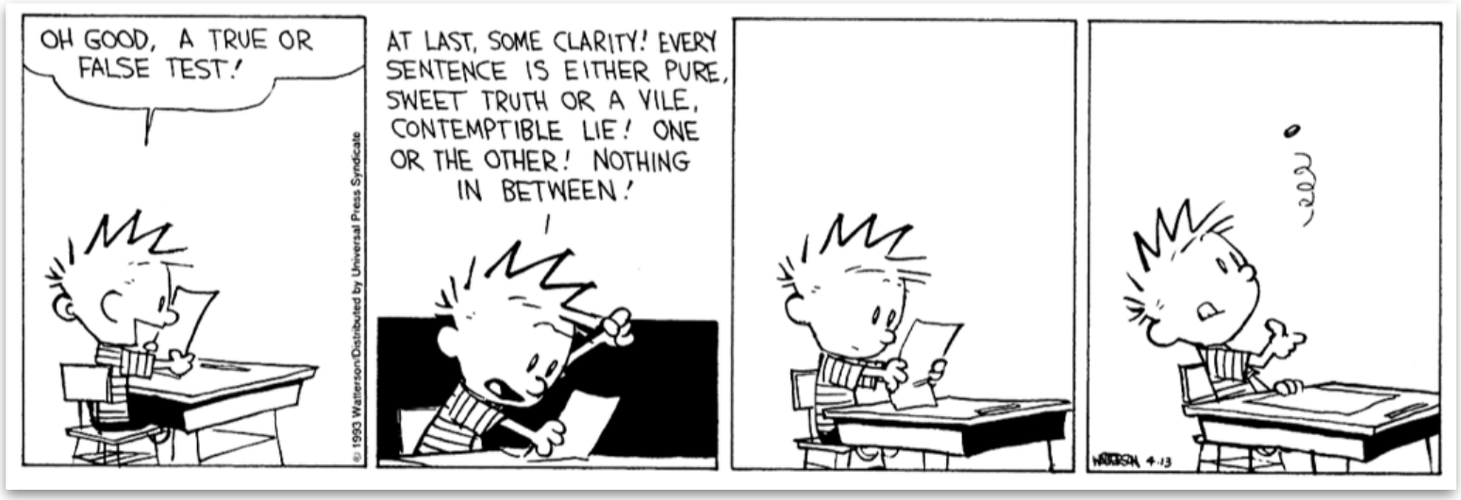
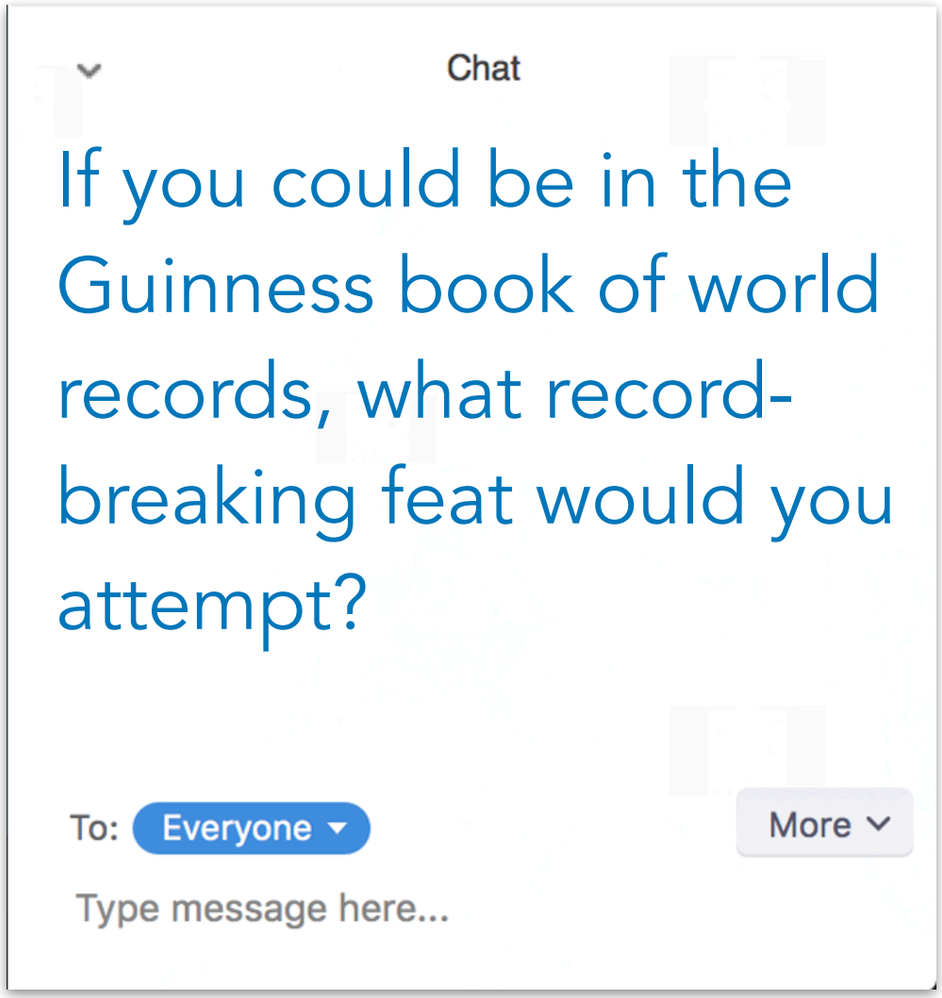
PSYCH 252: Statistical Methods for Behavioral and Social Sciences

Model comparison





We're listening to "INDUSTRY BABY" by "Lil Nas X, Jack Harlow" submitted by Sarah Wu

02/07/2022

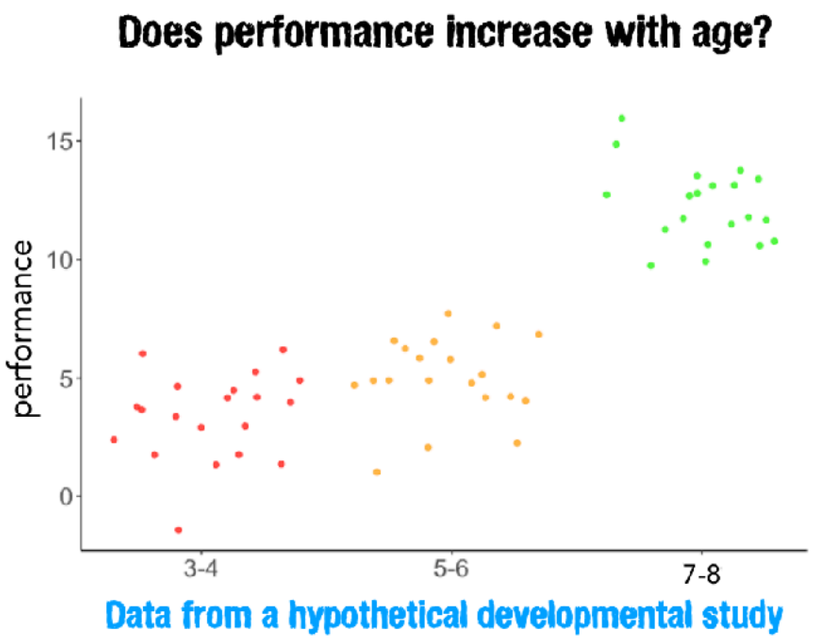
Plan for today

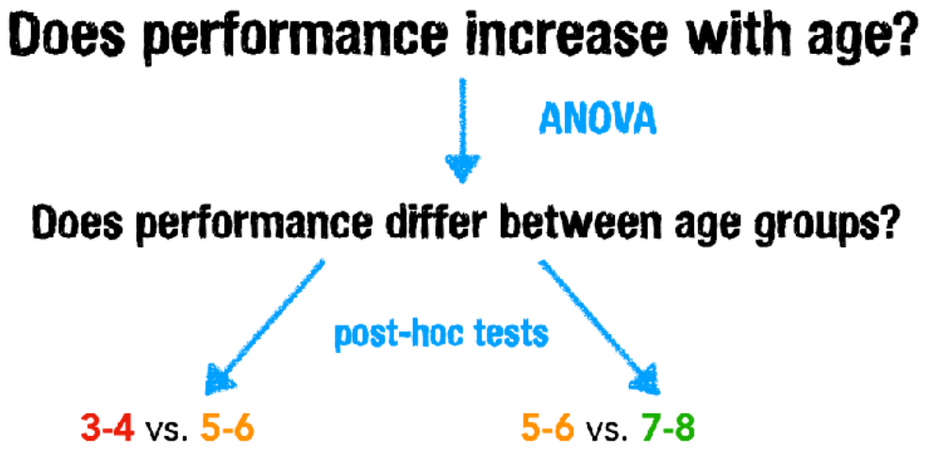
- Quick recap
- Simulating a power analysis
  - Demonstration in RStudio
- Model comparison
  - Cross-validation
  - AIC and BIC
- Linear mixed effects models

Quick recap

Quick recap: Linear contrasts

Contrasts





Is there are more direct way of asking this question with a statistical model?

Linear contrasts in R

```
1  library("emmeans") # for calculating contrasts
2
3  #  fit the linear model
4  fit = lm(formula = performance ~ group,
5           data = df.development)
6
7  # check factor levels
8  levels(df.development$group) [1] "3-4" "5-6" "7-8"
9
10 # define the contrasts of interest
11 contrasts = list(young_vs_old = c(-0.5, -0.5, 1),
12                  three_vs_five = c(-0.5, 0.5, 0))
13
14 # compute significance test on contrasts
15 fit %>%
16   emmeans("group",
17           contr = contrasts,
18           adjust = "bonferroni") %>%
19   pluck("contrasts")
```

compute the results

```
[1] "3-4" "5-6" "7-8"
 contrast       estimate        SE df t.ratio p.value
 young_vs_old  16.293541 0.4742322 57  33.936  <.0001
 three_vs_five  1.606009 0.5475962 57   2.933  0.0097

P value adjustment: bonferroni method for 2 tests
```


Post hoc tests

```
1 fit = lm(formula = performance ~ group,
2          data = df.development)
3
4 # pairwise differences between all the groups
5 fit %>%
6   emmeans(pairwise ~ group) %>%
7   pluck("contrasts")
```

all pairwise tests between groups

```
contrast    estimate        SE df t.ratio p.value
 3-4 - 5-6  -1.606009 0.5475962 57  -2.933  0.0145
 3-4 - 7-8 -16.896546 0.5475962 57 -30.856  <.0001
 5-6 - 7-8 -15.290537 0.5475962 57 -27.923  <.0001

P value adjustment: bonferroni method for 3 tests
```

Quick recap: Unbalanced designs

Beware of unbalanced designs

```
1 lm(formula = balance ~ skill + hand, data = df.poker.unbalanced) %>%
2   anova()
```

```
Analysis of Variance Table

Response: balance
           Df Sum Sq Mean Sq F value  Pr(>F)
skill       1   74.3   74.28  4.2904 0.03922 *
hand        2 2385.1 1192.57 68.8827 < 2e-16 ***
Residuals 286 4951.5   17.31
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

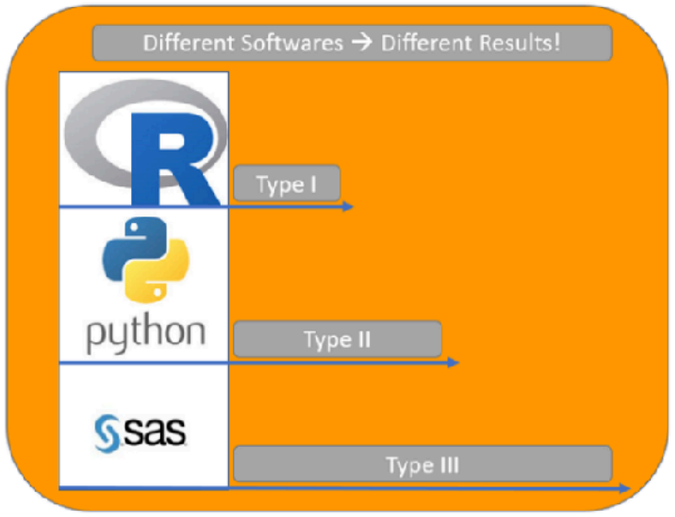
flipped the order

```
1 lm(formula = balance ~ hand + skill, data = df.poker.unbalanced) %>%
2   anova()
```

```
Analysis of Variance Table

Response: balance
           Df Sum Sq Mean Sq F value  Pr(>F)
hand        2 2419.8 1209.92 69.8845 <2e-16 ***
skill       1   39.6   39.59  2.2867 0.1316
Residuals 286 4951.5   17.31
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Default sums of squares ...



Default Types of Sums of Squares for different programming languages

not great for reproducibility ...

Route I: Using "afex"

```
1 library("afex")
2
3 fit = aov_ez(id = "participant",
4               dv = "balance",
5               data = df.poker.unbalanced,
6               between = c("hand", "skill"))
7 fit$Anova
```

```
Contrasts set to contr.sum for the following variables: hand, skill
Anova Table (Type III tests)

Response: dv
             Sum Sq  Df   F value     Pr(>F)
(Intercept) 27781.3   1 1676.9096 < 2.2e-16 ***
hand         2285.3   2   68.9729 < 2.2e-16 ***
skill          48.9   1    2.9540 0.0867525 .
hand:skill    246.5   2    7.4401 0.0007089 ***
Residuals    4705.0 284
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Route II: Using "emmeans"

preferred route!!

```
1 library("emmeans")
2
3 lm(formula = balance ~ hand + skill,
4    data = df.poker.unbalanced) %>%
5   joint_tests()
```

very handy function

```
model term df1 df2 F.ratio p.value
 hand        2 284  68.973  <.0001
 skill       1 284   2.954  0.0868
 hand:skill  2 284   7.440  0.0007
```

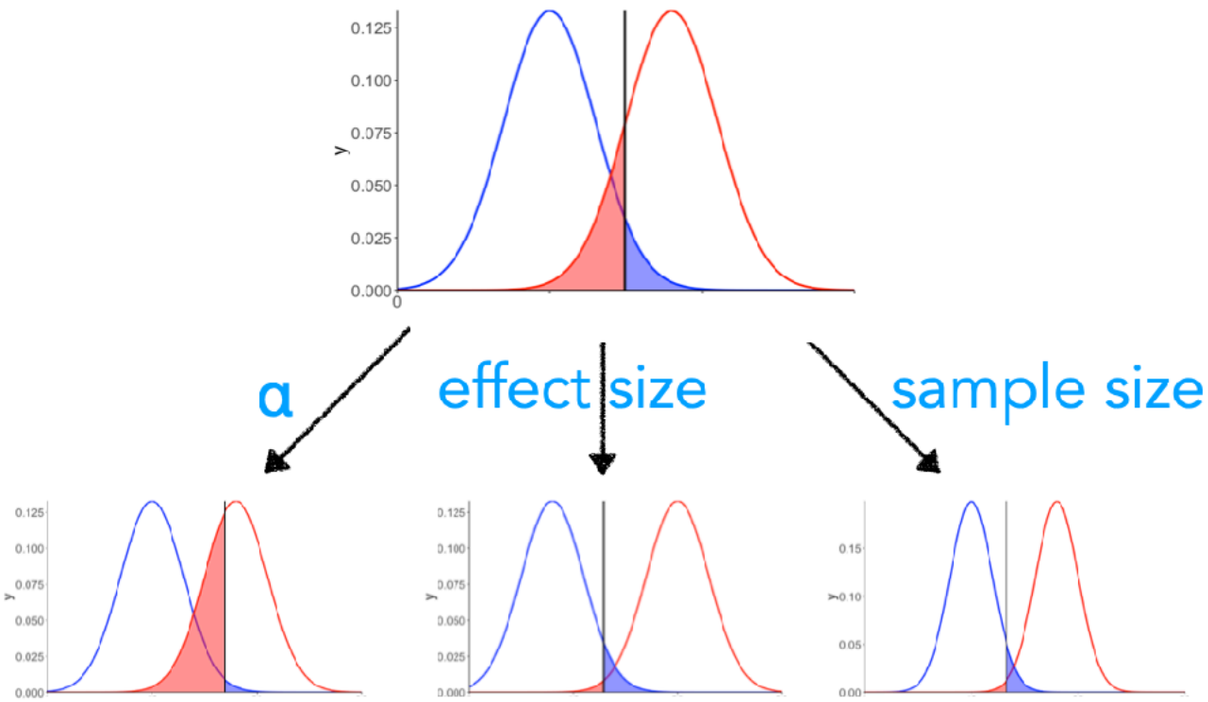
Quick recap: Power analysis

H_0: Not pregnant. H_1: Pregnant.

Type I Error: Falsely rejecting the null hypothesis (even though it is true).

Type II Error: Failing to reject the null hypothesis (even though it is false).

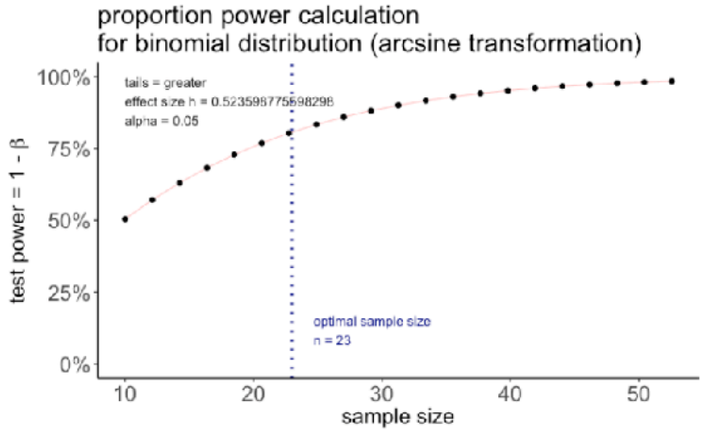
The knobs we can turn to affect power



"pwr" package in R

Option 2

```
1  library("pwr")
2  pwr.p.test(h = ES.h(p1 = 0.75, p2 = 0.50),
3             sig.level = 0.05,
4             power = 0.80,
5             alternative = "greater") %>%
6   plot()
```



Option 3

Power simulation recipe

- assume:
  - α, *n*, effect size
- simulate a large number of data sets of size *n* with the specified effect size
- for each data set, run a statistical test to calculate the p-value
- determine the probability of rejecting the H_0 (given that H_1 is true)

Simulating a power analysis

Power simulation recipe

- assume:
  - α, *n*, effect size
- simulate a large number of data sets of size *n* with the specified effect size
- for each data set, run a statistical test to calculate the p-value
- determine the probability of rejecting the H_0 (given that H_1 is true)

Let's simulate ...

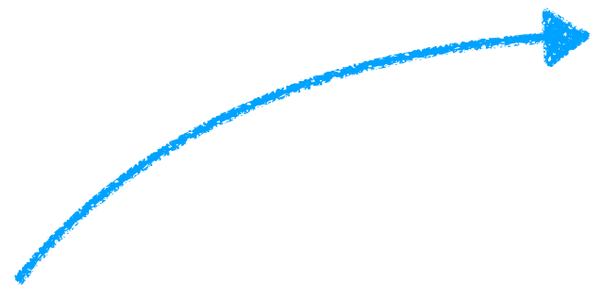
```r
# make reproducible
set.seed(1)

# number of simulations
n_simulations = 5

# run simulation
expand_grid(n = seq(10, 40, 2),
            simulation = 1:n_simulations,
            p = 0.75) %>%
  mutate(index = 1:n(),
         .before = n) %>%
  group_by(index, n, p, simulation) %>%
  mutate(response = rbinom(n = 1,
                           size = n,
                           prob = p),
         p.value = binom.test(x = response,
                              n = n,
                              p = 0.5,
                              alternative = "two.sided")$p.value) %>%
  group_by(n, p) %>%
  summarize(power = sum(p.value < 0.05) / n())
```

Let's simulate ...

```
 1 # make reproducible
 2 set.seed(1)
 3
 4 # number of simulations
 5 n_simulations = 5
 6
 7 # run simulation
 8 expand_grid(n = seq(10, 40, 2),
 9               simulation = 1:n_simulations,
10               p = 0.75) %>%
11   mutate(index = 1:n(),
12          .before = n) %>%
```



index	n	simulation	p
1	10	1	0.75
2	10	2	0.75
3	10	3	0.75
4	10	4	0.75
5	10	5	0.75
6	12	1	0.75
7	12	2	0.75
8	12	3	0.75
9	12	4	0.75
10	12	5	0.75

Let's simulate ...

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            p = 0.75) %>%
  mutate(index = 1:n(),
         .before = n) %>%
group_by(index, n, p, simulation) %>%
mutate(response = rbinom(n = 1,
                         size = n,
                         prob = p),
```

index	n	simulation	p	response
1	10	1	0.75	8
2	10	2	0.75	7
3	10	3	0.75	8
4	10	4	0.75	8
5	10	5	0.75	7
6	12	1	0.75	10
7	12	2	0.75	8
8	12	3	0.75	11
9	12	4	0.75	10
10	12	5	0.75	11

Let's simulate ...

index	n	simulation	p	response	p.value
1	10	1	0.75	8	0.11
2	10	2	0.75	7	0.34
3	10	3	0.75	8	0.11
4	10	4	0.75	8	0.11
5	10	5	0.75	7	0.34
6	12	1	0.75	10	0.04
7	12	2	0.75	8	0.39

```r
# make reproducible
set.seed(1)

# number of simulations
n_simulations = 5

# run simulation
expand_grid(n = seq(10, 40, 2),
            simulation = 1:n_simulations,
            p = 0.75) %>%
  mutate(index = 1:n(),
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  group_by(index, n, p, simulation) %>%
  mutate(response = rbinom(n = 1,
                           size = n,
                           prob = p),
         p.value = binom.test(x = response,
                              n = n,
                              p = 0.5,
                              alternative = "two.sided")$p.value) %>%
```

Let's simulate ...

```r
# make reproducible
set.seed(1)

# number of simulations
n_simulations = 5

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                           size = n,
                           prob = p),
         p.value = binom.test(x = response,
                              n = n,
                              p = 0.5,
                              alternative = "two.sided")$p.value) %>%
  group_by(n, p) %>%
  summarize(power = sum(p.value < 0.05) / n())
```
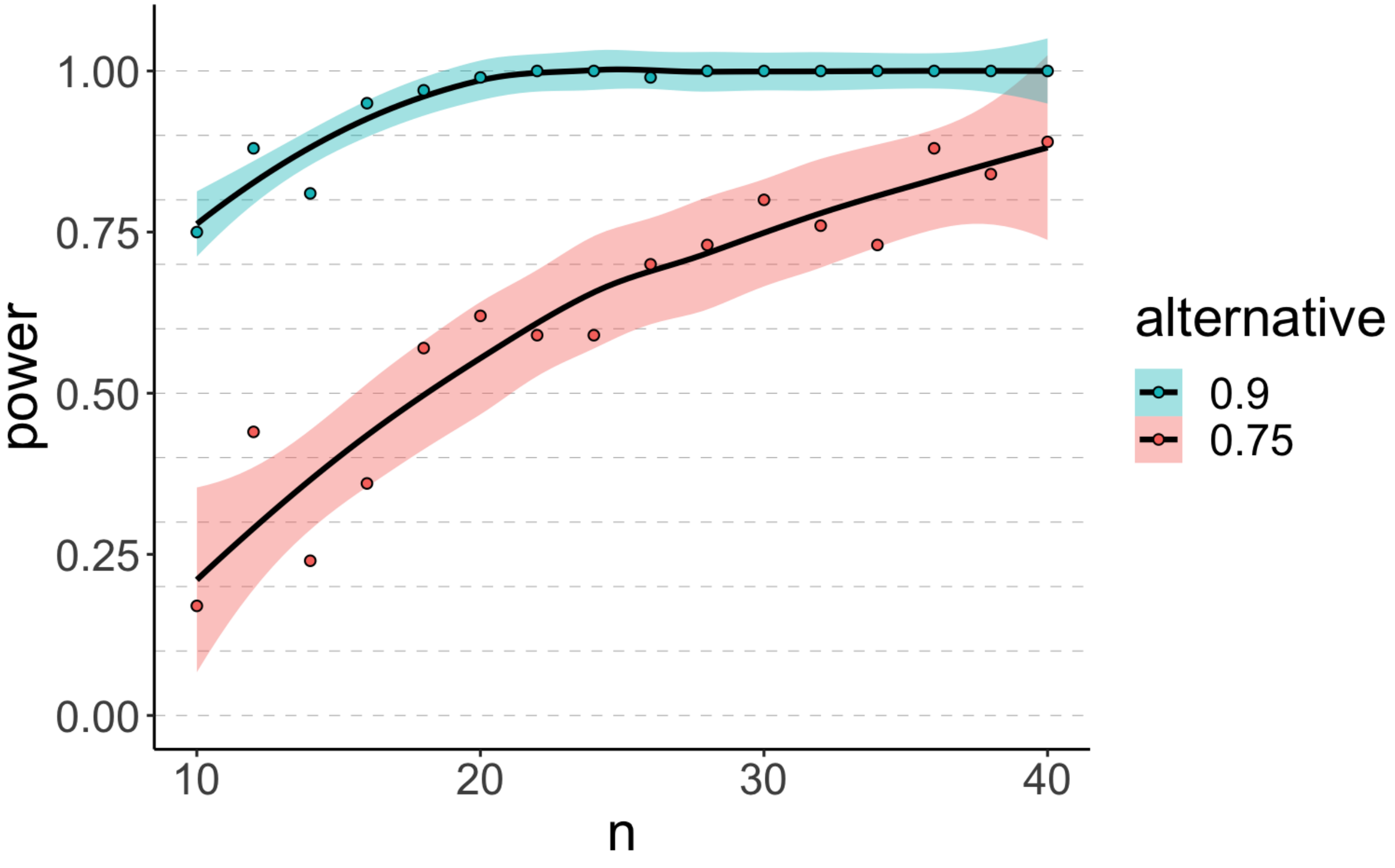

n	p	power
10	0.75	0.2
12	0.75	0.2
14	0.75	0.4
16	0.75	0.2
18	0.75	0.6
20	0.75	0.8
22	0.75	0.6
24	0.75	0.4
26	0.75	0.6
28	0.75	0.8
30	0.75	0.8

Let's simulate ...

in this example, I looked at the power for two different alternative hypotheses



Let's simulate ...

- here, I've used a simple example (Binomial test)
- but: we can use the same recipe for any statistical test that we are planning on running

Power simulation recipe

- assume:
  - α, n, effect size
- simulate a large number of data sets of size n with the specified effect size
- for each data set, run a statistical test to calculate the p-value for a given α
- determine the probability of rejecting the H_0 (given that H_1 is true)

time

Model comparison

The general procedure

1. Define H_0 as Model C (compact) and H_1 as Model A (augmented)
2. Fit model parameters to the data
3. Calculate the proportional reduction of error (PRE) in our sample
4. Decide whether the augmented model is **worth it** by comparing the observed PRE in our sample to the sampling distribution of PRE (assuming that H_0 is true)

Any problems with our approach?

sometimes it doesn't work ...

Model C

$$\text{balance}_i = \beta_0 + \epsilon_i$$

$$\text{balance}_i = \beta_0 + \beta_1 \cdot \text{student}_i + \epsilon_i$$

$$\text{balance}_i = \beta_0 + \beta_1 \cdot \text{student}_i + \epsilon_i$$

$$\text{balance}_i = \beta_0 + \beta_1 \cdot \text{student}_i + \epsilon_i$$

Model A

$$\text{balance}_i = \beta_0 + \beta_1 \cdot \text{student}_i + \beta_2 \cdot \text{age}_i + \epsilon_i$$ ✓

$$\text{balance}_i = \beta_0 + \beta_1 \cdot \text{student}_i + \beta_2 \cdot \text{age}_i + \epsilon_i$$ ✓

$$\text{balance}_i = \beta_0 + \beta_1 \cdot \text{age}_i + \epsilon_i$$ ✗

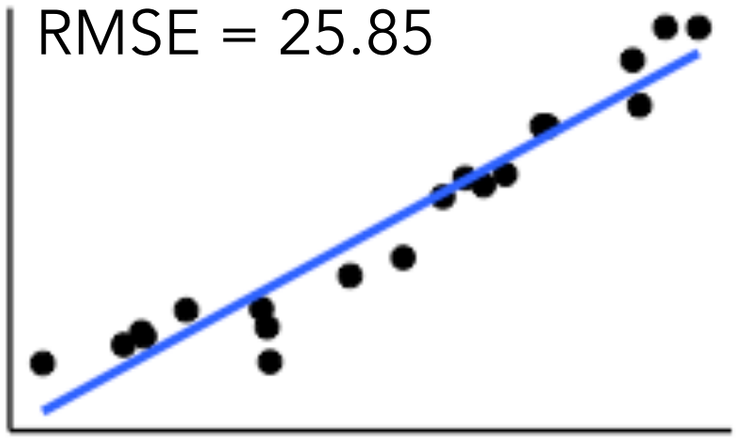
$$\text{balance}_i = \beta_0 + \beta_1 \cdot \text{age}_i + \beta_2 \cdot \text{degree}_i + \epsilon_i$$ ✗

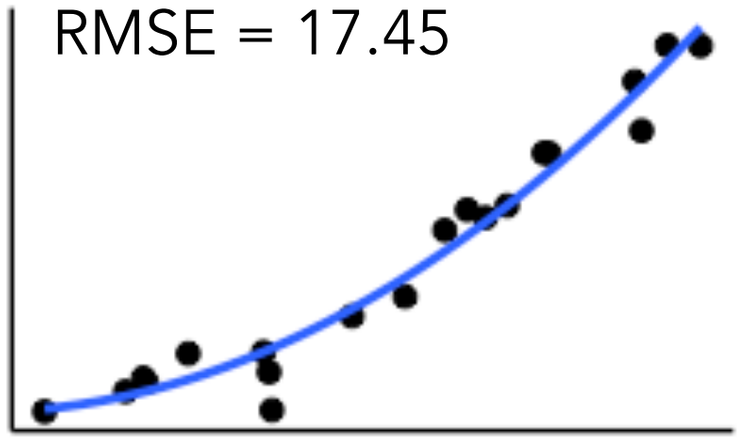
Tools for model comparison

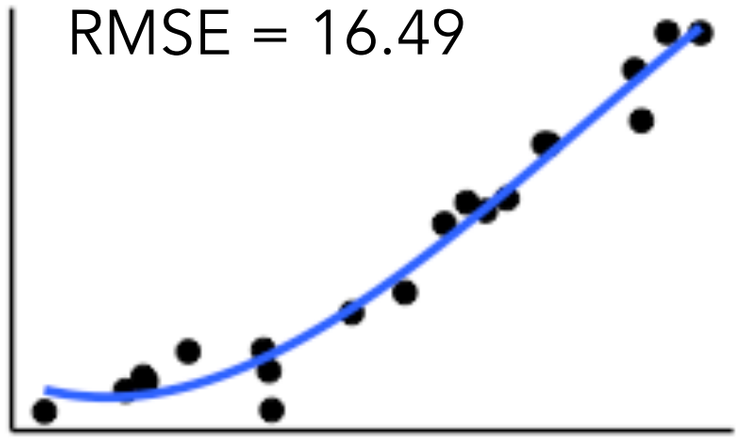
- **`anova()`:** compare a compact model with an augmented model via the F-test
  - problem: only works for nested models (where the augmented model contains all the predictors of the compact model and more)
- **What if we want to compare models that aren't nested?**
  - Cross-validation
  - AIC and BIC
  - Bayesian data analysis (we'll get there soon)

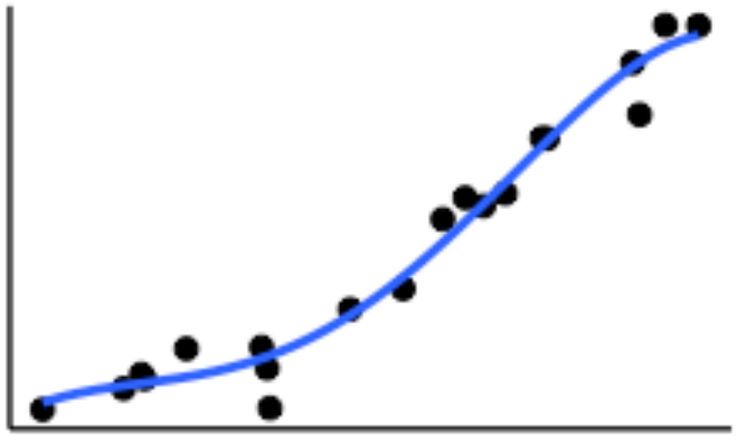
Cross-validation

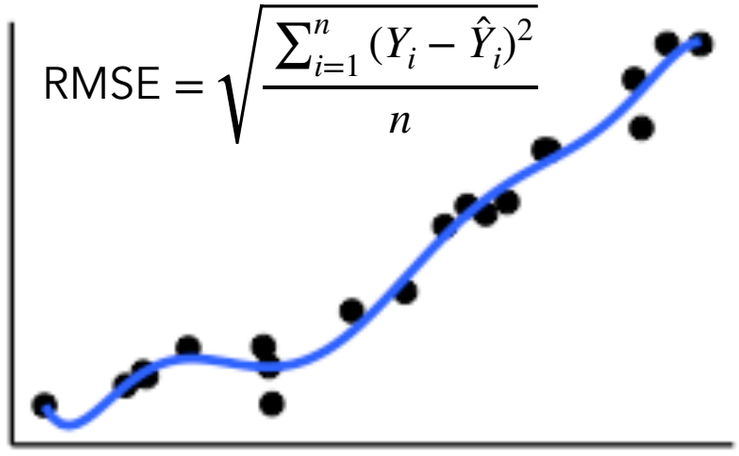
Which model describes the data best?

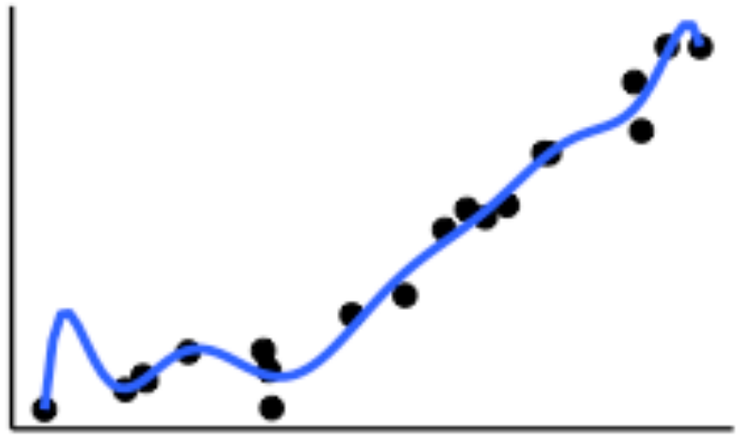


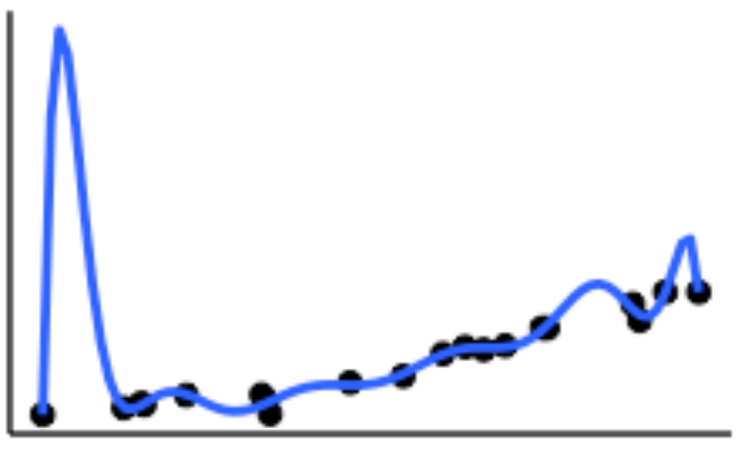


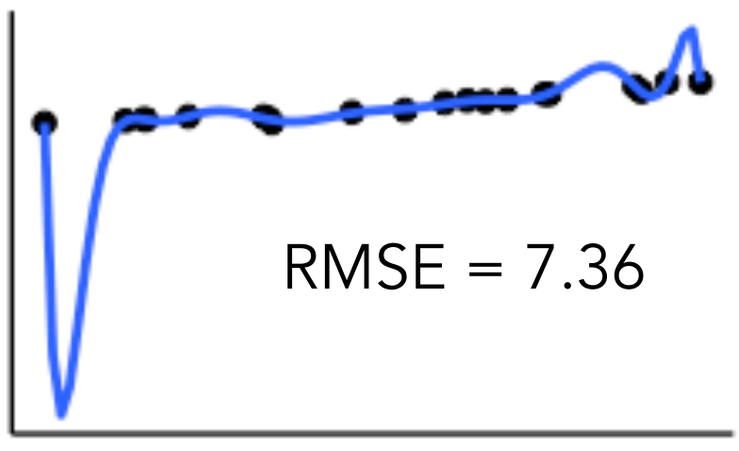


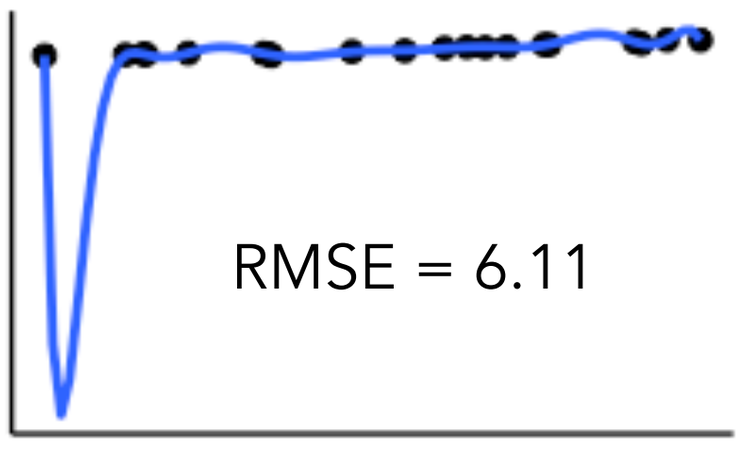








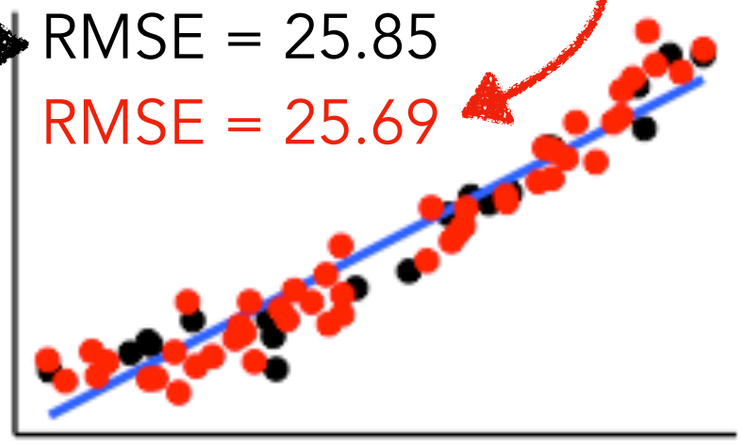




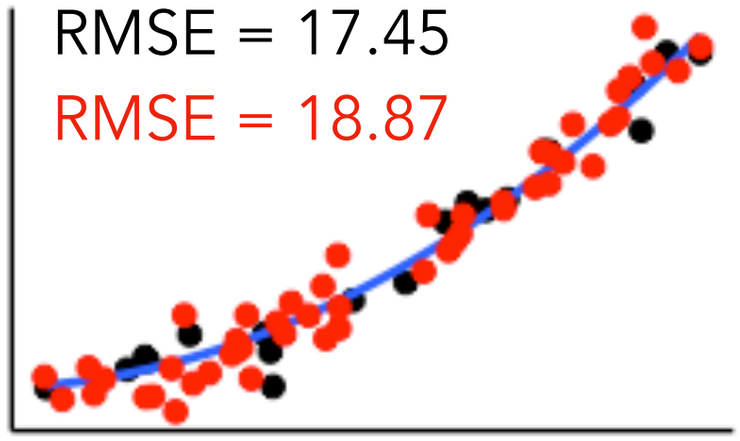
Which model describes the data best?

training error validation error

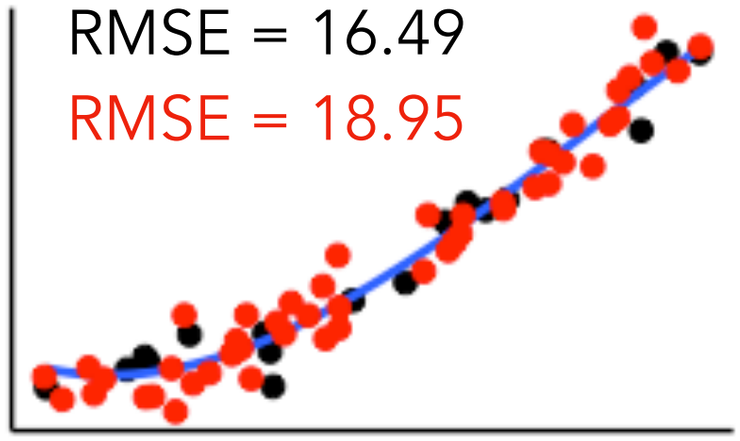
RMSE = 25.85
RMSE = 25.69

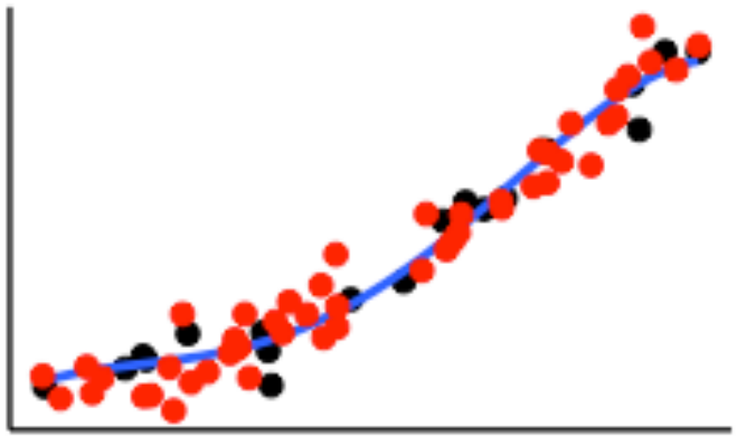


RMSE = 17.45
RMSE = 18.87

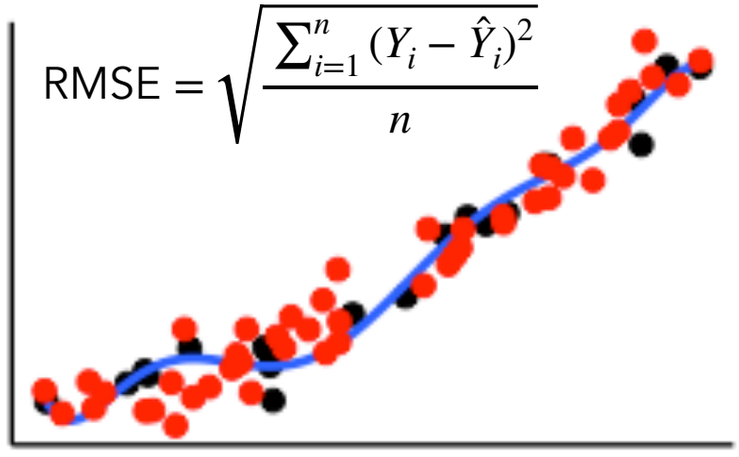


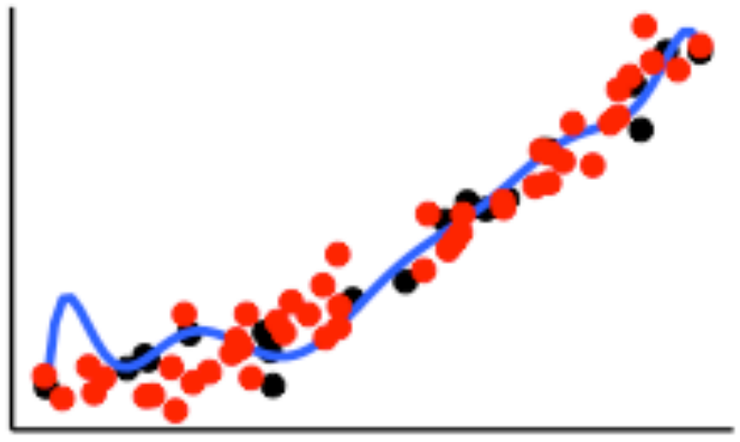
RMSE = 16.49
RMSE = 18.95

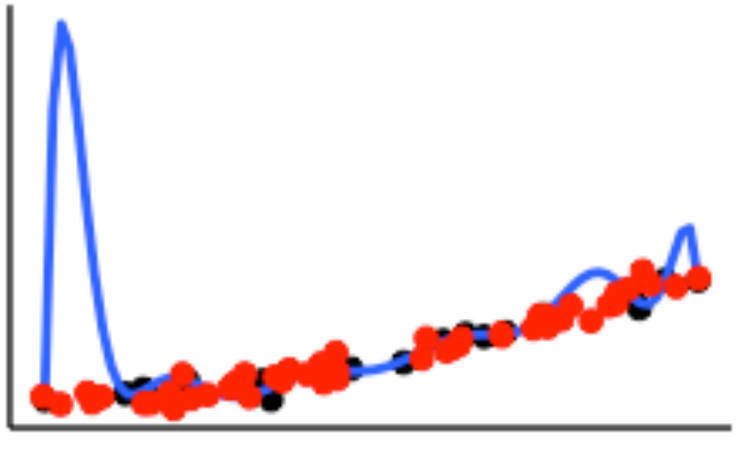




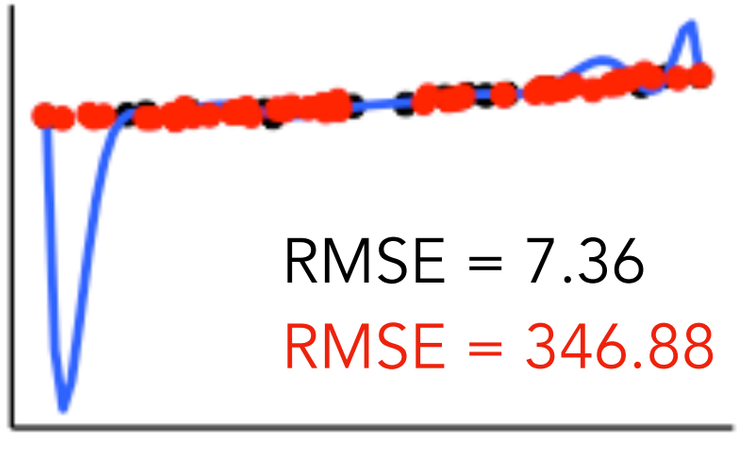
$$\text{RMSE} = \sqrt{\frac{\sum_{i=1}^{n}(Y_i - \hat{Y}_i)^2}{n}}$$



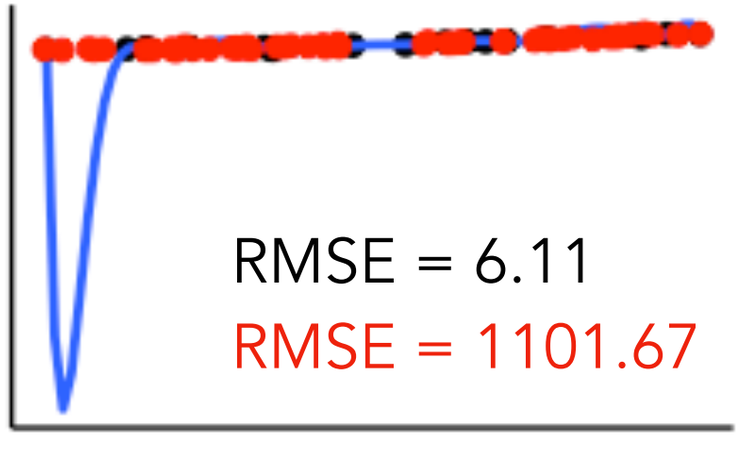




RMSE = 7.36
RMSE = 346.88



RMSE = 6.11
RMSE = 1101.67



Underfitting vs. Overfitting

ONE WAY TO EXPLAIN UNDERFITTING

Underfitting vs. Overfitting

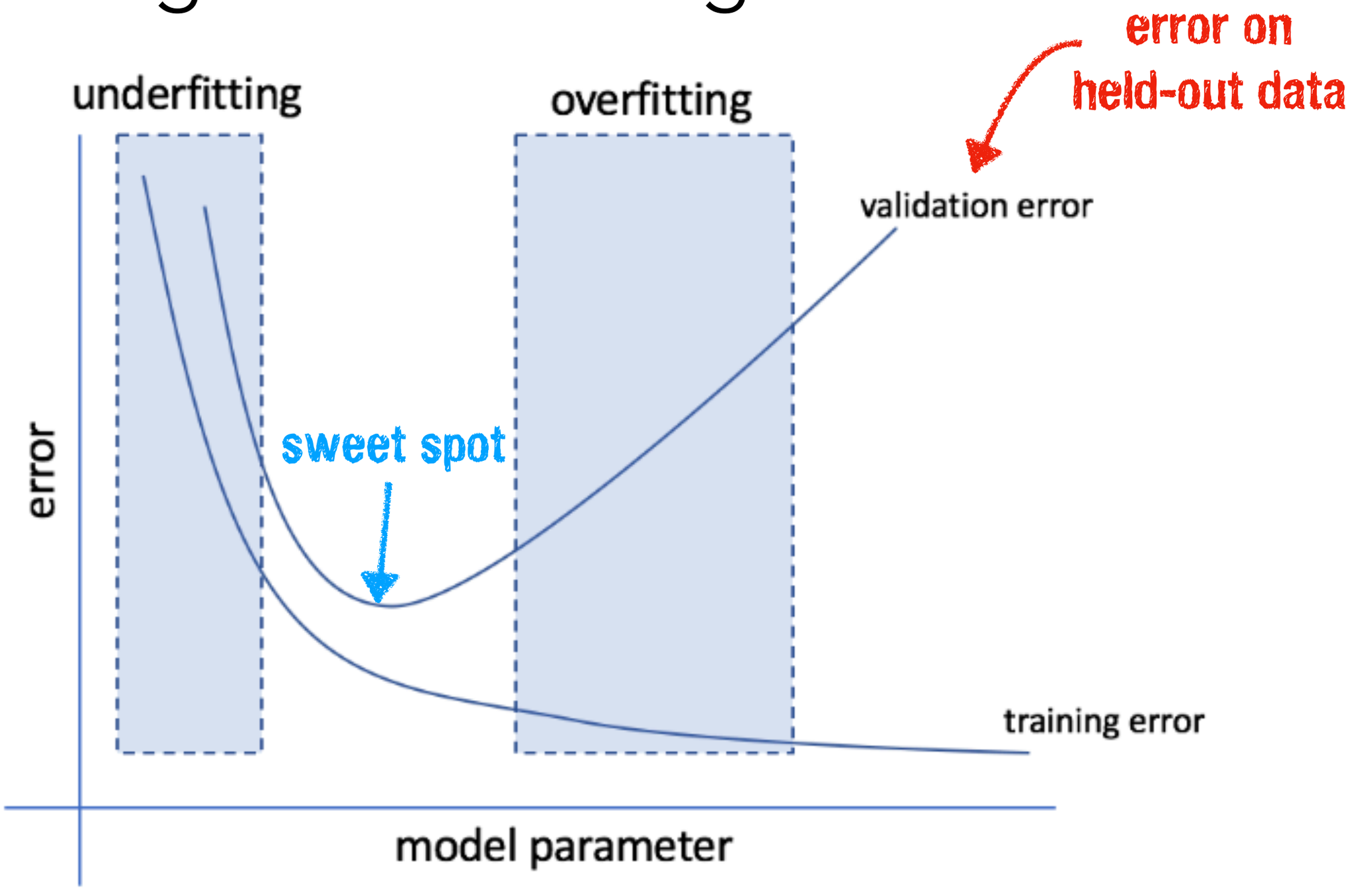
- **a good model should**:
  - explain the actual data well
  - predict future data well
- **bias-variance tradeoff**:
  - **bias** = error from erroneous assumptions in the model, high bias can cause a model to miss the relevant relations between predictors and outcome

underfitting

- **variance** = error from sensitivity to small fluctuations in the data, high variance can cause a model to fit the random noise in the data

overfitting

Underfitting vs. Overfitting



the goal is to find the **sweet spot** between underfitting and overfitting

Leave-one-out crossvalidation

LOO

Leave One Out

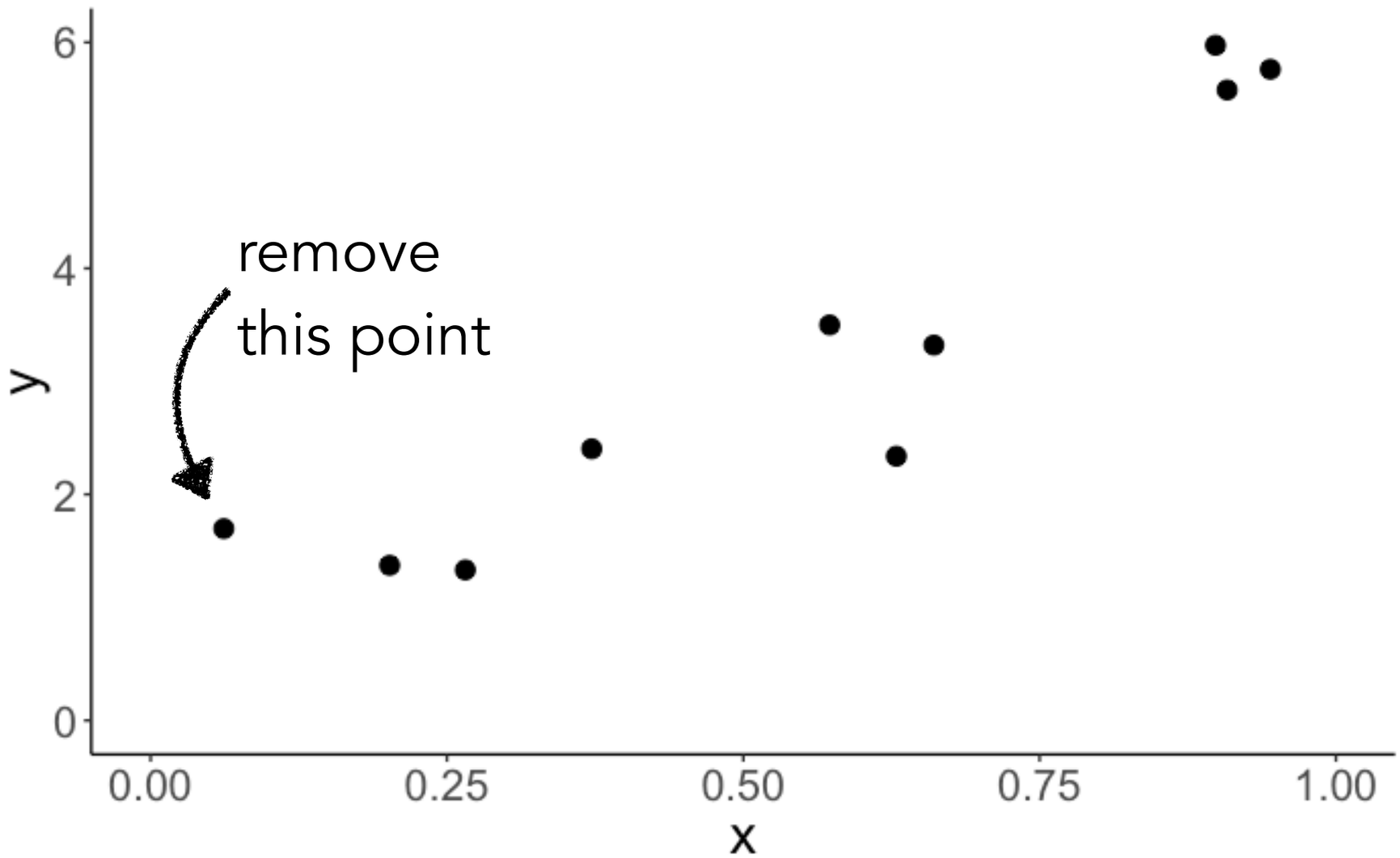
non-inspirational quote

Leave one out cross-validation

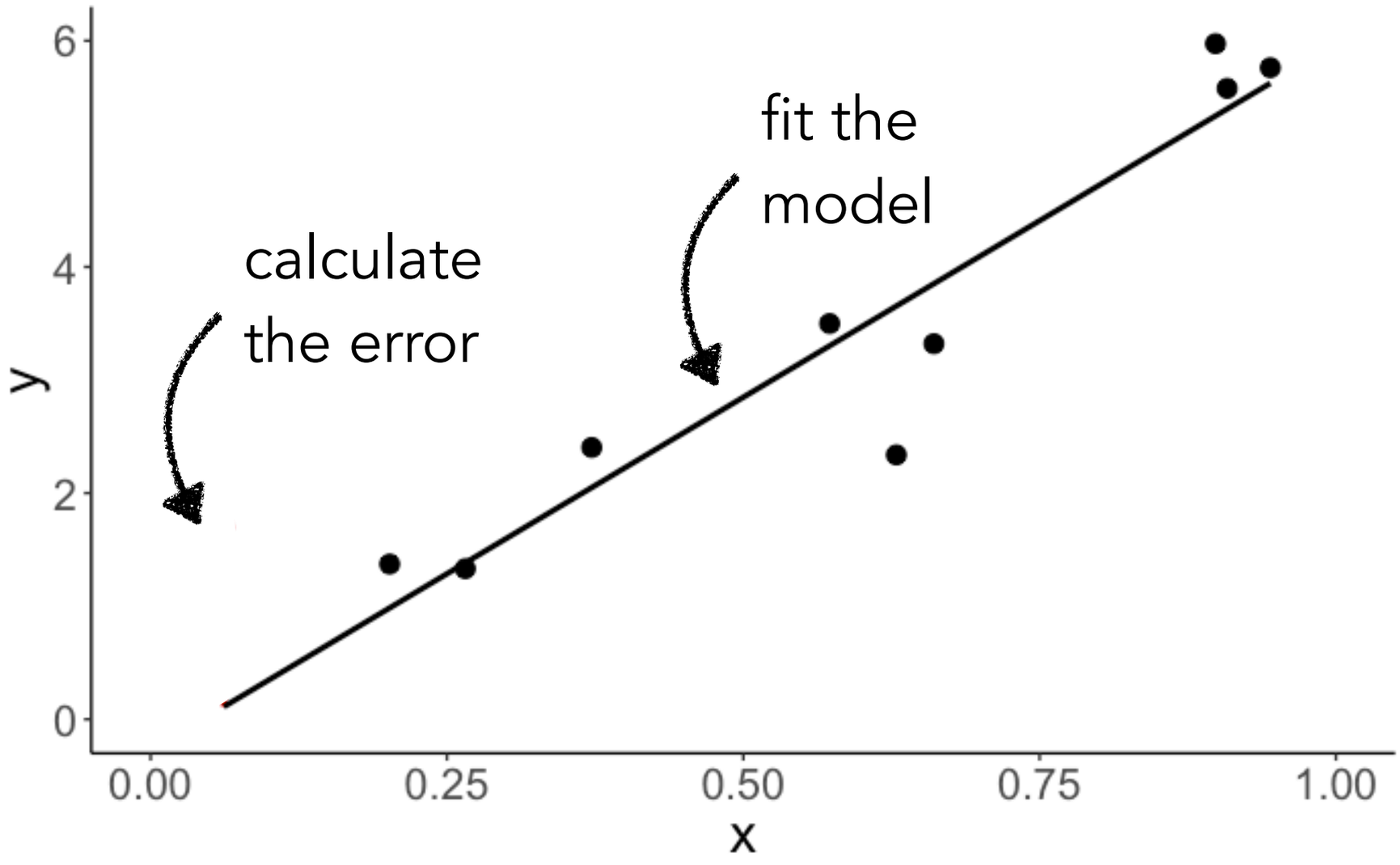
- train the model on all the data points except for one
- calculate the prediction error for the held-out data point

repeat for all data points

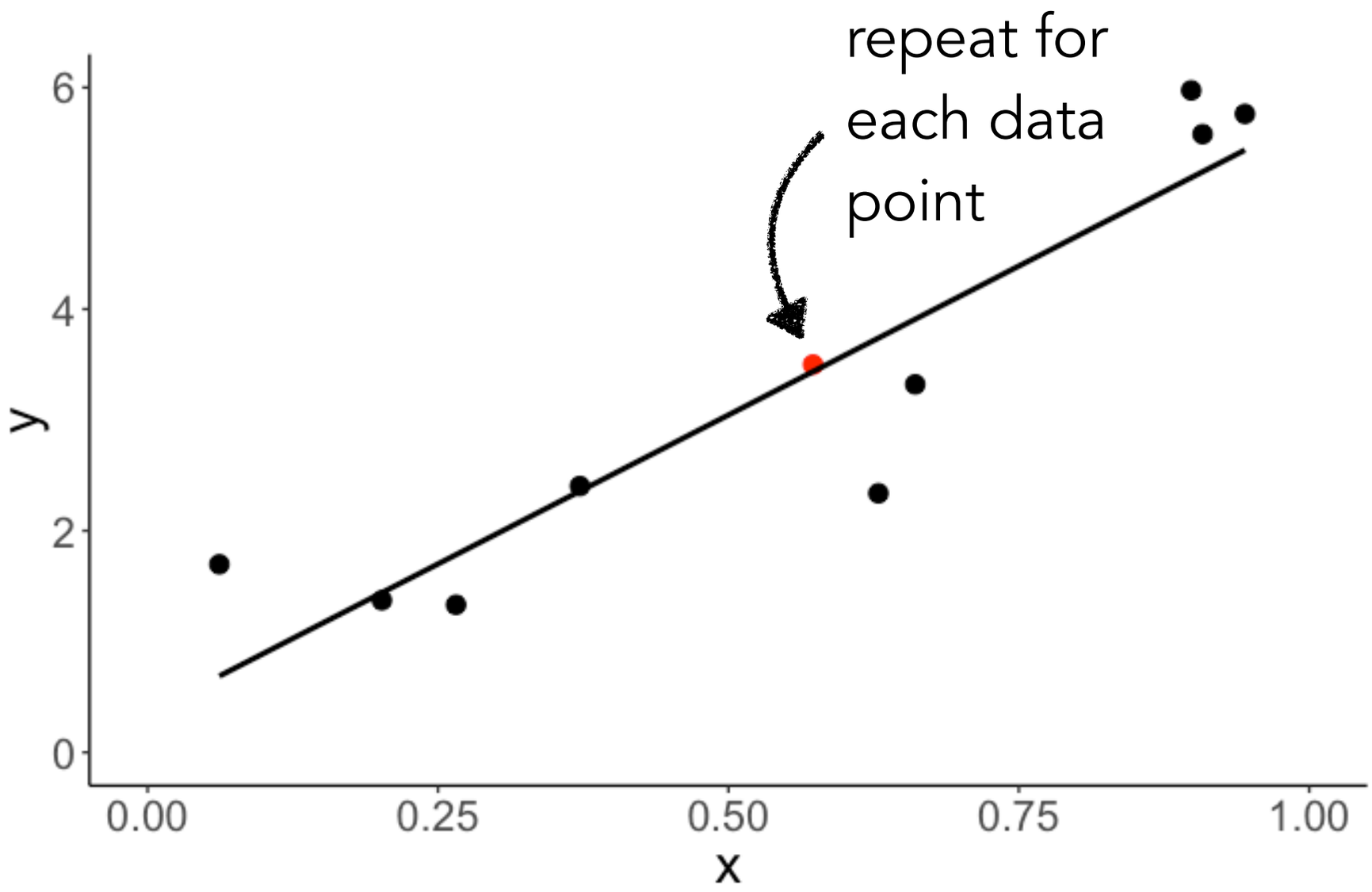
Leave one out cross-validation



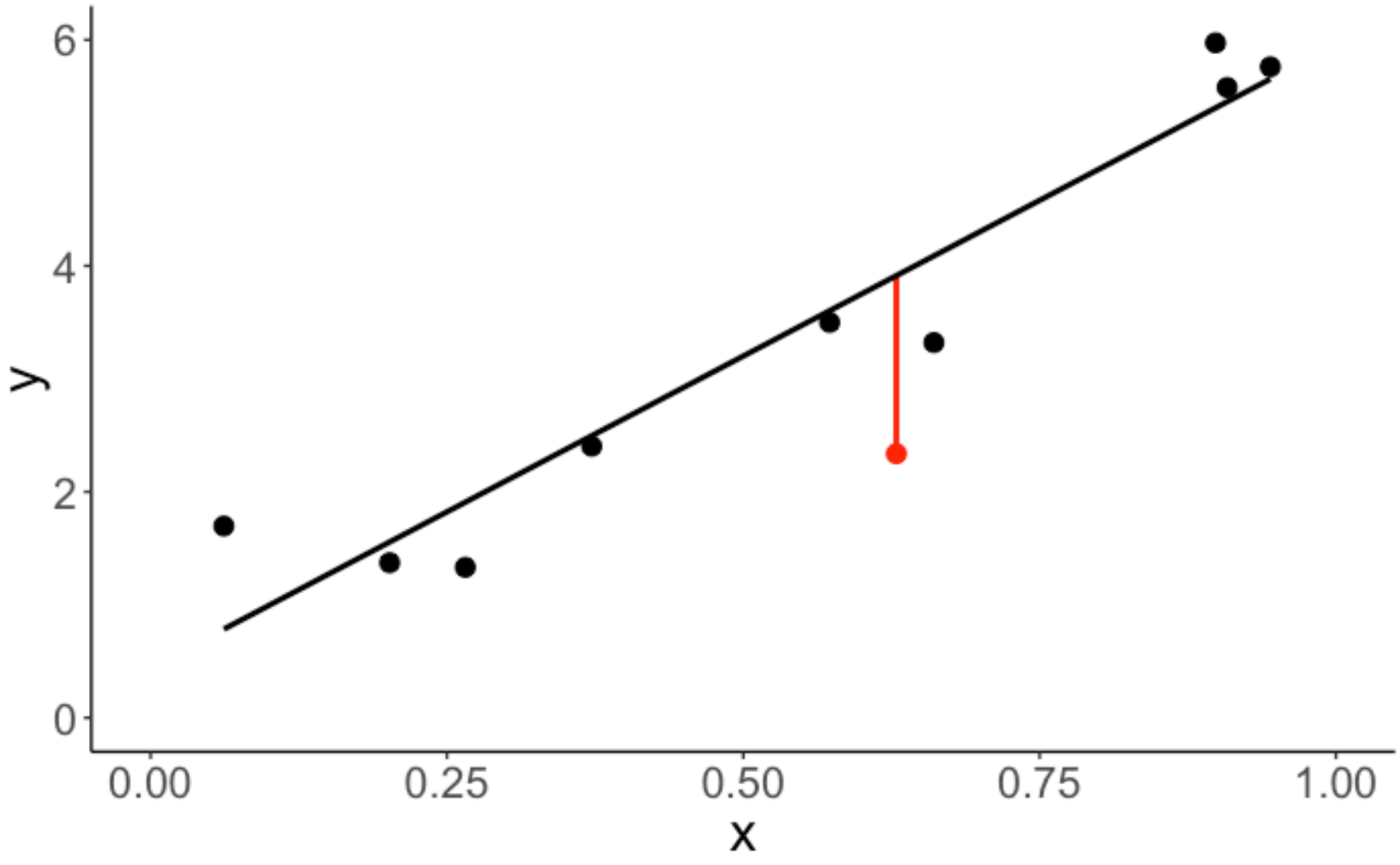
Leave one out cross-validation



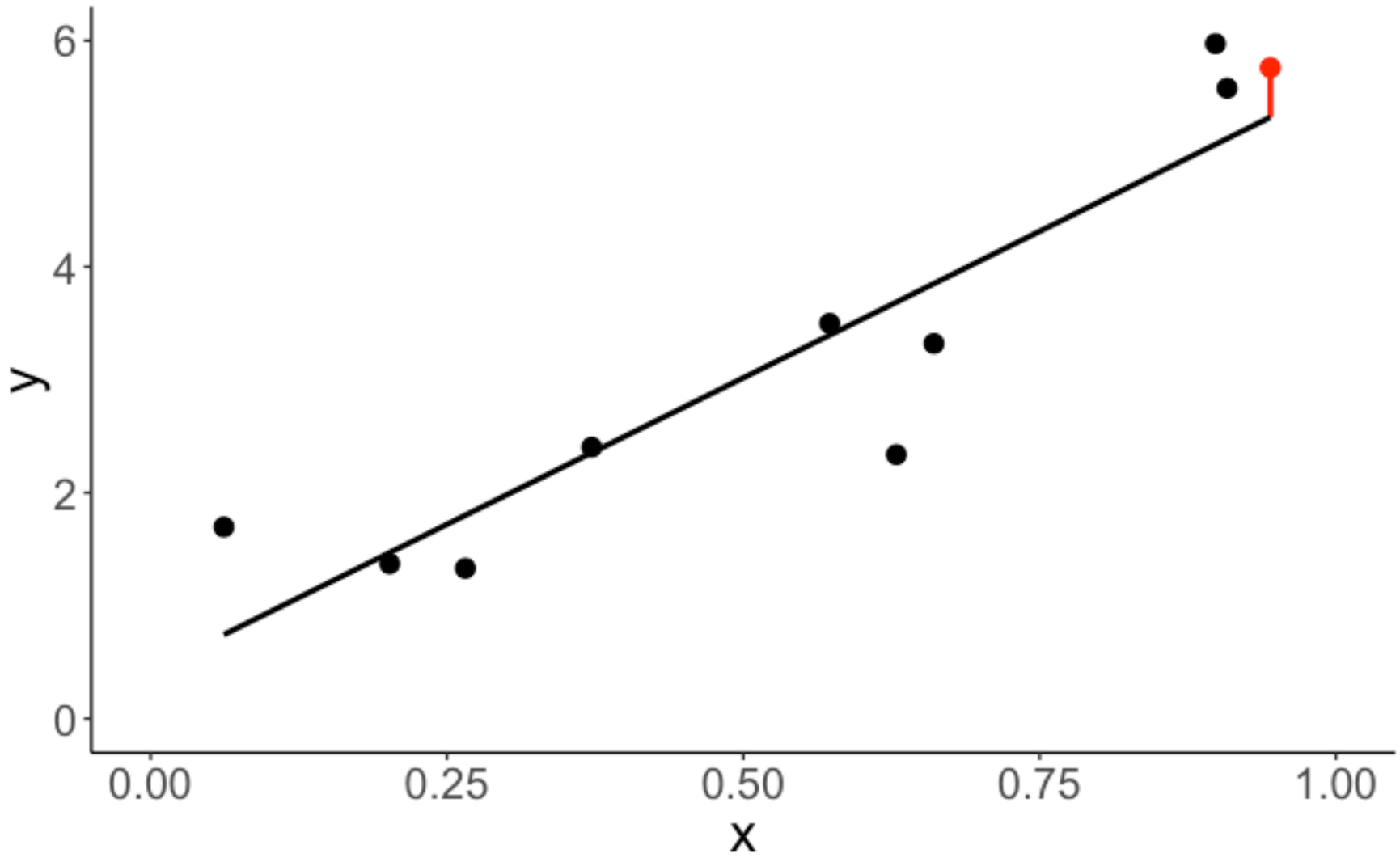
Leave one out cross-validation



Leave one out cross-validation

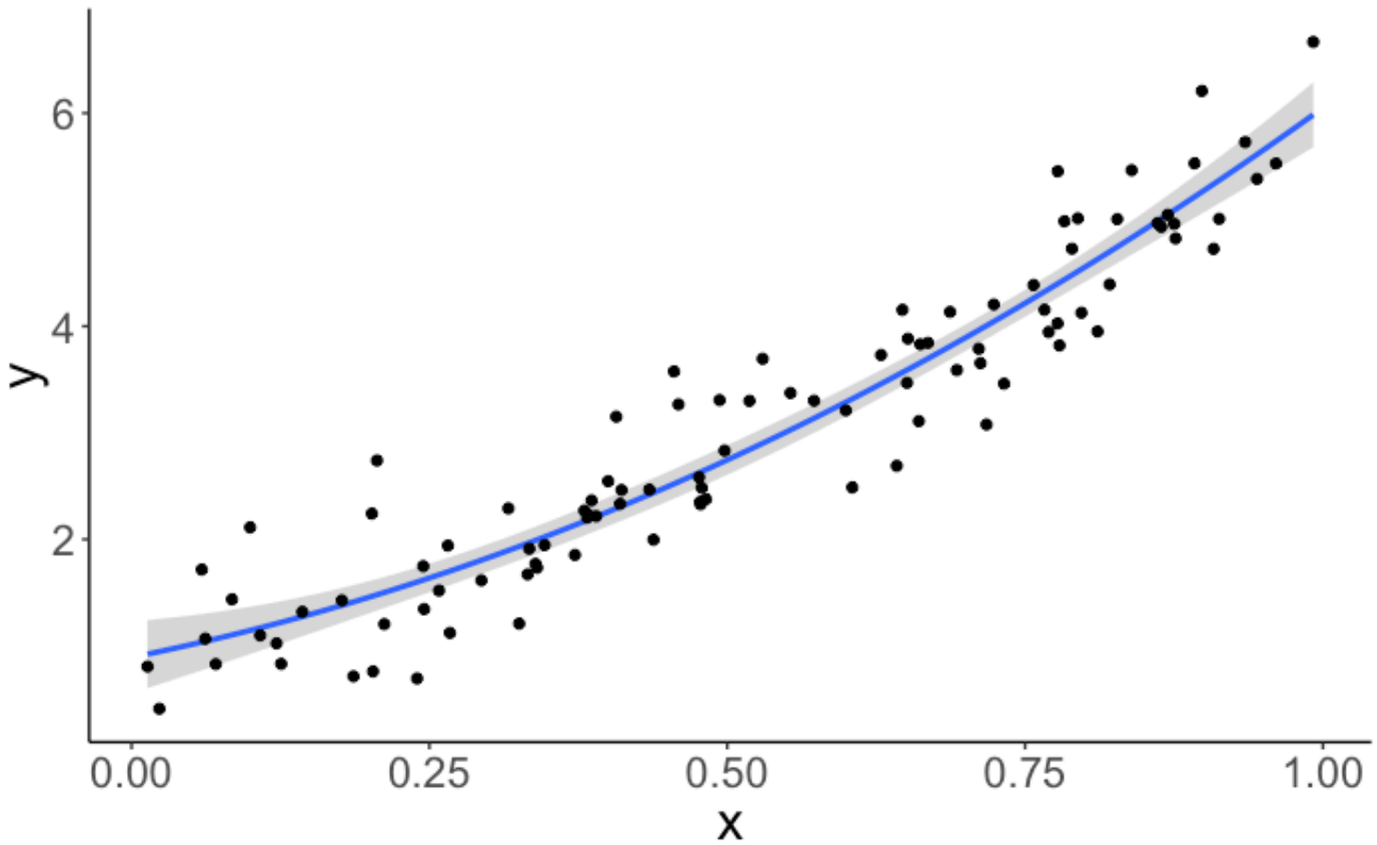


Leave one out cross-validation



Leave-one out crossvalidation

```r
# make example reproducible
set.seed(1)

# parameters
sample_size = 100
b0 = 1
b1 = 2
b2 = 3
sd = 0.5
```



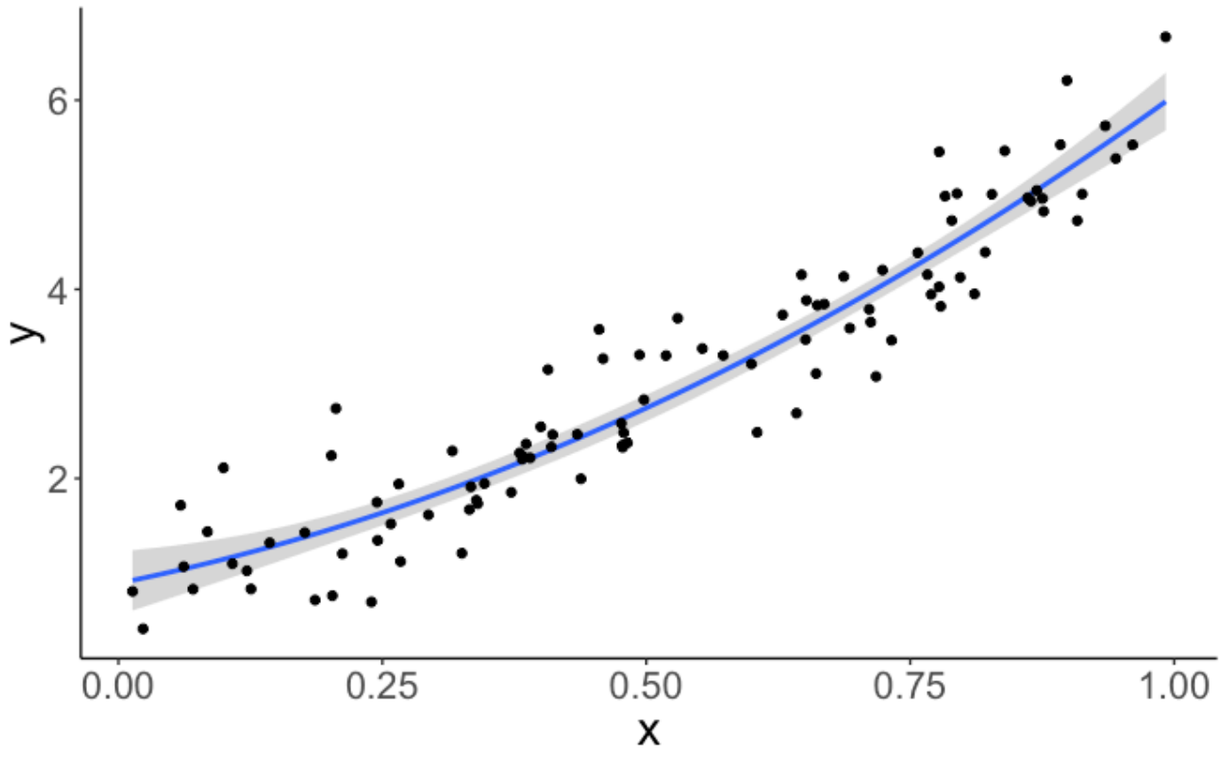

```r

# sample
df.data = tibble(
  participant = 1:sample_size,
  x = runif(sample_size, min = 0, max = 1),
  y = b0 + b1*x + b2*x^2 + rnorm(sample_size, sd = sd)
)
```

Leave-one out crossvalidation

ground truth

$$y_i = 1 + 2 \cdot x_i + 3 \cdot x_i^2 + e$$

$$e \sim \mathcal{N}(\text{mean} = 0,\ \text{sd} = 0.5)$$



candidate models

simple $\hat{y}_i = b_0 + b_1 \cdot x_i$

correct $\hat{y}_i = b_0 + b_1 \cdot x_i + b_2 \cdot x_i^2$

complex $\hat{y}_i = b_0 + b_1 \cdot x_i + b_2 \cdot x_i^2 + b_3 \cdot x_i^3$

we could do an F-test here since the models are nested ...

Leave-one out crossvalidation

```
1  library("modelr")
2
3  df.cross = df.data %>%
4    crossv_loo() %>% # function which generates training and test data sets
5    mutate(model_simple = map(train, ~ lm(y ~ 1 + x, data = .)),
6           model_correct = map(train, ~ lm(y ~ 1 + x + I(x^2), data = .)),
7           model_complex = map(train, ~ lm(y ~ 1 + x + I(x^2) + I(x^3), data = .))) %>%
8    pivot_longer(cols = contains("model"),
9                 names_to = "index",
10                values_to = "model") %>%
11   mutate(rmse = map2_dbl(.x = model, .y = test, .f = ~ rmse(.x, .y)))
```

nice package for basic cross-validation

index	mean_rmse
simple	0.65
correct	0.42
complex	0.41

complex model has the lowest error on the training data

Leave-one out crossvalidation

```
1 library("modelr")
2
3 df.cross = df.data %>%
4   crossv_loo() %>%
```

splits the data set into training and test

	train	test	.id
1	list(data = list(participant = 1:10, x = c(0.265508663…	list(data = list(participant = 1:10, x = c(0.265508663…	1
2	list(data = list(participant = 1:10, x = c(0.265508663…	list(data = list(participant = 1:10, x = c(0.265508663…	2
3	list(data = list(participant = 1:10, x = c(0.265508663…	list(data = list(participant = 1:10, x = c(0.265508663…	3
4	list(data = list(participant = 1:10, x = c(0.265508663…	list(data = list(participant = 1:10, x = c(0.265508663…	4
5	list(data = list(participant = 1:10, x = c(0.265508663…	list(data = list(participant = 1:10, x = c(0.265508663…	5
6	list(data = list(participant = 1:10, x = c(0.265508663…	list(data = list(participant = 1:10, x = c(0.265508663…	6
7	list(data = list(participant = 1:10, x = c(0.265508663…	list(data = list(participant = 1:10, x = c(0.265508663…	7
8	list(data = list(participant = 1:10, x = c(0.265508663…	list(data = list(participant = 1:10, x = c(0.265508663…	8
9	list(data = list(participant = 1:10, x = c(0.265508663…	list(data = list(participant = 1:10, x = c(0.265508663…	9
10	list(data = list(participant = 1:10, x = c(0.265508663…	list(data = list(participant = 1:10, x = c(0.265508663…	10

each entry is simply a pointer to the data set plus some indices `.idx` for the filtered data points

Leave-one out crossvalidation

```
1 library("modelr")
2
3 df.cross = df.data %>%
4   crossv_loo() %>%
5   mutate(model_simple = map(train, ~ lm(y ~ 1 + x, data = .)),
6          model_correct = map(train, ~ lm(y ~ 1 + x + I(x^2), data = .)),
7          model_complex = map(train, ~ lm(y ~ 1 + x + I(x^2) + I(x^3), data = .))) %>%
```

fit three different models to the training data set

Leave-one out crossvalidation

```
library("modelr")

df.cross = df.data %>%
  crossv_loo() %>%
  mutate(model_simple = map(train, ~ lm(y ~ 1 + x, data = .)),
         model_correct = map(train, ~ lm(y ~ 1 + x + I(x^2), data = .)),
         model_complex = map(train, ~ lm(y ~ 1 + x + I(x^2) + I(x^3), data = .))) %>%
  pivot_longer(cols = contains("model"),
               names_to = "index",
               values_to = "model") %>%
  mutate(rmse = map2_dbl(.x = model, .y = test, .f = ~ rmse(.x, .y)))
```

calculate the root mean squared error for each model on the test data set

```
df.cross %>%
  group_by(index) %>%
  summarize(mean_rmse = mean(rmse))
```

index	mean_rmse
simple	0.65
correct	0.48
complex	0.70

the correct model has the lowest prediction error

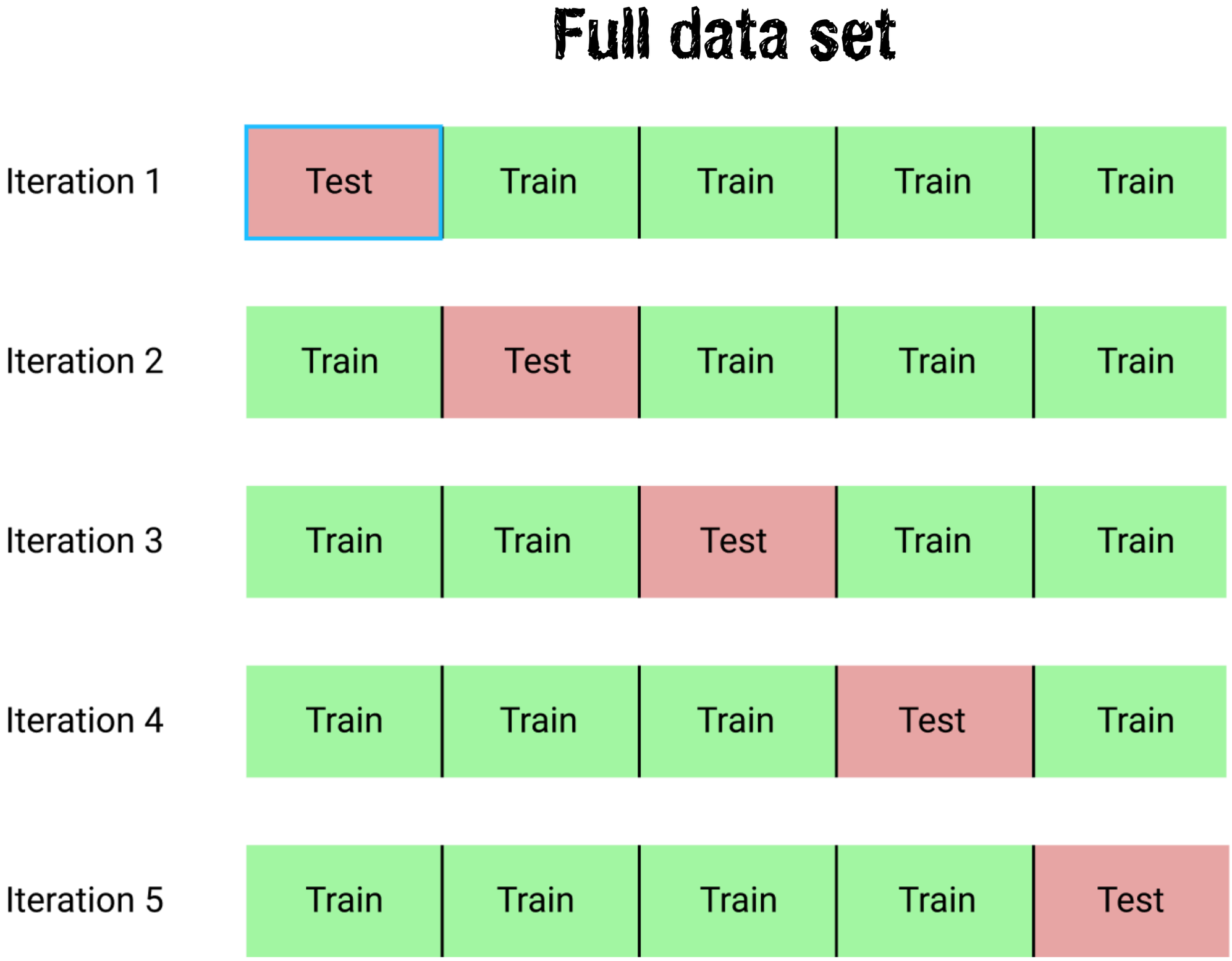
Leave-one out crossvalidation

Any potential problems with LOO?

can be computationally expensive since it requires fitting the model `n` times (once for each data point) ...

k-fold cross validation

k-fold crossvalidation



k-fold crossvalidation

k-fold crossvalidation

```
df.cross = df.data %>%
  crossv_kfold(k = 10) %>%
  mutate(model_simple = map(.x = train,
                            .f = ~ lm(y ~ 1 + x, data = .)),
         model_correct = map(.x = train,
                             .f = ~ lm(y ~ 1 + x + I(x^2), data = .)),
         model_complex = map(.x = train,
                             .f = ~ lm(y ~ 1 + x + I(x^2) + I(x^3), data = .))) %>%
  pivot_longer(cols = contains("model"),
               names_to = "model",
               values_to = "fit") %>%
  mutate(rsquare = map2_dbl(.x = fit,
                            .y = test,
                            .f = ~ rsquare(.x, .y)))
```

using R^2 as a measure

why didn't we use R^2 for LOO?

this wouldn't work for LOO since we only have one data point in the test data...

index	median_rsquare
simple	0.839
correct	0.865
complex	0.860

the correct model accounts for the most variance in the test data

k-fold vs. leave-one-out crossvalidation

- **LOO**:
  - trained on **more** data
    - more variance
    - less bias
- **k-fold**:
  - trained on **less** data
    - less variance
    - more bias

Monte Carlo crossvalidation

Monte Carlo crossvalidation

random splits into training and test data

```
crossv_mc(n = 50, test = 0.5)
```

number of training-test splits

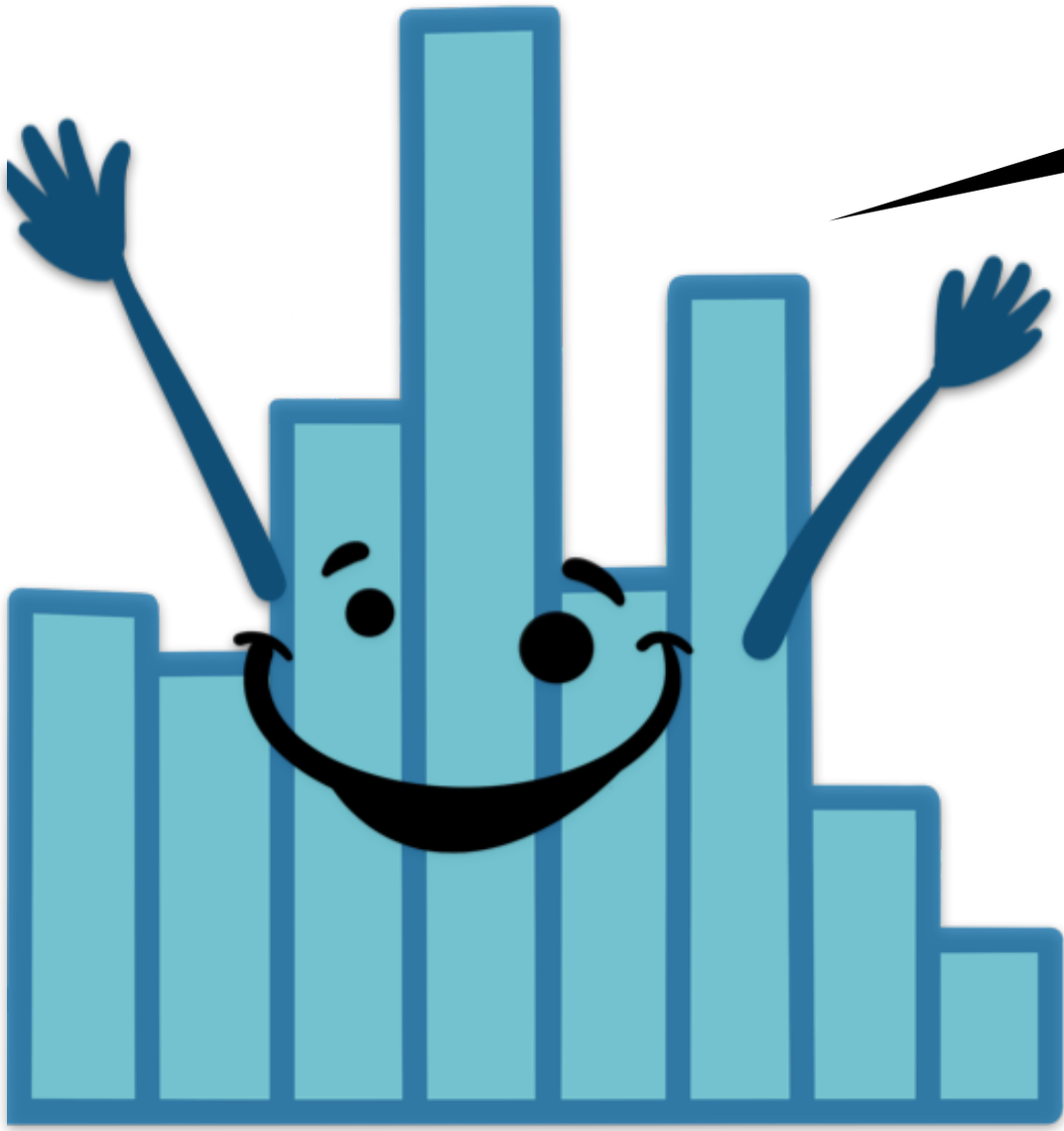
proportion of test data in each split

- splits can also be done in a **stratified** way (check out the `tidymodels` package)
- for example, generate training data that has the same percentage of cases from each group
- fit data from some participants, test on data from other participants, ...

We're listening to "Liability" by "Tape Machines, Astyn Turr" submitted by Sarah Wu

02:00

stretch break!

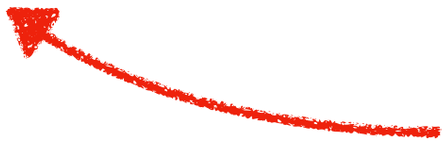


time

AIC and BIC

AIC and BIC

- AIC = Akaike Information Criterion
- BIC = Bayesian Information Criterion



not that much Bayesian about it ...

$$\mathrm{AIC} = 2k - 2\ln(L)$$

$$\mathrm{BIC} = \ln(n)k - 2\ln(\hat{L})$$

$\hat{L}$ = maximized value of the likelihood function of the model

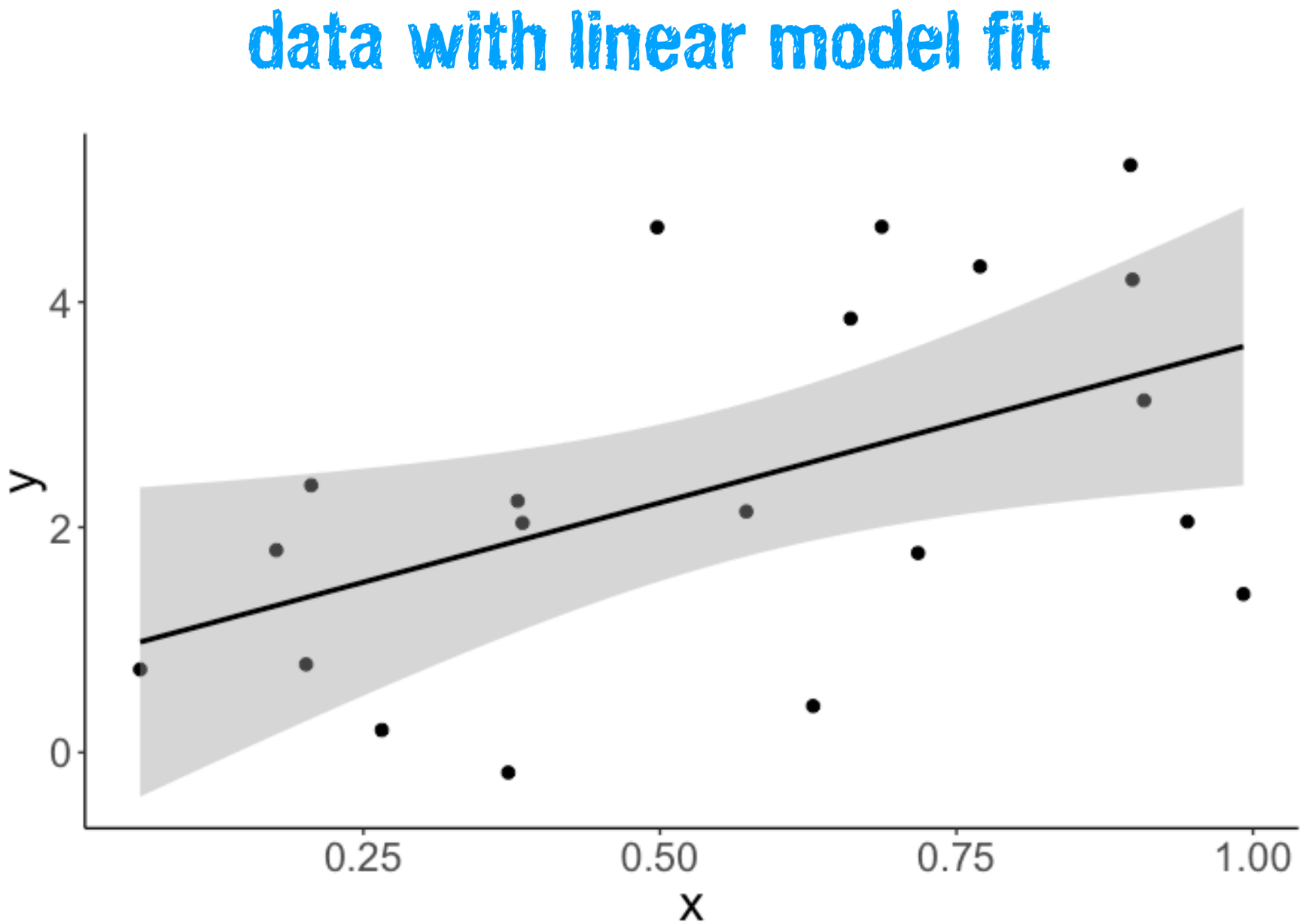
k = number of parameters in the model

n = number of observations

AIC and BIC

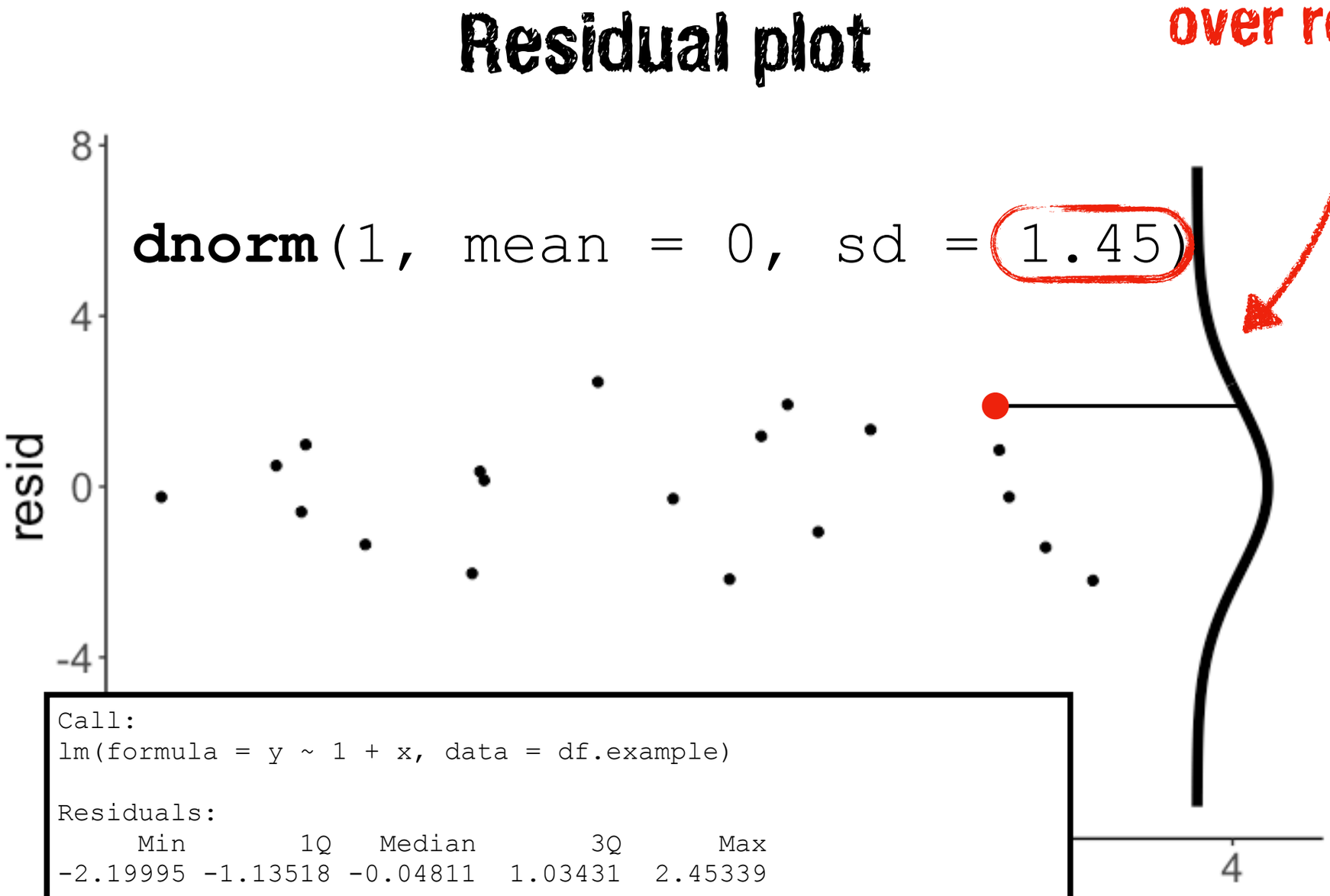
- How do we get the likelihood of our model?
  - in a linear regression, minimizing least squares is equivalent to maximizing the likelihood of the data given the model
- Assumptions of the linear model:
  - residuals are normally distributed with:
    - `mean = 0` and `sd = sigma`
  - calculate overall likelihood by computing the likelihood of each residual, and then multiplying

AIC and BIC



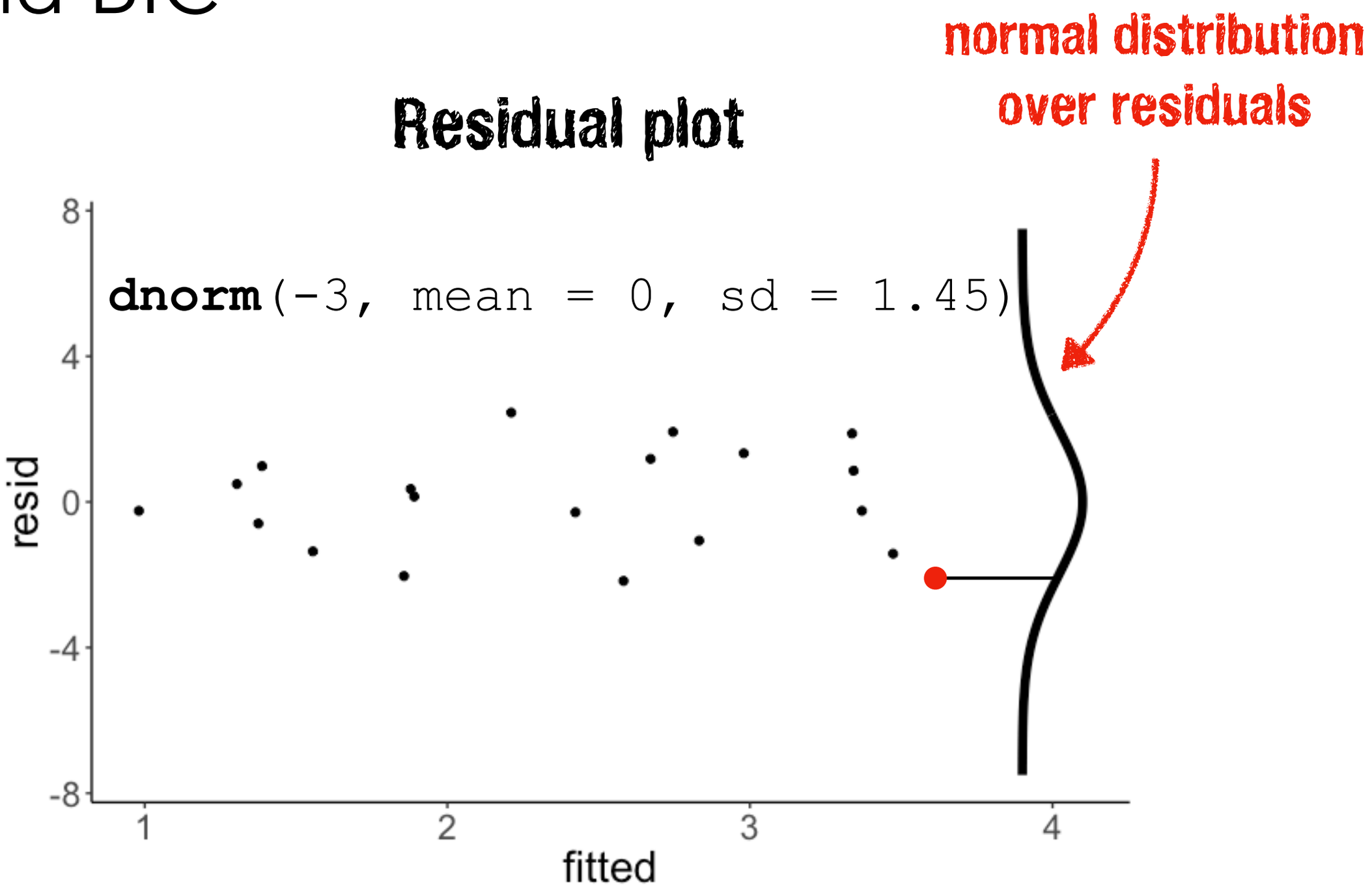
AIC and BIC

normal distribution over residuals




```
Call:
lm(formula = y ~ 1 + x, data = df.example)

Residuals:
     Min       1Q   Median       3Q      Max
-2.19995 -1.13518 -0.04811  1.03431  2.45339

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   0.8062     0.7157   1.126   0.2748
x             2.8232     1.1374   2.482   0.0232 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 1.449 on 18 degrees of freedom
Multiple R-squared:  0.255,Adjusted R-squared:  0.2136
F-statistic: 6.161 on 1 and 18 DF,  p-value: 0.02315
```

AIC and BIC



since the data points are independent, we can calculate the overall likelihood by multiplying the likelihood of each observation

AIC and BIC

```
dnorm(1.88, mean = 0, sd = 1.45) = 0.12
```

```
 1 # generate some data
 2 df.like = tibble(
 3   x = runif(20, min = 0, max = 1),
 4   y = 1 + 3 * x + rnorm(20, sd = 2)
 5 )
 6
 7 # fit the model
 8 fit = lm(formula = y ~ x,
 9           data = df.like)
10
11 # model summary
12 fit %>%
13   glance()
```

x	y	fitted	resid	likelihood
0.90	5.22	3.34	1.88	0.12
0.27	0.20	1.56	-1.36	0.18
0.37	-0.18	1.86	-2.04	0.10
0.57	2.14	2.42	-0.28	0.27
0.91	3.13	3.37	-0.24	0.27
0.20	0.78	1.38	-0.59	0.25
0.90	4.20	3.34	0.86	0.23
0.94	2.05	3.47	-1.42	0.17
0.66	3.85	2.67	1.18	0.20
0.63	0.41	2.58	-2.17	0.09

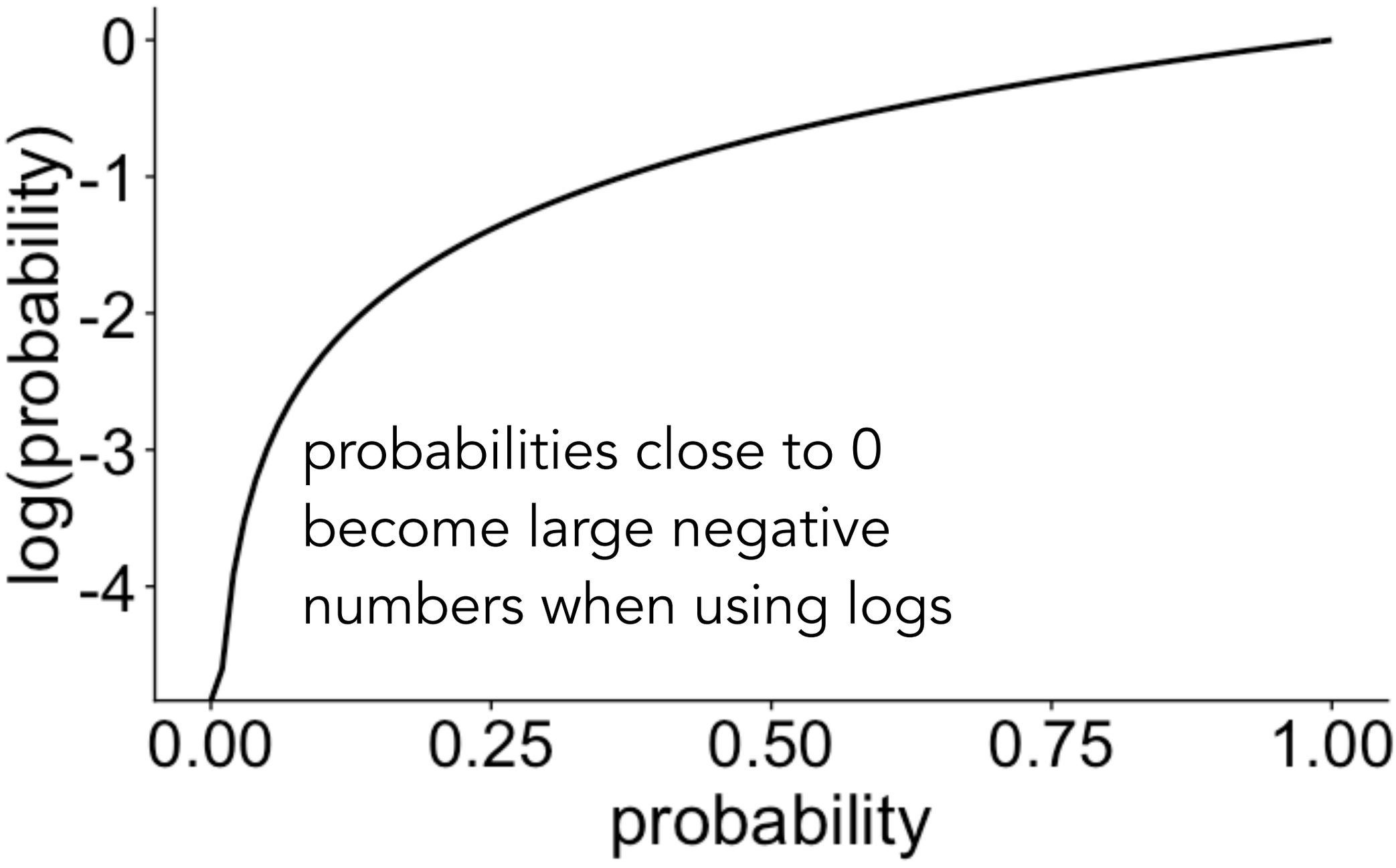
$$\sum_{i=1}^{n} \ln(\text{likelihood})$$

inferred standard deviation of the error

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual
0.25	0.21	1.45	6.16	0.02	2	-34.74	75.47	78.46	37.77	18

$$e \sim \mathcal{N}(\text{mean} = 0,\ \text{sd} = 1.45)$$

`log()` is your friend!



Clue guide to probability

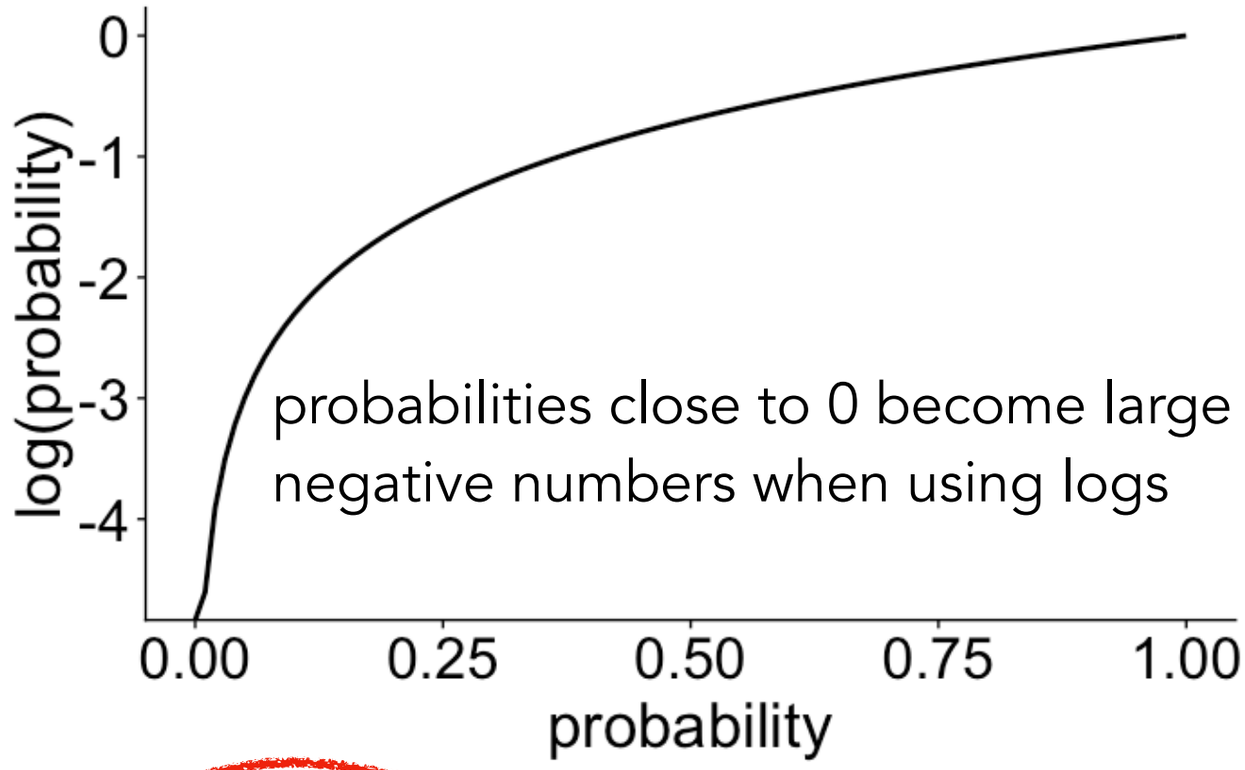
- *joint probability*:
- if A and B are independent then
- **Definition**: $p(A, B) = p(A) \cdot p(B)$

- $p(\text{Prof Plum, candle stick}) =$
  $p(\text{Prof Plum}) \cdot p(\text{candle stick}) =$
  $\frac{1}{6} \cdot \frac{1}{6} = \frac{1}{36}$

Who?

What?

`log()` is your friend!



multiplying probabilities

$$0.01 \cdot 0.01 \cdot 0.01 \cdot 0.01 = 0.00000001$$

number becomes extremely small quickly

take log()

`log(0.01)= -4.60517`

number becomes large but that's ok

summing logs

$$(-4.60517) + (-4.60517) + (-4.60517) + (-4.60517) = -18.42068$$

transform back into probability

`exp(-18.42068)= 0.00000001`

often not necessary since we just use logLikelihood

AIC and BIC

dnorm(1.88, mean = 0, sd = 1.45) = 0.12

```
# generate some data
df.like = tibble(
   x = runif(20, min = 0, max = 1),
   y = 1 + 3 * x + rnorm(20, sd = 2)
)

# fit the model
fit = lm(formula = y ~ x,
         data = df.like)

# model summary
fit %>%
   glance()
```

x	y	fitted	resid	likelihood
0.90	5.22	3.34	1.88	0.12
0.27	0.20	1.56	-1.36	0.18
0.37	-0.18	1.86	-2.04	0.10
0.57	2.14	2.42	-0.28	0.27
0.91	3.13	3.37	-0.24	0.27
0.20	0.78	1.38	-0.59	0.25
0.90	4.20	3.34	0.86	0.23
0.94	2.05	3.47	-1.42	0.17
0.66	3.85	2.67	1.18	0.20
0.63	0.41	2.58	-2.17	0.09

inferred standard deviation of the error

$$\sum_{i=1}^{n} \ln(\text{likelihood})$$

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual
0.25	0.21	1.45	6.16	0.02	2	-34.74	75.47	78.46	37.77	18

$$e \sim \mathcal{N}(\text{mean} = 0,\ \text{sd} = 1.45)$$

AIC and BIC

$$\text{AIC} = 2k - 2\ln(\hat{L})$$

$$\text{BIC} = \ln(n)k - 2\ln(\hat{L})$$

$\ln(\hat{L})$ = maximized value of the likelihood function of the model **-34.74**

k = number of parameters in the model **3**

n = number of observations **20**

the `sd` of the normal distribution modeling the residuals counts as a parameter

```
lm(formula = y ~ 1 + x, data = df.example)
```

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual
0.25	0.21	1.45	6.16	0.02	2	-34.74	75.47	78.46	37.77	18

AIC and BIC

$$\text{AIC} = 2k - 2\ln(\hat{L}) = 2 \cdot 3 - 2 \cdot (-34.74) = 75.47$$

$$\text{BIC} = \ln(n)k - 2\ln(\hat{L}) = \ln(20) \cdot 3 - 2 \cdot (-34.74) = 78.46$$

$\ln(\hat{L})$ = maximized value of the likelihood function of the model **-34.74**

k = number of parameters in the model **3**

n = number of observations **20**

the `sd` of the normal distribution modeling the residuals counts as a parameter

```
lm(formula = y ~ 1 + x, data = df.example)
```

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual
0.25	0.21	1.45	6.16	0.02	2	-34.74	75.47	78.46	37.77	18

AIC and BIC

$$\mathrm{AIC} = 2k - 2\ln(\hat{L})$$

$$\mathrm{BIC} = \ln(n)k - 2\ln(\hat{L})$$

ΔBIC	Evidence against higher BIC
0 to 2	Not worth more than a bare mention
2 to 6	Positive
6 to 10	Strong
>10	Very Strong

- for both AIC and BIC, *lower* is better!
- neither provide a test of a model in the sense of testing a null hypothesis
  - AIC or BIC tell us nothing about the absolute quality of a model, only the quality relative to other models
- BIC generally penalizes free parameters more strongly than AIC (though it depends on the size of *n*)

What shall I use when?

- Use it all!
- ideally, the different measures provide converging evidence

Table 2
Summary of the model results. Values for *r* and RMSE indicate means (with 5% and 95% quantiles in parentheses) based on 100 split-half cross-validation runs. BIC scores are based on running the models on the full data set.

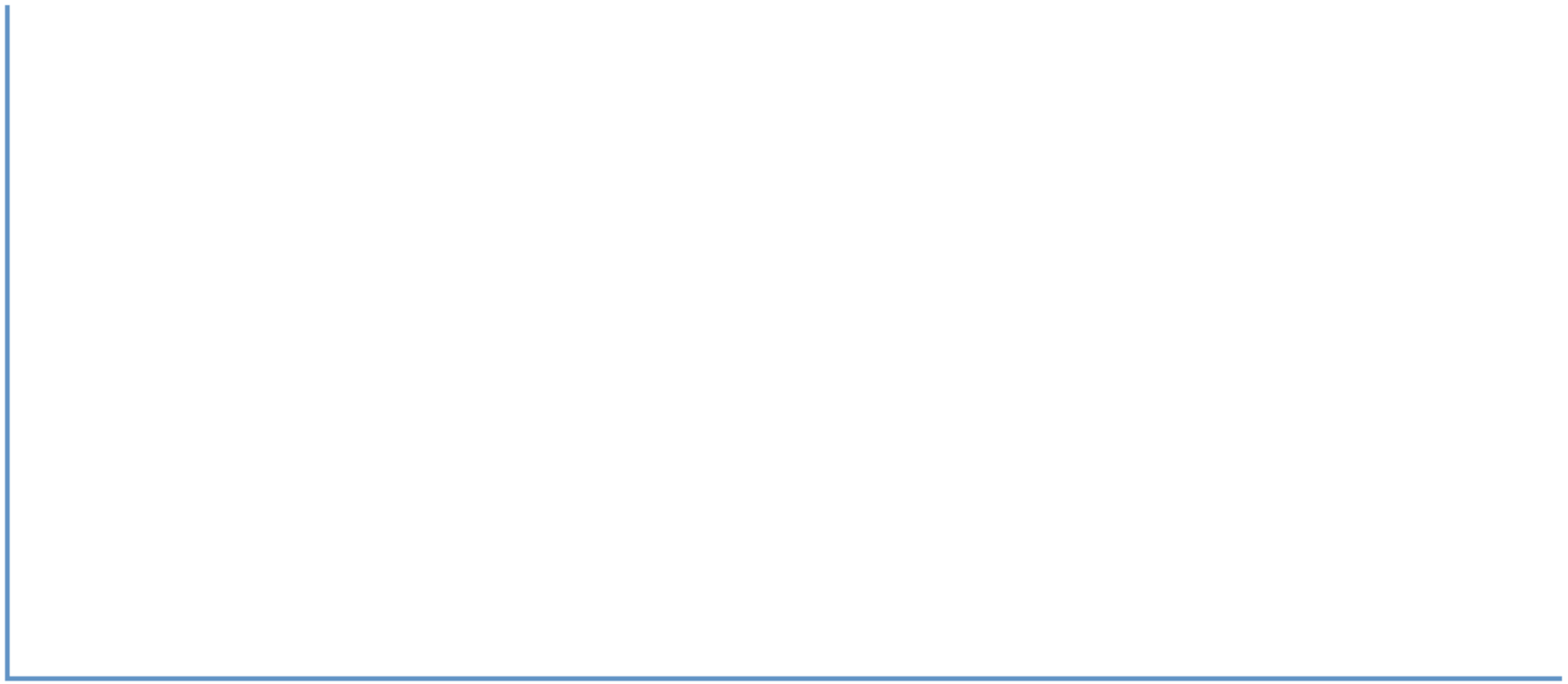
Model	*r*	RMSE	BIC
Difference & pivotality	.86 (.66, .95)	10.56 (6.17, 17.21)	158.59
Difference	.70 (.30, .90)	26.92 (16.4, 40.6)	209.74
Pivotality	.63 (.41, .77)	14.23 (11.39, 17.54)	199.53
Optimality	.66 (.42, .84)	14.55 (10.54, 17.91)	199.47

Note: BIC = Bayesian Information Criterion (lower values indicate better model performance).

Plan for today

- Quick recap
- Simulating a power analysis
  - Demonstration in RStudio
- Model comparison
  - Cross-validation
  - AIC and BIC
- Linear mixed effects models

How was the pace of today's class?



much too slow

a little too slow

just right

a little too fast

much too fast

How happy were you with today's class overall?

What did you like about today's class? What could be improved next time?

Thank you!