

**Welcome to week 14!**

**A quicky review!**

**Emphasis on Final will be material  
listed here & in todays lecture.**

# Hypothesis Testing Framework (Ch. 4-6)

The general outline of the process:

1. Set the hypotheses.

For a single proportion this will look like:

$H_0: p = \text{null value}$

$H_A: p < \text{or } > \text{ or } \neq \text{ null value}$

2. Check assumptions and conditions

3. Calculate a test statistic and a p-value

4. Make a decision, and interpret it in context

- If p-value  $< \alpha$ , reject  $H_0$ ,  
there is sufficient evidence for  $[H_A]$
- If p-value  $> \alpha$ , do not reject  $H_0$ ,  
there is not sufficient for evidence for  $[H_A]$

Provides a rigorous way  
to determine the answer  
with a specific level of  
confidence.

English



Math



English

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(a) normal, large sample

(b) normal?, small sample

(c) observations & theory

## Test Statistics

(a) Z-score  $\rightarrow P(Z)$

(b) T-Score  $\rightarrow P(T)$

(c)  $\chi^2 \rightarrow P(\chi^2)$

# Anatomy of a test statistic

The general form of a test statistic is

Only tricks are:  
(1) picking what the point and null values are based on our hypotheses

$$\frac{\text{point estimate} - \text{null value}}{\text{SE of point estimate}}$$

(2) what the form of the standard errors is based on what our underlying distribution looks like (normal, t-distribution,  $\chi^2$ )

This construction is based on

- identifying the difference between a point estimate and an expected value if the null hypothesis was true, and
- standardizing that difference using the standard error of the point estimate.

These two ideas will help in the construction of an appropriate test statistic for count data.

# Decision errors (cont.)

There are two competing hypotheses: the null and the alternative. In a hypothesis test, we make a decision about which might be true, but our choice might be incorrect.

		Decision	
		fail to reject $H_0$	reject $H_0$
Truth	$H_0$ true	✓	Type 1 Error
	$H_A$ true	Type 2 Error	✓

A **Type 1 Error** is rejecting the null hypothesis when  $H_0$  is true.

A **Type 2 Error** is failing to reject the null hypothesis when  $H_A$  is true.

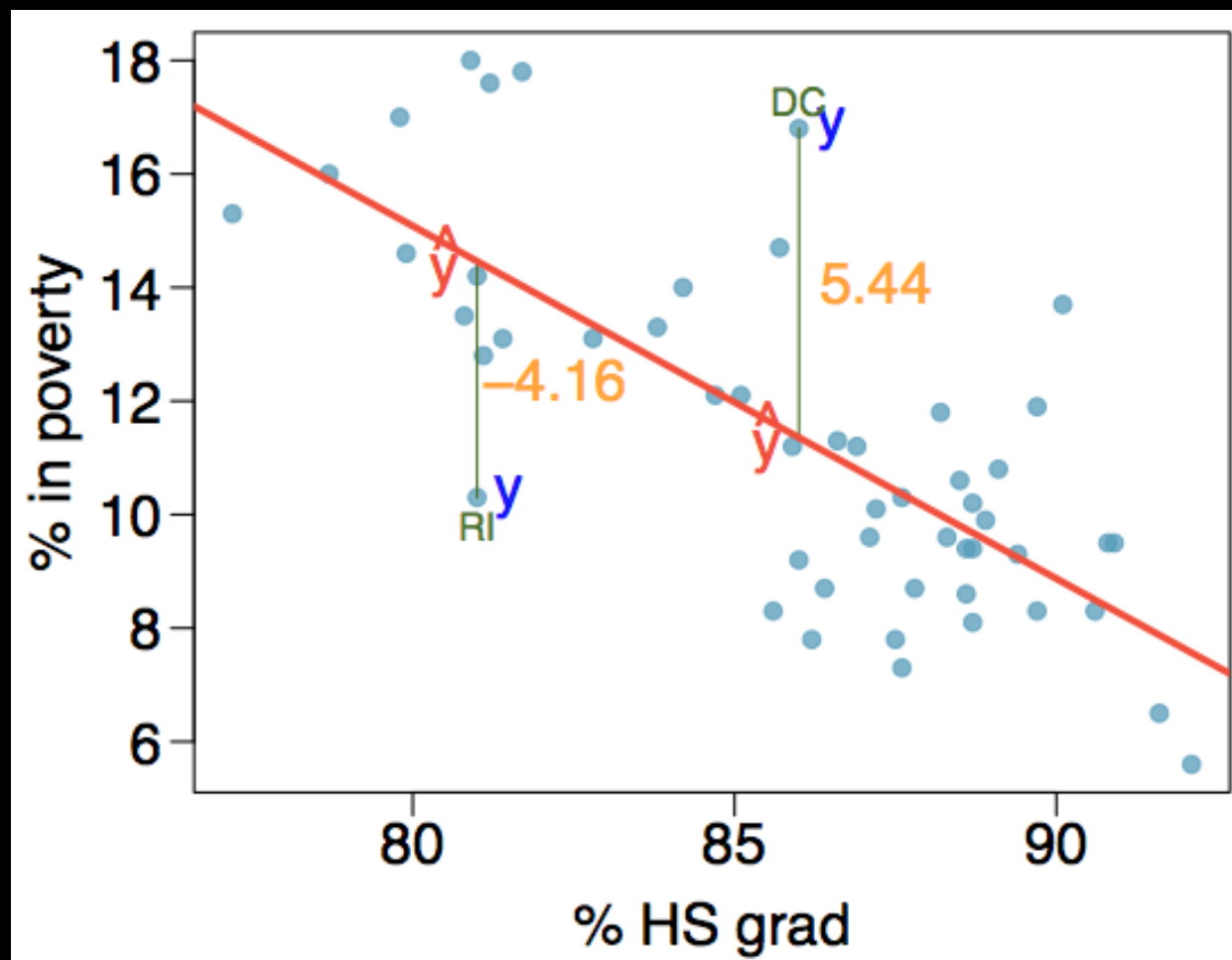
We (almost) never know if  $H_0$  or  $H_A$  is true, but we need to consider all possibilities.

# Residuals

**Residuals** are the leftovers from the model fit:  $\text{Data} = \text{Fit} + \text{Residual}$

Aka a **residual** is the difference between the observed ( $y_i$ ) and predicted  $\hat{y}_i$ .

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



Here is a depiction of the residuals - how far each point is from our fitted line.

# p-values for Linear Regression

What's really going on here? Just the same calculations we've been doing the past few weeks!

p-value > 0.05  
so we fail to reject  $H_0$

```
> summary(myLine)

Call:
lm(formula = BAC ~ Beers, data = BB)

Residuals:
    Min       1Q   Median       3Q      Max
-0.027118 -0.017350  0.001773  0.008623  0.041027

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.012701   0.012638  -1.005    0.332
Beers        0.017964   0.002402   7.480 2.97e-06 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.02044 on 14 degrees of freedom
Multiple R-squared:  0.7998,    Adjusted R-squared:  0.7855
F-statistic: 55.94 on 1 and 14 DF,  p-value: 2.969e-06
```

$H_0$ : There is no relation between Beers and BAC - slope = 0

$H_A$ : There is a relationship between Beers and BAC - slope  $\neq 0$



# Conditions to use MLR

1. Independence of observations of responses
2. Linearity of *\*all\** variables - linear relationship between response variable and each of the explanatory variables
3. Multicollinearity checked for - does not mean we cannot use MLR, but we should be aware of how predictor/explanatory variables are related when quoting our results
4. Constant variance
5. Normality of Residuals
6. No influential points (outliers with strong leverage)

# Logistic Regression: A Morbid Example

Logistic regression is a GLM used to model a binary categorical variable using numerical and categorical predictors.

We assume a binomial distribution produced the outcome variable and we therefore want to model  $p$  the probability of success for a given set of predictors.

To finish specifying the Logistic model we just need to establish a reasonable link function that connects  $\eta$  to  $p$ . There are a variety of options but the most commonly used is the logit function.

$$\text{logit}(p) = \log \left( \frac{p}{1-p} \right), \text{ for } 0 \leq p \leq 1$$

# Logistic Regression: A Morbid Example

Ok, so what does the totality of our model look like?

$$y_i \sim \text{Binom}(p_i)$$

$$\eta = \beta_0 + \beta_1 x_1 + \cdots + \beta_n x_n$$

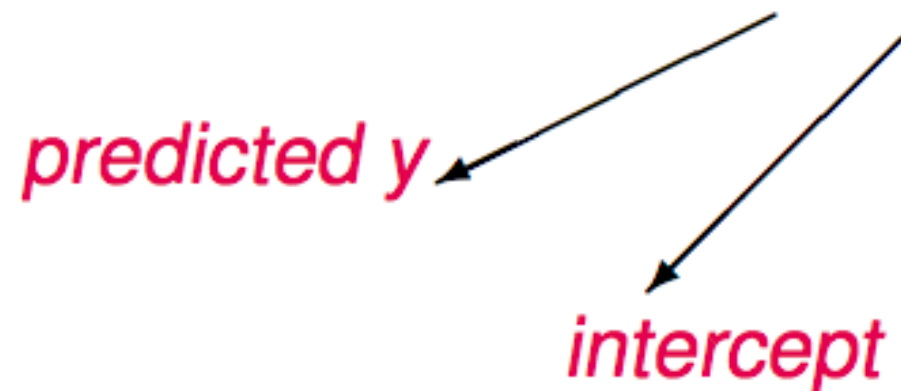
$$\text{logit}(p) = \eta$$

From which we back out the probability of survival based on parameters 1-n, for the  $i$ th observation:

$$p_i = \frac{\exp(\beta_0 + \beta_1 x_{1,i} + \cdots + \beta_n x_{n,i})}{1 + \exp(\beta_0 + \beta_1 x_{1,i} + \cdots + \beta_n x_{n,i})}$$

# So far...

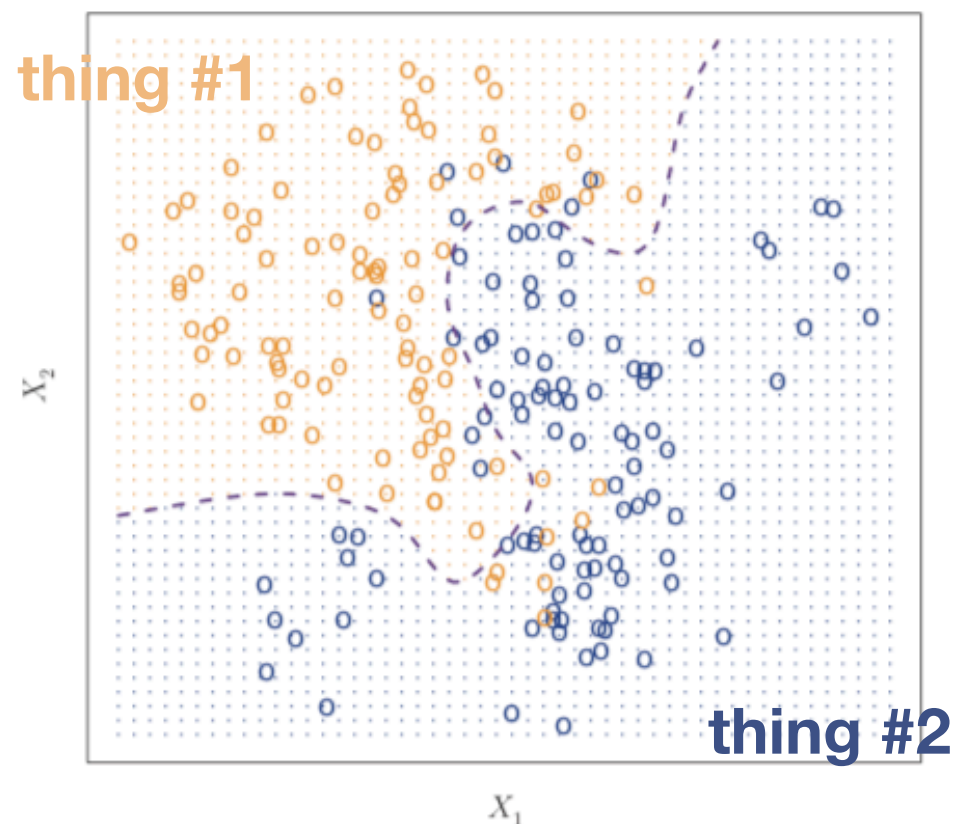
$$\hat{y} = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \dots + \beta_n x_n$$



So far we've been saying:  
"I have a basic idea of what the functional form of y looks like (a line or a logit) - computer go find the parameters of that functional form."

This is nice because we have some hope of gaining intuition from our models.

# Now we classify...



"I want to know where thing #1 and thing #2 live in some 2D space - computer, go figure out the boundary between these two things and let me know"

This is nice because we don't have to assume some model beforehand.

# Bias-Variance Trade-Off (First Glance)

$$E \left( y_0 - \hat{f}(x_0) \right)^2 = \text{Var}(\hat{f}(x_0)) + [\text{Bias}(\hat{f}(x_0))]^2 + \text{Var}(\epsilon)$$

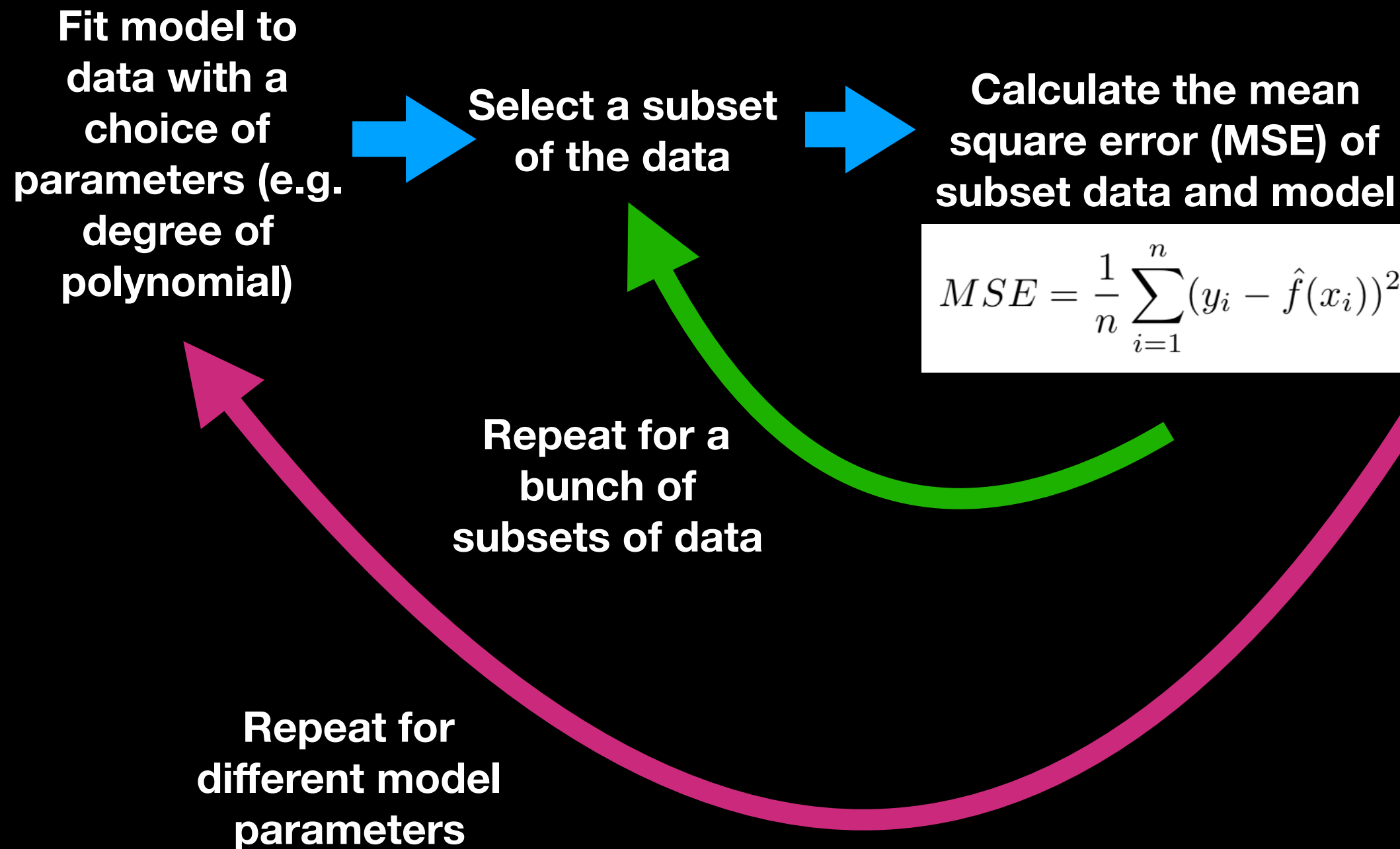
**mean square error** if we kept estimating response variable  $y$  by our fitted function of our explanatory variables,  $f(x)$  with different sample datasets at point  $x_0$

how much our function,  $f$ , changes if we use a different random sample  
(**variance**)

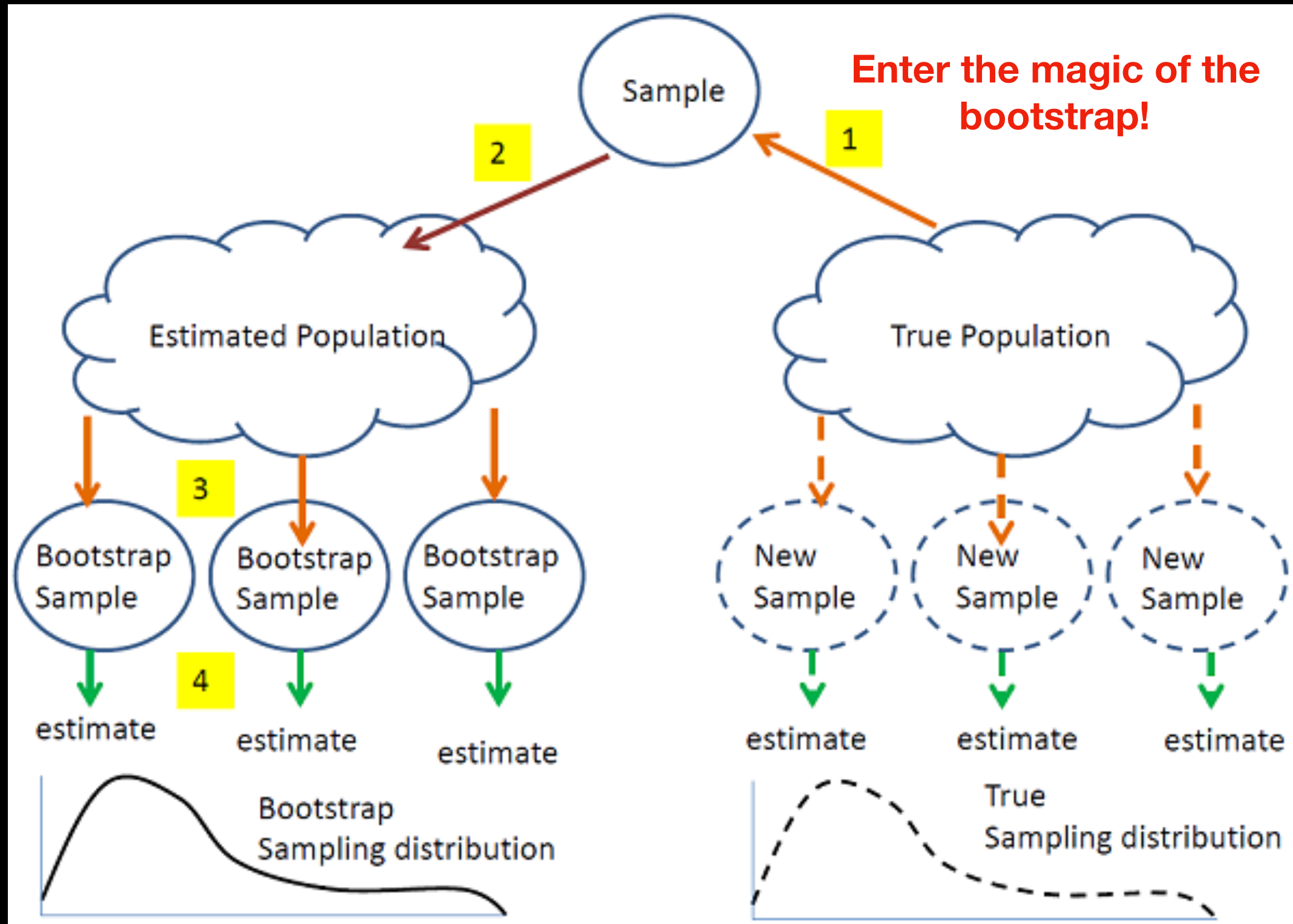
Inherent error (**bias**) in the fact that any model is only an approximation to reality

Inherent error in our measurements

# Cross-Validation Methods



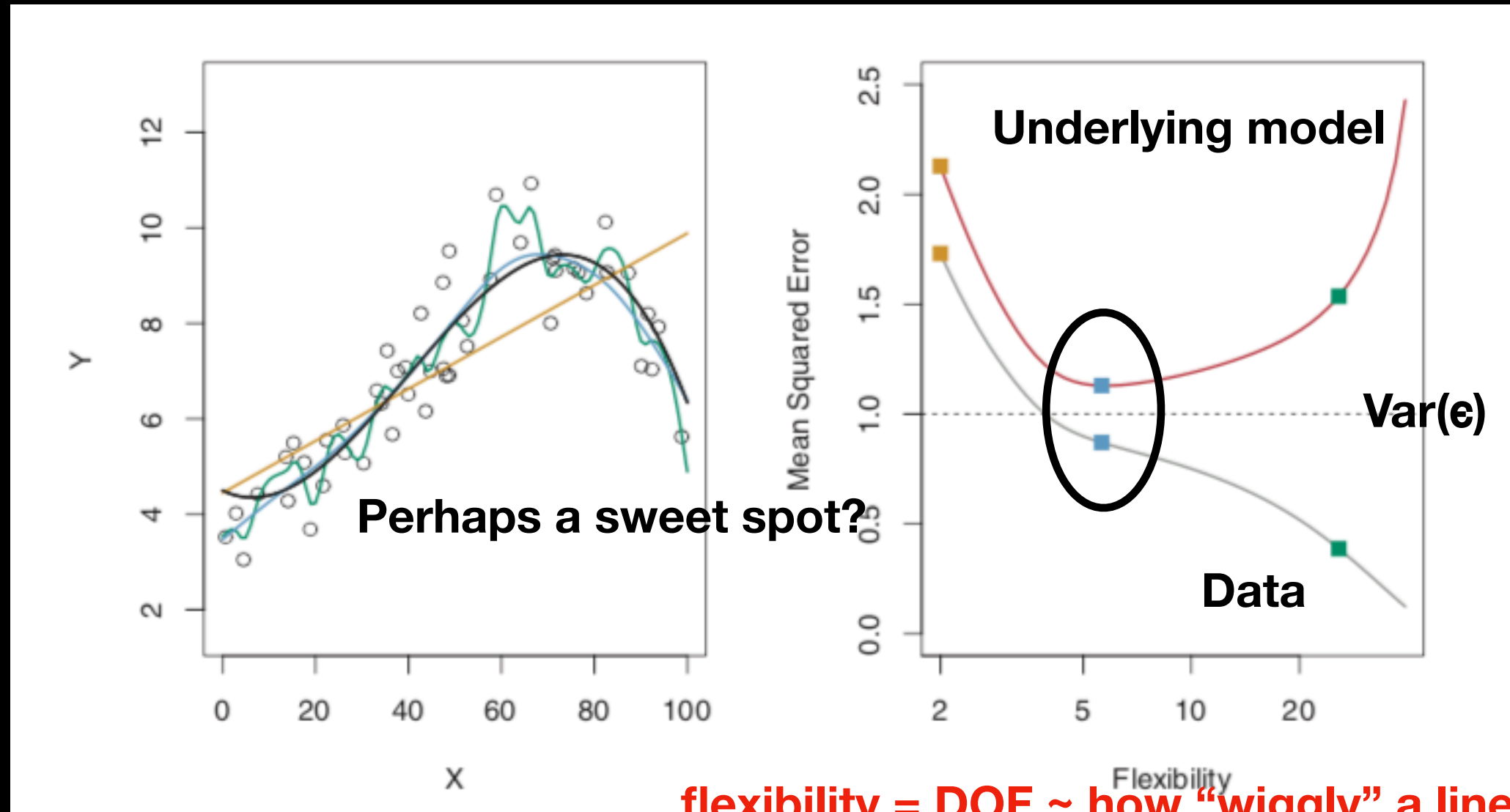
# Bootstrapping



Distribution of means, proportions, etc

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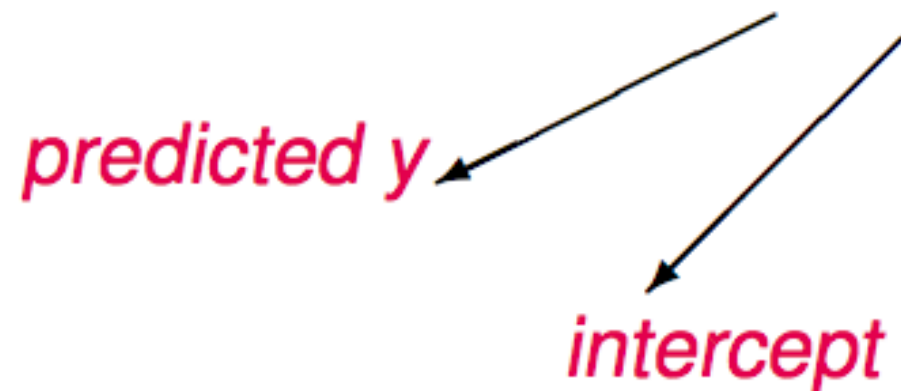
- Actual underlying function -  $y$
- o Simulated data with added error ( $\epsilon$ )
- Linear fit
- Low “flexibility” smooth spline
- High “flexibility” smooth spline

fits data well, but underlying model badly



# So far...

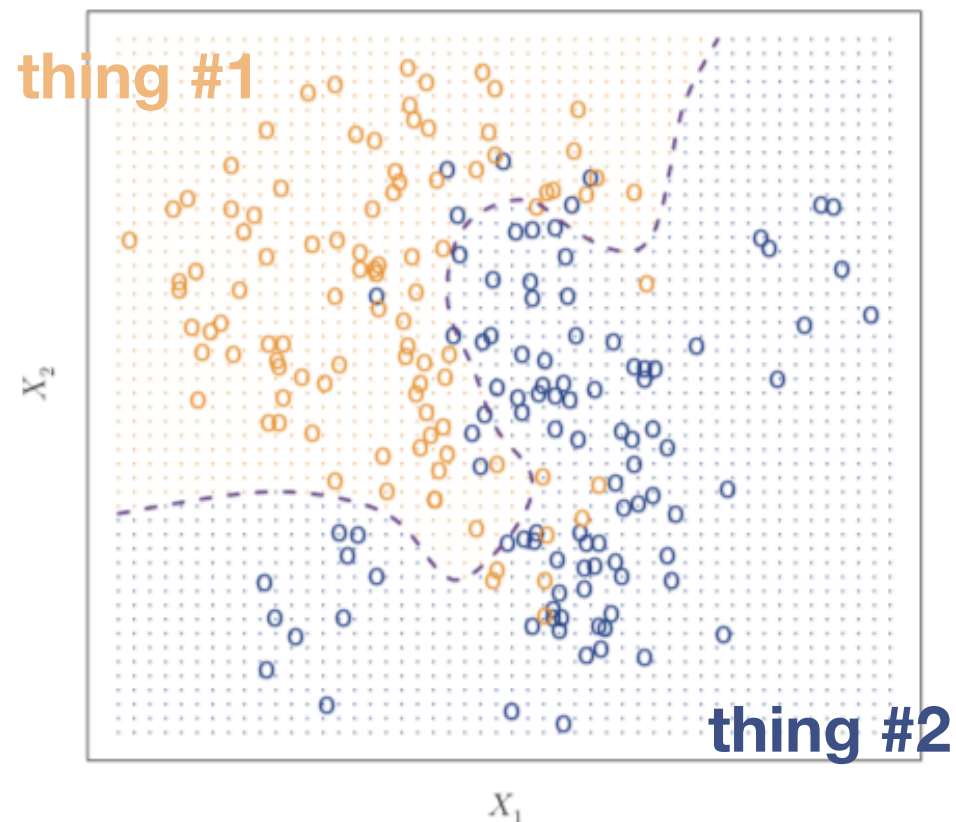
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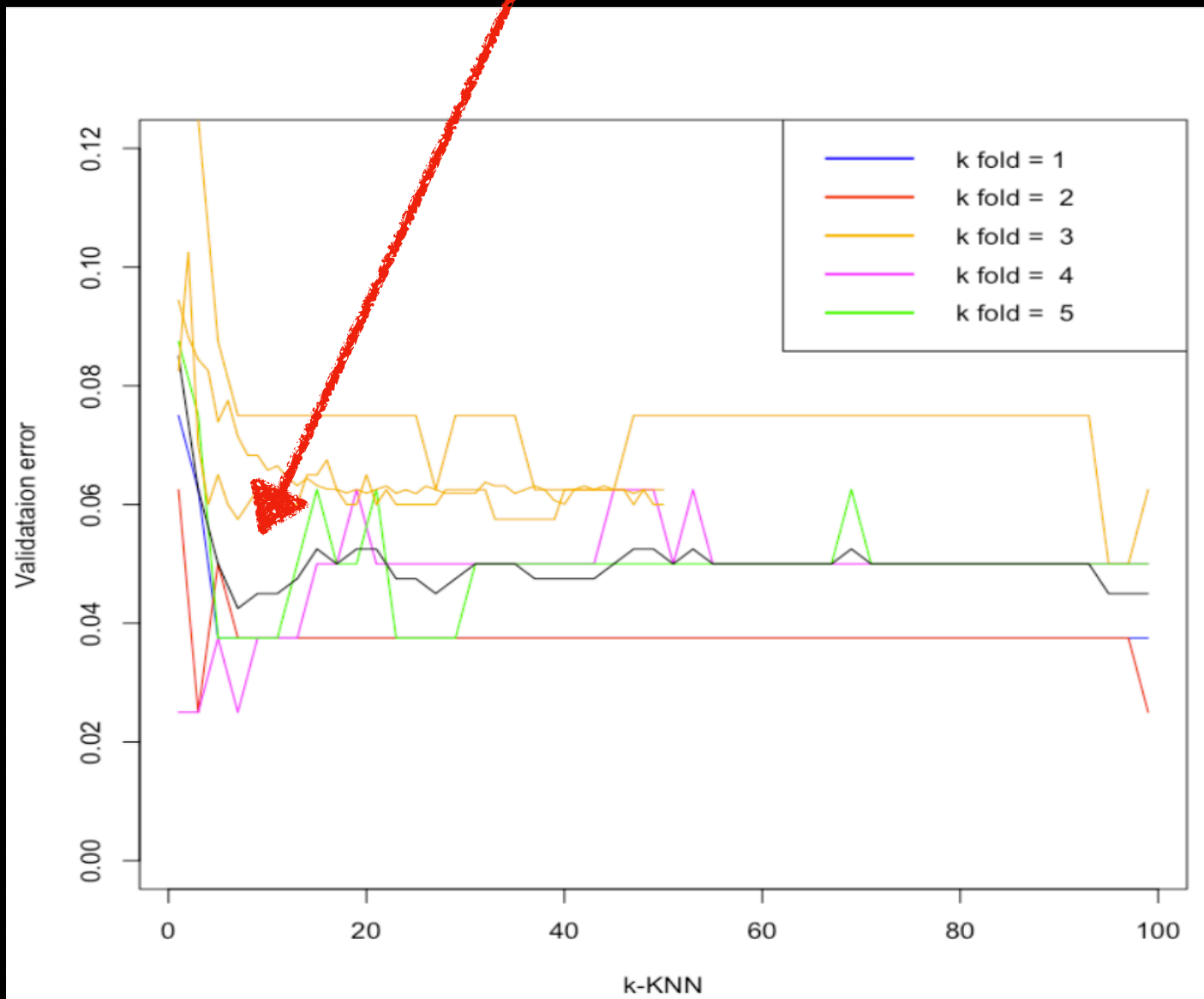


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But we are only able to calculate the test error because we know the background distribution.

Cross-Validation  
(Ch. 5)

Regularization  
(Ch. 6)

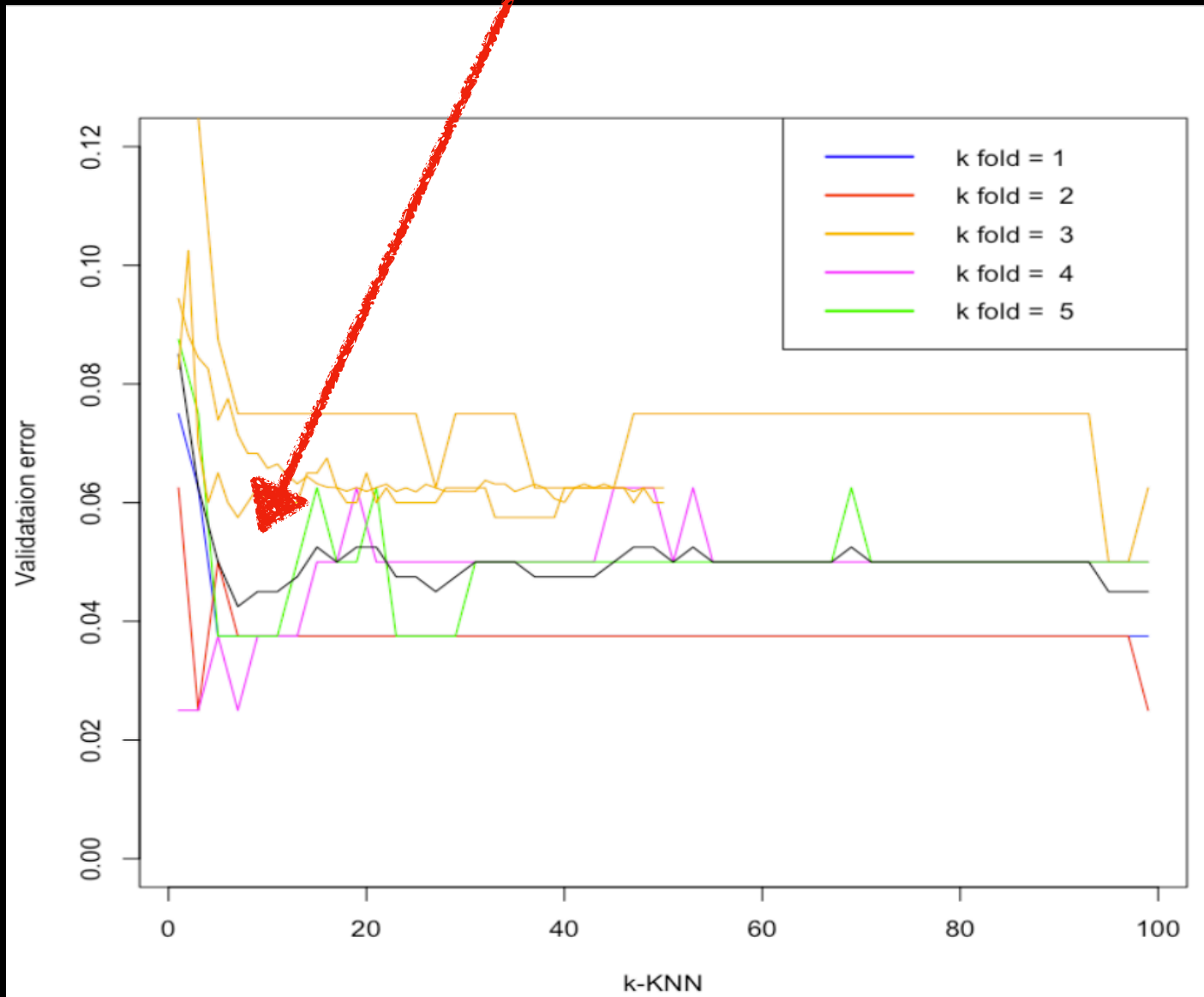
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Use math to  
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Last Week

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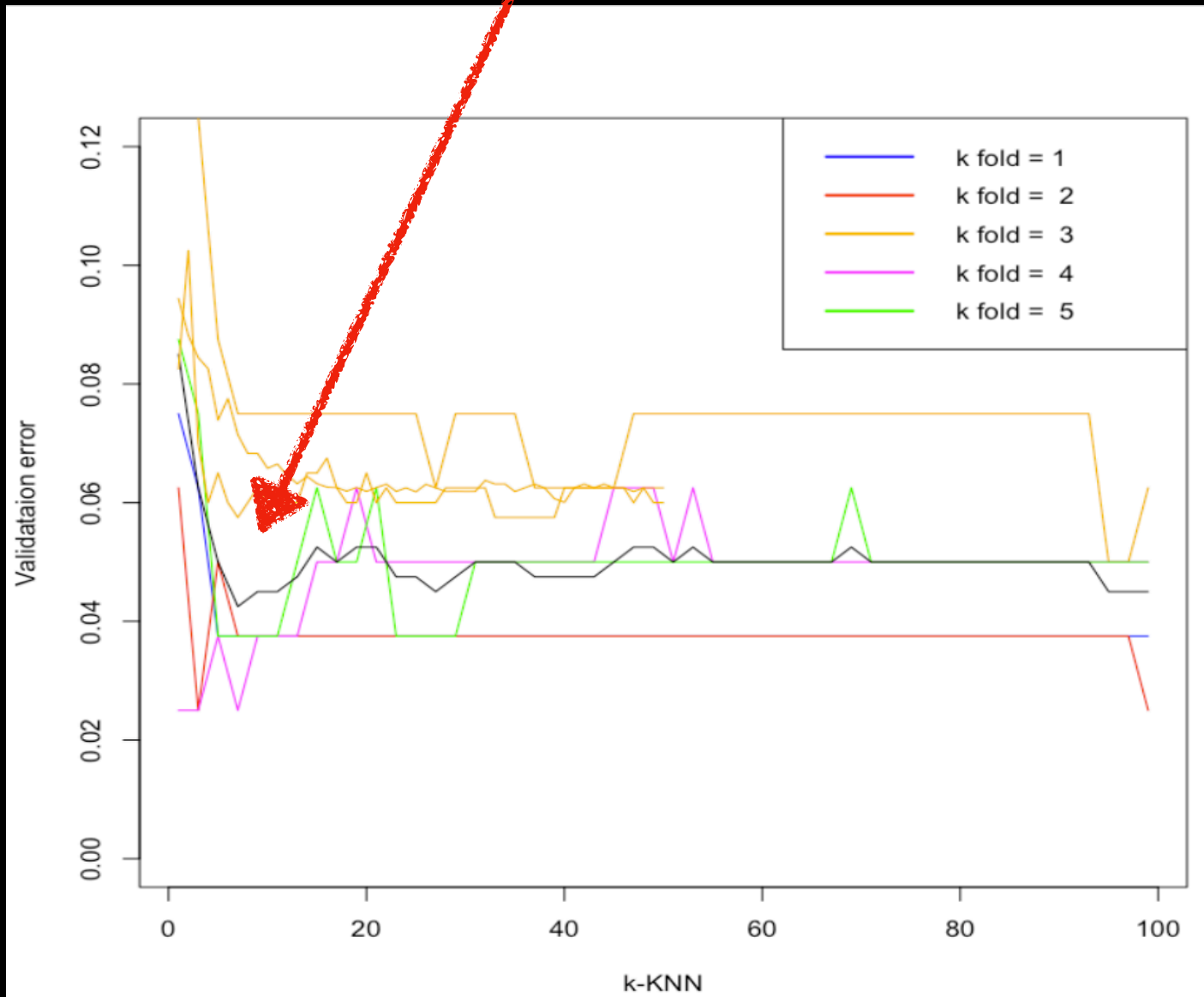
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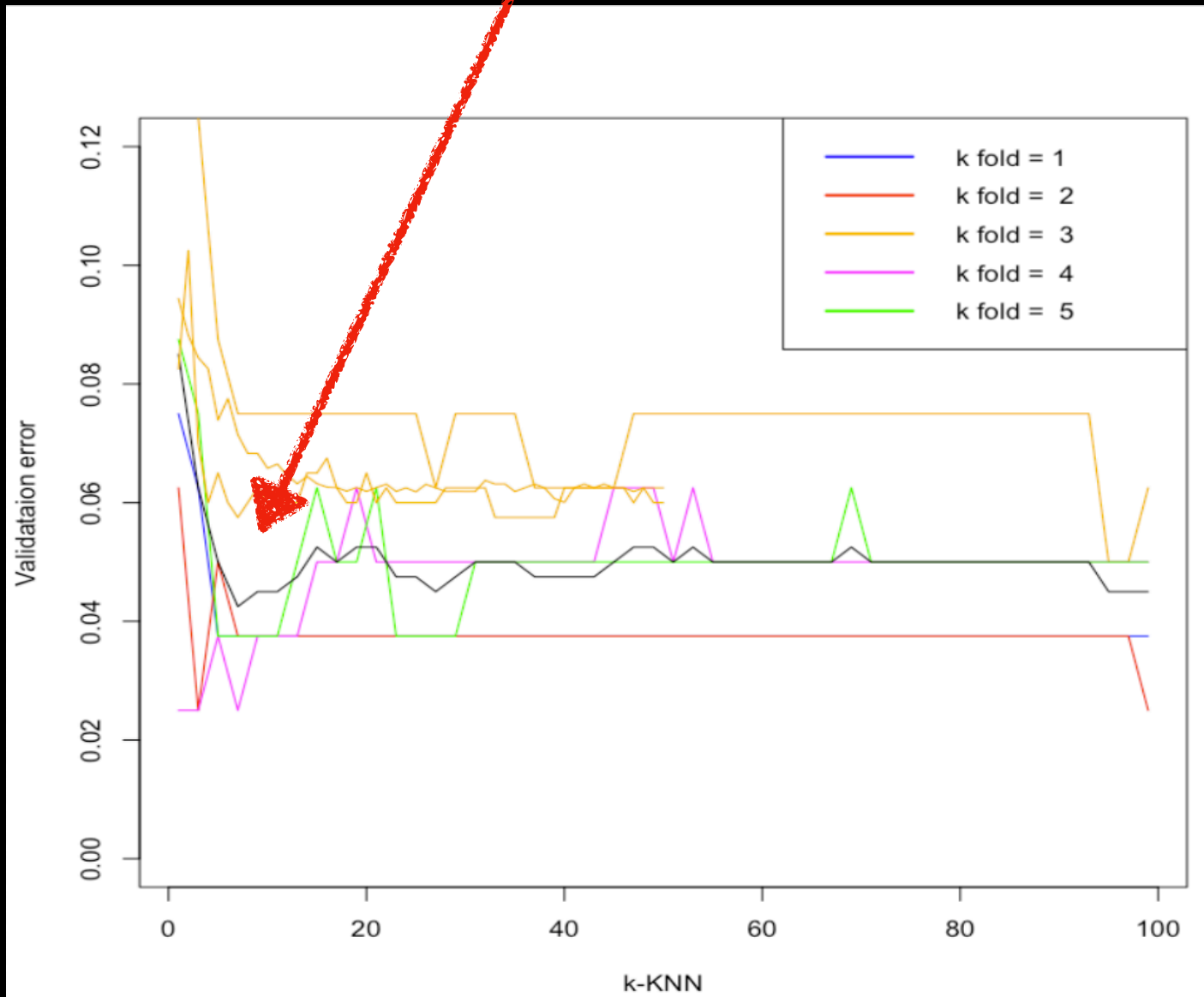
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# Improvements on the Linear Model

• **Linear regression** is a **linear model** that uses a **linear function** to predict the **output** of a **target variable** based on the **input** of a **feature variable**.

• The **linear function** is defined by the **intercept** and the **slope** of the line.

• The **intercept** is the **value** of the **output** when the **input** is **zero**.

• The **slope** is the **rate of change** of the **output** with respect to the **input**.

• The **linear function** can be written as  $y = \beta_0 + \beta_1 x$ , where  $y$  is the **output**,  $x$  is the **input**,  $\beta_0$  is the **intercept**, and  $\beta_1$  is the **slope**.

• The **linear model** can be used to predict the **output** of a **target variable** based on the **input** of a **feature variable**.

• The **linear model** is a **simple** and **easy** to use model.

• The **linear model** is a **good** starting point for more complex models.

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**Prediction Accuracy:** especially when  $p > n$ , to control the variance.

**Model Interpretability:** By removing irrelevant features — that is, by setting the corresponding coefficient estimates to zero — we can obtain a model that is more easily interpreted. We will present some approaches for automatically performing **feature selection**.

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**A few more details...**

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We identify a subset of the  $p$  predictors (of  $k$  possible) that we believe to be related to the response. We then fit a model using least squares on the reduced set of variables.

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2. For  $k = 1, 2, \dots, p$ :
  - (a) Fit all  $\binom{p}{k}$  models that contain exactly  $k$  predictors.
  - (b) Pick the best among these  $\binom{p}{k}$  models, and call it  $M_k$ . Here **best** is defined as having the smallest RSS, or equivalently largest  $R^2$ .

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$$\text{RSS} = \sum_{i=1}^n \left( y_i - \beta_0 - \sum_{j=1}^p \beta_j x_{ij} \right)^2$$

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this number can get big  $\sim 2^p$   
 $p=2$ : 4 (including null)  
 $p=3$ : 8  
...  
 $p=10$ : 1024
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**Great news: we already covered this!**

# Subset selection: Forward & Backward (Review)

Forward selection: start with an empty model and add the variable that most improves the fit at each step.

Backward selection: start with a full model and remove the variable that least improves the fit at each step.

Both methods stop when no further improvement can be made.

Forward selection is generally preferred to backward selection because it is less computationally intensive.

Both methods can be used to select the best subset of variables for a given model.

Forward selection is a greedy algorithm, meaning that it makes locally optimal choices at each step.

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- Like forward stepwise selection, **backward stepwise selection** provides an efficient alternative to best subset selection.
- However, unlike forward stepwise selection, it begins with the full least squares model containing all  $p$  predictors, and then iteratively removes the least useful predictor, one-at-a-time.

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- *Neither are guaranteed to find the best possible model out of all  $2^p$  models containing subsets of the  $p$  predictors.*
- Backward selection requires that the **number of samples  $n$  is larger than the number of variables  $p$**  (so that the full model can be fit). In contrast, forward stepwise can be used even when  $n < p$ , and so is the only viable subset method when  $p$  is very large.

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$$C_p = \frac{1}{n} (\text{RSS} + 2d\hat{\sigma}^2)$$

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$$\text{AIC} = \frac{1}{n\hat{\sigma}^2} (\text{RSS} + 2d\hat{\sigma}^2)$$

Idea here is to get a measurement of the mean square error that accounts for # of parameters in a model

$$\text{BIC} = \frac{1}{n\hat{\sigma}^2} (\text{RSS} + \log(n)d\hat{\sigma}^2)$$

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Or: large values as  $R_{\text{adj}}^2$

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## Optional R notes.



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**Least squares minimization (i.e. minimize RSS)**

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In contrast, the **Ridge** or **Lasso** regression coefficient estimates  $\beta^R$  and  $\beta^L$  are the values that minimize

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where  $\lambda \geq 0$  is a **tuning parameter**, to be determined separately.

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Don't panic, its just a bit more math (and we'll get R to do it for us)

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# Shrinkage Methods

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**Why would we make our  
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# Shrinkage Methods

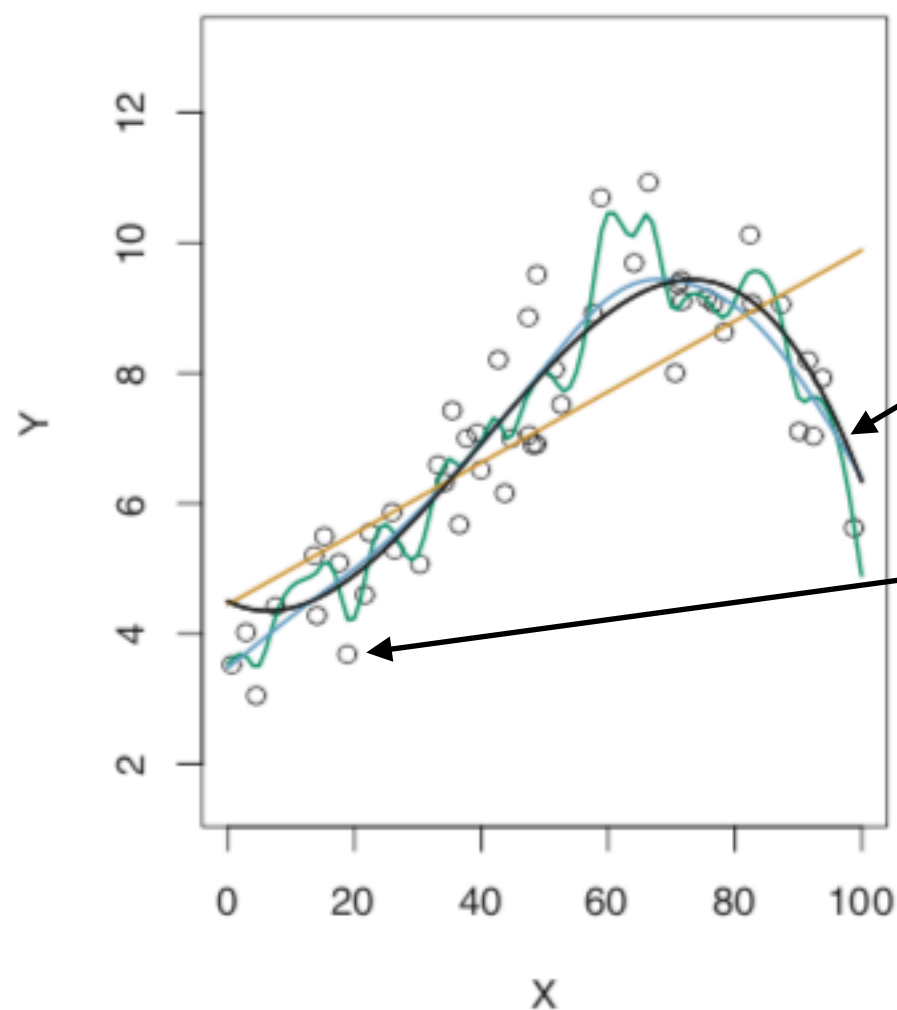
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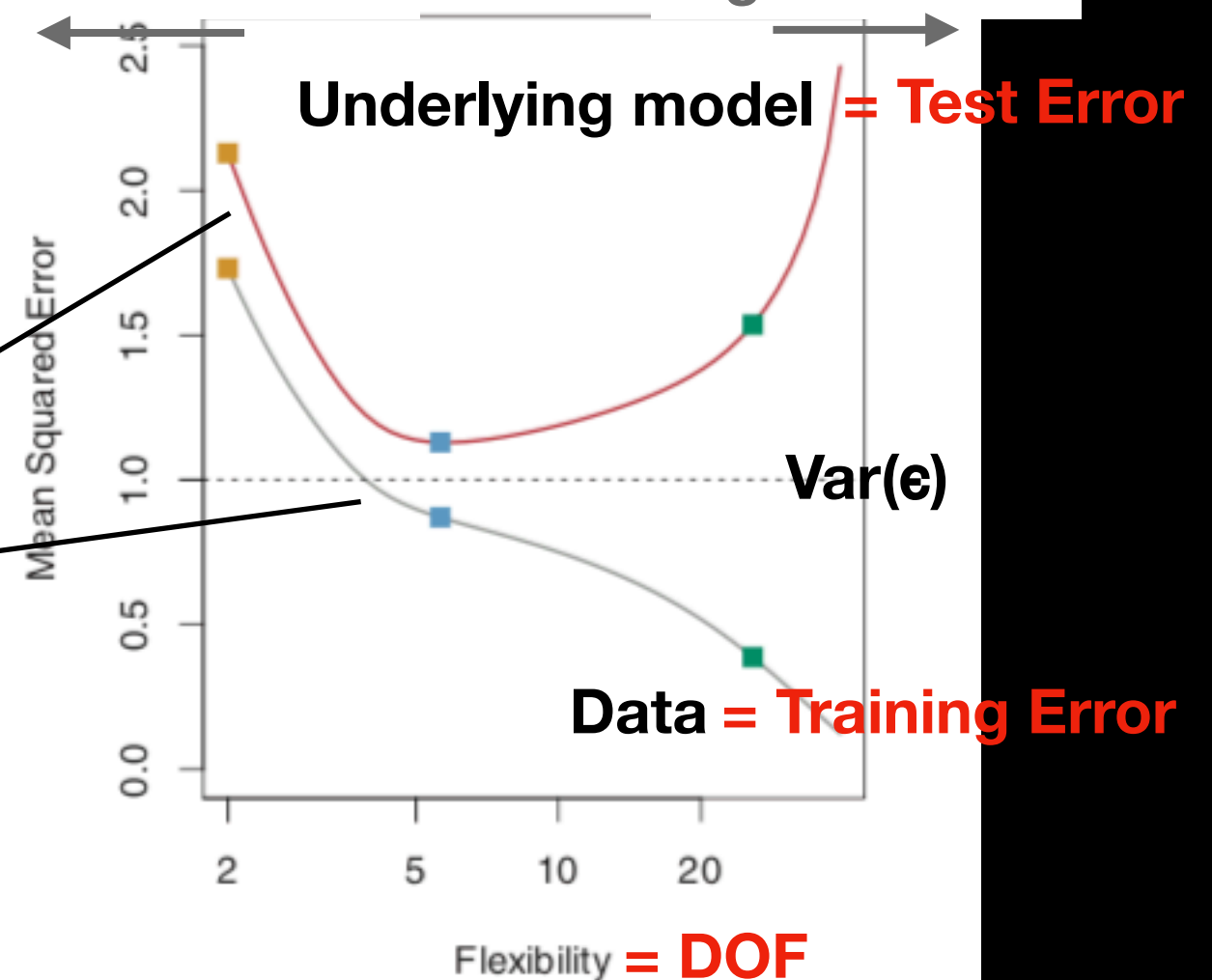
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High Bias  
Low Variance

Low Bias  
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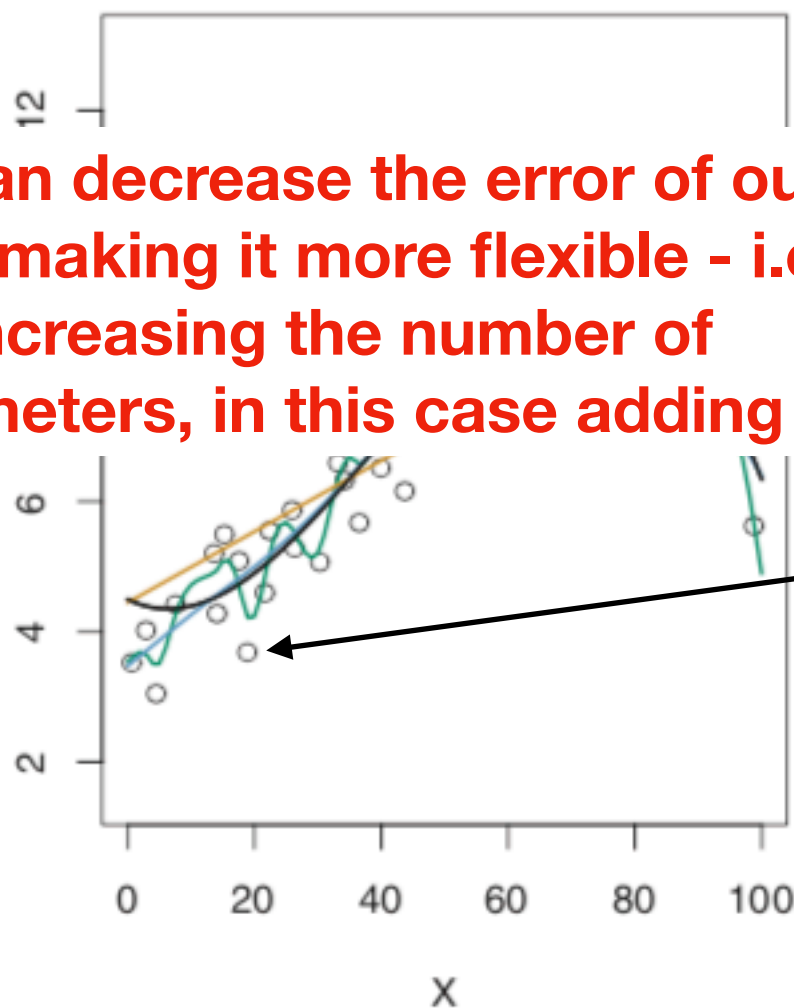
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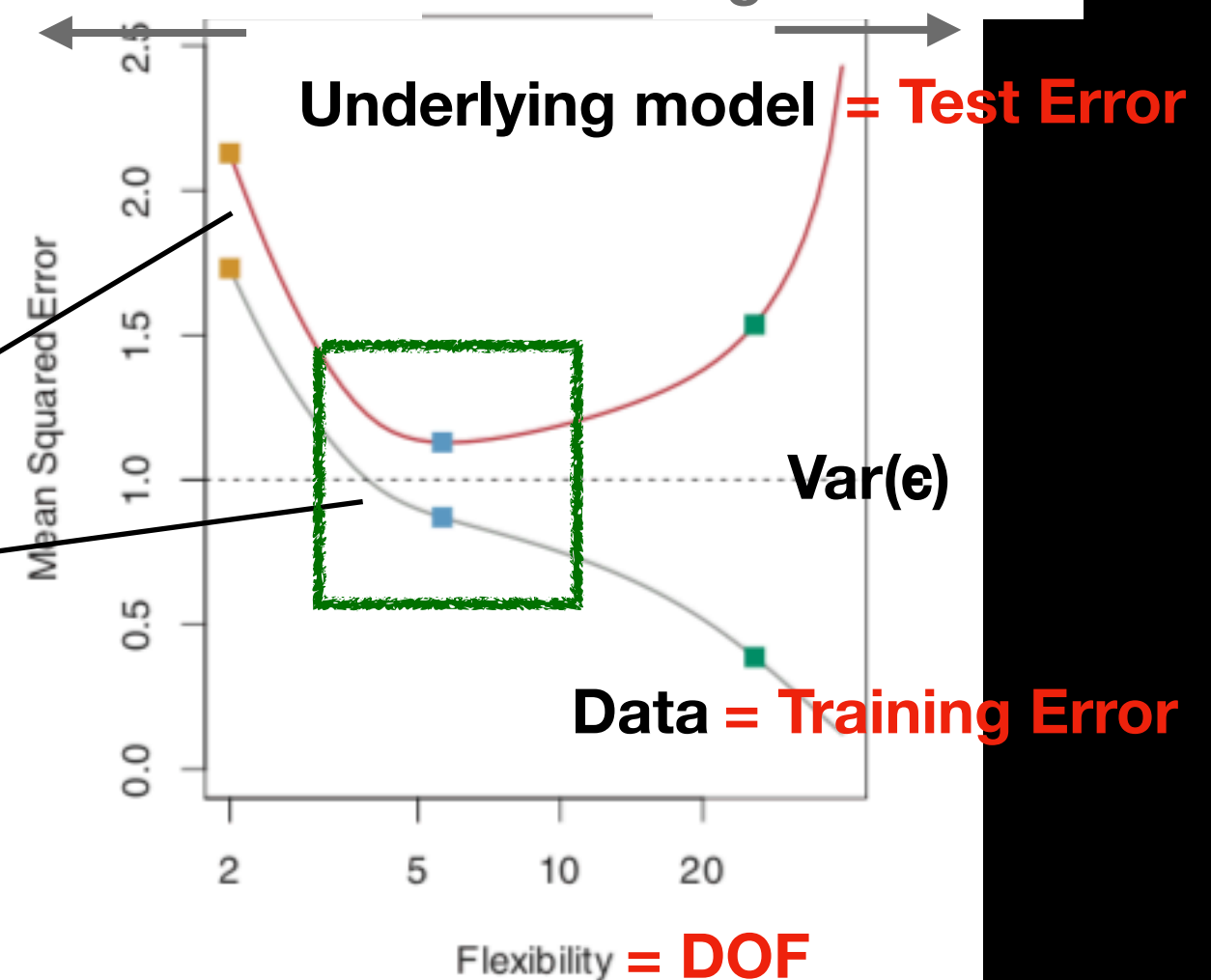
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We can decrease the error of our fit by making it more flexible - i.e. increasing the number of parameters, in this case adding  $\lambda$



High Bias  
Low Variance

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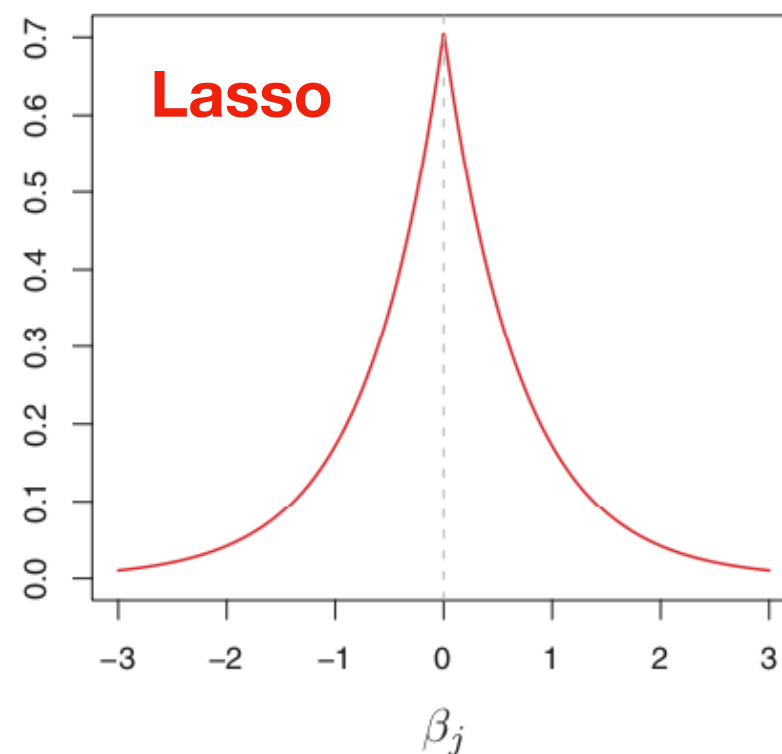
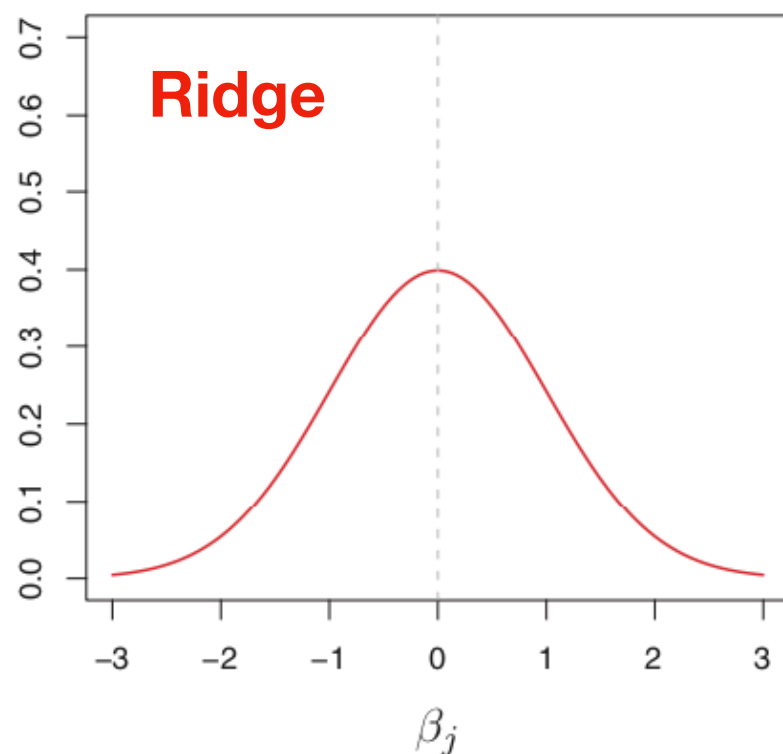
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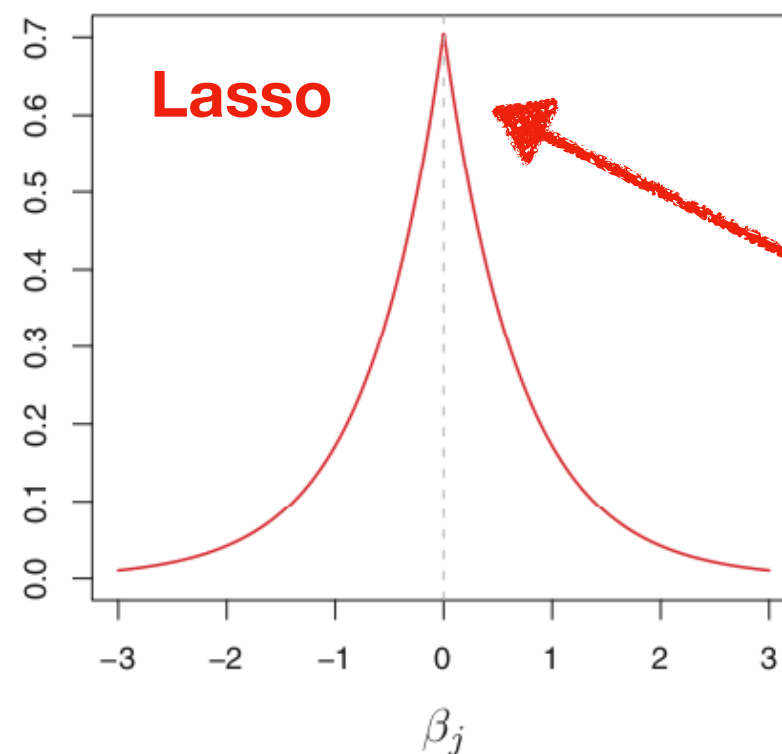
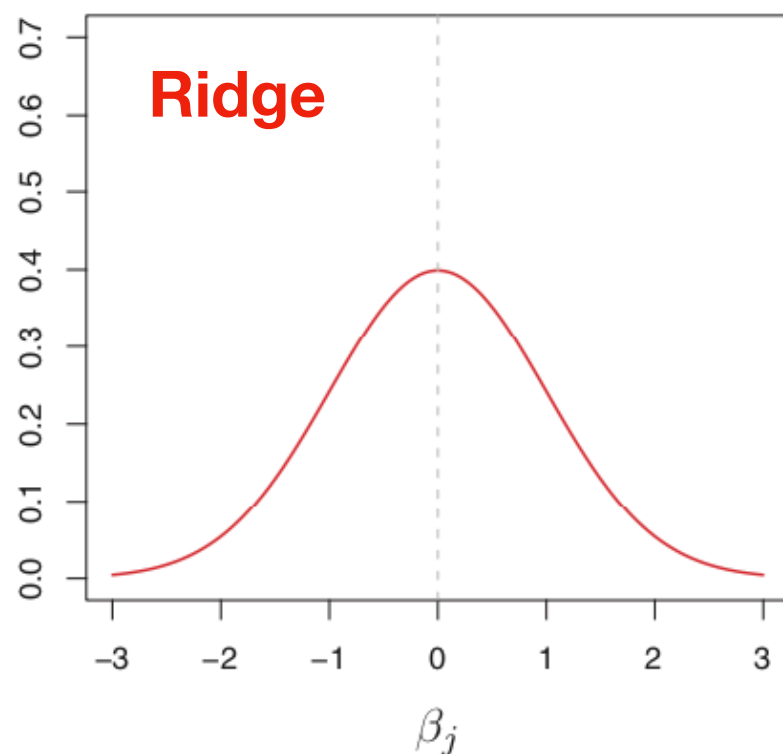
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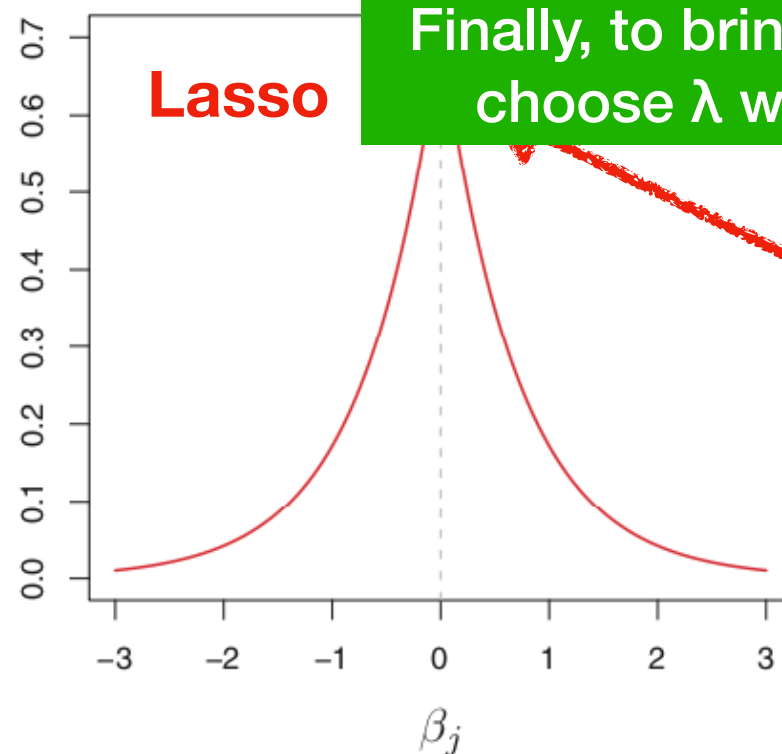
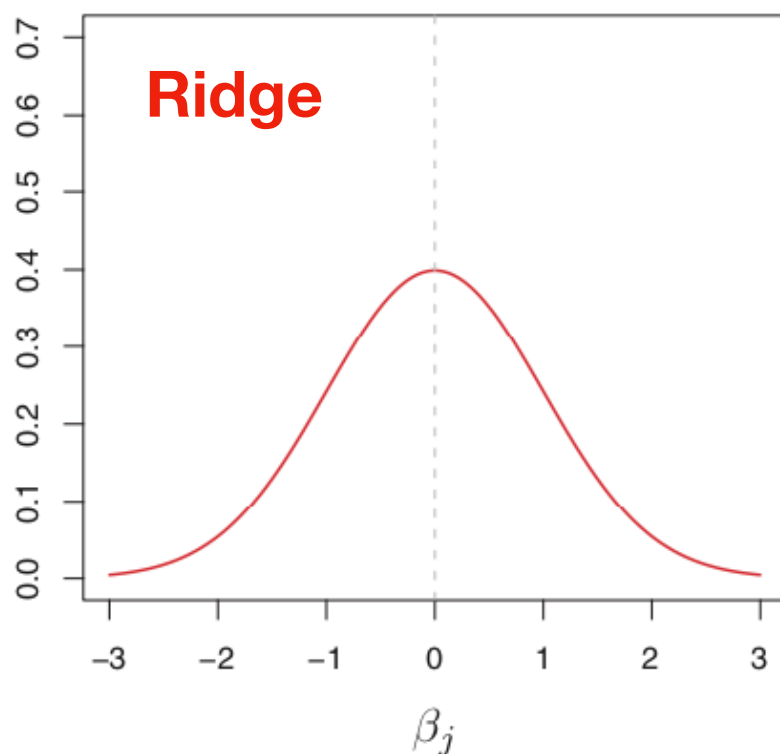
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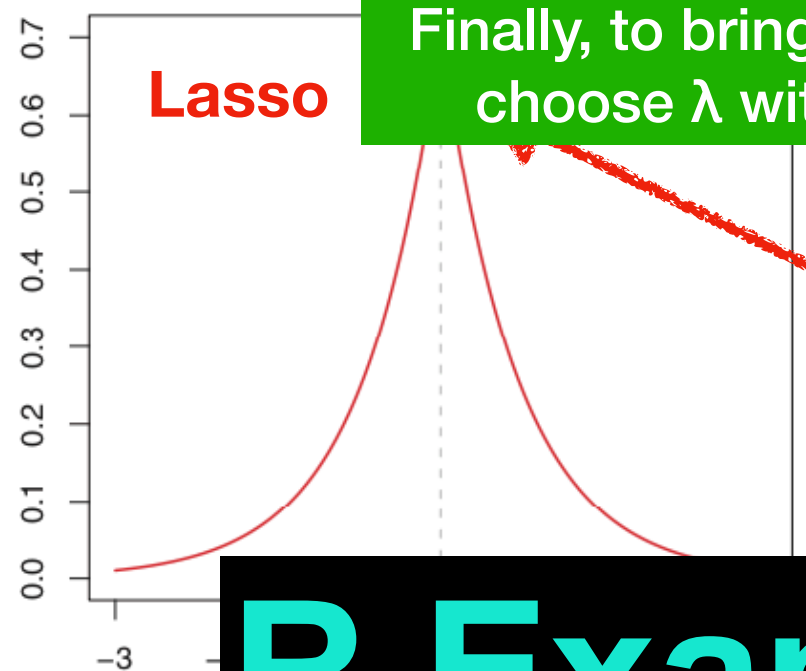
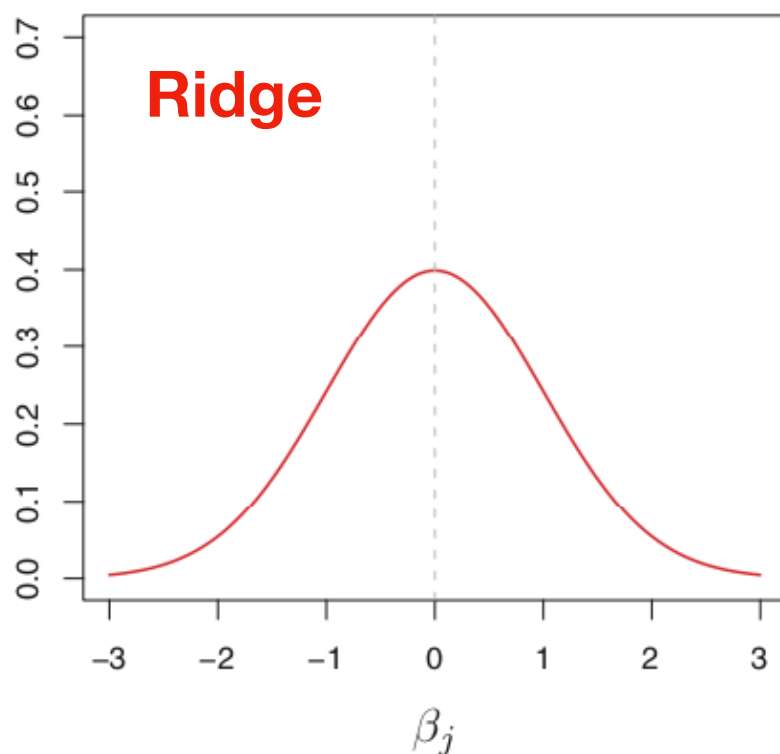
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# R Examples!











# **Unsupervised Learning:**

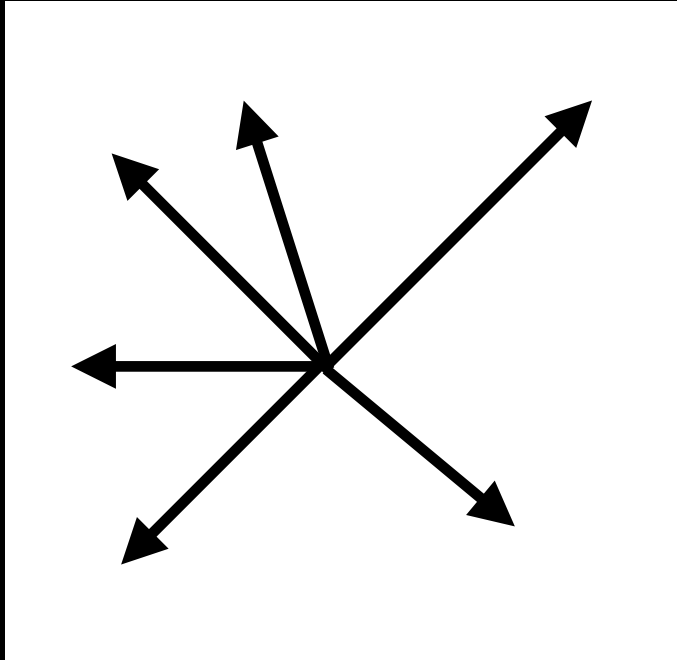
## **An intro to Principle Component Analysis**

# **Unsupervised Learning:**

## **An intro to Principle Component Analysis**

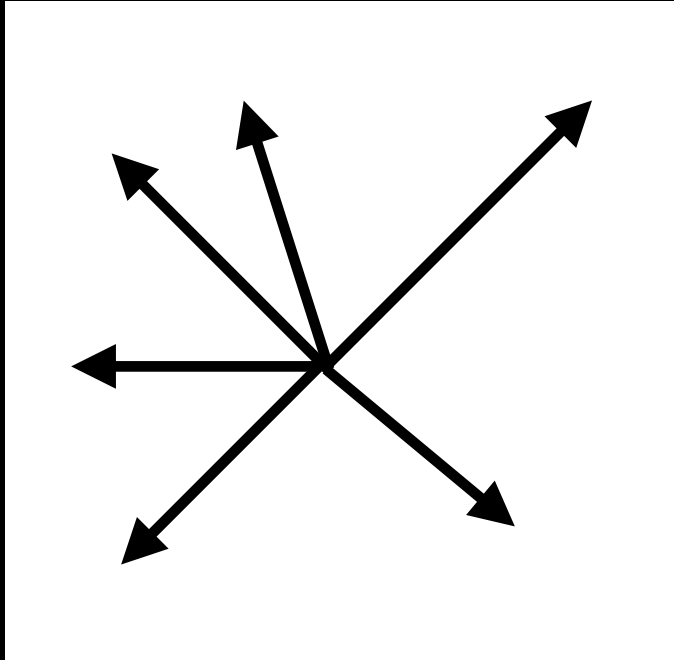
**... what do we do when we don't know anything**

# Principle Component Analysis: In Pictures

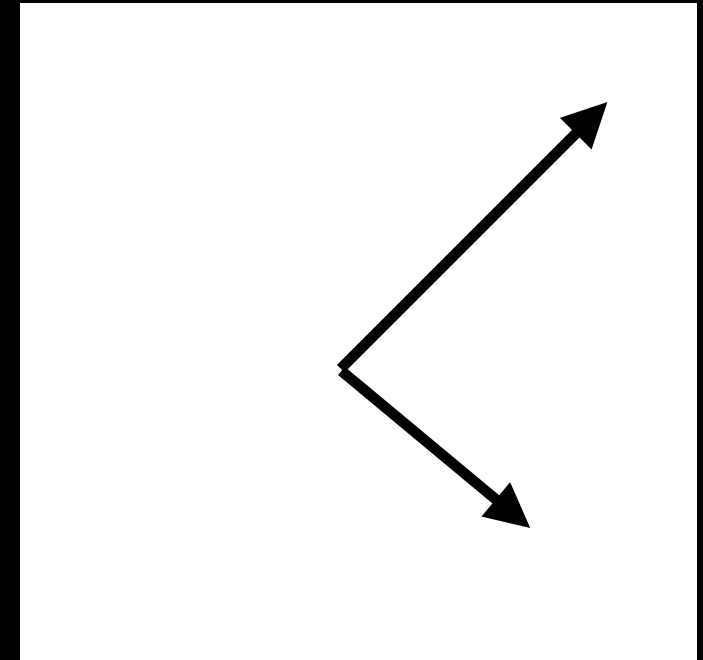
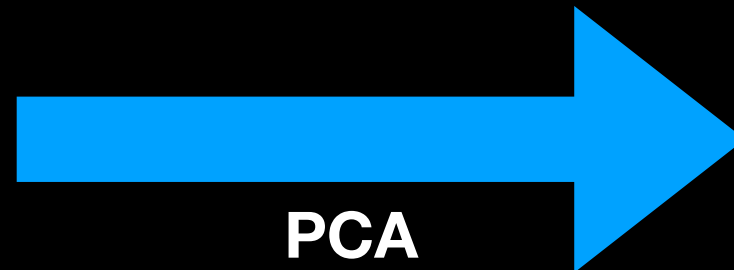


**How many vectors do I  
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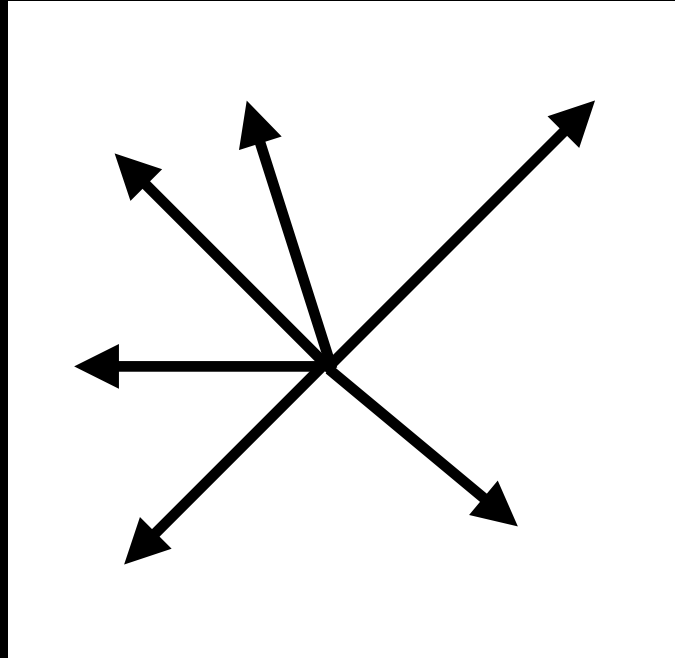


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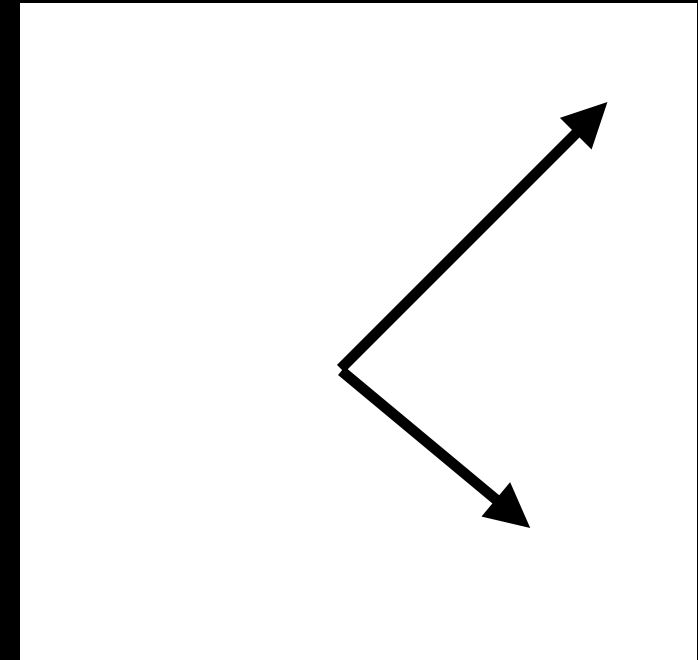
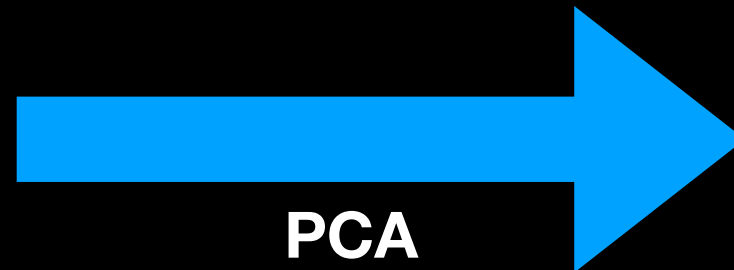


**Minimum number of  
vectors to define a space  
in a certain number of  
dimensions**

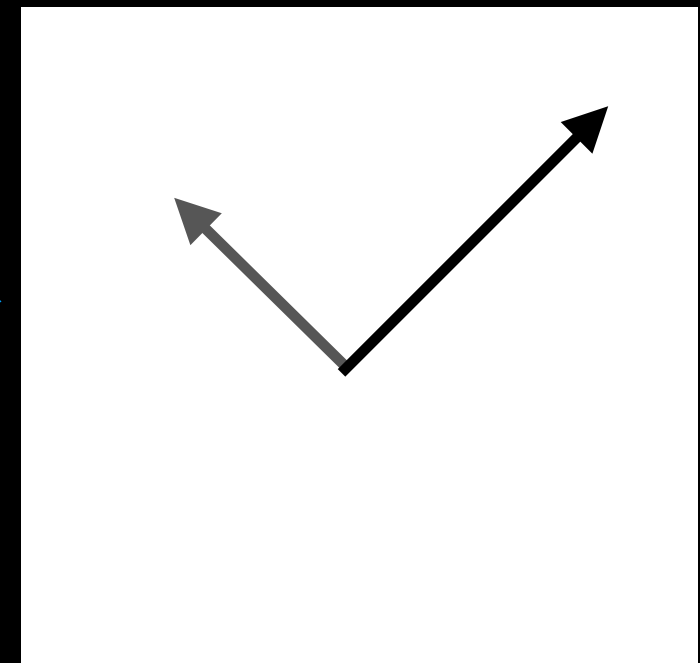
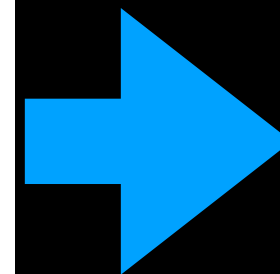
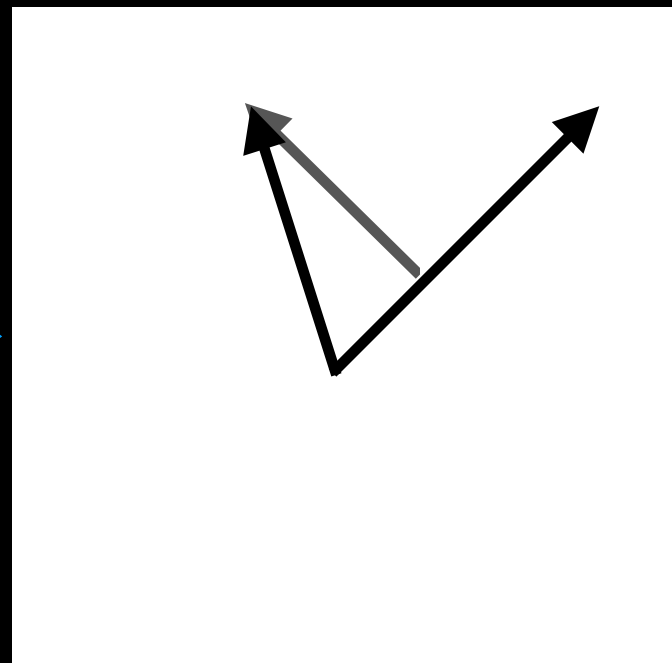
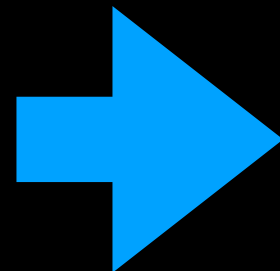
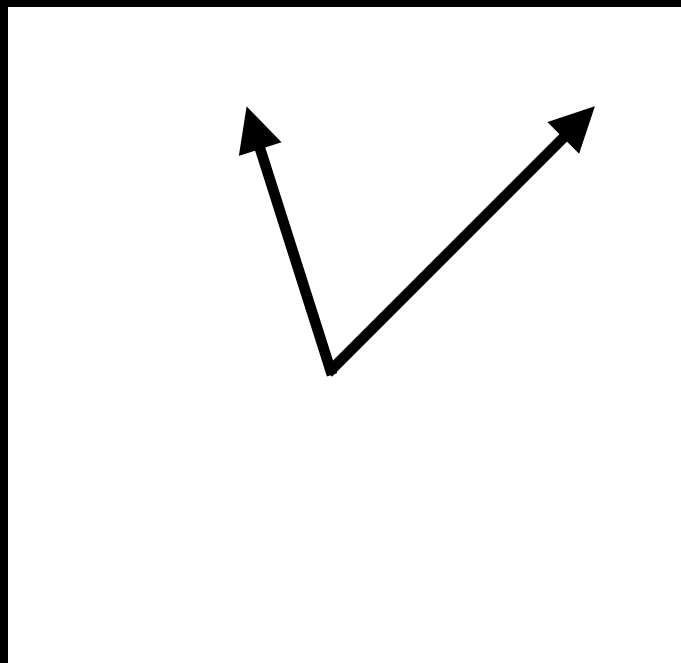
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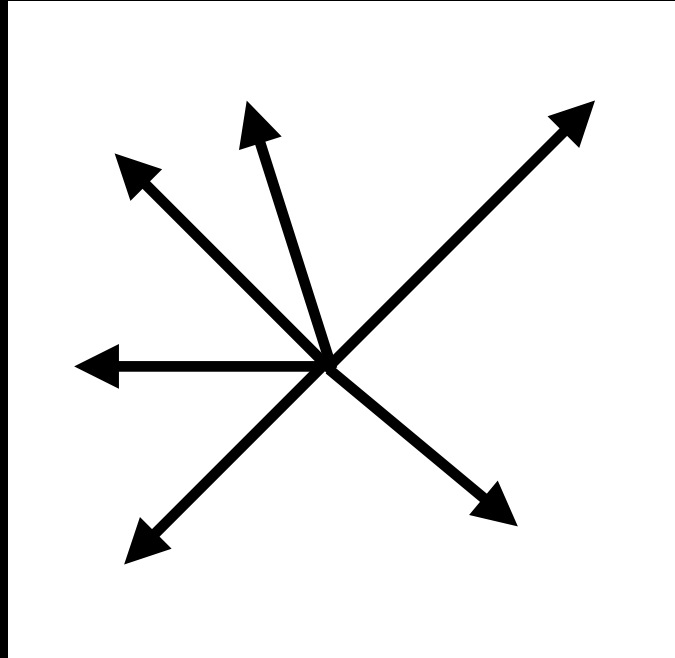
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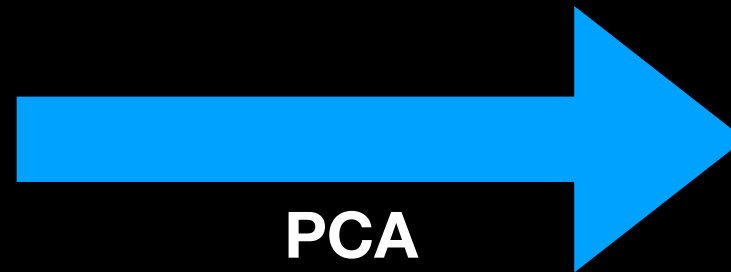
Constructing orthogonal vectors



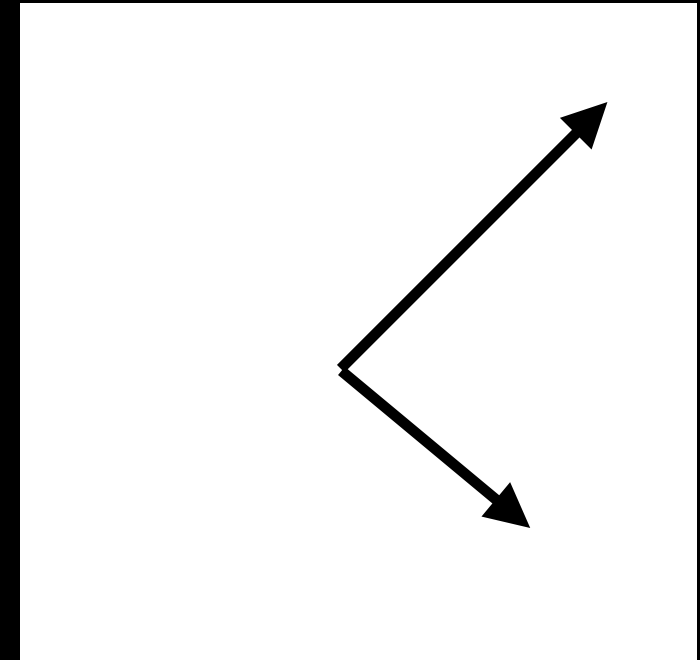
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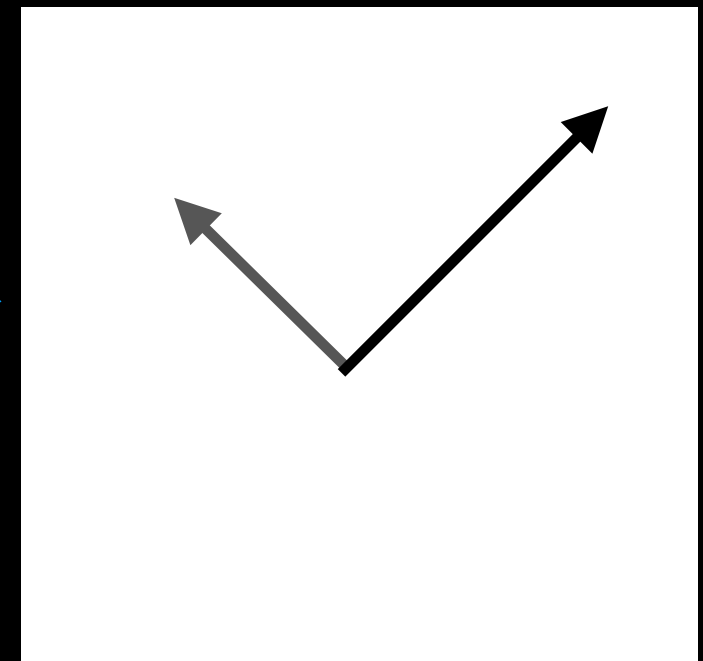
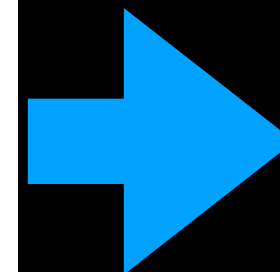
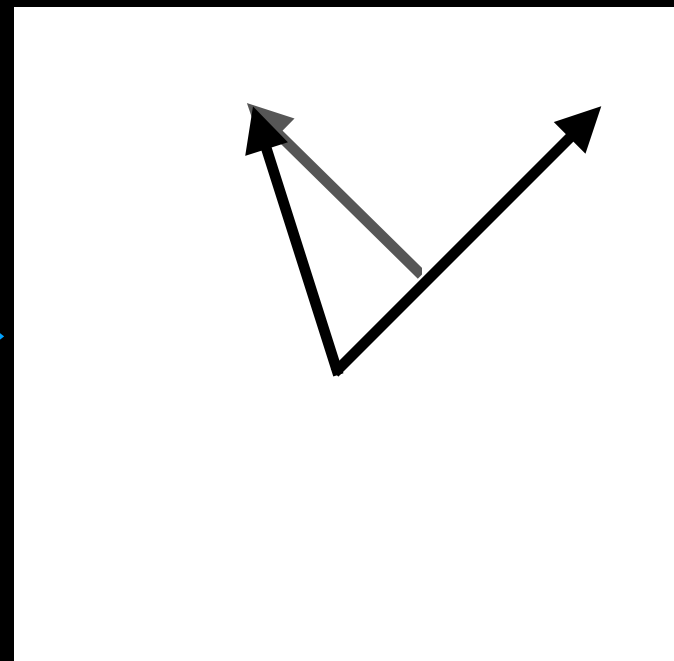
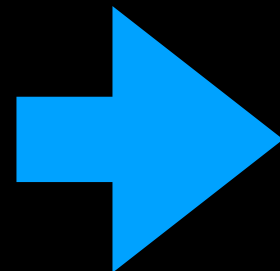
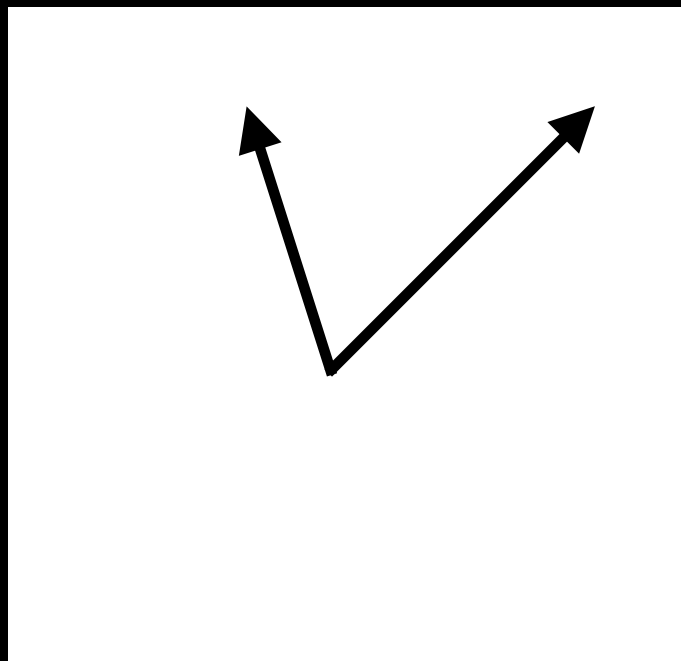
How many vectors do I need to define a 2D space?



The “dimensions” of our space is dictated by the number of parameters we have

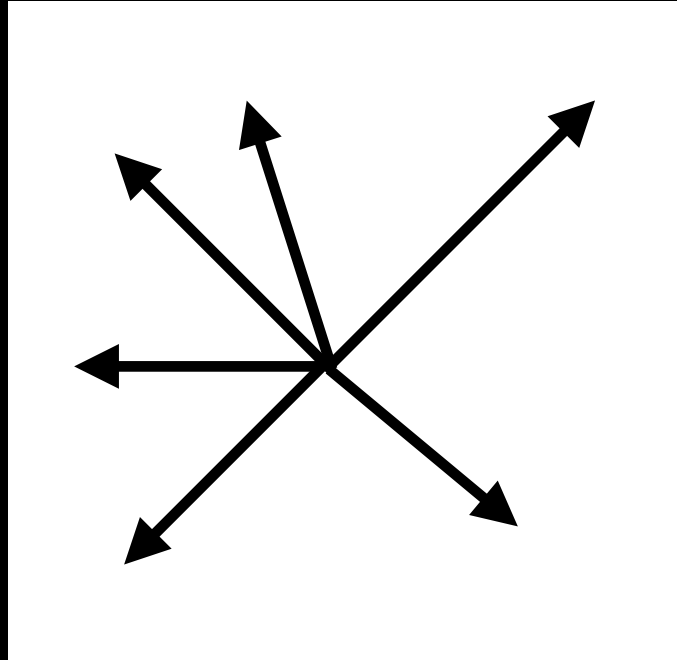


Minimum number of vectors to define a space in a certain number of dimensions

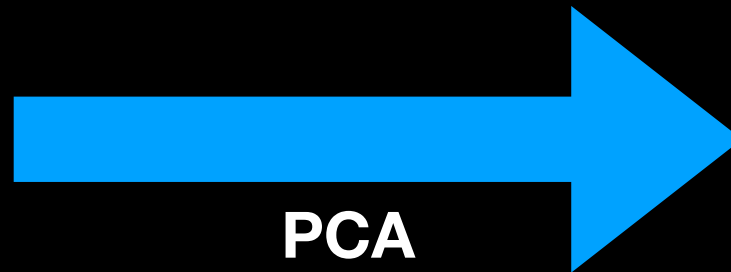


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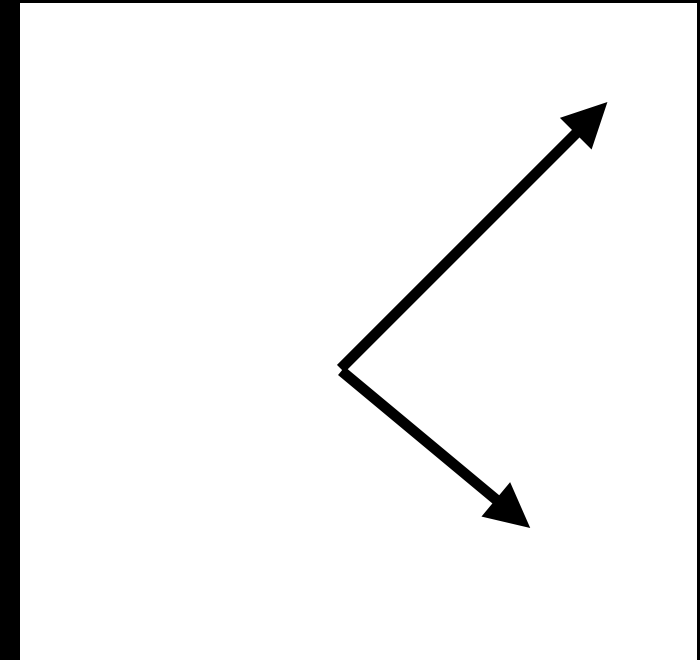


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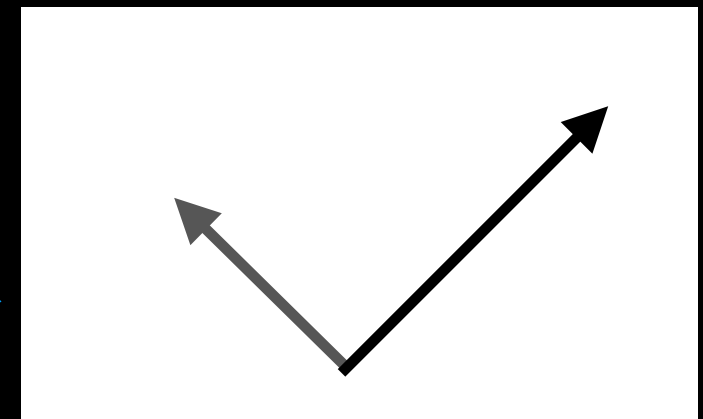
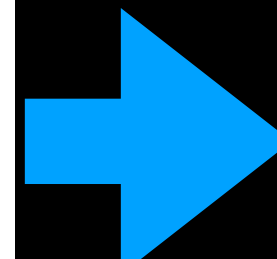
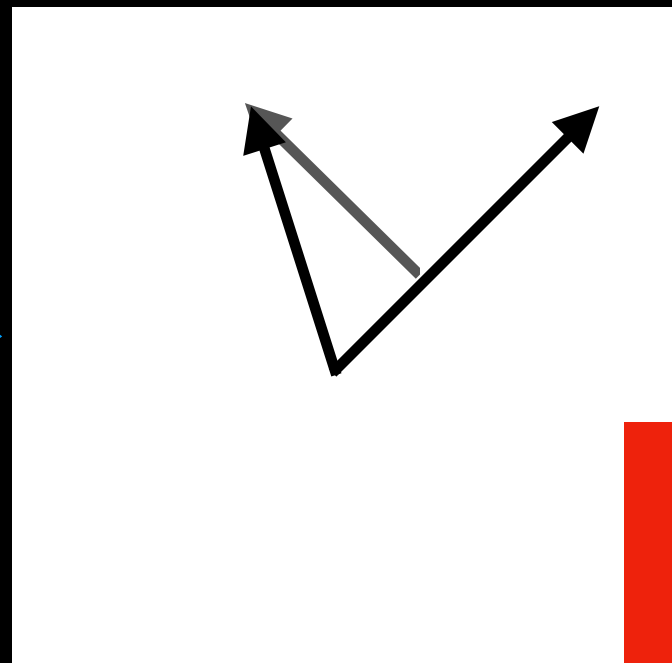
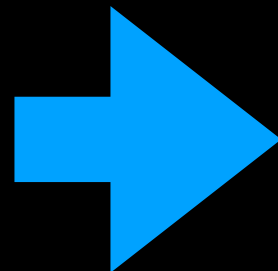
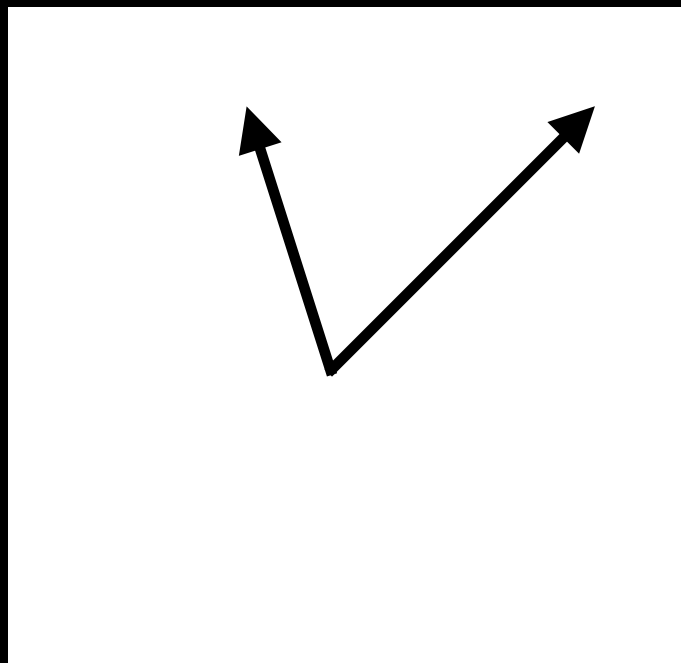


PCA

The “dimensions” of our space is dictated by the number of parameters we have



Minimum number of vectors to define a space in a certain number of dimensions



Aside: these are also called “eigenvectors” and are used a lot in physics - for example to express states of atoms in quantum mechanics

Constructing orthogonal vectors

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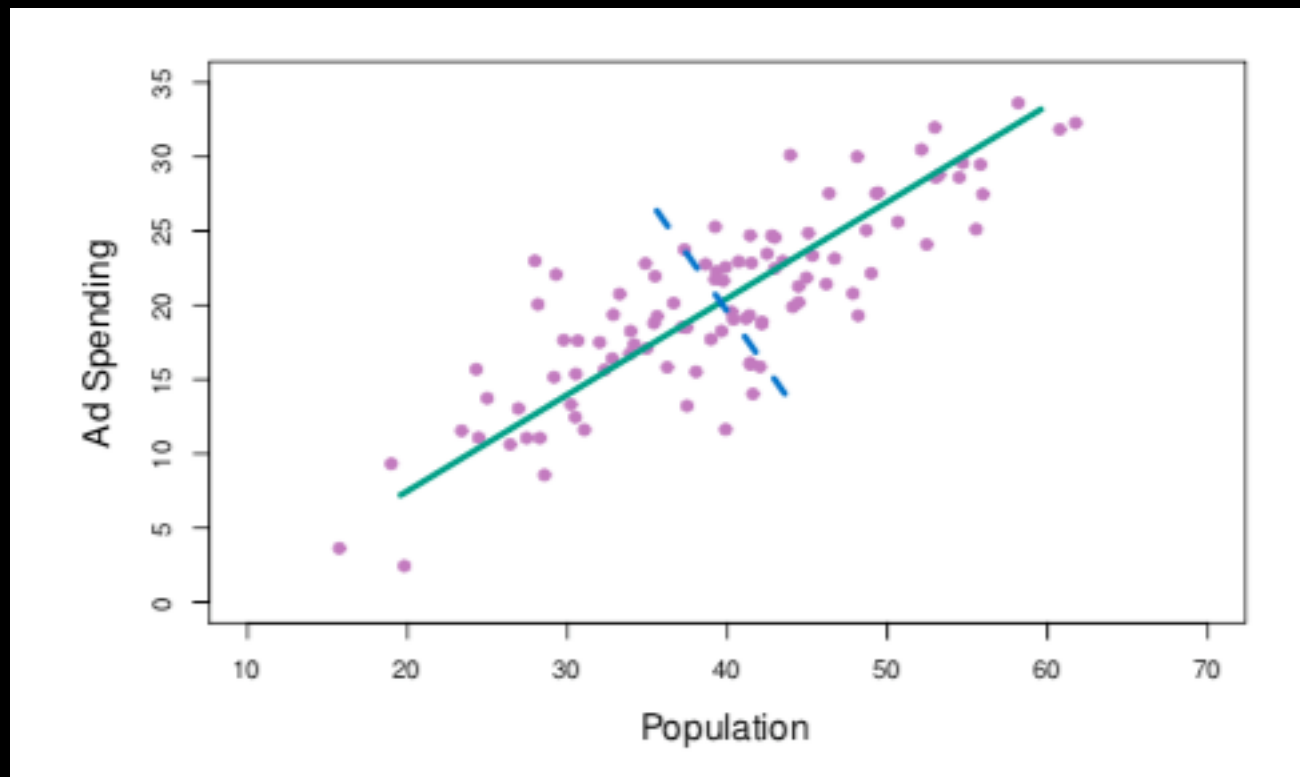
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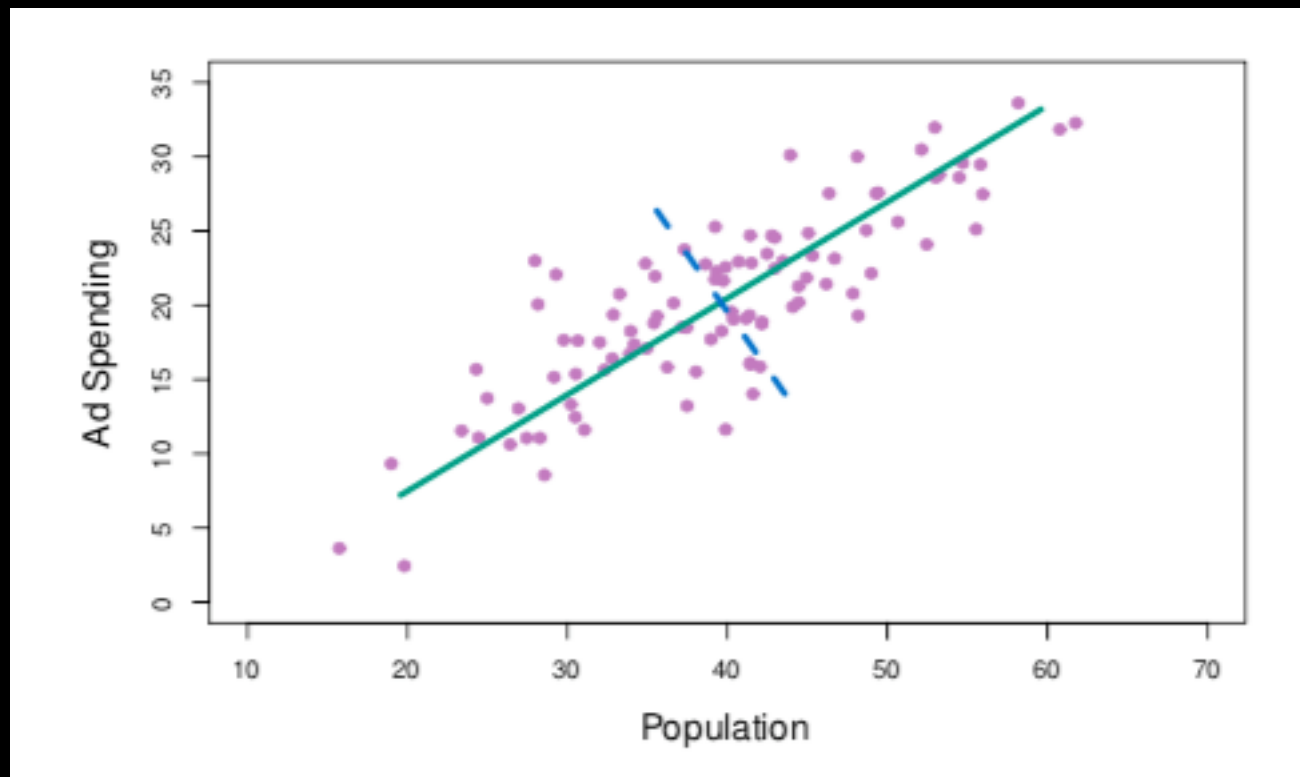


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**Quick R example!**



