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

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http://bit.ly/frod_san

Introduction to linear models

Modern statistics are easier than this

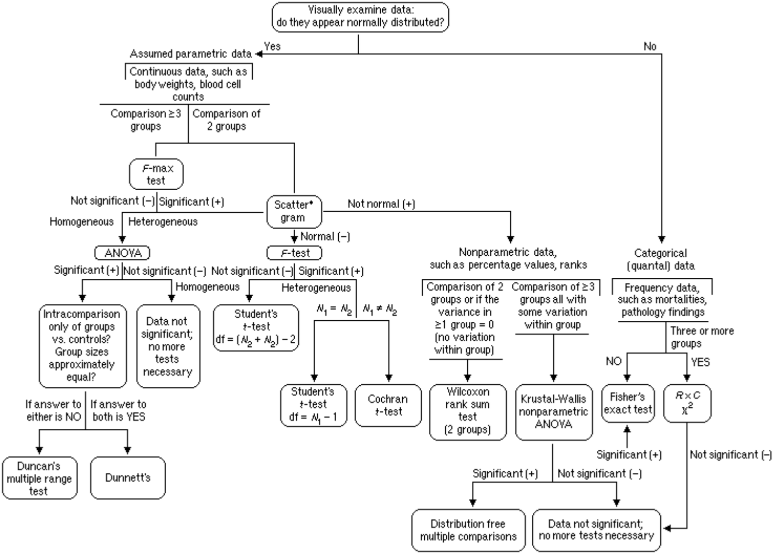
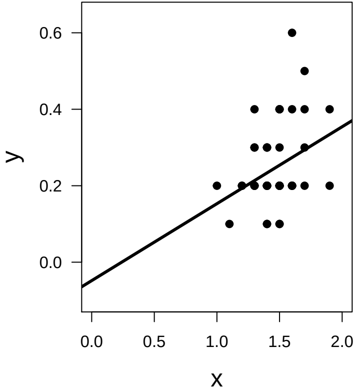

Visually examine data: do they appear normally distributed?
Yes
No
Assumed parametric data
Continuous data, such as body weights, blood cell counts
Comparison ≥3 groups
Comparison of 2 groups
F-max test
Not significant (−)
Significant (+)
Homogeneous
Heterogeneous
Scatter* gram
Not normal (+)
Normal (−)
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 = (N1 + N2) − 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 (−)

Figure 1:

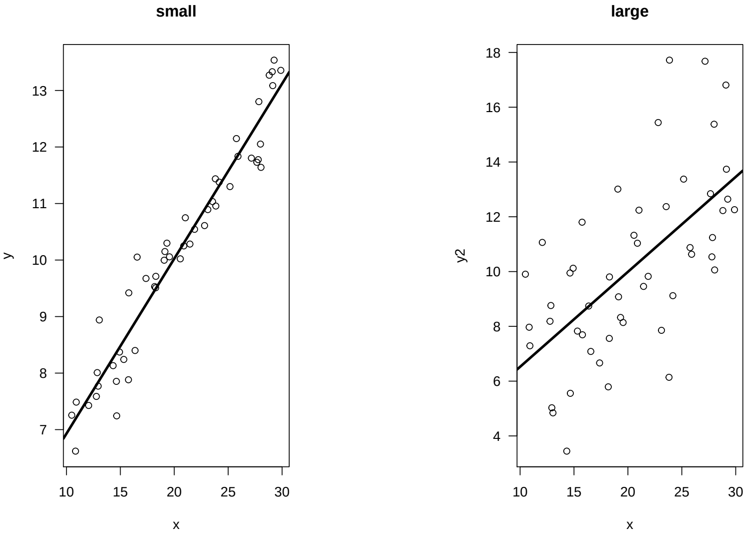
Our overarching regression framework

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



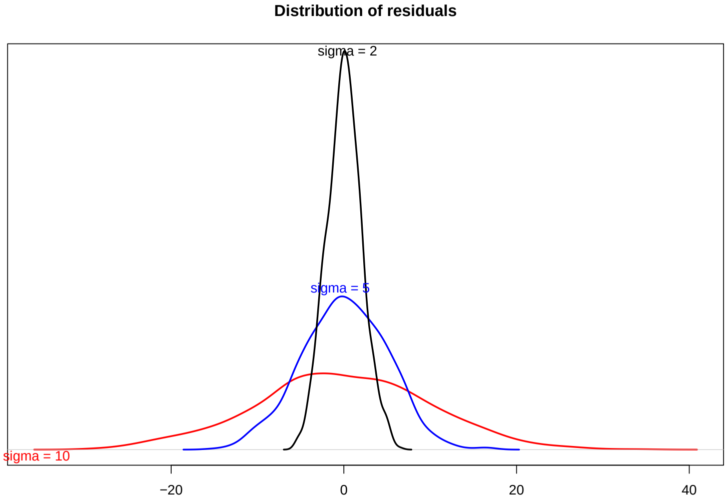
Data
y = response variable
x = predictor
Parameters
a = intercept
b = slope
σ = residual variation
ε = residuals

Residual variation (error)



Residual variation

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



In a Normal distribution

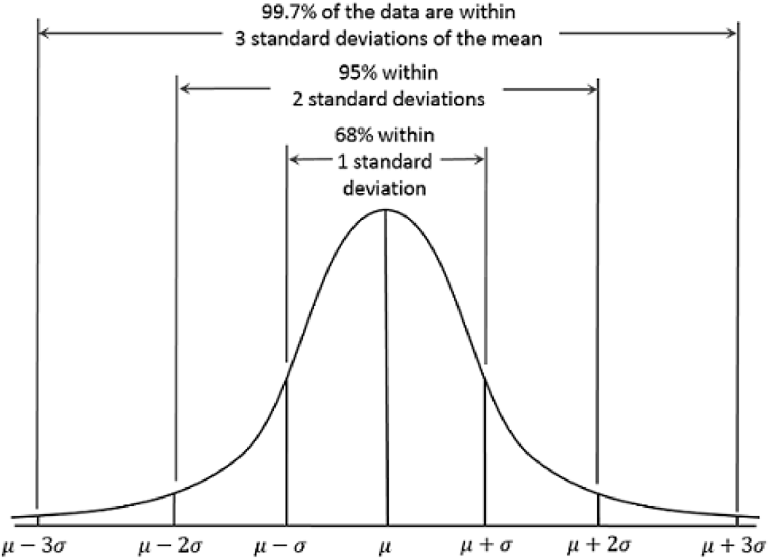


Figure 2:

Linear models

Example dataset: forest trees

- Go to https://tinyurl.com/treesdata

```r
trees <- read.csv("data-raw/trees.csv")
head(trees)
```

```
  plot   dbh height    sex dead
1    4 29.68   36.1   male    0
2    5 33.29   42.3   male    0
3    2 28.03   41.9 female    0
4    5 39.86   46.5 female    0
5    1 47.94   43.9 female    0
6    1 10.82   26.2   male    0
```

Example dataset: forest trees

- Go to https://tinyurl.com/treesdata
- Download zip file and uncompress (within your project folder!)

```
trees <- read.csv("data-raw/trees.csv")
head(trees)
```

```
  plot   dbh height    sex dead
1    4 29.68   36.1   male    0
2    5 33.29   42.3   male    0
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5    1 47.94   43.9 female    0
6    1 10.82   26.2   male    0
```

Questions

- What is the relationship between DBH and height?

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- Do taller trees have bigger trunks?

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- What is the relationship between DBH and height?
- Do taller trees have bigger trunks?
- Can we predict height from DBH? How well?

Always plot your data first!

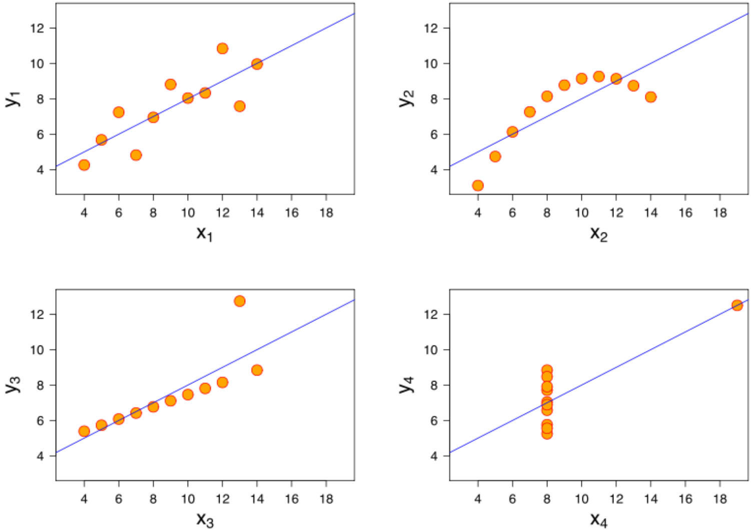
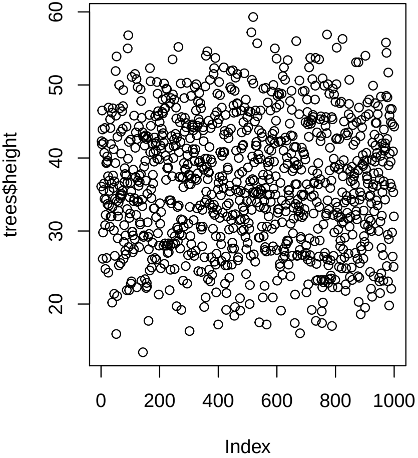


Figure 3:

Exploratory Data Analysis (EDA)

Outliers

```
plot(trees$height)
```



Outliers impact on regression

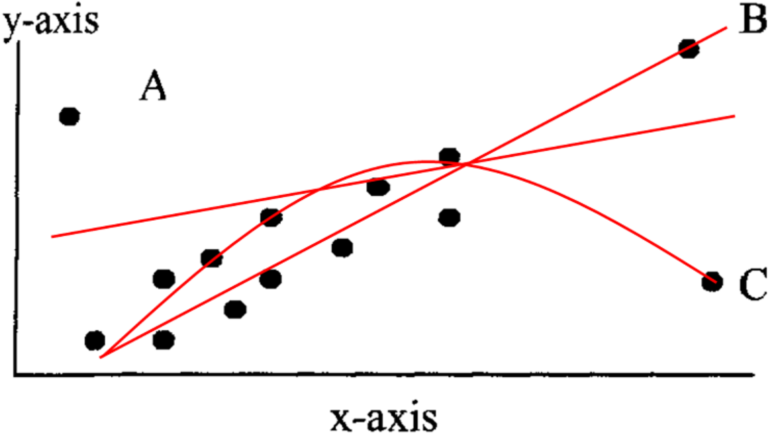
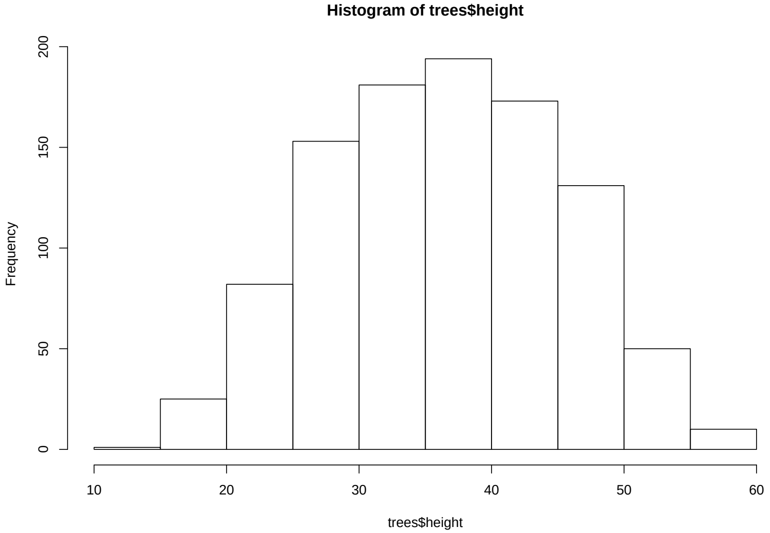


Figure 4:

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

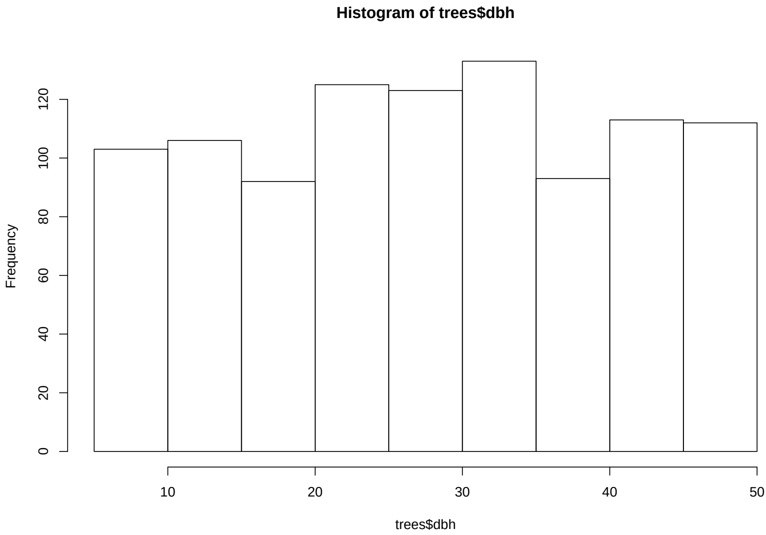
Histogram of response variable

```r
hist(trees$height)
```



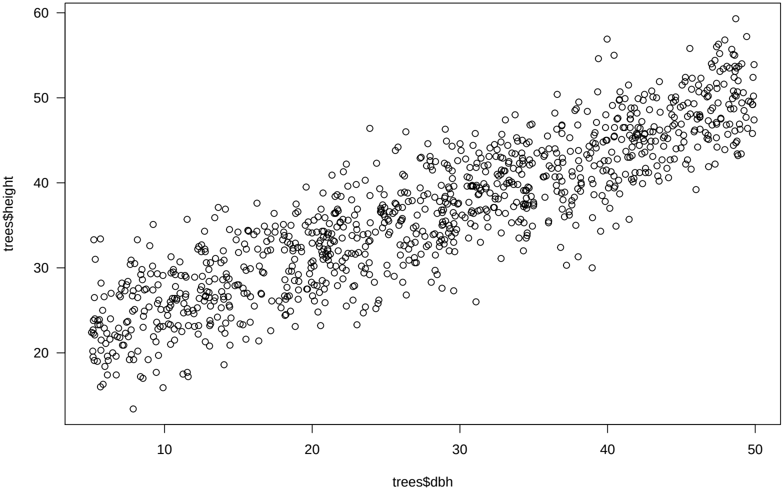
Histogram of predictor variable

```r
hist(trees$dbh)
```



Scatterplot

```
plot(trees$dbh, trees$height, las = 1)
```



Now fit model

Hint: `lm`

Now fit model

Hint: `lm`

```r
m1 <- lm(height ~ dbh, data = trees)
```

What does this mean?

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

Residuals:
     Min       1Q   Median       3Q      Max 
-13.3270  -2.8978   0.1057   2.7924  12.9511 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 19.33920    0.31064   62.26   <2e-16 ***
dbh          0.61570    0.01013   60.79   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.093 on 998 degrees of freedom
Multiple R-squared:  0.7874,    Adjusted R-squared:  0.7871 
F-statistic:  3695 on 1 and 998 DF,  p-value: < 2.2e-16
```

Retrieving model coefficients

```r
coef(m1)
```

```
(Intercept)         dbh
 19.3391968   0.6157036
```

Confidence intervals

```r
confint(m1)
```

```
                2.5 %    97.5 %
(Intercept) 18.7296053 19.948788
dbh          0.5958282  0.635579
```

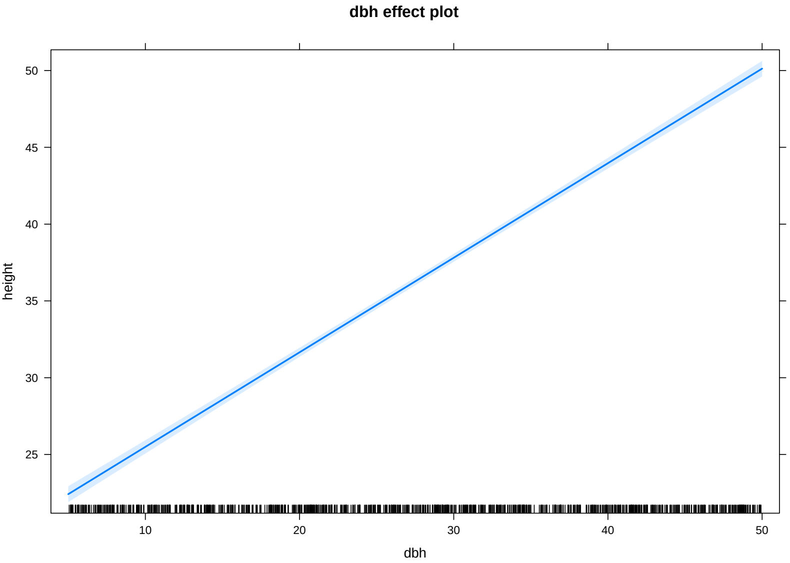
Using effects package

```r
library(effects)
summary(allEffects(m1))
```

```
 model: height ~ dbh

 dbh effect
dbh
       5       20       30       40       50 
22.41771 31.65327 37.81030 43.96734 50.12438 

 Lower 95 Percent Confidence Limits
dbh
       5       20       30       40       50 
21.89682 31.35487 37.55287 43.61733 49.61669 

 Upper 95 Percent Confidence Limits
dbh
       5       20       30       40       50 
22.93861 31.95167 38.06774 44.31735 50.63207 
```

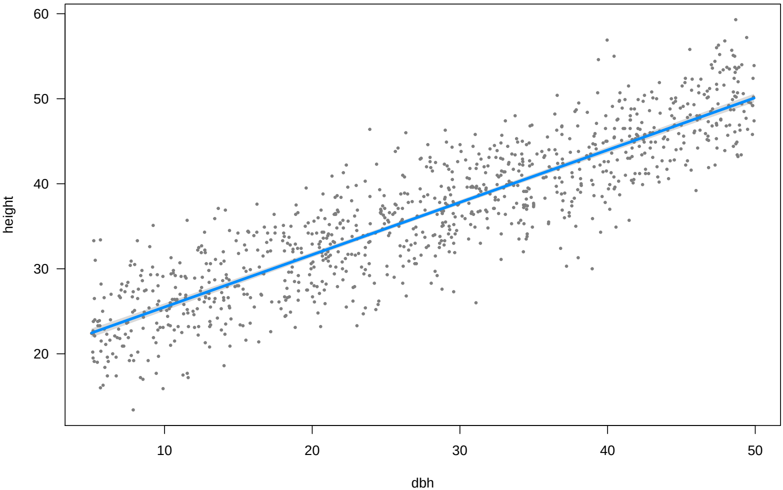
Plot effects

```
plot(allEffects(m1))
```



Plot model (visreg)

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



Linear model assumptions

- Linearity (transformations, GAM...)

Linear model assumptions

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- Residuals:

Linear model assumptions

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- Residuals:
  - Independent

Linear model assumptions

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

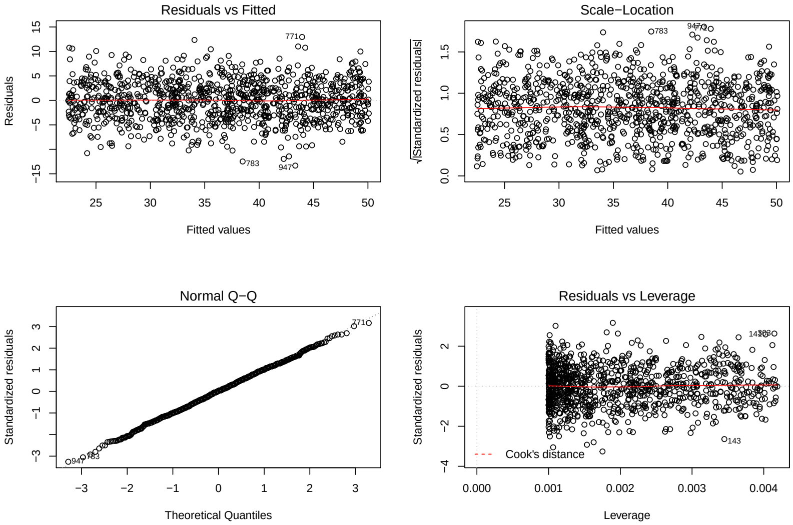
Linear model assumptions

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

Linear model assumptions

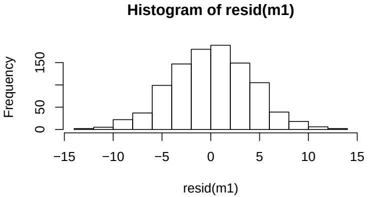
- Linearity (transformations, GAM. . .)
- Residuals:
  - Independent
  - Equal variance
  - Normal
- No measurement error in predictors

Model checking: residuals



Are residuals normal?

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



```
lm(formula = height ~ dbh, data = trees)
            coef.est coef.se
(Intercept) 19.34     0.31  
dbh          0.62     0.01  
---
n = 1000, k = 2
residual sd = 4.09, R-Squared = 0.79
```

SD of residuals = 4.09 coincides with estimate of `sigma`.

How good is the model in predicting tree height?

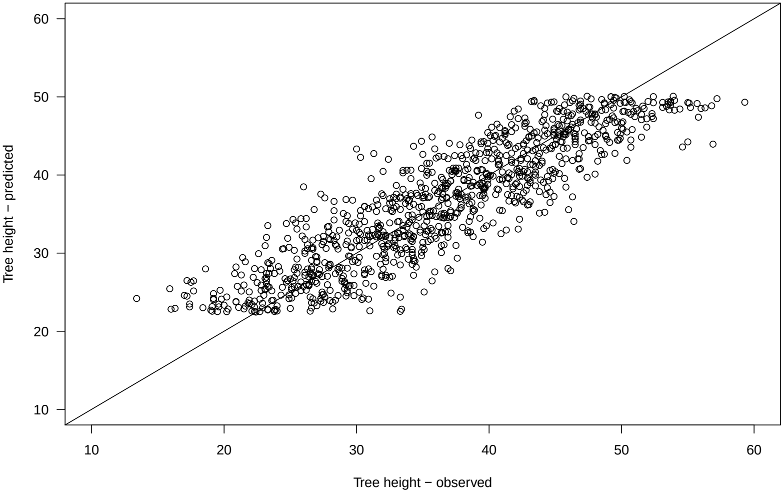
`fitted` gives predictions for each observation

```
trees$height.pred <- fitted(m1)
head(trees)
```

```
  plot   dbh height    sex dead height.pred
1    4 29.68   36.1   male    0    37.61328
2    5 33.29   42.3   male    0    39.83597
3    2 28.03   41.9 female    0    36.59737
4    5 39.86   46.5 female    0    43.88114
5    1 47.94   43.9 female    0    48.85603
6    1 10.82   26.2   male    0    26.00111
```

Calibration plot: Observed vs Predicted values

```
plot(trees$height, trees$height.pred, xlab = "Tree height - obse
```



Using fitted model for prediction

Q: Expected tree height if DBH = 39 cm?

```
new.dbh <- data.frame(dbh = c(39))
predict(m1, new.dbh, se.fit = TRUE)
```

```
$fit
       1
43.35164

$se.fit
[1] 0.1715514

$df
[1] 998

$residual.scale
[1] 4.092629
```

Important functions

- `plot`

Important functions

- `plot`
- `summary`

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

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

Important functions

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

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

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

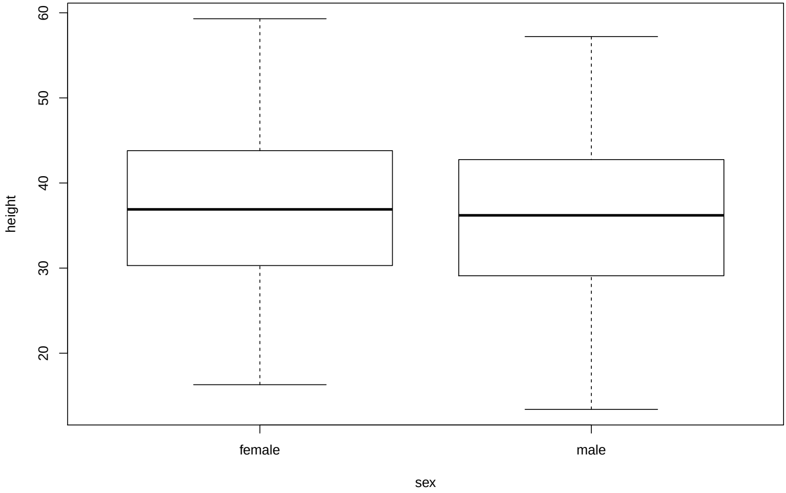
Important functions

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

Categorical predictors (factors)

Q: Does tree height vary with sex?

```
plot(height ~ sex, data = trees)
```



Model height ~ sex

```r
m2 <- lm(height ~ sex, data = trees)
```

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

Residuals:
     Min       1Q   Median       3Q      Max
-22.6881  -6.7881  -0.0097   6.7261  22.3687

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  36.9312     0.3981  92.778   <2e-16 ***
sexmale      -0.8432     0.5607  -1.504    0.133
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.865 on 998 degrees of freedom
Multiple R-squared:  0.002261,  Adjusted R-squared:  0.001261
F-statistic: 2.261 on 1 and 998 DF,  p-value: 0.133
```

Linear model with categorical predictors

$$
\begin{aligned}
y_i &= a + bx_i + \varepsilon_i \\
y_i &= a + b_{male} + \varepsilon_i
\end{aligned}
$$

Model height ∼ sex

```r
m2 <- lm(height ~ sex, data = trees)
```

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

Residuals:
     Min       1Q   Median       3Q      Max 
-22.6881  -6.7881  -0.0097   6.7261  22.3687 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)  36.9312     0.3981  92.778   <2e-16 ***
sexmale      -0.8432     0.5607  -1.504    0.133    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.865 on 998 degrees of freedom
Multiple R-squared:  0.002261,  Adjusted R-squared:  0.001261 
F-statistic: 2.261 on 1 and 998 DF,  p-value: 0.133
```

Effects: Height $\sim$ sex

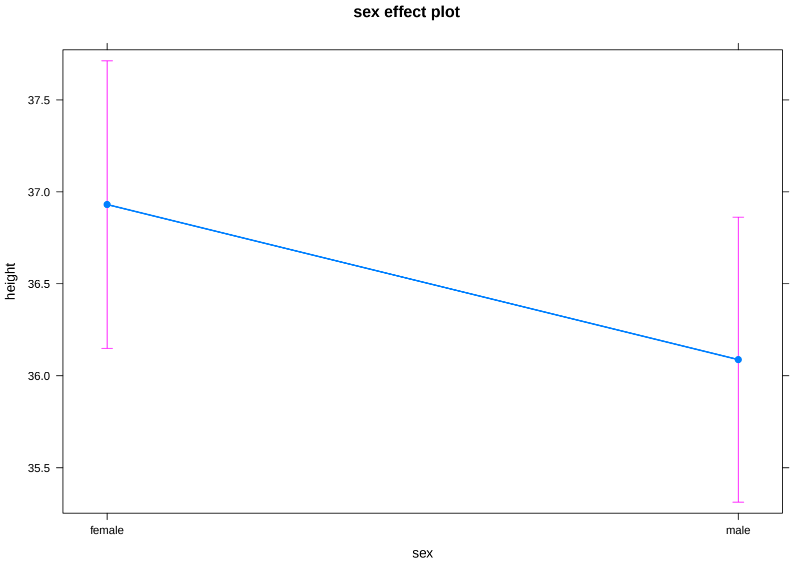
Compare CIs

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

```
 model: height ~ sex

 sex effect
sex
  female     male
36.93125 36.08810

 Lower 95 Percent Confidence Limits
sex
  female     male
36.15012 35.31319

 Upper 95 Percent Confidence Limits
sex
  female     male
37.71238 36.86300
```

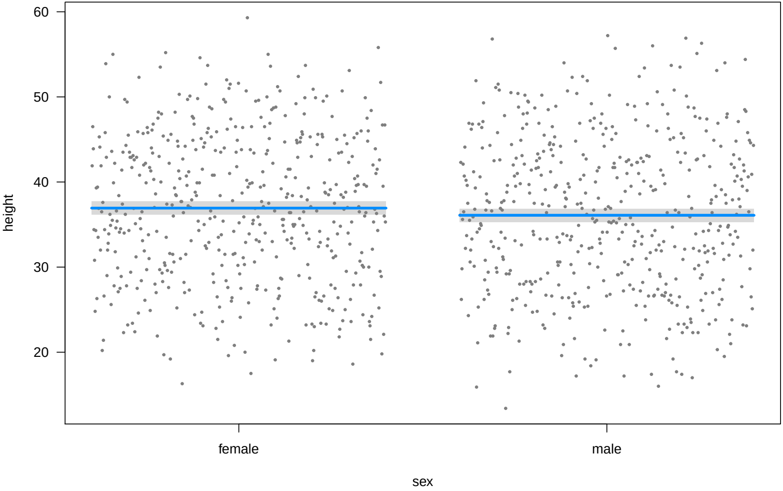
Plot

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

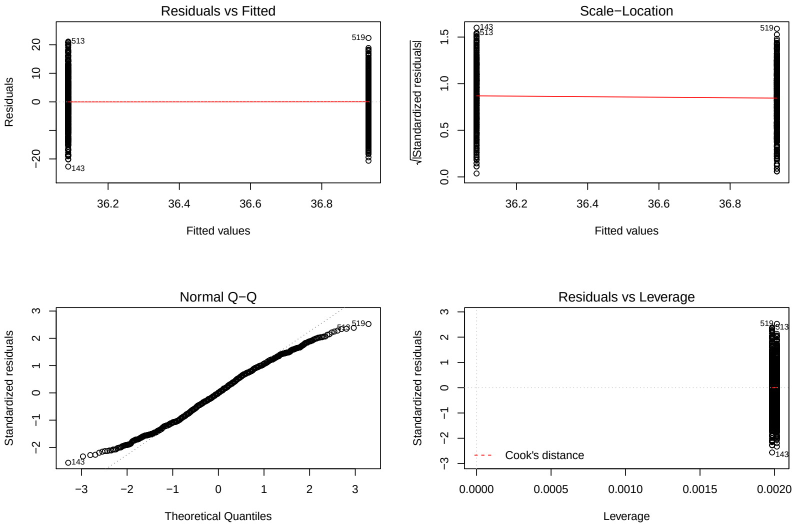


Plot (visreg)

```
visreg(m2)
```

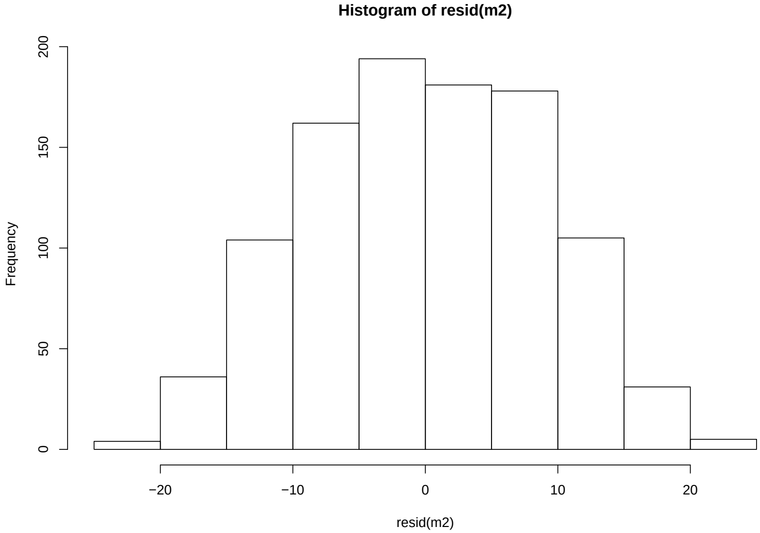


Model checking: residuals



Model checking: residuals

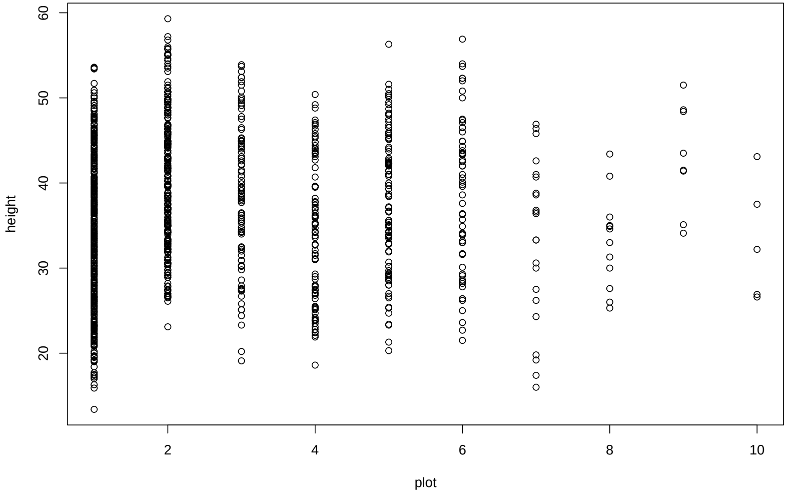
```
hist(resid(m2))
```



Q: Does height differ among field plots?

Plot data first

```
plot(height ~ plot, data = trees)
```



Linear model with categorical predictors

$$y_i = a + bx_i + \varepsilon_i$$
$$y_i = a + b_{plot2} + c_{plot3} + d_{plot4} + e_{plot5} + ... + \varepsilon_i$$

Model Height ~ Plot

All right here?

```
m3 <- lm(height ~ plot, data = trees)
```

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

Residuals:
     Min       1Q   Median       3Q      Max
-22.4498  -6.7049   0.0709   6.7537  23.0640

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  35.4636     0.4730  74.975  < 2e-16 ***
plot          0.3862     0.1413   2.733  0.00639 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.842 on 998 degrees of freedom
Multiple R-squared:  0.007429,  Adjusted R-squared:  0.006435
```

Plot is a factor!

```r
trees$plot <- as.factor(trees$plot)
```

Model Height ~ Plot

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

Residuals:
     Min       1Q   Median       3Q      Max 
-20.4416  -6.9004   0.0379   6.3051  19.7584 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)  33.8416     0.4266  79.329  < 2e-16 ***
plot2         6.3411     0.7126   8.899  < 2e-16 ***
plot3         4.9991     0.9828   5.086 4.36e-07 ***
plot4         0.5329     0.9872   0.540  0.58949    
plot5         4.3723     0.9425   4.639 3.97e-06 ***
plot6         4.7601     1.1709   4.065 5.18e-05 ***
plot7        -0.7416     1.8506  -0.401  0.68871    
plot8        -0.6832     2.4753  -0.276  0.78258    
plot9         9.1709     3.0165   3.040  0.00243 ** 
plot10       -0.5816     3.8013  -0.153  0.87843    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.446 on 990 degrees of freedom
Multiple R-squared:  0.1016,    Adjusted R-squared:  0.09344 
F-statistic: 12.44 on 9 and 990 DF,  p-value: < 2.2e-16
```

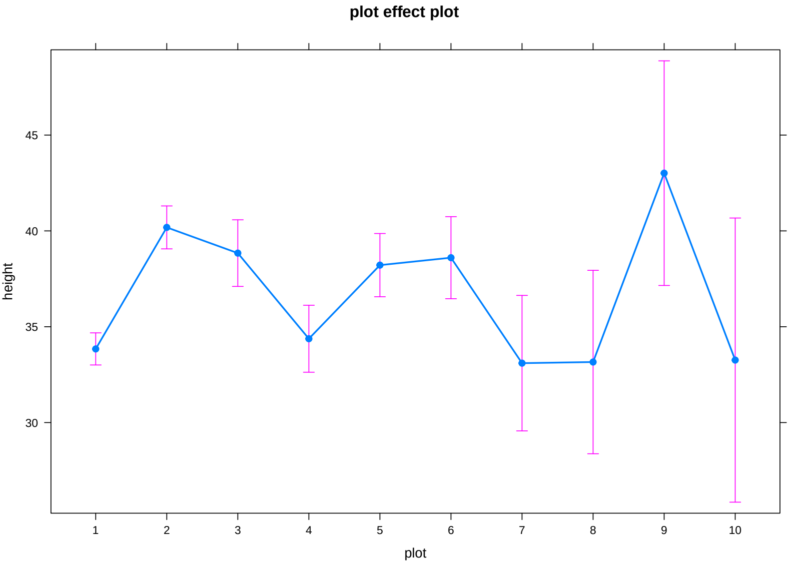
Estimated tree heights for each site

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

```
 model: height ~ plot

 plot effect
plot
       1        2        3        4        5        6        7        8 
33.84158 40.18265 38.84066 34.37444 38.21386 38.60167 33.10000 33.15833 
       9       10 
43.01250 33.26000 

 Lower 95 Percent Confidence Limits
plot
       1        2        3        4        5        6        7        8 
33.00444 39.06264 37.10317 32.62733 36.56463 36.46190 29.56629 28.37367 
       9       10 
37.15251 25.84764 

 Upper 95 Percent Confidence Limits
plot
       1        2        3        4        5        6        7        8 
34.67872 41.30265 40.57814 36.12156 39.86309 40.74143 36.63371 37.94299 
       9       10 
48.87249 40.67236 
```

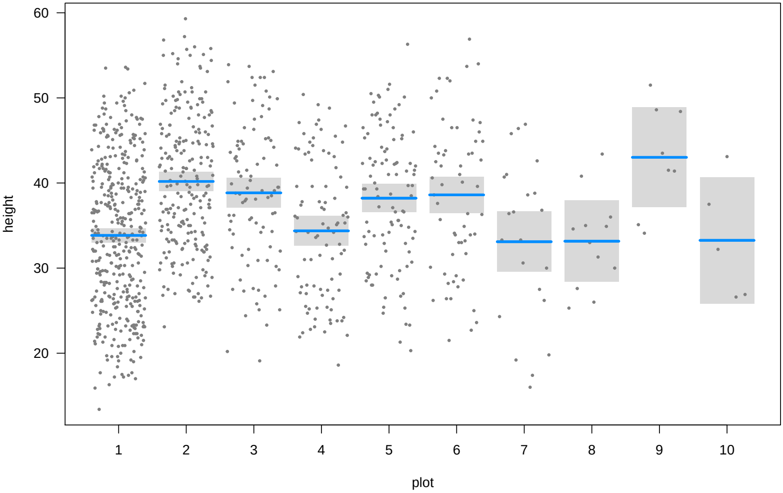
Plot

```
plot(allEffects(m3))
```

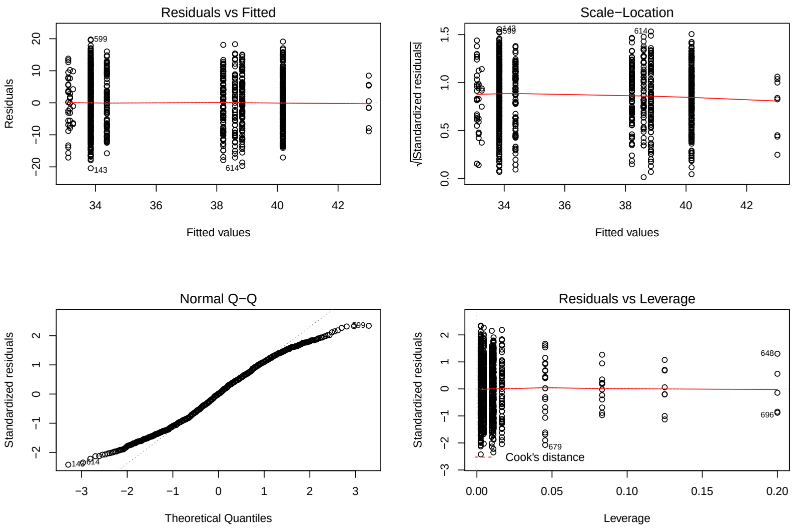


Plot (visreg)

```
visreg(m3)
```



Model checking: residuals



Combining continuous and categorical predictors

Predicting tree height based on dbh and site

$$y_i = a + bx_i + \varepsilon_i$$
$$y_i = a + b_{plot2} + c_{plot3} + d_{plot4} + e_{plot5} + ... + k \cdot DBH_i + \varepsilon_i$$

Predicting tree height based on dbh and site

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

Residuals:
     Min       1Q   Median       3Q      Max 
-10.1130  -1.9885   0.0582   2.0314  11.3320 

Coefficients:
             Estimate Std. Error t value Pr(>|t|)    
(Intercept) 16.699037   0.260565  64.088  < 2e-16 ***
plot2        6.504303   0.256730  25.335  < 2e-16 ***
plot3        4.357457   0.354181  12.303  < 2e-16 ***
plot4        1.934650   0.356102   5.433 6.98e-08 ***
plot5        3.637432   0.339688  10.708  < 2e-16 ***
plot6        4.204511   0.421906   9.966  < 2e-16 ***
plot7       -0.176193   0.666772  -0.264   0.7916    
plot8       -5.312648   0.893603  -5.945 3.82e-09 ***
plot9        5.437049   1.087766   4.998 6.84e-07 ***
plot10       2.263338   1.369986   1.652   0.0988 .  
dbh          0.617075   0.007574  81.473  < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.043 on 989 degrees of freedom
Multiple R-squared:  0.8835,    Adjusted R-squared:  0.8823 
F-statistic:   750 on 10 and 989 DF,  p-value: < 2.2e-16
```

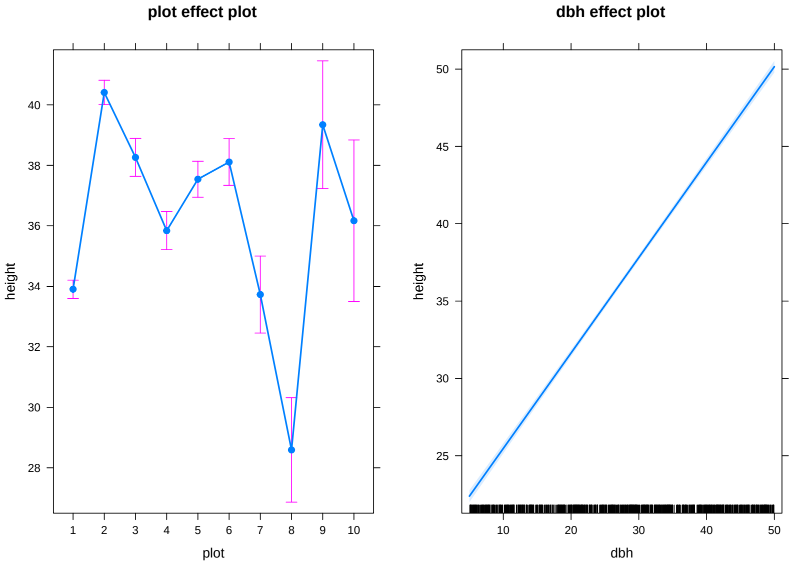
Estimated tree heights for each site

```r
summary(allEffects(multreg))
```

```
 model: height ~ plot + dbh

 plot effect
plot
       1        2        3        4        5        6        7        8
33.90437 40.40868 38.26183 35.83902 37.54181 38.10889 33.72818 28.59173
       9       10
39.34142 36.16771

 Lower 95 Percent Confidence Limits
plot
       1        2        3        4        5        6        7        8
33.60276 40.00512 37.63569 35.20858 36.94739 37.33787 32.45495 26.86438
       9       10
37.22831 33.49623

 Upper 95 Percent Confidence Limits
plot
       1        2        3        4        5        6        7        8
34.20599 40.81223 38.88798 36.46947 38.13622 38.87990 35.00141 30.31907
       9       10
41.45454 38.83919

 dbh effect
dbh
       5       20       30       40       50
22.38634 31.64246 37.81321 43.98396 50.15471
```

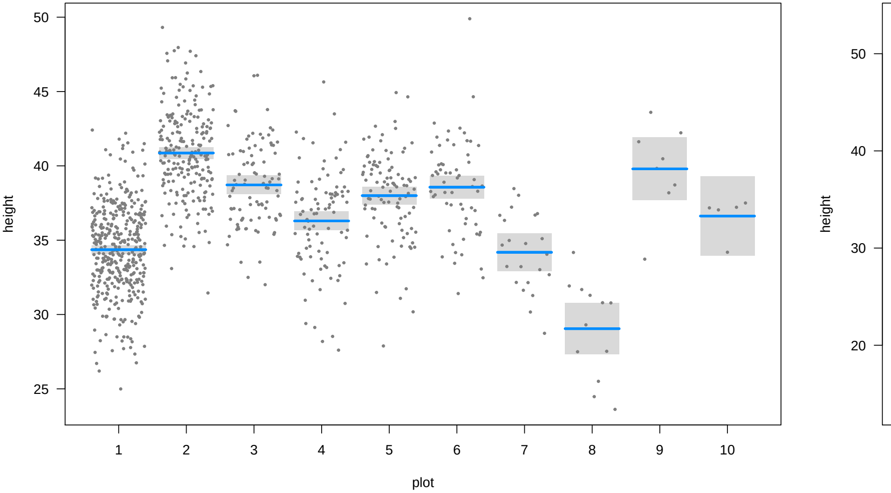
Plot

```
plot(allEffects(multreg))
```

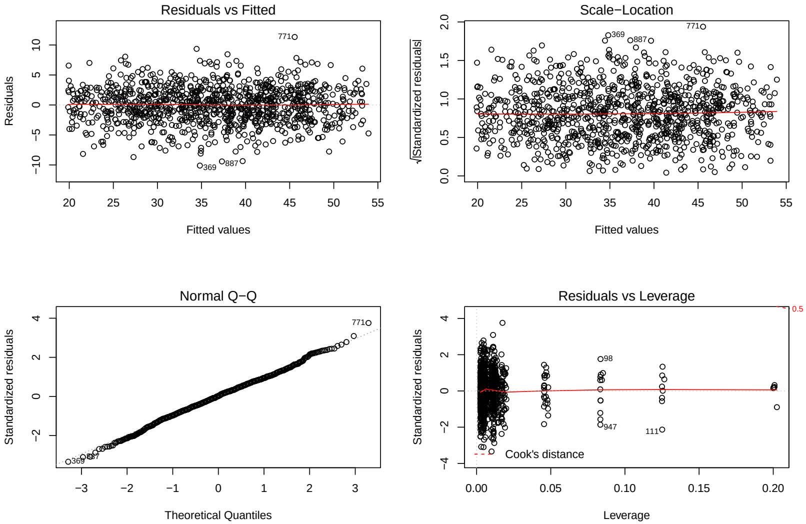


Plot (visreg)

```r
visreg(multreg)
```



Model checking: residuals



Extra exercises

- paperplanes: How does flight distance differ with age, gender or paper type?

Extra exercises

- paperplanes: How does flight distance differ with age, gender or paper type?
- mammal sleep: Are sleep patterns related to diet?

Extra exercises

- paperplanes: How does flight distance differ with age, gender or paper type?
- mammal sleep: Are sleep patterns related to diet?
- iris: Predict petal length $\sim$ petal width and species

Generalised Linear Models: Logistic regression

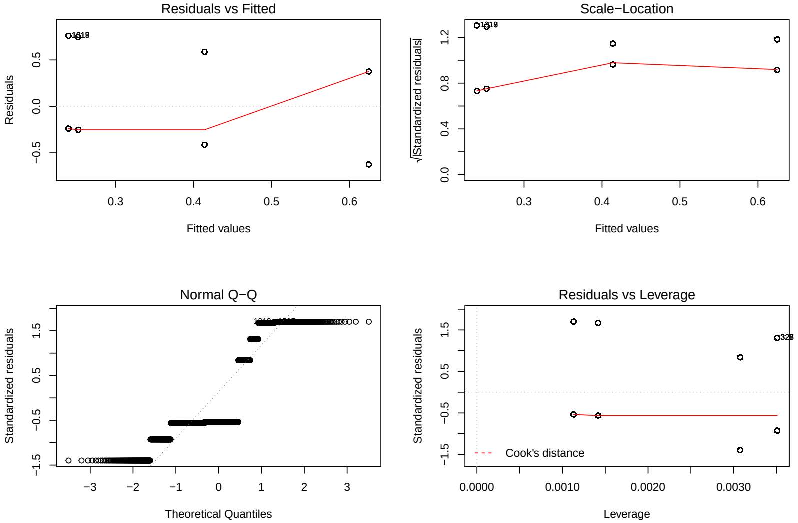
Q: Survival of passengers on the Titanic $\sim$ Class

Read `titanic_long.csv` dataset.

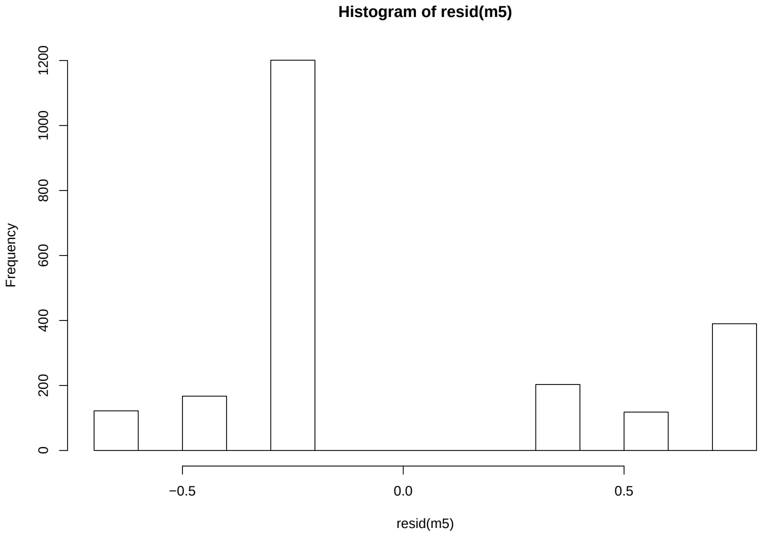
```
  class   age  sex survived
1 first adult male        1
2 first adult male        1
3 first adult male        1
4 first adult male        1
5 first adult male        1
6 first adult male        1
```

Let's fit linear model:

```r
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

1. **Response variable** - distribution `family`
    - Bernouilli - Binomial
    - Poisson

Generalised Linear Models

1. **Response variable** - distribution `family`
   - Bernouilli - Binomial
   - Poisson
   - Gamma

Generalised Linear Models

1. **Response variable** - distribution `family`
   - Bernouilli - Binomial
   - Poisson
   - Gamma
   - etc

Generalised Linear Models

1. **Response variable** - distribution `family`
   - Bernouilli - Binomial
   - Poisson
   - Gamma
   - etc
2. **Predictors** (continuous or categorical)

Generalised Linear Models

1. **Response variable** - distribution `family`
   - Bernouilli - Binomial
   - Poisson
   - Gamma
   - etc
2. **Predictors** (continuous or categorical)
3. **Link function**

Generalised Linear Models

1. **Response variable** - distribution `family`
    - Bernouilli - Binomial
    - Poisson
    - Gamma
    - etc
2. **Predictors** (continuous or categorical)
3. **Link function**
    - Gaussian: identity

Generalised Linear Models

1. **Response variable** - distribution `family`
   - Bernouilli - Binomial
   - Poisson
   - Gamma
   - etc
2. **Predictors** (continuous or categorical)
3. **Link function**
   - Gaussian: identity
   - Binomial: logit, probit

Generalised Linear Models

1. **Response variable** - distribution `family`
   - Bernouilli - Binomial
   - Poisson
   - Gamma
   - etc
2. **Predictors** (continuous or categorical)
3. **Link function**
   - Gaussian: identity
   - Binomial: logit, probit
   - Poisson: log. . .

Generalised Linear Models

1. **Response variable** - distribution `family`
   - Bernouilli - Binomial
   - Poisson
   - Gamma
   - etc
2. **Predictors** (continuous or categorical)
3. **Link function**
   - Gaussian: identity
   - Binomial: logit, probit
   - Poisson: log. . .
   - See `family`.

The modelling process

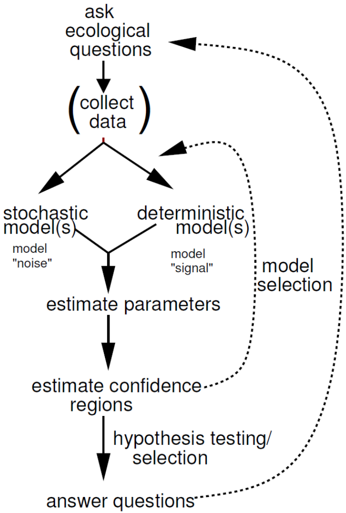


Figure 1.5 Flow of the modeling process.

Figure 5:

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

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

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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tapply(titanic$survived, titanic$class, length)
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```
  crew  first second  third 
   885    325    285    706 
```

How many survived?

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
```

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

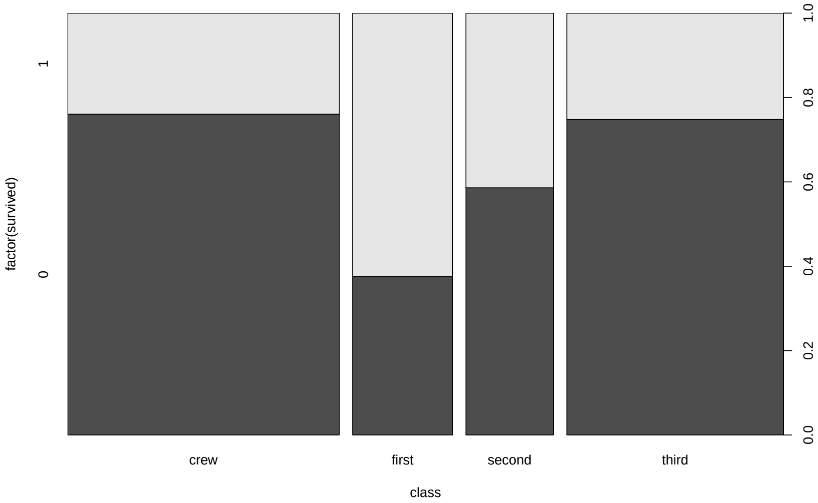
```
library(dplyr)
titanic %>%
  group_by(class, survived) %>%
  summarise(count = n())
```

```
# A tibble: 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 classsecond  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
```

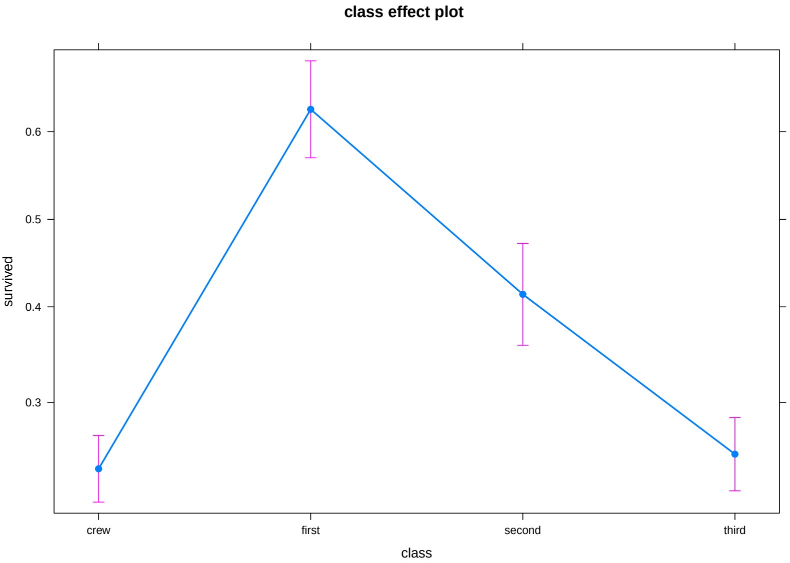
Model interpretation using effects package

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

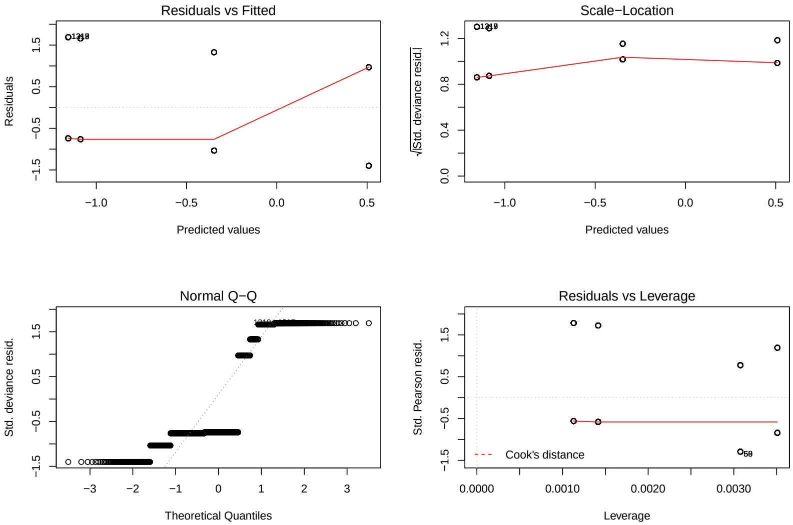
```
 model: survived ~ class

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

Effects plot

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



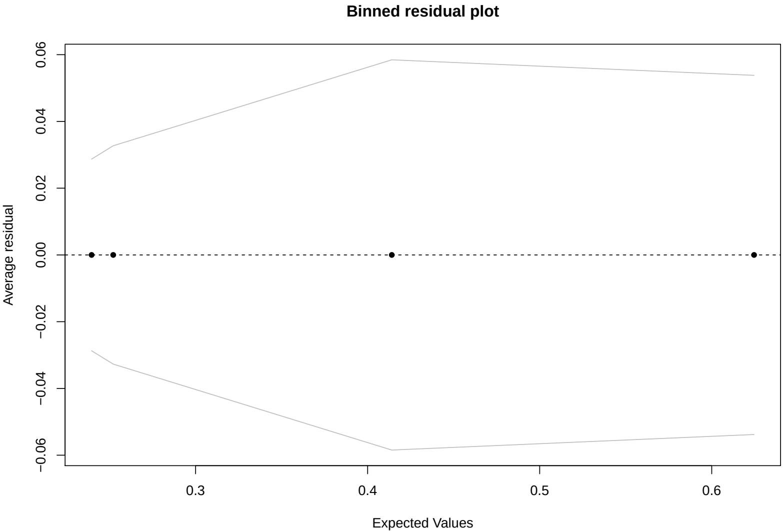
Logistic regression: model checking



Not very useful.

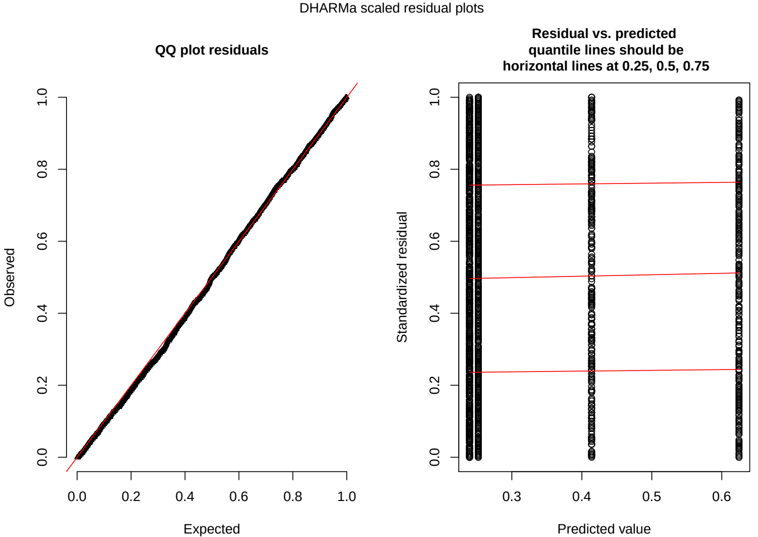
Binned residual plots for logistic regression

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



Residual diagnostics with DHARMa

```r
library(DHARMa)
simulateResiduals(tit.glm, plot = TRUE)
```



Recapitulating

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

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2. Check data: `summary`

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4. Fit model: `glm`. Don't forget to specify `family`!

Recapitulating

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

1. Import data: `read.table` or `read.csv`
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5. Examine models: `summary`
6. Use `plogis` to apply back-transformation (*invlogit*) to parameter estimates (`coef`). Alternatively, use `allEffects` from `effects` package.

Recapitulating

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7. Plot model: `plot(allEffects(model))`. Or use `visreg`.

Recapitulating

1. Import data: `read.table` or `read.csv`
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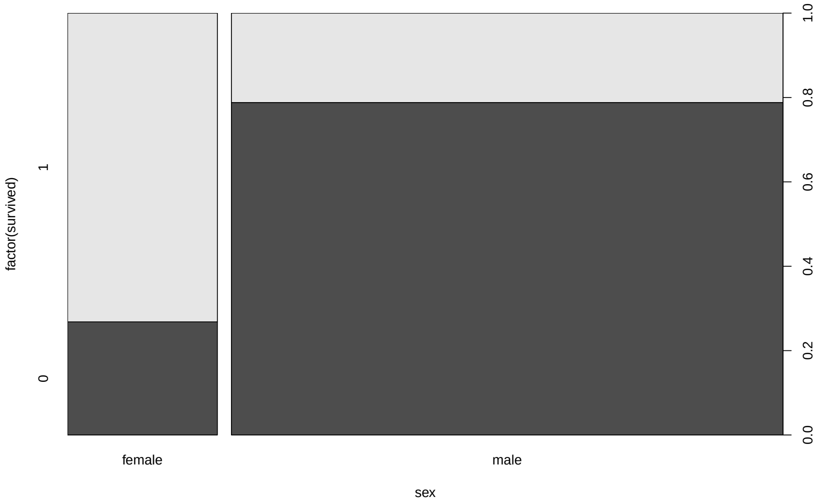
5. Examine models: `summary`
6. Use `plogis` to apply back-transformation (*invlogit*) to parameter estimates (`coef`). Alternatively, use `allEffects` from `effects` package.
7. Plot model: `plot(allEffects(model))`. Or use `visreg`.
8. Examine residuals: use `arm::binnedplot` or `DHARMa::simulateResiduals`.

Q: Did men have higher survival than women?

Plot first

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



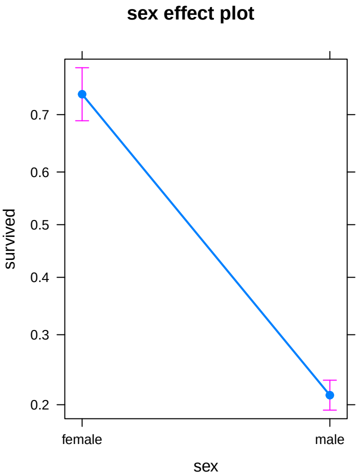
Fit model

```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. . .

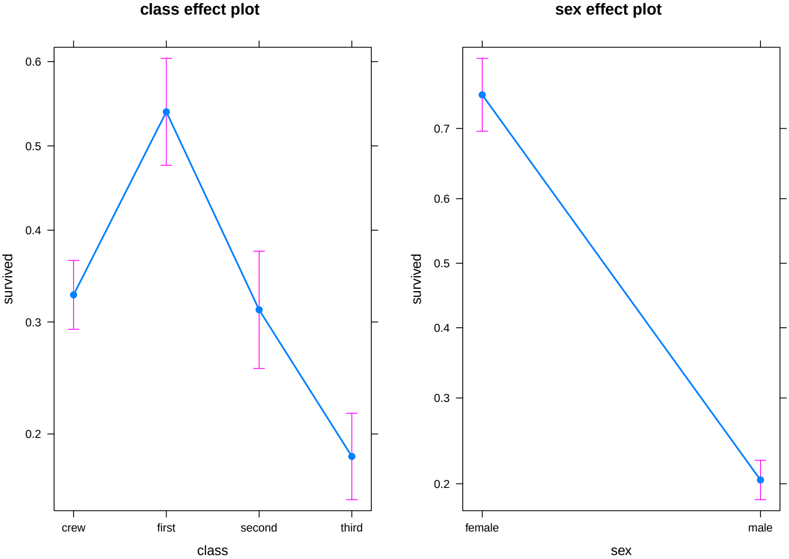
Fit additive model with both factors

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

```
glm(formula = survived ~ class + sex, family = binomial, data =
            coef.est coef.se
(Intercept)  1.19     0.16
classfirst   0.88     0.16
classsecond -0.07     0.17
classthird  -0.78     0.14
sexmale     -2.42     0.14
---
  n = 2201, k = 5
  residual deviance = 2228.9, null deviance = 2769.5 (difference
```

Plot additive model

```
plot(allEffects(tit.sex.class))
```



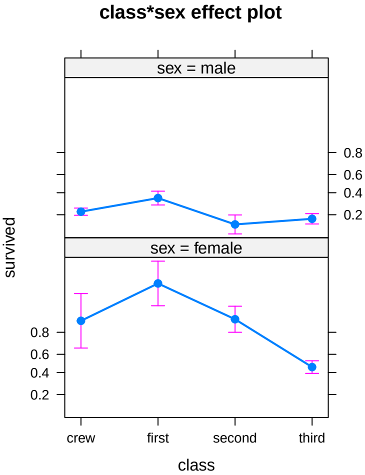
Fit model with both factors (interactions)

```
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 Yes
1 1   1st Female Adult   4 140
2 2   1st Female Child   0   1
3 3   1st   Male Adult 118  57
4 4   1st   Male Child   0   5
5 5   2nd Female Adult  13  80
6 6   2nd Female Child   0  13
```

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!

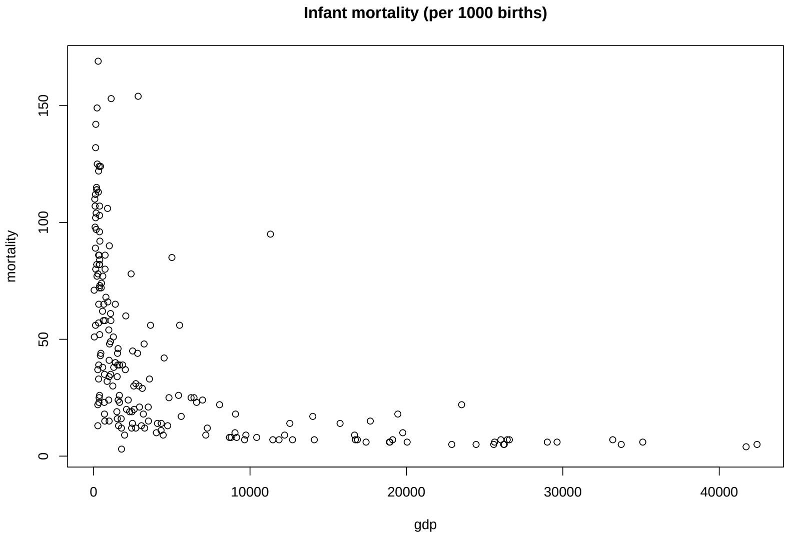
Logistic regression with continuous predictors

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

```r
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)
```

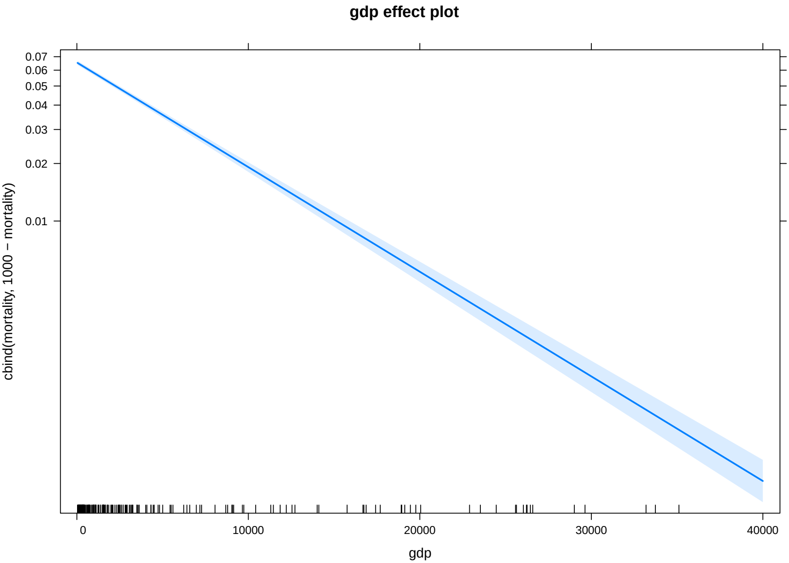
Effects

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

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

 gdp effect
gdp
          40        10000        20000        30000        40000
0.0652177296 0.0191438829 0.0054028095 0.0015096074 0.0004206154
```

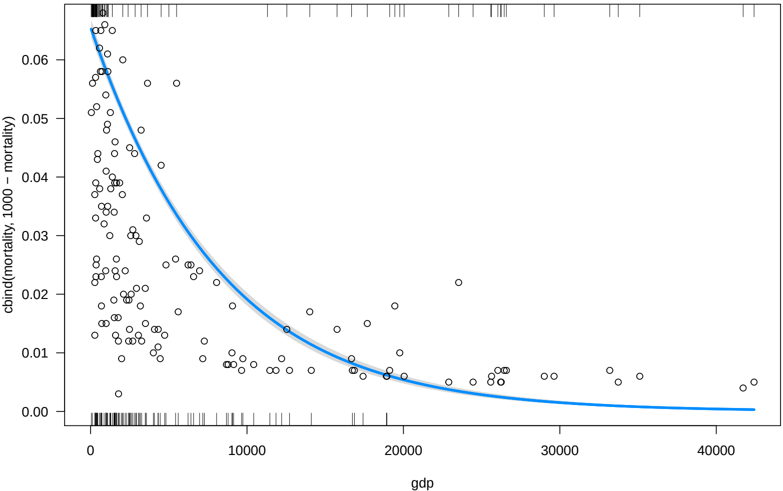
Effects plot

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



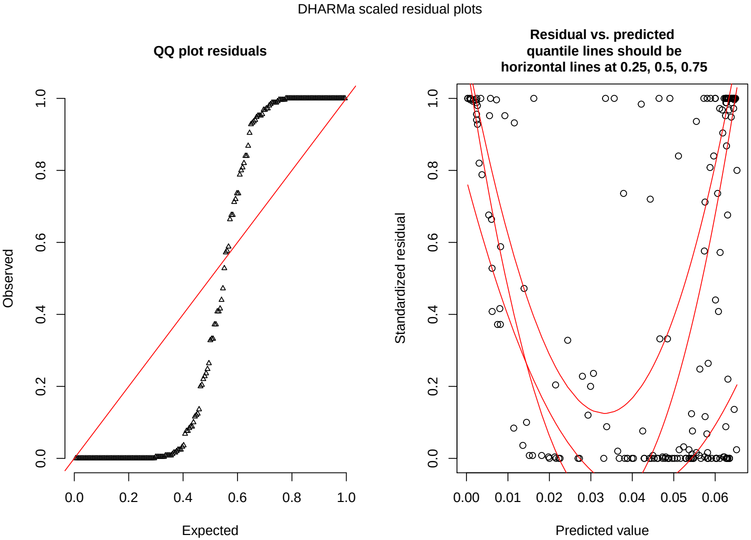
Plot model using visreg:

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



Residuals diagnostics with DHARMa

```
simulateResiduals(gdp.glm, plot = TRUE)
```



Overdispersion

Testing for overdispersion (DHARMa)

```
simres <- simulateResiduals(gdp.glm, refit = TRUE)
testOverdispersion(simres)
```

```

    DHARMa nonparametric overdispersion test via comparison to
    simulation under H0 = fitted model

data:  simres
dispersion = 20.761, p-value < 2.2e-16
alternative hypothesis: overdispersion
```

Overdispersion in logistic regression with proportion data

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

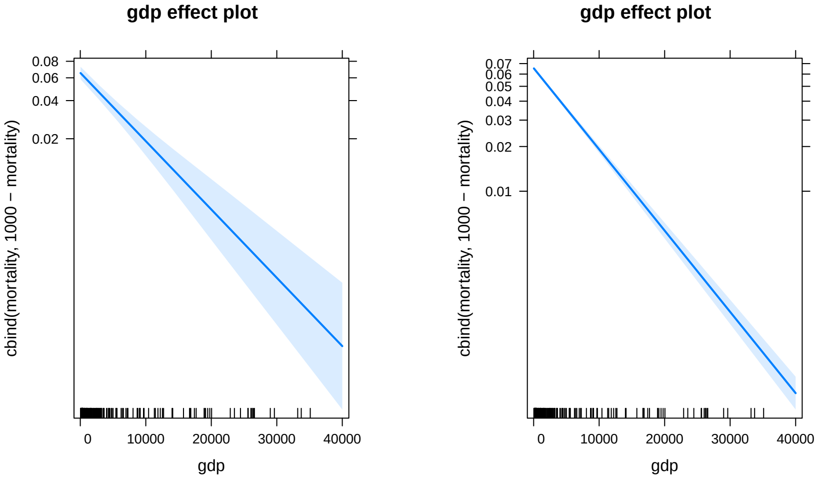
```
Call:
glm(formula = cbind(mortality, 1000 - mortality) ~ gdp, family =
    data = gdp)

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

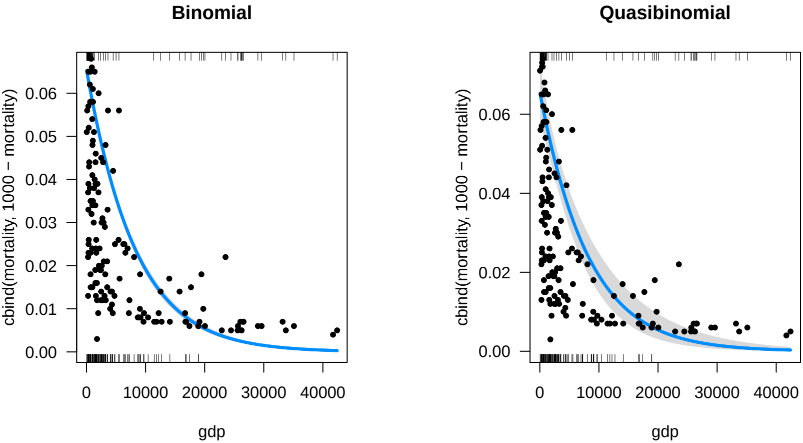
```
 model: cbind(mortality, 1000 - mortality) ~ gdp

 gdp effect
gdp
          40        10000        20000        30000        40000 
0.0652177296 0.0191438829 0.0054028095 0.0015096074 0.0004206154 
```

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

 gdp effect
gdp
          40        10000        20000        30000        40000 
0.0652177296 0.0191438829 0.0054028095 0.0015096074 0.0004206154 
```

But standard errors (uncertainty) do!



Plot model and data

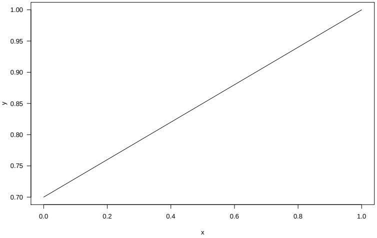


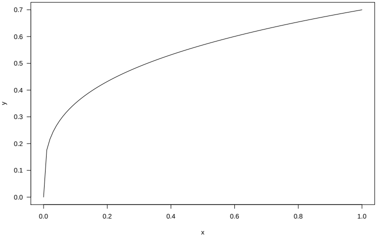
Overdispersion

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

Think about the shape of relationships

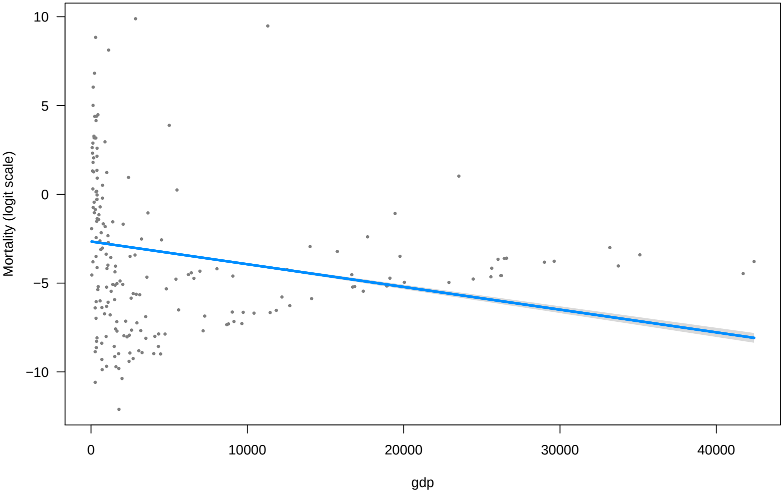
y ~ x + z
Really? Not everything has to be linear! Actually, it often is not.
Think about shape of relationship. See chapter 3 in Bolker's book.



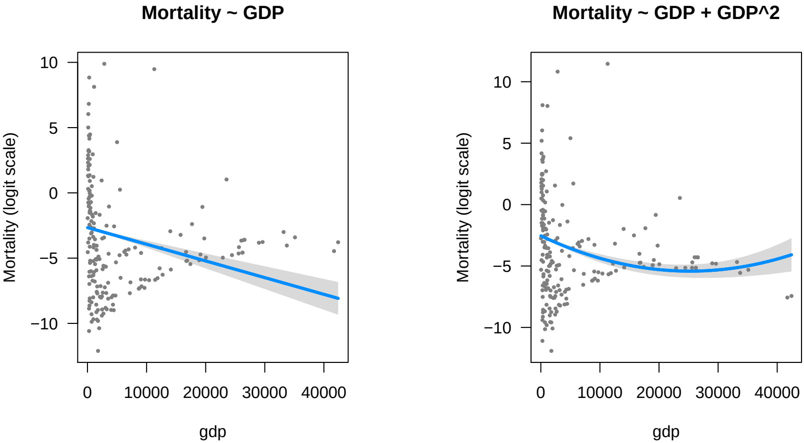


Think about the shape of relationships

```
visreg(gdp.glm, ylab = "Mortality (logit scale)")
```



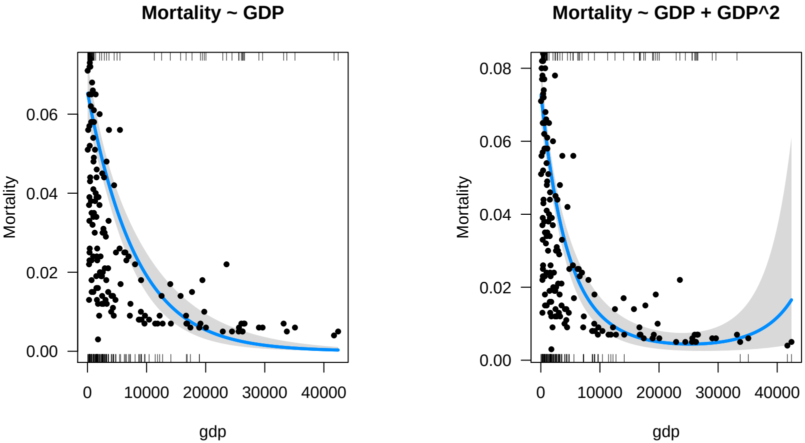
Think about the shape of relationships



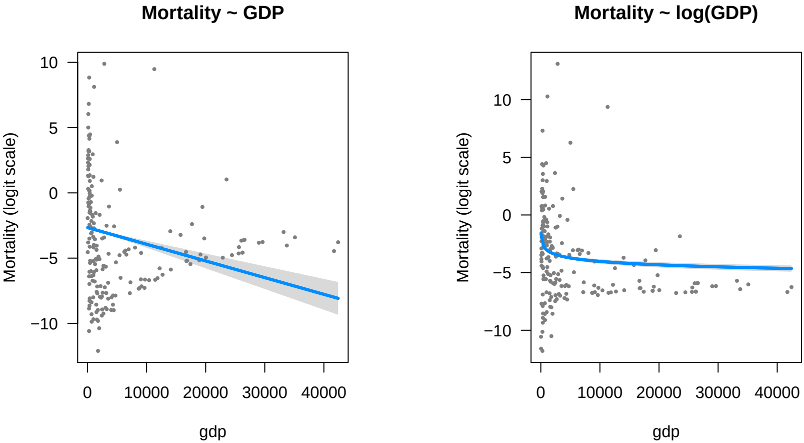
Mortality ~ GDP

Mortality ~ GDP + GDP^2

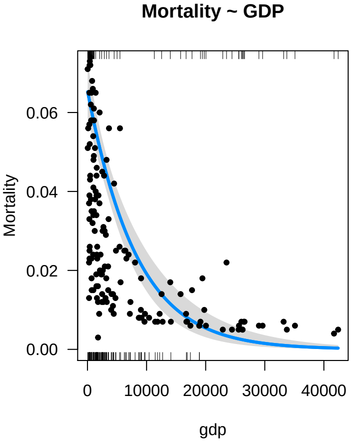
Think about the shape of relationships

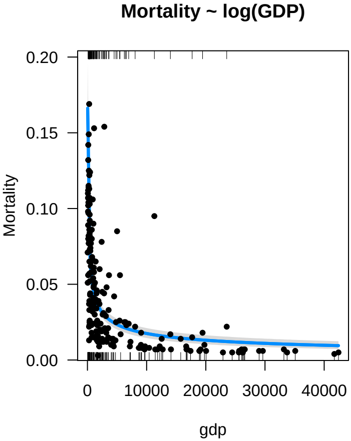


Think about the shape of relationships



Think about the shape of relationships





GLM 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

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

Example dataset: Seedling counts in quadrats

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

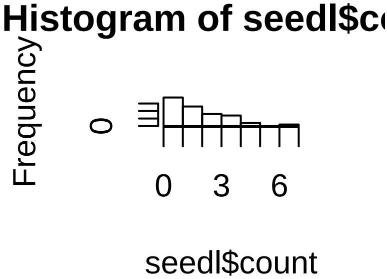
```
       X             count           row         col      
 Min.   : 1.00   Min.   :0.00   Min.   :1   Min.   : 1.0  
 1st Qu.:13.25   1st Qu.:1.00   1st Qu.:2   1st Qu.: 3.0  
 Median :25.50   Median :2.00   Median :3   Median : 5.5  
 Mean   :25.50   Mean   :2.14   Mean   :3   Mean   : 5.5  
 3rd 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             area     
 Min.   : 2.571   Min.   :0.25  
 1st Qu.:26.879   1st Qu.:0.25  
 Median :47.493   Median :0.50  
 Mean   :47.959   Mean   :0.62  
 3rd Qu.:67.522   3rd Qu.:1.00  
 Max.   :99.135   Max.   :1.00  
```

EDA

```r
table(seedl$count)
```

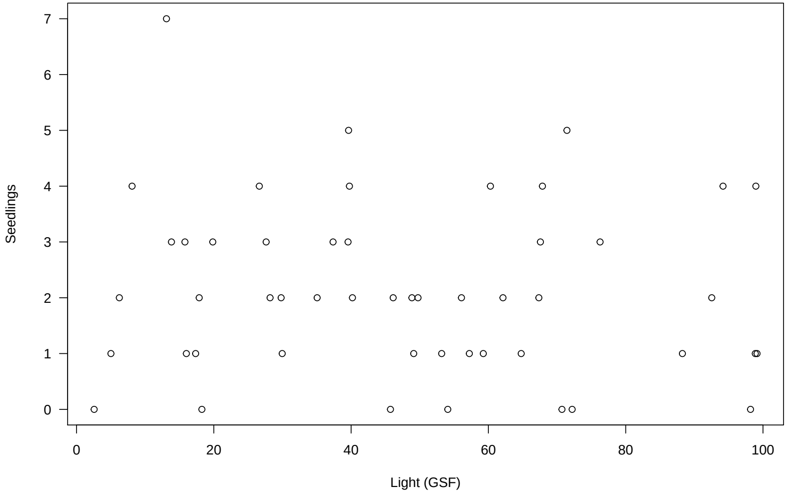
```

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

```r
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 
```

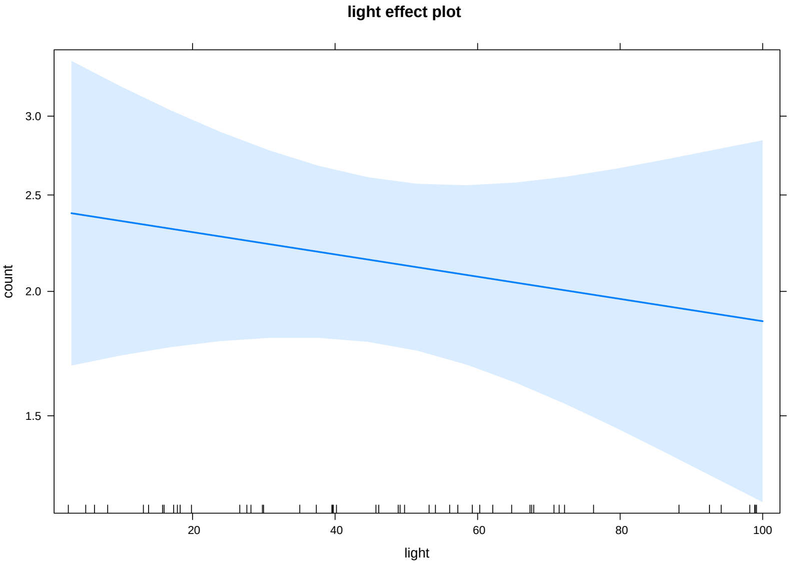
We need to back-transform: apply the inverse of the logarithm

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

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

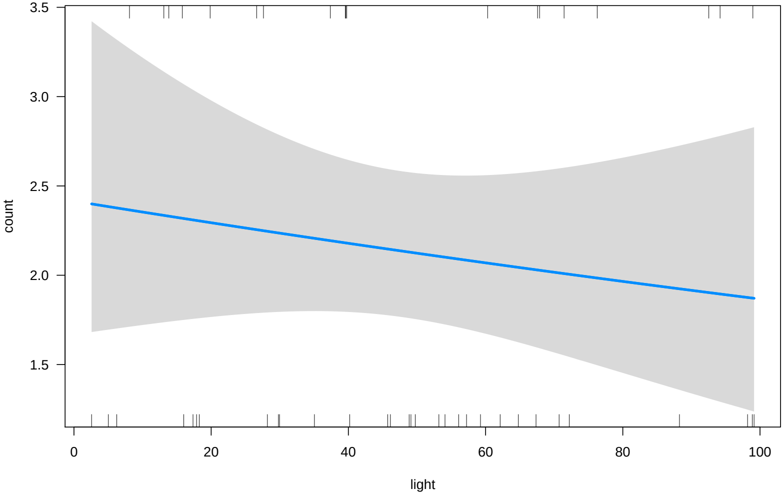
So what's the relationship between Nseedlings and light?

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

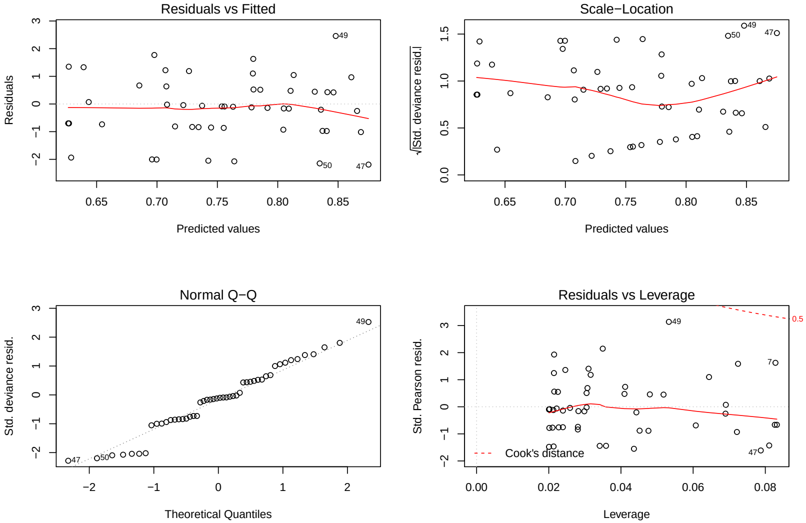


Using visreg

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

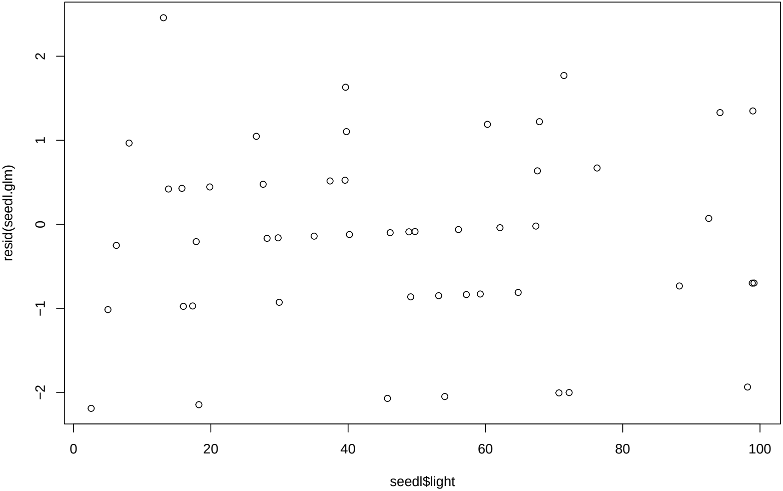


Poisson regression: model checking



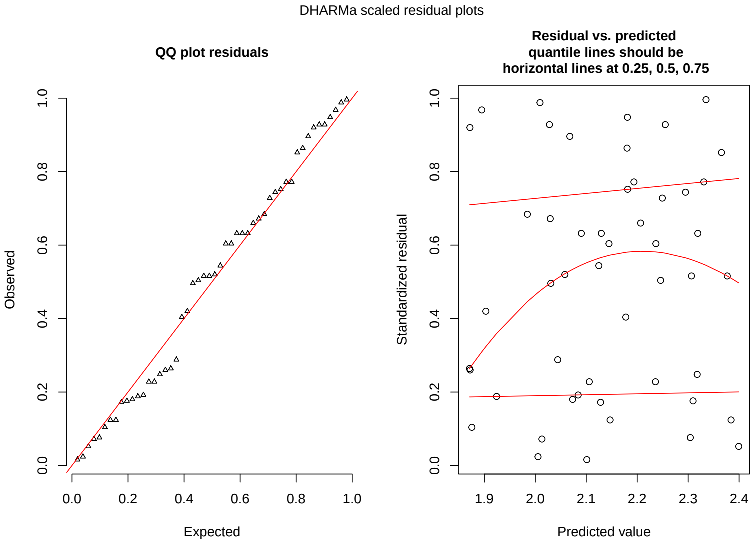
Is there pattern of residuals along predictor?

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



Residuals diagnostics with DHARMa

```
simulateResiduals(seedl.glm, plot = TRUE)
```



Poisson regression: Overdispersion

Always check overdispersion with count data

```r
simres <- simulateResiduals(seedl.glm, refit = TRUE)
testOverdispersion(simres)
```

```

	DHARMa nonparametric overdispersion test via comparison to
	simulation under H0 = fitted model

data:  simres
dispersion = 1.1574, p-value = 0.196
alternative hypothesis: overdispersion
```

Accounting for overdispersion in count data

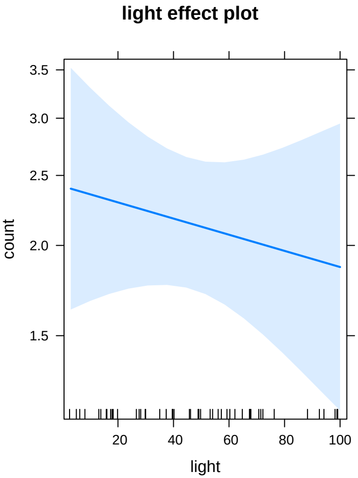
Use family quasipoisson

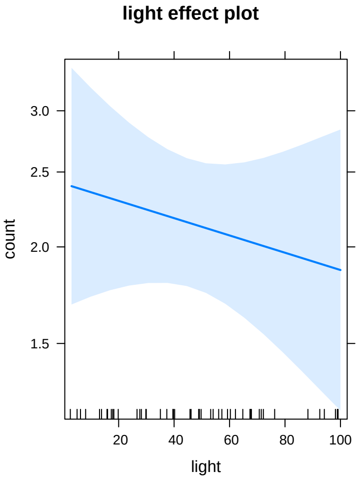
```
Call:
glm(formula = count ~ light, family = quasipoisson, data = seedl

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
       3       30       50       70      100
2.396665 2.235657 2.123408 2.016794 1.866826

 model: count ~ light

 light effect
light
       3       30       50       70      100
2.396665 2.235657 2.123408 2.016794 1.866826
```

But standard errors may change

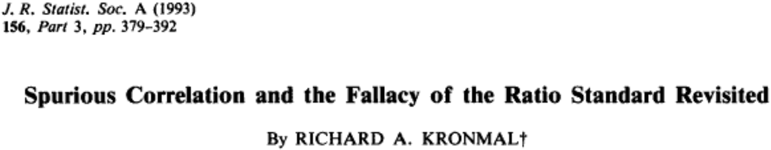




What if survey plots have different area?

Avoid regression of ratios

seedlings/area $\sim$ light



J. R. Statist. Soc. A (1993)
156, *Part* 3, *pp*. 379–392

Spurious Correlation and the Fallacy of the Ratio Standard Revisited

By RICHARD A. KRONMAL†

Figure 6:

Use offset to standardise response variables in GLMs

```
seedl.offset <- glm(count ~ light, offset = seedl$area, data = s
summary(seedl.offset)
```

```
Call:
glm(formula = count ~ light, family = poisson, data = seedl,
    offset = seedl$area)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.6926  -0.8532   0.1491   0.5211   3.1051

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.299469   0.185468   1.615    0.106
light       -0.004498   0.003441  -1.307    0.191

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 70.263  on 49  degrees of freedom
```

Note estimates now referred to area units

```
exp(coef(seedl.offset))
```

```
(Intercept)       light
  1.3491422   0.9955123
```

Mixed / Multilevel models

Example dataset: trees

- Data on 1000 trees from 10 plots.

```
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.

```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
```

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

A simple linear model

```r
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
```

Remember our model structure

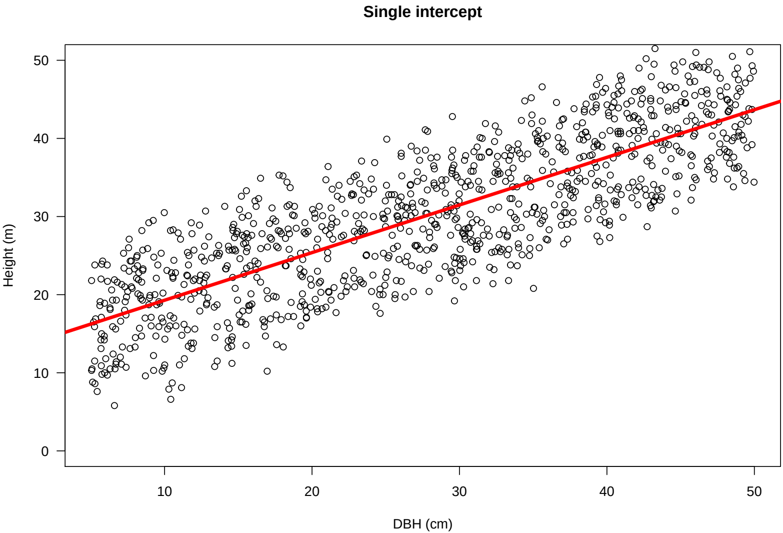
$$y_i \sim N(\mu_i, \sigma^2)$$
$$\mu_i = \alpha + \beta x_i$$

In this case:

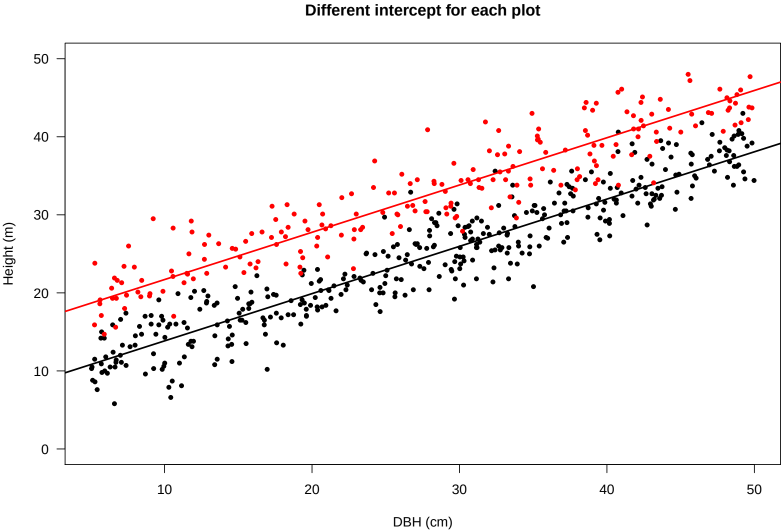
$$Height_i \sim N(\mu_i, \sigma^2)$$
$$\mu_i = \alpha + \beta DBH_i$$

α: expected height when DBH = 0
β: how much height increases with every unit increase of DBH

There is only one intercept



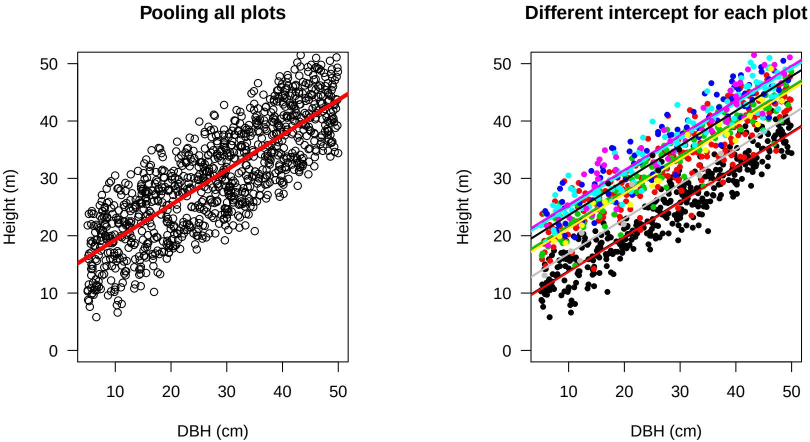
What if allometry varies among plots?



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

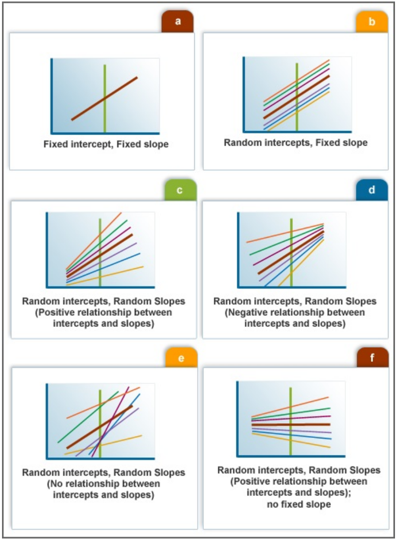

a
Fixed intercept, Fixed slope
b
Random intercepts, Fixed slope
c
Random intercepts, Random Slopes (Positive relationship between intercepts and slopes)
d
Random intercepts, Random Slopes (Negative relationship between intercepts and slopes)
e
Random intercepts, Random Slopes (No relationship between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

Figure 7:

Mixed models enable us to account for variability

- Varying intercepts
- Varying slopes

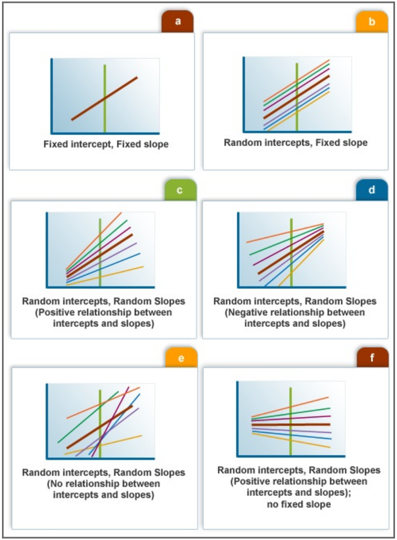

a
Fixed intercept, Fixed slope
b
Random intercepts, Fixed slope
c
Random intercepts, Random Slopes (Positive relationship between intercepts and slopes)
d
Random intercepts, Random Slopes (Negative relationship between intercepts and slopes)
e
Random intercepts, Random Slopes (No relationship between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

Figure 7:

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.

Hence there's gradient between

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

Hence there's gradient between

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

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))`

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.

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))`

Random vs Fixed effects?

1. Fixed effects constant across individuals, random effects vary.

http://andrewgelman.com/2005/01/25/why_i_dont_use/

Random vs Fixed effects?

1. Fixed effects constant across individuals, random effects vary.
2. Effects are fixed if they are interesting in themselves; random if interest in the underlying population.

http://andrewgelman.com/2005/01/25/why_i_dont_use/

Random vs Fixed effects?

1. Fixed effects constant across individuals, random effects vary.
2. Effects are fixed if they are interesting in themselves; random if interest in the underlying population.
3. Fixed when sample exhausts the population; random when the sample is small part of the population.

http://andrewgelman.com/2005/01/25/why_i_dont_use/

Random vs Fixed effects?

1. Fixed effects constant across individuals, random effects vary.
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4. Random effect if it's assumed to be a realized value of random variable.

http://andrewgelman.com/2005/01/25/why_i_dont_use/

Random vs Fixed effects?

1. Fixed effects constant across individuals, random effects vary.
2. Effects are fixed if they are interesting in themselves; random if interest in the underlying population.
3. Fixed when sample exhausts the population; random when the sample is small part of the population.
4. Random effect if it's assumed to be a realized value of random variable.
5. Fixed effects estimated using least squares or maximum likelihood; random effects estimated with shrinkage.

http://andrewgelman.com/2005/01/25/why_i_dont_use/

What is a random effect, really?

1. Varies by group

Random effects are estimated with partial pooling, while fixed effects are not (infinite variance).

What is a random effect, really?

1. Varies by group
2. Variation estimated with probability model

Random effects are estimated with partial pooling, while fixed effects are not (infinite variance).

Shrinkage improves parameter estimation

Especially for groups with low sample size

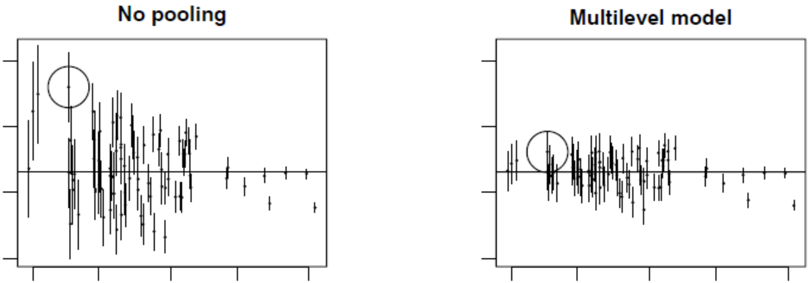


Figure 8:

From Gelman & Hill p. 253

Fitting mixed/multilevel models

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

```
lmer(formula = height ~ dbh + (1 | plot), data = trees)
            coef.est coef.se
(Intercept) 14.80     1.44
dbh          0.61     0.01

Error terms:
 Groups   Name        Std.Dev.
 plot     (Intercept) 4.45
 Residual             2.89
---
number of obs: 1000, groups: plot, 10
AIC = 5015.6, DIC = 4996.4
deviance = 5002.0
```

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"
```

Broom: model estimates in tidy form

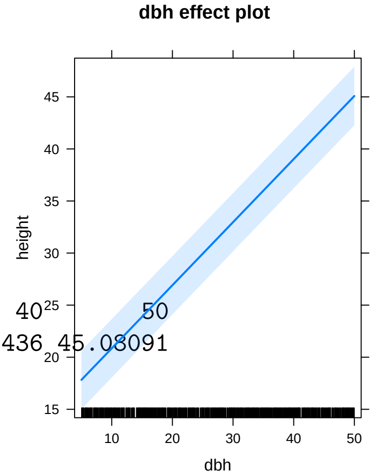
```r
library(broom)
tidy(mixed)
```

```
                     term   estimate  std.error statistic    gr
1             (Intercept) 14.7981641 1.437421280  10.29494    fi
2                     dbh  0.6056549 0.007040079  86.02956    fi
3      sd_(Intercept).plot  4.4535702          NA        NA     p
4 sd_Observation.Residual  2.8852942          NA        NA Resid
```

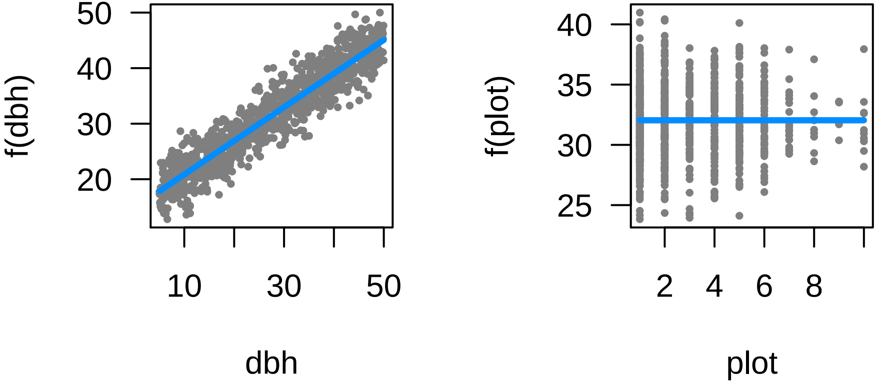
Visualising model: `allEffects`

```
 model: height ~ dbh

 dbh effect
dbh
       5       20       30       40       50 
17.82644 26.91126 32.96781 39.02436 45.08091 
```

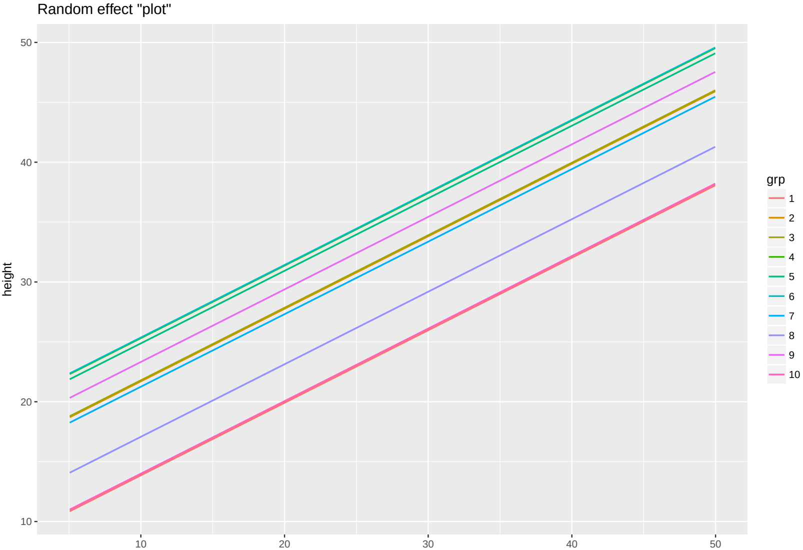


Visualising model: `visreg`



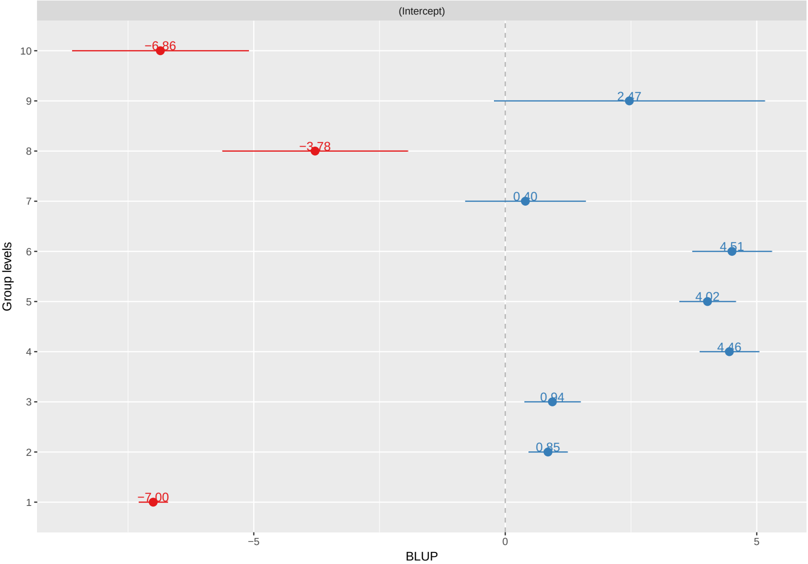
Visualising model: `sjPlot`

```r
library(sjPlot)
sjp.lmer(mixed, type = "ri.slope")
```



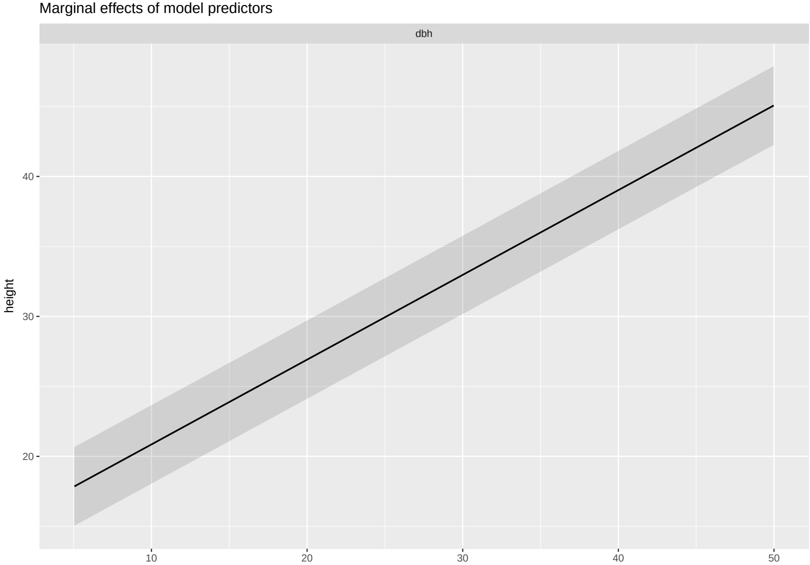
Visualising model: `sjPlot`

```
sjp.lmer(mixed)
```



Visualising model: sjPlot

```
sjp.lmer(mixed, type = "eff", show.ci = TRUE)
```

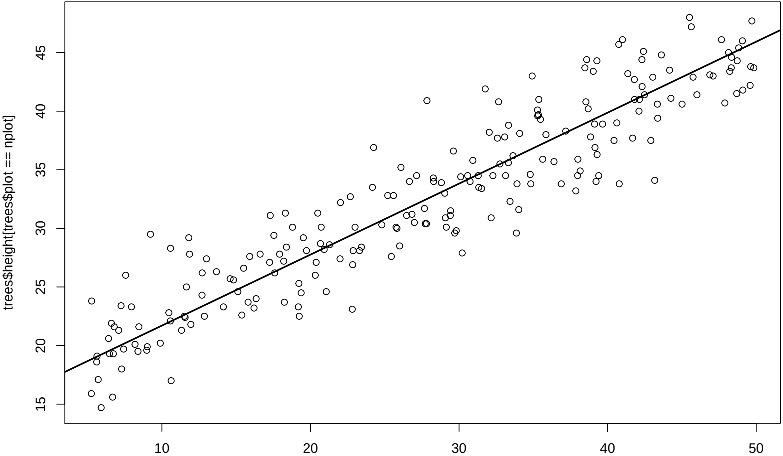


Using merTools to understand fitted model

```
library(merTools)
shinyMer(mixed)
```

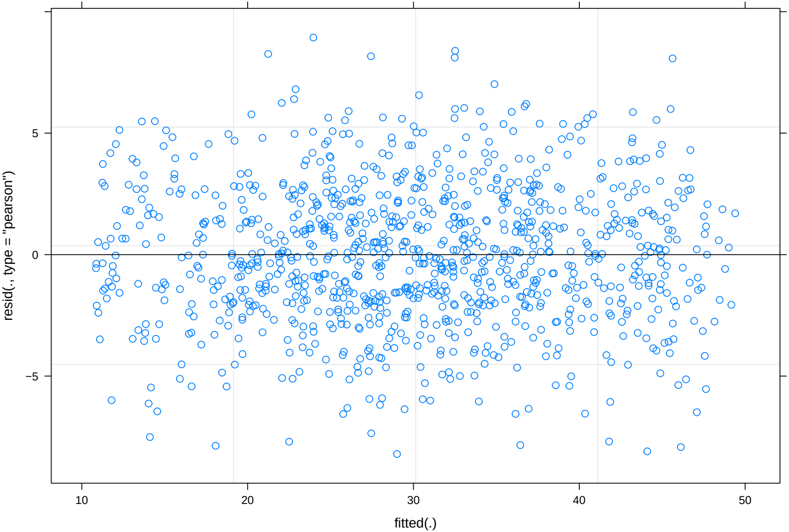
Plotting regression for individual forest plots

```
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
```



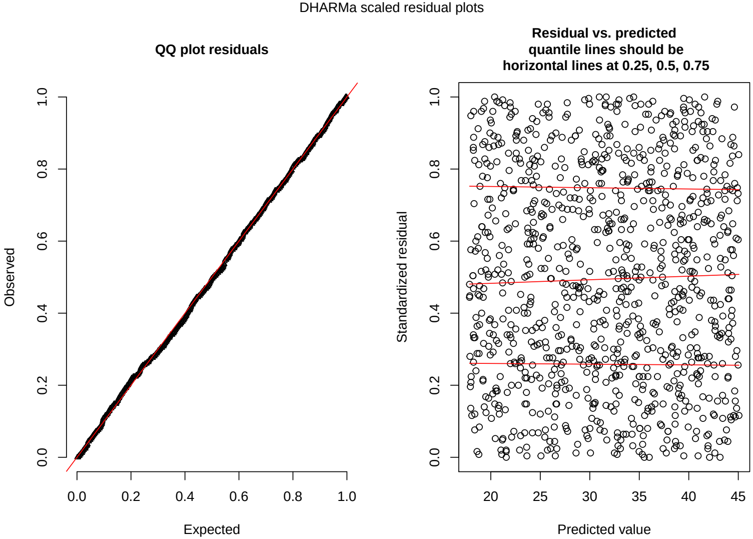
Checking residuals

```
plot(mixed)
```



Checking residuals (DHARMa)

```
simulateResiduals(mixed, plot = TRUE, use.u = TRUE)
```



Growing the hierarchy: adding plot-level predictors

Model with group-level predictors

We had:

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

Now

$$\begin{aligned} y_i &= a_j + bx_i + \varepsilon_i \\ a_j &\sim N(\mu_j, \tau^2) \\ \mu_j &= \gamma + \delta \cdot predictor_j \\ \varepsilon_i &\sim N(0, \sigma^2) \end{aligned}$$

Merging trees and plot data

```r
plotdata <- read.csv("data-raw/plotdata.csv")
trees.full <- merge(trees, plotdata, by = "plot")
head(trees.full)
```

```
  plot   dbh height    sex dead  dbh.c temp
1    1 28.63   22.1 female    0   3.63 15.1
2    1 44.71   39.0 female    0  19.71 15.1
3    1 28.31   29.0 female    0   3.31 15.1
4    1 19.33   19.1   male    0  -5.67 15.1
5    1  9.25   12.2 female    0 -15.75 15.1
6    1 30.02   23.1 female    0   5.02 15.1
```

Centre continuous variables

Plot temperatures referred as deviations from 15ºC

```
trees.full$temp.c <- trees.full$temp - 15
```

Fit multilevel model

```
group.pred <- lmer(height ~ dbh + (1 | plot) + temp.c, data = tr
arm::display(group.pred)
```

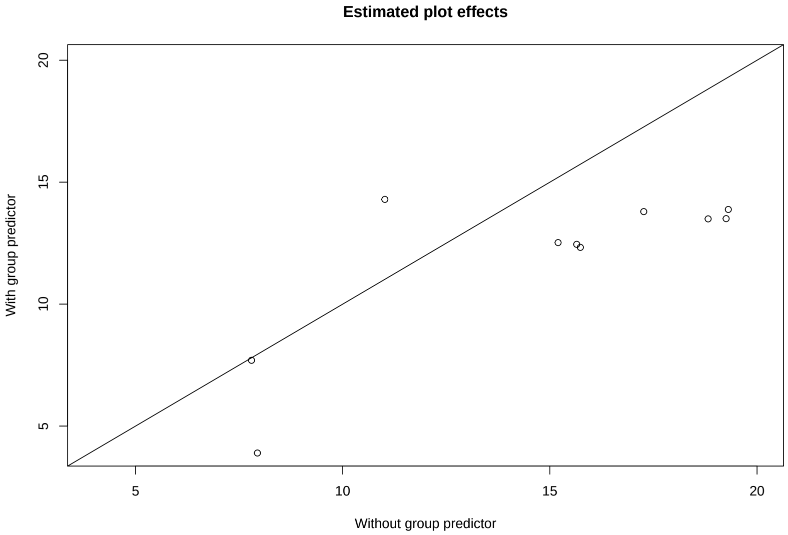
```
lmer(formula = height ~ dbh + (1 | plot) + temp.c, data = trees.
            coef.est coef.se
(Intercept) 11.79     1.75
dbh          0.61     0.01
temp.c       1.07     0.46

Error terms:
 Groups   Name        Std.Dev.
 plot     (Intercept) 3.61
 Residual             2.89
---
number of obs: 1000, groups: plot, 10
AIC = 5012.8, DIC = 4991
deviance = 4996.9
```

Examine model with merTools

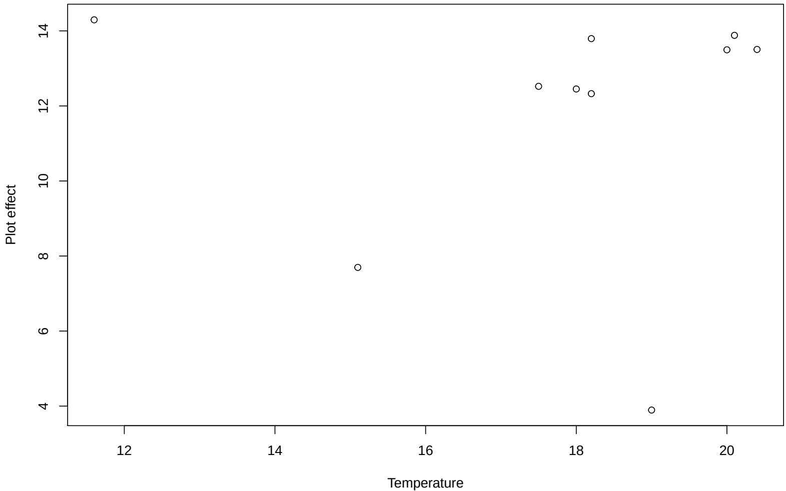
```r
shinyMer(group.pred)
```

Comparing plot effects with and without group predictor



Are plot effects related to temperature?

```
plot(plotdata$temp, coef(group.pred)$plot[,1],
     xlab = "Temperature", ylab = "Plot effect")
```



Varying intercepts and slopes

Varying intercepts and slopes

- There is overall difference in height among plots (different intercepts)

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

Varying intercepts and slopes

- There is overall difference in height among plots (different intercepts)
- AND

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

Varying intercepts and slopes

- There is overall difference in height among plots (different intercepts)
- AND
- Relationship between DBH and Height varies among plots (different slopes)

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

Varying intercepts and slopes

```
lmer(formula = height ~ dbh + (1 + dbh | plot), data = trees)
            coef.est coef.se
(Intercept) 14.82     1.48  
dbh          0.60     0.01  

Error terms:
 Groups   Name        Std.Dev. Corr 
 plot     (Intercept) 4.57          
          dbh         0.01     -0.41
 Residual             2.88          
---
number of obs: 1000, groups: plot, 10
AIC = 5018.6, DIC = 4995.9
deviance = 5001.3
```

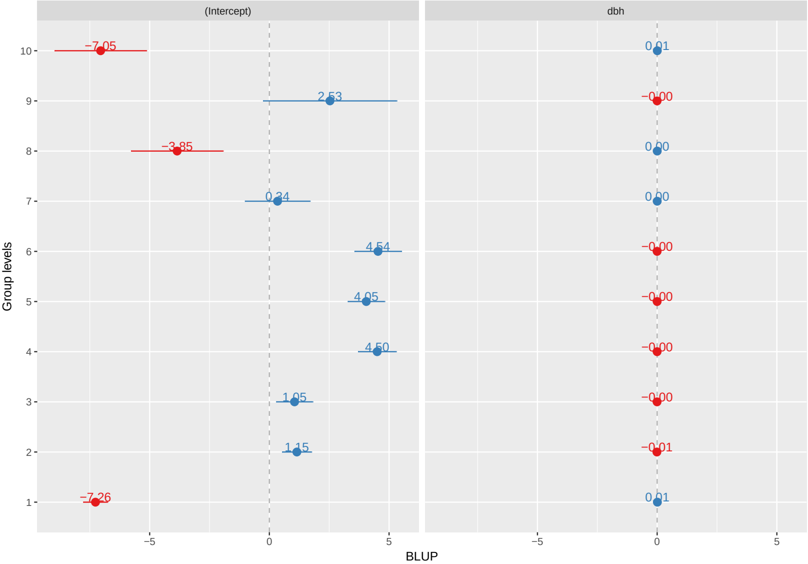
Varying intercepts and slopes

```
$plot
   (Intercept)       dbh
1     7.554578 0.6144452
2    15.966915 0.5942836
3    15.868969 0.6008673
4    19.321161 0.6031855
5    18.866370 0.6039353
6    19.355009 0.6038332
7    15.159258 0.6067449
8    10.965429 0.6080747
9    17.348840 0.6024600
10    7.769135 0.6109349

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

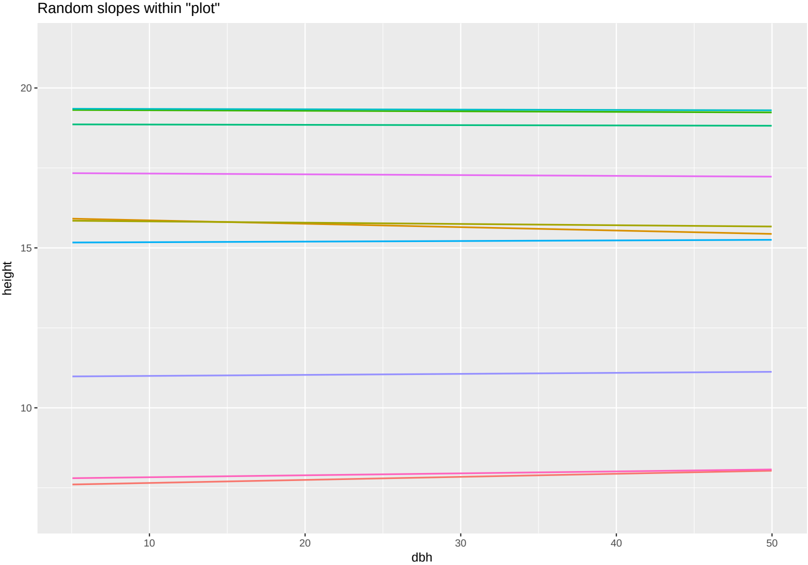
Visualising model: `sjPlot`

```
sjp.lmer(mixed.slopes)
```



Visualising model: `sjPlot`

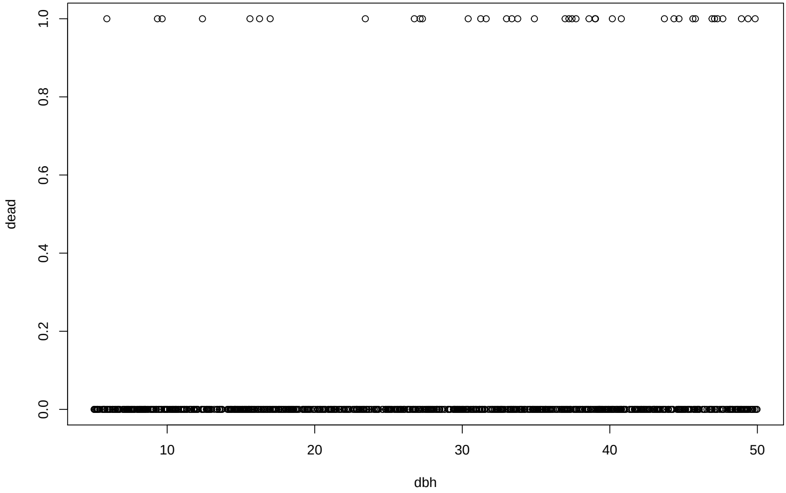
```r
sjp.lmer(mixed.slopes, type = "rs.ri")
```



Multilevel logistic regression

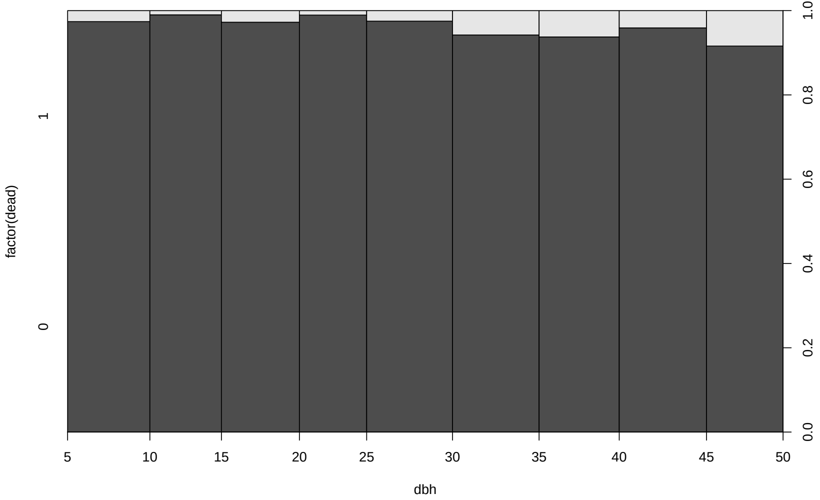
Q: Relationship between tree size and mortality

```r
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
```

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
factor(plot)7    0.03126    1.06064   0.029   0.9765
```

Fit multilevel logistic regression

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

```
glmer(formula = dead ~ dbh + (1 | plot), data = trees, family =
            coef.est coef.se
(Intercept) -4.47     0.49
dbh          0.04     0.01

Error terms:
 Groups   Name        Std.Dev.
 plot     (Intercept) 0.00
 Residual             1.00
---
number of obs: 1000, groups: plot, 10
AIC = 325.9, DIC = 319.9
deviance = 319.9
```

Retrieve model coefficients

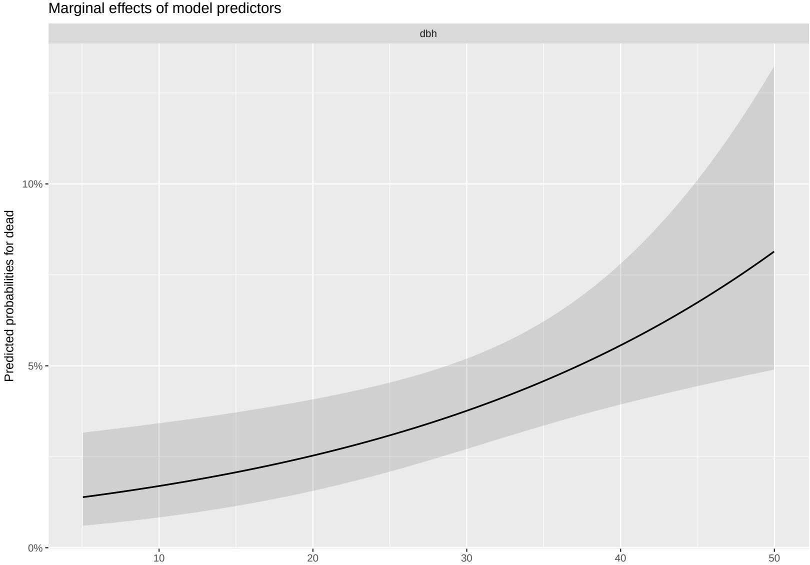
```
coef(mixed.logis)
```

```
$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
8    -4.469446 0.04093806
9    -4.469446 0.04093806
10   -4.469446 0.04093806

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

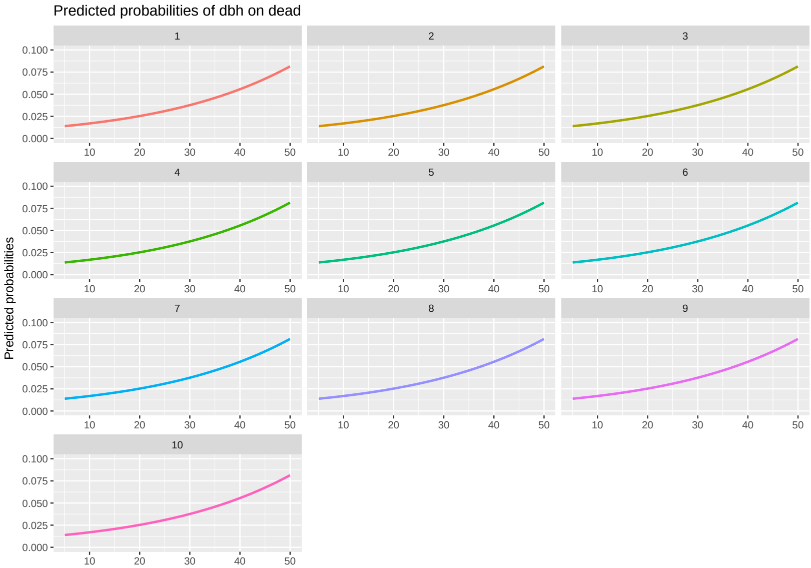
Visualising model: `sjPlot`

```
sjp.glmer(mixed.logis, type = "eff", show.ci = TRUE)
```



Visualising model: sjPlot

```
sjp.glmer(mixed.logis, type = "ri.slope")
```



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- Perfect for structured data (space-time)

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- Predictors enter at the appropriate level
- Accommodate variation in treatment effects
- More efficient inference of regression parameters
- Using all the data to perform inferences for groups with small sample size

Formula syntax for different models

```
y ~ x + (1 | group) # varying intercepts
y ~ x + (1 + x | group) # varying intercepts and slopes
y ~ x + (1 | group/subgroup) # nested
y ~ x + (1 | group1) + (1 | group2) # varying intercepts, crossed
y ~ x + (1 + x | group1) + (1 + x | group2) # varying intercepts and slopes, crossed
```

END

Figure 9:

Source code and materials:
https://github.com/Pakillo/LM-GLM-GLMM-intro