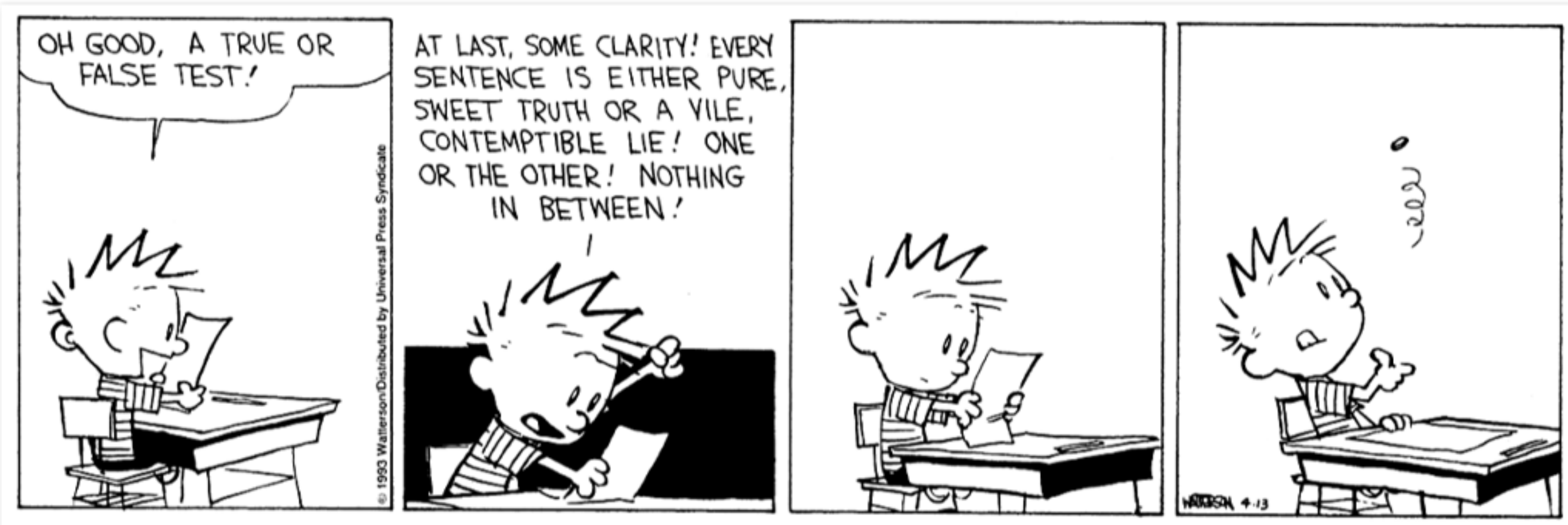
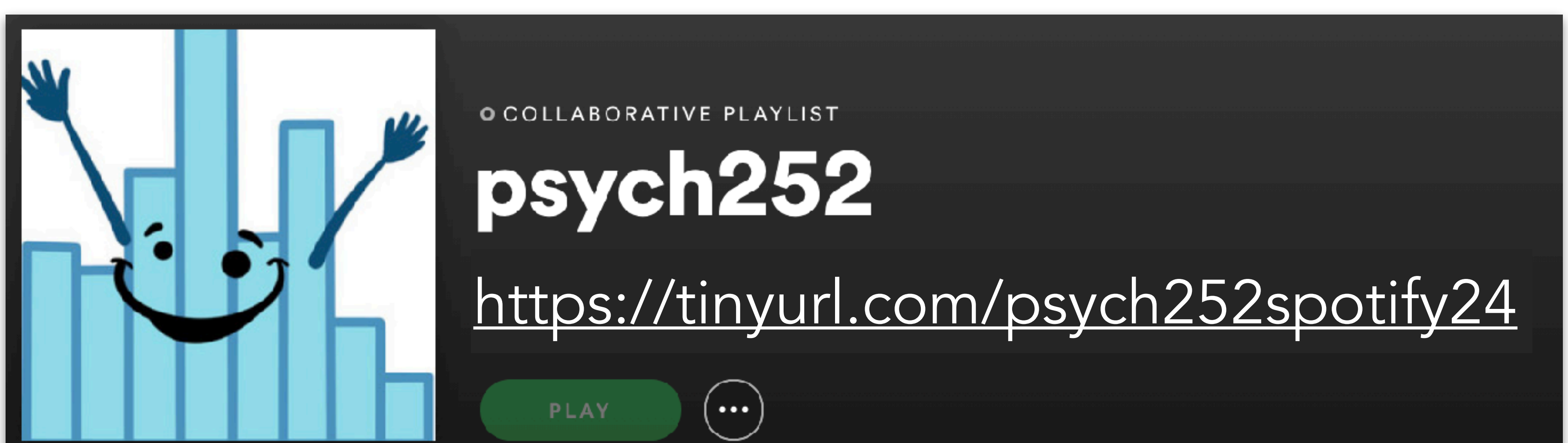
Model comparison





02/12/2024

Logistics

Midterm

Clarification on question 14/15 #40

A

Ari Beller STAFF
22 hours ago in Midterm

PIN STAR WATCH 15 VIEWS

1

A clarification from Tobi on the power analysis question for the midterm:

"In Question 14, you're asked to consider samples sizes from 10 to **50** in steps of 5.

The waypoint in Question 15 (`load ("data/lm_results2.RData")`) reads in a data frame with samples sizes from 10 to **60** in steps of 5.

We'll make this consistent next time. For now, don't worry about the differences. If you'd like to avoid using the waypoint, you can either use the data frame from Question 14 with samples sizes from 10 to 50 or change it to compute one with sample sizes from 10 to 60."

Comment Edit Delete Endorse •••

Add comment

Recordings updated

Lecture recordings 2022

- Introduction
- Visualization I
- Visualization II
- Data wrangling I
- Data wrangling II
- Probability
- Simulation I
- Simulation II
- Modeling data
- Linear model I
- Linear model II
- Linear model III
- Linear model IV
- Power analysis
- Model comparison

contains another simulated
power analysis example

Homework 3 solutions

HW3 Solutions? #41

Anonymous
14 hours ago in **Homework – HW3**

PIN STAR WATCH 12 VIEWS

Hi, I'm wondering when the solutions to homework 3 will be posted? Thanks!

Comment Edit Delete Endorse •••

1 Answer

Tobi Gerstenberg STAFF
2 hours ago

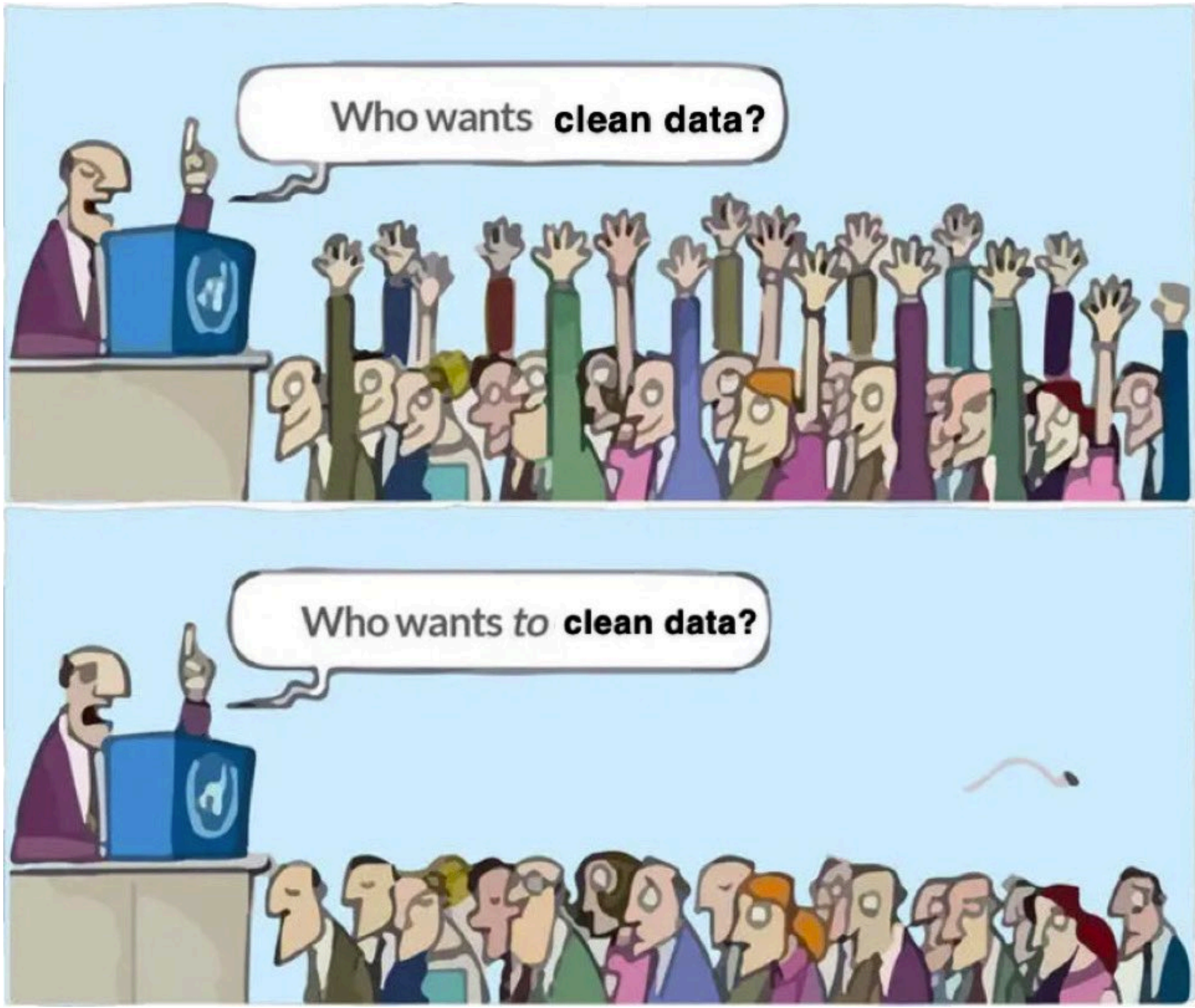
The solutions are up now. Sorry about the delay and thanks for the ping!

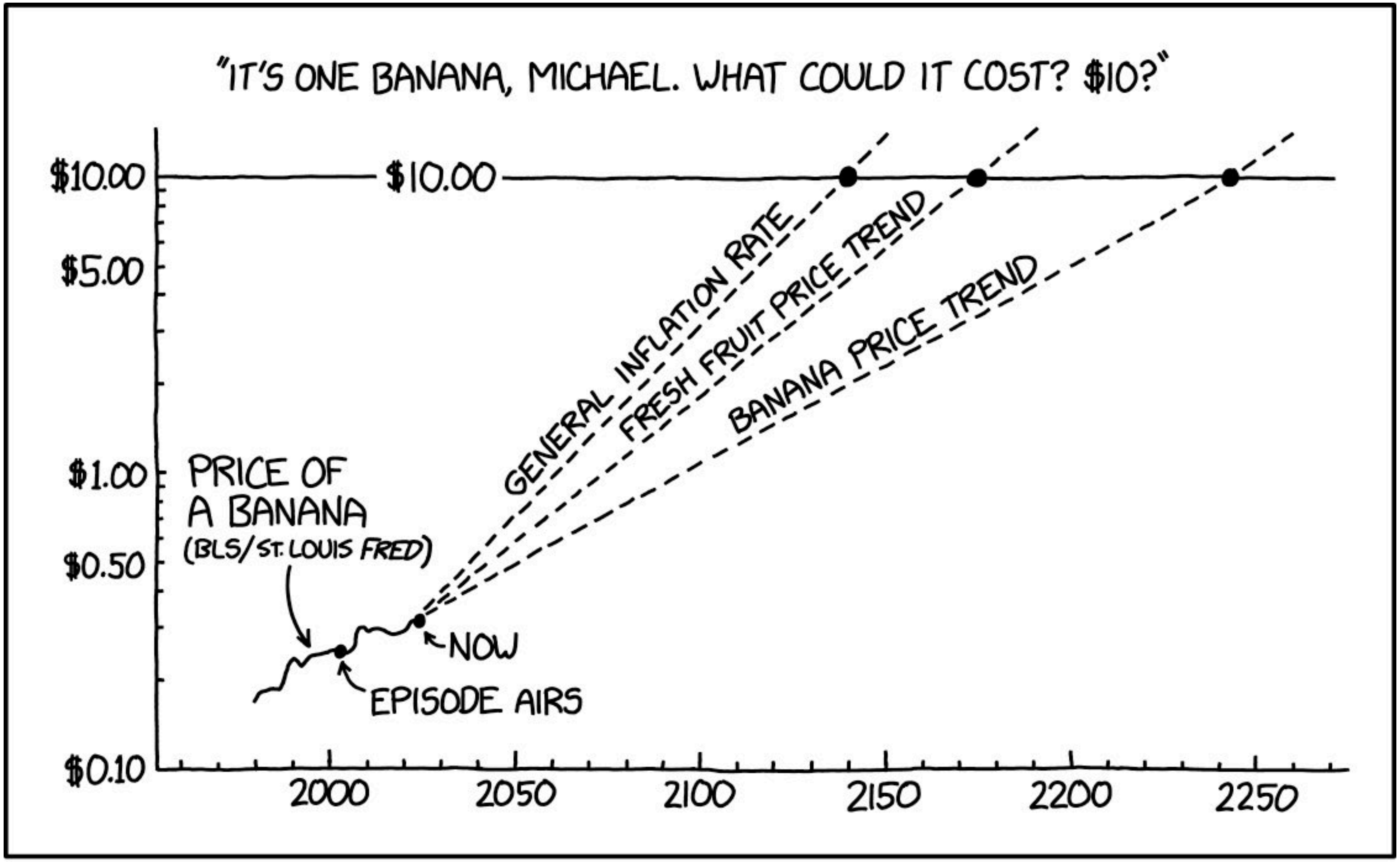
1

Comment Edit Delete Endorse •••

Add comment

Things that came up


Who wants clean data?
Who wants to clean data?

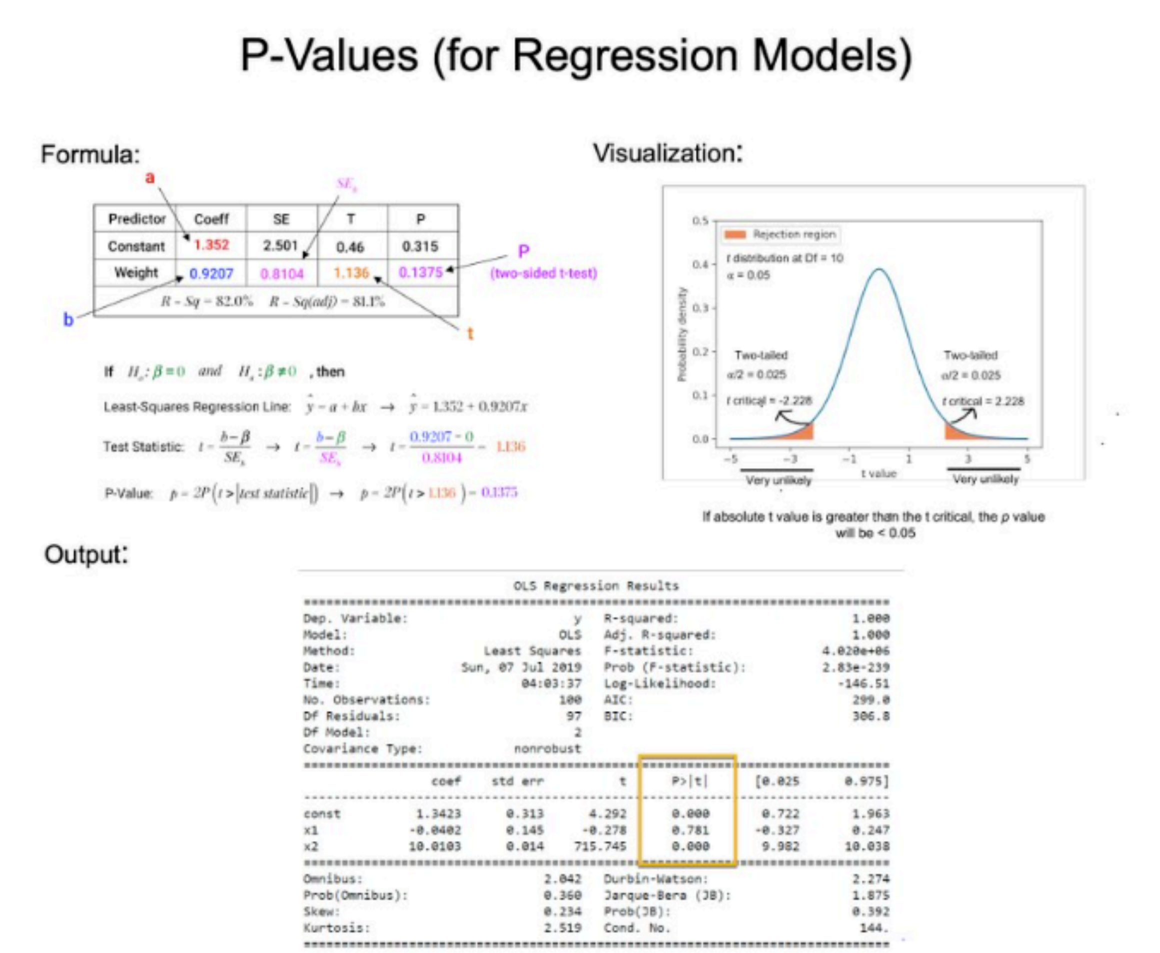


THAT LINE PROBABLY HAS ANOTHER CENTURY OR SO LEFT.

M. Bolton
@5_utr

Oh god another "data science influencer" claiming p-values are a measure of strength of the evidence against a null hypothesis, shoot me now 🙄

> **Matt Dancho (Business Science)** @mdancho84 · Feb 10
> Understanding P-Values is essential for improving regression models. In 2 minutes, learn what took me 2 years to figure out.
>
> 1. The p-value: A p-value, in statistics, is a measure used to assess the strength of the evidence against a null hypothesis....
> Show more



5:12 AM · Feb 11, 2024 · **152.7K** Views

18 28 383 298

$$P(D \mid H_0)$$

this is the p-value

$$P(H_0 \mid D)$$

this is ideally what we'd like to know

Plan for today

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

Quick recap

Quick recap: Unbalanced designs

Beware of unbalanced designs

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

```
Analysis of Variance Table

Response: balance
           Df Sum Sq Mean Sq F value  Pr(>F)
skill       1   74.3   74.28  4.2304 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
```

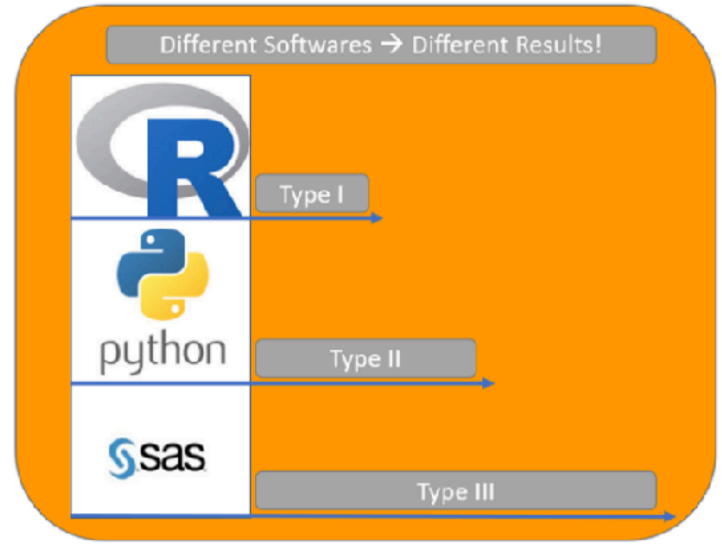
flipped the order

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

```
library("afex")

fit = aov_ez(id = "participant",
             dv = "balance",
             data = df.poker.unbalanced,
             between = c("hand", "skill"))
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!!

```
library("emmeans")

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

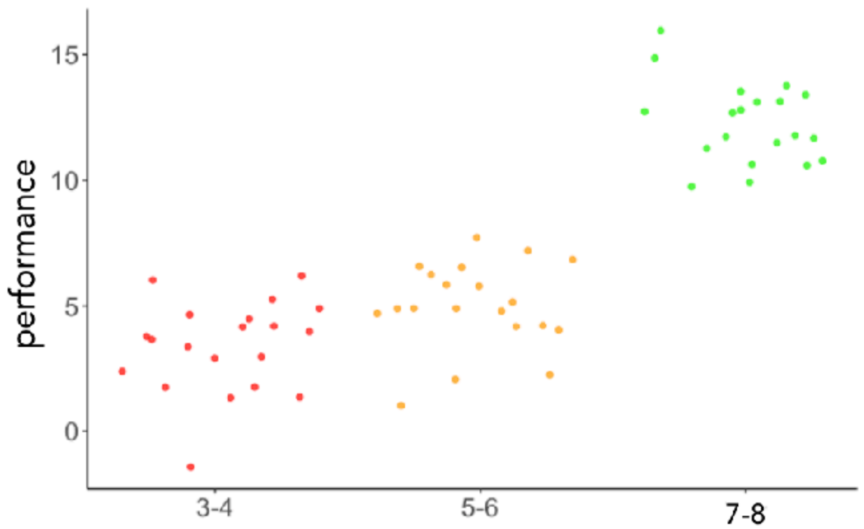
very handy function

```
model term dfl 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: Linear contrasts

Contrasts

Does performance increase with age?



Data from a hypothetical developmental study

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Does performance increase with age?

ANOVA

Does performance differ between age groups?

post-hoc tests

3-4 vs. 5-6

5-6 vs. 7-8

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

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Linear contrasts in R

```r
library("emmeans") # for calculating contrasts

#  fit the linear model
fit = lm(formula = performance ~ group,
         data = df.development)

# check factor levels
levels(df.development$group) [1] "3-4" "5-6" "7-8"

# define the contrasts of interest
contrasts = list(young_vs_old = c(-0.5, -0.5, 1),
                 three_vs_five = c(-0.5, 0.5, 0))

# compute significance test on contrasts
fit %>%
  emmeans("group",
          contr = contrasts,
          adjust = "bonferroni") %>%
  pluck("contrasts")
```

compute the results

```
[1] "3-4" "5-6" "7-8"
 contrast      estimate        SE df t.ratio p.value
 young_vs_old  16.093541 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
```

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Post hoc tests

```r
fit = lm(formula = performance ~ group,
         data = df.development)

# pairwise differences between all the groups
fit %>%
  emmeans(pairwise ~ group) %>%
  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
```

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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).

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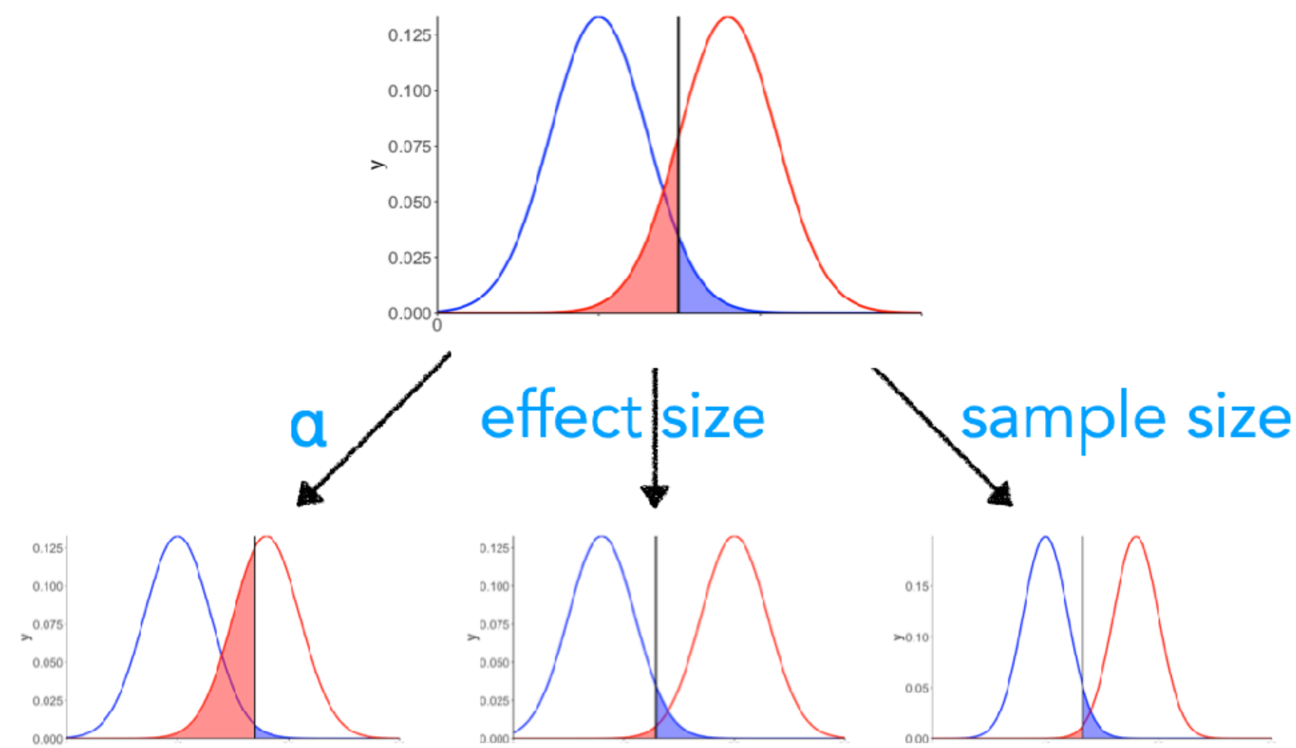
The knobs we can turn to affect power

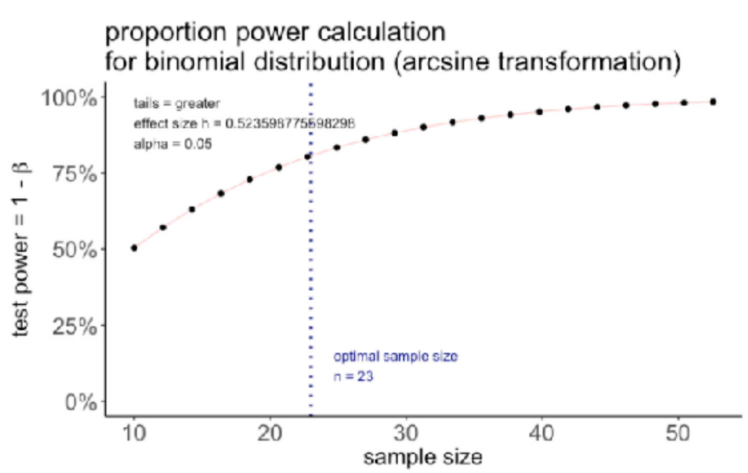


54

"pwr" package in R

Option 2

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



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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)

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Quick recap: Power analysis

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())
```

Simulating a power analysis

RStudio® 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 ...

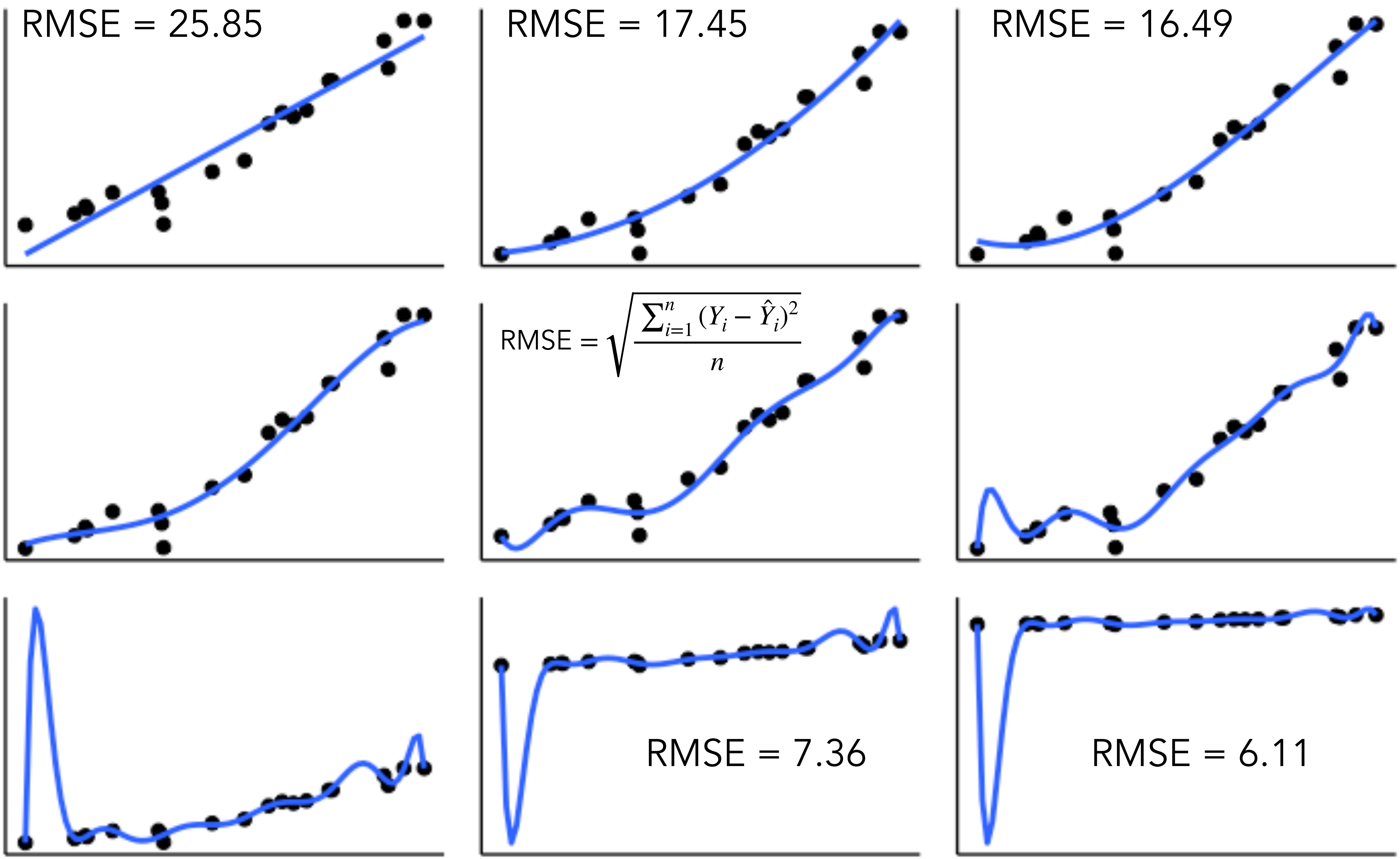
Model C	Model A
$\text{balance}_i = \beta_0 + \epsilon_i$	$\text{balance}_i = \beta_0 + \beta_1 \cdot \text{student}_i + \beta_2 \cdot \text{age}_i + \epsilon_i$ ✓
$\text{balance}_i = \beta_0 + \beta_1 \cdot \text{student}_i + \epsilon_i$	$\text{balance}_i = \beta_0 + \beta_1 \cdot \text{student}_i + \beta_2 \cdot \text{age}_i + \epsilon_i$ ✓
$\text{balance}_i = \beta_0 + \beta_1 \cdot \text{student}_i + \epsilon_i$	$\text{balance}_i = \beta_0 + \beta_1 \cdot \text{age}_i + \epsilon_i$ ✗
$\text{balance}_i = \beta_0 + \beta_1 \cdot \text{student}_i + \epsilon_i$	$\text{balance}_i = \beta_0 + \beta_1 \cdot \text{age}_i + \beta_2 \cdot \text{degree}_i + \epsilon_i$ ✗

Tools for model comparison

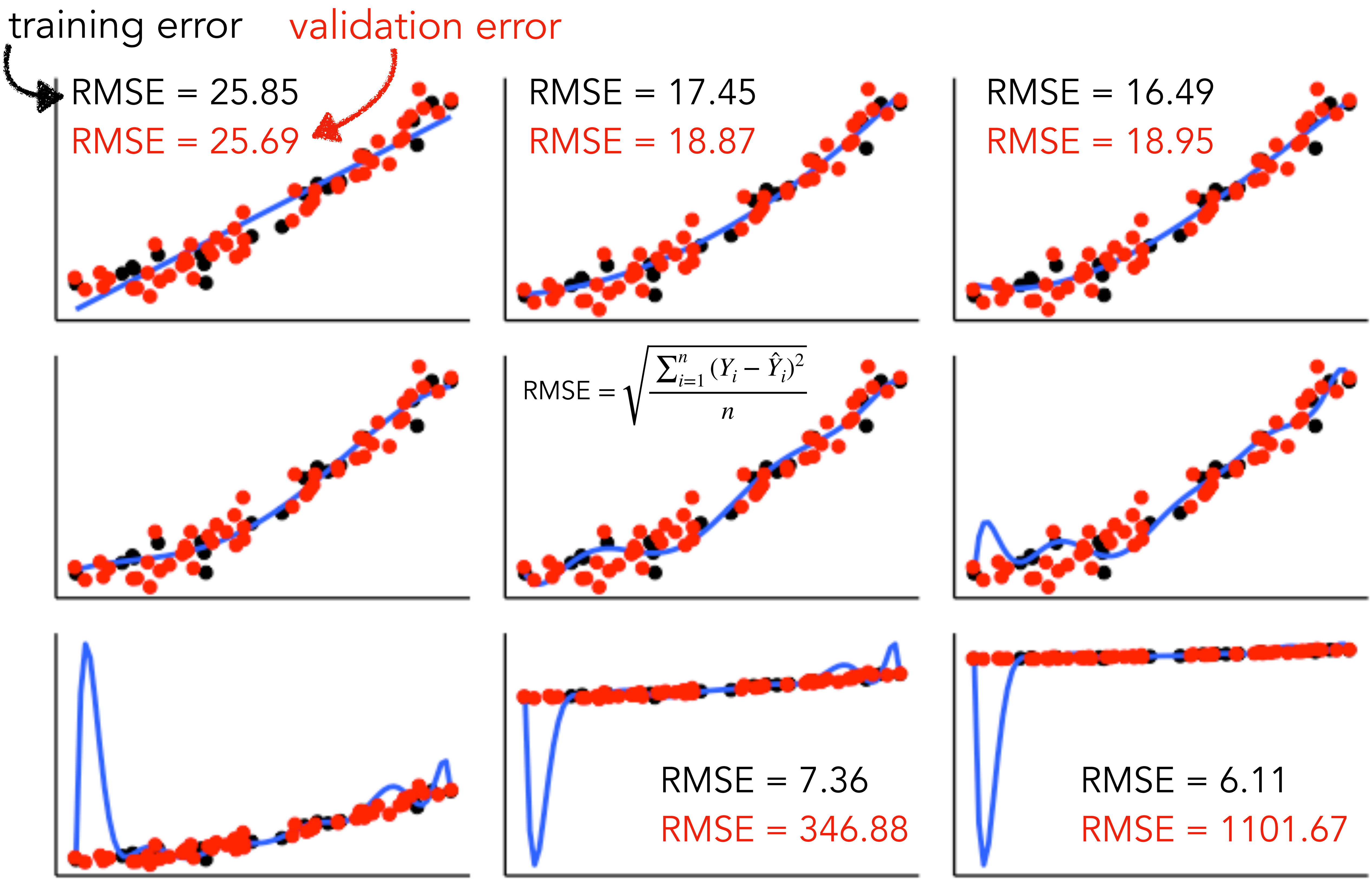
- **`anova()`**: compare a compact model with an augmented model via the F-test
  - problem: only works for nested models (where the augmented model contains all the predictors of the compact model and more)
- **What if we want to compare models that aren't nested?**
  - Cross-validation
  - AIC and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

Cross-validation

Which model describes the data best?

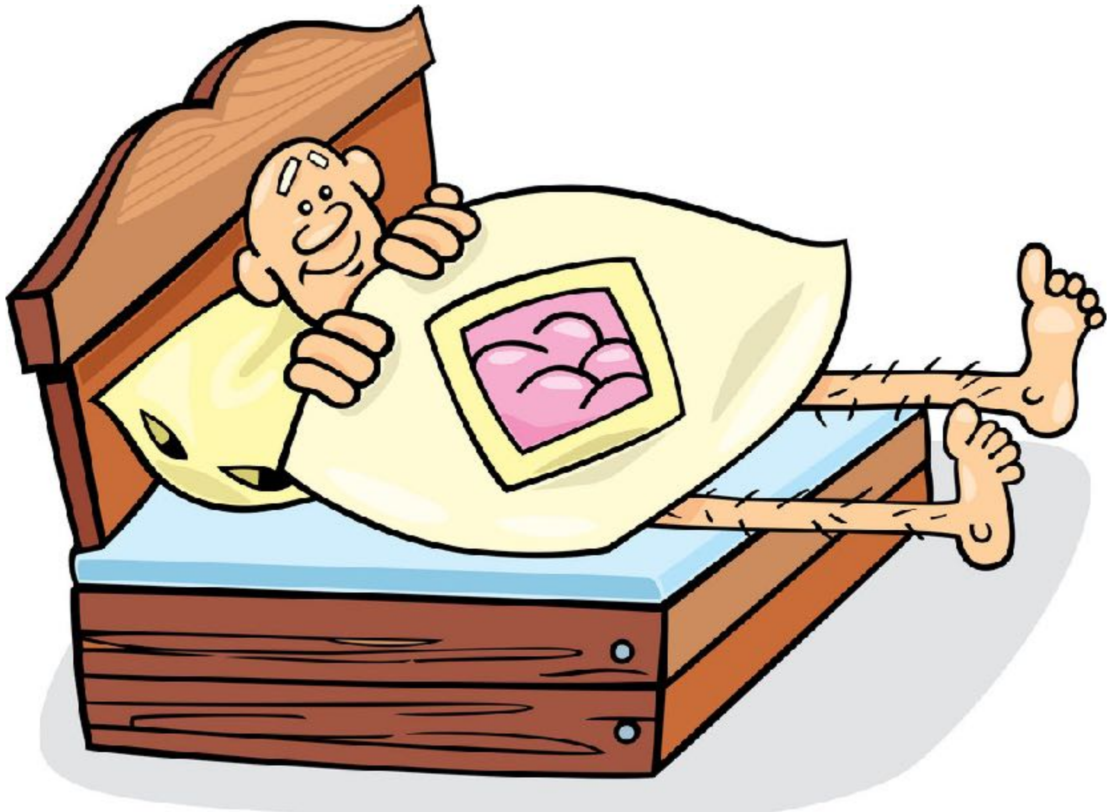


Which model describes the data best?



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

Underfitting vs. Overfitting



ONE WAY TO EXPLAIN UNDERFITTING

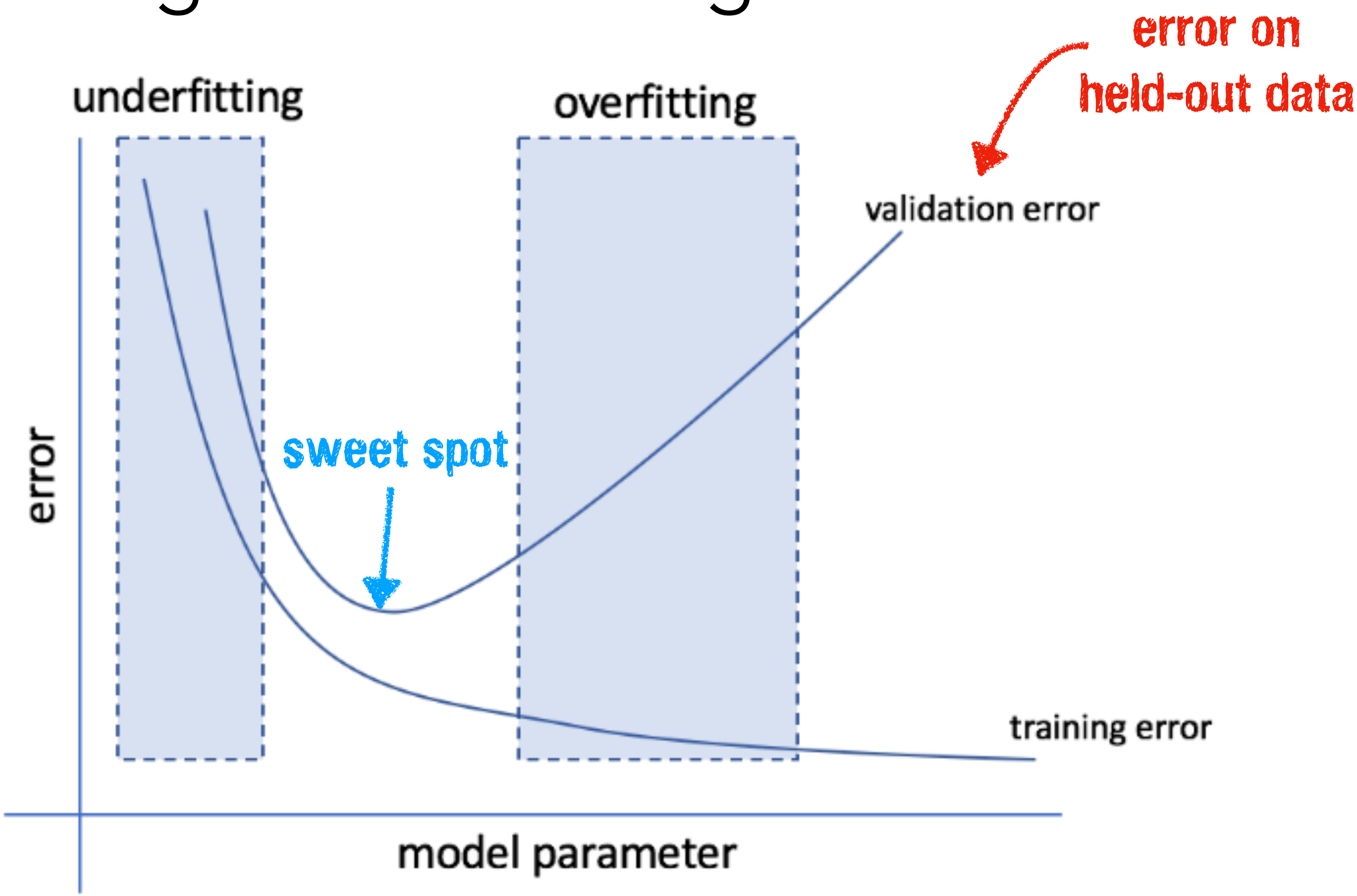
Underfitting vs. Overfitting

- **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

non-inspirational quote

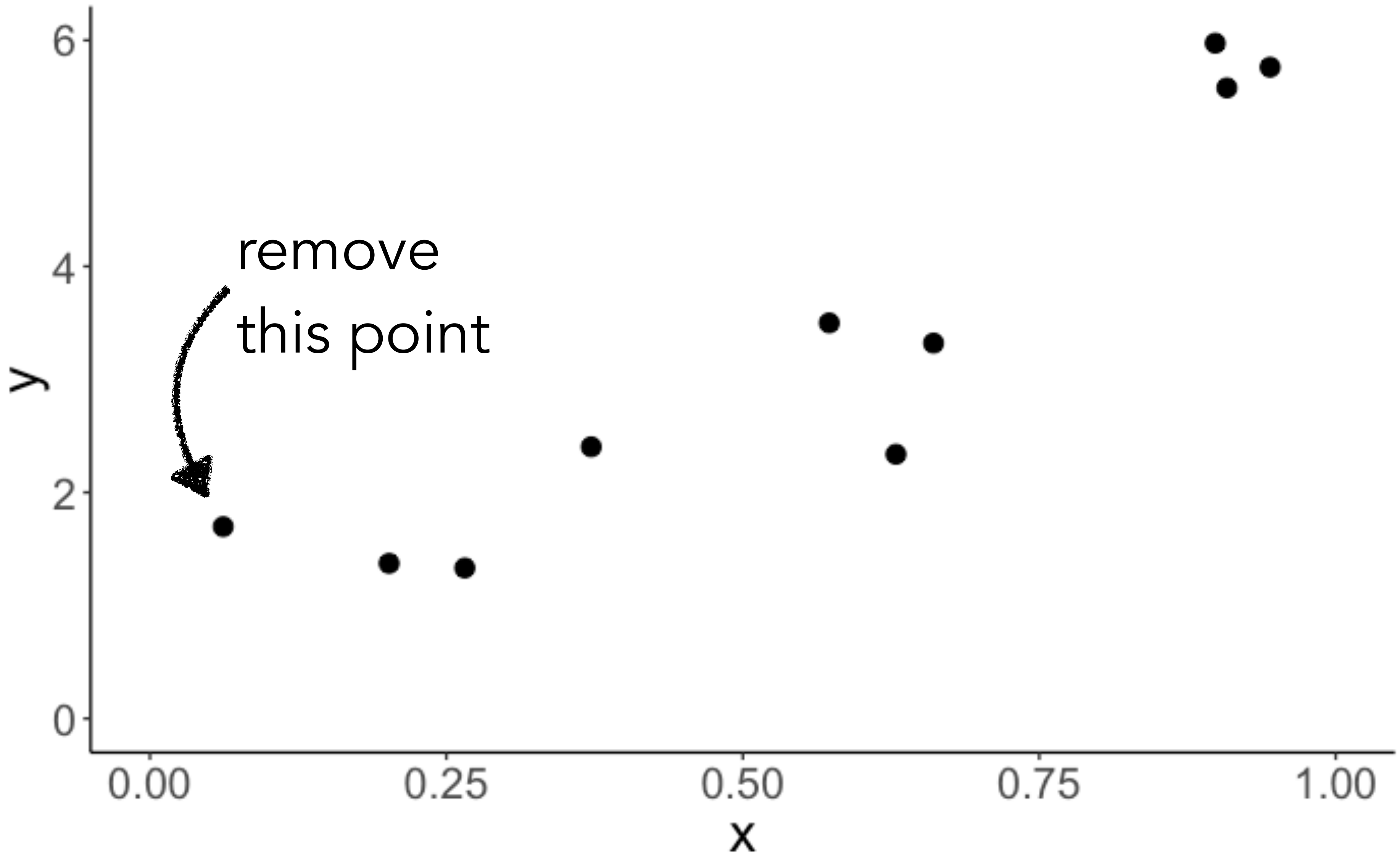
LOO

Leave one out cross-validation

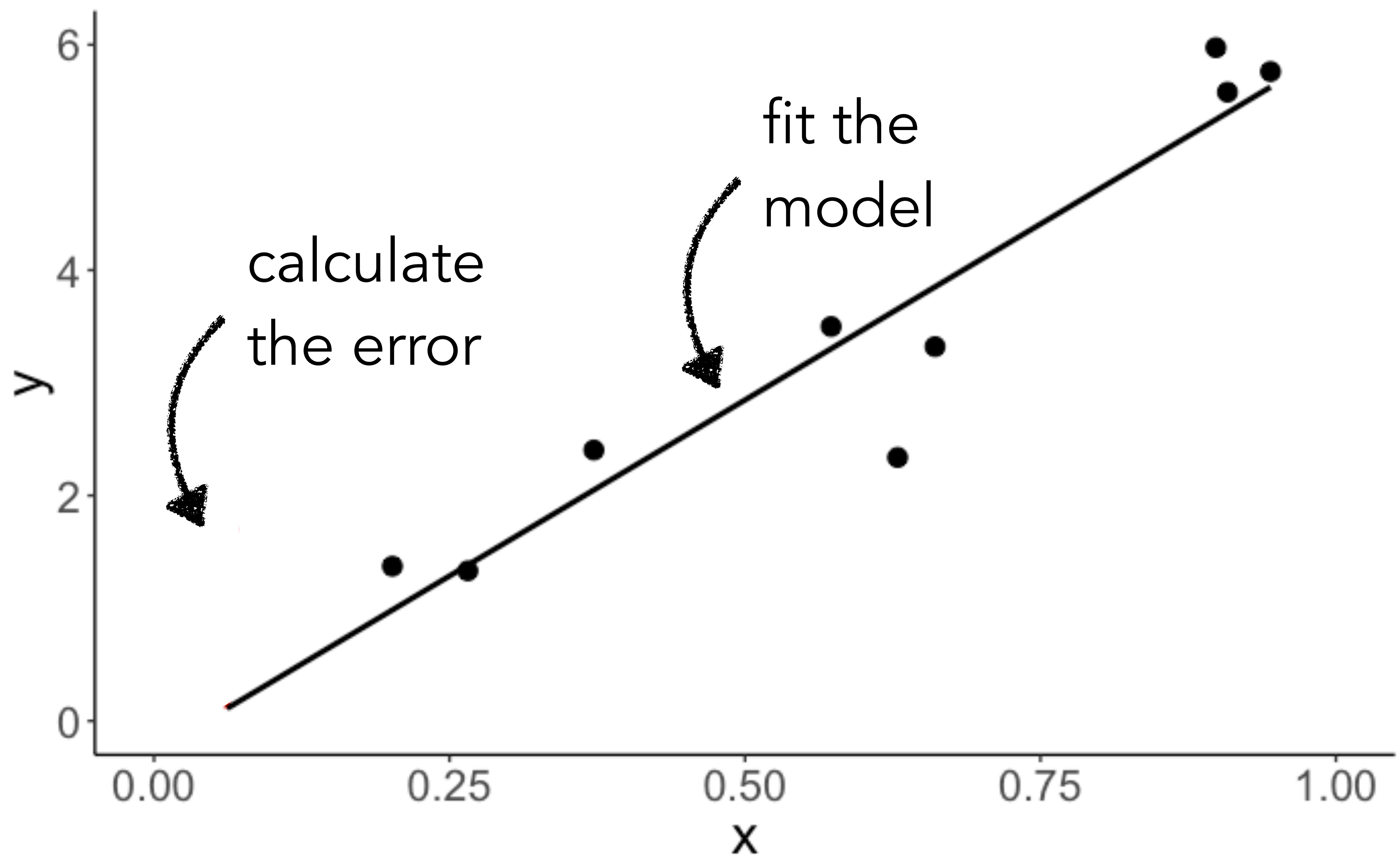
- train the model on all the data points except for one
- calculate the prediction error for the held-out data point

repeat for all data points

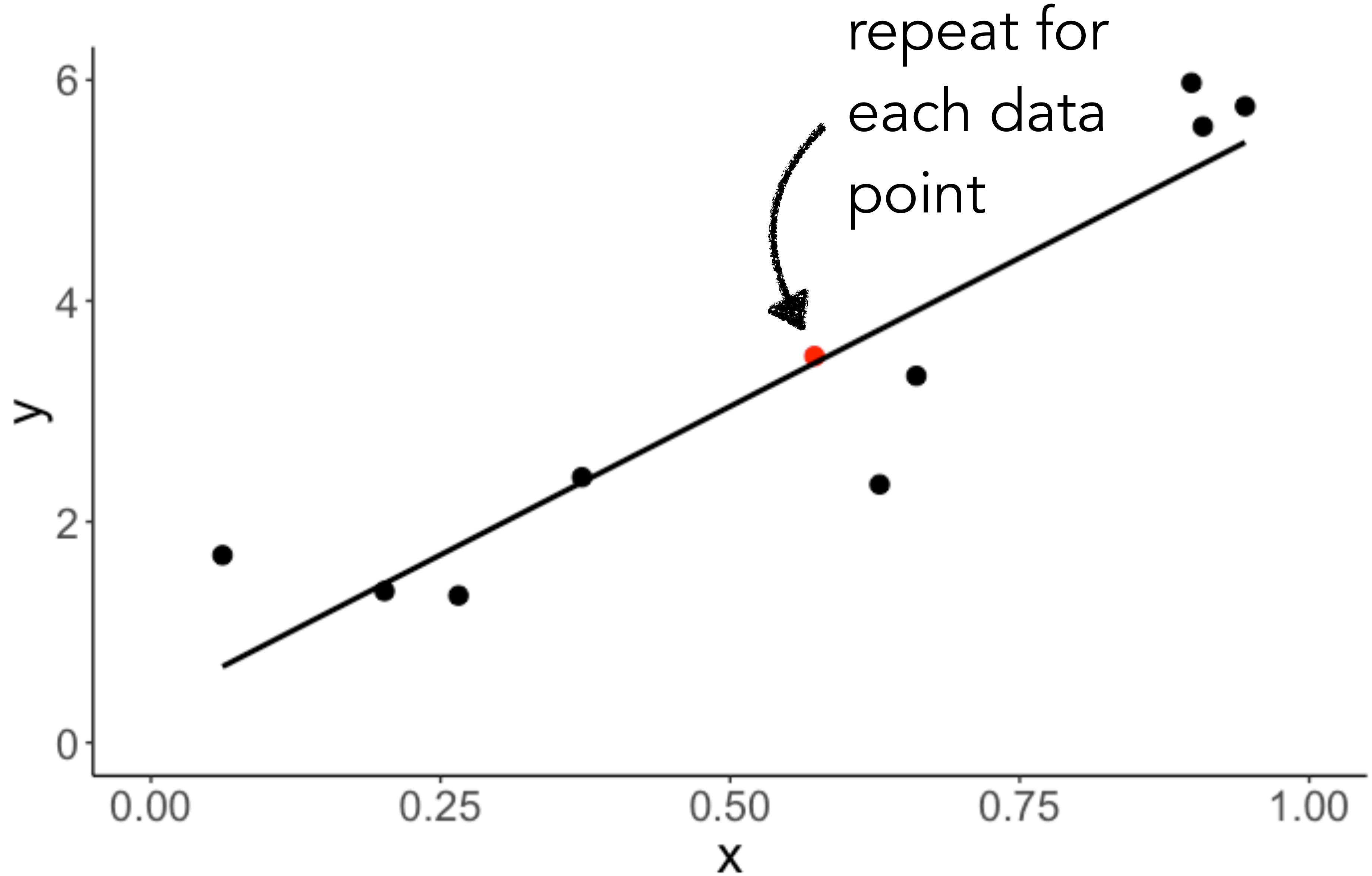
Leave one out cross-validation



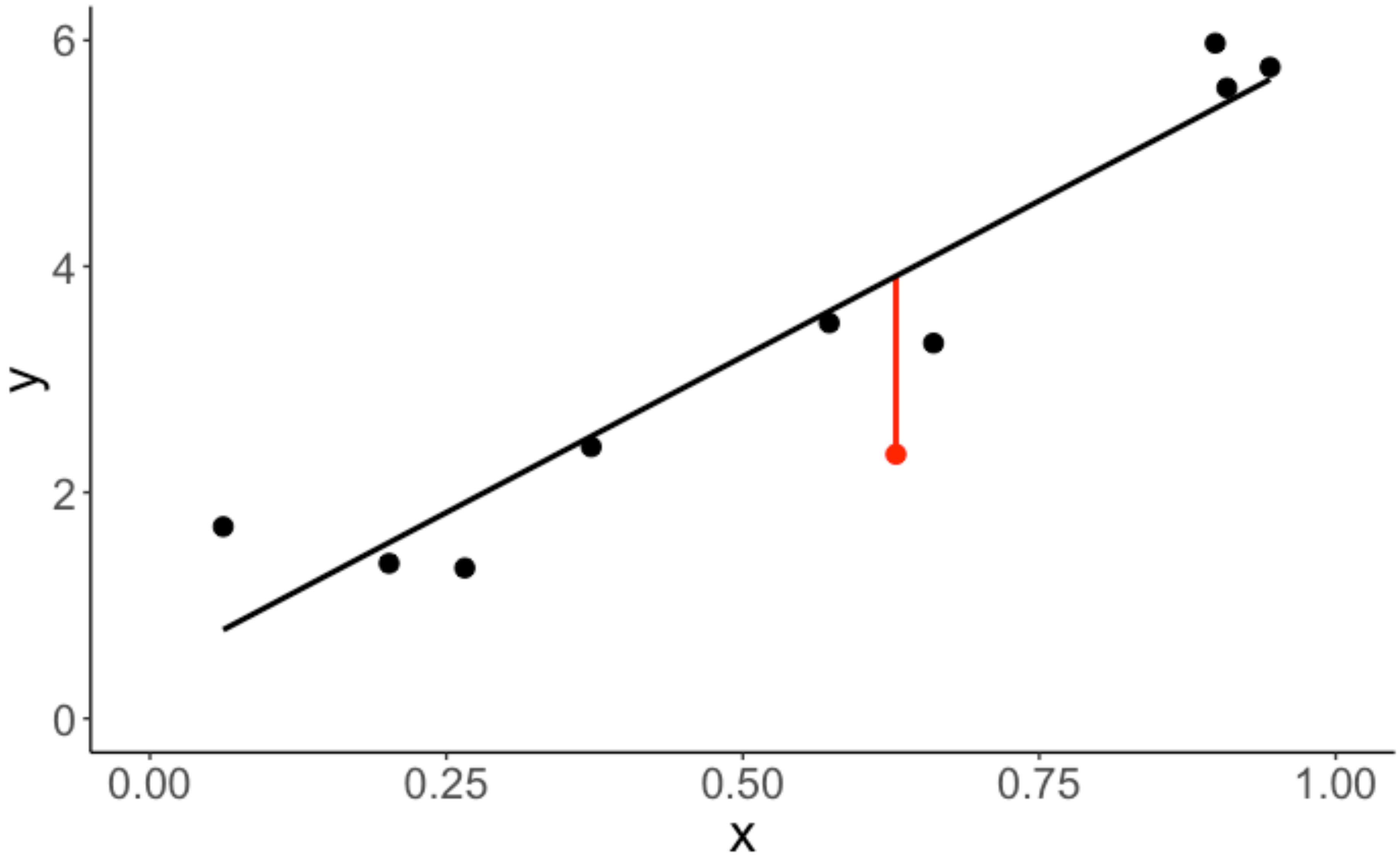
Leave one out cross-validation



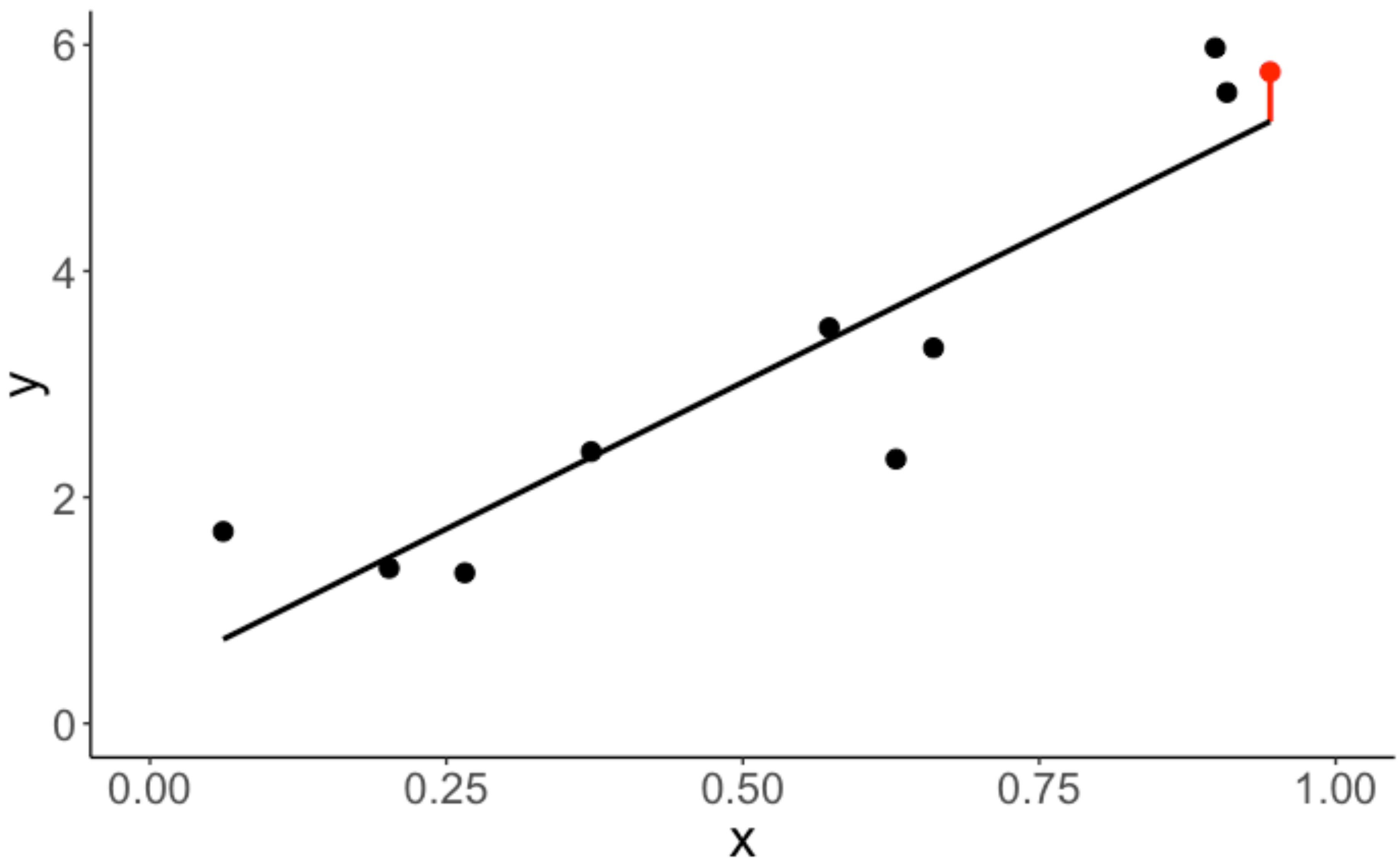
Leave one out cross-validation



Leave one out cross-validation

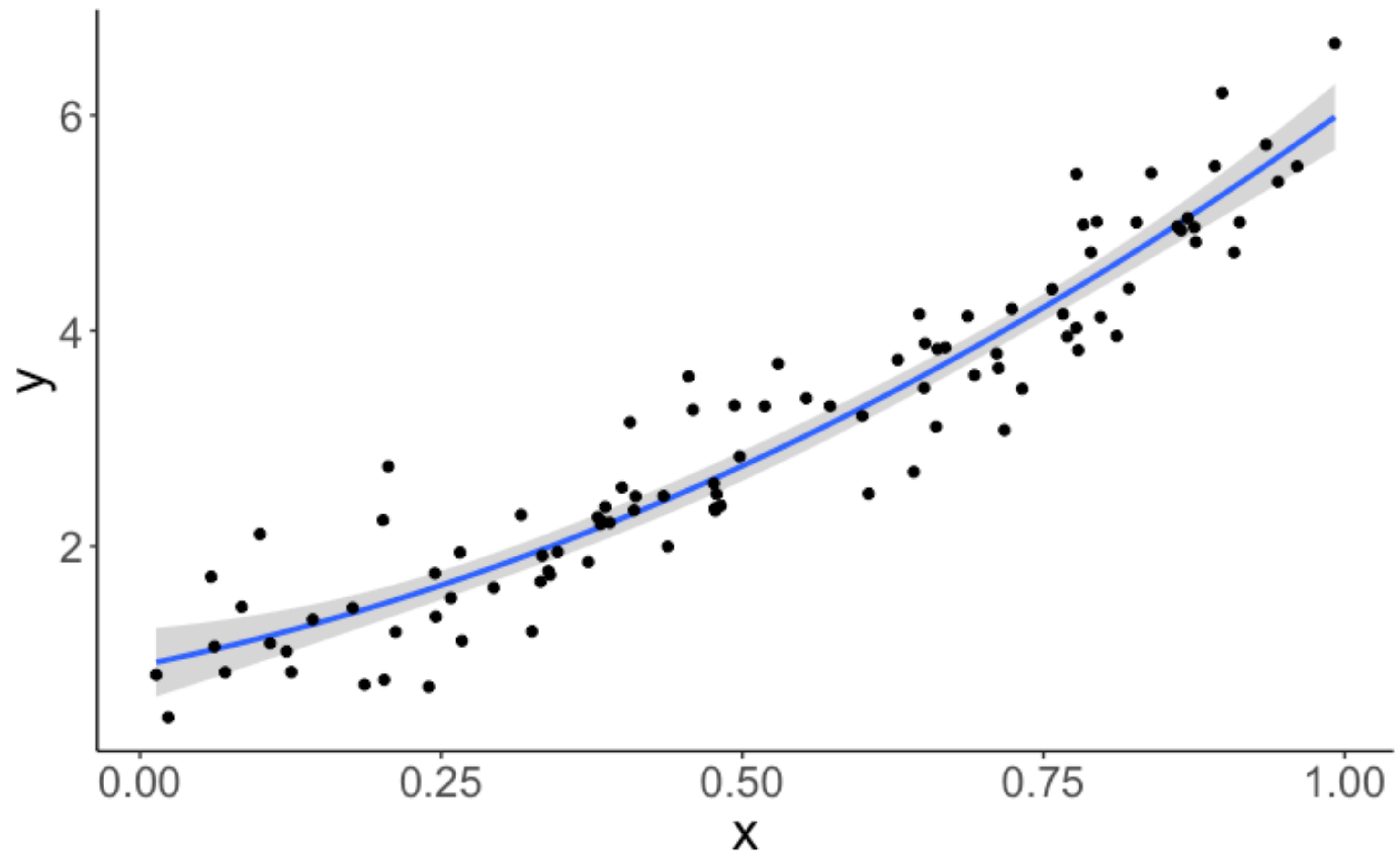


Leave one out cross-validation



Leave-one out crossvalidation

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

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



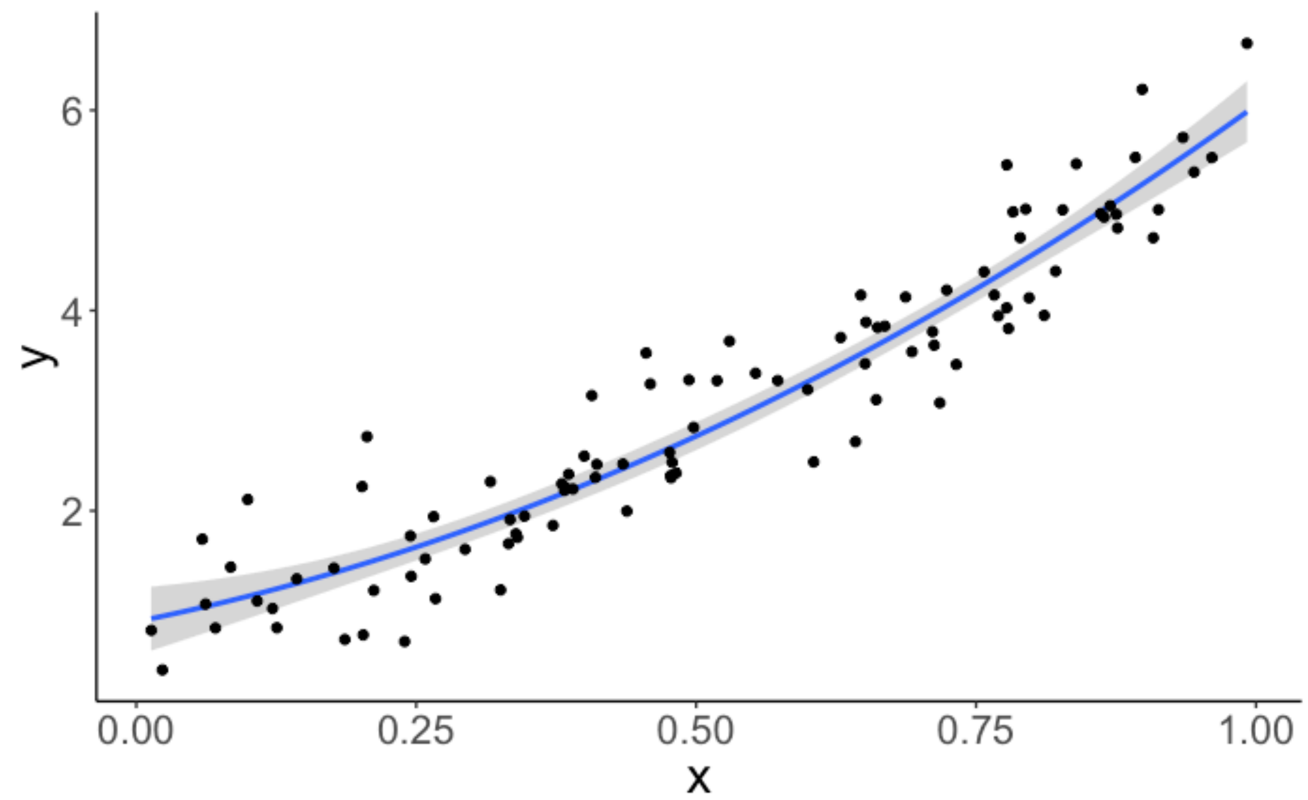

```r

# 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 $\widehat{y}_i = b_0 + b_1 \cdot x_i$

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

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

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

Leave-one out crossvalidation

```r
library("modelr")

df.cross = df.data %>%
  crossv_loo() %>% # function which generates training and test data sets
  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)))
```

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

```r
library("modelr")

df.cross = df.data %>%
  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

```
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 = .))) %>%
```

fit three different models to the training data set

Leave-one out crossvalidation

```r
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

```r
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?

$\boxed{\textbf{XX}}$

k-fold cross validation

k-fold crossvalidation

Full data set

Iteration 1	Test	Train	Train	Train	Train
Iteration 2	Train	Test	Train	Train	Train
Iteration 3	Train	Train	Test	Train	Train
Iteration 4	Train	Train	Train	Test	Train
Iteration 5	Train	Train	Train	Train	Test

k-fold crossvalidation

k-fold crossvalidation

```r
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)
```

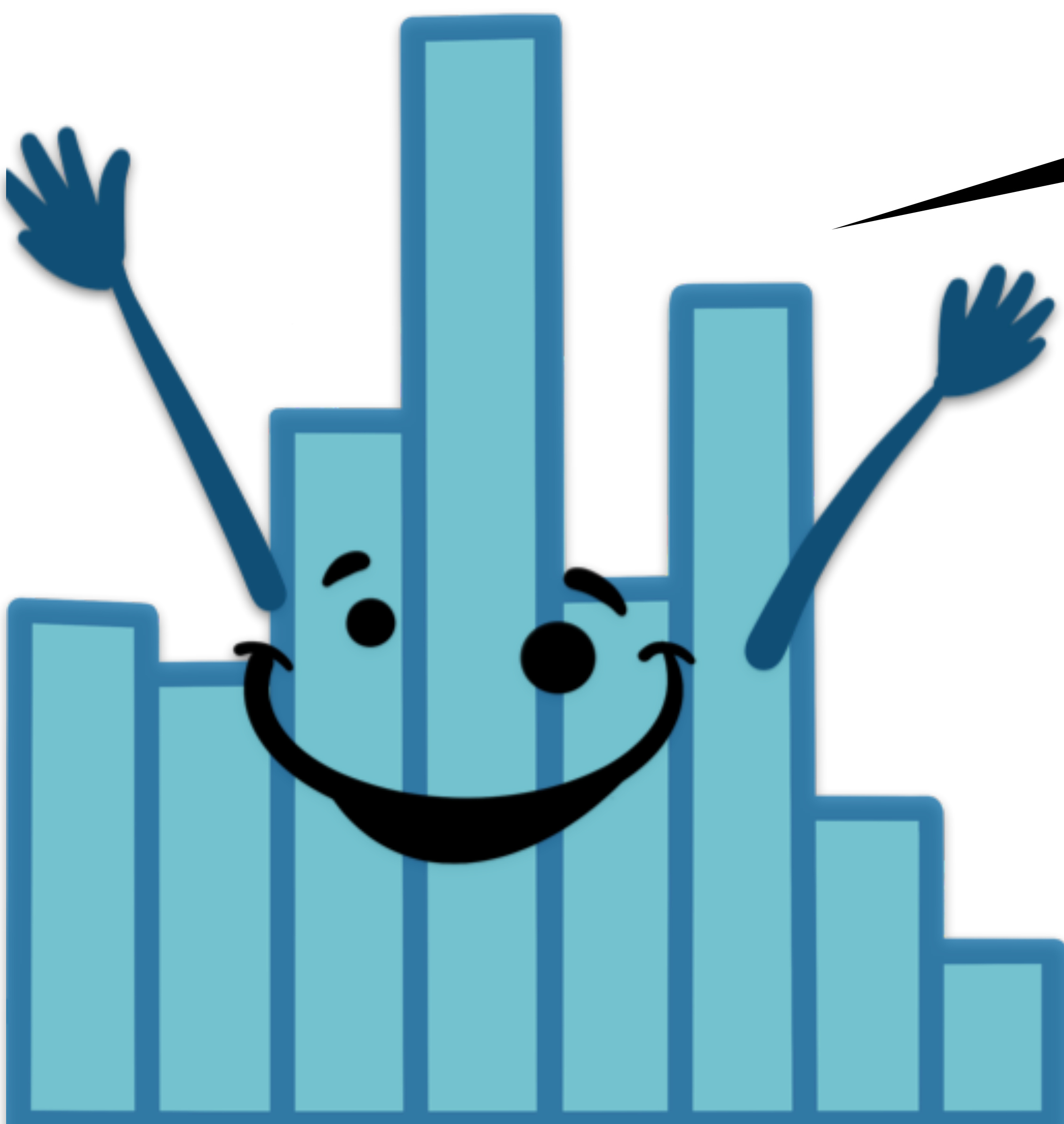
number of
training-test splits

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, ...

02:00

stretch break!



RStudio®

time

AIC and BIC

AIC and BIC

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

not that much Bayesian about it ...

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

?

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

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

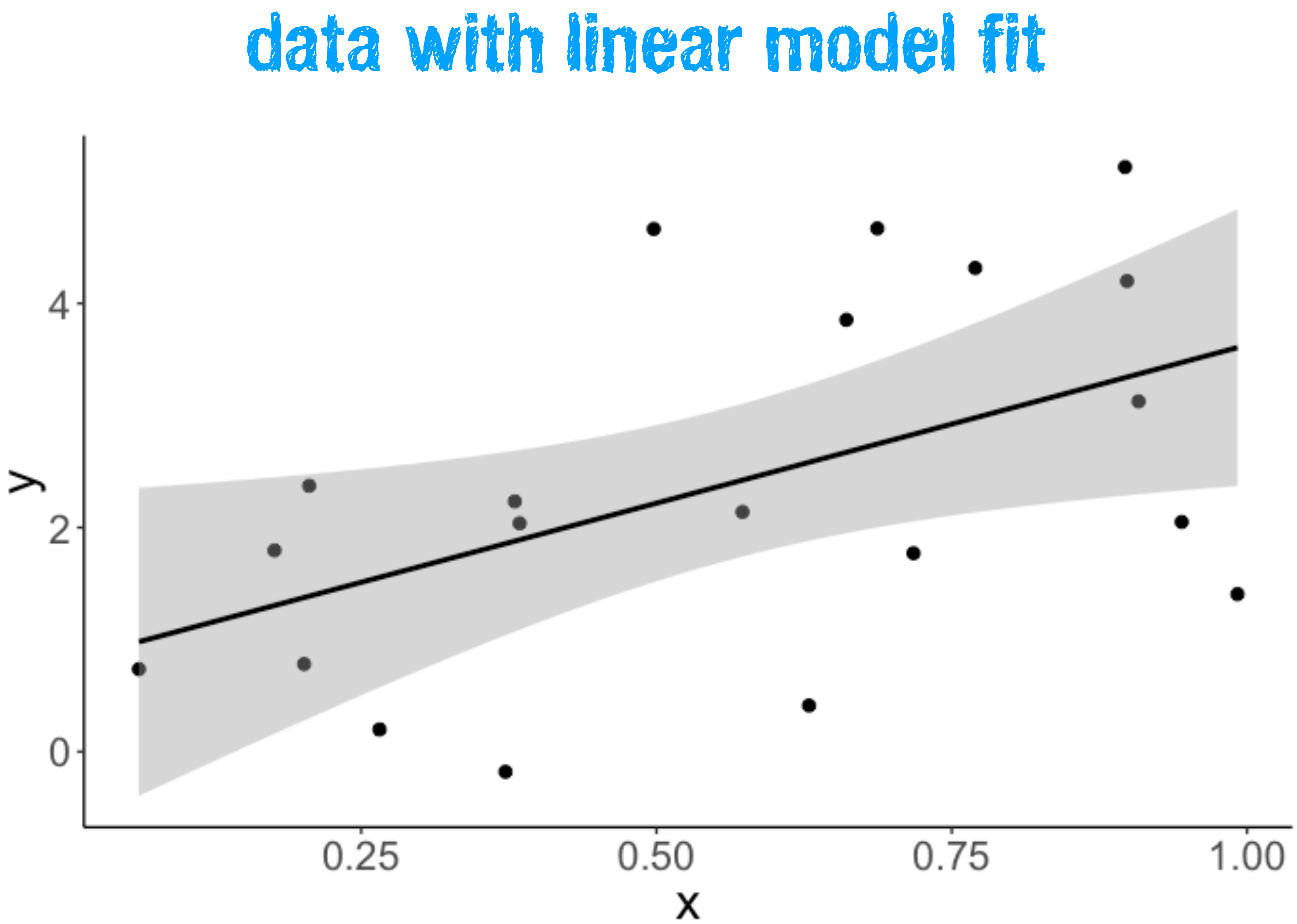
k = number of parameters in the model

n = number of observations

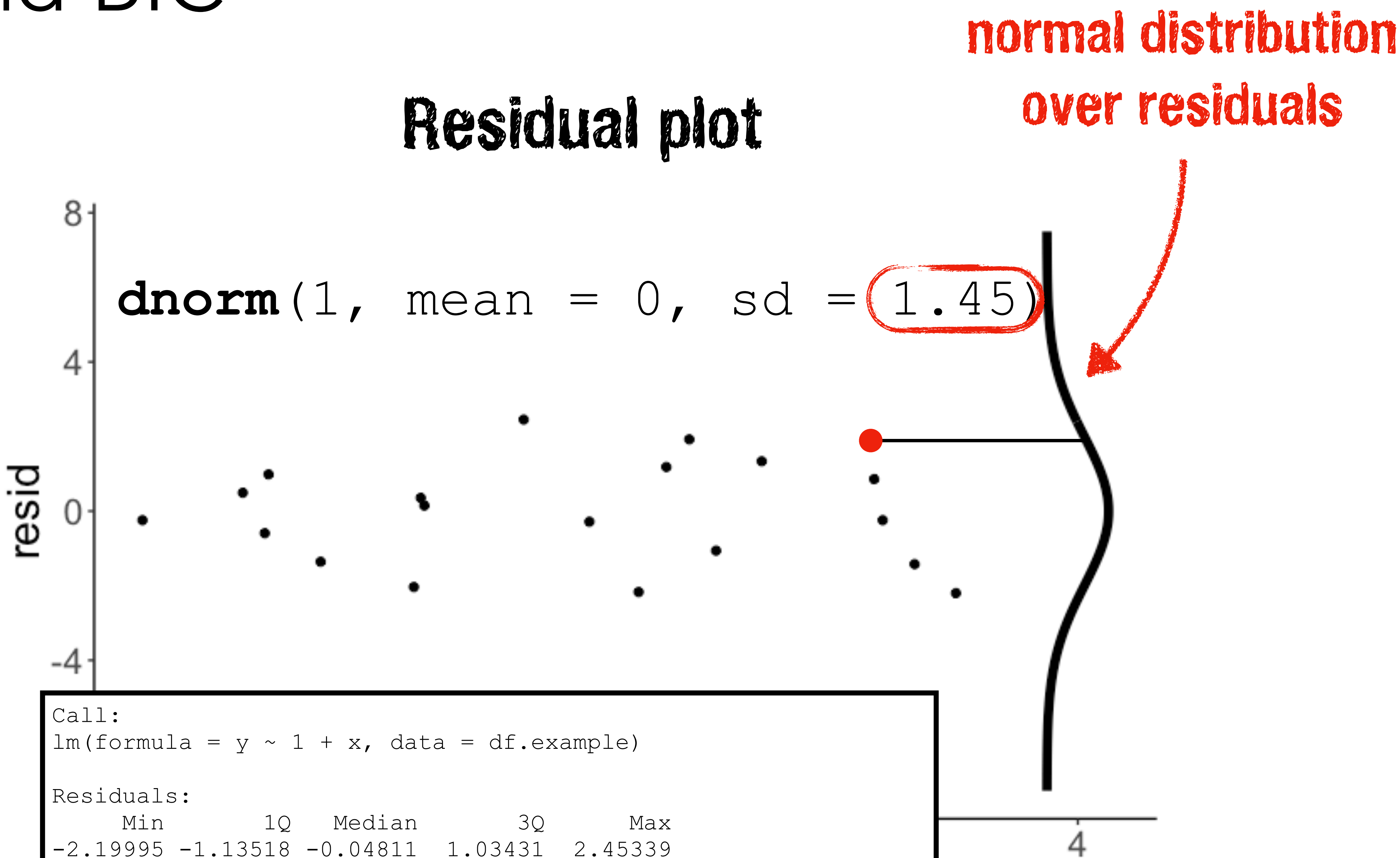
AIC and BIC

- 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

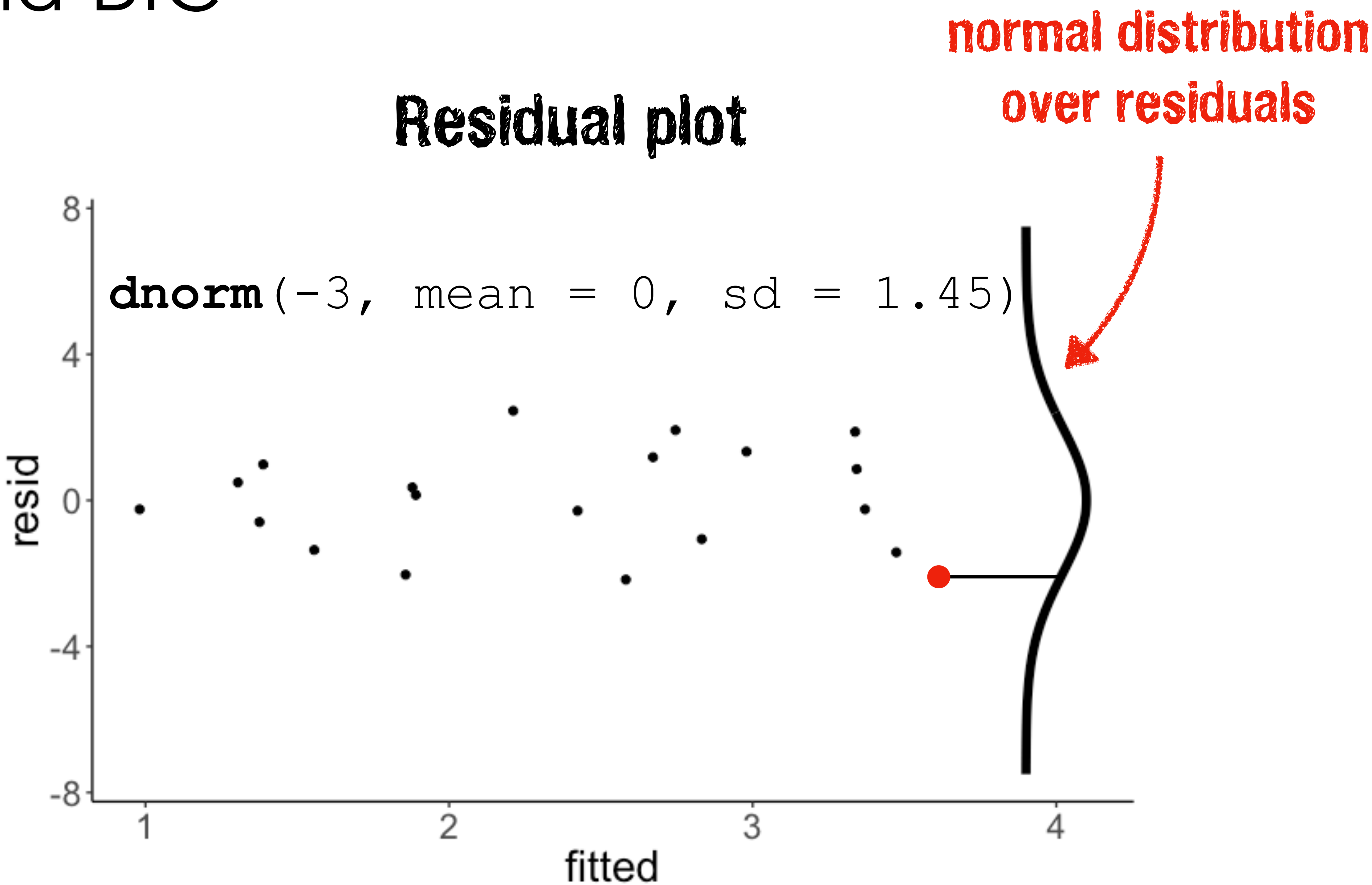


AIC and BIC




```
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
```

```r
# 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

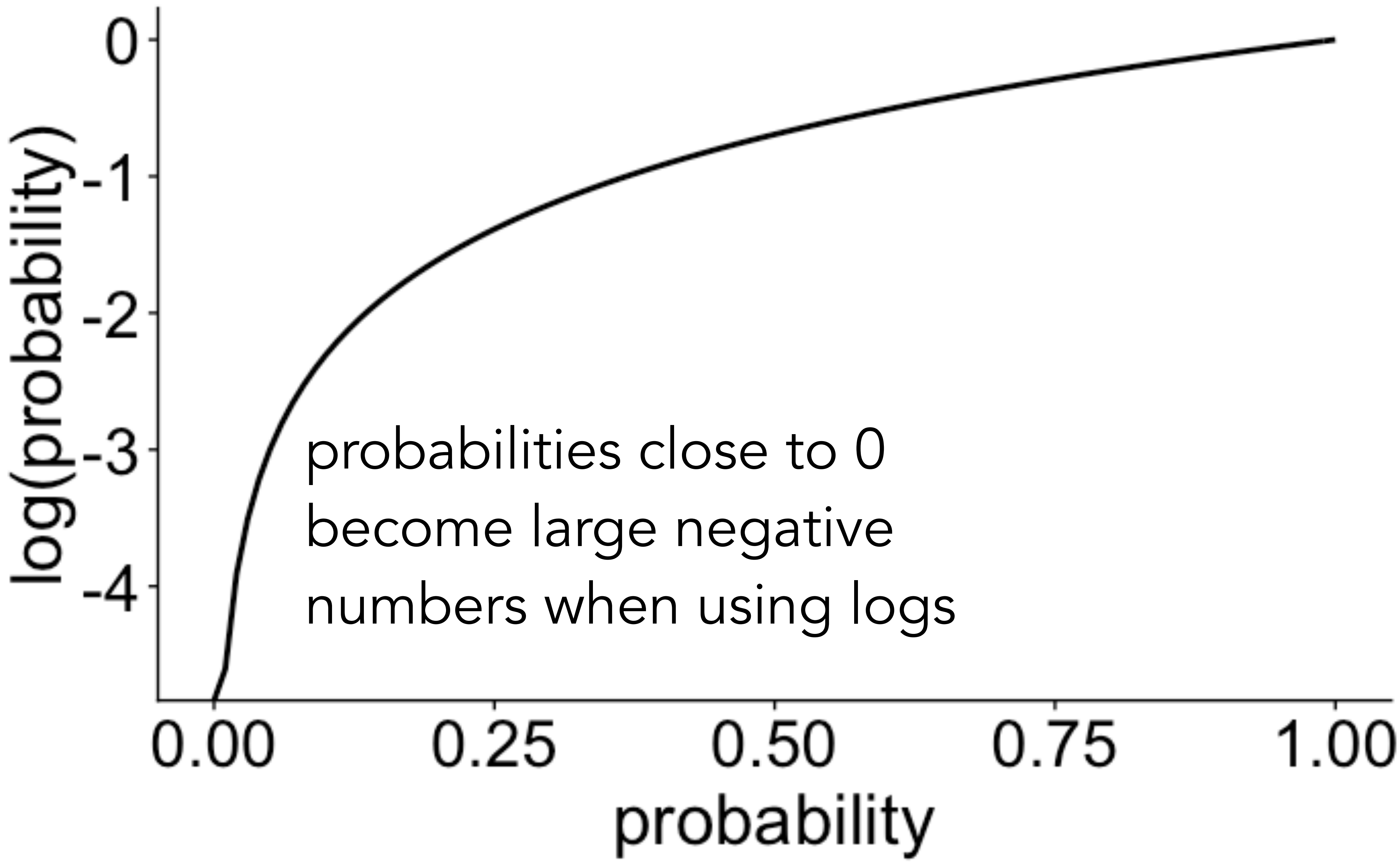
inferred standard deviation of the error

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

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

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

`log()` is your friend!



Clue guide to probability

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

- $p(\text{Prof Plum, candle stick}) =$

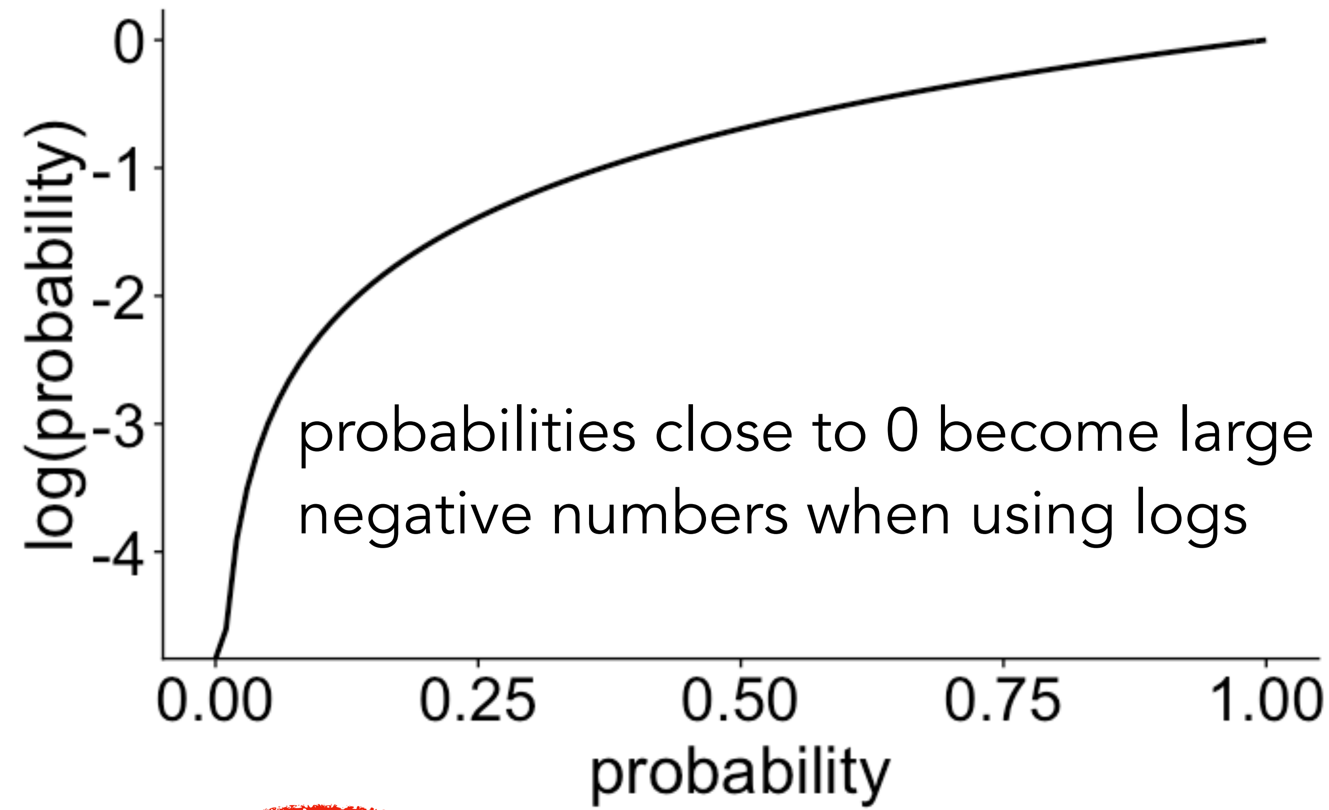
  $p(\text{Prof Plum}) \cdot p(\text{candle stick}) =$

$$\frac{1}{6} \cdot \frac{1}{6} = \frac{1}{36}$$

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`

summing logs

number becomes large but that's ok

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

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`

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

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)
```

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AIC and BIC

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

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

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.

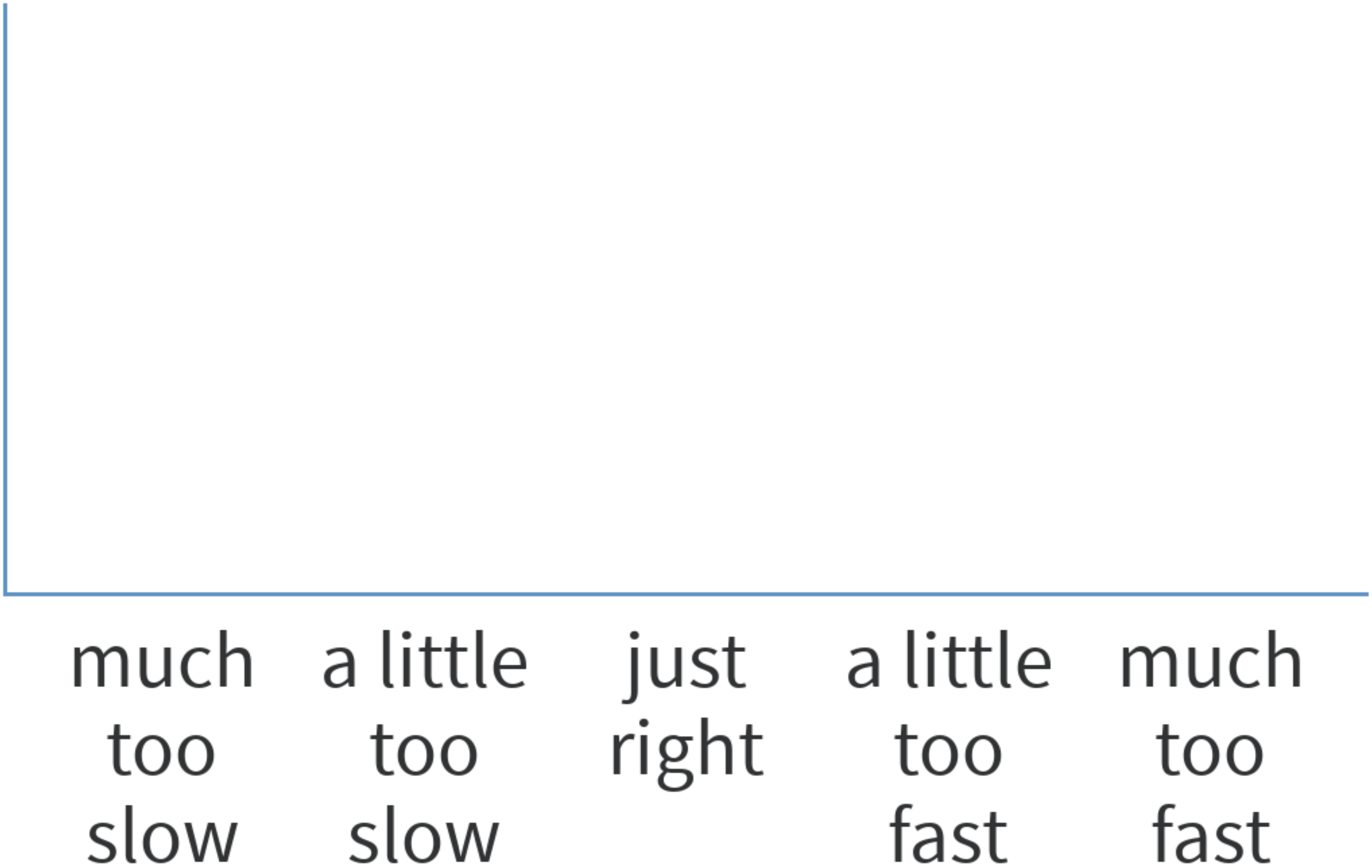
Model	*r*	RMSE	BIC
Difference & pivotality	.86 (.66, .95)	10.56 (6.17, 17.21)	158.59
Difference	.70 (.30, .90)	26.92 (16.4, 40.6)	209.74
Pivotality	.63 (.41, .77)	14.23 (11.39, 17.54)	199.53
Optimality	.66 (.42, .84)	14.55 (10.54, 17.91)	199.47

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

How was the pace of today's class?



How happy were you with today's class overall?

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

Answers to this poll are anonymous

Thank you!