Generalised Linear Models: Logistic regression

Q: Survival of passengers on the Titanic ∼ Class

Read `titanic_long.csv` dataset and fit linear model (survival ∼ class).

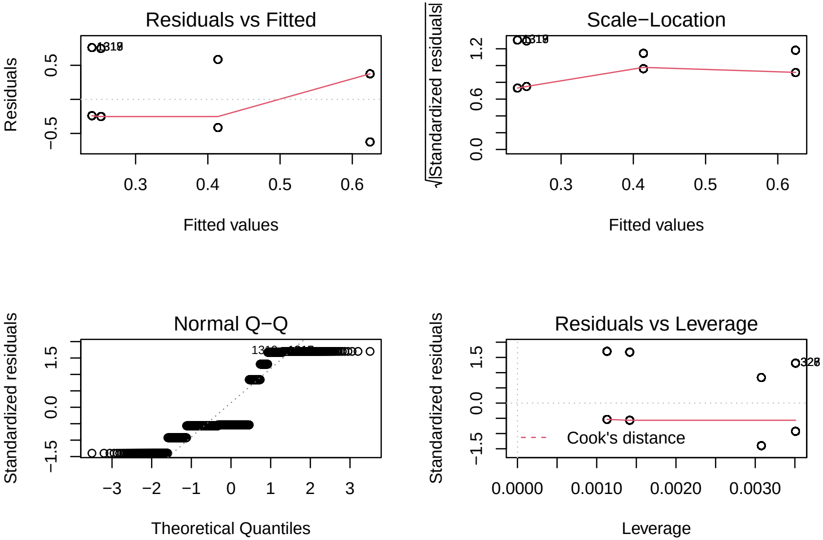
```
  class   age  sex survived
1 first adult male        1
2 first adult male        1
3 first adult male        1
4 first adult male        1
5 first adult male        1
6 first adult male        1
```

Quiz

https://pollev.com/franciscorod726

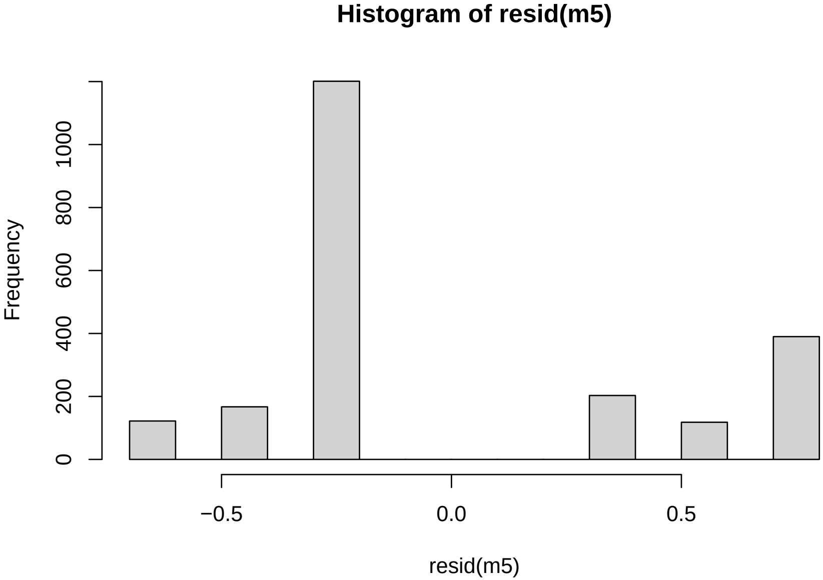
Let's check linear model:

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



```
null device
          1
```

Weird residuals!



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

Binary variables (0/1)

Counts (0, 1, 2, 3, …)

Generalised Linear Models to the rescue!

Generalised Linear Models

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

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   - Bernouilli - Binomial

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   - Poisson

Generalised Linear Models

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    - Gamma

Generalised Linear Models

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

Generalised Linear Models

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

Generalised Linear Models

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   - Bernouilli - Binomial
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   - etc
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3. **Link function**

Generalised Linear Models

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   - etc
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   - Gaussian: identity

Generalised Linear Models

1. **Response variable** - distribution `family`
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   - etc
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   - Binomial: logit, probit

Generalised Linear Models

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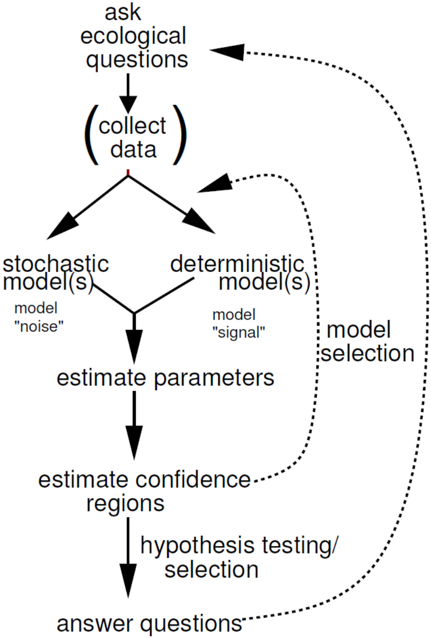
   - Binomial: logit, probit
   - Poisson: log...

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



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 survived in each class?

```
table(titanic$class, titanic$survived)
```

```
          0   1
  crew   673 212
  first  122 203
  second 167 118
  third  528 178
```

Back to survival of Titanic passengers (dplyr)

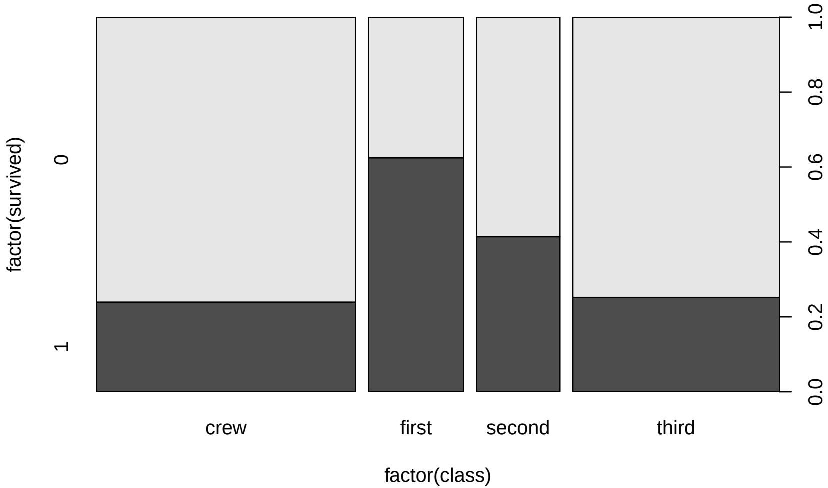
Passenger survival according to class

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

```
# A tibble: 8 x 3
# Groups:   class [4]
  class  survived count
  <chr>     <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
```

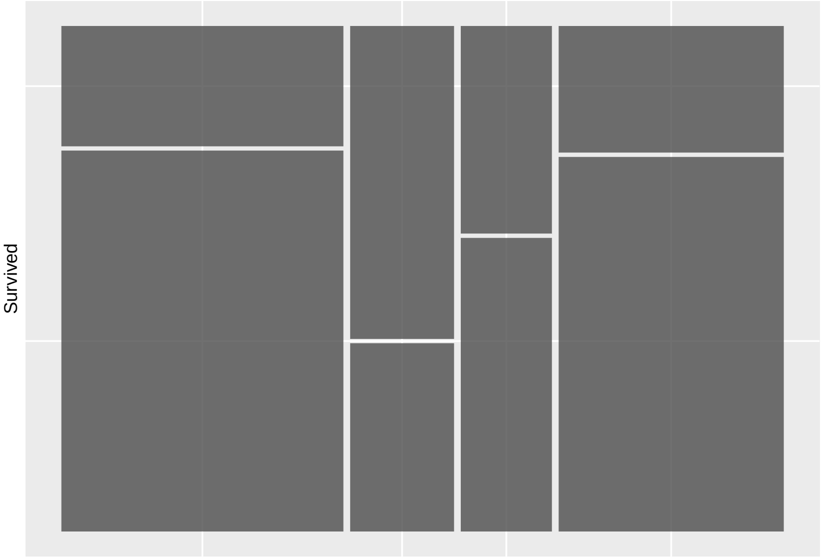
Or graphically...

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



Mosaic plots (ggplot2)

```
ggplot(titanic) +
  geom_mosaic(aes(x = product(survived, class))) +
  labs(x = "", y = "Survived")
```



Fitting GLMs in R: `glm`

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

which corresponds to

$$logit(Pr(survival)_i) = a + b \cdot class_i$$

$$logit(Pr(survival)_i) = a + b_{first} + c_{second} + d_{third}$$

Fitting GLMs in R: glm

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

```
Call:
glm(formula = survived ~ class, family = binomial, data = titanic)

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)

    Null deviance: 2769.5  on 2200  degrees of freedom
Residual deviance: 2588.6  on 2197  degrees of freedom
AIC: 2596.6

Number of Fisher Scoring iterations: 4
```

These estimates are in logit scale!

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?

Must add intercept (baseline) to the parameter estimate:

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

```
(Intercept)
  0.6246154
```

Again this value matches the data:

```r
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 
```

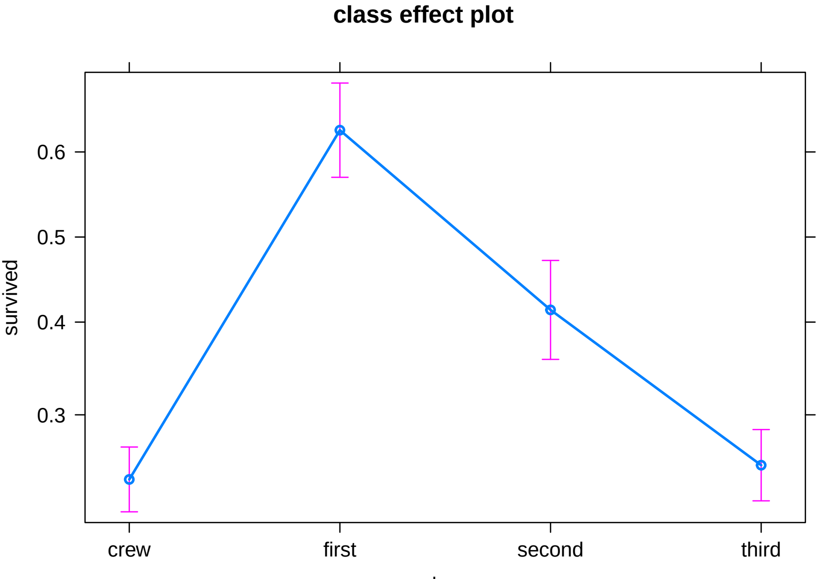
Presenting model results

```r
kable(xtable::xtable(tit.glm), digits = 2)
```

	Estimate	Std. Error	z value	Pr(>|z|)
(Intercept)	-1.16	0.08	-14.67	0.00
classfirst	1.66	0.14	11.97	0.00
classsecond	0.81	0.14	5.62	0.00
classthird	0.07	0.12	0.58	0.56

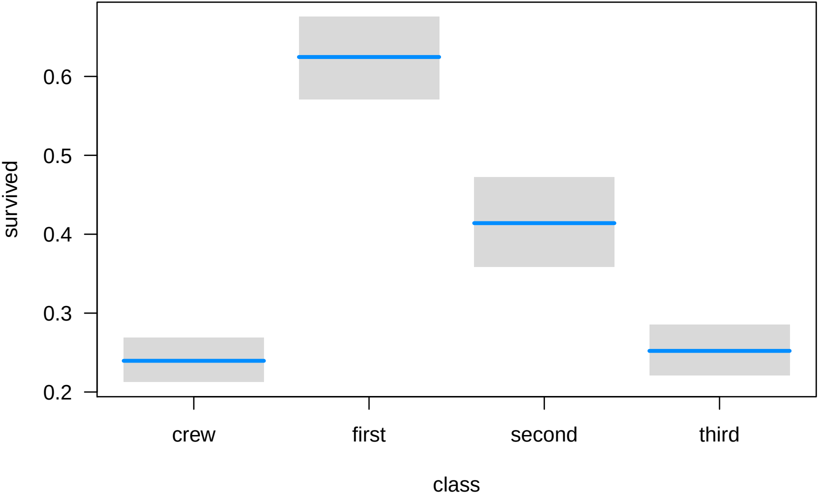
Visualising model: `effects` package

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



Visualising model: visreg package

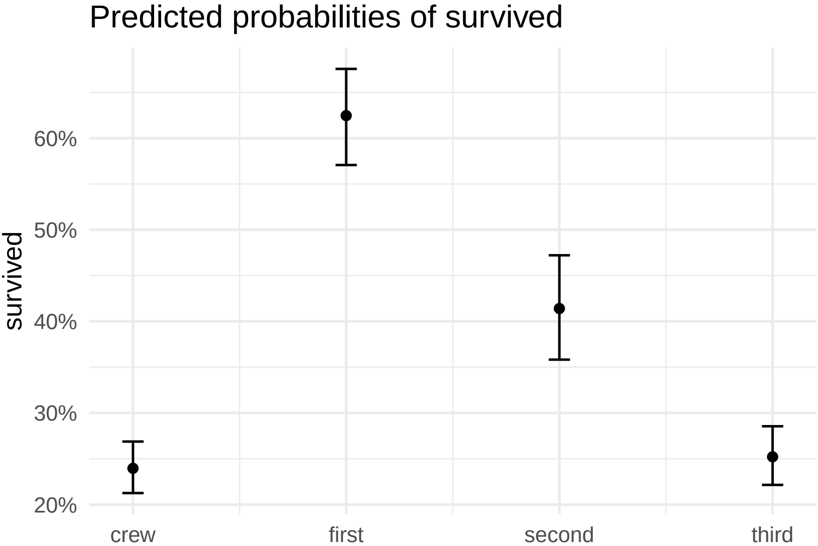
```r
visreg(tit.glm, scale = "response", rug = FALSE)
```



Visualising model: `sjPlot` package

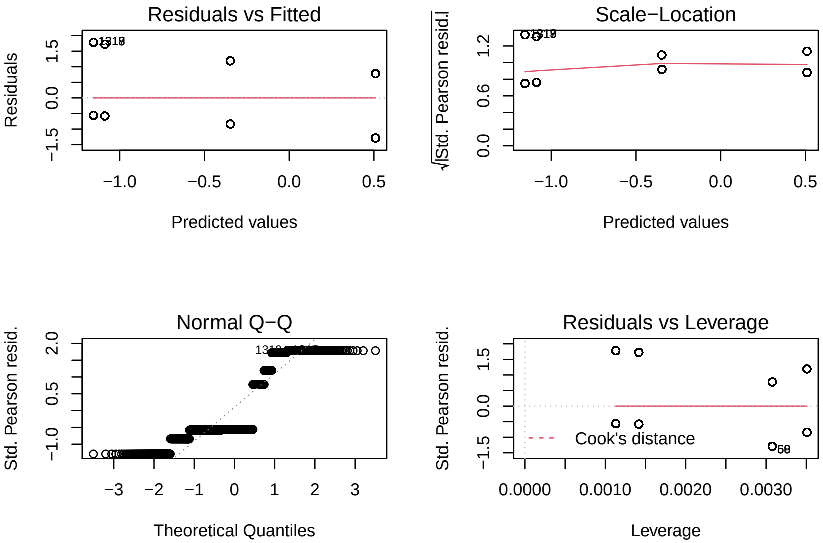
```
sjPlot::plot_model(tit.glm, type = "eff")
```

```
$class
```



Logistic regression: model checking

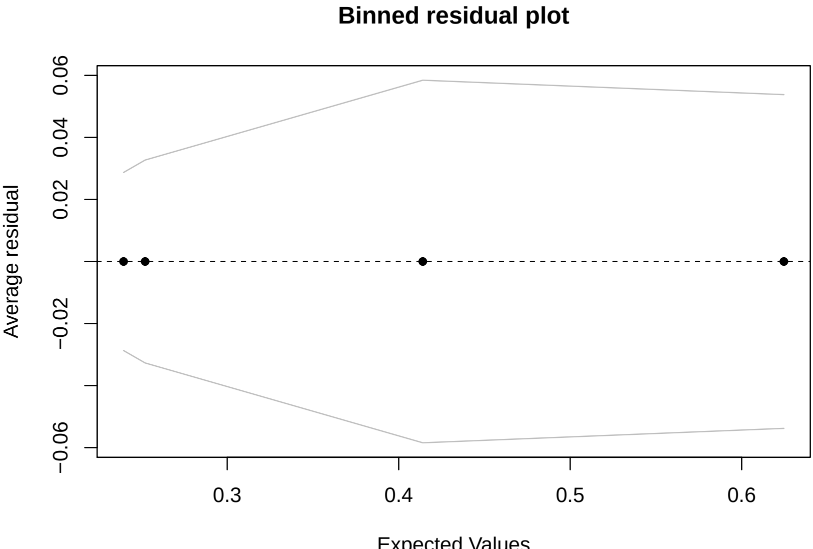
Not very useful



```
null device
```

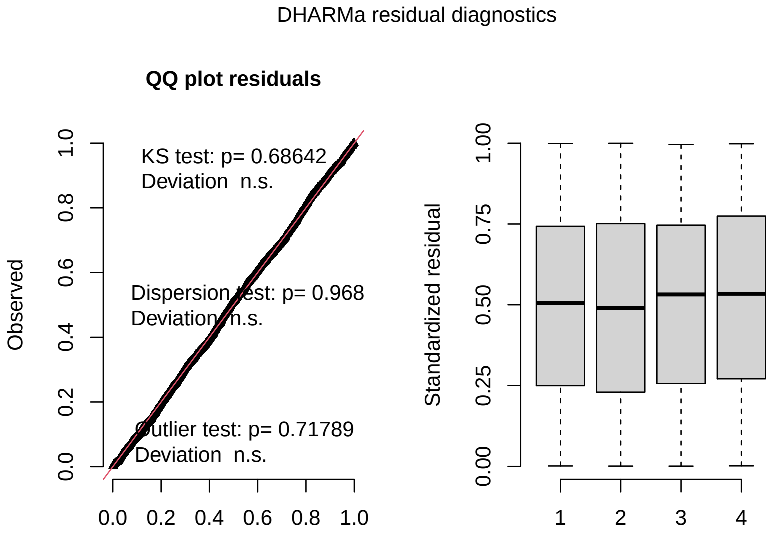
Binned residual plots for logistic regression

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



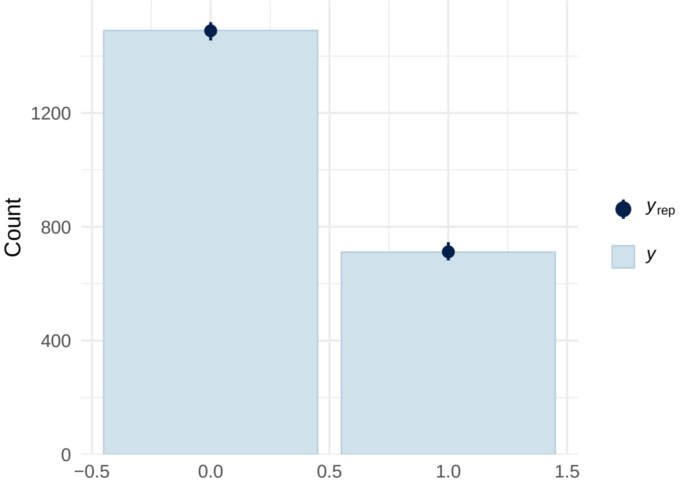
Residual diagnostics with DHARMa

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



Model checking with simulated data

```r
library(bayesplot)
sims <- simulate(tit.glm, nsim = 100)
ppc_bars(titanic$survived, yrep = t(as.matrix(sims)))
```



Pseudo R-squared for GLMs

```r
library(performance)
r2(tit.glm)
```

```
$R2_Tjur
 Tjur's R2
0.08650663
```

But many caveats apply! (e.g. see here and here)

Recapitulating

1. **Visualise data**

Recapitulating

1. **Visualise data**
2. **Fit model**: `glm`. Don't forget to specify `family`!

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3. **Examine model**: `summary`

Recapitulating

1. **Visualise data**
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4. **Back-transform parameters** from *logit* into probability scale (e.g. `allEffects`)

Recapitulating

1. **Visualise data**
2. **Fit model**: `glm`. Don't forget to specify `family`!
3. **Examine model**: `summary`
4. **Back-transform parameters** from *logit* into probability scale (e.g. `allEffects`)
5. **Plot model**: `plot(allEffects(model))`, `visreg`, `plot_model`...

Recapitulating

1. **Visualise data**
2. **Fit model**: `glm`. Don't forget to specify `family`!
3. **Examine model**: `summary`
4. **Back-transform parameters** from *logit* into probability scale (e.g. `allEffects`)
5. **Plot model**: `plot(allEffects(model))`, `visreg`, `plot_model`...
6. **Examine residuals**: `DHARMa::simulateResiduals`.

Q: Did men have higher survival than women?

Quiz

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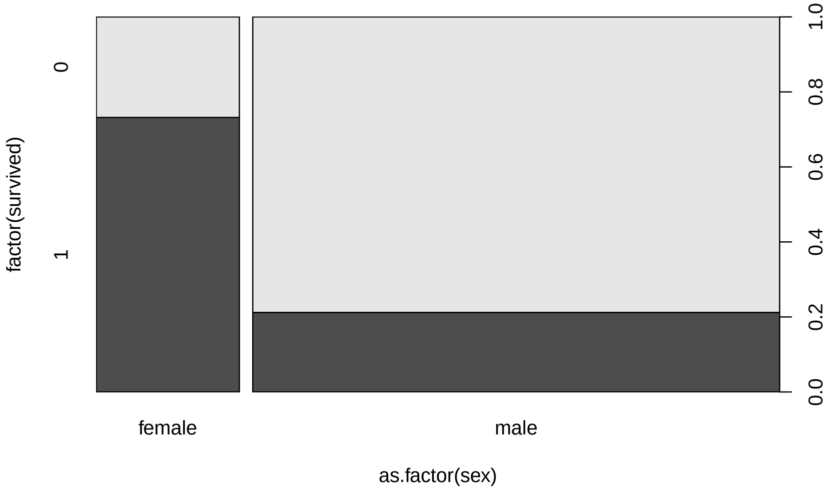
Plot first

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

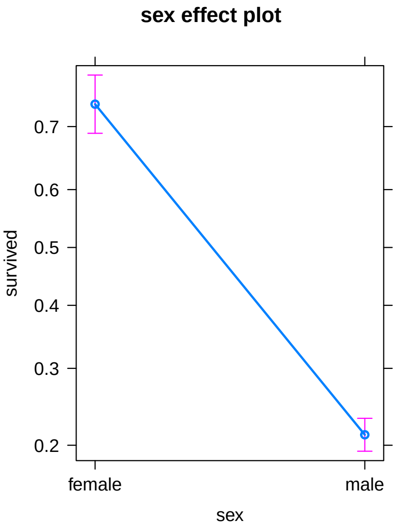


Fit model

```
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
Residual deviance: 2335.0  on 2199  degrees of freedom
AIC: 2339
```

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

```r
table(titanic$class, titanic$survived, titanic$sex)
```

```
, ,  = female

        
           0   1
  crew     3  20
  first    4 141
  second  13  93
  third  106  90

, ,  = male

        
           0   1
  crew   670 192
  first  118  62
  second 154  25
  third  422  88
```

Mmmm...

Quiz

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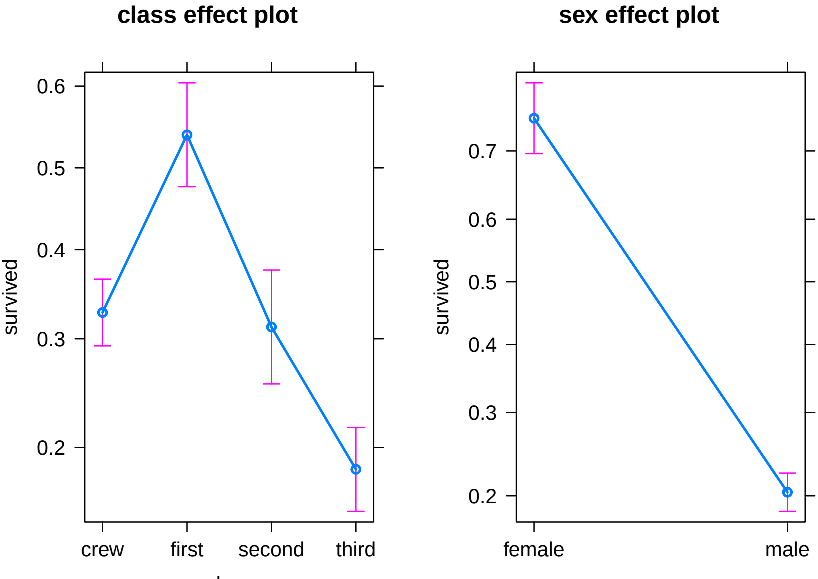
Fit additive model with both factors

```r
tit.sex.class <- glm(survived ~ class + sex, family = binomial,
```

```
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))
```



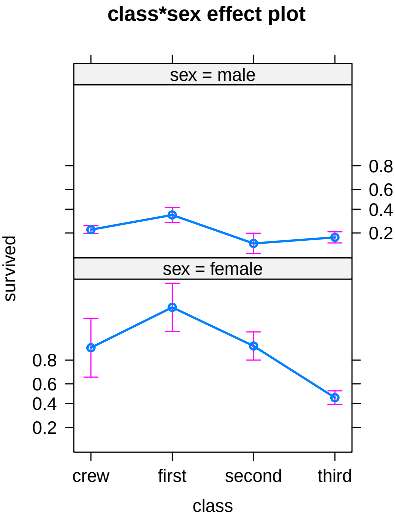
Fit model with both factors (interactions)

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

```
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

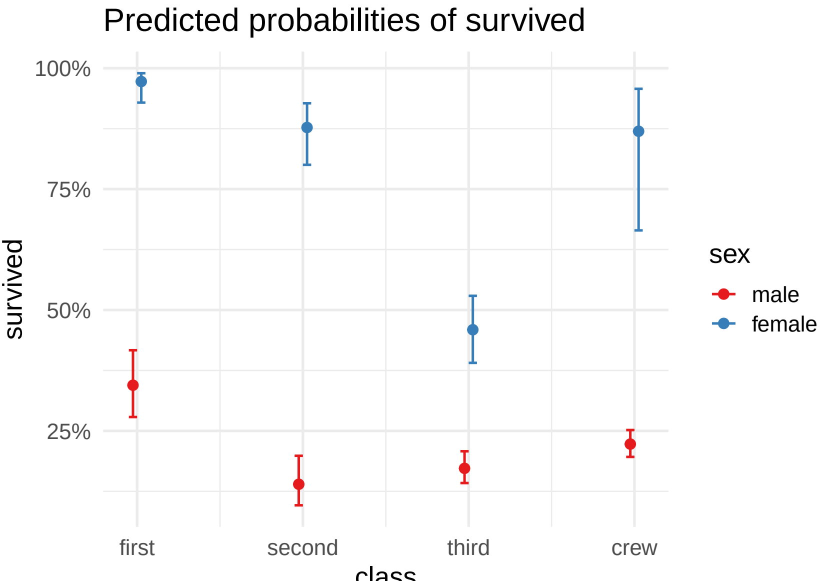
```
 model: survived ~ class * sex

 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**.

Effects (sjPlot)

```
plot_model(tit.sex.class, type = "int")
```



Extra exercises:

Is survival related to age?
Are age effects dependent on sex?

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
 Length:207         Min.   :  2.00   Min.   :   36
 Class :character   1st Qu.: 12.00   1st Qu.:  442
 Mode  :character   Median : 30.00   Median : 1779
                    Mean   : 43.48   Mean   : 6262
                    3rd Qu.: 66.00   3rd Qu.: 7272
                    Max.   :169.00   Max.   :42416
                    NA's   :6        NA's   :10
```

Q: Is infant mortality related to GDP?

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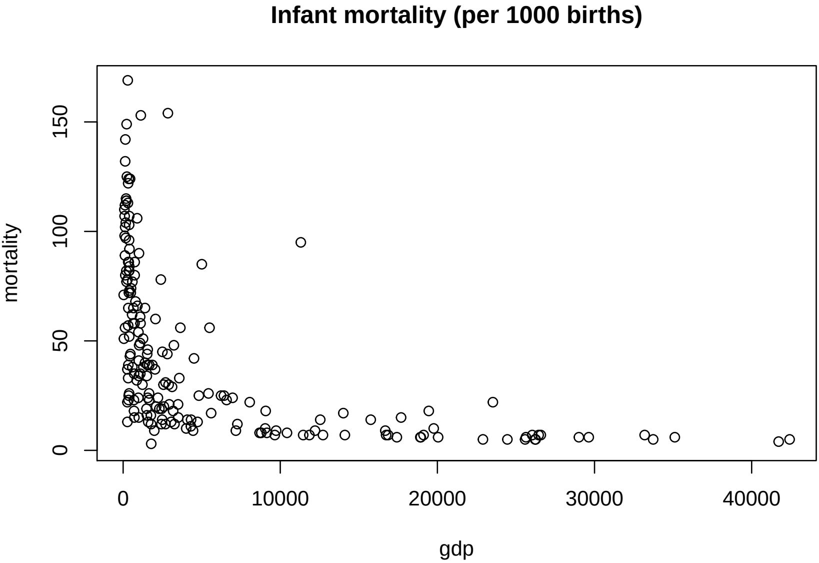
EDA

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



Fit model

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

```

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

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

Coefficients:
              Estimate Std. Error z value Pr(>|z|)    
(Intercept) -2.657e+00  1.311e-02 -202.76   <2e-16 ***
gdp         -1.279e-04  3.458e-06  -36.98   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)
```

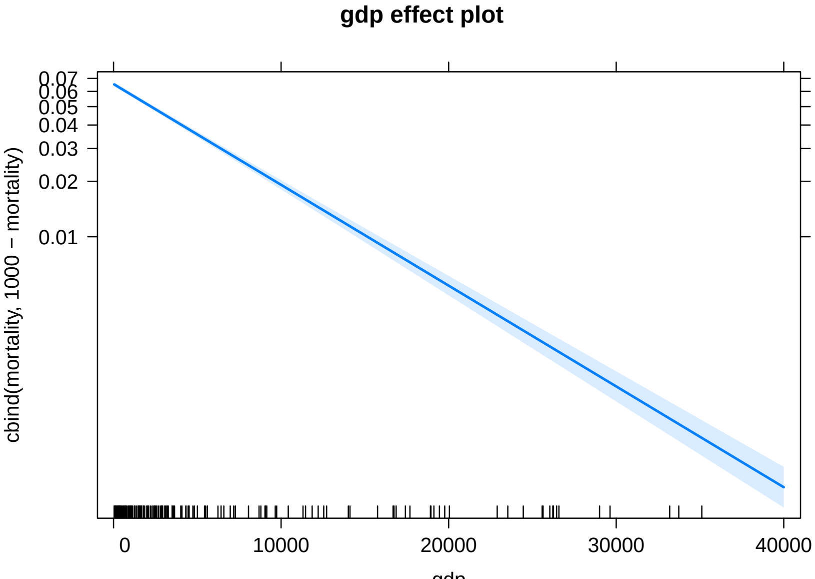
Effects

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

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

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

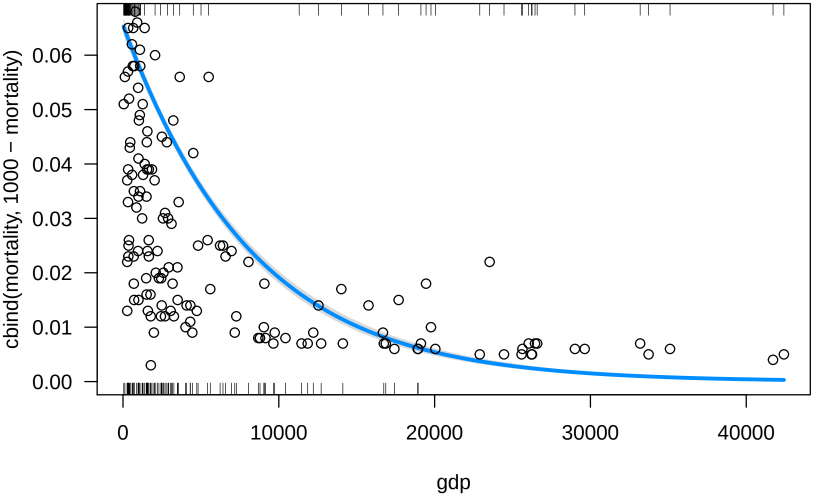
Effects plot

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



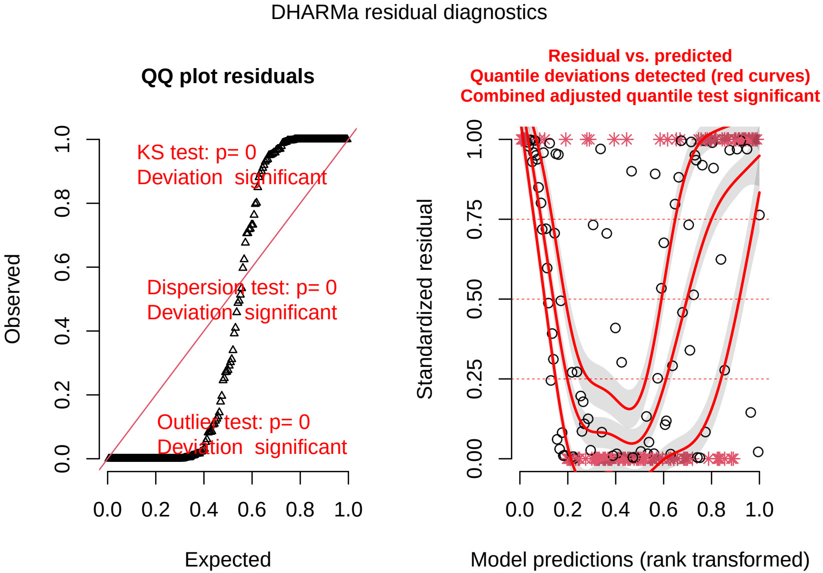
Plot model using visreg:

```
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)

```r
simres <- simulateResiduals(gdp.glm, refit = TRUE)
testDispersion(simres, plot = FALSE)
```

```
	DHARMa nonparametric dispersion test via mean deviance resid
	vs. simulated-refitted

data:  simres
dispersion = 21, p-value < 2.2e-16
alternative hypothesis: two.sided
```

Overdispersion in logistic regression with proportion data

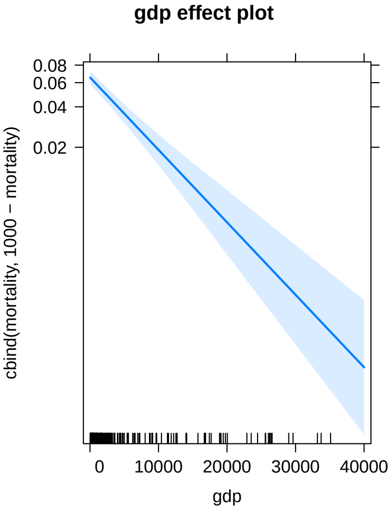
```
gdp.overdisp <- glm(cbind(mortality, 1000 - mortality) ~ gdp,
                    data = gdp, family = quasibinomial)
```

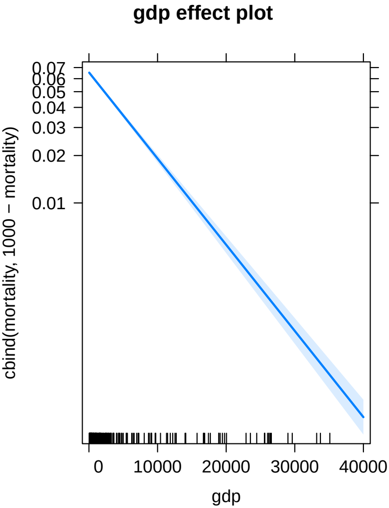
```
Call:
glm(formula = cbind(mortality, 1000 - mortality) ~ gdp, family =
    data = gdp)

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

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept) -2.657e+00  5.977e-02 -44.465  < 2e-16 ***
gdp         -1.279e-04  1.577e-05  -8.111 5.96e-14 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for quasibinomial family taken to be 20.79
```

Mean estimates do not change after accounting for overdispersion

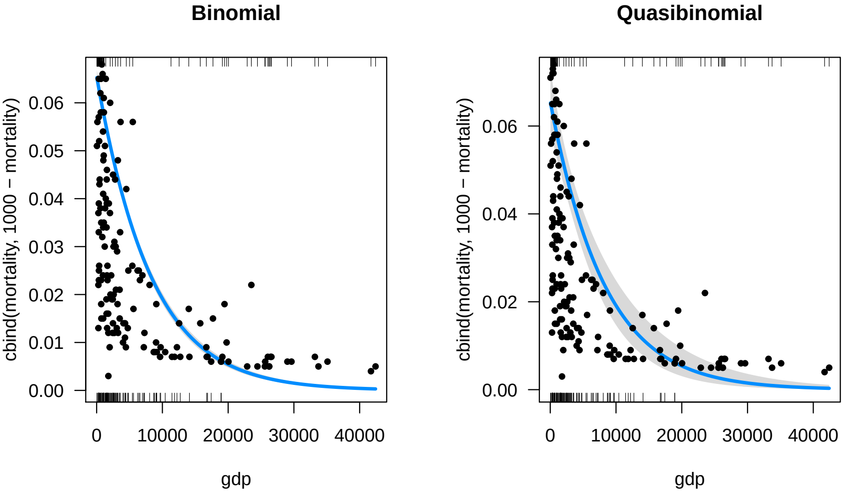
```
 model: cbind(mortality, 1000 - mortality) ~ gdp

 gdp effect
gdp
         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

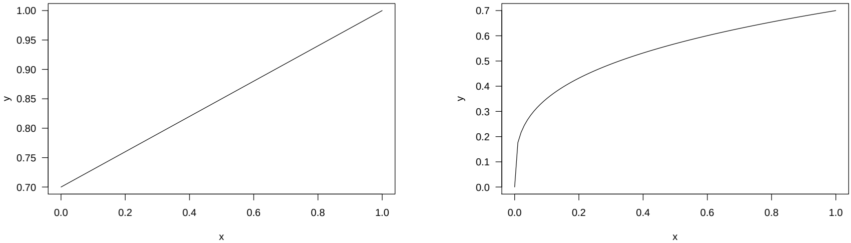


Overdispersion

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

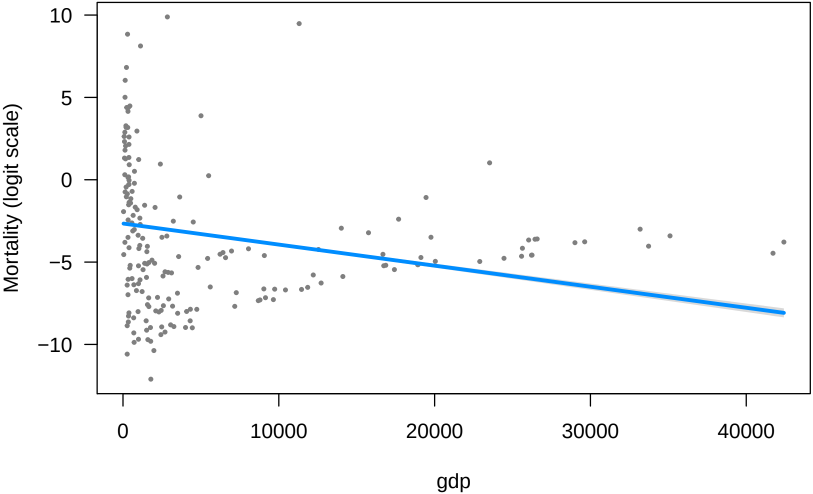
Think about the shape of relationships

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

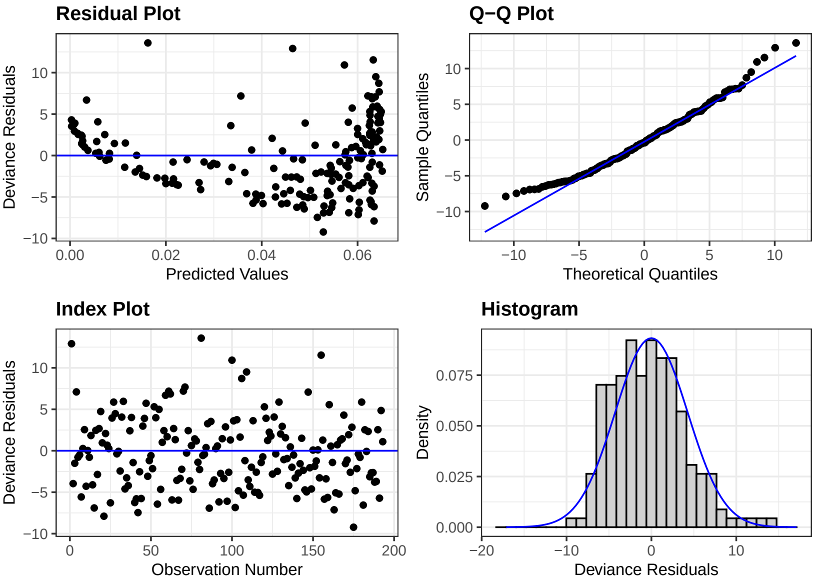


Think about the shape of relationships

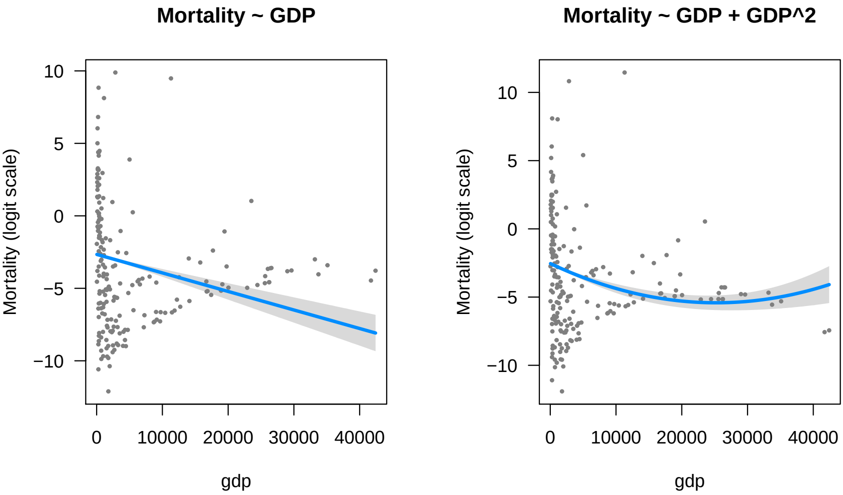
```
visreg(gdp.glm, ylab = "Mortality (logit scale)")
```



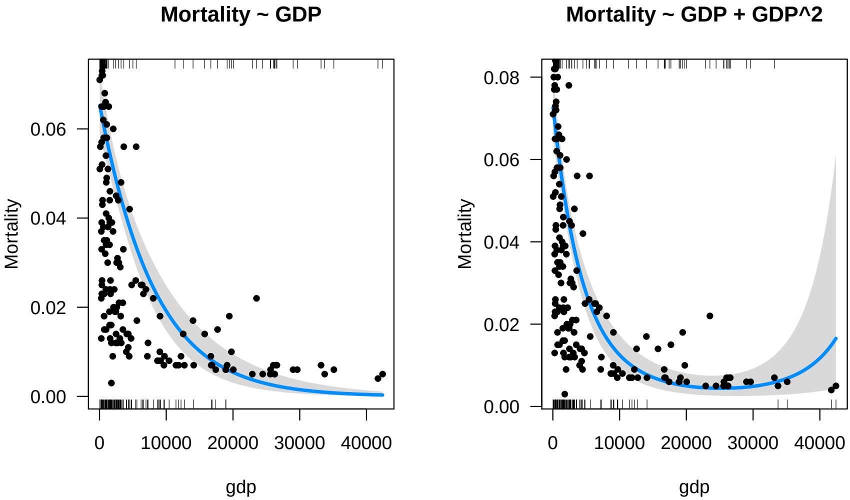
Think about the shape of relationships



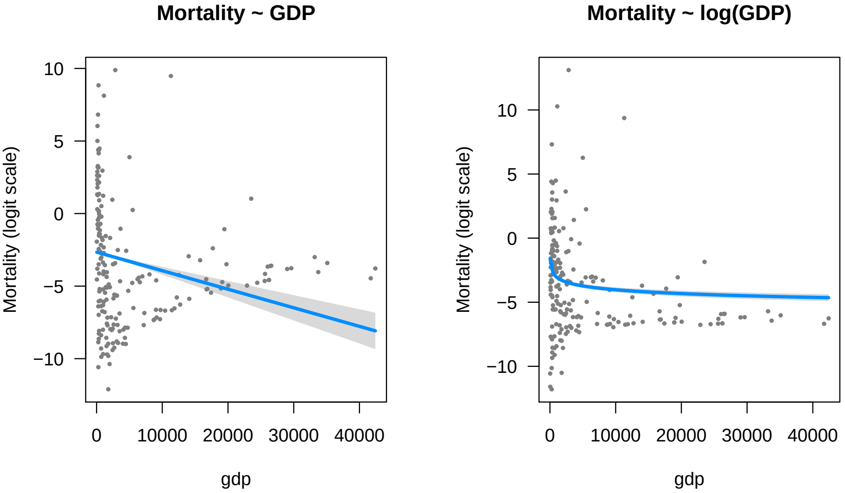
Think about the shape of relationships



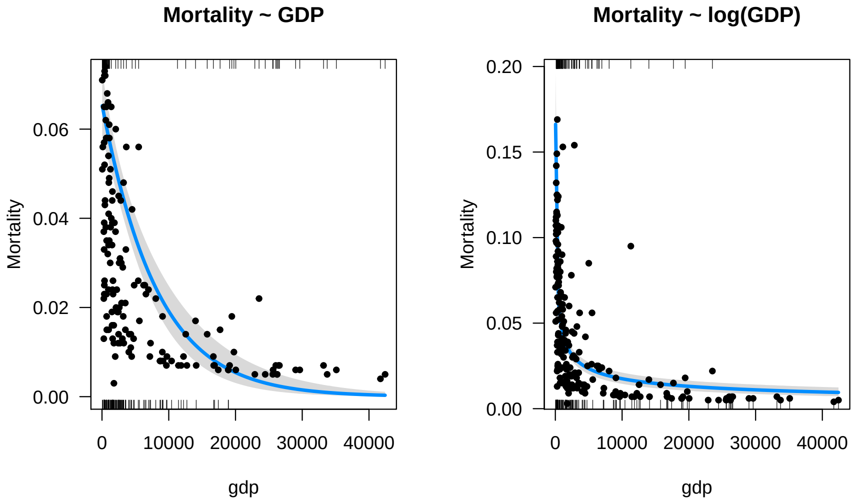
Think about the shape of relationships



Think about the shape of relationships



Think about the shape of relationships



```
gdp.log <- glm(cbind(mortality, 1000 - mortality) ~ log(gdp),
```

More examples

- seedset.csv: Comparing seed set among plants (Data from Harder et al. 2011)

Seed set among plants

```r
seed <- readr::read_csv("data/seedset.csv")
head(seed)
```

```
# A tibble: 6 x 6
  species    plant pcmass fertilized seeds ovulecnt
  <chr>      <dbl>  <dbl>      <dbl> <dbl>    <dbl>
1 ferruginea     2  0             70    52      330
2 ferruginea     2  0.2          321   188      461
3 ferruginea     2  0.485        351   278      435
4 ferruginea     2  0.737        386   301      430
5 ferruginea     2  1            367   342      419
6 ferruginea     3  0            185    39      470
```

```r
seed$plant <- as.factor(seed$plant)
```

Questions:

https://pollev.com/franciscorod726

- Is seed set related to proportion of outcross pollen (pcmass)?

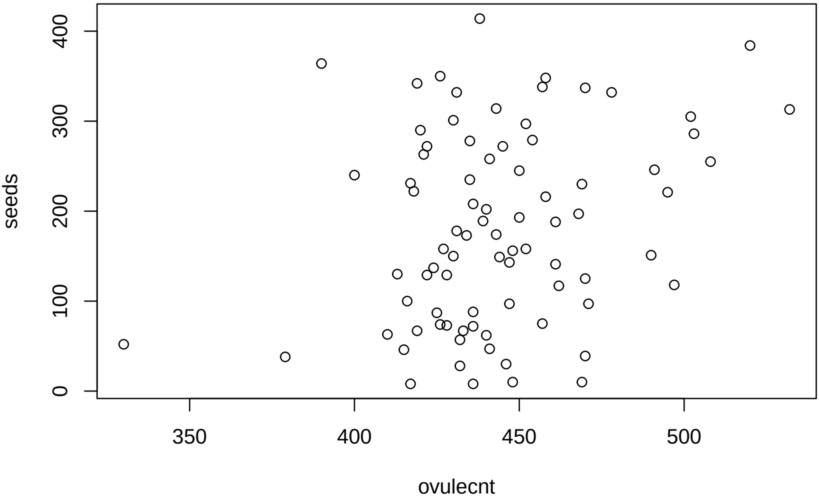
Questions:

https://pollev.com/franciscorod726

- Is seed set related to proportion of outcross pollen (pcmass)?
- Which plant had lower seed set?

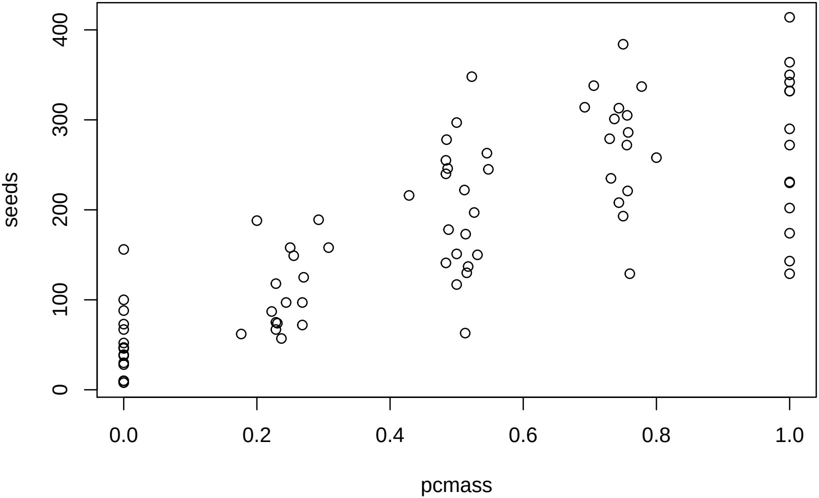
Number of seeds vs Number of ovules

```r
plot(seeds ~ ovulecnt, data = seed)
```

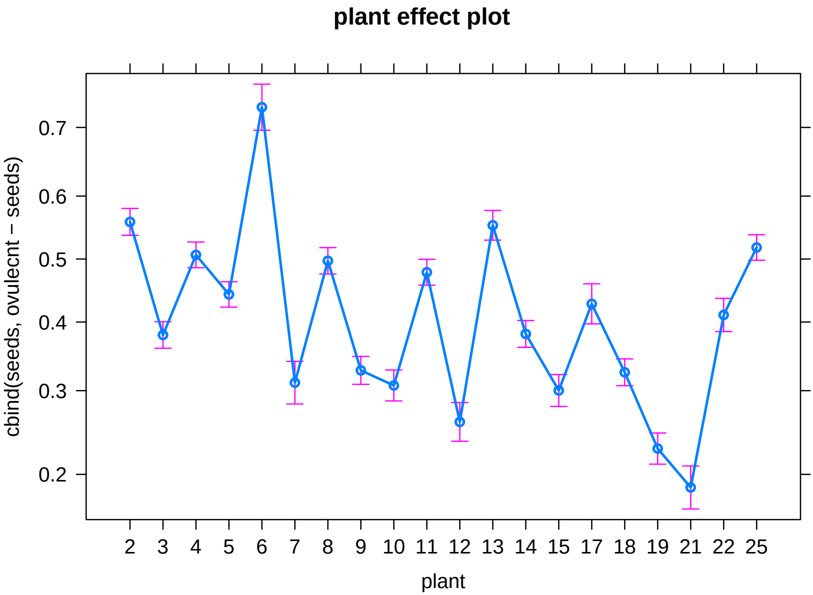


Number of seeds vs Proportion outcross pollen

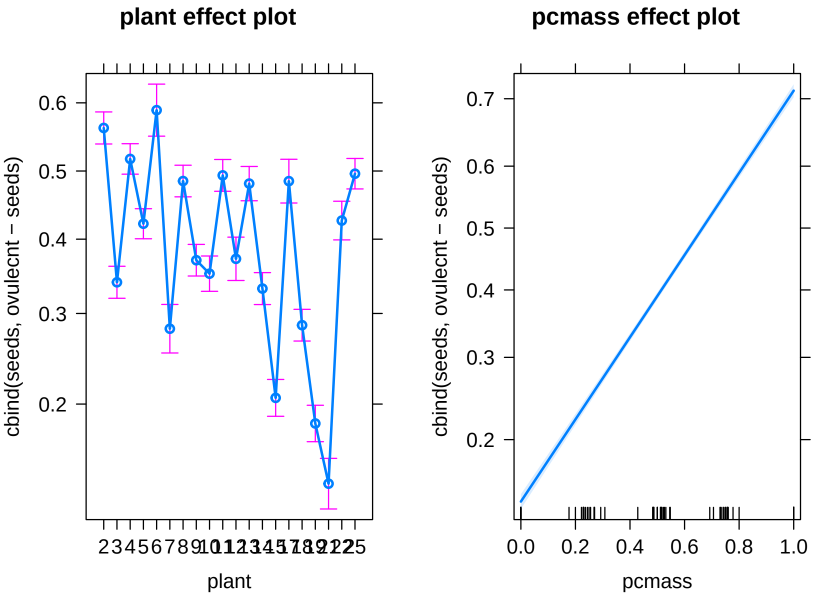
```
plot(seeds ~ pcmass, data = seed)
```



Seed set across plants



Seed set ~ outcross pollen


plant effect plot
cbind(seeds, ovulecnt − seeds)
plant
pcmass effect plot
cbind(seeds, ovulecnt − seeds)
pcmass