Linear, Generalized, and Mixed/Multilevel models - an introduction with R

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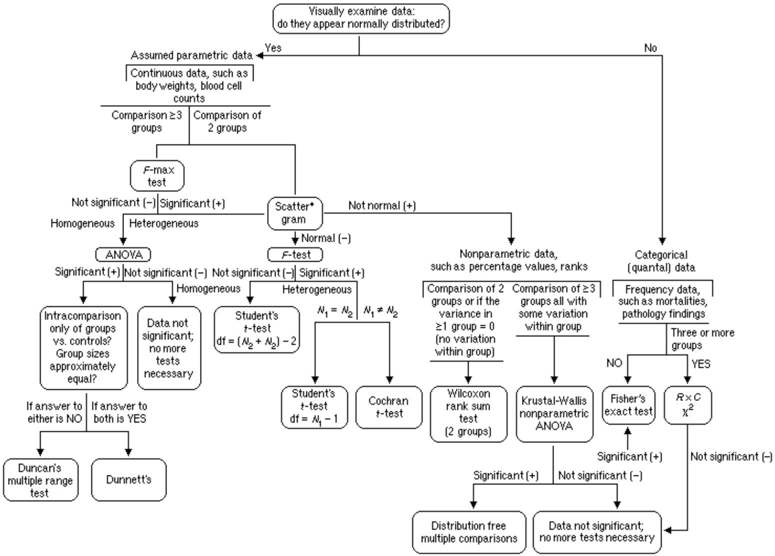
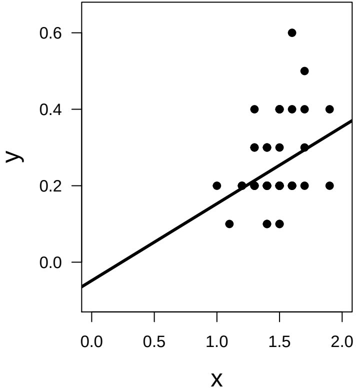
http://bit.ly/frod_san

Modern statistics are easier than this


Visually examine data:
do they appear normally distributed?
Yes
No
Assumed parametric data
Continuous data, such as body weights, blood cell counts
Comparison ≥3 groups
Comparison of 2 groups
F-max test
Not significant (−)
Significant (+)
Homogeneous
Heterogeneous
Scatter•gram
Not normal (+)
Normal (−)
ANOVA
F-test
Significant (+)
Not significant (−)
Not significant (−)
Significant (+)
Homogeneous
Heterogeneous
Intracomparison only of groups vs. controls? Group sizes approximately equal?
Data not significant; no more tests necessary
Student's t-test df = (N2 + N1) − 2
N1 = N2
N1 ≠ N2
Student's t-test df = N1 − 1
Cochran t-test
If answer to either is NO
If answer to both is YES
Duncan's multiple range test
Dunnett's
Nonparametric data, such as percentage values, ranks
Comparison of 2 groups or if the variance in ≥1 group = 0 (no variation within group)
Comparison of ≥3 groups all with some variation within group
Wilcoxon rank sum test (2 groups)
Krustal-Wallis nonparametric ANOVA
Significant (+)
Not significant (−)
Distribution free multiple comparisons
Data not significant; no more tests necessary
Categorical (quantal) data
Frequency data, such as mortalities, pathology findings
Three or more groups
NO
YES
Fisher's exact test
R × C χ2
Significant (+)
Not significant (−)

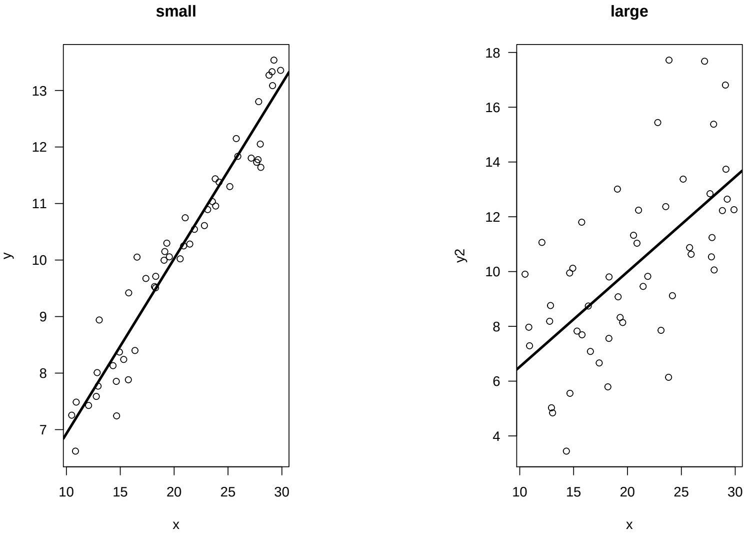
Our overarching regression framework

$$y_i = a + bx_i + \varepsilon_i$$
$$\varepsilon_i \sim N\left(0, \sigma^2\right)$$



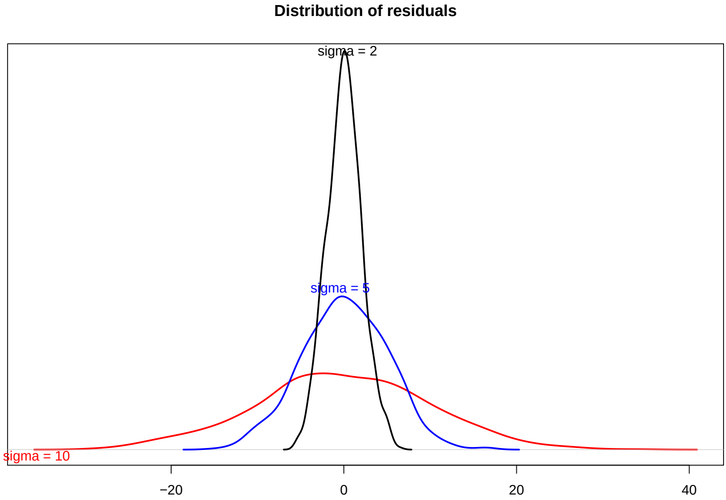
Data
y = response variable
x = predictor
Parameters
a = intercept
b = slope
σ = residual variation
ε = residuals

Residual variation (error)

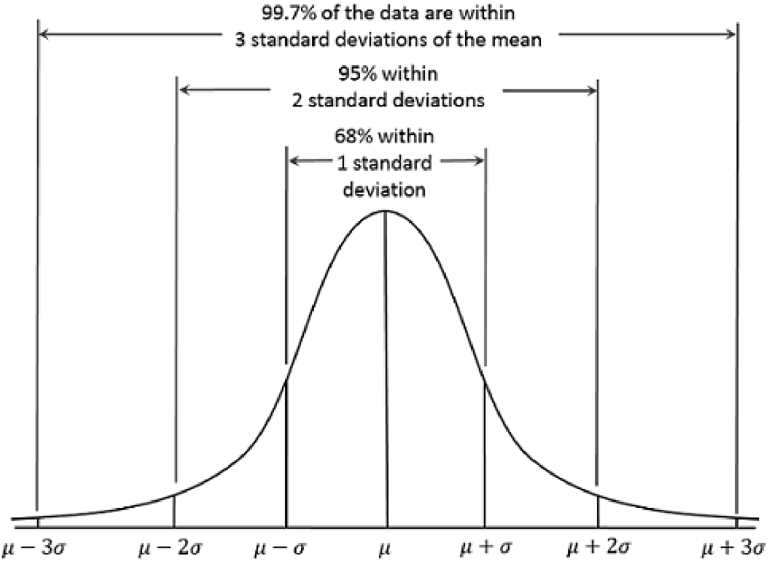


Residual variation

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



In a Normal distribution



Quick refresher of linear models

- Download datasets from `http://bit.ly/DEAD_datasets`

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- Load `iris` data into R

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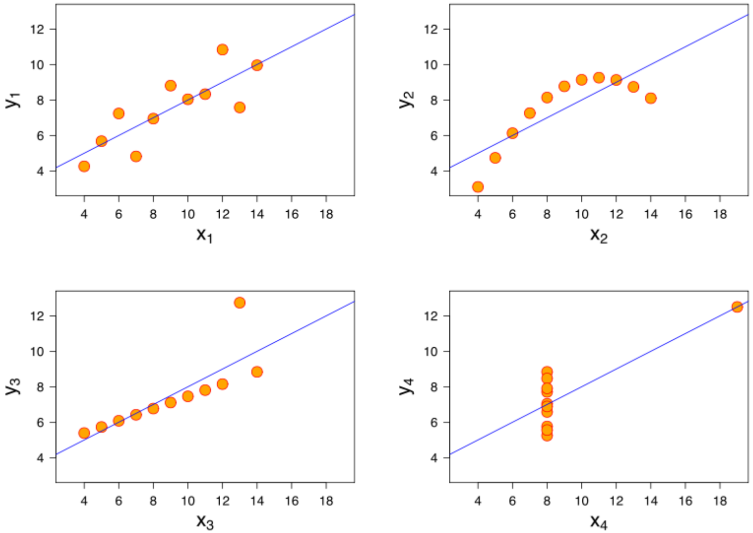
- Load `iris` data into R
- Q: What is the relationship between petal width and length in *Iris setosa*?

Iris dataset

```
str(setosa)
```

```
'data.frame':	50 obs. of  5 variables:
 $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
 $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
 $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ..
 $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ..
 $ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1
```

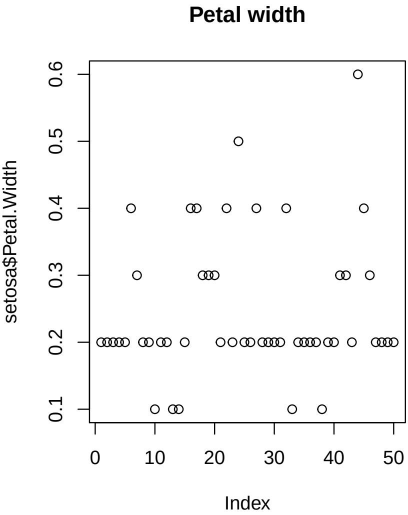
Always plot your data first!



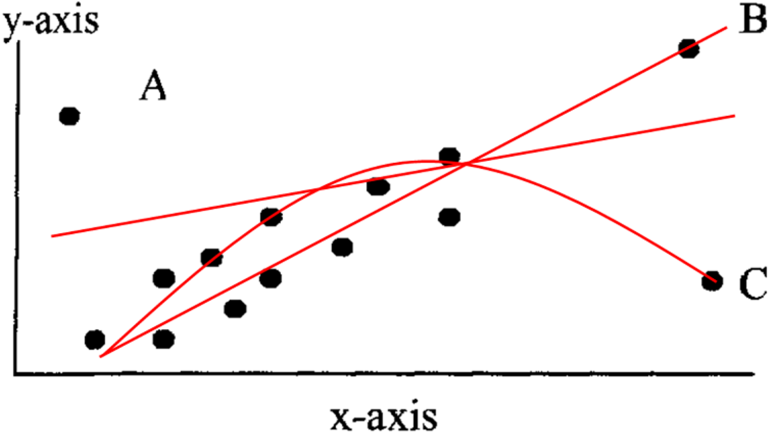
Exploratory Data Analysis (EDA)

Outliers

```
plot(setosa$Petal.Width, main = "Petal width")
```



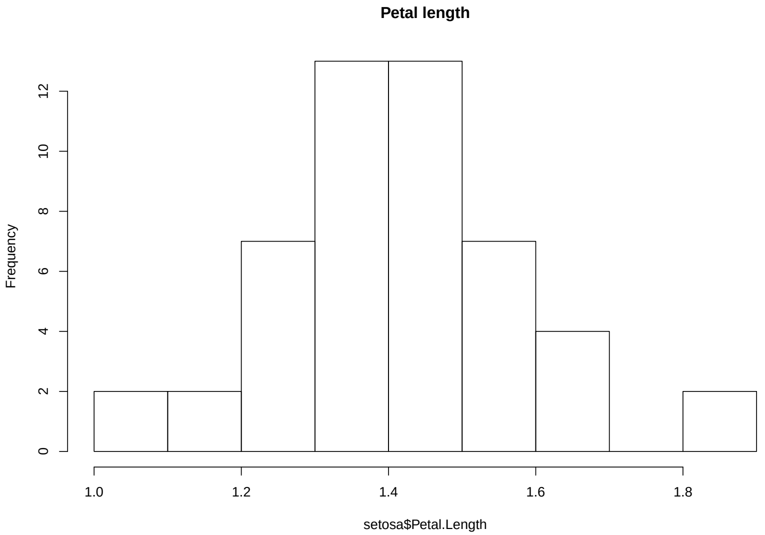
Outliers impact on regression



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

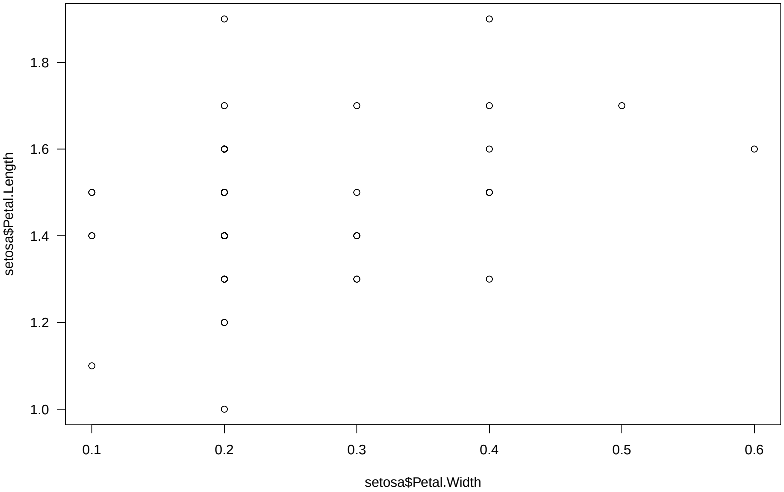
Histogram

```
hist(setosa$Petal.Length, main = "Petal length")
```



Scatterplot

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



Now fit model

Hint: `lm`

Now fit model

Hint: `lm`

```r
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
```

Retrieving model coefficients

```r
coef(m1)
```

```
(Intercept) Petal.Width
  1.3275634   0.5464903
```

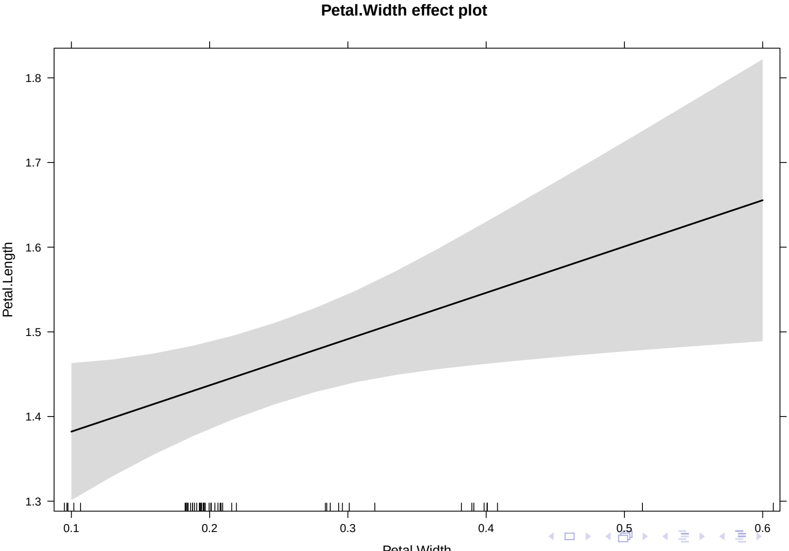
Confidence intervals

```
confint(m1)
```

```
                 2.5 %    97.5 %
(Intercept) 1.20700694 1.4481199
Petal.Width 0.09531905 0.9976615
```

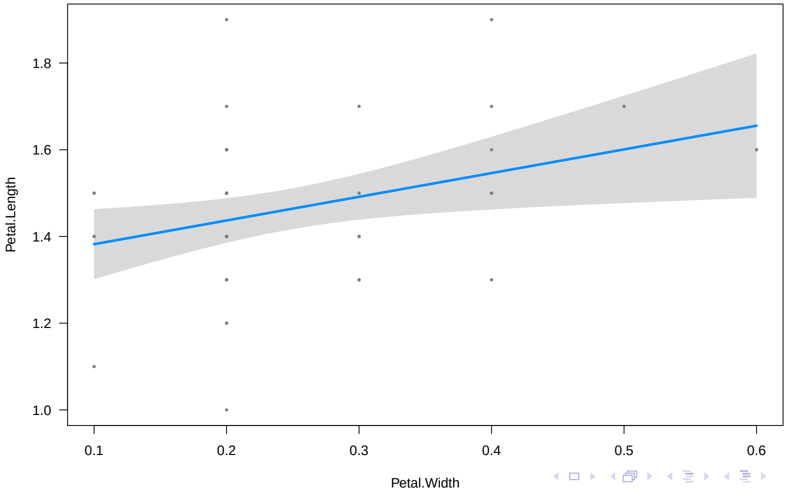
Plot effects

```
library(effects)
plot(allEffects(m1))
```



Plot model (visreg)

```r
library(visreg)
visreg(m1)
```



Linear model assumptions

- Linearity (transformations, GAM. . .)

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- Residuals:

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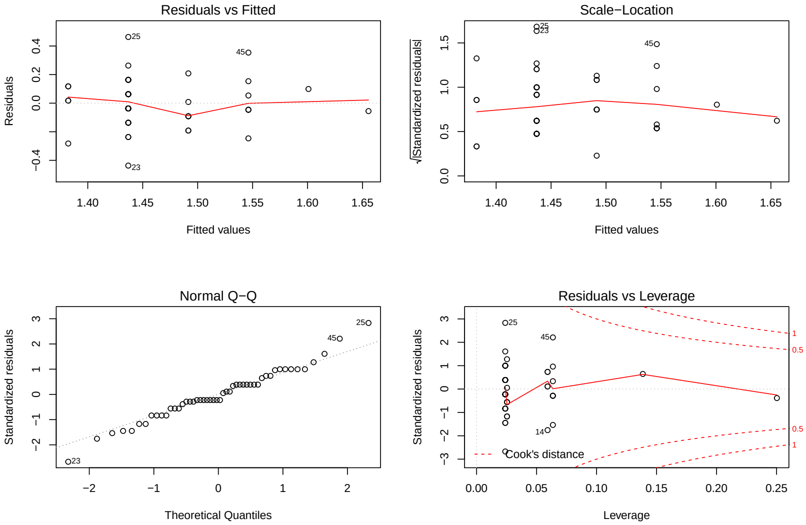
  - Normal

Linear model assumptions

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

Model checking: residuals



Residuals vs Fitted

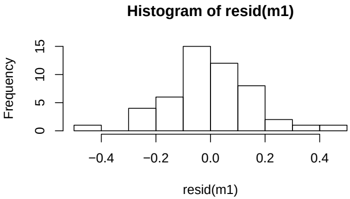
Scale−Location

Normal Q−Q

Residuals vs Leverage

Are residuals normal?

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



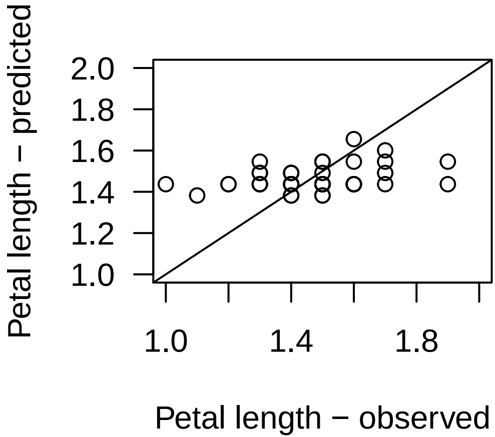
```
lm(formula = Petal.Length ~ Petal
             coef.est coef.se
(Intercept) 1.33     0.06
Petal.Width 0.55     0.22
---
n = 50, k = 2
residual sd = 0.17, R-Squared =
```

SD of residuals = 0.16 coincides with estimate of `sigma`.

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?

```r
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`

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- `plot`
- `summary`
- `coef`

Important functions

- `plot`
- `summary`
- `coef`
- `confint`

Important functions

- `plot`
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- `fitted`

Important functions

- `plot`
- `summary`
- `coef`
- `confint`
- `fitted`
- `resid`

Important functions

- `plot`
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- `coef`
- `confint`
- `fitted`
- `resid`
- `allEffects`

Important functions

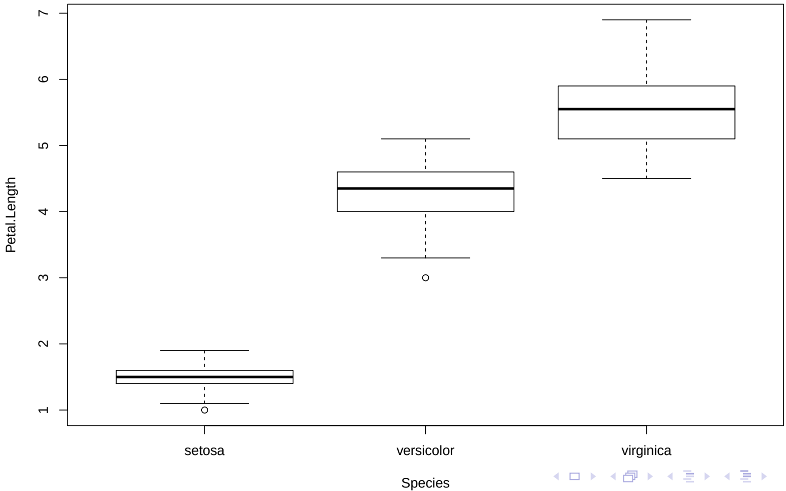
- `plot`
- `summary`
- `coef`
- `confint`
- `fitted`
- `resid`
- `allEffects`
- `predict`

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

$$
\begin{aligned}
y_i &= a + bx_i + \varepsilon_i \\
y_i &= a + b_{versicolor} + c_{virginica} + \varepsilon_i
\end{aligned}
$$

Model

```r
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
```

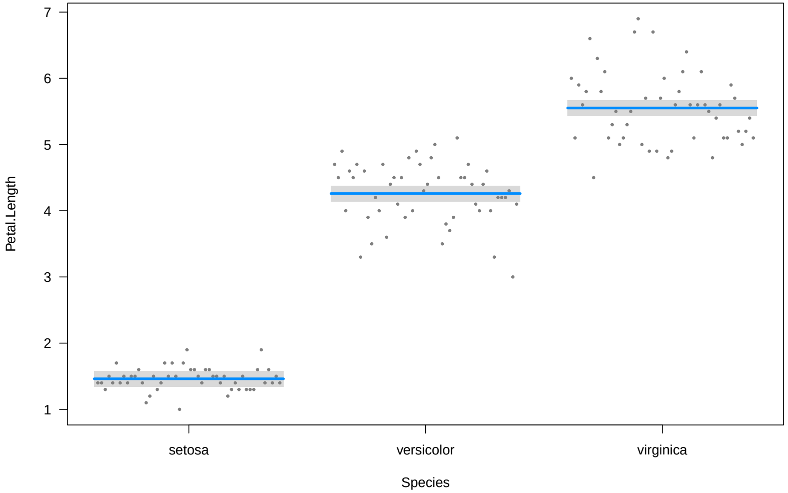
Alternatively, no intercept

```r
m3 <- lm(Petal.Length ~ Species - 1, data = iris)
```

```

Call:
lm(formula = Petal.Length ~ Species - 1, 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|)
Speciessetosa      1.46200    0.06086   24.02   <2e-16 ***
Speciesversicolor  4.26000    0.06086   70.00   <2e-16 ***
Speciesvirginica   5.55200    0.06086   91.23   <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:  0.9895,	Adjusted R-squared:  0.9892
```

Petal length differences across 3 *Iris* species

```
visreg(m3)
```



Are differences statistically significant?

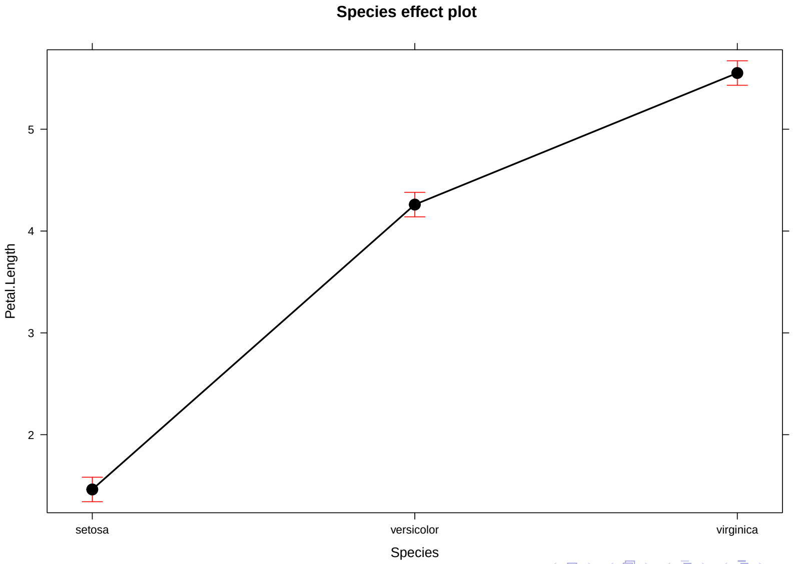
Compare CIs

```
summary(allEffects(m3))
```

```
 model: Petal.Length ~ Species - 1

 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(m3))
```



Combining continuous and categorical predictors

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

$$\begin{aligned} y_i &= a + bx_i + \varepsilon_i \\ y_i &= a + b_{versicolor} + c_{virginica} + \varepsilon_i \\ y_i &= a + b_{versicolor} + c_{virginica} + d \cdot PetalWidth_i + \varepsilon_i \end{aligned}$$

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)

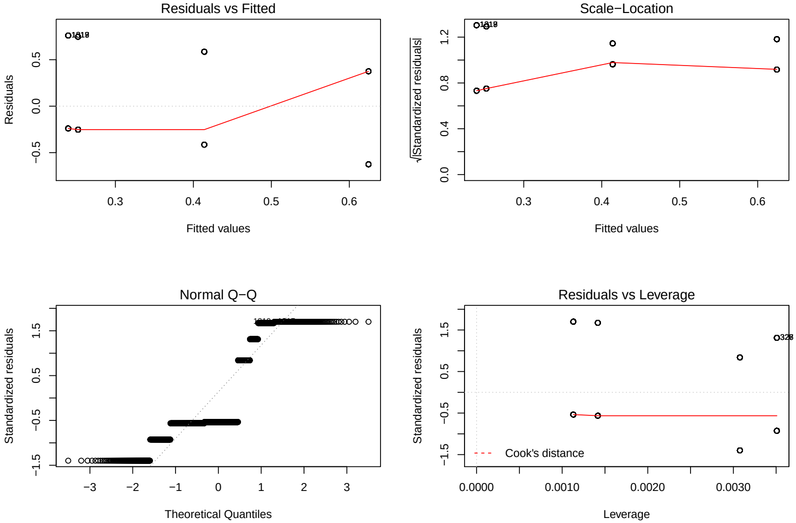
Q: Survival of passengers on the Titanic ∼ Class

Read `titanic_long.csv` dataset.

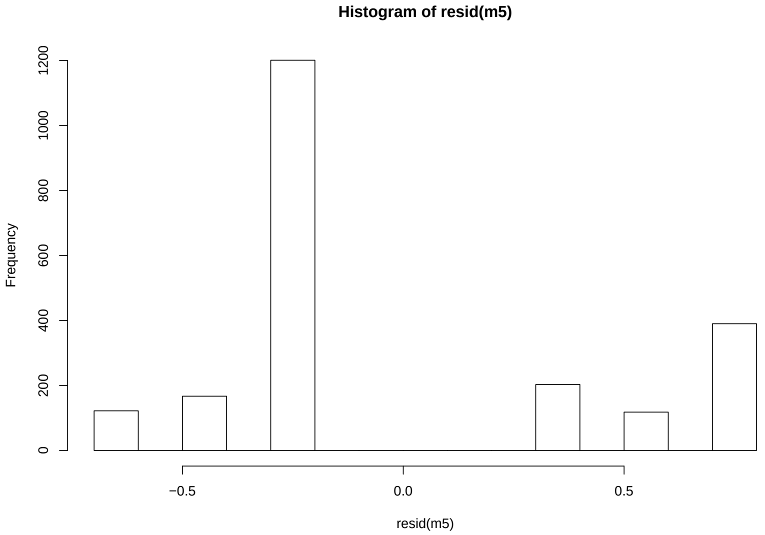
```
  class   age  sex survived
1 first adult male        1
2 first adult male        1
3 first adult male        1
4 first adult male        1
5 first adult male        1
6 first adult male        1
```

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

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   - Bernouilli - Binomial

Generalised Linear Models

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Generalised Linear Models

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Generalised Linear Models

1. **Response variable** - distribution `family`
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   - etc

Generalised Linear Models

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Generalised Linear Models

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   - etc
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3. **Link function**

Generalised Linear Models

1. **Response variable** - distribution `family`
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   - etc
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   - Gaussian: identity

Generalised Linear Models

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Generalised Linear Models

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Generalised Linear Models

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2. **Predictors** (continuous or categorical)
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   - Gaussian: identity
   - Binomial: logit, probit
   - Poisson: log. . .
   - See `family`.

The modelling process

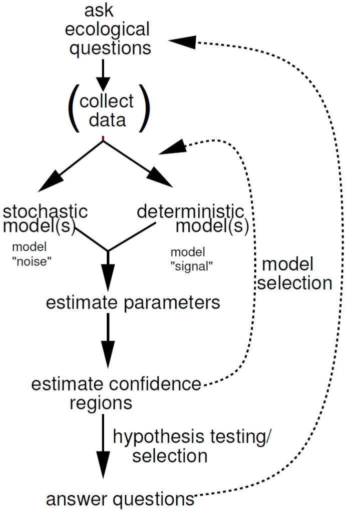

Figure 1.5 Flow of the modeling process.

Bolker 2008

Bernouilli - Binomial distribution (Logistic regression)

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

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

Then

$$\begin{aligned} Pr(alive) &= a + bx \\ logit(Pr(alive)) &= a + bx \\ Pr(alive) = invlogit(a + bx) &= \frac{e^{a+bx}}{1 + e^{a+bx}} \end{aligned}$$

Bernouilli - Binomial distribution (Logistic regression)

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

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

Then

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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?

```r
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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How many survived?

Back to survival of Titanic passengers

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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?

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tapply(titanic$survived, titanic$class, length)
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  crew  first second  third
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```

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

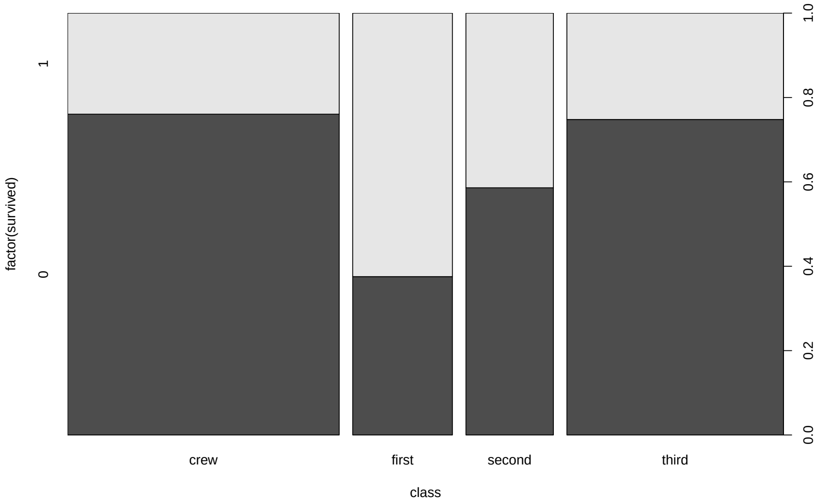
```
library(dplyr)
titanic %>%
  group_by(class, survived) %>%
  summarise(count = n())
```

```
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 =

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 classsecond  classthird 
-1.15515905  1.66434399  0.80784987  0.06784632 
```

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

```r
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
```

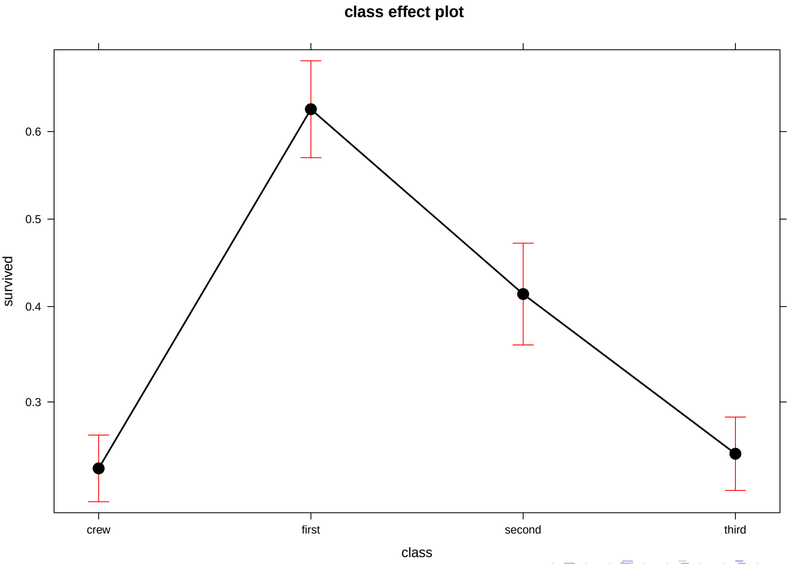
Model interpretation using effects package

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

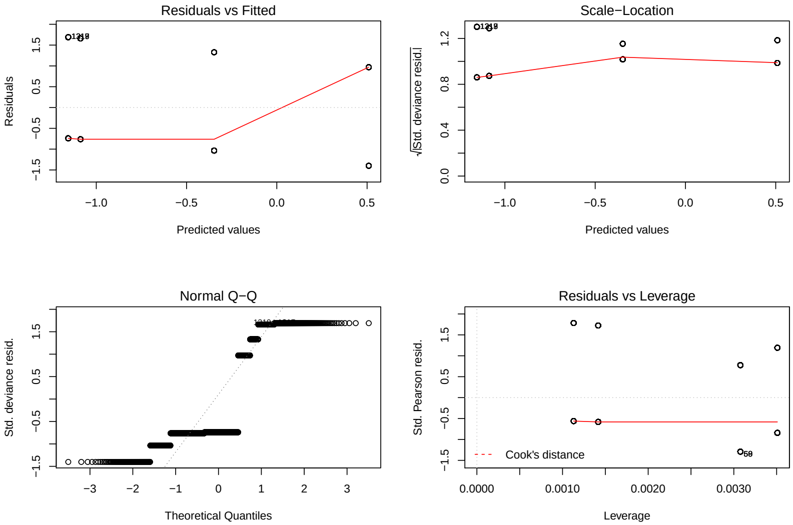
```
 model: survived ~ class

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

Effects plot

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



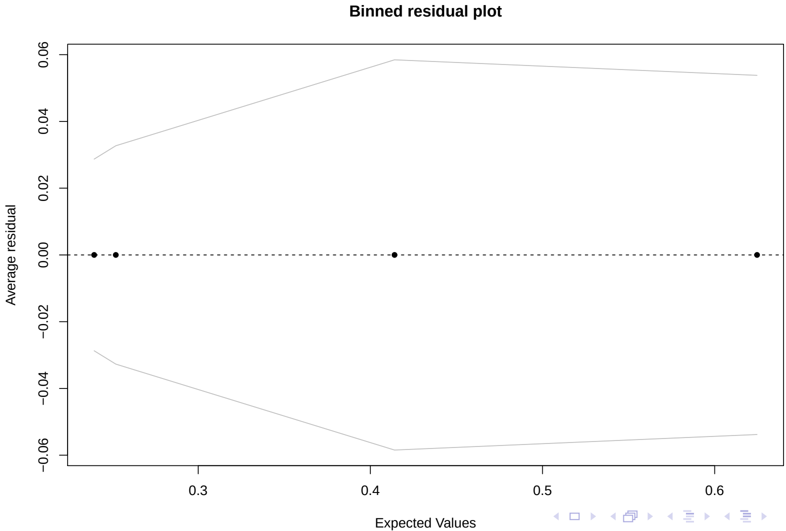
Logistic regression: model checking



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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Recapitulating

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5. Examine models: `summary`
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Recapitulating

1. Import data: `read.table` or `read.csv`
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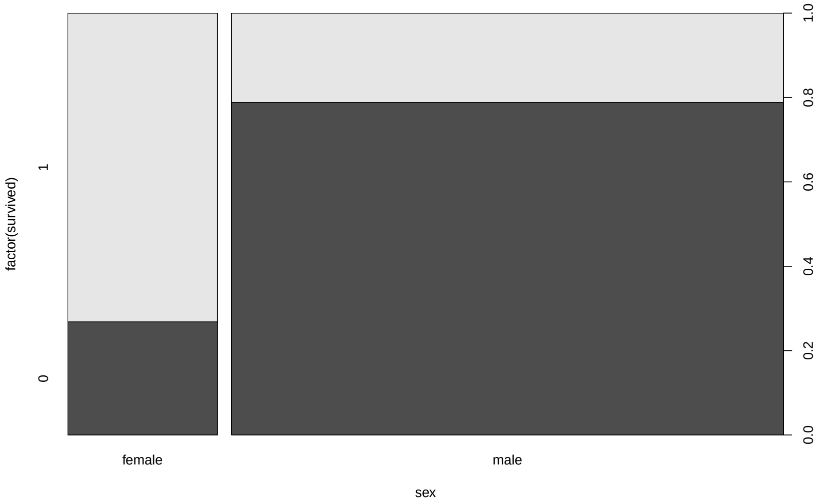
7. Plot model: `plot(allEffects(model))`. Or use `visreg`.
8. Examine residuals: `binnedplot` from package `arm`. Use `predict` to obtain predicted values for each obs.

Q: Did men have higher survival than women?

Plot first

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



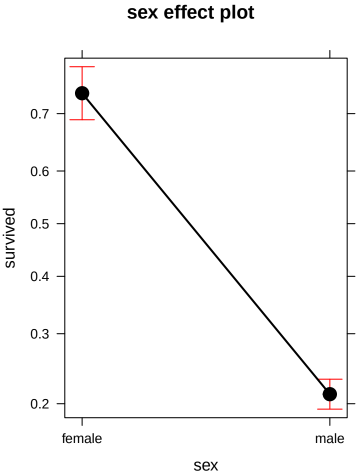
Fit model

```r
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`

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

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

Mmmm...

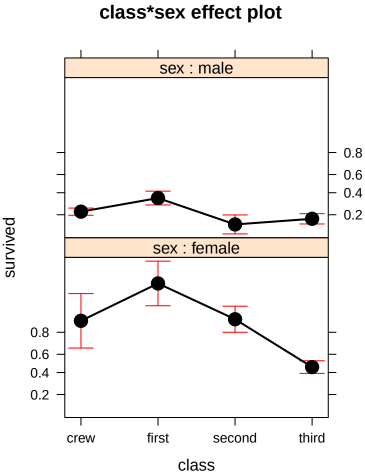
Fit model with both factors (interactions)

```r
tit.sex.class <- glm(survived ~ class * sex, data = titanic, fam
```

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

Effects

```
 model: survived ~ class * sex

 class*sex effect
        sex
class         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
```

```
Call:
glm(formula = cbind(Yes, No) ~ Class, family = binomial, data =

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!

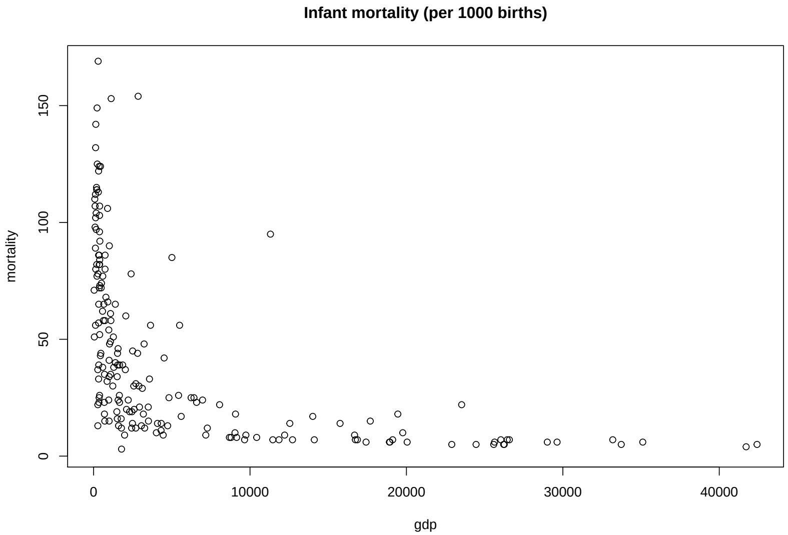
Logistic regression with continuous predictors

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)
```

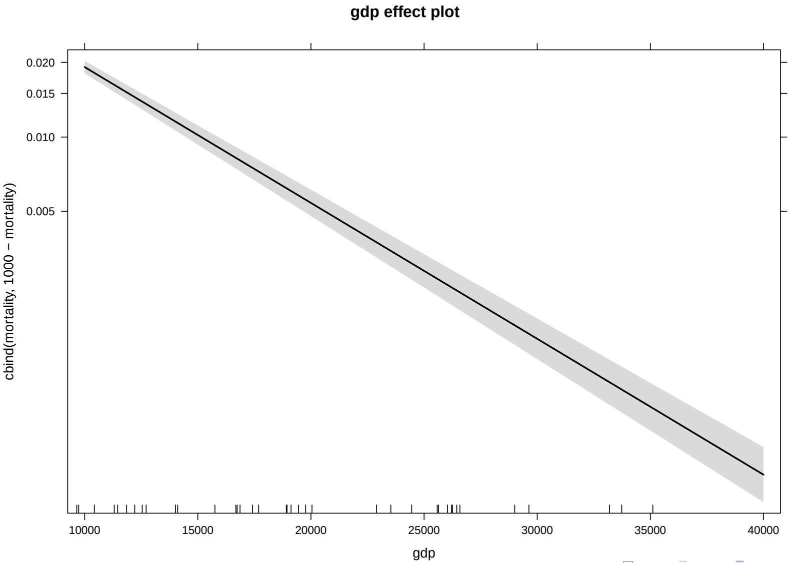
Effects

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

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

 gdp effect
gdp
       10000        20000        30000        40000 
0.0191438829 0.0054028095 0.0015096074 0.0004206154 
```

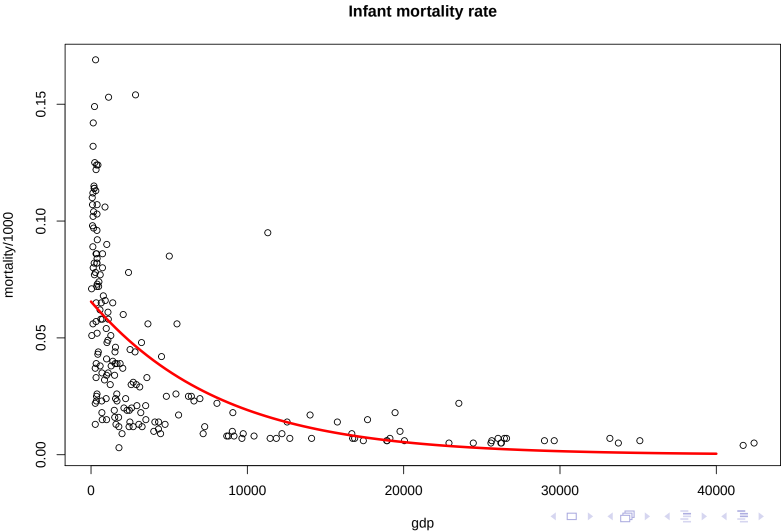
Effects plot

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



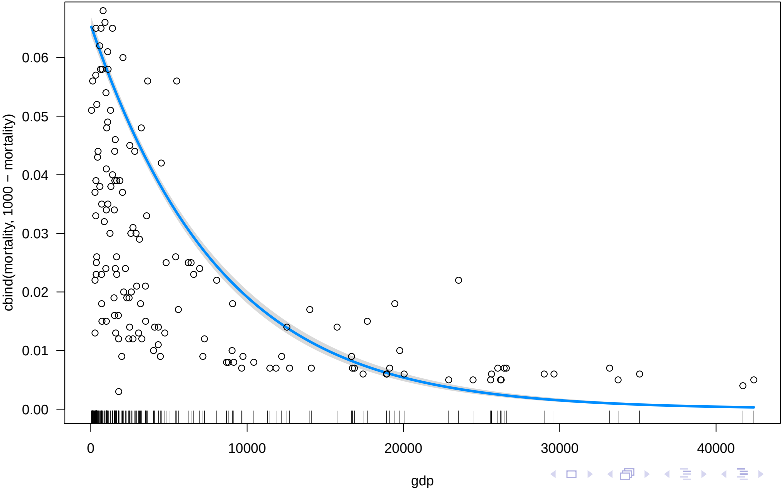
Plot model and data

```
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

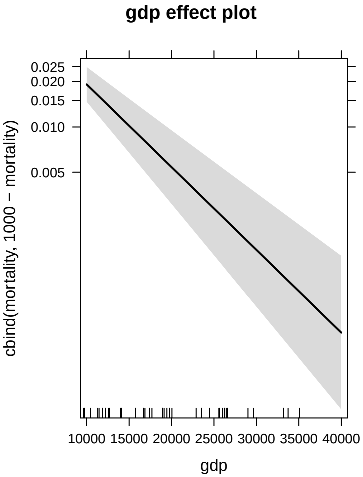
```r
gdp.overdisp <- glm(cbind(mortality, 1000 - mortality) ~ gdp,
               data = gdp, family = quasibinomial)
```

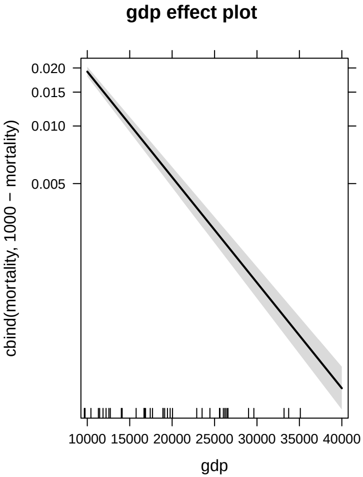
```

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

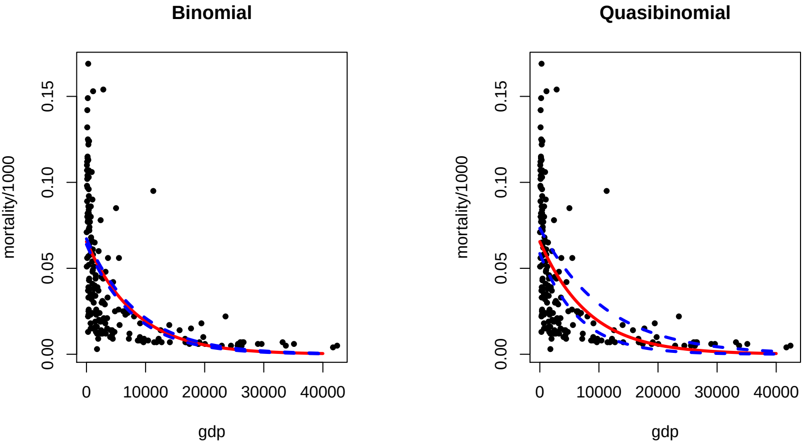
```
 model: cbind(mortality, 1000 - mortality) ~ gdp

 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

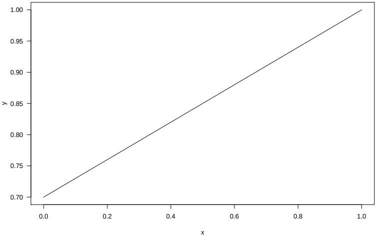


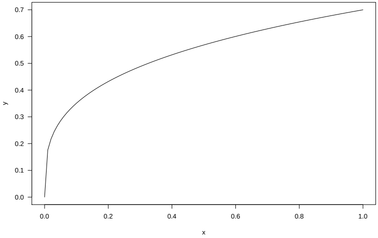
Overdispersion

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

$$\begin{aligned} log(N) &= a + bx \\ N &= e^{a+bx} \end{aligned}$$

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

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

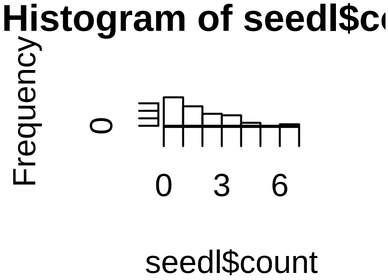
```
       X             count           row         col
 Min.   : 1.00   Min.   :0.00   Min.   :1   Min.   : 1.0
 1st Qu.:13.25   1st Qu.:1.00   1st Qu.:2   1st Qu.: 3.0
 Median :25.50   Median :2.00   Median :3   Median : 5.5
 Mean   :25.50   Mean   :2.14   Mean   :3   Mean   : 5.5
 3rd Qu.:37.75   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(seedl$count)
```

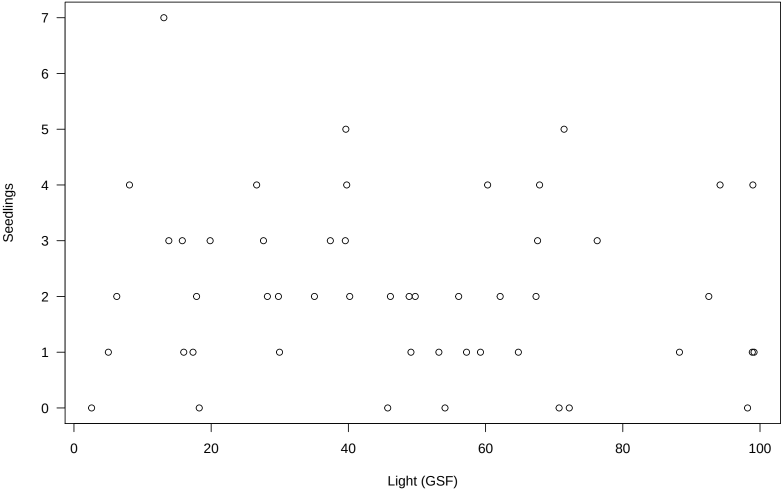
```
 0  1  2  3  4  5  7 
 7 12 13  8  7  2  1 
```

```
hist(seedl$count)
```



Q: Relationship between Nseedlings and light?

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



Let's fit model (Poisson regression)

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

```

Call:
glm(formula = count ~ light, family = poisson, data = seedl)

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(seedl.glm)
```

```
(Intercept)        light
0.881805022 -0.002575656
```

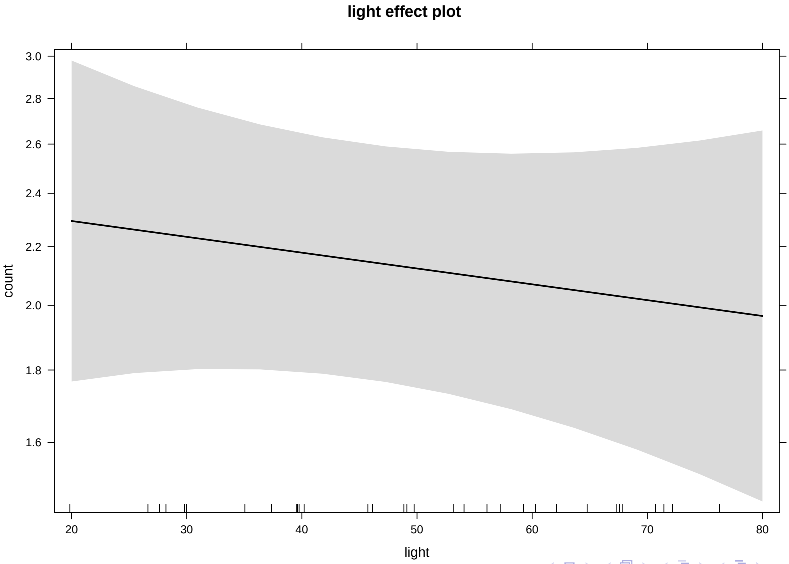
We need to back-transform: apply the inverse of the logarithm

```
exp(coef(seedl.glm))
```

```
(Intercept)       light
  2.4152554   0.9974277
```

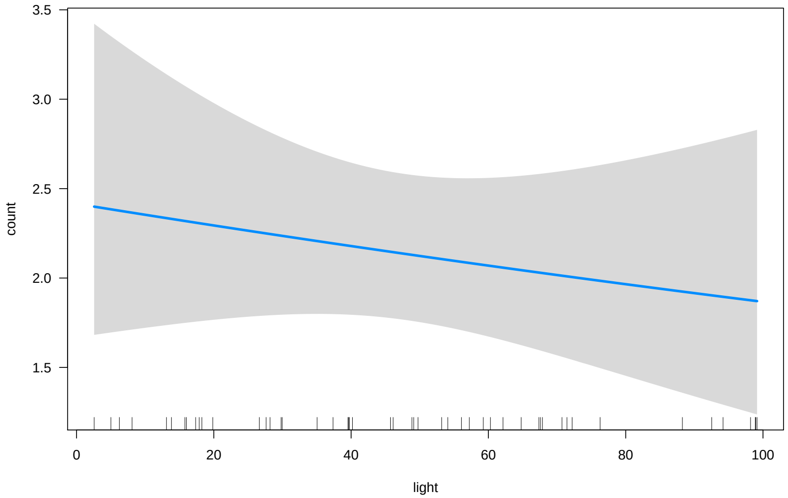
So what's the relationship between Nseedlings and light?

```
plot(allEffects(seedl.glm))
```

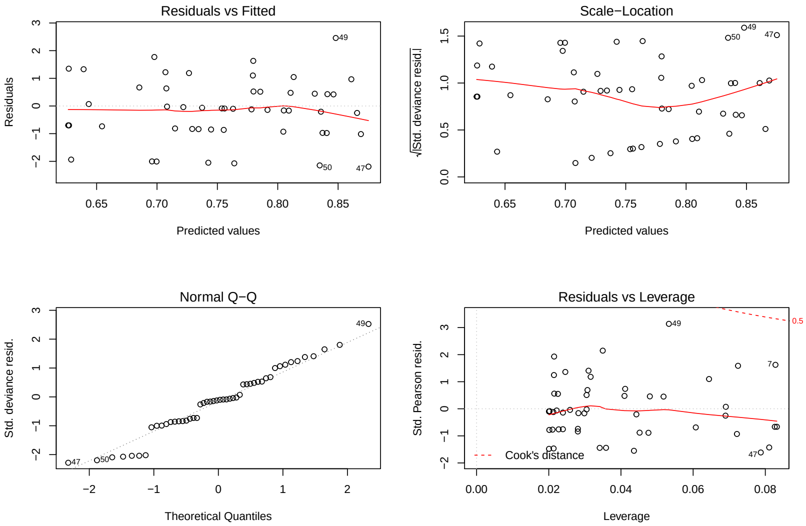


Using visreg

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

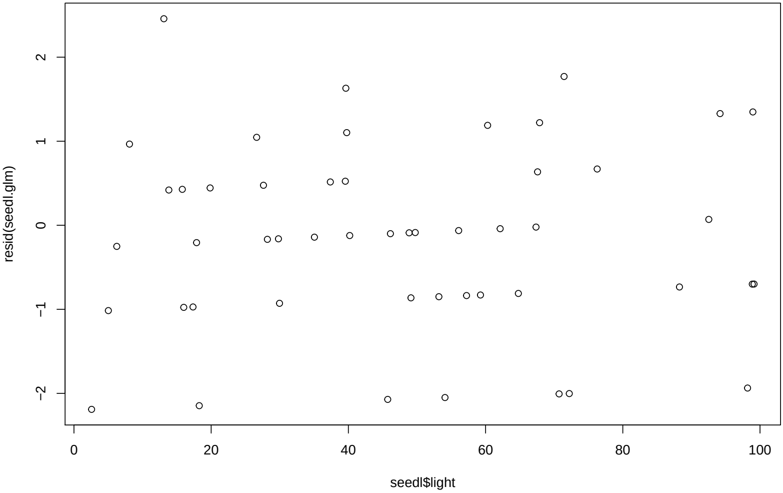


Poisson regression: model checking



Is there pattern of residuals along predictor?

```r
plot(seedl$light, resid(seedl.glm))
```



Poisson regression: Overdispersion

Always check overdispersion with count data

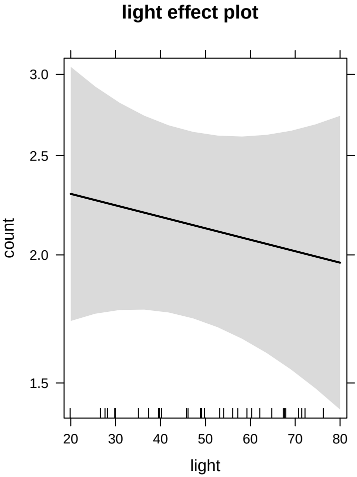
Use family quasipoisson

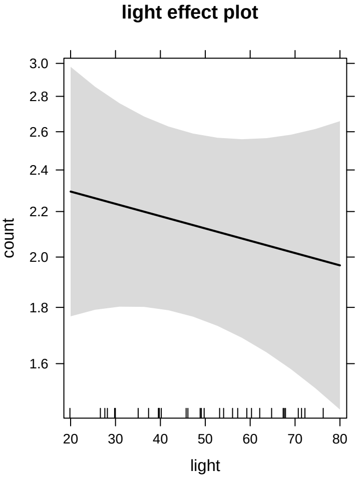
```
Call:
glm(formula = count ~ light, family = quasipoisson, data = seedl

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

Example dataset: trees

- Data on 1000 trees from 10 plots.

```r
head(trees)
```

```
  plot   dbh height    sex dead  dbh.c
1    2 38.85   37.8 female    0  13.85
2    4 26.05   38.1 female    0   1.05
3    5 42.66   50.2 female    0  17.66
4    2 20.72   30.1 female    0  -4.28
5    4 21.83   34.0 female    0  -3.17
6    4  8.23   21.9   male    0 -16.77
```

Example dataset: trees

- Data on 1000 trees from 10 plots.
- Trees per plot: 4 - 392.

```
head(trees)
```

```
  plot   dbh height    sex dead   dbh.c
1    2 38.85   37.8 female    0  13.85
2    4 26.05   38.1 female    0   1.05
3    5 42.66   50.2 female    0  17.66
4    2 20.72   30.1 female    0  -4.28
5    4 21.83   34.0 female    0  -3.17
6    4  8.23   21.9   male    0 -16.77
```

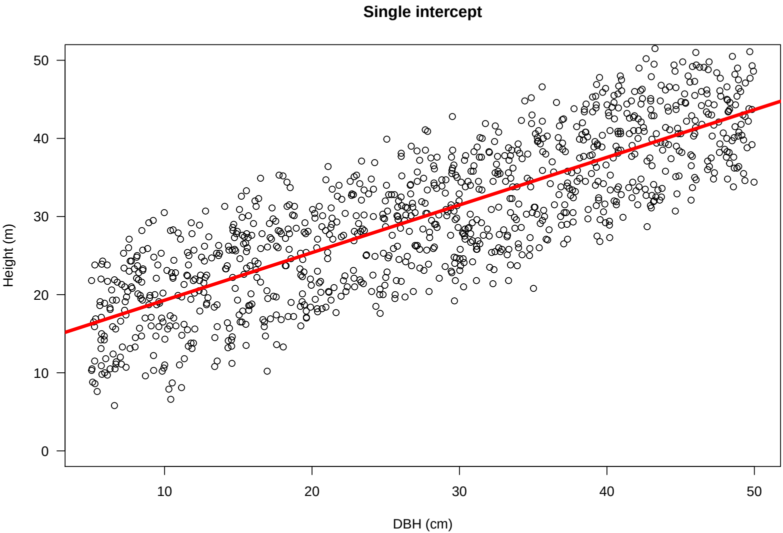
Q: What’s the relationship between tree diameter and height?

A simple linear model

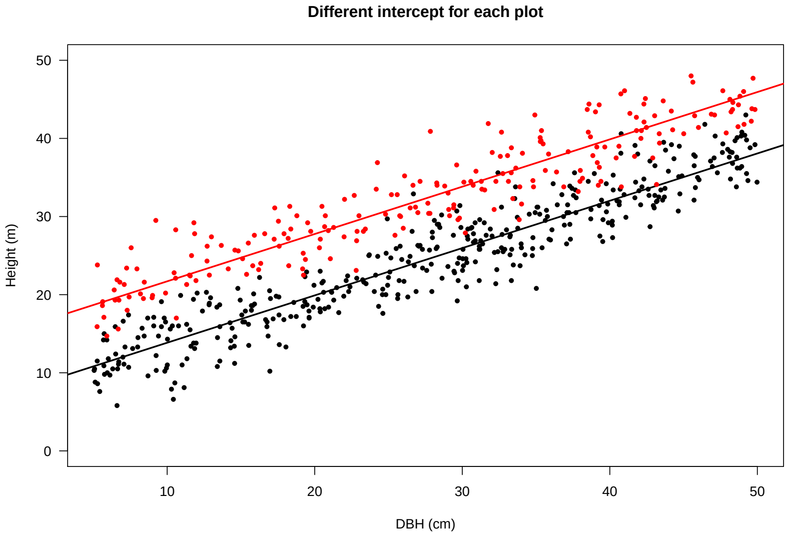
```
lm.simple <- lm(height ~ dbh, data = trees)
```

```

Call:
lm(formula = height ~ dbh, data = trees)

Residuals:
     Min       1Q   Median       3Q      Max 
-13.7384  -4.7652   0.4759   4.2931  13.5282 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 13.18767    0.41476   31.80   <2e-16 ***
dbh          0.60967    0.01351   45.14   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 5.549 on 998 degrees of freedom
Multiple R-squared:  0.6712,    Adjusted R-squared:  0.6709 
F-statistic:  2038 on 1 and 998 DF,  p-value: < 2.2e-16
```

There is only one intercept



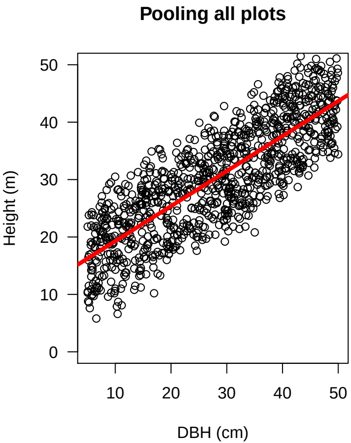
What if allometry varies among plots?

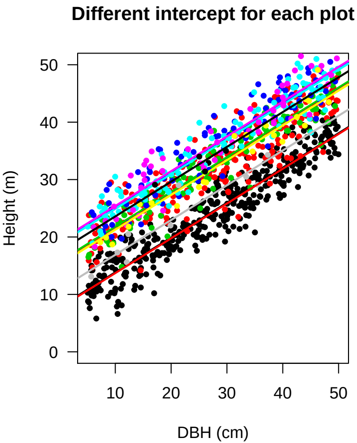


Fitting a varying intercepts model with lm

```
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
```

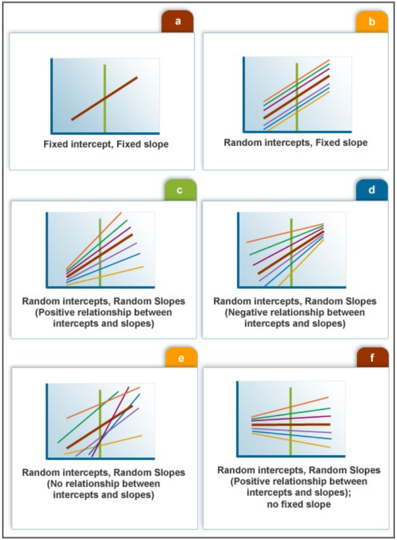
Single vs varying intercept





Mixed models enable us to account for variability

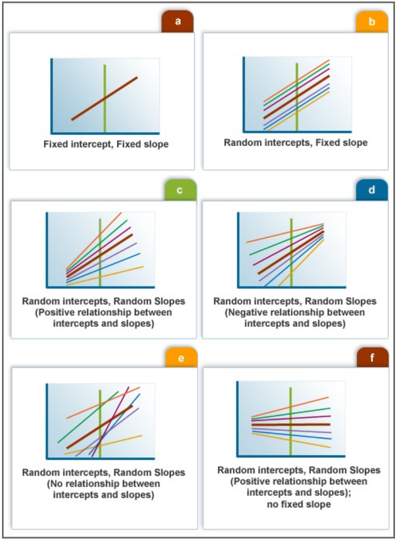
- Varying intercepts


a
Fixed intercept, Fixed slope
b
Random intercepts, Fixed slope
c
Random intercepts, Random Slopes (Positive relationship between intercepts and slopes)
d
Random intercepts, Random Slopes (Negative relationship between intercepts and slopes)
e
Random intercepts, Random Slopes (No relationship between intercepts and slopes)
f
Random intercepts, Random Slopes (Positive relationship between intercepts and slopes); no fixed slope

http://www.esourceresearch.org/

Mixed models enable us to account for variability

- Varying intercepts
- Varying slopes


a
Fixed intercept, Fixed slope
b
Random intercepts, Fixed slope
c
Random intercepts, Random Slopes (Positive relationship between intercepts and slopes)
d
Random intercepts, Random Slopes (Negative relationship between intercepts and slopes)
e
Random intercepts, Random Slopes (No relationship between intercepts and slopes)
f
Random intercepts, Random Slopes (Positive relationship between intercepts and slopes); no fixed slope

http://www.esourceresearch.org/

Mixed model with varying intercepts

$$\begin{aligned} y_i &= a_j + bx_i + \varepsilon_i \\ a_j &\sim N\left(0, \tau^2\right) \\ \varepsilon_i &\sim N\left(0, \sigma^2\right) \end{aligned}$$

En nuestro ejemplo:

$$\begin{aligned} Height_i &= plot_j + bDBH_i + \varepsilon_i \\ plot_j &\sim N\left(0, \tau^2\right) \\ \varepsilon_i &\sim N\left(0, \sigma^2\right) \end{aligned}$$

Mixed models estimate varying parameters (intercepts and/or slopes) with pooling among levels (rather than considering them fully independent)

Hence there’s gradient between

- **complete pooling**: Single overall intercept.

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- **complete pooling**: Single overall intercept.
  - `lm (height ~ dbh)`

Hence there's gradient between

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    - `lm (height ~ dbh)`
- **no pooling**: One *independent* intercept for each plot.

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  - `lm (height ~ dbh + factor(plot))`

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- **complete pooling**: Single overall intercept.
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- **no pooling**: One *independent* intercept for each plot.
  - `lm (height ~ dbh + factor(plot))`
- **partial pooling**: Inter-related intercepts.

Hence there's gradient between

- **complete pooling**: Single overall intercept.
  - `lm (height ~ dbh)`
- **no pooling**: One *independent* intercept for each plot.
  - `lm (height ~ dbh + factor(plot))`
- **partial pooling**: Inter-related intercepts.
  - `lmer(height ~ dbh + (1 | plot))`

Fitting mixed/multilevel models

```r
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

```r
coef(mixed)
```

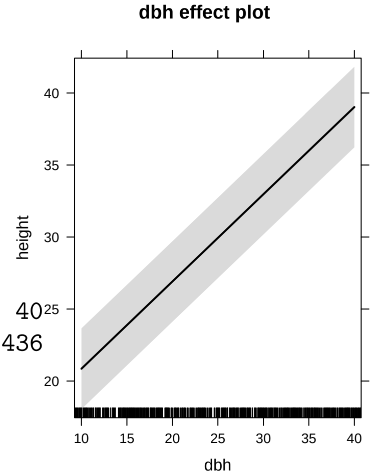
```
$plot
   (Intercept)       dbh
1     7.798373 0.6056549
2    15.647613 0.6056549
3    15.735397 0.6056549
4    19.253661 0.6056549
5    18.819467 0.6056549
6    19.306574 0.6056549
7    15.197908 0.6056549
8    11.016485 0.6056549
9    17.265447 0.6056549
10    7.940715 0.6056549

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

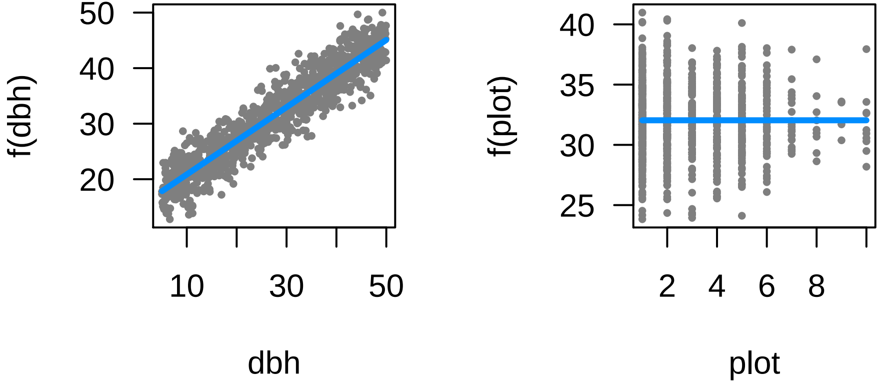
Visualising model: `allEffects`

```
 model: height ~ dbh

 dbh effect
dbh
      10       20       30       40
20.85471 26.91126 32.96781 39.02436
```

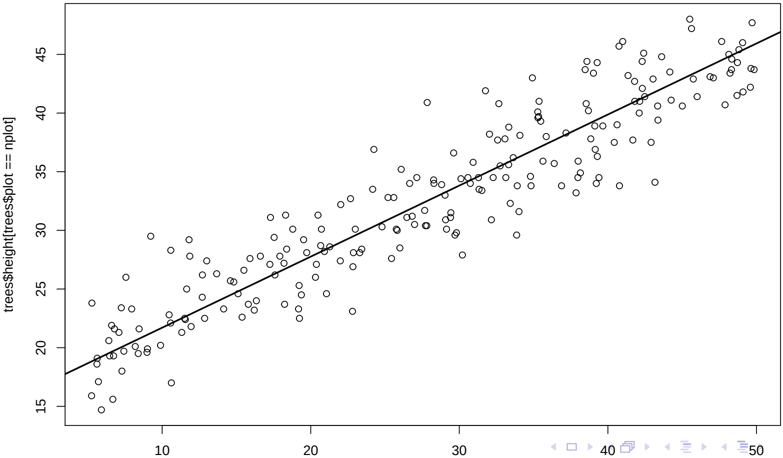


Visualising model: `visreg`



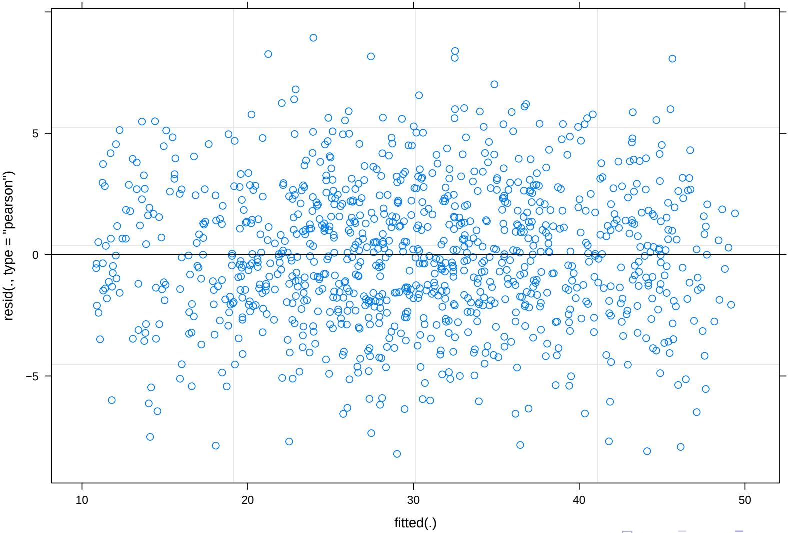
Plotting regression for individual forest plots

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



Checking residuals

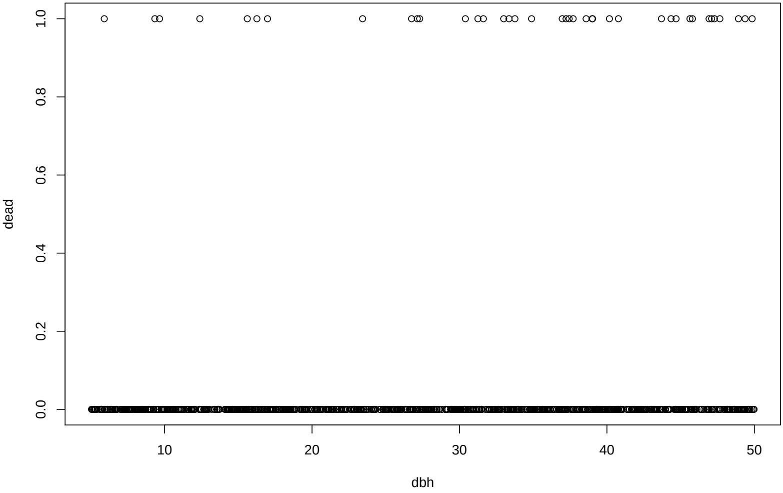
```
plot(mixed)
```



Multilevel logistic regression

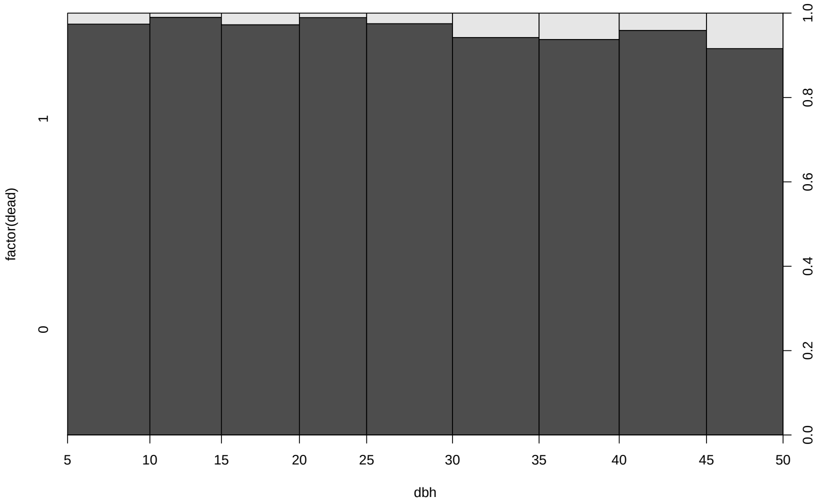
Q: Relationship between tree size and mortality

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



Q: Relationship between tree size and mortality

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



Fit simple logistic regression

```r
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 independent plot effects)

```
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
```

Fit multilevel logistic regression

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

```
Generalized linear mixed model fit by maximum likelihood (Laplac
  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

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

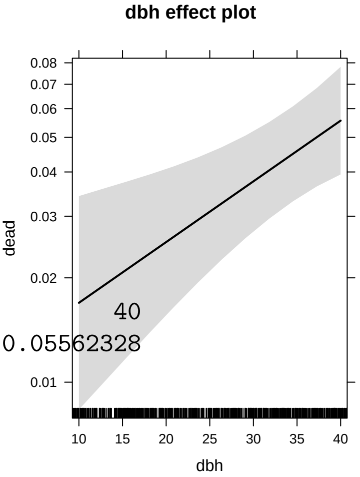
```
$plot
   (Intercept)        dbh
1     -4.469446 0.04093806
2     -4.469446 0.04093806
3     -4.469446 0.04093806
4     -4.469446 0.04093806
5     -4.469446 0.04093806
6     -4.469446 0.04093806
7     -4.469446 0.04093806
8     -4.469446 0.04093806
9     -4.469446 0.04093806
10    -4.469446 0.04093806

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

Visualising model: `allEffects`

```
 model: dead ~ dbh

 dbh effect
dbh
        10         20         30         40
0.01695545 0.02531581 0.03764063 0.05562328
```



END

:)

Source code and materials:

`https://github.com/Pakillo/LM-GLM-GLMM-intro`