

An introduction to statistical inference

Francisco Rodriguez-Sanchez

http://bit.ly/frod_san

Why statistics?

To answer questions like...

- ▶ what's the probability that something occurs?

To answer questions like...

- ▶ what's the probability that something occurs?
- ▶ does X influence Y? How much?

To ensure correct inferences

11	451	97	80	46	83	74	29	15	8.03	1.3
439	164	94	45	73	98	99	29	73	34.0	1.3
235	166	172	54	91	85	40	79	73	34.0	1.3
1.433	896	2.132	2.390	3.860	2.175	1.980	3.000	3.000	3.000	1.3
1.870	2.845	1.001	1.920	1.760	2.981	3.000	3.000	3.000	3.000	1.3
2.427	1.335	1.230	1.250	1.715	2.524	2.956	2.956	2.956	2.956	1.3
2.424	2.697	1.001	1.250	1.275	2.520	2.718	2.718	2.718	2.718	1.3
1.692	84	2.05	2.390	2.985	2.020	2.020	2.020	2.020	2.020	1.3
1.199	2.032	1.198	2.415	2.415	2.415	2.415	2.415	2.415	2.415	1.3
35	290	92	430	268	159	324	324	324	324	1.3
35	243	249	277	175	324	324	324	324	324	1.3
74	249	301	277	175	324	324	324	324	324	1.3
94	301	277	3.809	6.308	2.450	2.450	2.450	2.450	2.450	1.3

Inference



Bolker et al 2009 TREE:

'311 out of 537 GLMM analyses (58%) used these tools
inappropriately'

To get answers to tough problems

For example...

How many seeds do trees produce?



A. Torrenegra

Inferring tree fecundity



Course goals

- ▶ **Understand** statistical inference

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- ▶ Avoid **misconceptions**

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- ▶ Avoid **misconceptions**
- ▶ Promote **good practices**

Topics

- ▶ Descriptive statistics

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- ▶ Graphics

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- ▶ Sampling

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- ▶ Linear models & GLMs

Topics

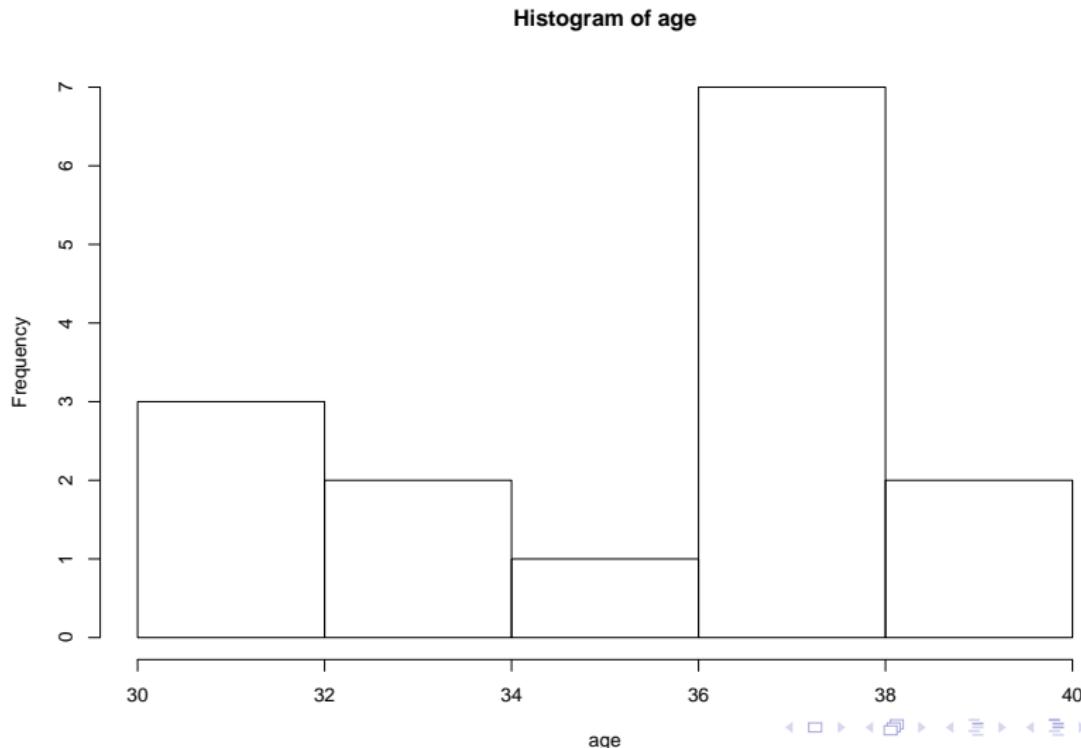
- ▶ Descriptive statistics
- ▶ Graphics
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- ▶ Experimental design
- ▶ Hypothesis testing
- ▶ Bayesian inference
- ▶ Linear models & GLMs
- ▶ Model selection

Descriptive statistics

Guess my age

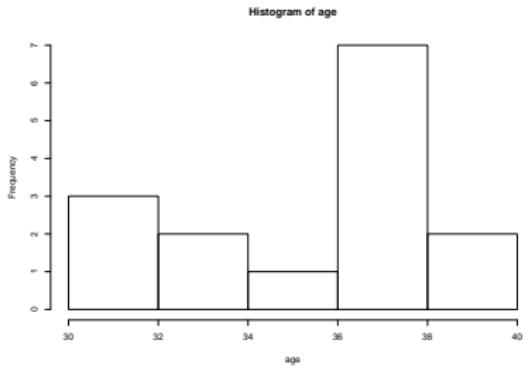
Graph your estimates

```
hist(age)
```



Summarise that distribution

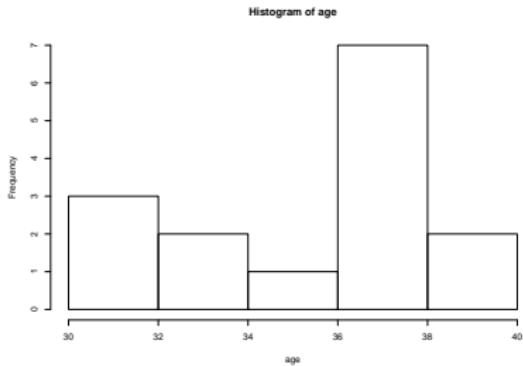
► Central tendency



Summarise that distribution

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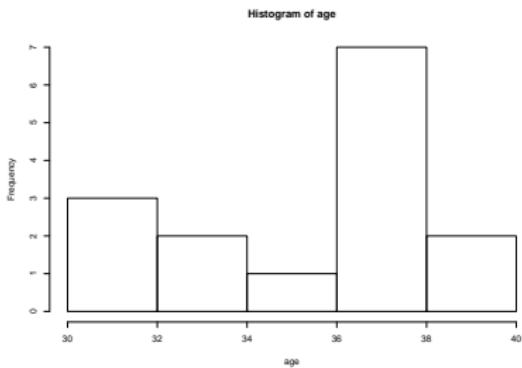
- mean



Summarise that distribution

► Central tendency

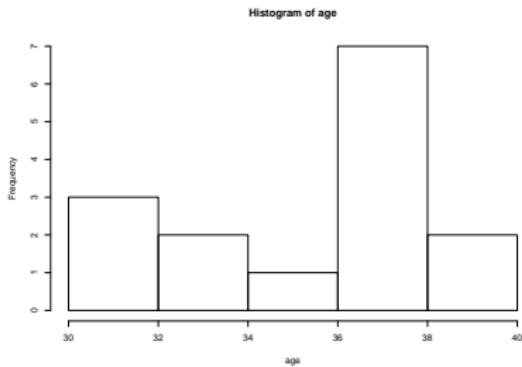
- ▶ mean
- ▶ median



Summarise that distribution

► Central tendency

- ▶ mean
- ▶ median
- ▶ mode

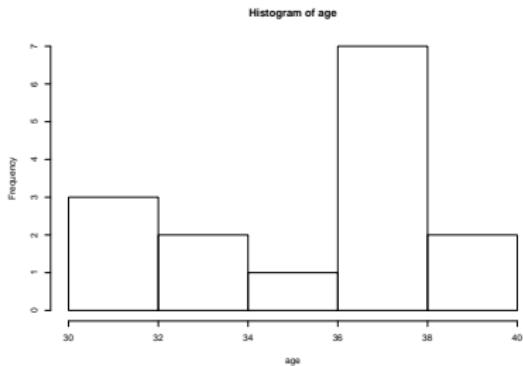


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- ▶ **Central tendency**

- ▶ mean
- ▶ median
- ▶ mode

- ▶ **Variation**



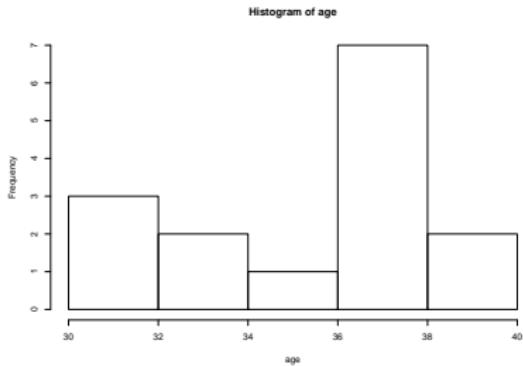
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- ▶ min, max, range



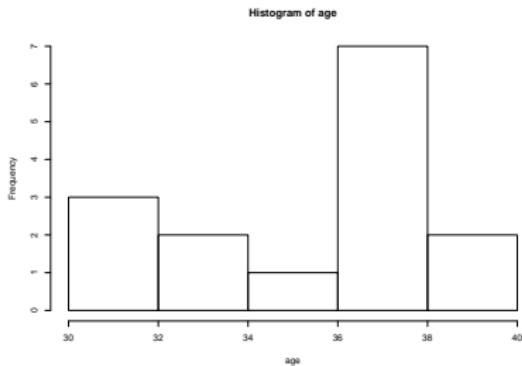
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- ▶ min, max, range
- ▶ quantiles



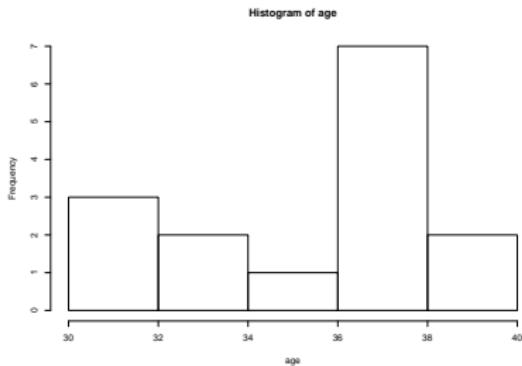
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► Variation

- ▶ min, max, range
- ▶ quantiles
- ▶ standard deviation



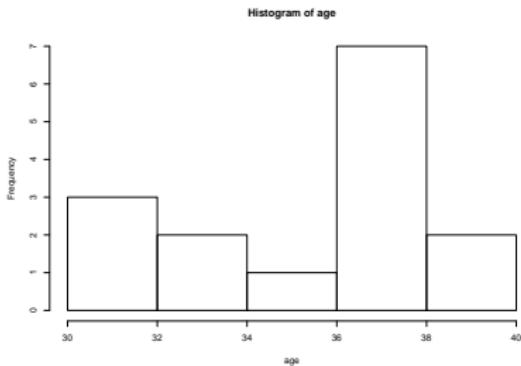
Summarise that distribution

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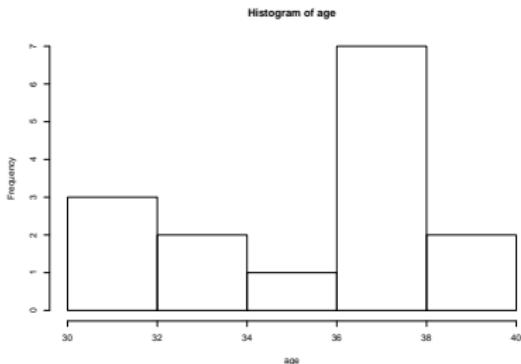
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- ▶ quantiles
- ▶ standard deviation
- ▶ standard error
- ▶ coefficient of variation



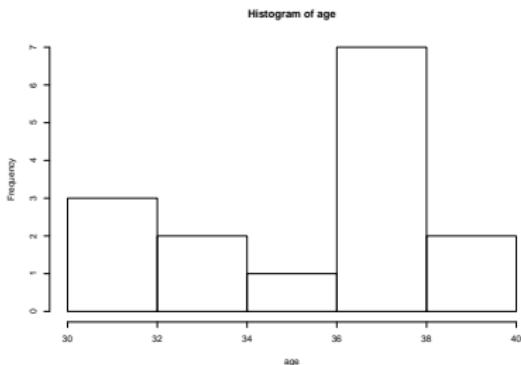
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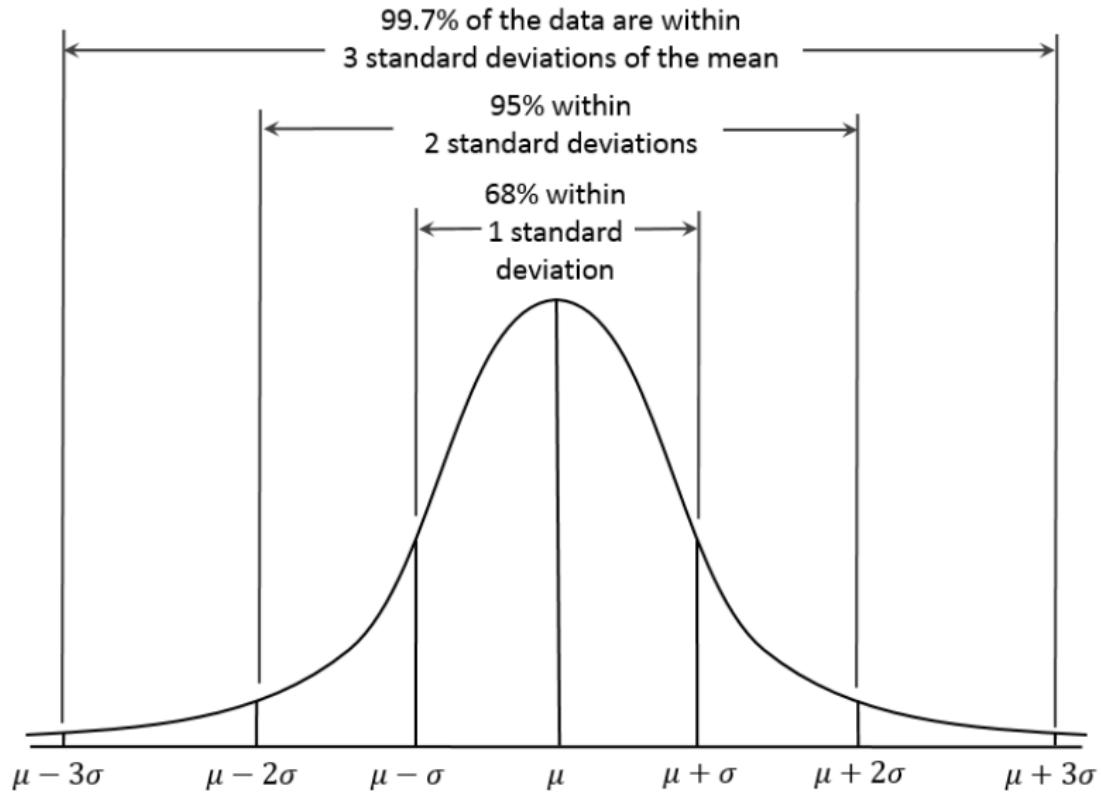
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► Variation

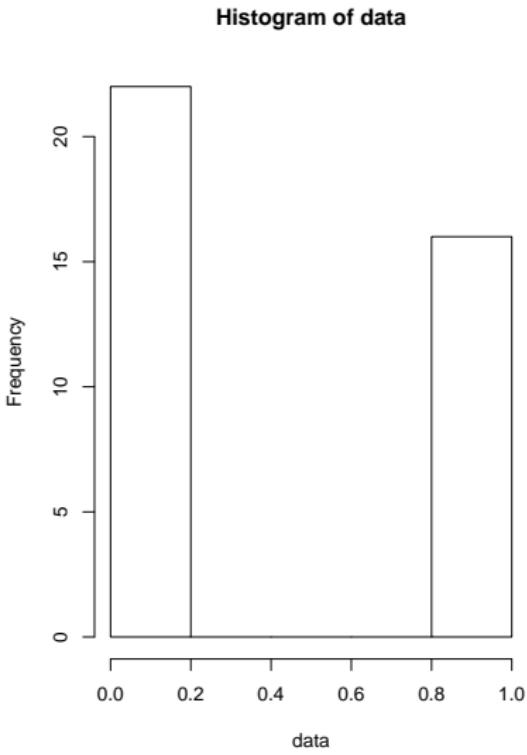
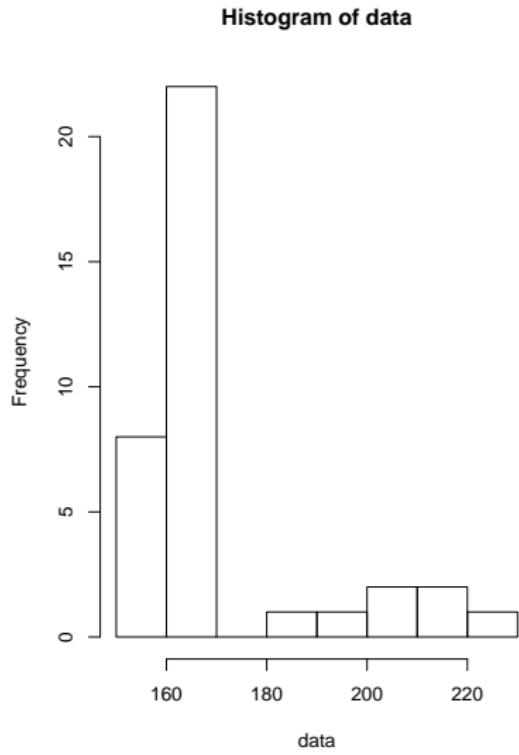
- ▶ min, max, range
- ▶ quantiles
- ▶ standard deviation
- ▶ standard error
- ▶ coefficient of variation
- ▶ confidence intervals



In a Normal distribution



What statistical descriptors are best? (and why)



Sampling

Inference: from samples to population

We rarely measure the whole **population**, but take **samples** instead.



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5. Do all CIs contain true mean height?

Understanding confidence intervals

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- ▶ To read more: Morey et al (2015)

What happens if we increase sample size?

- ▶ CI width decreases...

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- ▶ CI width decreases...
- ▶ but still 5% of CIs will NOT contain true mean!

Bayesian credible intervals

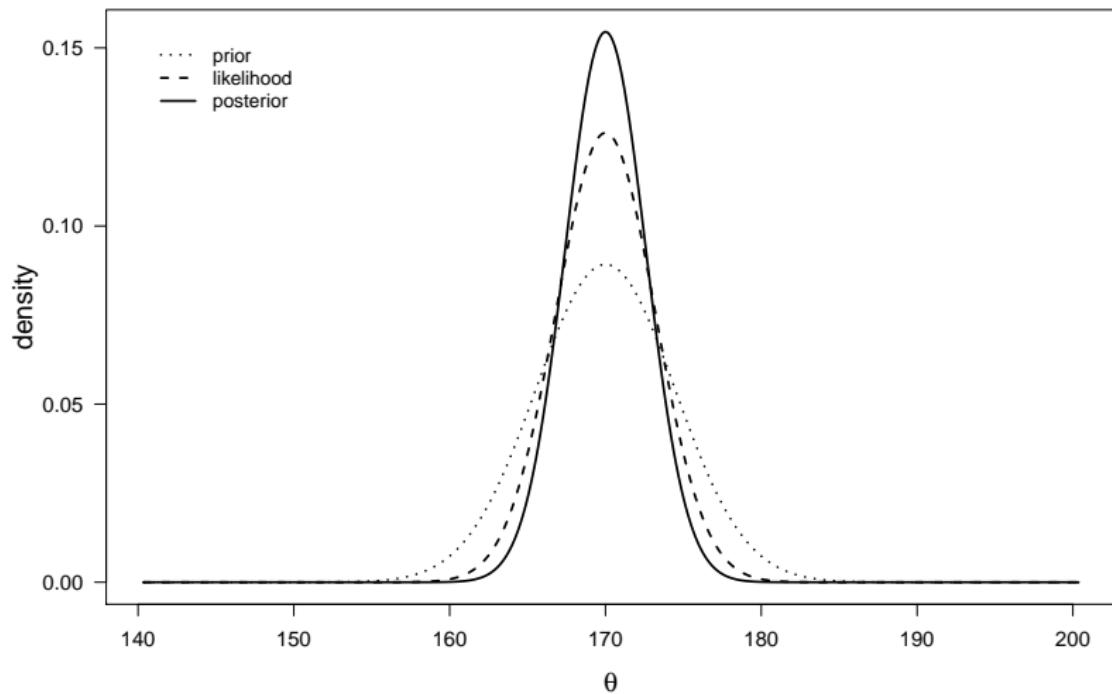
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Bayesian credible intervals

- ▶ Bayesian **credible** intervals do give the probability that true parameter value is contained within them.
- ▶ Frequentist CIs and Bayesian credible intervals can be similar, but not always.

Bayesian inference: prior, posterior, and Bayes' theorem

$$\text{Posterior} \propto \text{Likelihood} \times \text{Prior}$$



Experimental design

Eg. Evaluating fertilizer effect



Replication!



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- ▶ Determine sample size *a priori* according to wanted precision of estimates (power analysis).
- ▶ Traditionally, ecology studies have had too low sample sizes.
- ▶ Hence missing many subtle effects, and prone to bias.
- ▶ Complex models (w/ interactions etc) require **high** sample sizes.

Sample size is very important

See The evolution of correlations

Stopping rules:

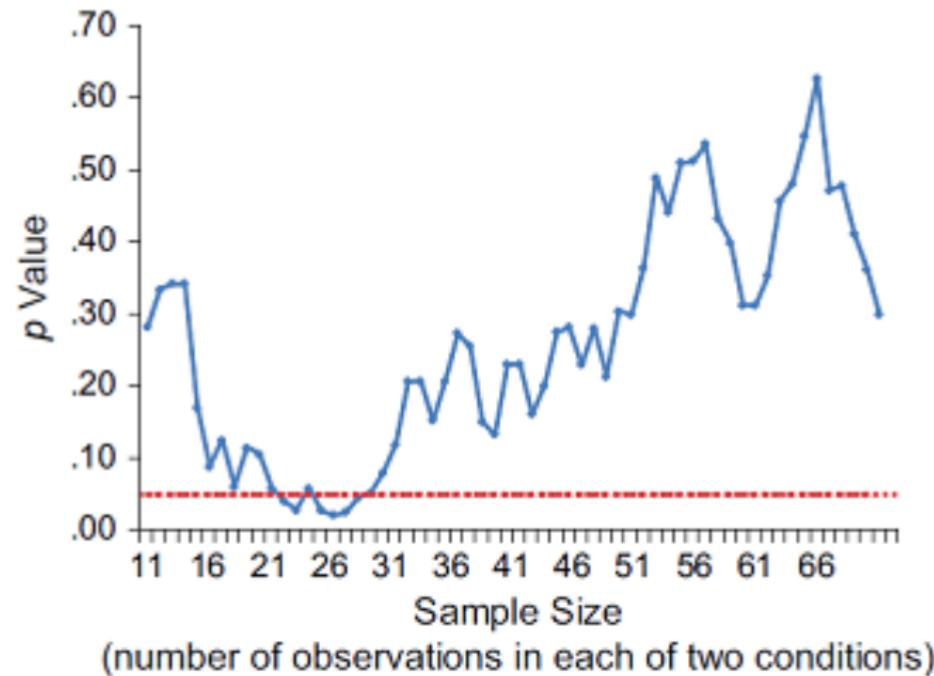


Fig. 2. Illustrative simulation of p values obtained by a researcher who continuously adds an observation to each of two conditions, conducting a t test after each addition. The dotted line highlights the conventional significance criterion of $p \leq .05$.

Randomization



Randomization

- ▶ Haphazard \neq Random

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- ▶ Stratify: randomize within groups (e.g. species, soil types)

Have controls

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- ▶ Untreated individuals, plots... (assigned randomly, of course).
- ▶ Must differ only in treatment (i.e. homogeneous environment).
- ▶ Measure before & after treatment.
- ▶ Consider blind designs to avoid observer bias.

Hypothesis testing

Does height differ between local and foreign students?

- ▶ Heights in Sevilla:

188 162 195 150 162

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
150.0	162.0	162.0	171.4	188.0	195.0

180 182 166 179 188 177 176 167 186 191

Min.	1st Qu.	Median	Mean	3rd Qu.	Max.
166.0	176.2	179.5	179.2	185.0	191.0

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- ▶ We know what happens in **our samples**, but want to extrapolate to the whole **population**.

If we sample students' heights in this class. . .

- ▶ Can we extrapolate results to

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- ▶ Can we extrapolate results to
 - ▶ this class?

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- ▶ Can we extrapolate results to
 - ▶ this class?
 - ▶ this university?
 - ▶ this city?
 - ▶ the world?
- ▶ What's the **suitable population** to make inferences given this sample?

NHST concepts

Null and alternative hypotheses



Null and alternative hypotheses

- ▶
- ▶ **Null hypothesis:** heights don't differ.

Null and alternative hypotheses

- ▶
- ▶ **Null hypothesis:** heights don't differ.
- ▶ **Alternative hypothesis:** heights are different.

P value



P value

- ▶
- ▶ Probability of observing data as or more extreme than these *if H₀ was true.*

P value

- ▶
- ▶ Probability of observing data as or more extreme than these *if H₀ was true.*
- ▶ Hence **the lower P the more unlikely H₀** (i.e. more likely there's a true difference).

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- ▶ If $p < 0.05$, we **reject** H_0 .

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- ▶ If $p < 0.05$, we **reject** H_0 .
- ▶ If $p > 0.05$, we **fail to reject** H_0
- ▶ (which is not the same as 'H₀ is true')

Let's do the test

```
t.test(h.sevi, h.out)
```

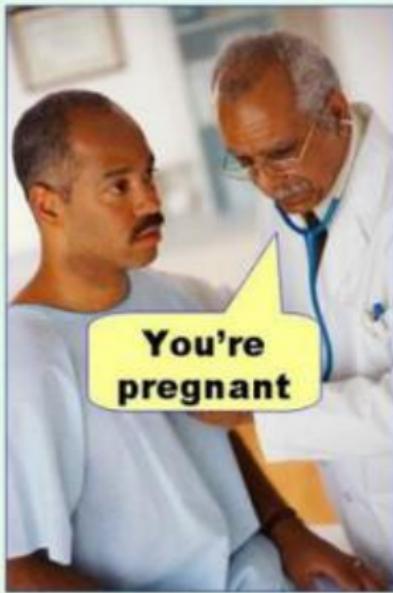
Welch Two Sample t-test

```
data: h.sevi and h.out
t = -0.87134, df = 4.7547, p-value = 0.4254
alternative hypothesis: true difference in means is not equal to
95 percent confidence interval:
-31.1728 15.5728
sample estimates:
mean of x mean of y
171.4      179.2
```

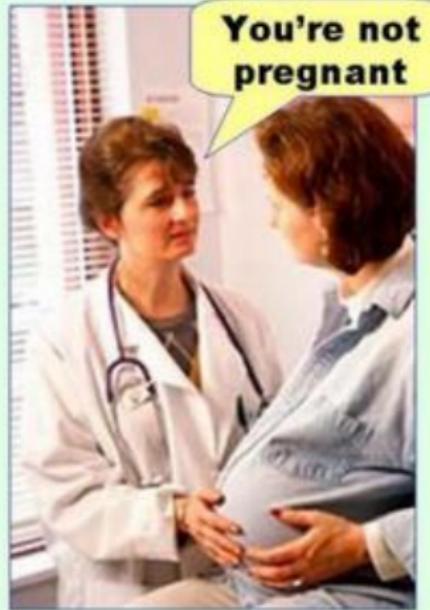
Are heights different then?

Rejecting hypotheses: two types of error

Type I error
(false positive)



Type II error
(false negative)



Rejecting hypotheses: two types of error

Statistics: Hypothesis Test	Null Hypothesis is True	Null Hypothesis is False
Reject Null Hypothesis	Type I Error	Correct
Fail to Reject Null Hypothesis	Correct	Type II Error

Power: Probability of detecting true difference (rejecting H₀ when it's false).

Understanding NHST

<http://rpsychologist.com/d3/NHST/>

Example: biased coin

```
[1] 0 0 1 0 0 1 1 1 1 0
```

```
1-sample proportions test without continuity correction
```

```
data: sum(coin) out of ntrials, null probability 0.5  
X-squared = 0, df = 1, p-value = 1
```

```
alternative hypothesis: true p is not equal to 0.5
```

```
95 percent confidence interval:
```

```
0.2365931 0.7634069
```

```
sample estimates:
```

```
p  
0.5
```

Correlation between variables

<http://rpsychologist.com/d3/correlation/>

Common pitfalls and good practice

Interesting reading

esa

ECOSPHERE

Applied statistics in ecology: common pitfalls and simple solutions

E. ASHLEY STEEL,^{1,†} MAUREEN C. KENNEDY,² PATRICK G. CUNNINGHAM,³ AND JOHN S. STANOVICK⁴

<http://dx.doi.org/10.1890/ES13-00160.1>

First things first

- ▶ Always

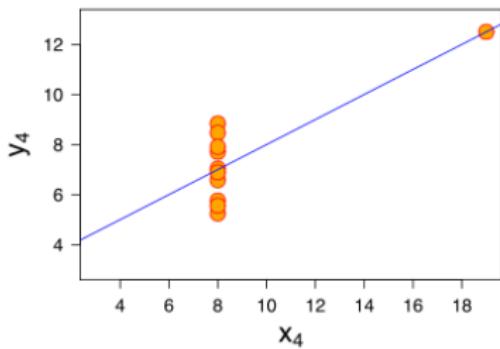
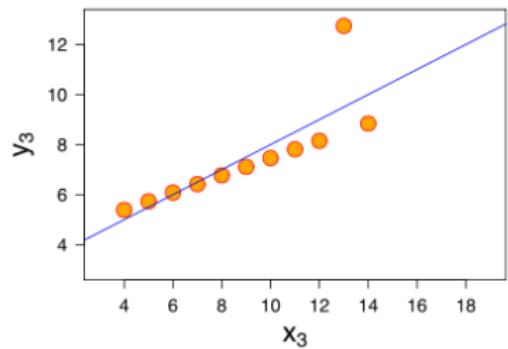
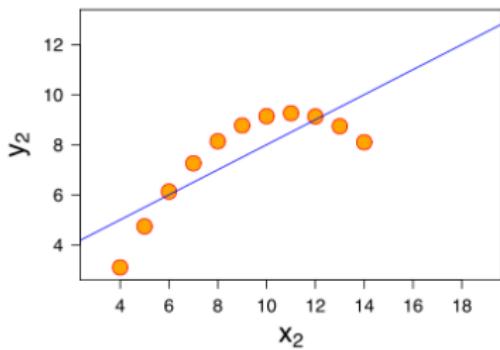
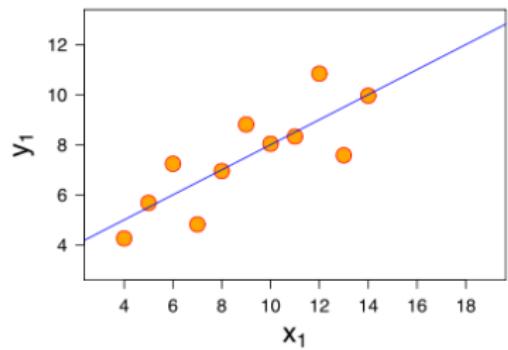
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Plot data and models



Plot. Check models. Plot. Check assumptions. Plot.

Lavine 2014 *Ecology*

News: Hamburgers increase risk of heart attack

- ▶ In a sample of 10,000 people, it was found that eating >2 hamburgers a week increased heart attacks by 50%.

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- ▶ In a sample of 10,000 people, it was found that eating >2 hamburgers a week increased heart attacks by 50%.
- ▶ **Do hamburgers increase heart attacks?**

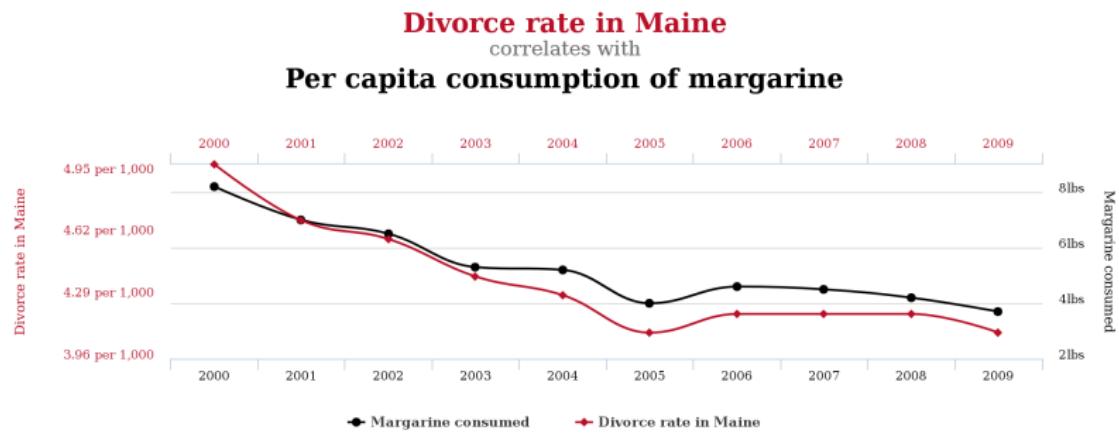
Bigger flowers increase reproductive success

- ▶ We found that plants with bigger flowers produced 30% more seeds...

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Correlation vs Causation

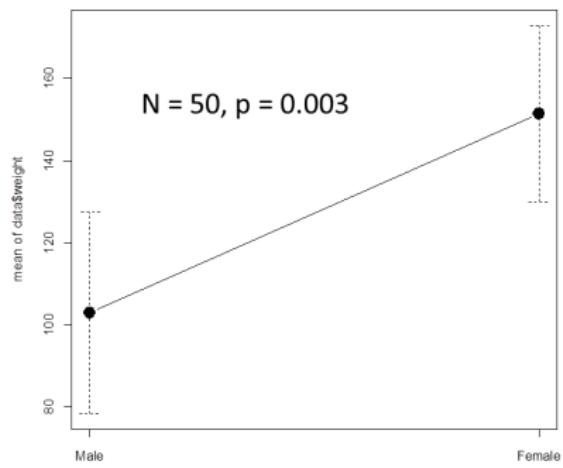
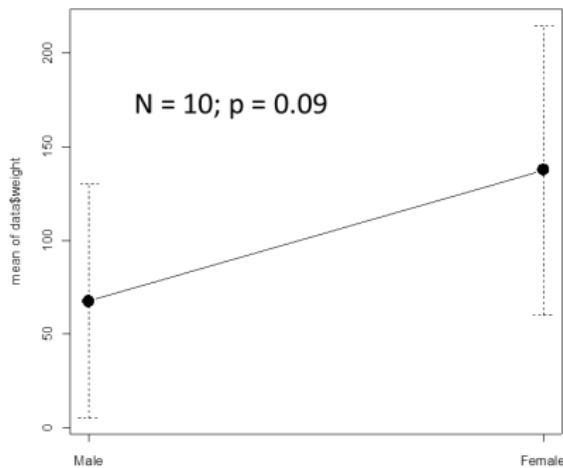


<http://tylervigen.com/spurious-correlations>

Statistically significant != biologically important

- ▶ Big real difference but low sample size:

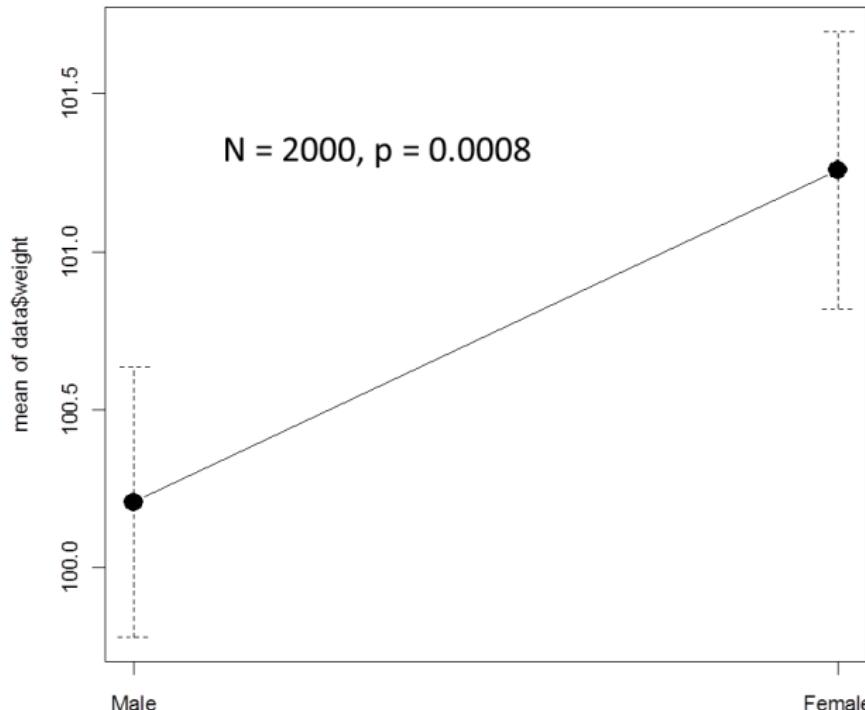
Real difference = 40 g



Statistically significant != biologically important

- Trivial difference, big sample size:

Real difference = 1 g



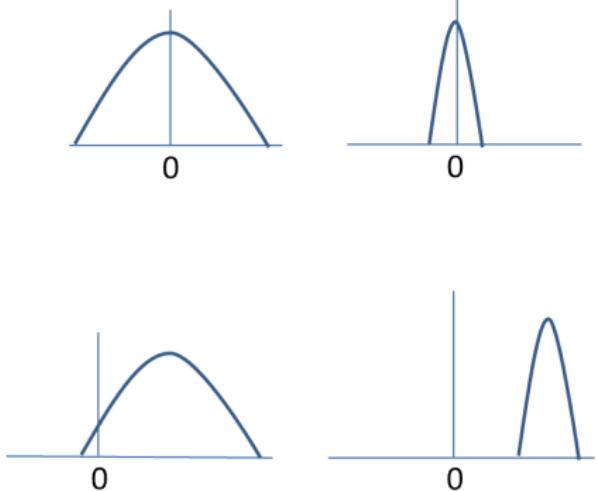
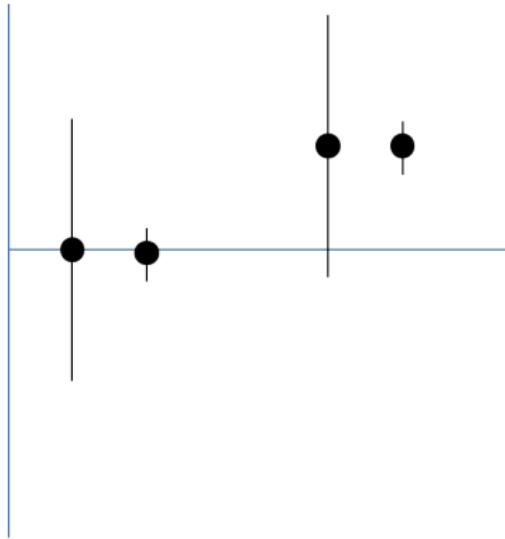
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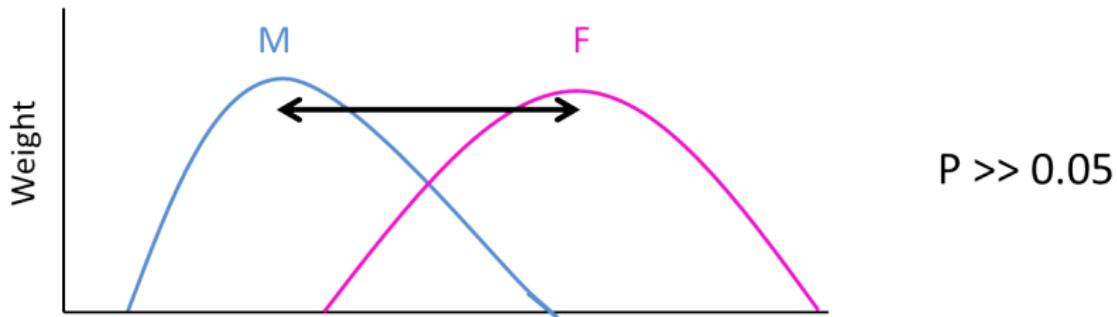
Statistically significant != biologically important

- ▶ P-value depends on sample size: with large n , everything can be significant.
- ▶ Suggested reading: significantly misleading

Not significant != there is no effect



Failure to reject H₀ != H₀ is true



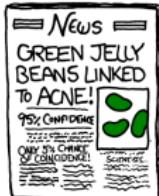
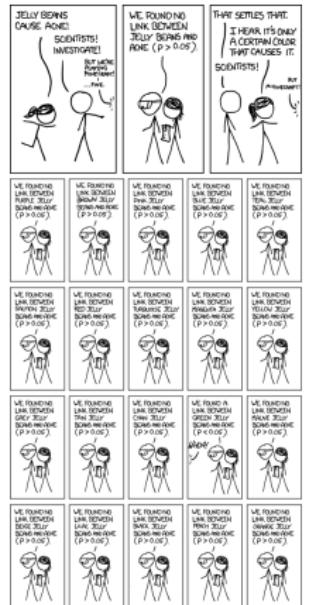
0.05 is an arbitrary threshold

The Difference Between “Significant” and “Not Significant” is not Itself Statistically Significant

Andrew GELMAN and Hal STERN

<http://dx.doi.org/10.1198/000313006X152649>

Multiple hypothesis testing



How to make your results significant

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 2. Artificially choose when to end your experiment.
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 4. Test different conditions (e.g. different levels of a factor) and report the ones you like.
- To read more: Simmons et al 2011

The New Statistics

Aim for estimation of effects and their uncertainty.



General Article

The New Statistics: Why and How

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<http://dx.doi.org/10.1177/0956797613504966>

How many types of errors?

- ▶ **Type I:** incorrect rejection of null hypothesis.

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- ▶ **Type S (Sign):** estimating effect in opposite direction.

How many types of errors?

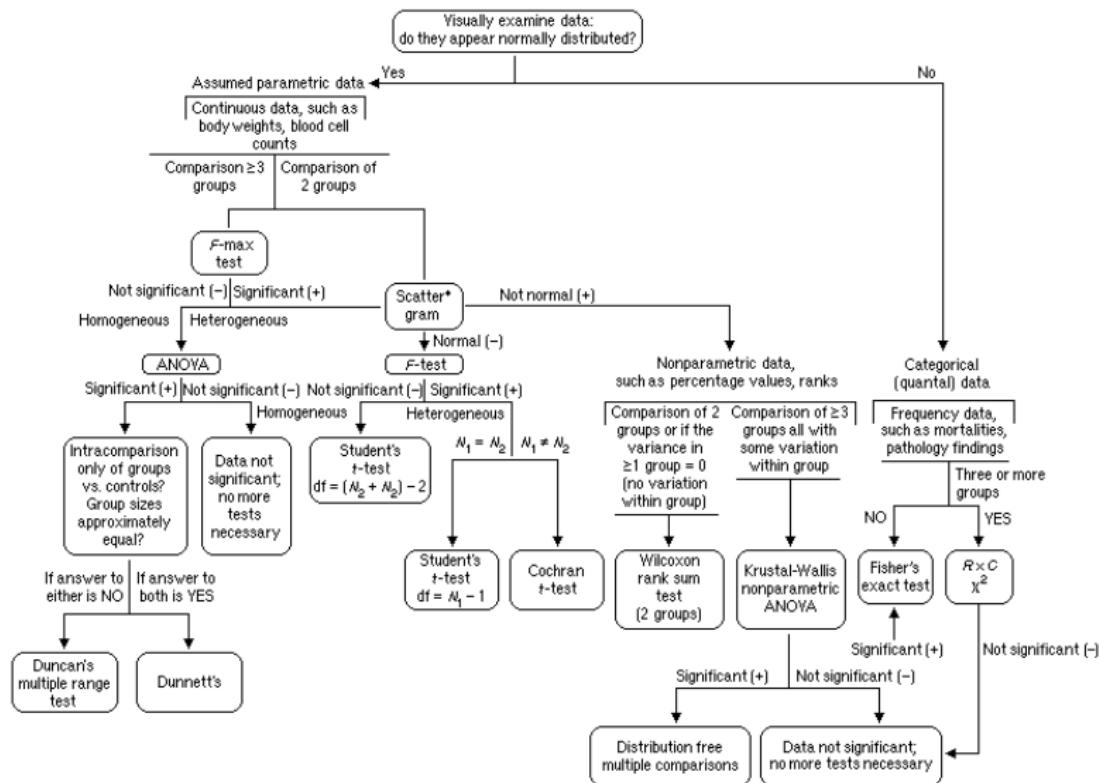
- ▶ **Type I:** incorrect rejection of null hypothesis.
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- ▶ **Type S (Sign):** estimating effect in opposite direction.
- ▶ **Type M (Magnitude):** Misestimating magnitude of the effect (under or overestimating).

How many types of errors?

- ▶ **Type I:** incorrect rejection of null hypothesis.
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- ▶ **Type S (Sign):** estimating effect in opposite direction.
- ▶ **Type M (Magnitude):** Misestimating magnitude of the effect (under or overestimating).
- ▶ **Type III:** finding right answer to the wrong question!

Introduction to statistical modelling

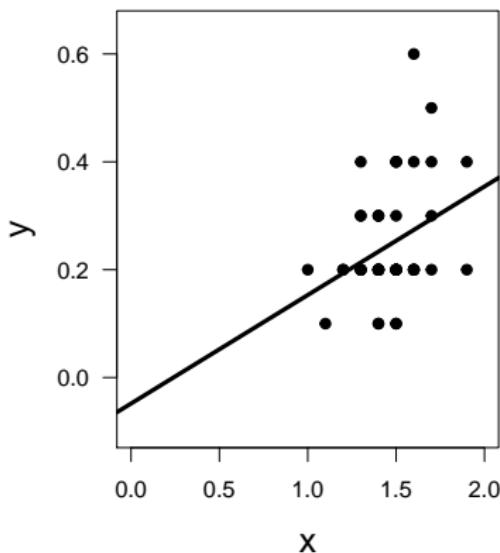
Modern statistics are easier than this



Our overarching regression framework

$$y_i = a + bx_i + \varepsilon_i$$

$$\varepsilon_i \sim N(0, \sigma^2)$$



Data

y = response variable

x = predictor

Parameters

a = intercept

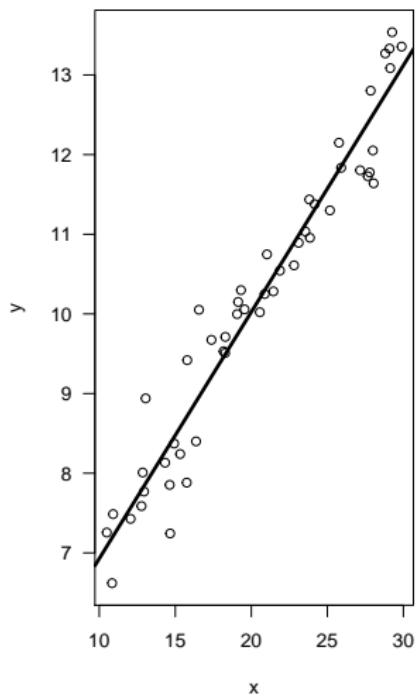
b = slope

σ = residual variation

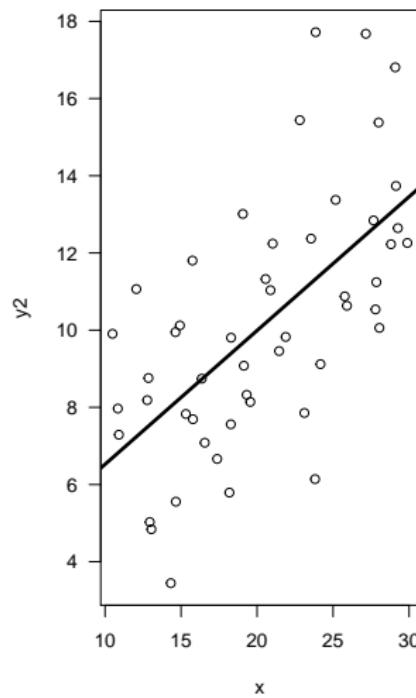
ε = residuals

Residual variation (error)

small



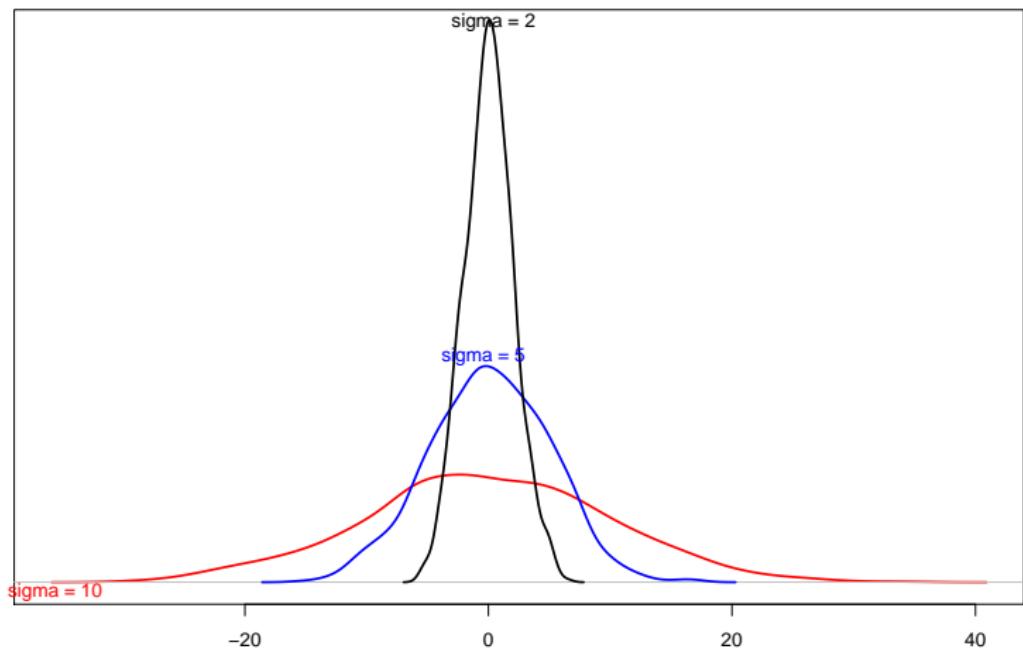
large



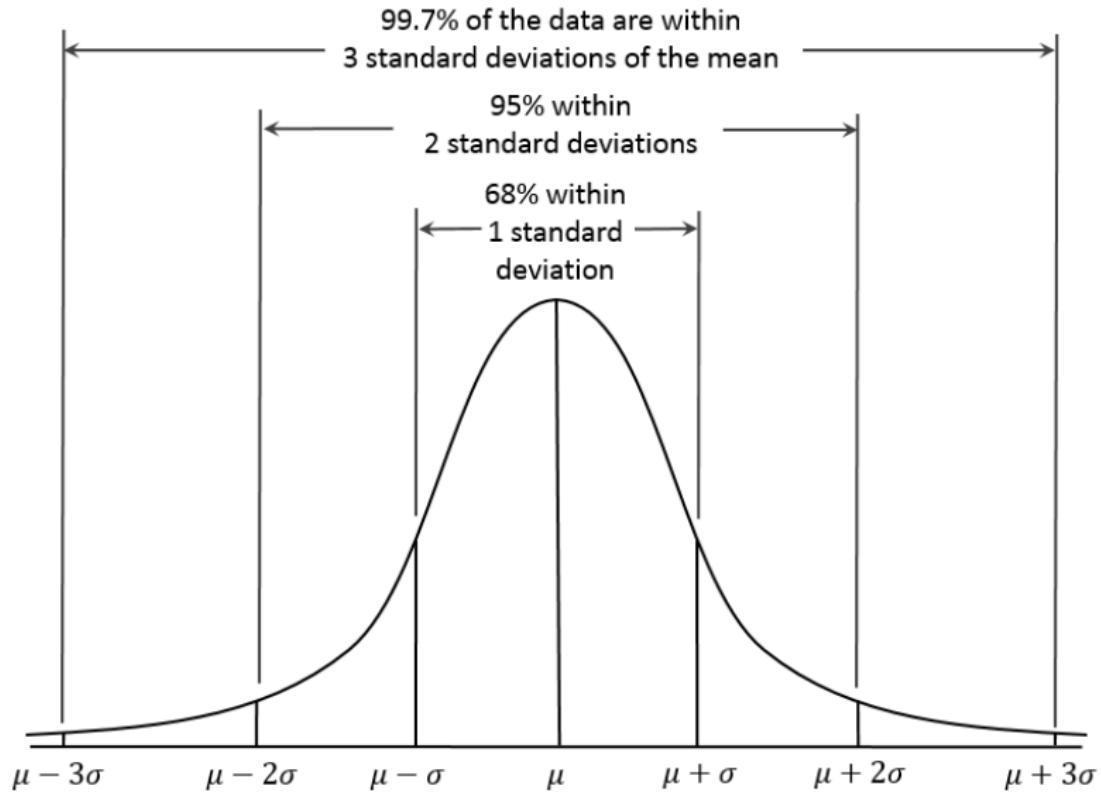
Residual variation

$$\varepsilon_i \sim N(0, \sigma^2)$$

Distribution of residuals



In a Normal distribution

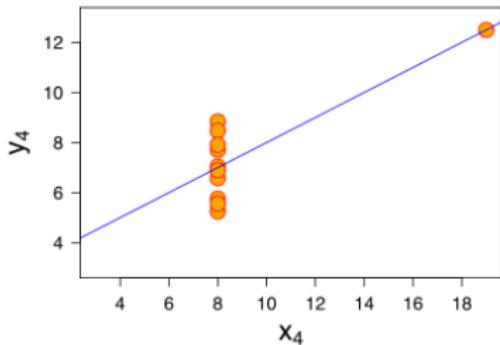
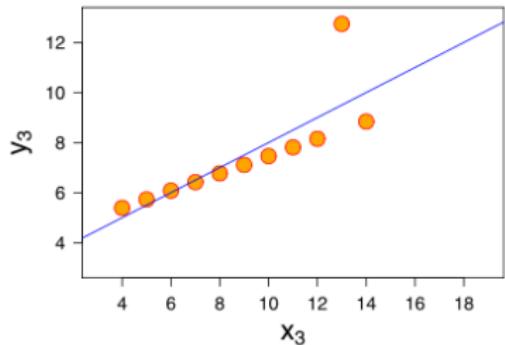
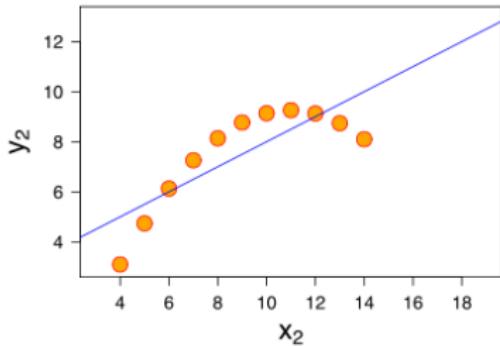
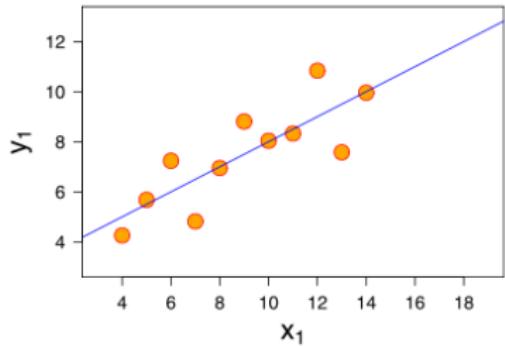


Let's do real data analysis

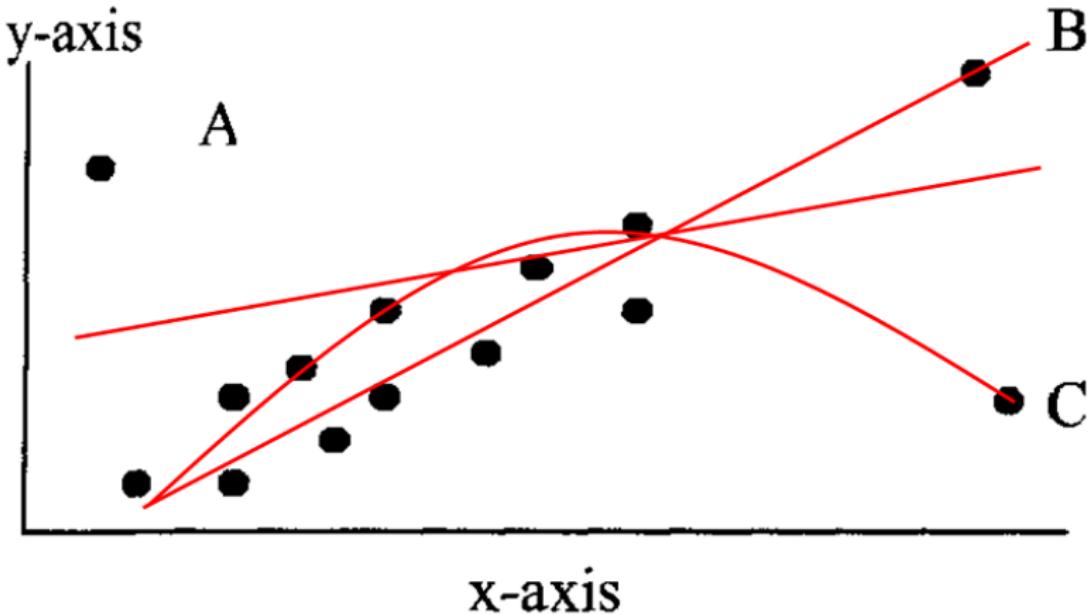
Q: What is the relationship between petal width and length in *Iris setosa*?

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa

Always plot your data first!



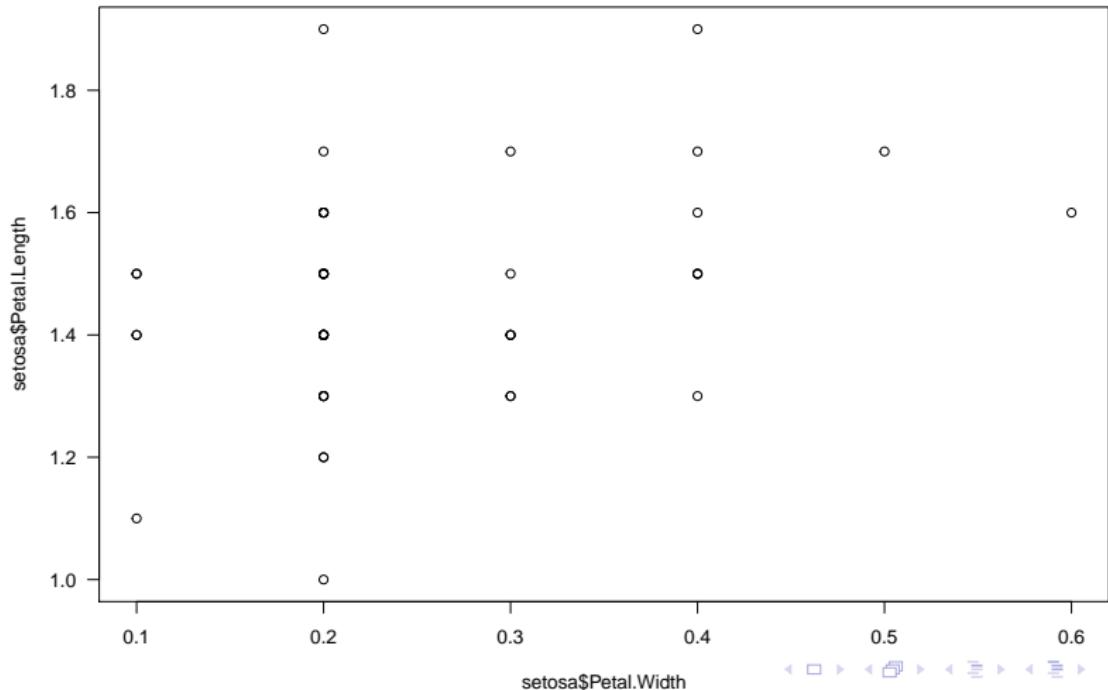
Outliers impact on regression



See <http://rpsychologist.com/d3/correlation/>

Scatterplot

```
plot(setosa$Petal.Width, setosa$Petal.Length, las = 1)
```



Now fit model

```
m1 <- lm(Petal.Length ~ Petal.Width, data = setosa)
```

What does this mean?

Call:

```
lm(formula = Petal.Length ~ Petal.Width, data = setosa)
```

Residuals:

Min	1Q	Median	3Q	Max
-0.43686	-0.09151	-0.03686	0.09018	0.46314

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	1.32756	0.05996	22.141	<2e-16 ***
Petal.Width	0.54649	0.22439	2.435	0.0186 *

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

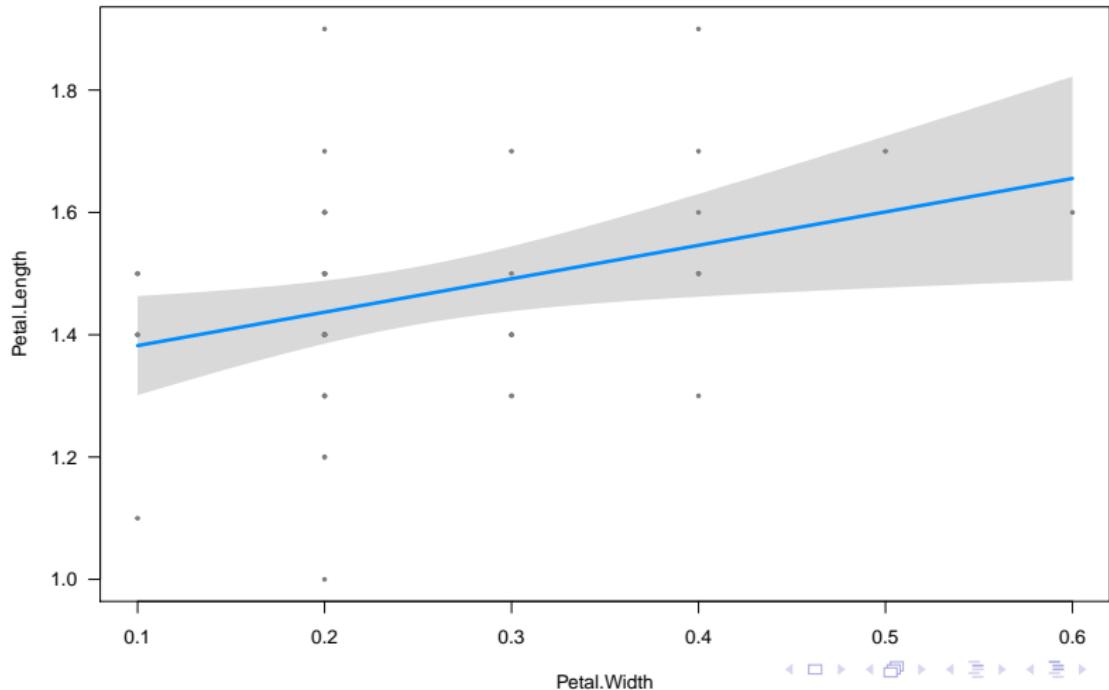
Residual standard error: 0.1655 on 48 degrees of freedom

Multiple R-squared: 0.11, Adjusted R-squared: 0.09144

F-statistic: 5.931 on 1 and 48 DF, p-value: 0.01864

Plot model (visreg)

```
visreg(m1)
```



Linear model assumptions

- ▶ Linearity (transformations, GAM...)

Linear model assumptions

- ▶ Linearity (transformations, GAM...)
- ▶ Residuals:

Linear model assumptions

- ▶ Linearity (transformations, GAM...)
- ▶ Residuals:
 - ▶ Independent

Linear model assumptions

- ▶ Linearity (transformations, GAM...)
- ▶ Residuals:
 - ▶ Independent
 - ▶ Equal variance

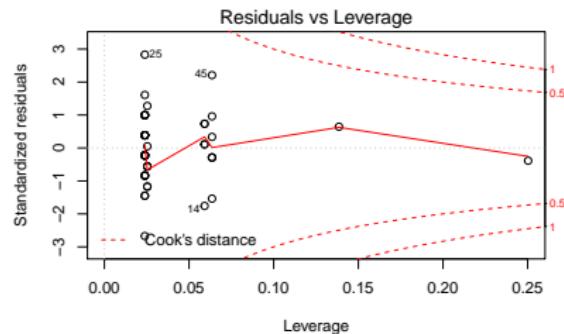
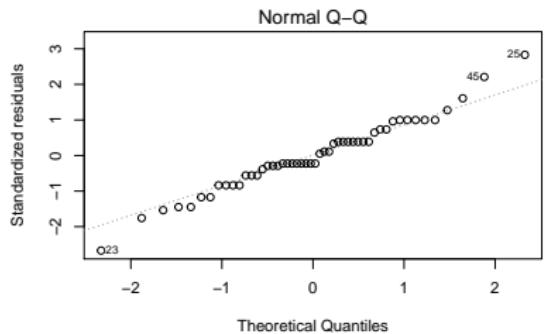
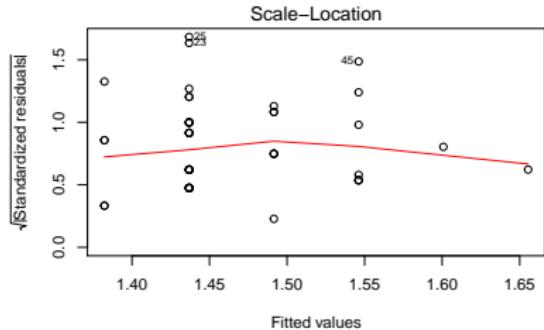
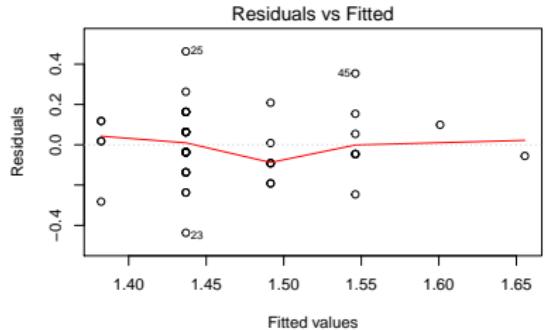
Linear model assumptions

- ▶ Linearity (transformations, GAM...)
- ▶ Residuals:
 - ▶ Independent
 - ▶ Equal variance
 - ▶ Normal

Linear model assumptions

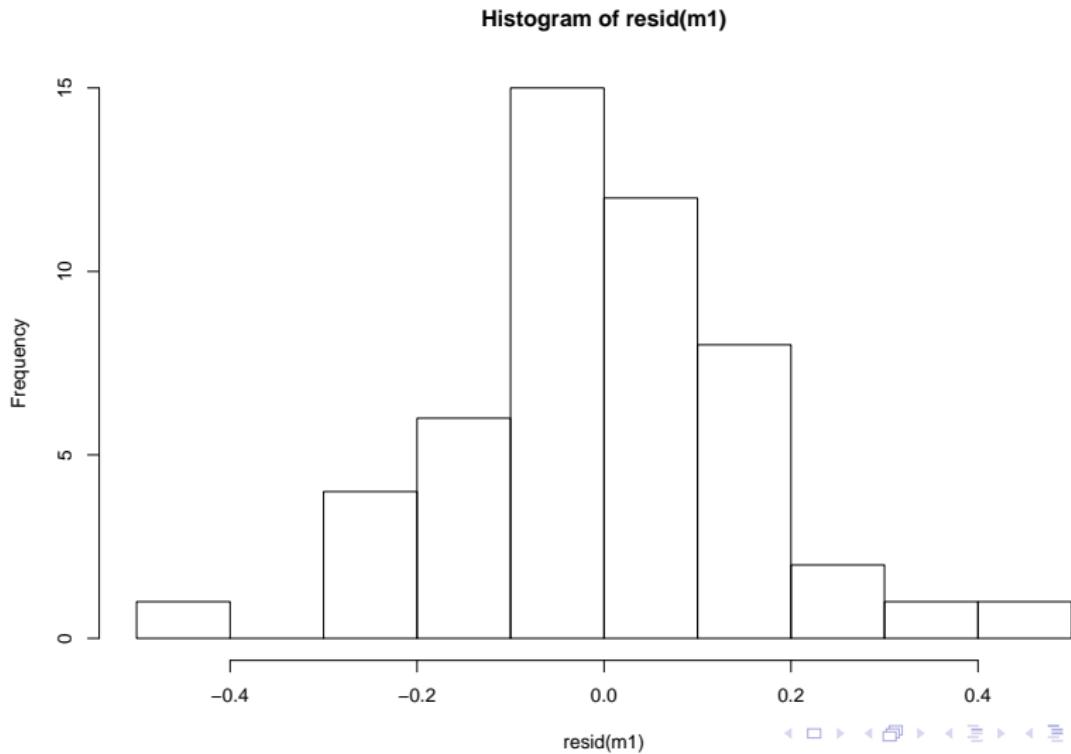
- ▶ Linearity (transformations, GAM...)
- ▶ Residuals:
 - ▶ Independent
 - ▶ Equal variance
 - ▶ Normal
- ▶ No measurement error in predictors

Model checking: residuals



Are residuals normal?

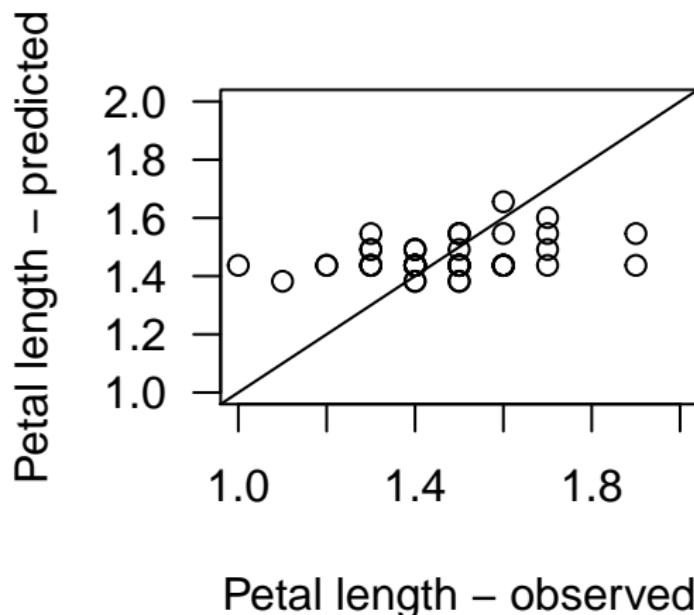
```
hist(resid(m1))
```



How good is the model in predicting petal length?

Observed vs Predicted values: use fitted.

```
plot(setosa$Petal.Length, fitted(m1), xlab = "Petal length - obs")
```



Using fitted model for prediction

Q: Expected petal length if width = 0.39?

Using fitted model for prediction

Q: Expected petal length if width = 0.39?

```
predict(m1, data.frame(Petal.Width = c(0.39)), se.fit = TRUE)
```

```
$fit
```

```
1
```

```
1.540695
```

```
$se.fit
```

```
[1] 0.03990149
```

```
$df
```

```
[1] 48
```

```
$residual.scale
```

```
[1] 0.1655341
```

Important functions

- ▶ plot

Important functions

- ▶ `plot`
- ▶ `summary`

Important functions

- ▶ `plot`
- ▶ `summary`
- ▶ `coef`

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- ▶ `resid`

Important functions

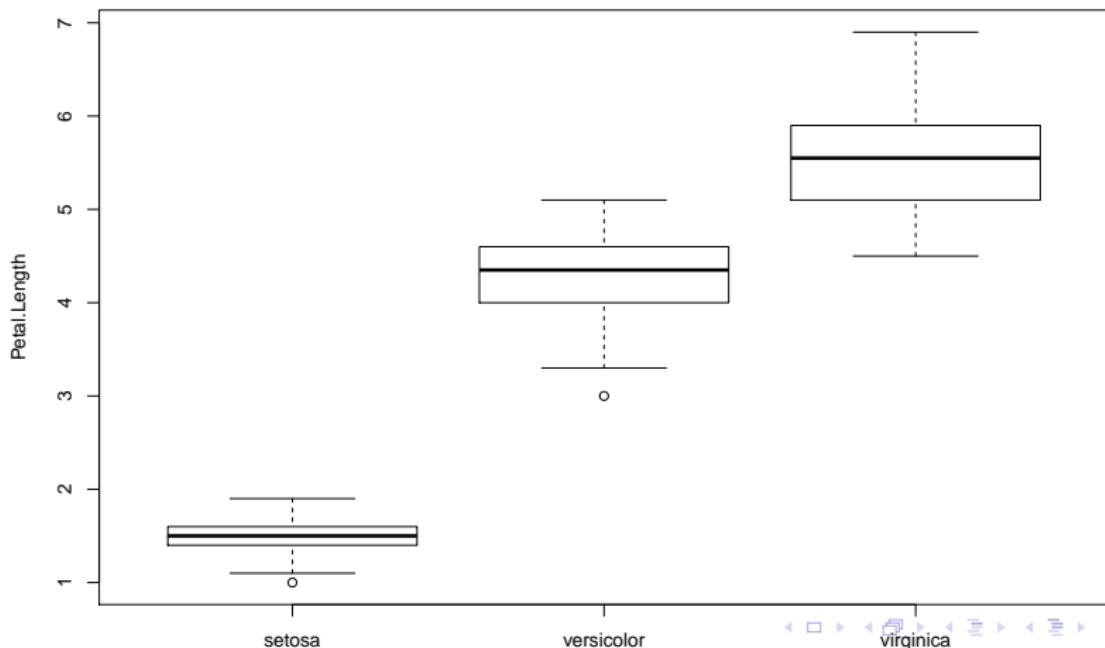
- ▶ plot
- ▶ summary
- ▶ coef
- ▶ confint
- ▶ fitted
- ▶ resid
- ▶ predict

Categorical predictors (factors)

Q: Does petal length vary among *Iris* species?

First, a plot:

```
plot(Petal.Length ~ Species, data = iris)
```



Linear model with categorical predictors

$$y_i = a + bx_i + \varepsilon_i$$

$$y_i = a + b_{versicolor} + c_{virginica} + \varepsilon_i$$

Model

```
m2 <- lm(Petal.Length ~ Species, data = iris)
```

Call:

```
lm(formula = Petal.Length ~ Species, data = iris)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.260	-0.258	0.038	0.240	1.348

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	1.46200	0.06086	24.02	<2e-16 ***
Speciesversicolor	2.79800	0.08607	32.51	<2e-16 ***
Speciesvirginica	4.09000	0.08607	47.52	<2e-16 ***

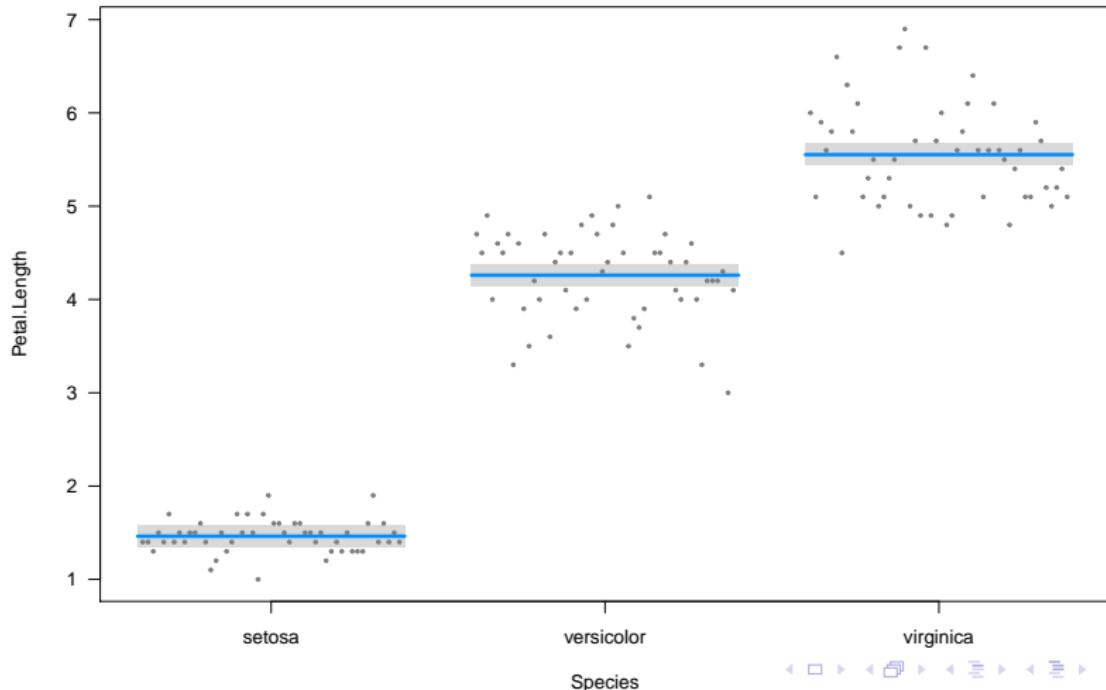
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.4303 on 147 degrees of freedom

Multiple R-squared: 0.9414, Adjusted R-squared: 0.9406 ↗ ↘

Petal length differences across 3 *Iris* species

```
visreg(m2)
```



Are differences statistically significant?

Compare CIs

```
summary(allEffects(m2))
```

model: Petal.Length ~ Species

Species effect

Species

	setosa	versicolor	virginica
	1.462	4.260	5.552

Lower 95 Percent Confidence Limits

Species

	setosa	versicolor	virginica
	1.341729	4.139729	5.431729

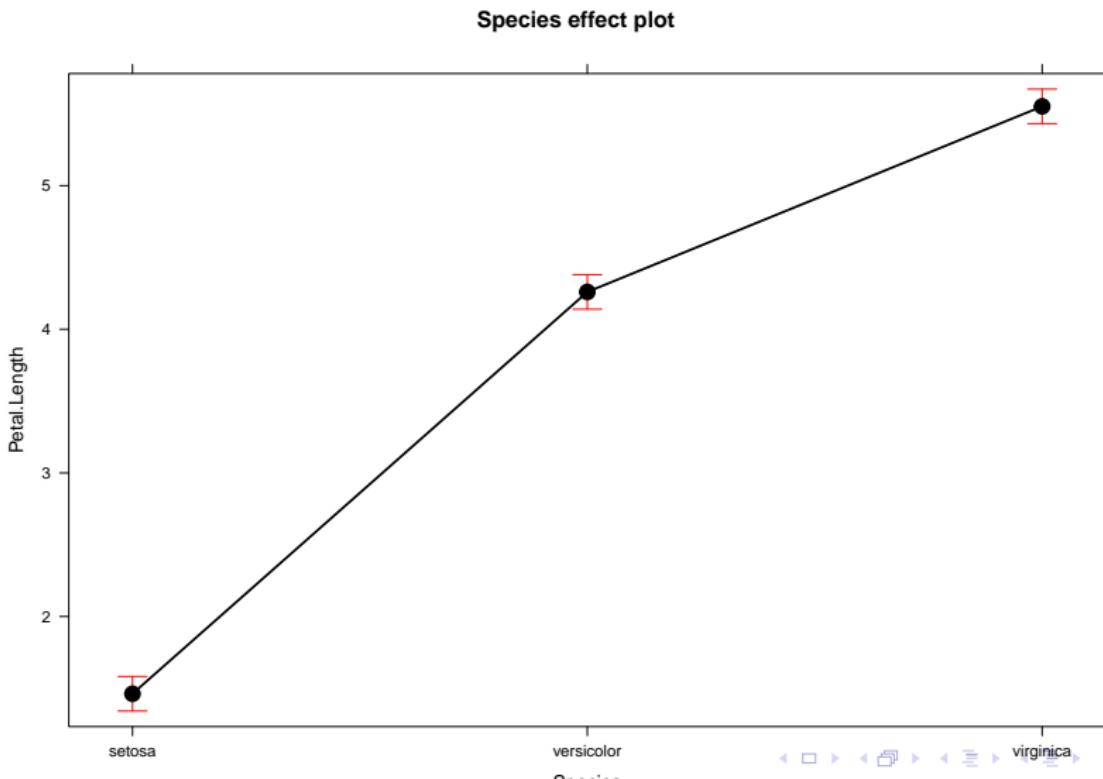
Upper 95 Percent Confidence Limits

Species

	setosa	versicolor	virginica
	1.582271	4.380271	5.672271

Plotting effects

```
plot(allEffects(m2))
```



Does height differ between local and foreign students?

Combining continuous and categorical predictors

Predicting *Iris* petal length according to species and petal width

$$y_i = a + bx_i + \varepsilon_i$$

$$y_i = a + b_{versicolor} + c_{virginica} + \varepsilon_i$$

$$y_i = a + b_{versicolor} + c_{virginica} + d \cdot PetalWidth_i + \varepsilon_i$$

Predicting *Iris* petal length according to species and petal width

Call:

```
lm(formula = Petal.Length ~ Species + Petal.Width, data = iris)
```

Residuals:

Min	1Q	Median	3Q	Max
-1.02977	-0.22241	-0.01514	0.18180	1.17449

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	1.21140	0.06524	18.568	< 2e-16 ***
Speciesversicolor	1.69779	0.18095	9.383	< 2e-16 ***
Speciesvirginica	2.27669	0.28132	8.093	2.08e-13 ***
Petal.Width	1.01871	0.15224	6.691	4.41e-10 ***

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

Residual standard error: 0.3777 on 146 degrees of freedom

Multiple R-squared: 0.9551, Adjusted R-squared: 0.9542

Generalised Linear Models (GLMs)

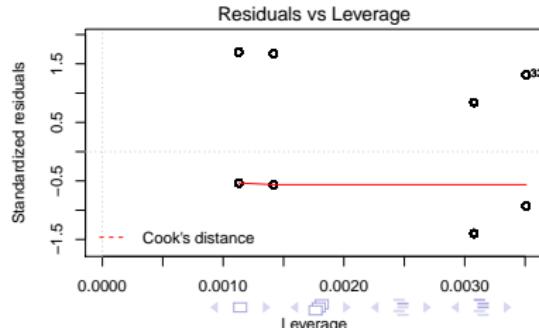
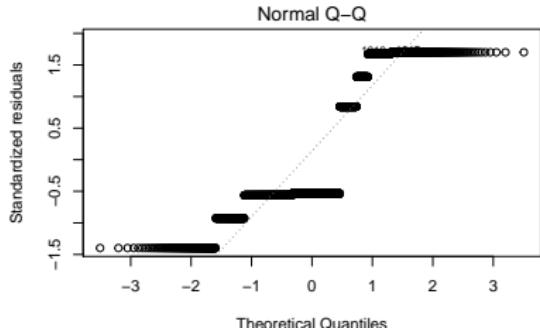
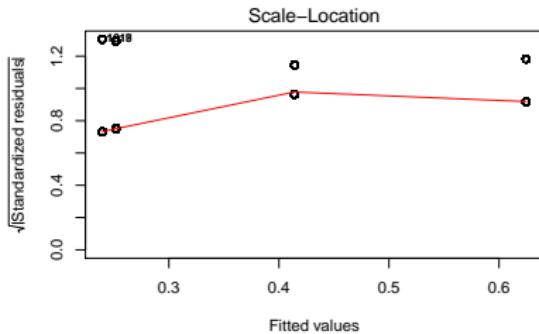
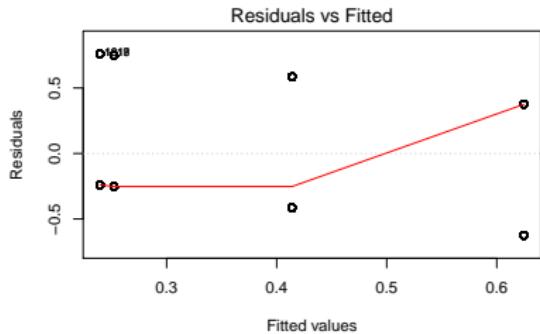
Q: Survival of passengers on the Titanic ~ Class

Read titanic_long.csv dataset.

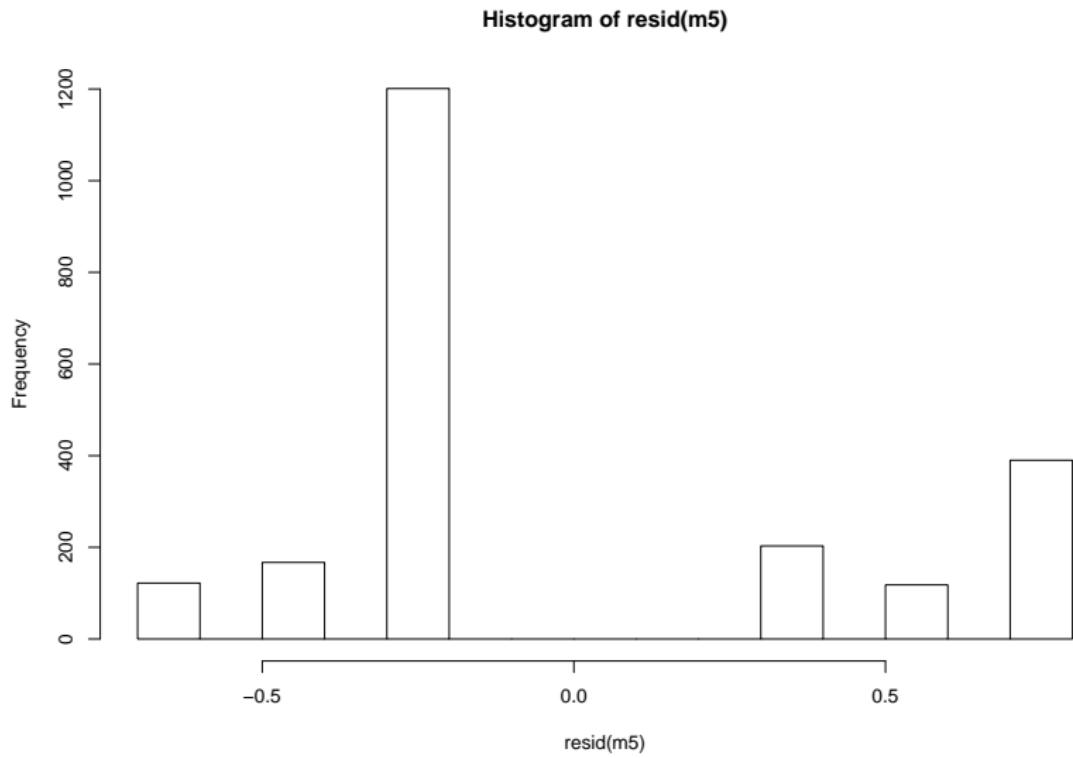
	class	age	sex	survived
1	first	adult	male	1
2	first	adult	male	1
3	first	adult	male	1
4	first	adult	male	1
5	first	adult	male	1
6	first	adult	male	1

Let's fit linear model:

```
m5 <- lm(survived ~ class, data = titanic)
```



Weird residuals!



What if your residuals are clearly non-normal? | And variance not constant (heteroscedasticity)?

- ▶ Binary variables (0/1)

What if your residuals are clearly non-normal? | And variance not constant (heteroscedasticity)?

- ▶ Binary variables (0/1)
- ▶ Counts (0, 1, 2, 3, ...)

Generalised Linear Models

1. **Response variable** - distribution family

Generalised Linear Models

1. Response variable - distribution family

- ▶ Bernouilli - Binomial

Generalised Linear Models

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Generalised Linear Models

1. Response variable - distribution family

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- ▶ etc

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2. Predictors (continuous or categorical)

Generalised Linear Models

1. Response variable - distribution family

- ▶ Bernouilli - Binomial
- ▶ Poisson
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- ▶ etc

2. Predictors (continuous or categorical)

3. Link function

Generalised Linear Models

1. Response variable - distribution family

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- ▶ Poisson
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- ▶ Gaussian: identity

Generalised Linear Models

1. Response variable - distribution family

- ▶ Bernouilli - Binomial
- ▶ Poisson
- ▶ Gamma
- ▶ etc

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3. Link function

- ▶ Gaussian: identity
- ▶ Binomial: logit, probit

Generalised Linear Models

1. Response variable - distribution family

- ▶ Bernouilli - Binomial
- ▶ Poisson
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- ▶ etc

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- ▶ Binomial: logit, probit
- ▶ Poisson: log...

Generalised Linear Models

1. Response variable - distribution family

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- ▶ Poisson
- ▶ Gamma
- ▶ etc

2. Predictors (continuous or categorical)

3. Link function

- ▶ Gaussian: identity
- ▶ Binomial: logit, probit
- ▶ Poisson: log...
- ▶ See `family`.

The modelling process

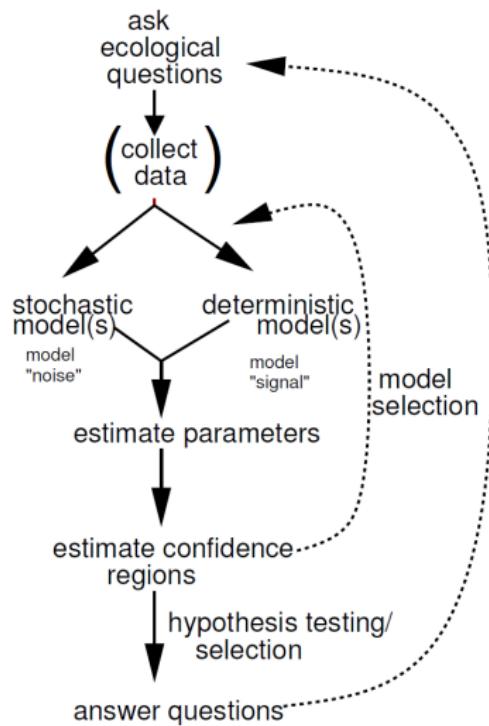


Figure 1.5 Flow of the modeling process.

Bolker 2008

Bernoulli - Binomial distribution (Logistic regression)

- ▶ Response variable: Yes/No (e.g. survival, sex, presence/absence)

$$\text{logit}(p) = \ln \left(\frac{p}{1-p} \right)$$

Then

$$Pr(\text{alive}) = a + bx$$

$$\text{logit}(Pr(\text{alive})) = a + bx$$

$$Pr(\text{alive}) = \text{invlogit}(a + bx) = \frac{e^{a+bx}}{1 + e^{a+bx}}$$

Bernoulli - Binomial distribution (Logistic regression)

- ▶ Response variable: Yes/No (e.g. survival, sex, presence/absence)
- ▶ Link function: logit (others possible, see `family`).

$$\text{logit}(p) = \ln \left(\frac{p}{1-p} \right)$$

Then

$$Pr(\text{alive}) = a + bx$$

$$\text{logit}(Pr(\text{alive})) = a + bx$$

$$Pr(\text{alive}) = \text{invlogit}(a + bx) = \frac{e^{a+bx}}{1 + e^{a+bx}}$$

Back to survival of Titanic passengers

How many passengers travelled in each class?

Back to survival of Titanic passengers

How many passengers travelled in each class?

```
tapply(titanic$survived, titanic$class, length)
```

	crew	first	second	third
	885	325	285	706

Back to survival of Titanic passengers

How many passengers travelled in each class?

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Back to survival of Titanic passengers

How many passengers travelled in each class?

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```

	crew	first	second	third
	885	325	285	706

How many survived?

```
tapply(titanic$survived, titanic$class, sum)
```

	crew	first	second	third
	212	203	118	178

Back to survival of Titanic passengers

How many passengers travelled in each class?

```
tapply(titanic$survived, titanic$class, length)
```

	crew	first	second	third
885	325	285	706	

How many survived?

```
tapply(titanic$survived, titanic$class, sum)
```

	crew	first	second	third
212	203	118	178	

What proportion survived in each class?

```
as.numeric(tapply(titanic$survived, titanic$class, mean))
```

```
[1] 0.2395480 0.6246154 0.4140351 0.2521246
```

Back to survival of Titanic passengers (dplyr)

Passenger survival according to class

```
library(dplyr)
titanic %>%
  group_by(class, survived) %>%
  summarise(count = n())
```

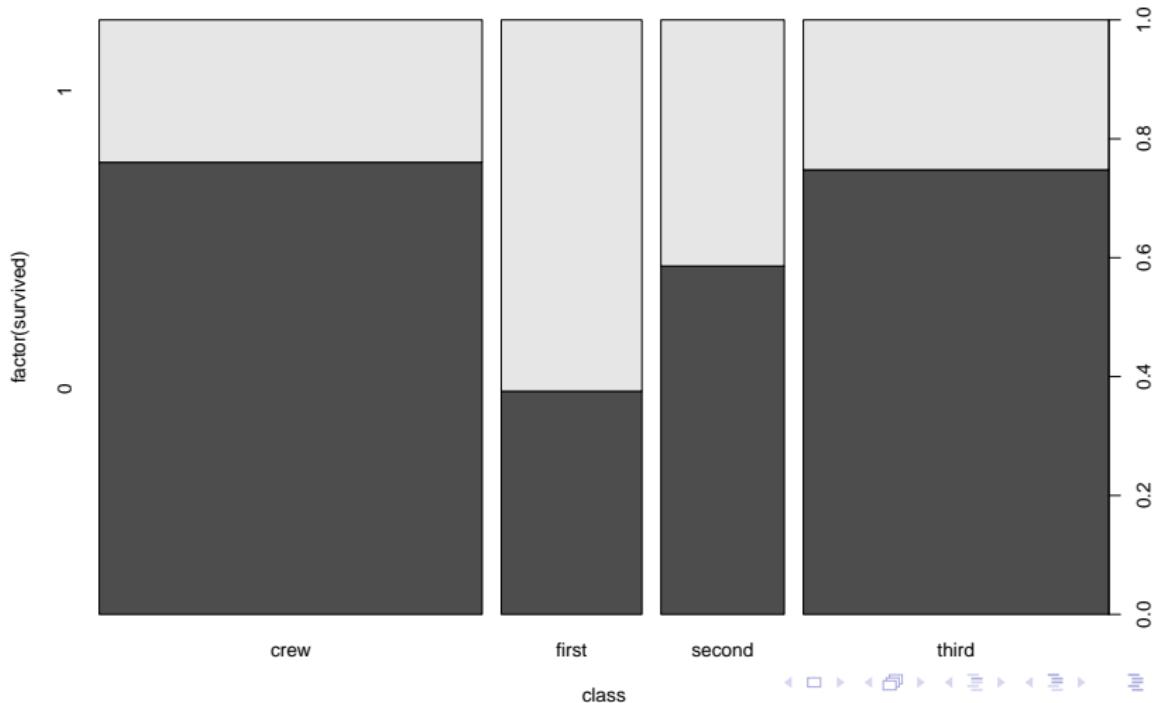
Source: local data frame [8 x 3]
Groups: class [?]

	class	survived	count
	(fctr)	(int)	(int)
1	crew	0	673
2	crew	1	212
3	first	0	122
4	first	1	203
5	second	0	167
6	second	1	118
7	third	0	528
8	third	1	178

Or `summarise(group_by(titanic, class, survived), count = n())`

Or graphically...

```
plot(factor(survived) ~ class, data = titanic)
```



Fitting GLMs in R: `glm`

```
tit.glm <- glm(survived ~ class, data=titanic, family=binomial)
```

Call:

```
glm(formula = survived ~ class, family = binomial, data = titani
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.3999	-0.7623	-0.7401	0.9702	1.6906

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-1.15516	0.07876	-14.667	< 2e-16 ***
classfirst	1.66434	0.13902	11.972	< 2e-16 ***
classsecond	0.80785	0.14375	5.620	1.91e-08 ***
classthird	0.06785	0.11711	0.579	0.562

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

(Dispersion parameter for binomial family taken to be 1)



Interpreting logistic regression output

Parameter estimates (logit-scale)

(Intercept)	classfirst	classesecond	classthird
-1.15515905	1.66434399	0.80784987	0.06784632

We need to back-transform: apply *inverse logit*
Crew probability of survival:

```
plogis(coef(tit.glm)[1])
```

(Intercept)
0.239548

Looking at the data, the proportion of crew who survived is

```
[1] 0.239548
```

Q: Probability of survival for 1st class passengers?

```
plogis(coef(tit.glm)[1] + coef(tit.glm)[2])
```

```
(Intercept)  
0.6246154
```

Needs to add intercept (baseline) to the parameter estimate. Again this value matches the data:

```
sum(titanic$survived[titanic$class == "first"]) /  
nrow(titanic[titanic$class == "first", ])
```

```
[1] 0.6246154
```

Model interpretation using effects package

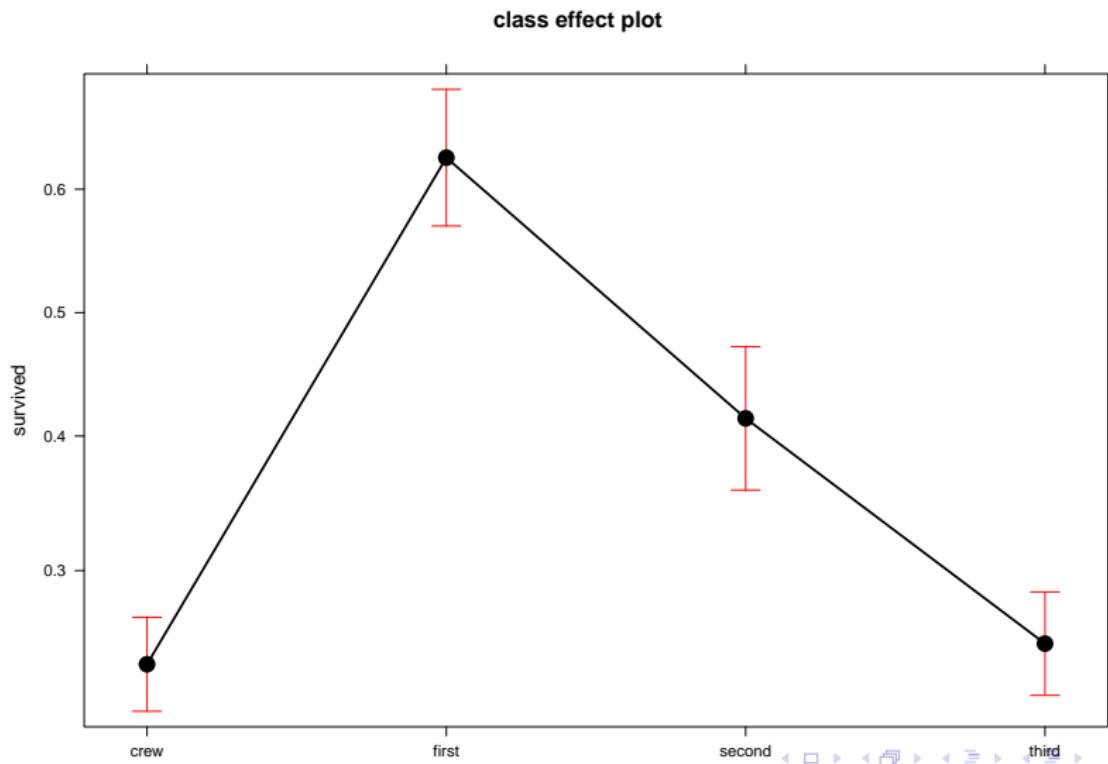
```
library(effects)
allEffects(tit.glm)

model: survived ~ class

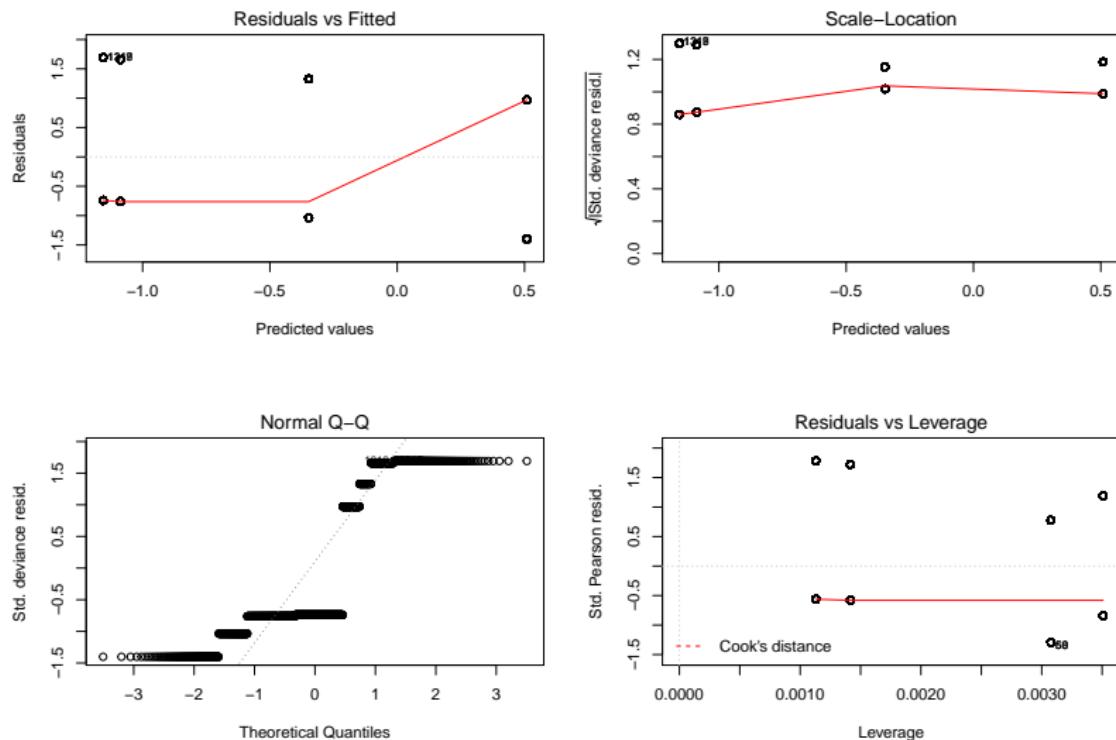
class effect
class
    crew      first     second     third
0.2395480 0.6246154 0.4140351 0.2521246
```

Effects plot

```
plot(allEffects(tit.glm))
```



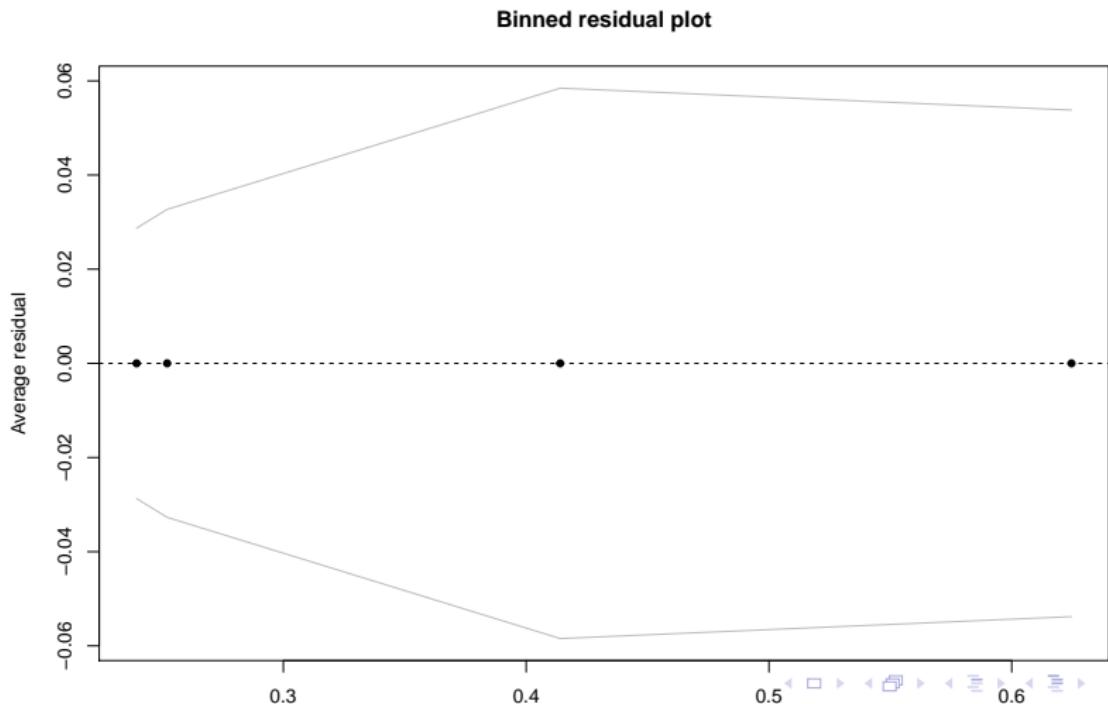
Logistic regression: model checking



Not very useful.

Binned residual plots for logistic regression

```
predvals <- predict(tit.glm, type="response")
arm::binnedplot(predvals, titanic$survived - predvals)
```



Recapitulating

1. Import data: `read.table` or `read.csv`

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2. Check data: `summary`

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Recapitulating

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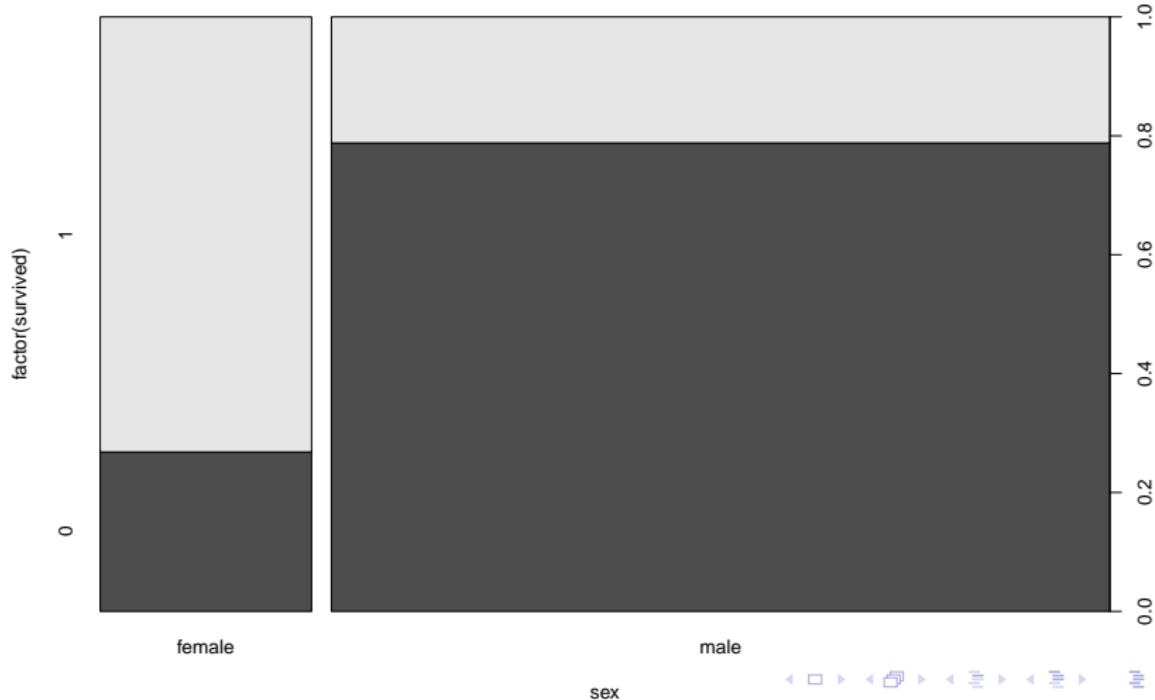
Recapitulating

1. Import data: `read.table` or `read.csv`
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6. Use `plogis` to apply back-transformation (*invlogit*) to parameter estimates (`coef`). Alternatively, use `allEffects` from `effects` package.
7. Plot model: `plot(allEffects(model))`. Or use `visreg`.
8. Examine residuals: `binnedplot` from package `arm`. Use `predict` to obtain predicted values for each obs.

Q: Did men have higher survival than women?

Plot first

```
plot(factor(survived) ~ sex, data = titanic)
```



Fit model

```
tit.sex <- glm(survived ~ sex, data = titanic, family = binomial)
```

Call:

```
glm(formula = survived ~ sex, family = binomial, data = titanic)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.6226	-0.6903	-0.6903	0.7901	1.7613

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.0044	0.1041	9.645	<2e-16 ***
sexmale	-2.3172	0.1196	-19.376	<2e-16 ***

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 2769.5 on 2200 degrees of freedom ▶ 🔍 ↻

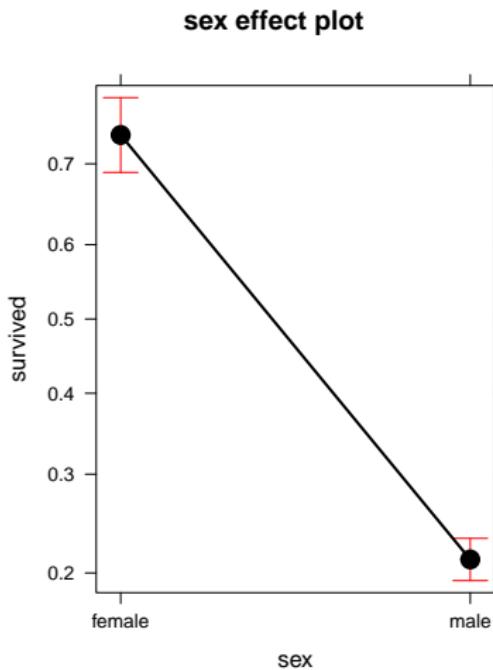
Effects

```
model: survived ~ sex
```

sex effect

sex

female	male
0.7319149	0.2120162



Q: Did women have higher survival because they travelled more in first class?

Let's look at the data

tapply

```
tapply(titanic$survived, list(titanic$class, titanic$sex), sum)
```

	female	male
crew	20	192
first	141	62
second	93	25
third	90	88

Mmmm...

Fit model with both factors (interactions)

```
tit.sex.class <- glm(survived ~ class * sex, data = titanic, family = binomial)

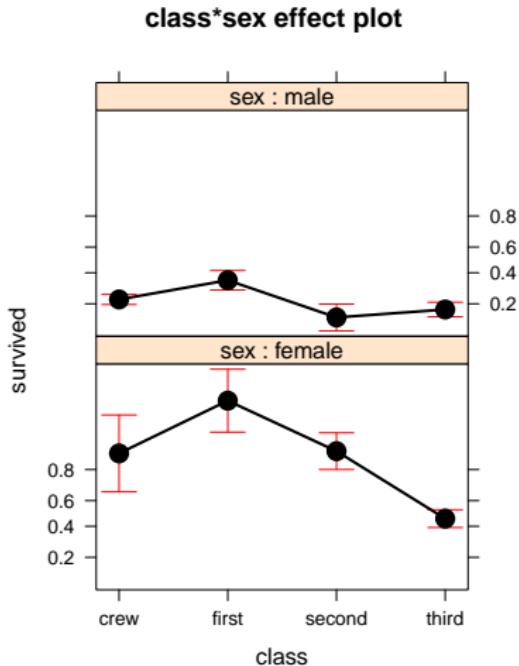
glm(formula = survived ~ class * sex, family = binomial, data = titanic)
    coef.est  coef.se
(Intercept)      1.90     0.62
classfirst       1.67     0.80
classsecond      0.07     0.69
classthird      -2.06     0.64
sexmale          -3.15     0.62
classfirst:sexmale -1.06     0.82
classsecond:sexmale -0.64     0.72
classthird:sexmale  1.74     0.65
---
n = 2201, k = 8
residual deviance = 2163.7, null deviance = 2769.5 (difference = 605.8)
```

Effects

```
model: survived ~ class * sex
```

class*sex effect

class	sex	
	female	male
crew	0.8695652	0.2227378
first	0.9724138	0.3444444
second	0.8773585	0.1396648
third	0.4591837	0.1725490



So, women had higher probability of survival than men, even within the same class.

Logistic regression for proportion data

Read Titanic data in different format

Read Titanic_prop.csv data.

X	Class	Sex	Age	No
Min. : 1.00	1st : 4	Female: 8	Adult: 8	Min. : 0.00
1st Qu.: 4.75	2nd : 4	Male : 8	Child: 8	1st Qu.: 0.00
Median : 8.50	3rd : 4			Median : 8.50
Mean : 8.50	Crew: 4			Mean : 93.12
3rd Qu.: 12.25				3rd Qu.: 96.25
Max. : 16.00				Max. : 670.00
Yes				
Min. : 0.00				
1st Qu.: 9.50				
Median : 14.00				
Mean : 44.44				
3rd Qu.: 75.25				
Max. : 192.00				

These are the same data, but summarized (see Freq variable).

Use cbind(n.success, n.failures) as response

```
prop.glm <- glm(cbind(Yes, No) ~ Class, data = tit.prop, family = binomial)
```

Call:

```
glm(formula = cbind(Yes, No) ~ Class, family = binomial, data = tit.prop)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-9.6404	-0.2915	1.5698	5.0366	10.1516

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.5092	0.1146	4.445	8.79e-06 ***
Class2nd	-0.8565	0.1661	-5.157	2.51e-07 ***
Class3rd	-1.5965	0.1436	-11.114	< 2e-16 ***
ClassCrew	-1.6643	0.1390	-11.972	< 2e-16 ***

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

(Dispersion parameter for binomial family taken to be 1)



Effects

```
model: cbind(Yes, No) ~ Class  
  
Class effect  
Class  
    1st      2nd      3rd      Crew  
0.6246154 0.4140351 0.2521246 0.2395480
```

Compare with former model based on raw data:

```
model: survived ~ class  
  
class effect  
class  
    crew      first     second     third  
0.2395480 0.6246154 0.4140351 0.2521246
```

Same results!

Logistic regression with continuous predictors

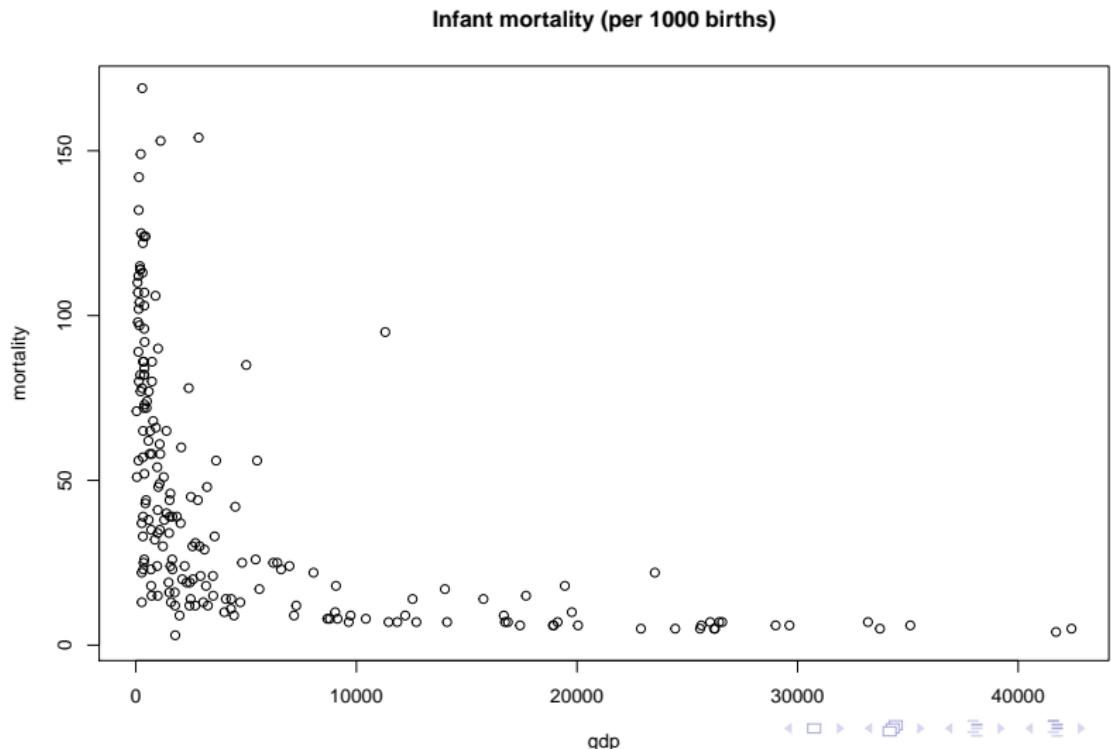
Example dataset: GDP and infant mortality

Read UN_GDP_infantmortality.csv.

	country	mortality	gdp
Afghanistan	: 1	Min. : 2.00	Min. : 36
Albania	: 1	1st Qu.: 12.00	1st Qu.: 442
Algeria	: 1	Median : 30.00	Median : 1779
American.Samoa	: 1	Mean : 43.48	Mean : 6262
Andorra	: 1	3rd Qu.: 66.00	3rd Qu.: 7272
Angola	: 1	Max. : 169.00	Max. : 42416
(Other)	: 201	NA's : 6	NA's : 10

EDA

```
plot(mortality ~ gdp, data = gdp, main = "Infant mortality (per
```



Fit model

```
gdp.glm <- glm(cbind(mortality, 1000 - mortality) ~ gdp,  
                 data = gdp, family = binomial)
```

Call:

```
glm(formula = cbind(mortality, 1000 - mortality) ~ gdp, family =  
     data = gdp)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-9.2230	-3.5163	-0.5697	2.4284	13.5849

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.657e+00	1.311e-02	-202.76	<2e-16 ***
gdp	-1.279e-04	3.458e-06	-36.98	<2e-16 ***

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

(Dispersion parameter for binomial family taken to be 1)



Effects

```
allEffects(gdp.glm)
```

```
model: cbind(mortality, 1000 - mortality) ~ gdp
```

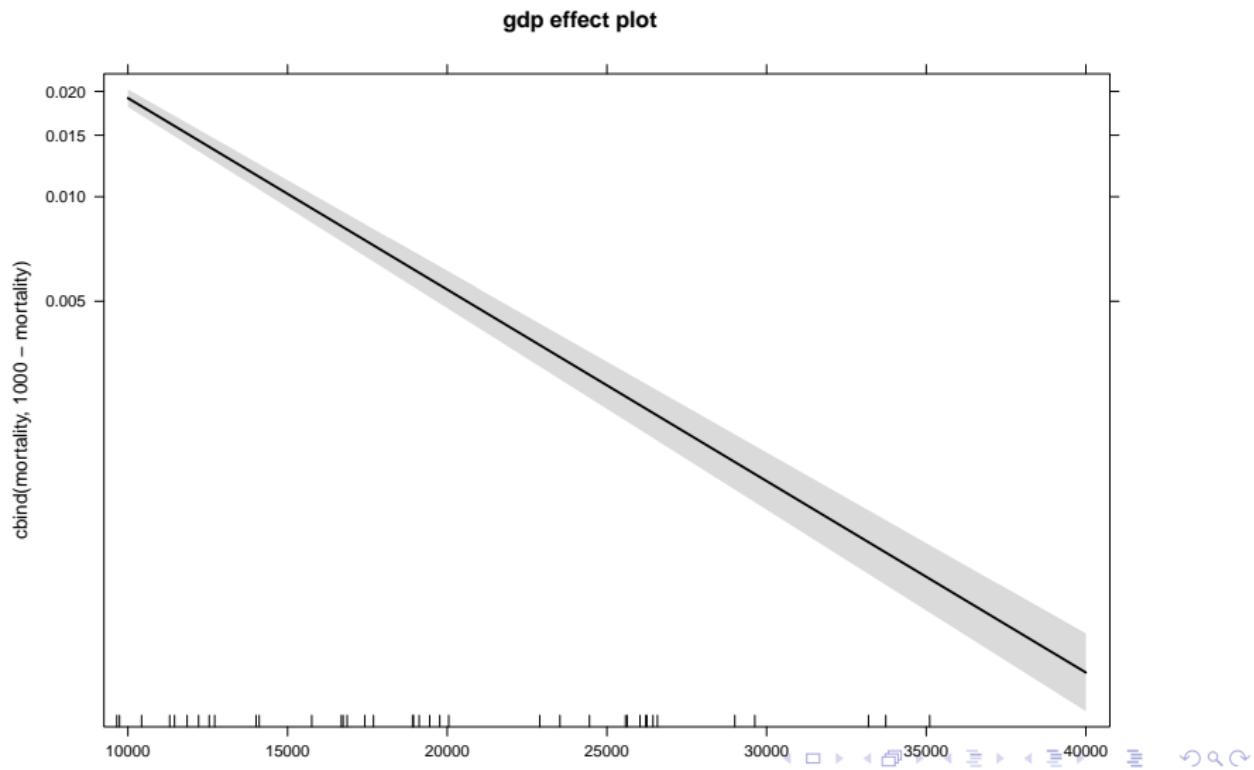
gdp effect

gdp

	10000	20000	30000	40000
0.0191438829	0.0054028095	0.0015096074	0.0004206154	

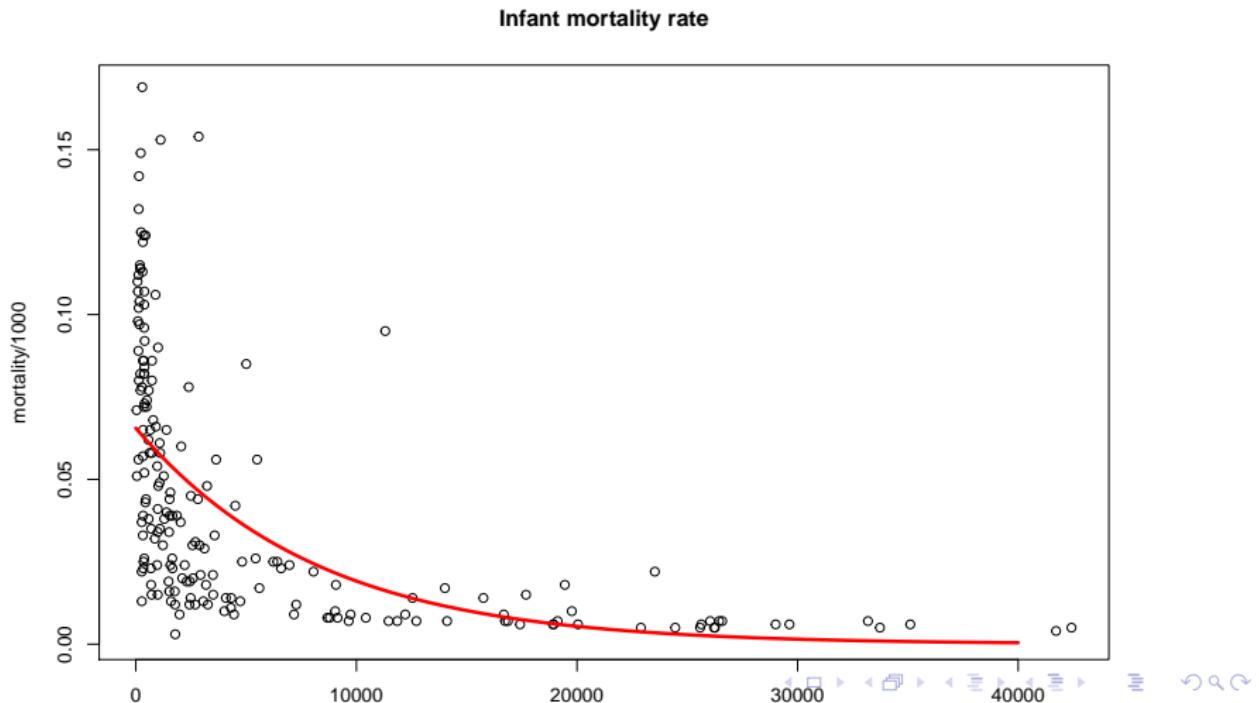
Effects plot

```
plot(allEffects(gdp.glm))
```



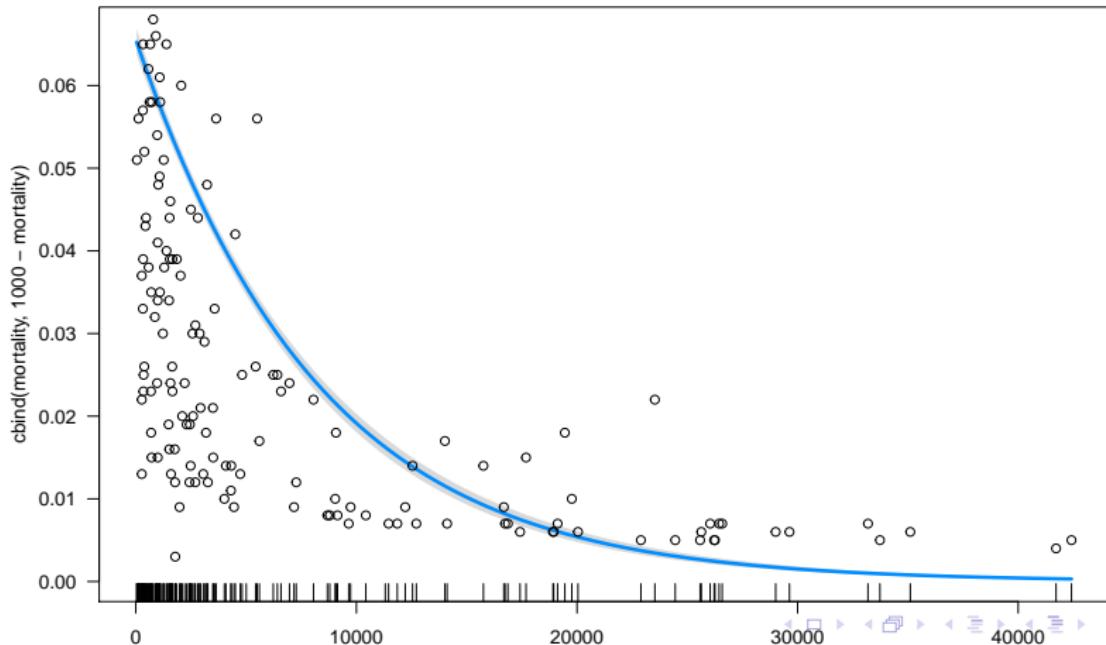
Plot model and data

```
plot(mortality/1000 ~ gdp, data = gdp, main = "Infant mortality  
curve(plogis(coef(gdp.glm)[1] + coef(gdp.glm)[2]*x), from = 0, t
```



Or using visreg:

```
visreg(gdp.glm, scale = "response")
points(mortality/1000 ~ gdp, data = gdp)
```



Overdispersion

Overdispersion in logistic regression with proportion data

```
gdp.overdisp <- glm(cbind(mortality, 1000 - mortality) ~ gdp,  
                     data = gdp, family = quasibinomial)
```

Call:

```
glm(formula = cbind(mortality, 1000 - mortality) ~ gdp, family =  
     data = gdp)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-9.2230	-3.5163	-0.5697	2.4284	13.5849

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-2.657e+00	5.977e-02	-44.465	< 2e-16 ***
gdp	-1.279e-04	1.577e-05	-8.111	5.96e-14 ***

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

(Dispersion parameter for quasibinomial family taken to be 20.79)

Mean estimates do not change after accounting for overdispersion

```
model: cbind(mortality, 1000 - mortality) ~ gdp
```

```
gdp effect  
gdp
```

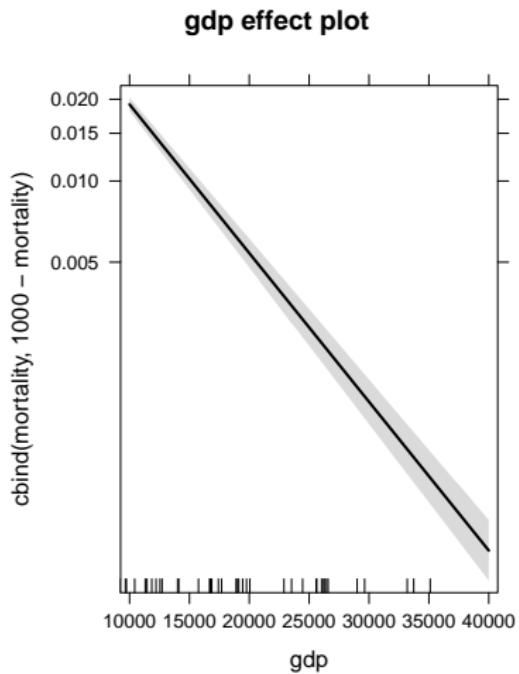
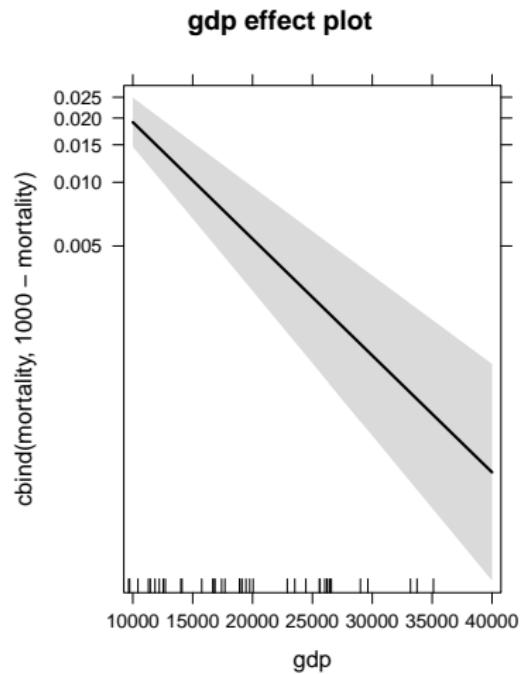
10000	20000	30000	40000
0.0191438829	0.0054028095	0.0015096074	0.0004206154

```
model: cbind(mortality, 1000 - mortality) ~ gdp
```

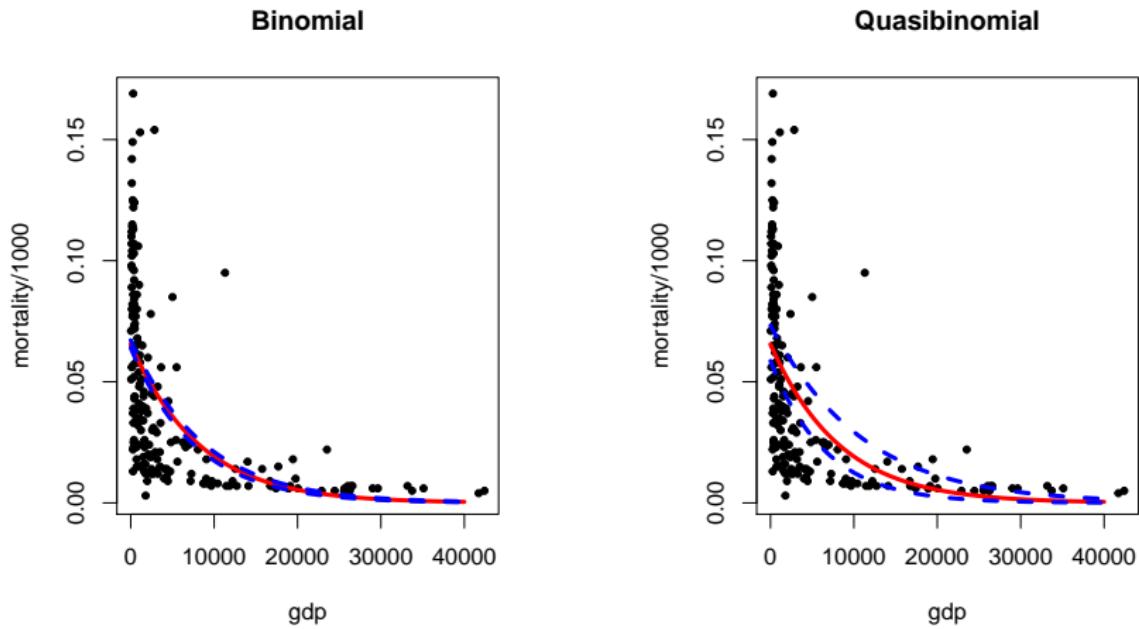
```
gdp effect  
gdp
```

10000	20000	30000	40000
0.0191438829	0.0054028095	0.0015096074	0.0004206154

But standard errors (uncertainty) do!



Plot model and data



Overdispersion

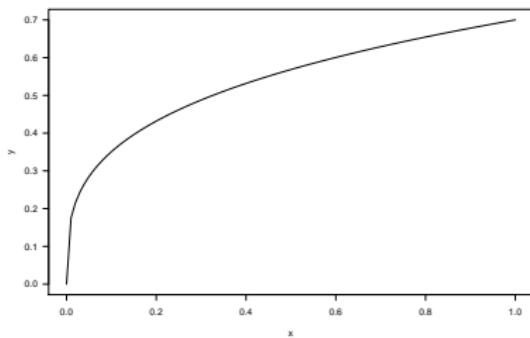
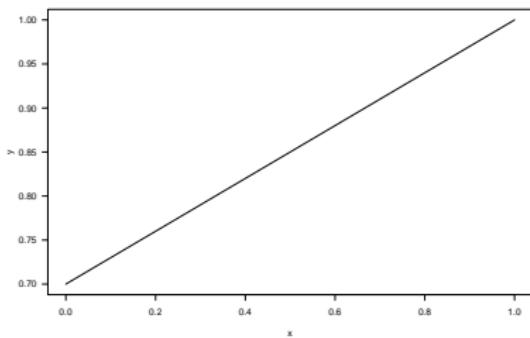
Whenever you fit logistic regression to **proportion** data, check family quasibinomial.

Think about the shape of relationships

$$y \sim x + z$$

Really? Not everything has to be linear! Actually, it often is not.

Think about shape of relationship. See chapter 3 in Bolker's book.



GLMs for count data: Poisson regression

Types of response variable

- ▶ Gaussian: lm

Types of response variable

- ▶ Gaussian: `lm`
- ▶ Bernouilli / Binomial: `glm` (family `binomial` / `quasibinomial`)

Types of response variable

- ▶ Gaussian: `lm`
- ▶ Bernouilli / Binomial: `glm` (family `binomial` / `quasibinomial`)
- ▶ Counts: `glm` (family `poisson` / `quasipoisson`)

Poisson regression

- ▶ Response variable: Counts (0, 1, 2, 3...) - discrete

Then

$$\log(N) = a + bx$$

$$N = e^{a+bx}$$

Poisson regression

- ▶ Response variable: Counts (0, 1, 2, 3...) - discrete
- ▶ Link function: log

Then

$$\log(N) = a + bx$$

$$N = e^{a+bx}$$

Example dataset: Seedling counts in 0.5 m² quadrats

```
seedl <- read.csv("data-raw/seedlings.csv")
```

X	count	row	col
Min. : 1.00	Min. : 0.00	Min. : 1	Min. : 1.0
1st Qu.:13.25	1st Qu.:1.00	1st Qu.:2	1st Qu.: 3.0
Median :25.50	Median :2.00	Median :3	Median : 5.5
Mean :25.50	Mean :2.14	Mean :3	Mean : 5.5
3rd Qu.:37.75	3rd Qu.:3.00	3rd Qu.:4	3rd Qu.: 8.0
Max. :50.00	Max. : 7.00	Max. :5	Max. :10.0
light			
Min. : 2.571			
1st Qu.:26.879			
Median :47.493			
Mean :47.959			
3rd Qu.:67.522			
Max. :99.135			

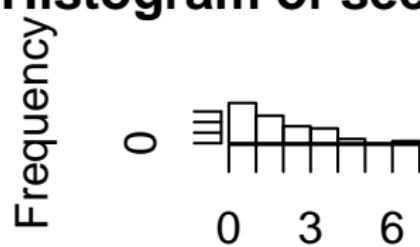
EDA

```
table(seed1$count)
```

0	1	2	3	4	5	7
7	12	13	8	7	2	1

```
hist(seed1$count)
```

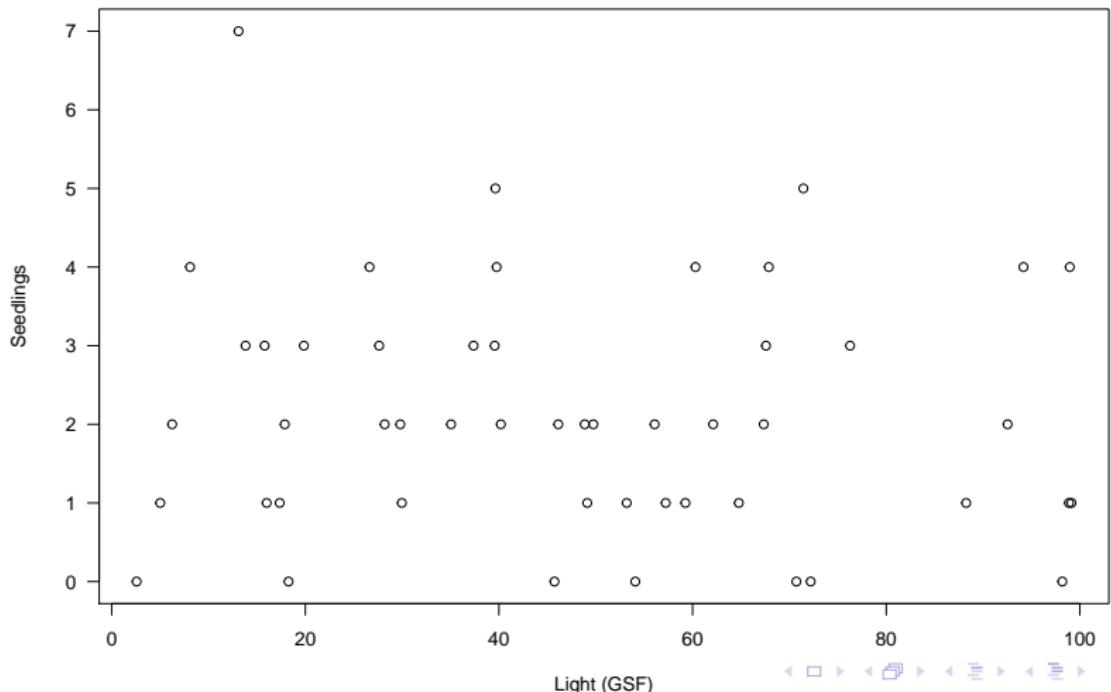
Histogram of seed1\$count



seed1\$count

Q: Relationship between Nseedlings and light?

```
plot(seed1$light, seed1$count, las = 1, xlab = "Light (GSF)", yl
```



Let's fit model (Poisson regression)

```
seed1.glm <- glm(count ~ light, data = seed1, family = poisson)  
summary(seed1.glm)
```

Call:

```
glm(formula = count ~ light, family = poisson, data = seed1)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.1906	-0.8466	-0.1110	0.5220	2.4577

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.881805	0.188892	4.668	3.04e-06 ***
light	-0.002576	0.003528	-0.730	0.465

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

(Dispersion parameter for poisson family taken to be 1)

Interpreting Poisson regression output

Parameter estimates (log scale):

```
coef(seed1.glm)
```

	light
(Intercept)	0.881805022
light	-0.002575656

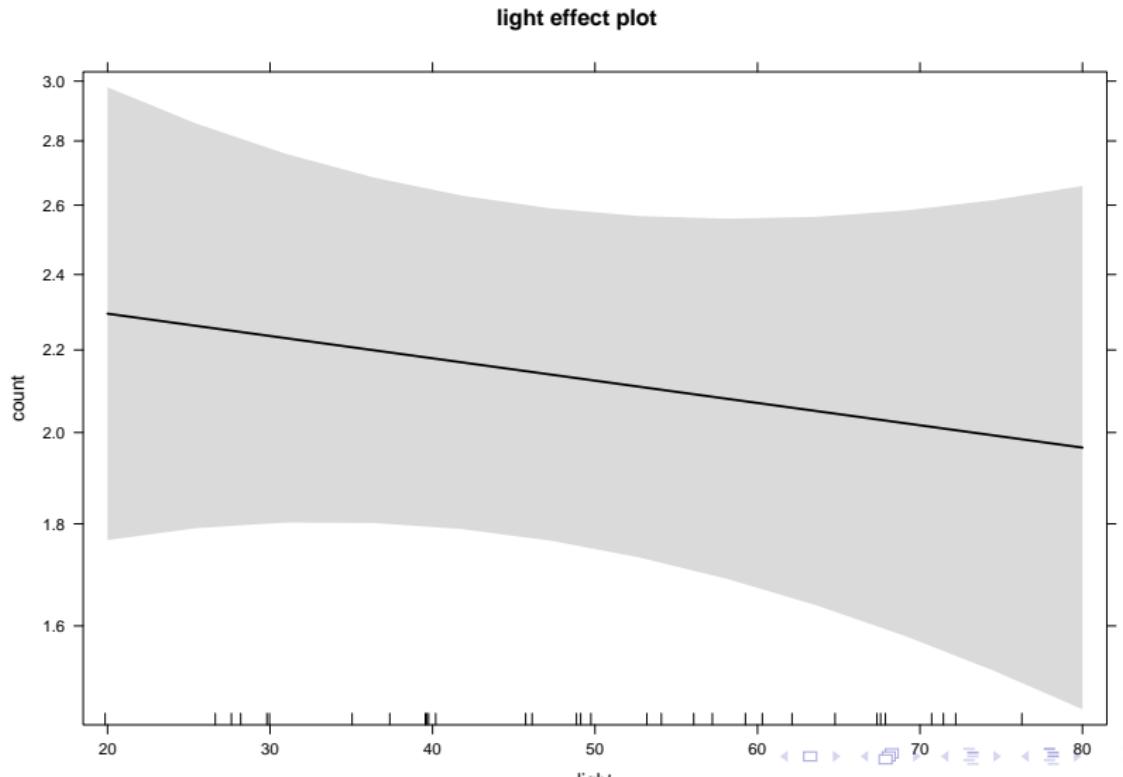
We need to back-transform: apply the inverse of the logarithm

```
exp(coef(seed1.glm))
```

	light
(Intercept)	2.4152554
light	0.9974277

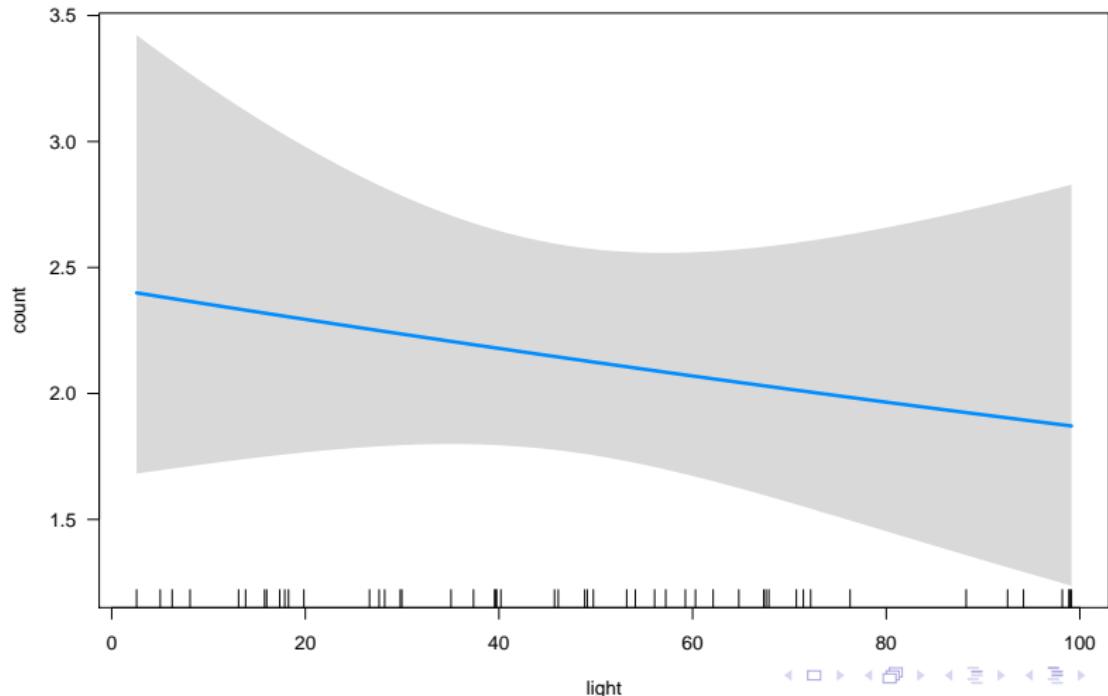
So what's the relationship between Nseedlings and light?

```
plot(allEffects(seed1.glm))
```

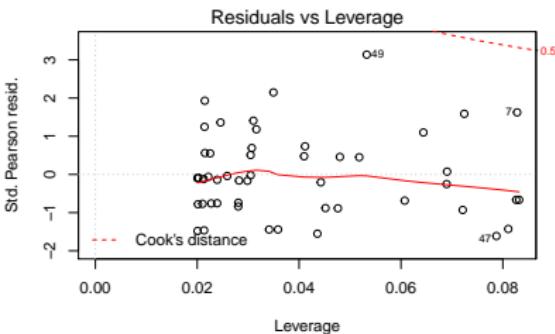
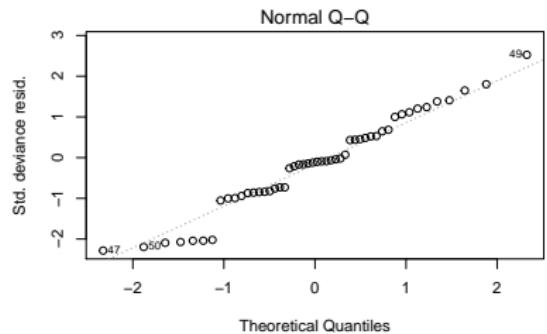
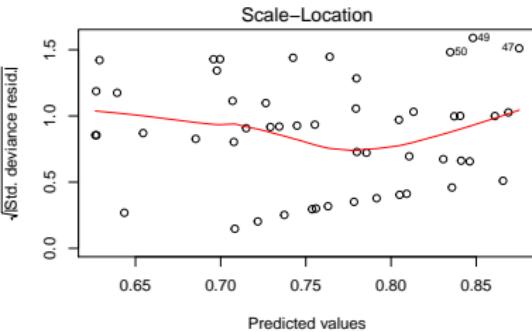
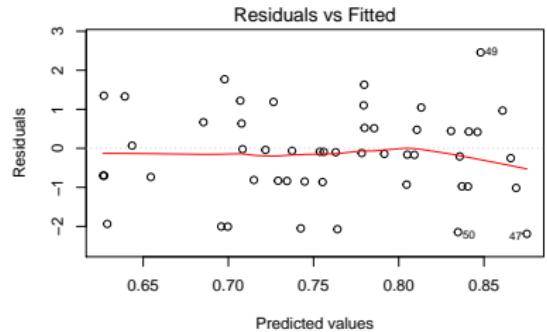


Using visreg

```
visreg(seed1.glm, scale = "response")
```

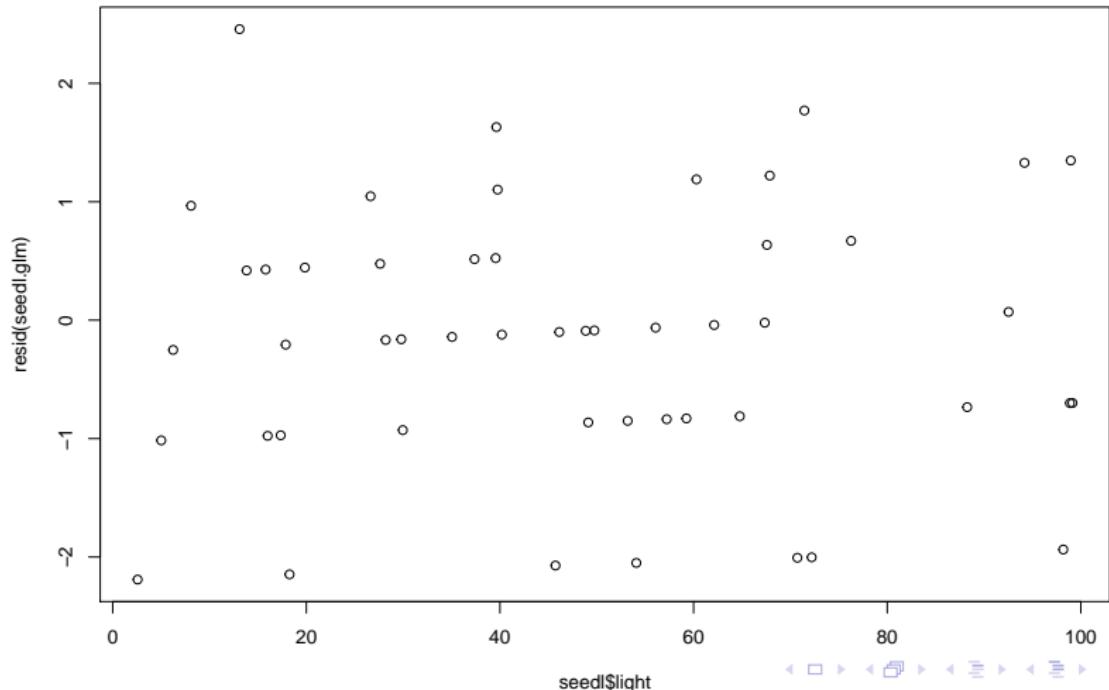


Poisson regression: model checking



Is there pattern of residuals along predictor?

```
plot(seed1$light, resid(seed1.glm))
```



Poisson regression: Overdispersion

Always check overdispersion with count data

Use family quasipoisson

Call:

```
glm(formula = count ~ light, family = quasipoisson, data = seedl)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.1906	-0.8466	-0.1110	0.5220	2.4577

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.881805	0.201230	4.382	6.37e-05 ***
light	-0.002576	0.003758	-0.685	0.496

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

(Dispersion parameter for quasipoisson family taken to be 1.1349)

Null deviance: 63.029 on 49 degrees of freedom

Residual deviance: 62.492 on 48 degrees of freedom

Mean estimates do not change after accounting for overdispersion

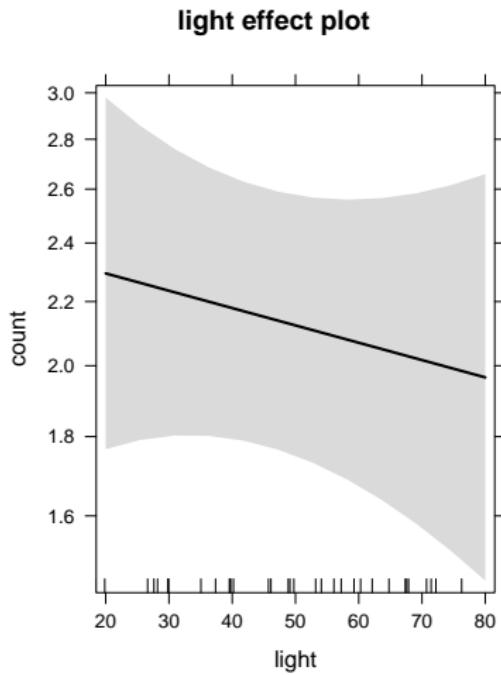
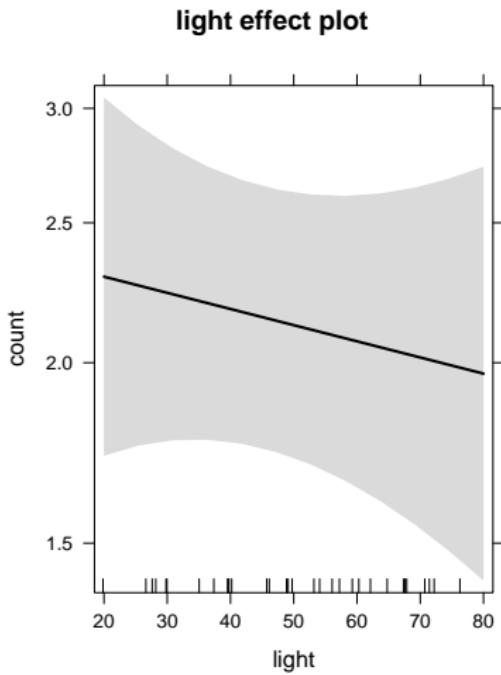
```
model: count ~ light
```

```
light effect  
light  
20      40      60      80  
2.293988 2.178810 2.069414 1.965512
```

```
model: count ~ light
```

```
light effect  
light  
20      40      60      80  
2.293988 2.178810 2.069414 1.965512
```

But standard errors may change



Mixed / Multilevel Models

Mixed models enable us to account for variability

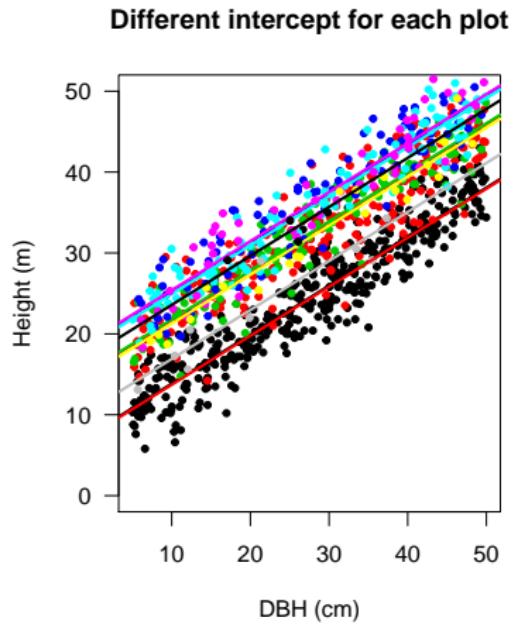
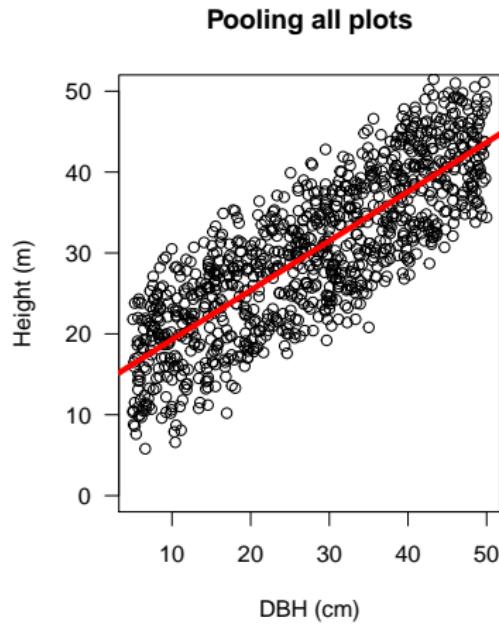
- ▶ Varying intercepts

Mixed models enable us to account for variability

- ▶ Varying intercepts
- ▶ Varying slopes

Single vs varying intercept

Dataset: 1000 trees from 10 plots (trees per plot: 4 - 392).



Fitting a varying intercepts model with lm

```
lm(formula = height ~ factor(plot) + dbh, data = trees)
            coef.est  coef.se
(Intercept)    7.79     0.24
factor(plot)2   7.86     0.24
factor(plot)3   7.95     0.32
factor(plot)4  11.48     0.33
factor(plot)5  11.05     0.32
factor(plot)6  11.55     0.43
factor(plot)7   7.41     0.63
factor(plot)8   3.05     0.97
factor(plot)9   9.73     1.45
factor(plot)10 -0.14     0.92
dbh             0.61     0.01
---
n = 1000, k = 11
residual sd = 2.89, R-Squared = 0.91
```

Mixed model with varying intercepts

$$y_i = a_j + bx_i + \varepsilon_i$$

$$a_j \sim N(0, \tau^2)$$

$$\varepsilon_i \sim N(0, \sigma^2)$$

En nuestro ejemplo:

$$Height_i = plot_j + bDBH_i + \varepsilon_i$$

$$plot_j \sim N(0, \tau^2)$$

$$\varepsilon_i \sim N(0, \sigma^2)$$

Fitting mixed/multilevel models

```
library(lme4)
mixed <- lmer(height ~ dbh + (1|plot), data = trees)
```

Linear mixed model fit by REML ['lmerMod']
Formula: height ~ dbh + (1 | plot)
Data: trees

REML criterion at convergence: 5007.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.84491	-0.65574	-0.02247	0.69295	3.09733

Random effects:

Groups	Name	Variance	Std.Dev.
plot	(Intercept)	19.834	4.454
	Residual	8.325	2.885

Number of obs: 1000, groups: plot, 10

Fixed effects:

Retrieve model coefficients

```
coef(mixed)
```

```
$plot  
(Intercept) dbh  
1 7.798373 0.6056549  
2 15.647613 0.6056549  
3 15.735397 0.6056549  
4 19.253661 0.6056549  
5 18.819467 0.6056549  
6 19.306574 0.6056549  
7 15.197908 0.6056549  
8 11.016485 0.6056549  
9 17.265447 0.6056549  
10 7.940715 0.6056549
```

```
attr(,"class")  
[1] "coef.mer"
```

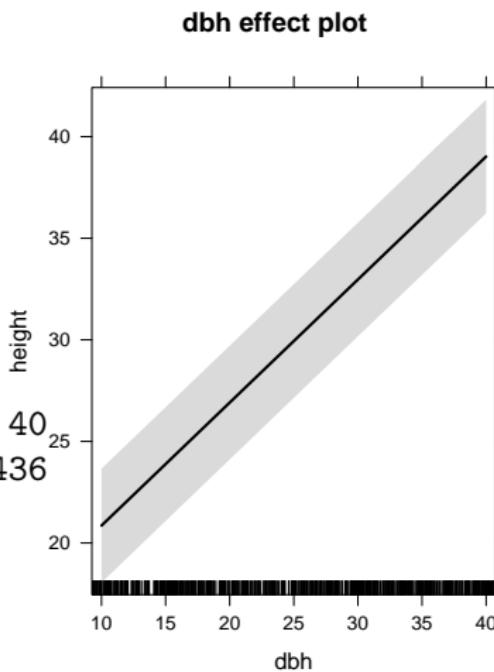
Visualising model: allEffects

model: height ~ dbh

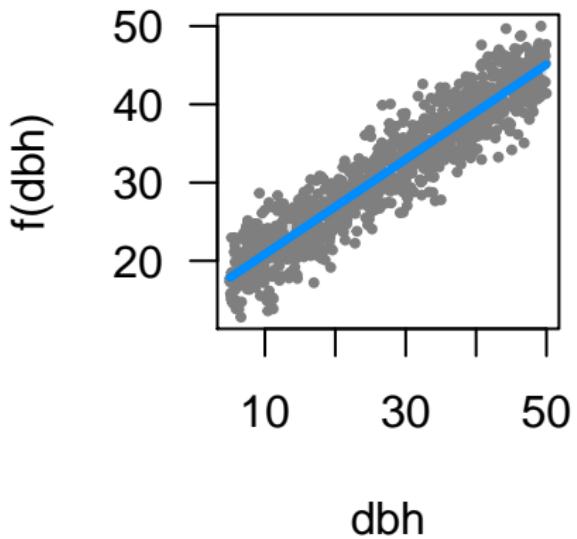
dbh effect

dbh

10	20	30	40
20.85471	26.91126	32.96781	39.02436

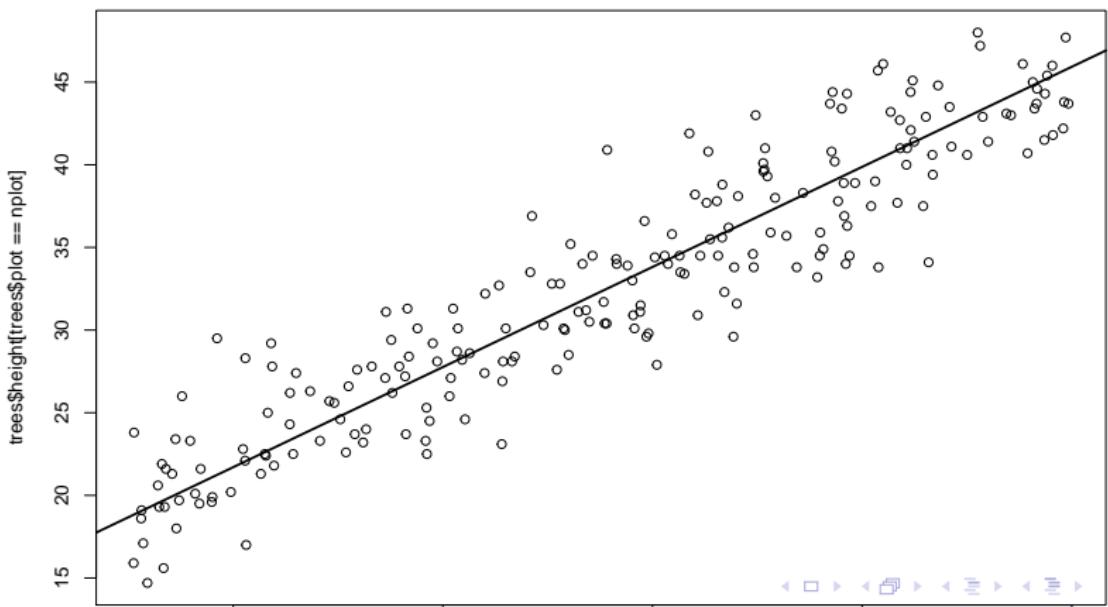


Visualising model: visreg



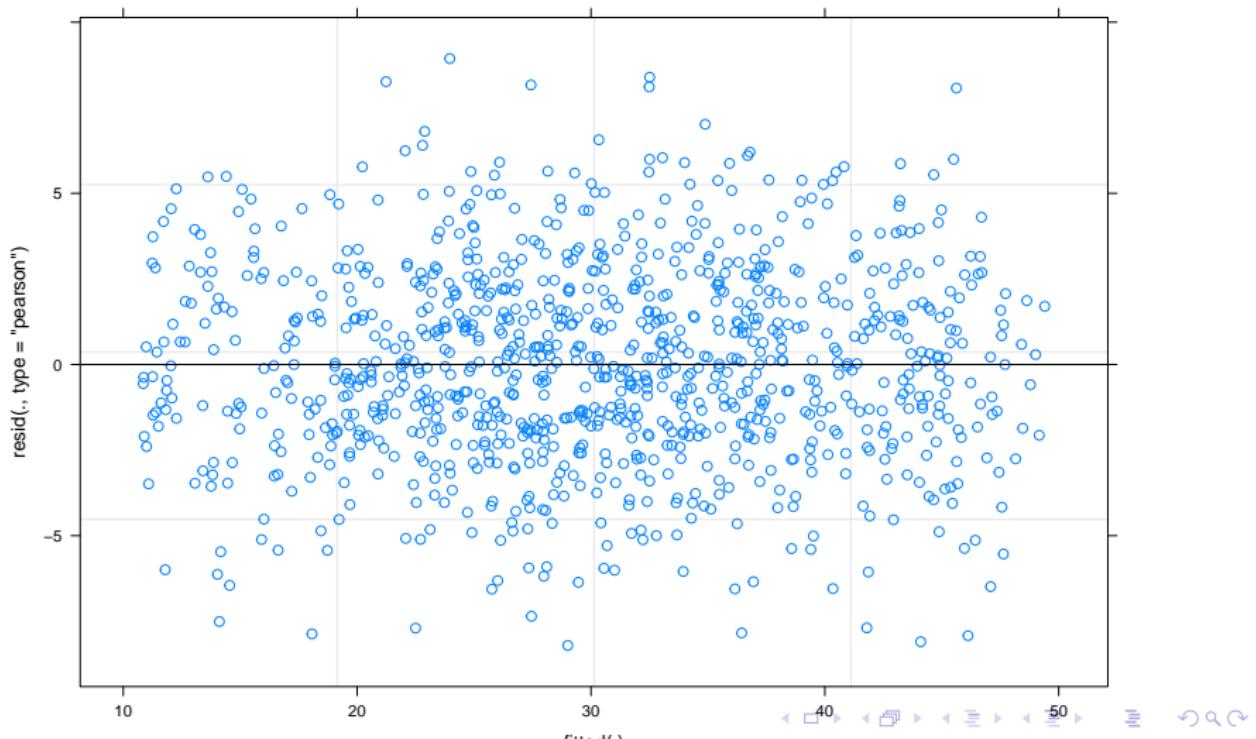
Plotting regression for individual forest plots

```
nplot <- 2  
plot(trees$dbh[trees$plot==nplot], trees$height[trees$plot==nplot]  
abline(a=coef(mixed)$plot[nplot, 1], b=coef(mixed)$plot[nplot, 2])
```



Checking residuals

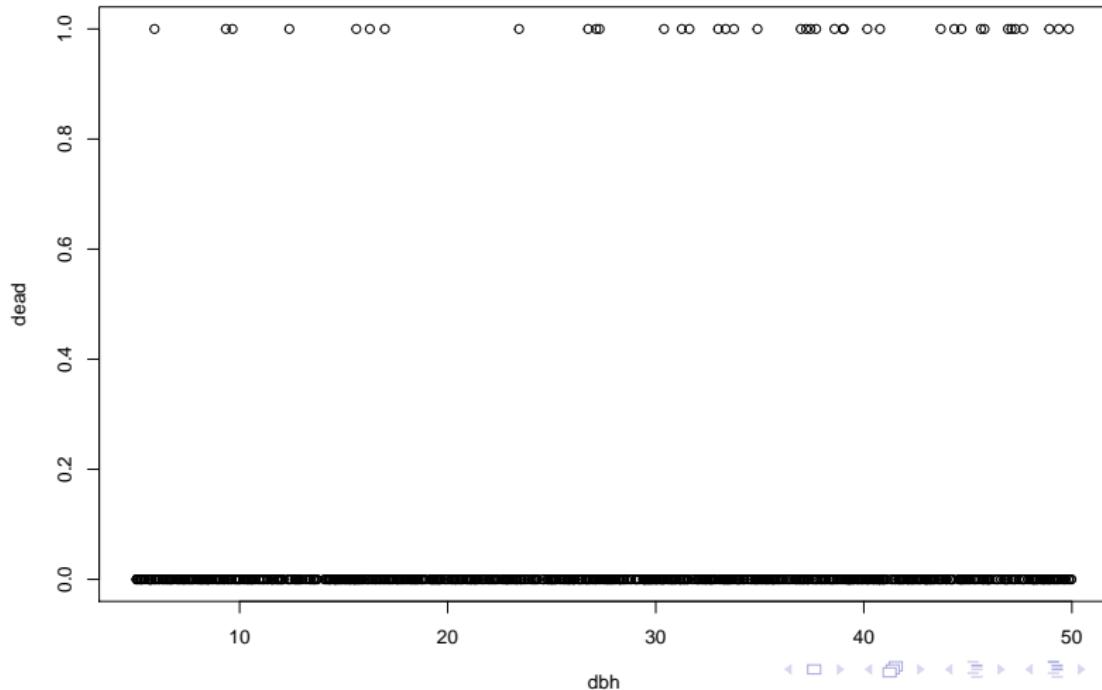
```
plot(mixed)
```



Multilevel logistic regression

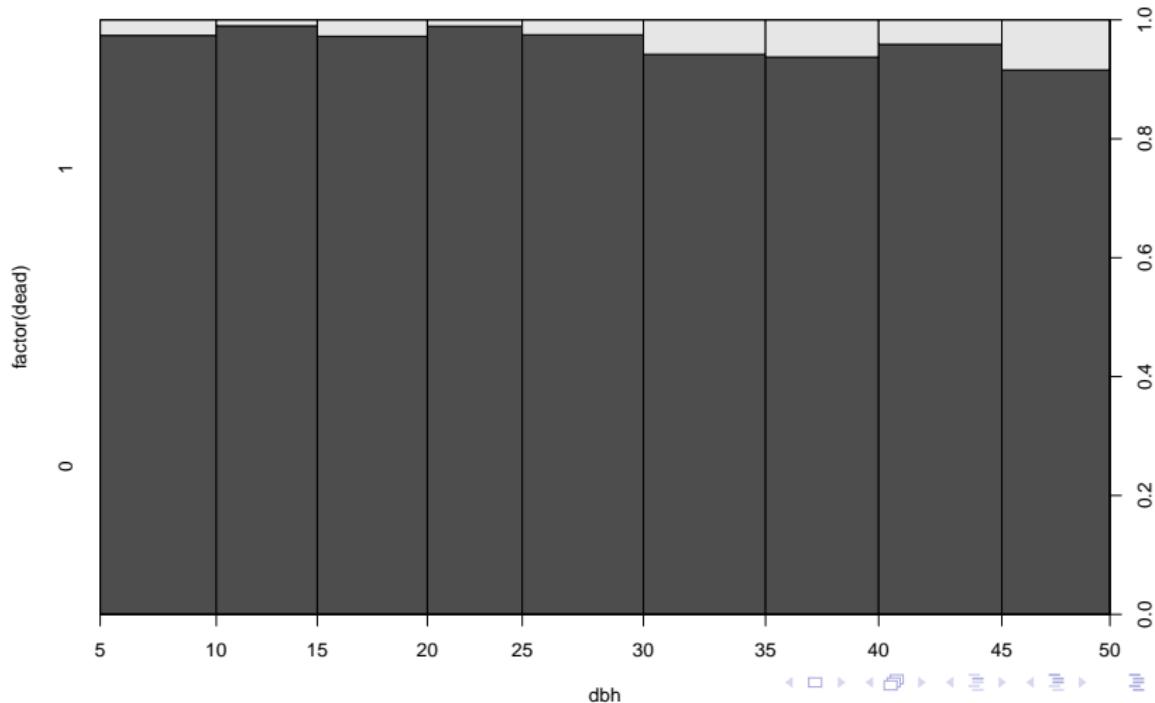
Q: Relationship between tree size and mortality

```
plot(dead ~ dbh, data = trees)
```



Q: Relationship between tree size and mortality

```
plot(factor(dead) ~ dbh, data = trees)
```



Fit simple logistic regression

```
simple.logis <- glm(dead ~ dbh, data = trees, family=binomial)
```

Call:

```
glm(formula = dead ~ dbh, family = binomial, data = trees)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.4121	-0.3287	-0.2624	-0.2048	2.9127

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-4.46945	0.49445	-9.039	< 2e-16 ***
dbh	0.04094	0.01380	2.967	0.00301 **

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 329.51 on 999 degrees of freedom

Fit simple logistic regression (with plots)

```
logis2 <- glm(dead ~ dbh + factor(plot), data = trees, family=bi
```

Call:

```
glm(formula = dead ~ dbh + factor(plot), family = binomial, data =
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.5923	-0.3198	-0.2549	-0.1940	2.8902

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)	
(Intercept)	-4.40106	0.52997	-8.304	<2e-16	***
dbh	0.04060	0.01386	2.929	0.0034	**
factor(plot)2	-0.59168	0.52132	-1.135	0.2564	
factor(plot)3	0.54576	0.47094	1.159	0.2465	
factor(plot)4	0.05507	0.57434	0.096	0.9236	
factor(plot)5	-0.38312	0.64222	-0.597	0.5508	
factor(plot)6	-0.08426	0.76908	-0.110	0.9128	
factor(plot)7	0.03126	1.06064	0.029	0.9765	■ ▶ ↻ 🔍

Fit multilevel logistic regression

```
mixed.logis <- glmer(dead ~ dbh + (1|plot), data=trees, family =
```

```
Generalized linear mixed model fit by maximum likelihood (Laplace  
Approximation) [glmerMod]  
Family: binomial ( logit )  
Formula: dead ~ dbh + (1 | plot)  
Data: trees
```

AIC	BIC	logLik	deviance	df.resid
325.9	340.6	-160.0	319.9	997

Scaled residuals:

Min	1Q	Median	3Q	Max
-0.2977	-0.2356	-0.1872	-0.1456	8.2792

Random effects:

Groups	Name	Variance	Std.Dev.
plot	(Intercept)	0	0

Number of obs: 1000, groups: plot, 10

Retrieve model coefficients

```
coef(mixed.logis)
```

```
$plot
  (Intercept)          dbh
1    -4.469446  0.04093806
2    -4.469446  0.04093806
3    -4.469446  0.04093806
4    -4.469446  0.04093806
5    -4.469446  0.04093806
6    -4.469446  0.04093806
7    -4.469446  0.04093806
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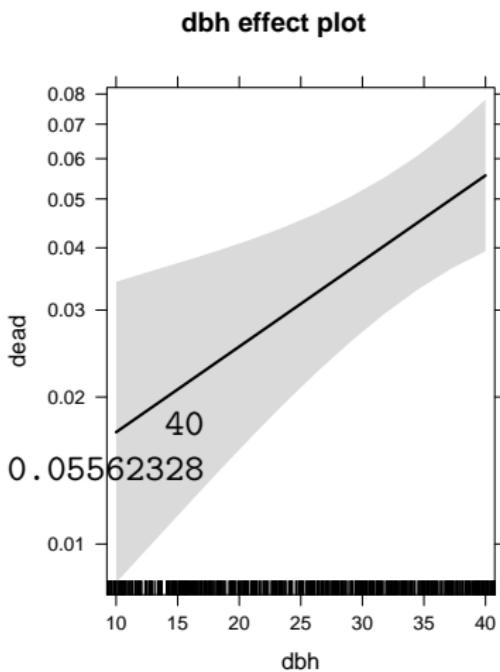
```
attr(,"class")
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Visualising model: allEffects

```
model: dead ~ dbh
```

```
dbh effect  
dbh
```

10	20	30
0.01695545	0.02531581	0.03764063



MODEL SELECTION

Why model selection?

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- ▶ *Non-nested models*: compare fit of different models (e.g. alternative hypotheses)
 - ▶ But building larger model might be better than choosing any of them!

Overfitting and balanced model complexity

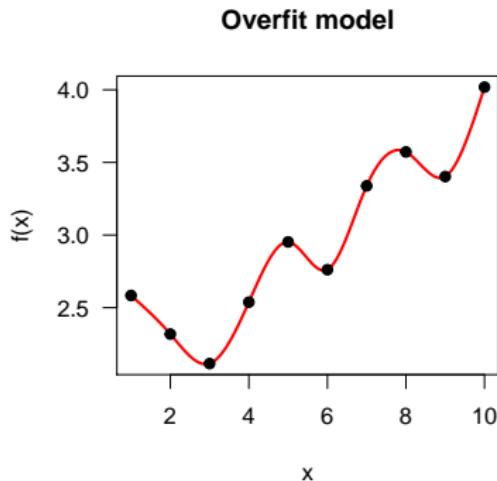


Figure 1: Overfitted model

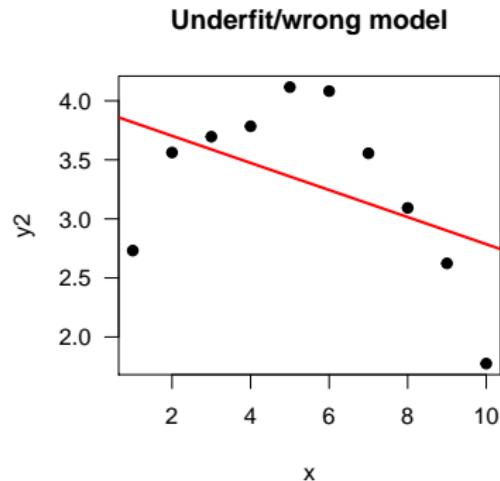
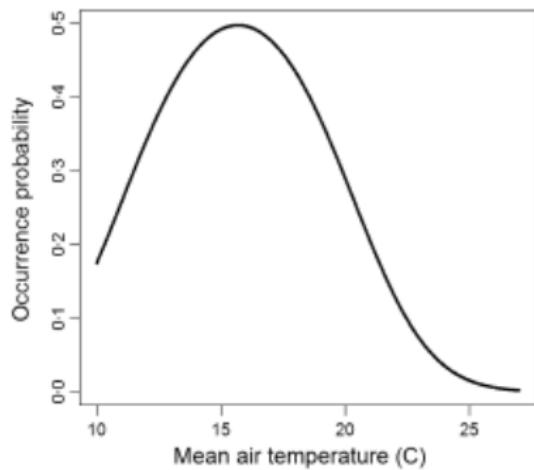


Figure 2: Wrong model

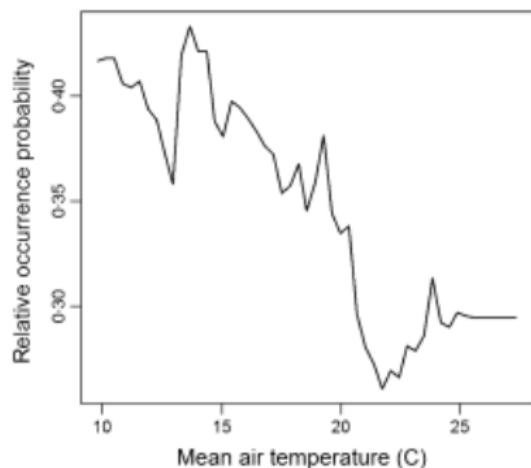
Overfitting: an example with niche modelling

Wenger & Olden (2012) Assessing transferability of ecological models: an underappreciated aspect of statistical validation. *Methods Ecol Evol.*

GLMM



Random forests (overfit)



So, two important aspects of model selection

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- ▶ On the other hand, we want to avoid overfitting and overly complex models.

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- ▶ All these methods have flaws!

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- ▶ Doesn’t work with hierarchical models or informative priors!

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- ▶ They give average out-of-sample prediction error, but prediction errors can differ substantially within the same dataset (e.g. populations, species).
- ▶ Sometimes better models rank poorly (Gelman et al. 2013). So, combine with thorough model checks.

So which variables should enter my model?

Choosing predictors

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- ▶ See also Zuur et al 2010.

Removing predictors

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- ▶ This includes stepAIC (e.g. Dahlgren 2010; Burnham et al 2011; Hegyi & Garamszegi 2011).

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(assuming only potentially relevant predictors have been selected a priori)

- ▶ NOT significant + expected sign = let it be.

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- ▶ Significant + expected sign = keep it!

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5. Always report effect sizes

END

:)

Source code and materials:

<https://github.com/Pakillo/stats-intro>

