

## Recoding variables (2), model validation

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## Cleaning messy data

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## Load messy titanic data

- From terminal: git pull
- In Rstudio: Open project, intermediate\_stats

```
# titanic<-read_csv('./slides/data/titanic_messy.csv')
```

## Data cleaning lab

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Break

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## Model comparison and validation

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- What is the goal of a regression model?

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$$y_i = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \varepsilon_i$$

What is the primary characteristic of the vector of  $\beta$  that the OLS method returns? (Hint: it involves the residuals)

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What does RSS mean in plain english?

What's the most common single measure you use to assess the goodness-of-fit of an OLS model?

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1. What is the numerator?
2. What is the denominator?
3. What does this ratio tell us?
4. When can we compare  $R^2$  across models?
5. What does RSS look like for logistic models?

## For more complex models

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Fun fact: For the normal likelihood model, OLS==MLE

## What is a likelihood?

A likelihood function is a function we use to identify parameters for a model given our data. It depends on the probability distribution we use to model our data.

We can think of a likelihood  $L(y|\theta)$  as describing the probability of observing our data given a set of parameters.

$R^2$  only describes the proportion of variance explained under a Normal likelihood model.

The likelihood ratio test is similar to comparing  $R^2$ . We can directly compare the likelihood of the data conditional on our estimated model for two models as:

$$LR = \frac{L(y|\theta_1)}{L(y|\theta_2)}$$

Conveniently, we can use a  $\chi^2$  distribution to perform a significance test on whether model 2 fits better than model 1.



## An example: returning to the titanic

```
titanic <- read_csv("./data/titanic.csv")
m0 <- glm(Survived ~ Sex, data = titanic, family = "binomial")
m1 <- glm(Survived ~ Sex + Age, data = titanic, family = "binomial")
anova(m0, m1, test = "LRT")
```

```
## Analysis of Deviance Table
##
## Model 1: Survived ~ Sex
## Model 2: Survived ~ Sex + Age
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1      885      916.12
## 2      884      916.00  1  0.12358  0.7252
```

## Likelihood ratio test Example (cont.)

```
m2 <- glm(Survived ~ Sex + Age + factor(Pclass), data = titanic, family = "binomial")
```

```
anova(m0, m2, test = "LRT")
```

```
## Analysis of Deviance Table
```

```
##
```

```
## Model 1: Survived ~ Sex
```

```
## Model 2: Survived ~ Sex + Age + factor(Pclass)
```

```
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
```

```
## 1      885      916.12
```

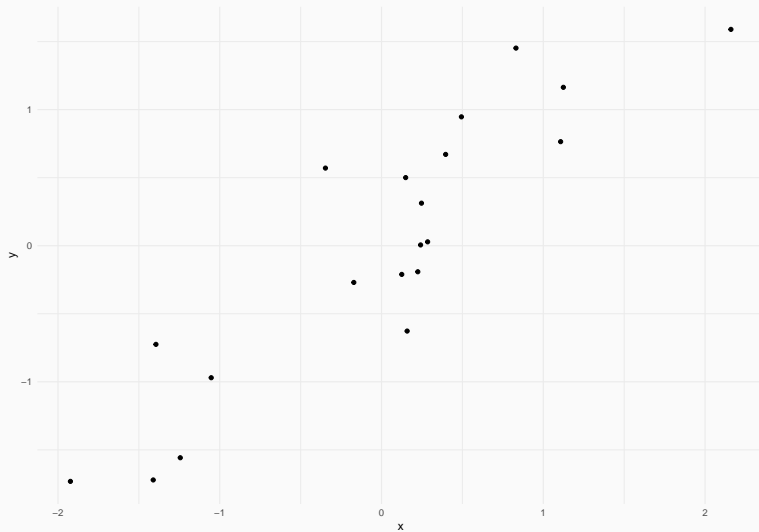
```
## 2      882      801.59  3   114.53 < 2.2e-16 ***
```

```
## ---
```

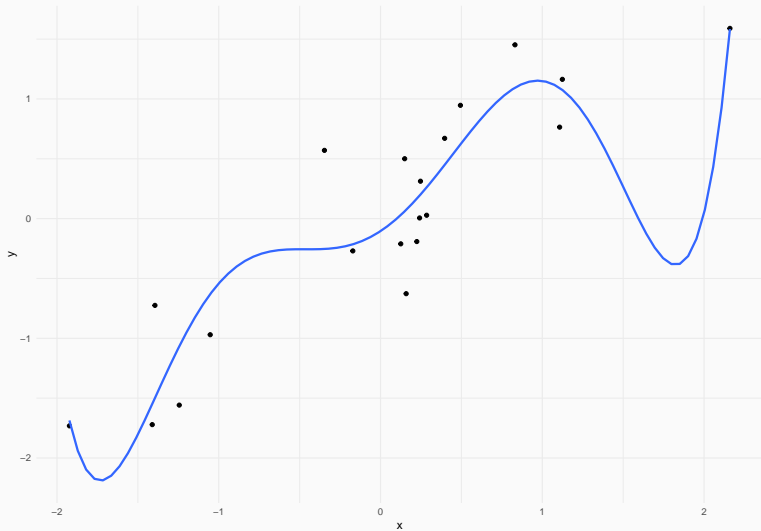
```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- Identical outcome variables
- Nested models (parameters in model A are a subset of parameters in model B)

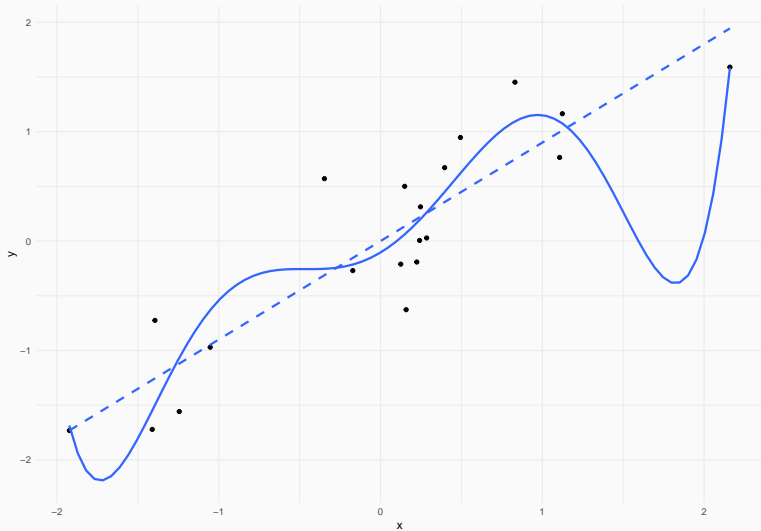
## Dangers of relying exclusively on goodness-of-fit measures



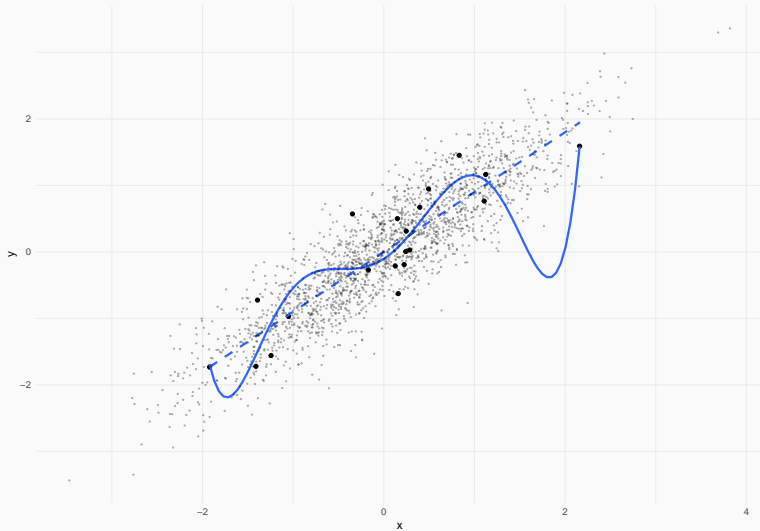
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## A more general approach: Bayesian Information Criteria

BIC is a general approach to comparing models estimated through MLE that is similar to a likelihood ratio test.

$$BIC = \ln(n)k - 2\ln(L)$$

Where  $n$  is the number of observations in our data,  $k$  is the number of parameters in the model, and  $L$  is the maximum of the likelihood function of our model.



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How does BIC differ from a likelihood ratio test?

- Directly compares goodness of fit
- Does not require nested models (does require identical outcomes)
- Easy to compare models
- Penalizes models for complexity, helps avoid overfitting

Models with low BIC fit better than models with high BIC

## BIC example

`BIC(m0)`

```
## [1] 929.6981
```

`BIC(m1)`

```
## [1] 936.3624
```

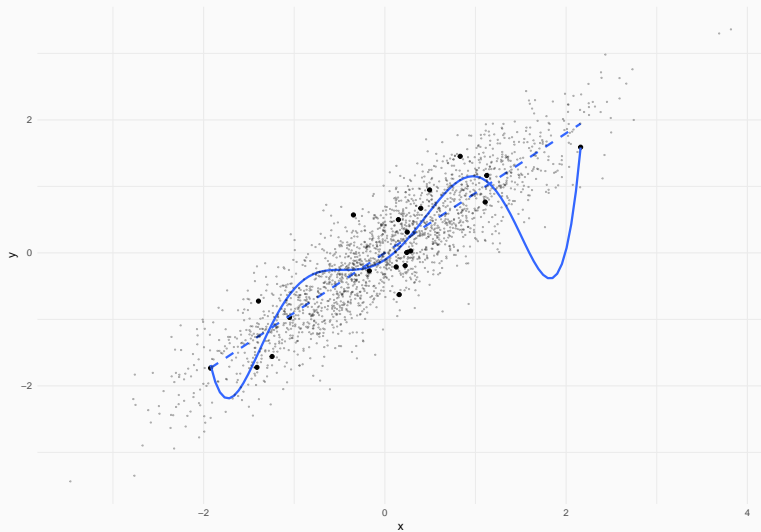
`BIC(m2)`

```
## [1] 835.5333
```

So we conclude that m2 is the better fit, because

$$BIC(m0) - BIC(m2) > BIC(m0) - BIC(m1)$$

## Returning to our overfit example



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```
formula(m_true)
```

```
## y ~ x
```

```
summary(m_true)$r.squared
```

```
## [1] 0.81
```

```
formula(m_of)
```

```
## y ~ x + I(x^2) + I(x^3) + I(x^4) + I(x^5) + I(x^6)
```

```
summary(m_of)$r.squared
```

```
## [1] 0.8400007
```

```
BIC(m_true)
```

```
## [1] 31.50425
```

```
BIC(m_of)
```

```
## [1] 43.04582
```