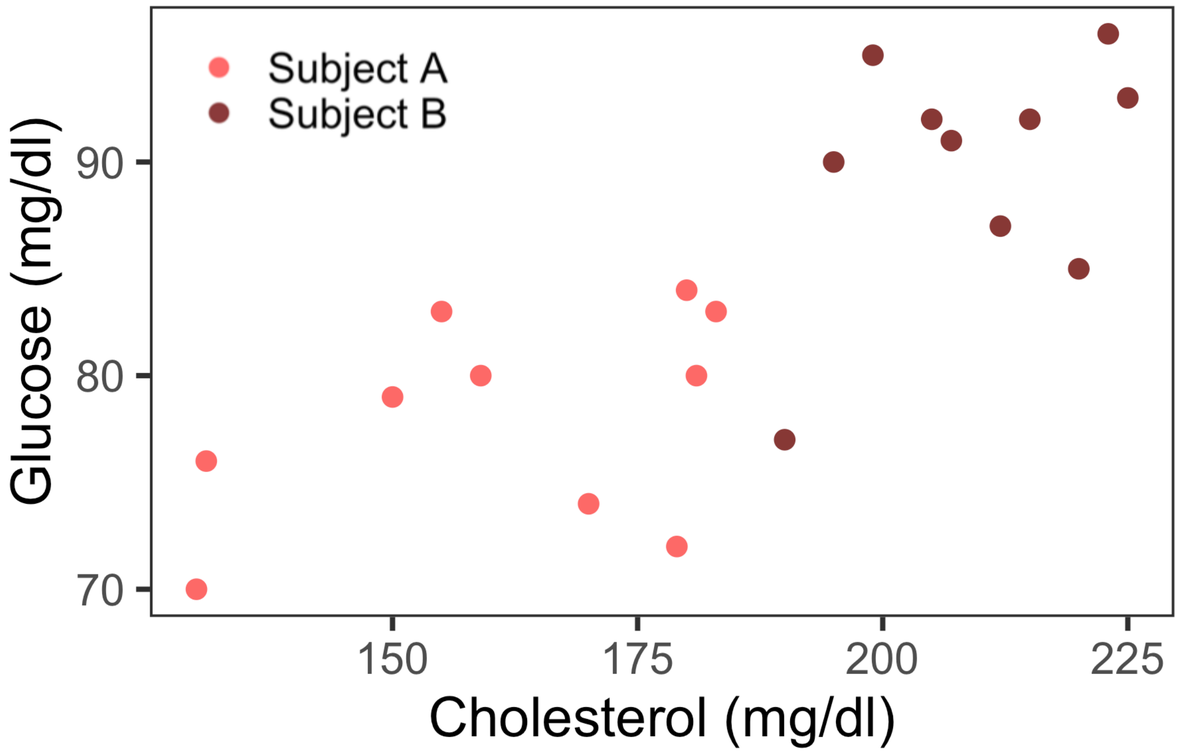



```
> lm(glucose ~ cholesterol)

   t = 5.330,
   df = 18,
   p-value = 4.57e-05
```

Multiple linear regression model

Is there a relationship between cholesterol and glucose?



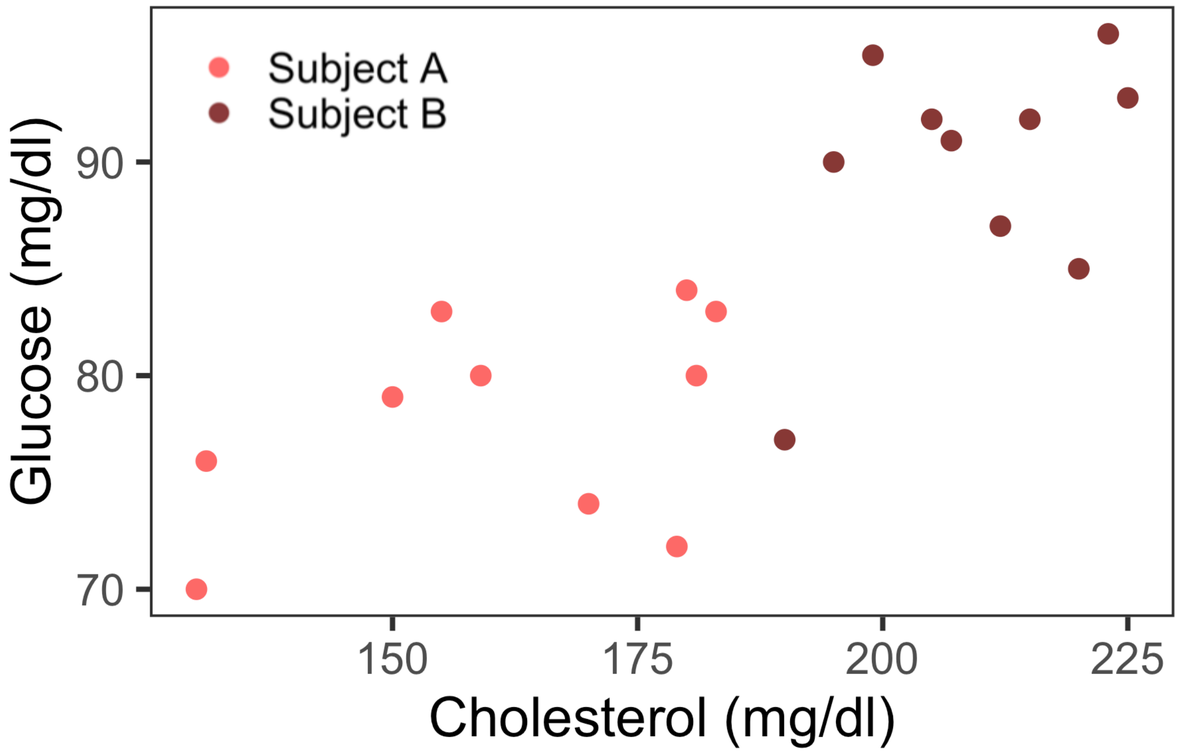

```
> lm(glucose ~ cholesterol + subject)

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 56.91808   11.40891   4.989 0.000112 ***
cholesterol  0.13091    0.06985   1.874 0.078206 .
subjectB     5.50776    3.96963   1.387 0.183218
---
```

When subject and cholesterol are 0, what is glucose? (Doesn't mean anything biologically in our data)

Multiple linear regression model

Is there a relationship between cholesterol and glucose?




```
> lm(glucose ~ cholesterol + subject)

Coefficients:
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(Intercept) 56.91808   11.40891   4.989 0.000112 ***
cholesterol  0.13091    0.06985   1.874 0.078206 .
subjectB     5.50776    3.96963   1.387 0.183218
---
```
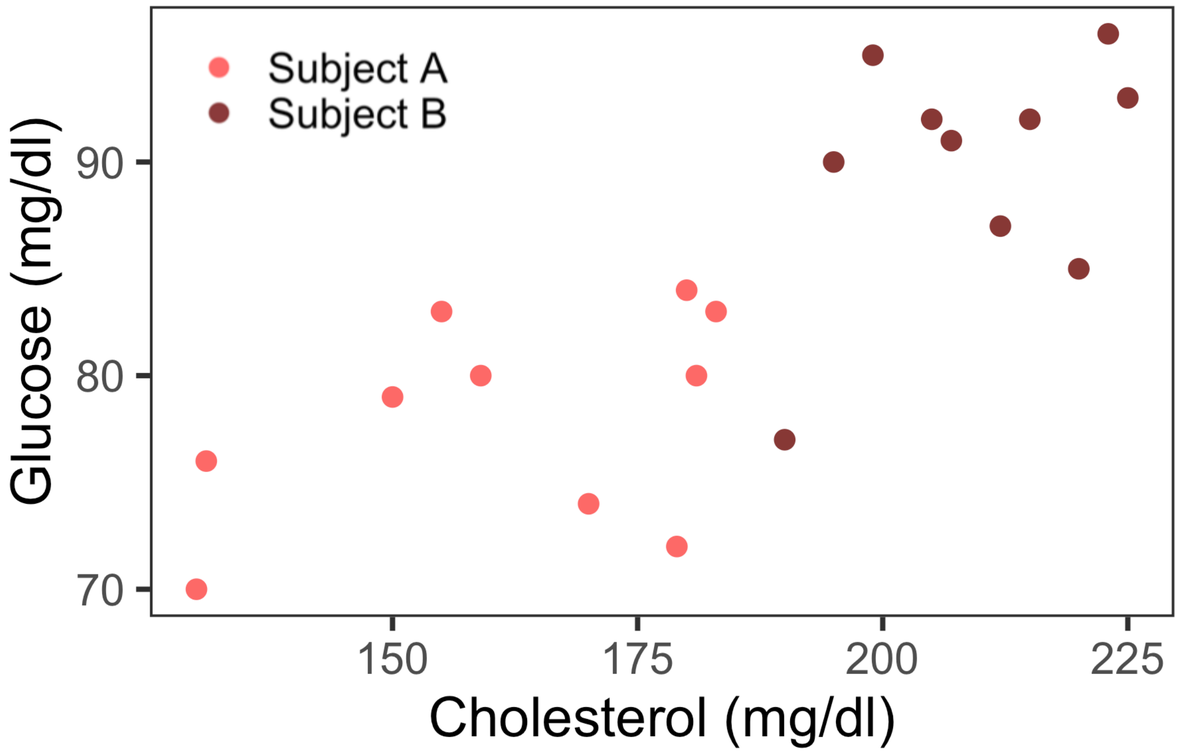

When cholesterol increases by one unit, glucose increases by 0.13 units

(β_1 for cholesterol)

Multiple linear regression model

Is there a relationship between cholesterol and glucose?



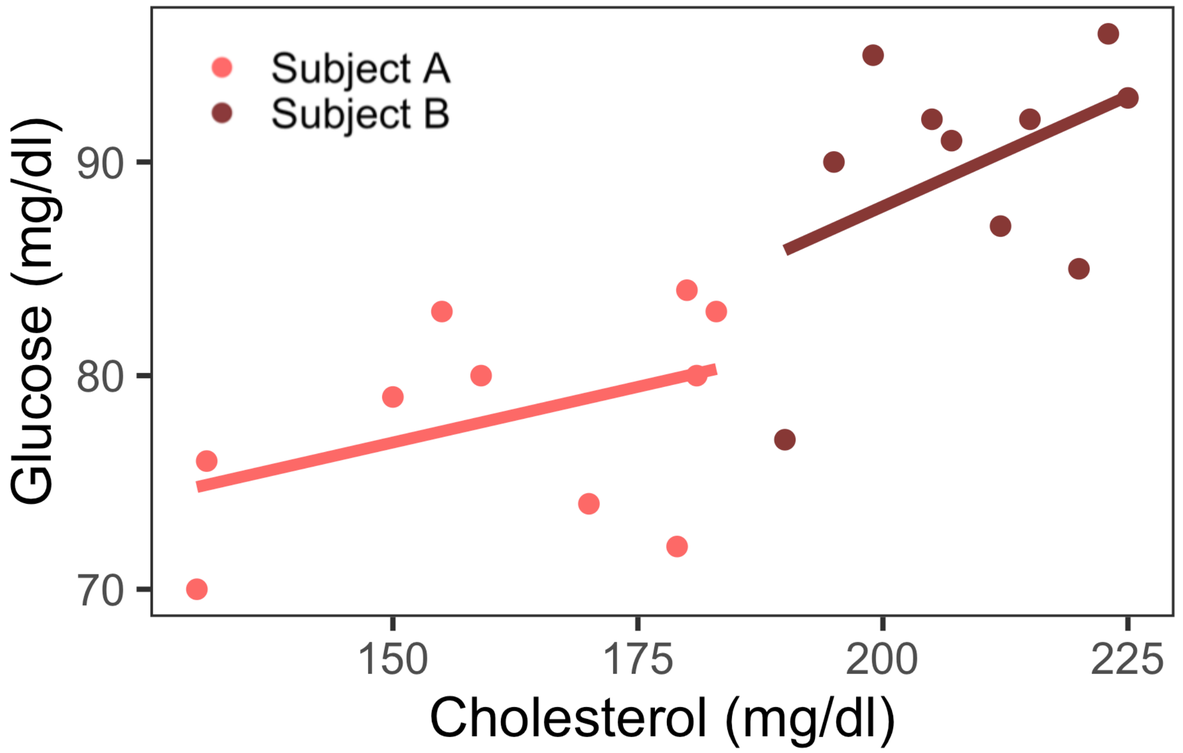

```
> lm(glucose ~ cholesterol + subject)

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 56.91808   11.40891   4.989 0.000112 ***
cholesterol  0.13091    0.06985   1.874 0.078206 .
subjectB     5.50776    3.96963   1.387 0.183218
---
```

When subject increases by one unit (i.e. from A to B), glucose increases by 5.5 units.

(β_1 **for subject)**

Multiple linear regression model

Is there a relationship between cholesterol and glucose?




```
> lm(glucose ~ cholesterol + subject)
```

```
Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 56.91808   11.40891   4.989 0.000112 ***
cholesterol  0.13091    0.06985   1.874 0.078206 .
subjectB     5.50776    3.96963   1.387 0.183218
---
```

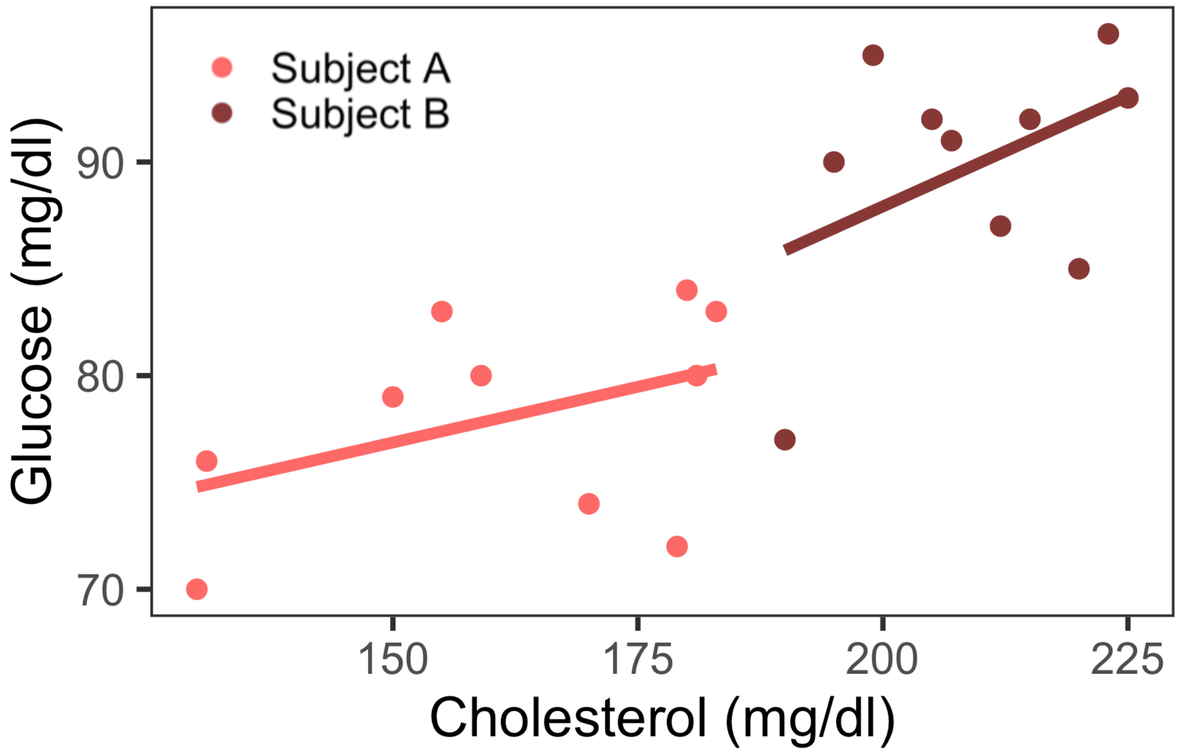
When subject increases by one unit (i.e. from A to B), glucose increases by 5.5 units.

(β_1 **for subject)**

$$G = 56.92 + 0.131(C) + 5.5(S)$$

Regression and the ***t*-test**

Is there a relationship between cholesterol and glucose (when controlling for subject)?



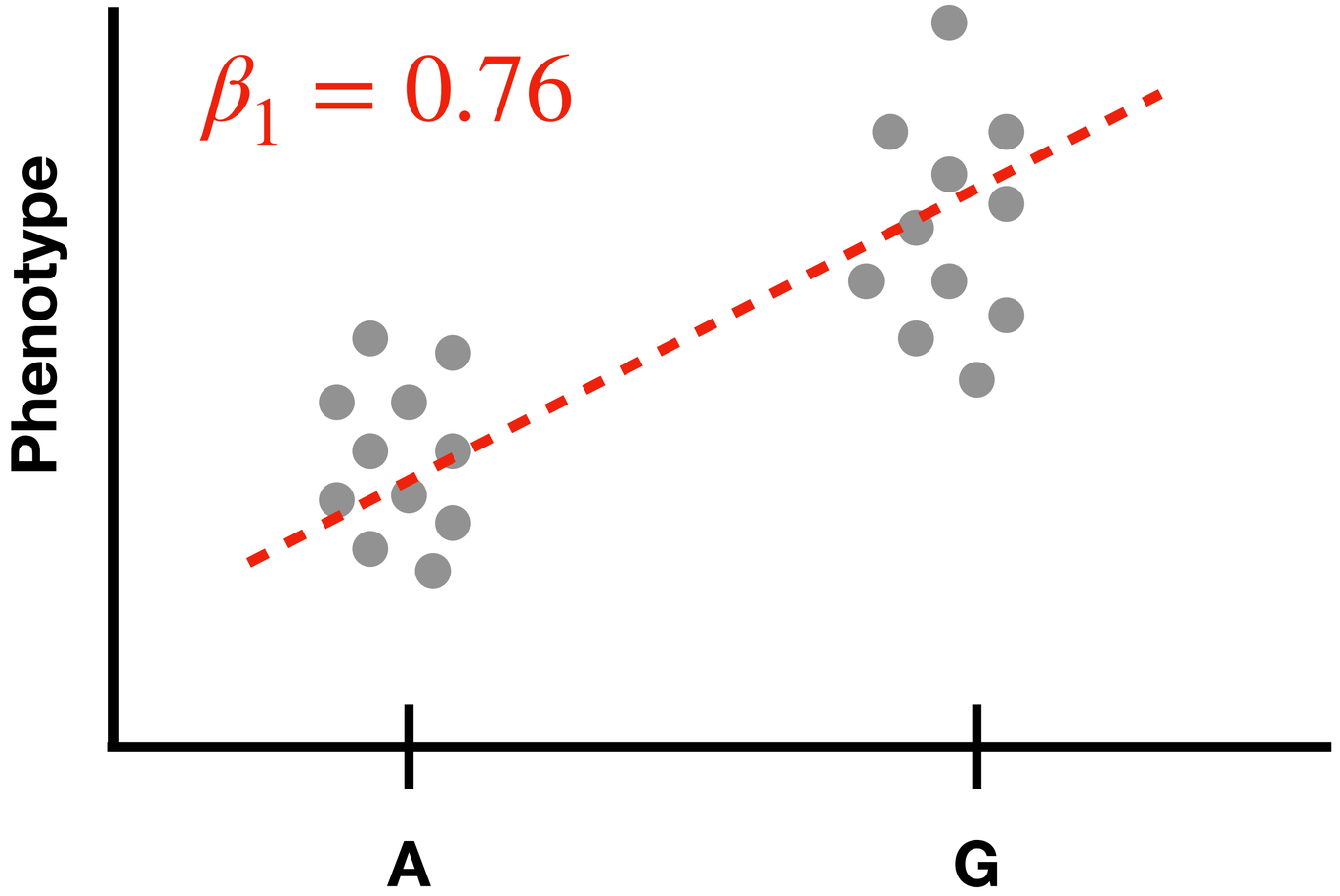

```
> lm(glucose ~ cholesterol)

   t = 1.396,
   b1 = 0.2,
   p-value = 0.20

> lm(glucose ~ cholesterol)

   t = 1.350,
   b1 = 0.1,
   p-value = 0.21411
```

Regression and the ***t*-test**

- When you have two groups (or a categorical variable), regression and t-test can mostly be used interchangeably
- When you have a quantitative (i.e. continuous) variable, regression is usually more appropriate
    - However, if you have biological reason to, you can split your quantitative variable into two groups and perform a t-test
- You can also perform a multiple regression by using two or more variables to predict responses (but be careful to make sure and only add variables of interest - models will be diluted down with each added variable)

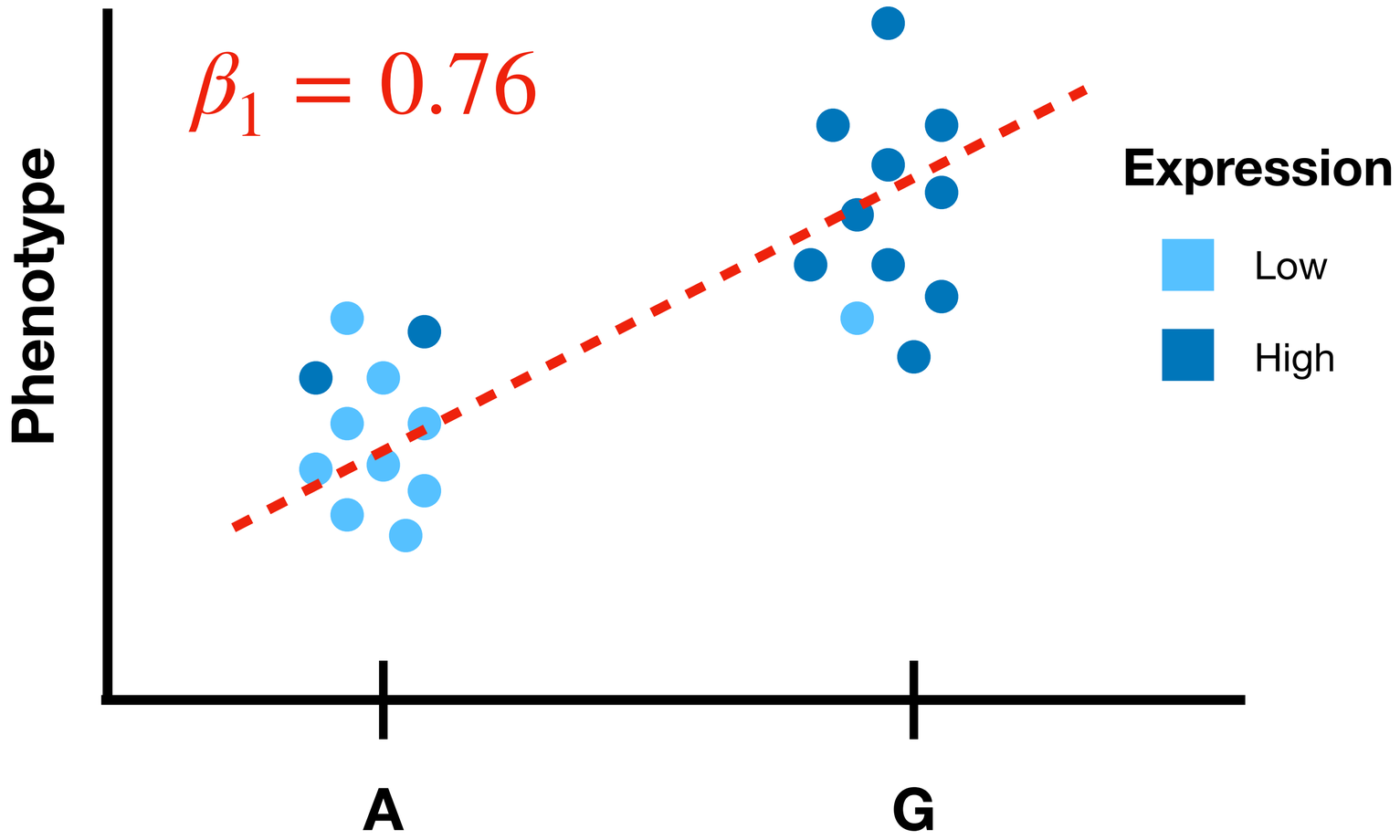
Using residual values to identify covariates

```
lm(phenotype ~ genotype)
```

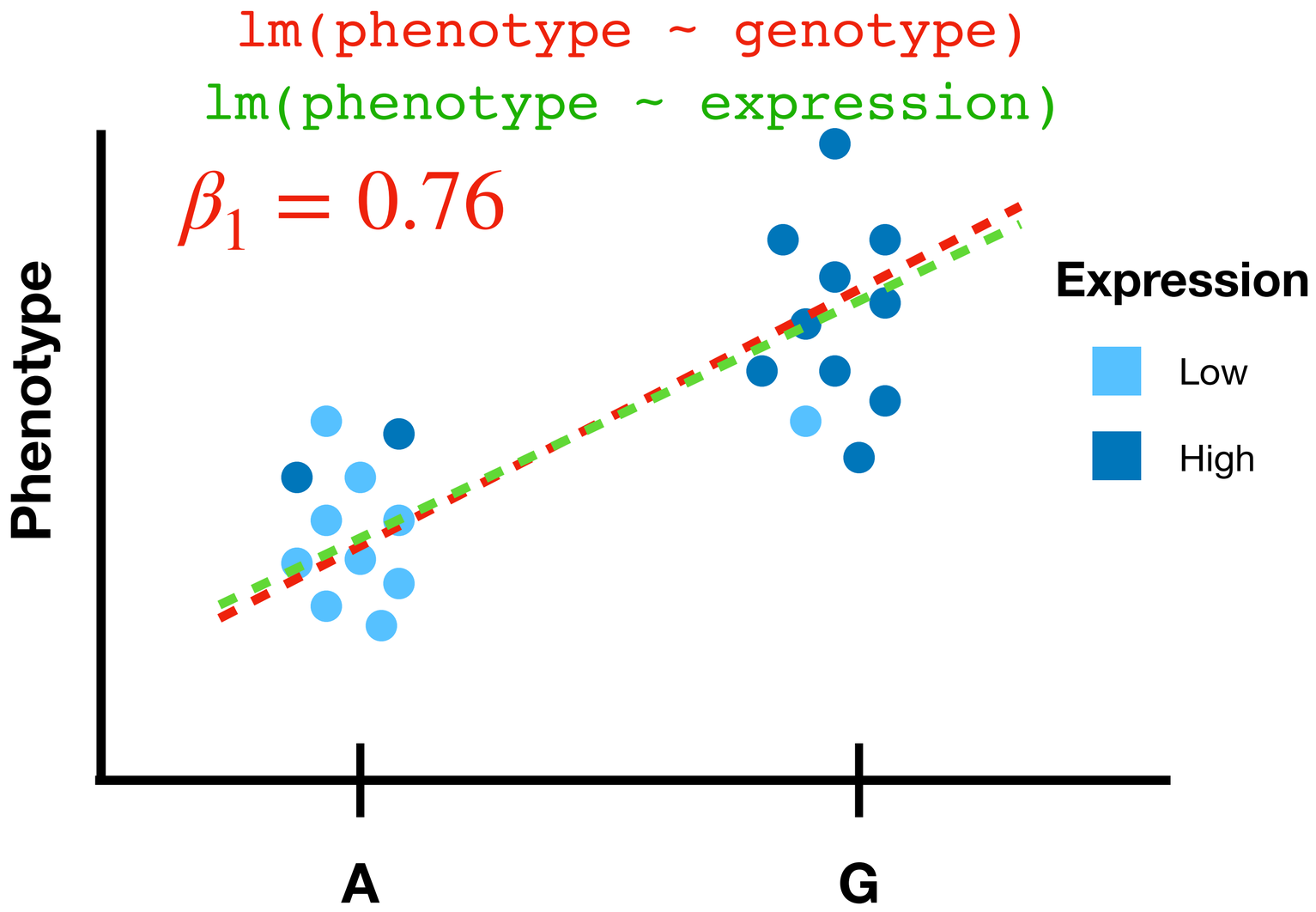


Using residual values to identify covariates

```
lm(phenotype ~ genotype)
```

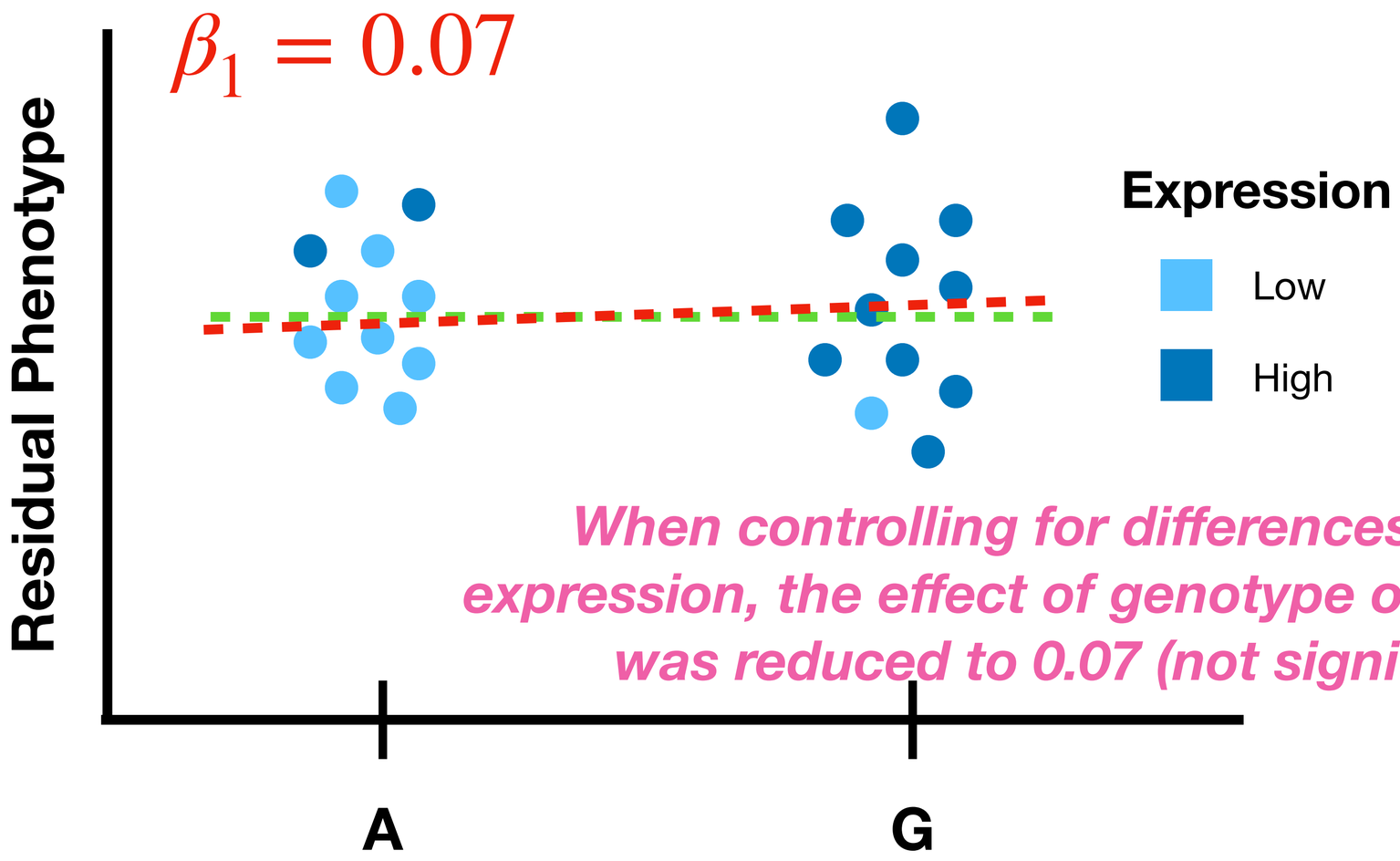


Using residual values to identify covariates



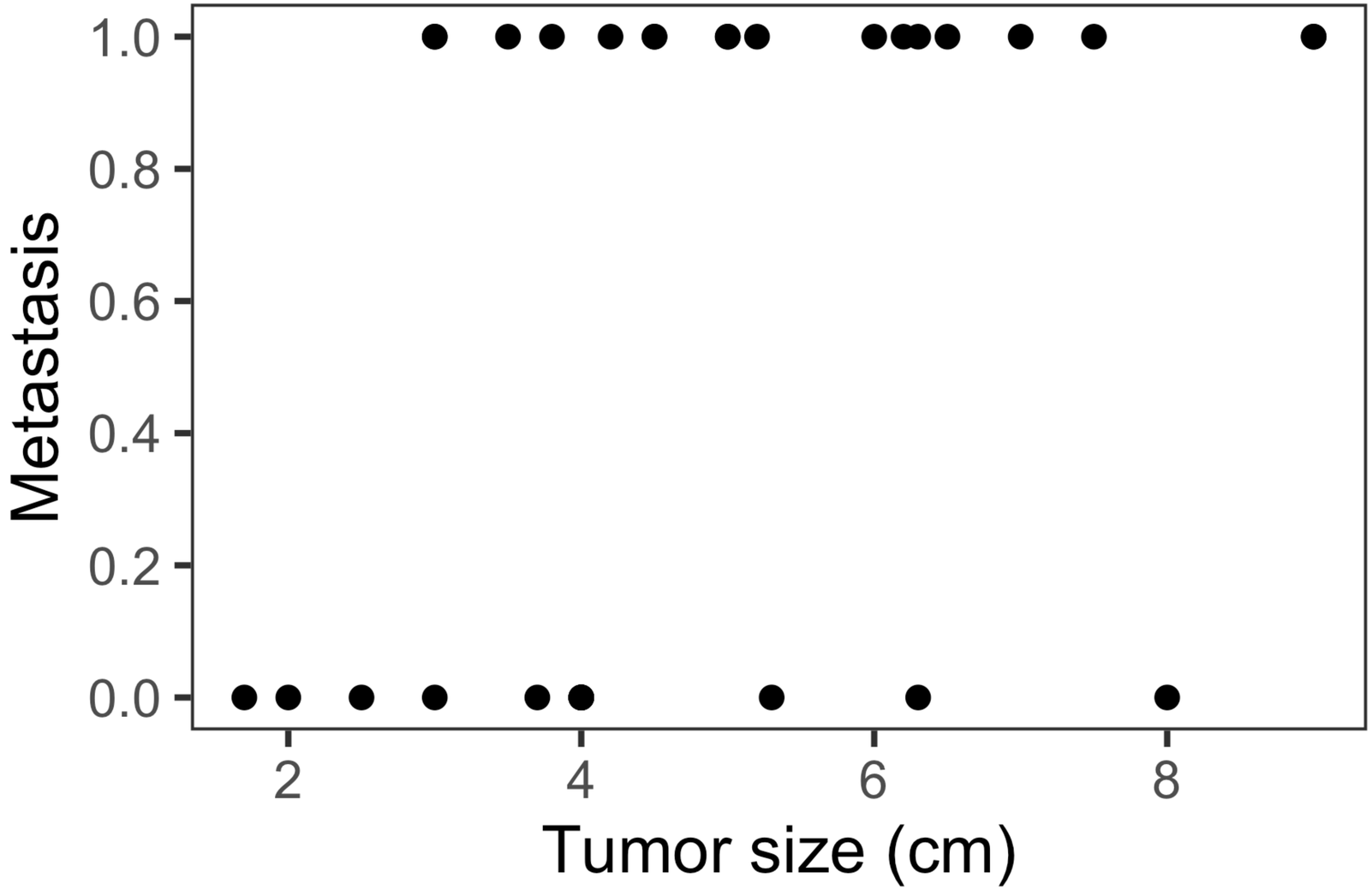
Using residual values to identify covariates

```
lm(phenotype ~ genotype + expression)
```



When controlling for differences in gene expression, the effect of genotype on phenotype was reduced to 0.07 (not significant).

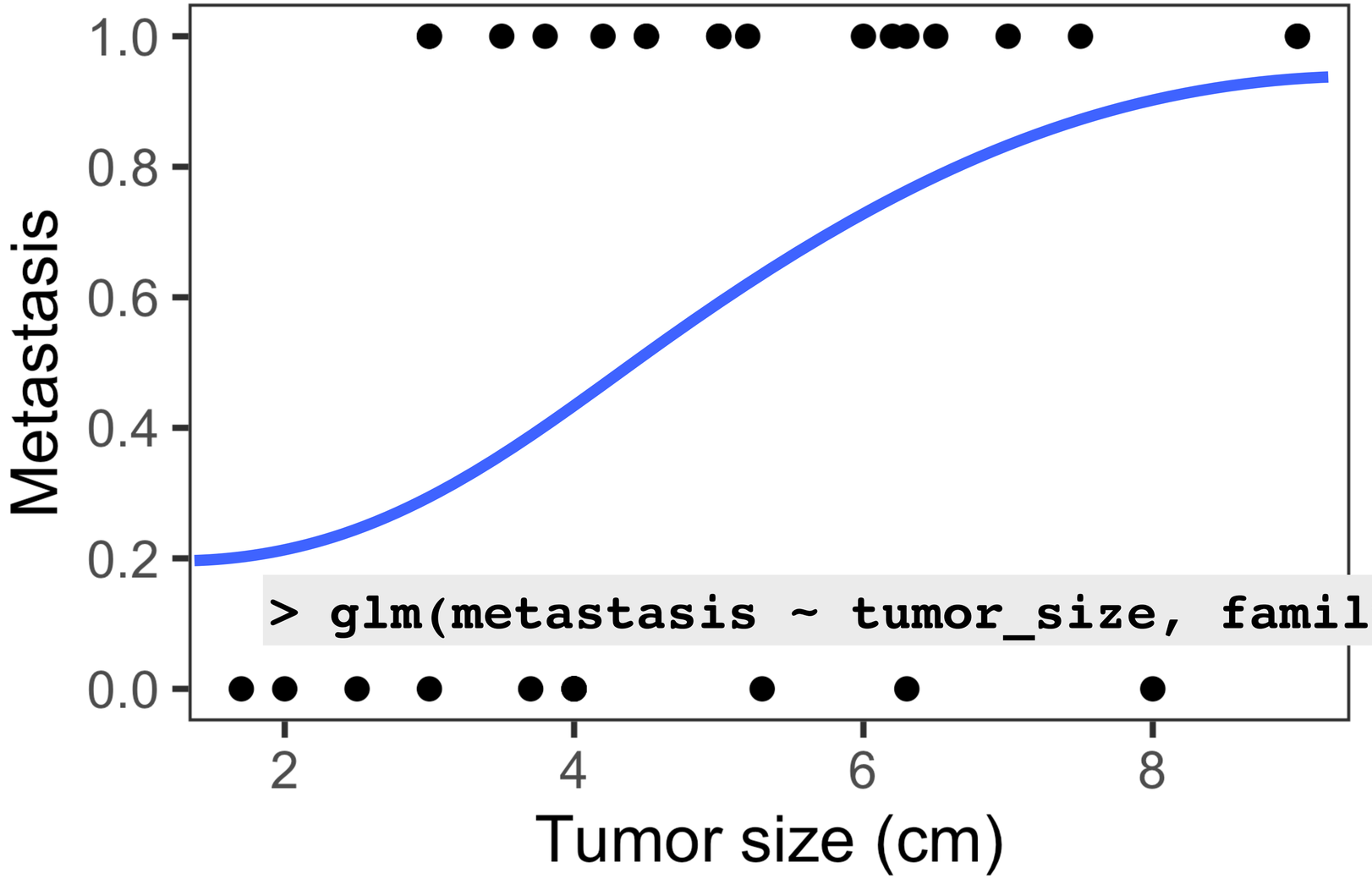
Introduction to logistic regression



Introduction to logistic regression

- Model relationship between X and Y by fitting a response curve that is always between 0 and 1
- Probability that Y = 1 (metastasis) for a given value of X (tumor size)
- **Linear function does not remain between 0 and 1**
- Logistic regression will have an “S” shape
- No error term: modeling the probability of an event directly
- **`glm(Y ~ X, family = “binomial”)`**

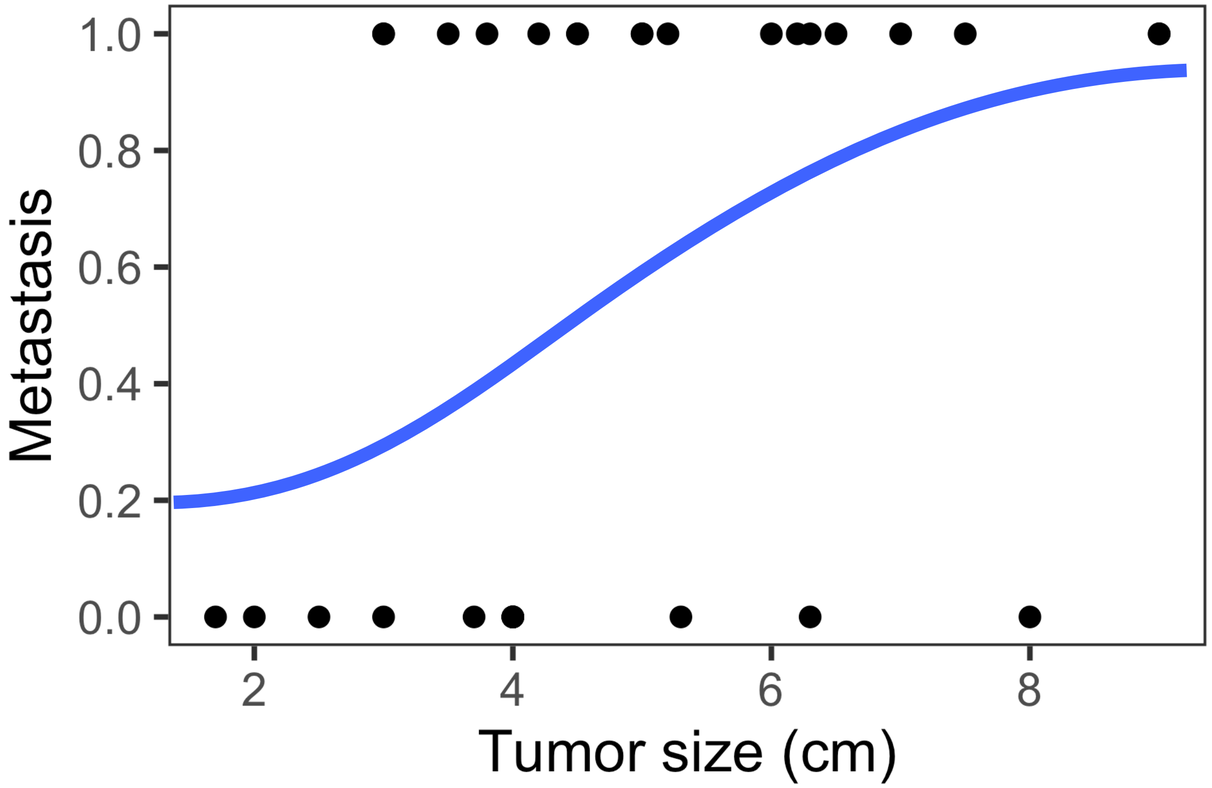
Introduction to logistic regression




```
> glm(metastasis ~ tumor_size, family = "binomial")
```

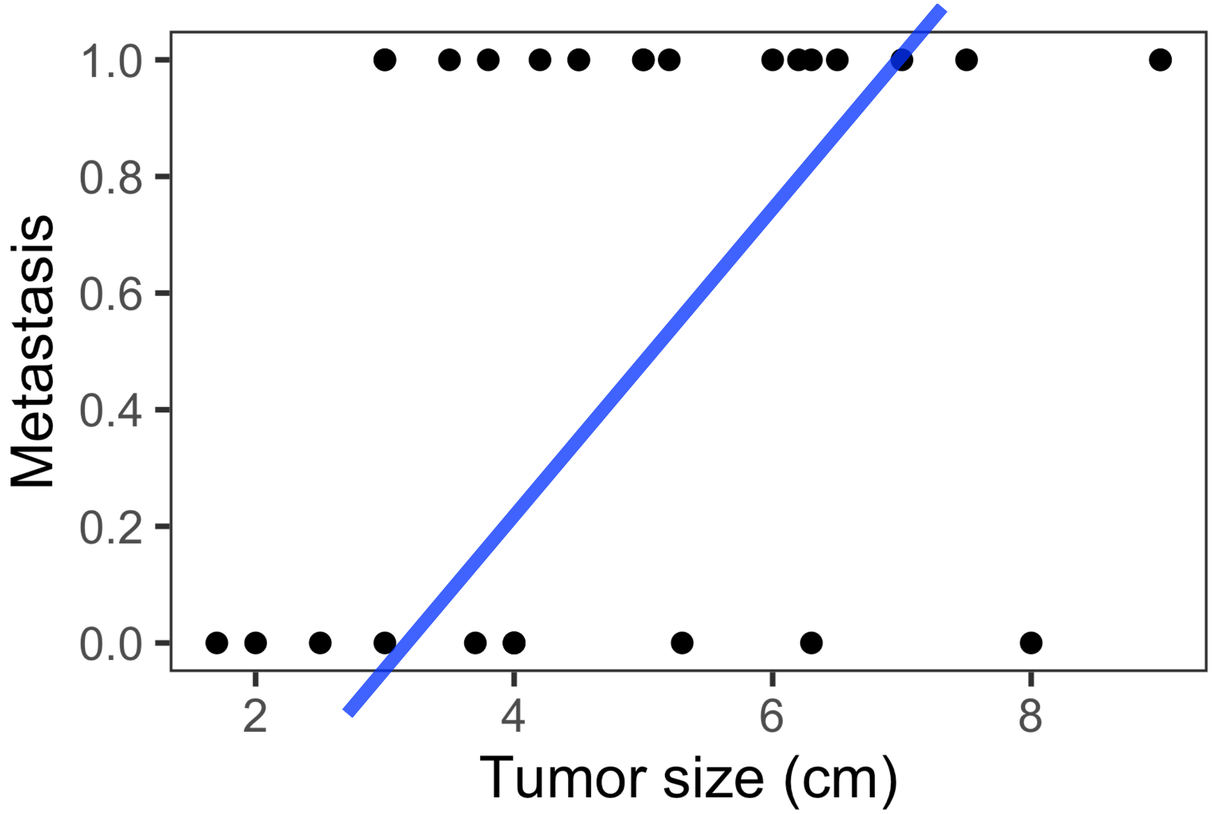
Introduction to logistic regression

Logistic regression



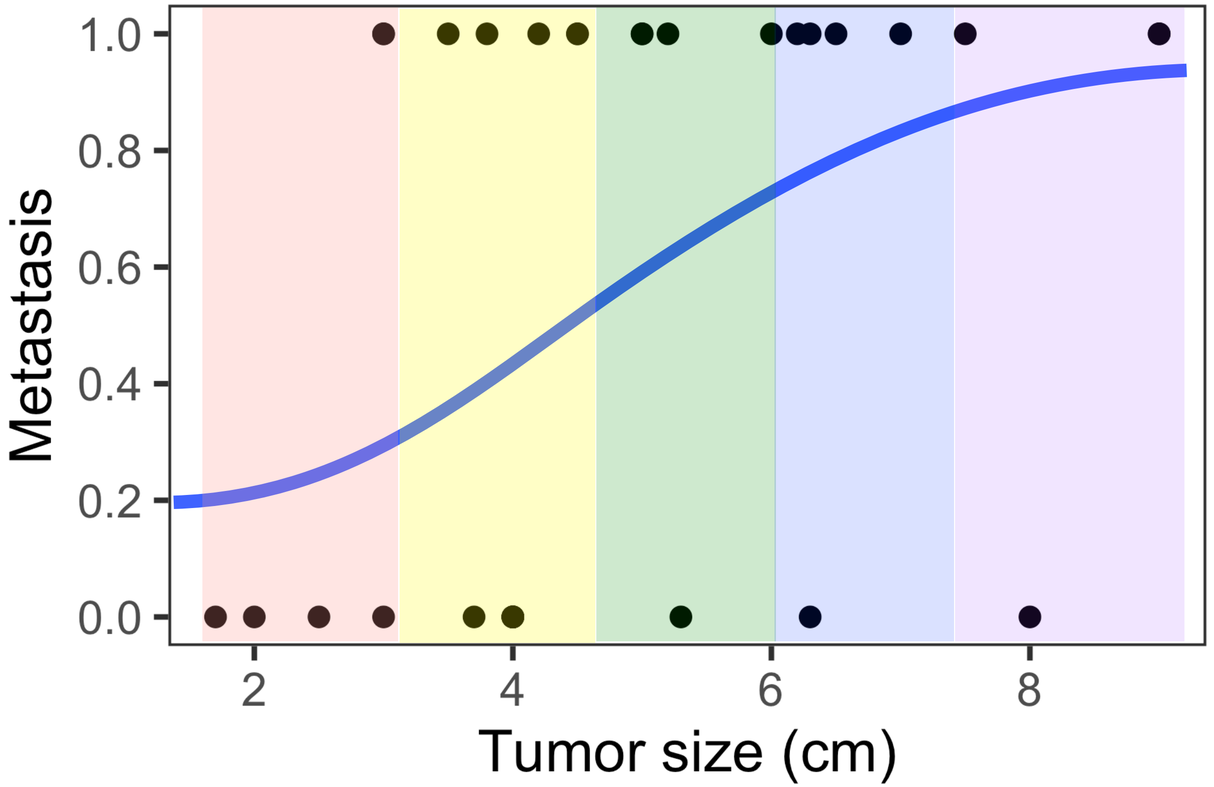
Predicted Y within 0-1 range

Linear regression



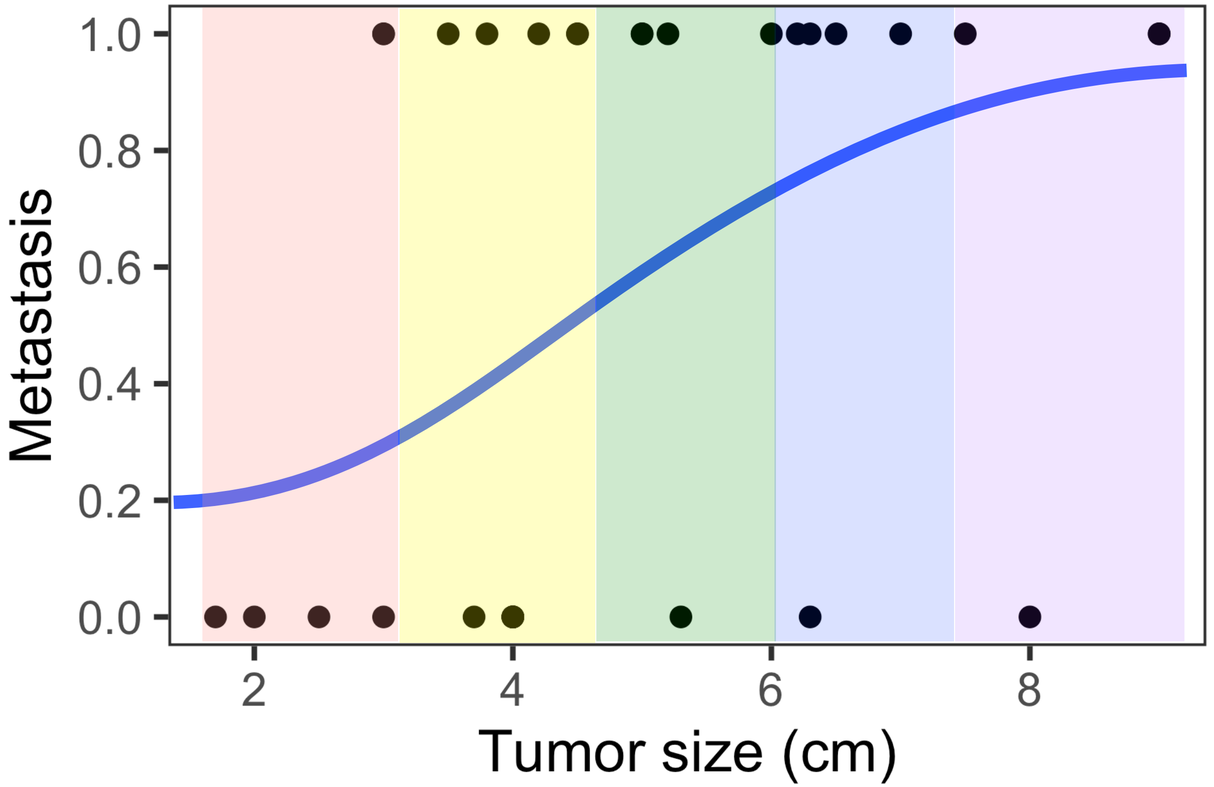
Predicted Y can exceed 0-1 range

Introduction to logistic regression



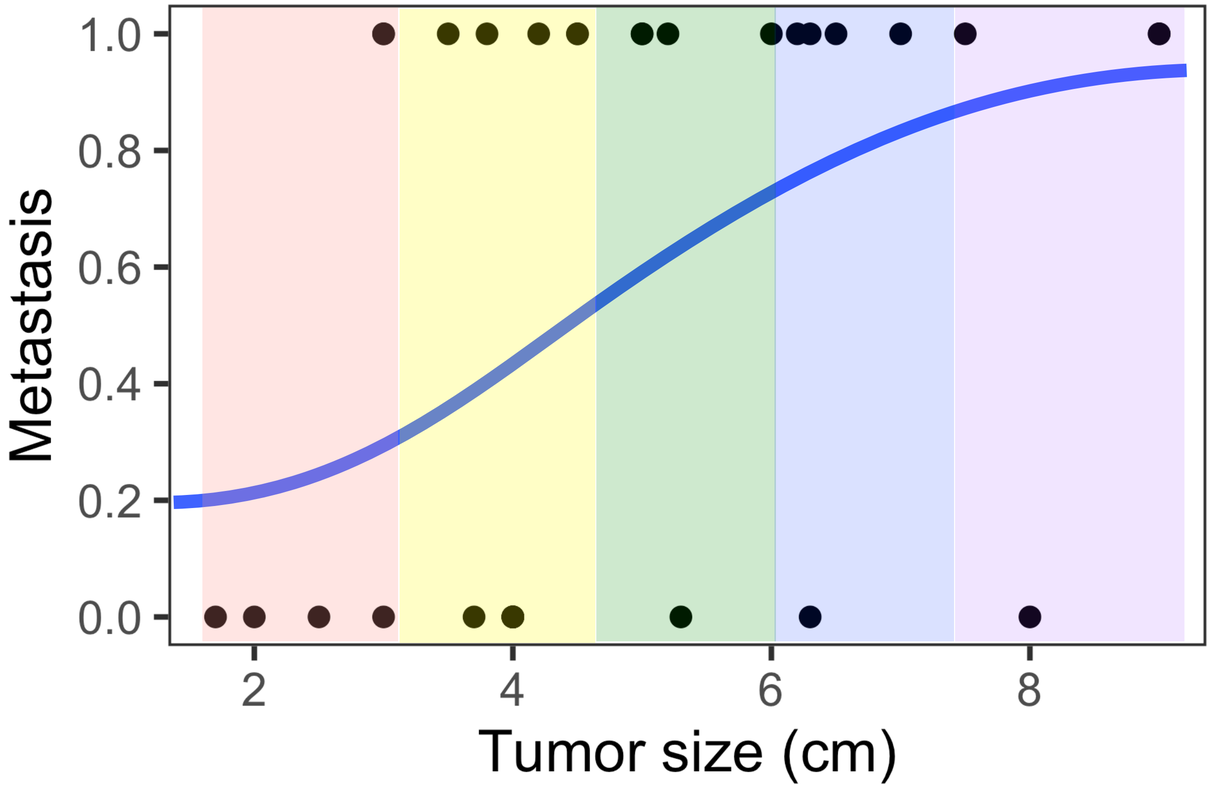
Size range	Points with Y = 1	Points with Y = 0	Fraction Y = 1	Proportion Y = 1
(1.5, 3.0]				
(3.0, 4.5]				
(4.5, 6.0]				
(6.0, 7.5]				
(7.5, 9.0]				

Introduction to logistic regression



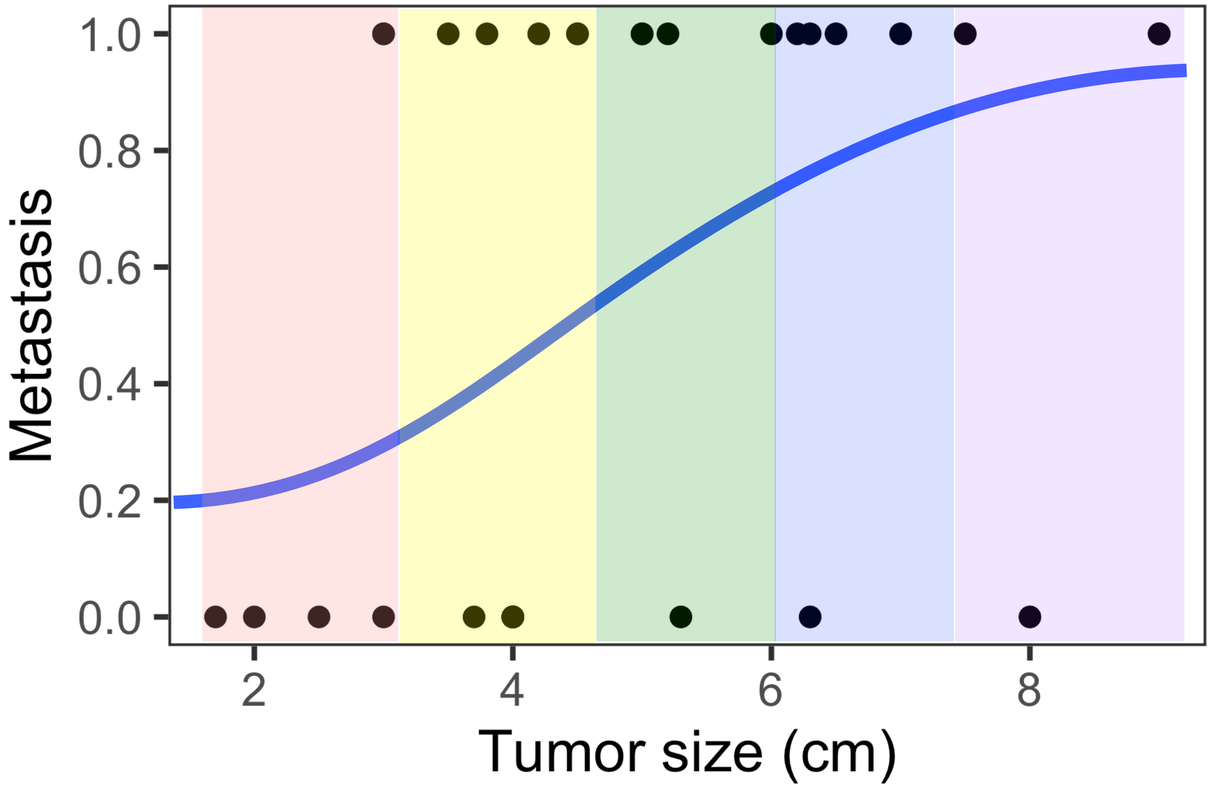
Size range	Points with Y = 1	Points with Y = 0	Fraction Y = 1	Proportion Y = 1
(1.5, 3.0]	2	4		
(3.0, 4.5]	5	6		
(4.5, 6.0]	4	1		
(6.0, 7.5]	5	1		
(7.5, 9.0]	2	1		

Introduction to logistic regression



Size range	Points with Y = 1	Points with Y = 0	Fraction Y = 1	Proportion Y = 1
(1.5, 3.0]	2	4	2/6	
(3.0, 4.5]	5	6	5/11	
(4.5, 6.0]	4	1	4/5	
(6.0, 7.5]	5	1	5/6	
(7.5, 9.0]	2	1	2/3	

Introduction to logistic regression



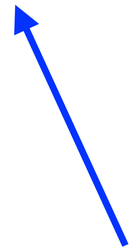
Size range	Points with Y = 1	Points with Y = 0	Fraction Y = 1	Proportion Y = 1
(1.5, 3.0]	2	4	2/6	0.33
(3.0, 4.5]	5	6	5/11	0.45
(4.5, 6.0]	4	1	4/5	0.80
(6.0, 7.5]	5	1	5/6	0.83
(7.5, 9.0]	2	1	2/3	0.67

https://www.datacamp.com/community/tutorials/logistic-regression-R

Introduction to logistic regression

```
> summary(glm(metastasis ~ tumor_size, family = “binomial”))
```

```
Call:
glm(formula = Metastasis ~ Size, family = "binomial", data = metastasis)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.0657  -1.1288   0.5657   0.9844   1.4185

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -2.0858     1.2256  -1.702   0.0888 .
Size          0.5117     0.2561   1.998   0.0457 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 42.165  on 30  degrees of freedom
Residual deviance: 37.002  on 29  degrees of freedom
AIC: 41.002

Number of Fisher Scoring iterations: 4
```



Default is linear

Real life examples of logistic models

Spam email detection

Extracts info like sender, typos, key phrases and produces probability

Credit card fraud

Extracts info like when/where purchase, how much, produces probability of fraud

Tumor prediction

Like the example we had!

Marketing

Will this user like this particular advertisement?

Final project notes

- t-tests need numerical continuous (i.e. quantitative) data. Count data will not work! If you have count data, chi-square test is more appropriate
- Make sure to review paired vs. unpaired tests. Paired tests are **only** appropriate under certain circumstances (think: measuring a phenotype before/after drug treatment)
- Some of you planned to use testing for normality as one of your statistical analyses. This is okay as long as you do it fully. **But if you have another test you could do with your data, I would prefer that, as testing for normality is really just checking an assumption** for using a t-test and not really a unique "test"
- If you are unsure or have questions, **reach out to me or the TAs earlier** rather than later.
    - Along those lines, I would recommend trying to get your data into R soon too in case there are unforeseen issues (as there always are with data science)

Announcements

Mon	Tue	Wed	Thu	Fri	Sat	Sun
22	23 **HW #8** Homework Due! **Lecture 15: AN...** Lecture	24	25 **No class: Than...** NO CLASS	26	27	28
29	30 **Practicum 3: M...** Practicum	Dec 1	2 **Q&A: "Overflo...** Review	3 **HW #9/Practic...** Homework Due!	4	5
6	7 **Final Exam** Exam	8	9	10 **Final project** Project Due!	11	12

R example