

Generalised Linear Models

Logistic regression

Francisco Rodríguez-Sánchez

<https://frodriguezsanchez.net>

Q: Survival of passengers on the Titanic ~ Class

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

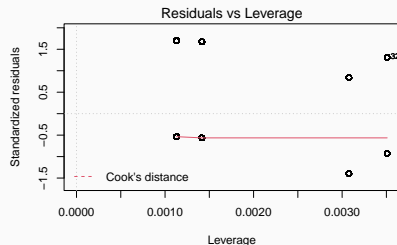
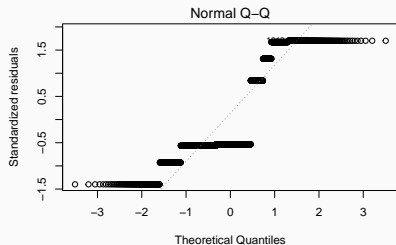
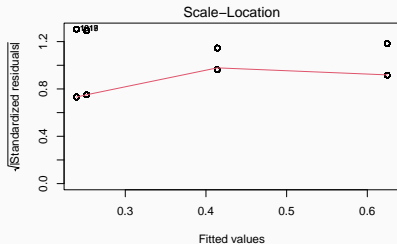
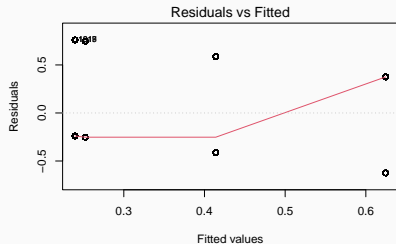
	class	age	sex	survived
1	first	adult	male	1
2	first	adult	male	1
3	first	adult	male	1
4	first	adult	male	1
5	first	adult	male	1
6	first	adult	male	1

Quiz: Did passenger class influence survival?

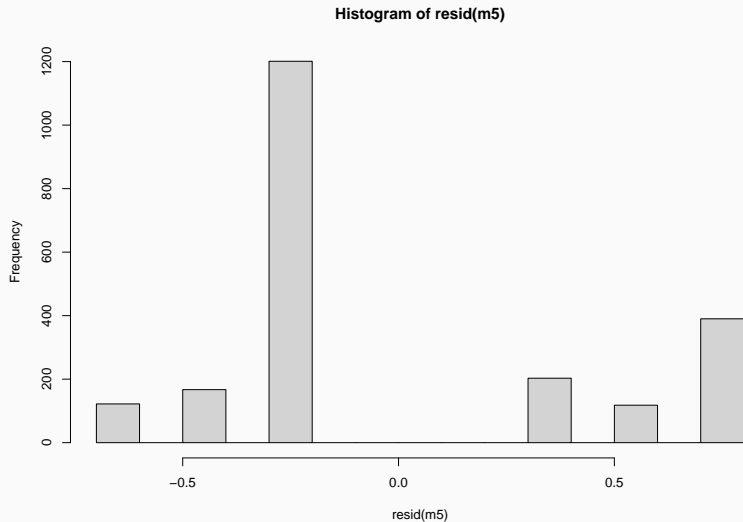
<https://pollev.com/franciscorod726>

Let's check linear model:

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



Weird residuals!



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

Binary variables (0/1)

Counts (0, 1, 2, 3, ...)

Categories (“small”, “medium”, “large”...)

Generalised Linear Models to the rescue!

1. Response variable - distribution family

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- Bernoulli - Binomial

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- Bernoulli - Binomial
- Poisson

1. Response variable - distribution family

- Bernoulli - Binomial
- Poisson
- Gamma

1. Response variable - distribution family

- Bernoulli - Binomial
- Poisson
- Gamma
- etc

1. Response variable - distribution family

- Bernoulli - Binomial
- Poisson
- Gamma
- etc

2. Predictors (continuous or categorical)

1. Response variable - distribution family

- Bernoulli - Binomial
- Poisson
- Gamma
- etc

2. Predictors (continuous or categorical)

3. Link function

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- Bernoulli - Binomial
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- Gaussian: identity

1. Response variable - distribution family

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2. Predictors (continuous or categorical)

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- Gaussian: identity
- Binomial: logit, probit

1. Response variable - distribution family

- Bernoulli - Binomial
- Poisson
- Gamma
- etc

2. Predictors (continuous or categorical)

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

1. Response variable - distribution family

- Bernoulli - Binomial
- Poisson
- Gamma
- etc

2. Predictors (continuous or categorical)

3. Link function

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

The modelling process

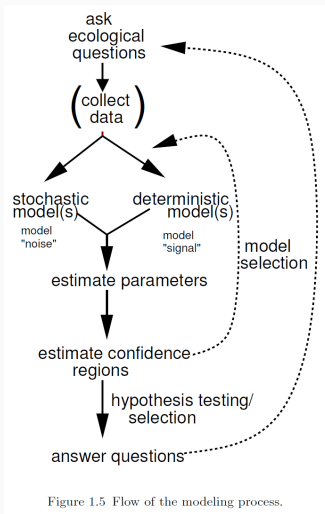


Figure 1.5 Flow of the modeling process.

Bernoulli - Binomial distribution (Logistic regression)

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

Canonical link function: **logit** (*log odds*), but others possible (see **family**)

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

Then

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

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

Where is the variance?

In a Gaussian GLM

$$y \sim \text{Normal}(\mu, \sigma)$$

In a Binomial GLM

$$y \sim \text{Binomial}(n, p)$$

n = number of trials

p = probability of success

$$\text{Var}(y) = np(1 - p)$$

(maximum variance when **p** around 0.5)

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

How many survived in each class? (*dplyr*)

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

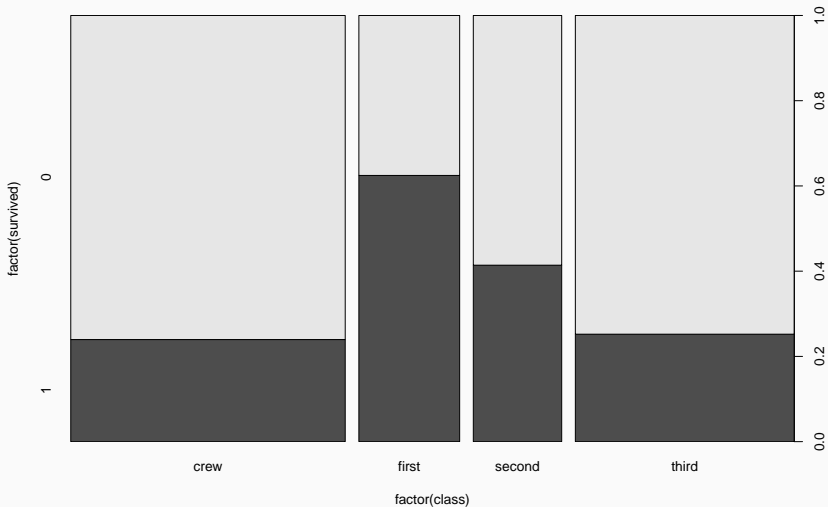
```
# A tibble: 8 x 3
```

```
# 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

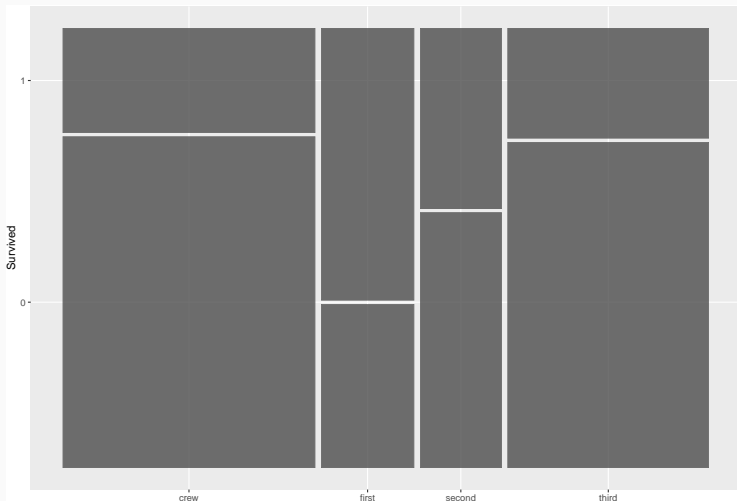
Data visualisation (mosaic plot)

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



Mosaic plots (ggplot2)

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



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

which corresponds to

$$\text{logit}(P(\text{survival})_i) = a + b \cdot \text{class}_i$$

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

Interpreting binomial GLM

```
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 ***
classecond	0.80785	0.14375	5.620	1.91e-08 ***
classtthird	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

Binomial GLM estimates are in `logit` scale!

We need to **back-transform** (apply *inverse logit*):

- Manually: `plogis`

Binomial GLM estimates are in `logit` scale!

We need to **back-transform** (apply *inverse logit*):

- Manually: `plogis`
- Automatically: `effects`, `modelbased`, etc.

Interpreting logistic regression output (effects pkg)

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

```
model: survived ~ class
```

```
class effect
```

```
class
```

	crew	first	second	third
	0.2395480	0.6246154	0.4140351	0.2521246

Interpreting logistic regression output (effects pkg)

Including confidence intervals:

```
summary(allEffects(tit.glm))
```

```
model: survived ~ class
```

```
class effect
```

```
class
```

	crew	first	second	third
	0.2395480	0.6246154	0.4140351	0.2521246

```
Lower 95 Percent Confidence Limits
```

```
class
```

	crew	first	second	third
	0.2125668	0.5706887	0.3582390	0.2214588

```
Upper 95 Percent Confidence Limits
```

```
class
```

	crew	first	second	third
	0.2687850	0.6756185	0.4721282	0.2854798

Interpreting logistic regression output (modelbased)

```
library("modelbased")  
estimate_means(tit.glm)
```

Estimated Marginal Means

class	Probability	SE	95% CI
first	0.62	0.03	[0.57, 0.68]
second	0.41	0.03	[0.36, 0.47]
third	0.25	0.02	[0.22, 0.29]
crew	0.24	0.01	[0.21, 0.27]

Marginal means estimated for class

Analysing differences among factor levels (class)

```
library("modelbased")  
estimate_contrasts(tit.glm)
```

Marginal Contrasts Analysis

Level1	Level2	Difference	95% CI	SE	df	z

first	crew	1.66	[1.30, 2.03]	0.14	Inf	11.97
first	second	0.86	[0.42, 1.29]	0.17	Inf	5.16
first	third	1.60	[1.22, 1.98]	0.14	Inf	11.11
second	crew	0.81	[0.43, 1.19]	0.14	Inf	5.62
second	third	0.74	[0.35, 1.13]	0.15	Inf	4.99
third	crew	0.07	[-0.24, 0.38]	0.12	Inf	0.58

Marginal contrasts estimated for class
p-value adjustment method: Holm (1979)

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

```
# R2 for Logistic Regression  
Tjur's R2: 0.087
```

But there are caveats (e.g. see [here](#) and [here](#))

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

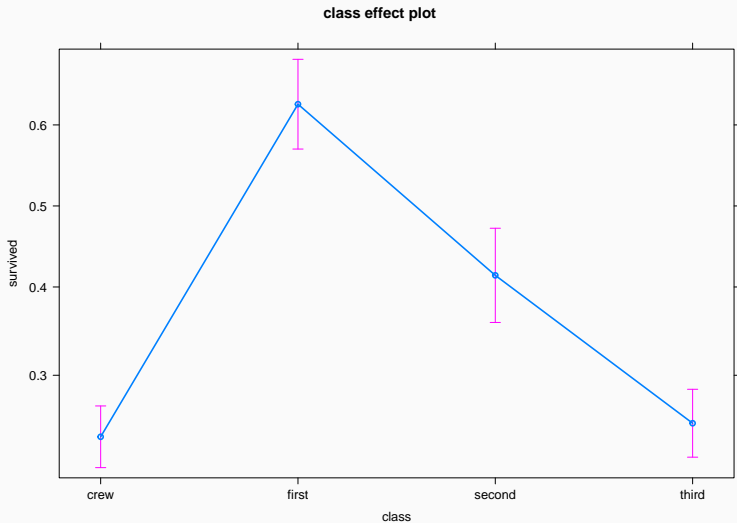
	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-1.16	0.08	-14.67	0.00
classfirst	1.66	0.14	11.97	0.00
classecond	0.81	0.14	5.62	0.00
classtthird	0.07	0.12	0.58	0.56

Presenting model results

```
library("modelsummary")  
modelsummary(tit.glm)
```

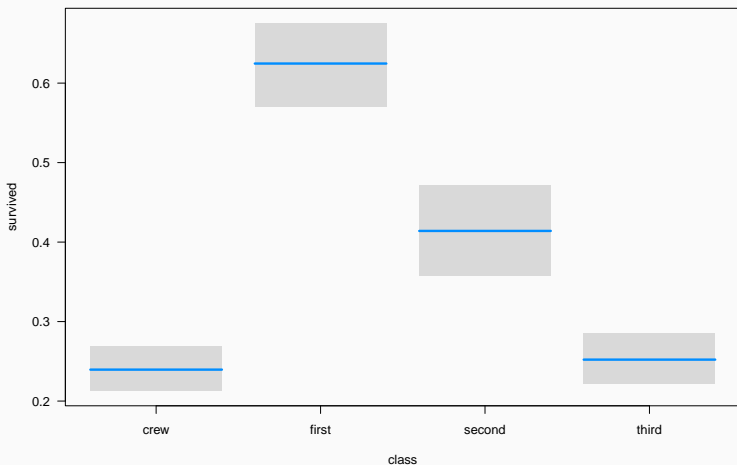
Visualising model: effects package

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



Visualising model: visreg package

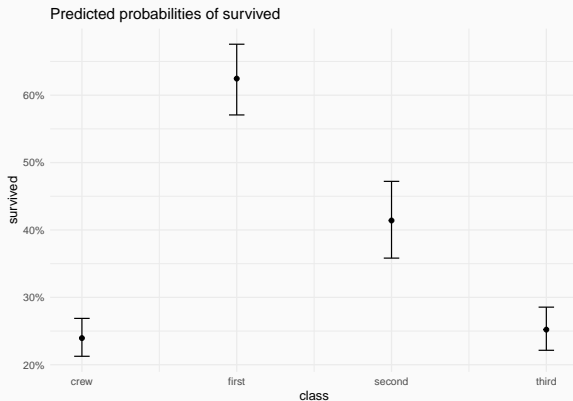
```
visreg(tit.glm, scale = "response", rug = FALSE)
```



Visualising model: sjPlot package

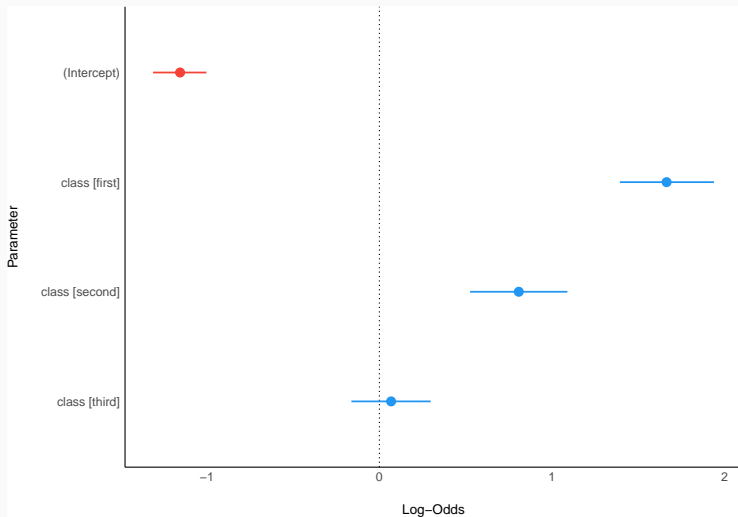
```
sjPlot::plot_model(tit.glm, type = "eff")
```

`$class`



Visualising model: see package

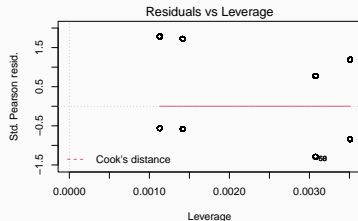
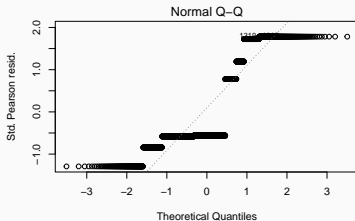
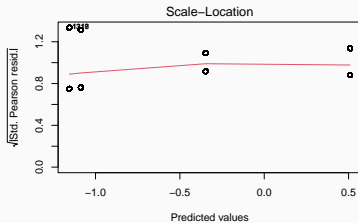
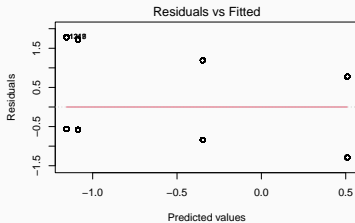
```
plot(parameters(tit.glm), show_intercept = TRUE)
```



Model checking

plot(model) not very useful with binomial GLM

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



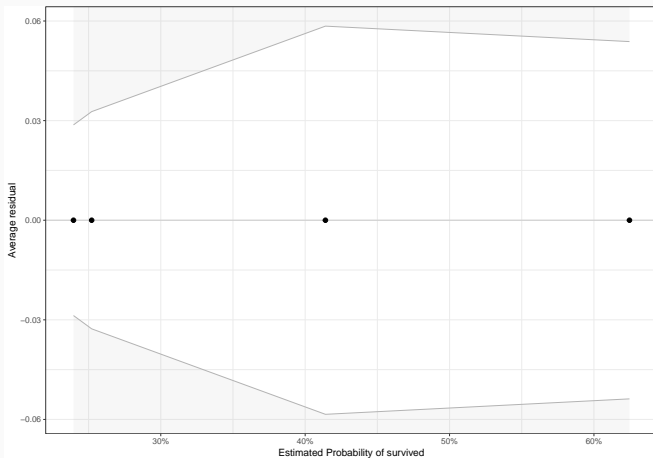
null device

1

Binned residual plots for logistic regression

```
binned_residuals(tit.glm)
```

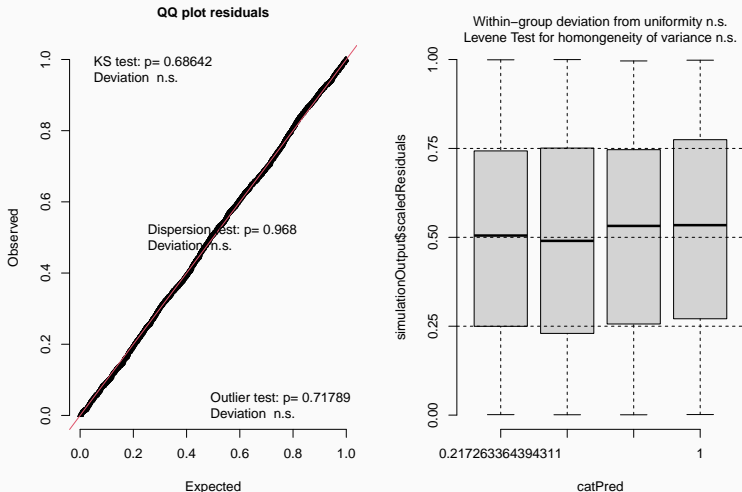
Ok: About 100% of the residuals are inside the error bounds.



Residual diagnostics with DHARMa

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

DHARMa residual diagnostics

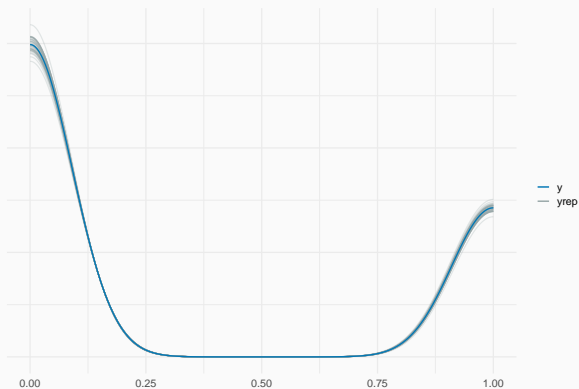


Posterior predictive checking

Simulate data from fitted model (**yrep**) and compare with observed data (**y**)

```
pp_check(tit.glm)
```

Posterior Predictive Check



1. Visualise data

Recapitulating

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

Recapitulating

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

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`)

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`...

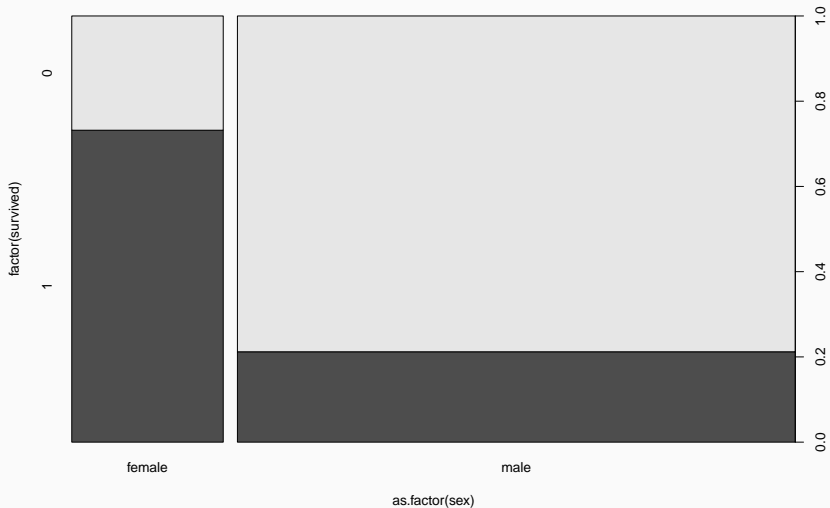
Recapitulating

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?

<https://pollev.com/franciscorod726>

First, visualise data



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

Number of Fisher Scoring iterations: 4

Model interpretation

```
model: survived ~ sex
```

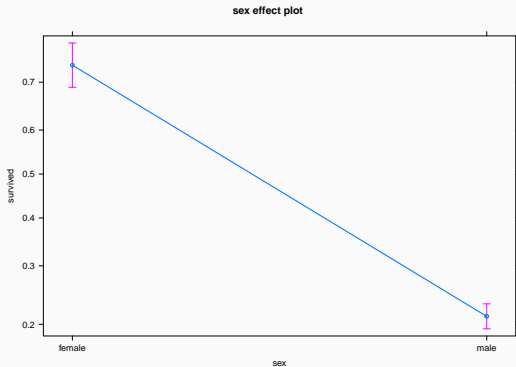
```
sex effect
```

```
sex
```

```
female
```

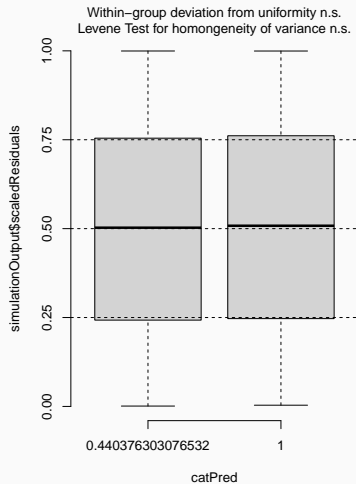
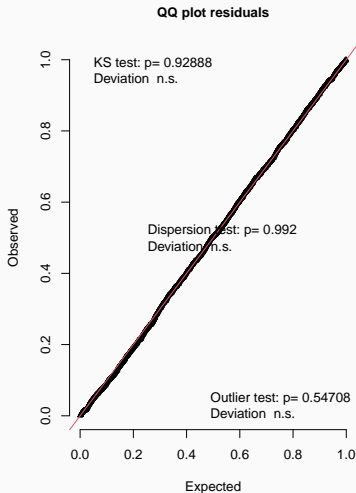
```
male
```

```
0.7319149 0.2120162
```




```
simulateResiduals(tit.sex, plot = TRUE)
```

DHARMA residual diagnostics



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

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



Let's look at the data

```
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

<https://pollev.com/franciscorod726>

Fit additive model with both factors

Call:

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

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.0915	-0.7149	-0.5012	0.7297	2.0673

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.18740	0.15747	7.541	4.68e-14 ***
classfirst	0.88081	0.15697	5.611	2.01e-08 ***
classecond	-0.07178	0.17093	-0.420	0.675
classtthird	-0.77742	0.14231	-5.463	4.69e-08 ***
sexmale	-2.42133	0.13909	-17.408	< 2e-16 ***

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

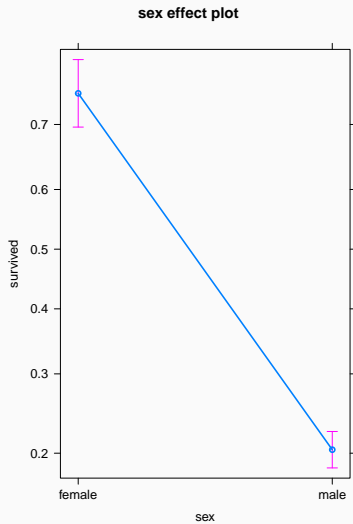
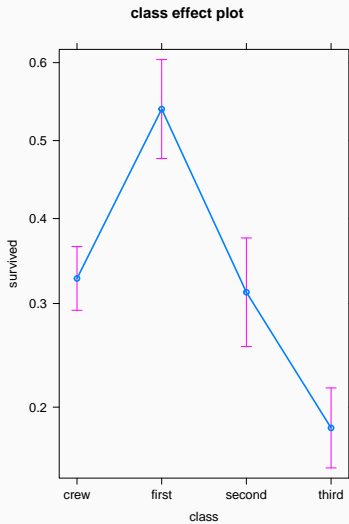
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 2769.5 on 2200 degrees of freedom

Residual deviance: 2228.9 on 2196 degrees of freedom

AIC: 2238.9

Plot additive model



Fit model with the interaction of both factors

Call:

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

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.6797	-0.7099	-0.6155	0.5115	1.9842

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.89712	0.61914	3.064	0.00218 **
classfirst	1.66535	0.80026	2.081	0.03743 *
classecond	0.07053	0.68630	0.103	0.91815
classtthird	-2.06075	0.63551	-3.243	0.00118 **
sexmale	-3.14690	0.62453	-5.039	4.68e-07 ***
classfirst:sexmale	-1.05911	0.81959	-1.292	0.19627
classecond:sexmale	-0.63882	0.72402	-0.882	0.37760
classtthird:sexmale	1.74286	0.65139	2.676	0.00746 **

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

(Dispersion parameter for binomial family taken to be 1)

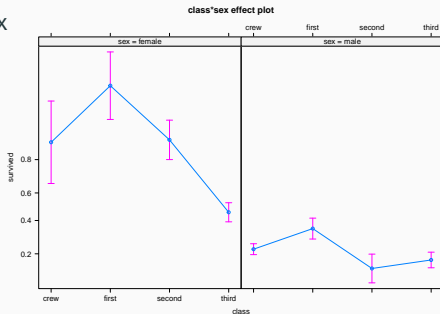
Women had higher survival than men, even within the same class

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

```
class*sex effect
```

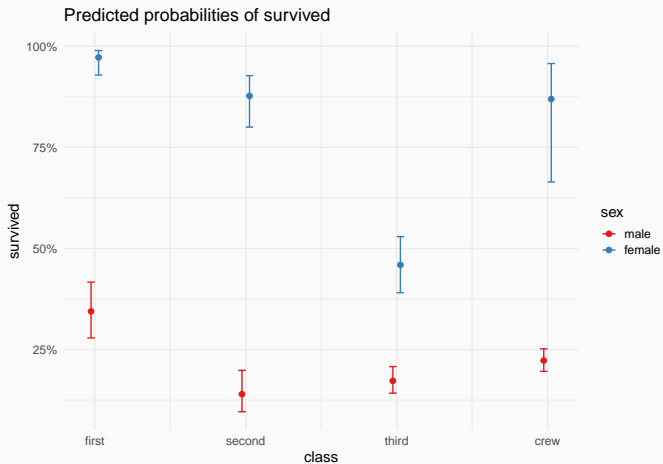
```
sex
```

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



Visualising model (sjPlot)

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



Comparing models

```
library("performance")
compare_performance(tit.sex.class.add, tit.sex.class.int)
```

Comparison of Model Performance Indices

Name	Model	AIC	BIC	Tjur's R2	RMSE	Sigma	Log_L
tit.sex.class.add	glm	2238.913	2267.396	0.248	0.405	1.007	0.
tit.sex.class.int	glm	2179.733	2225.306	0.271	0.399	0.993	0.

Comparing parameters

```
compare_parameters(tit.sex.class.add, tit.sex.class.int)
```

Parameter	tit.sex.class.add	tit.sex.class.int
(Intercept)	1.19 (0.88, 1.50)	1.90 (0.68, 3.11)
class (first)	0.88 (0.57, 1.19)	1.67 (0.10, 3.23)
class (second)	-0.07 (-0.41, 0.26)	0.07 (-1.27, 1.42)
class (third)	-0.78 (-1.06, -0.50)	-2.06 (-3.31, -0.82)
sex (male)	-2.42 (-2.69, -2.15)	-3.15 (-4.37, -1.92)
class (first) * sex (male)		-1.06 (-2.67, 0.55)
class (second) * sex (male)		-0.64 (-2.06, 0.78)
class (third) * sex (male)		1.74 (0.47, 3.02)
Observations	2201	2201

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 = binomial)
```

Call:

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

Deviance Residuals:

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

Coefficients:

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

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 671.96 on 13 degrees of freedom
Residual deviance: 491.06 on 10 degrees of freedom

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 binary data:

```
model: survived ~ class
```

class effect

class

	crew	first	second	third
	0.2395480	0.6246154	0.4140351	0.2521246

Logistic regression with continuous predictors

Example dataset: GDP and infant mortality

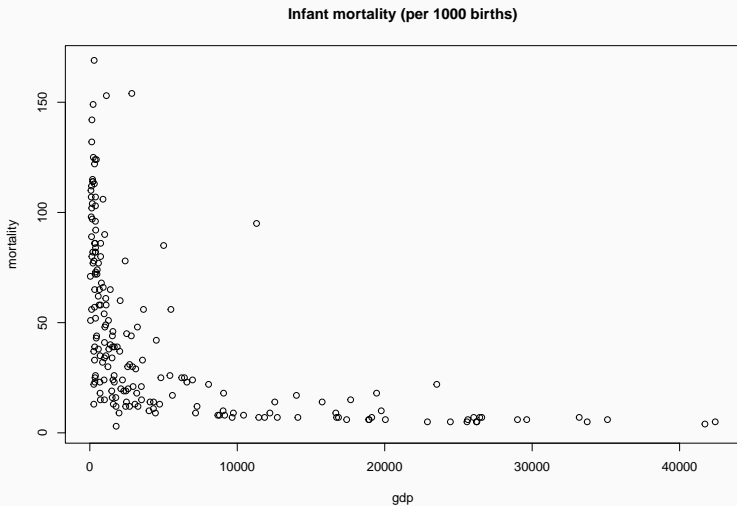
Read UN_GDP_infantmortality.csv.

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?

<https://pollev.com/franciscorod726>

Visualising data



Fit model

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

Call:

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

Null deviance: 6430.2 on 192 degrees of freedom
Residual deviance: 3530.2 on 191 degrees of freedom

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

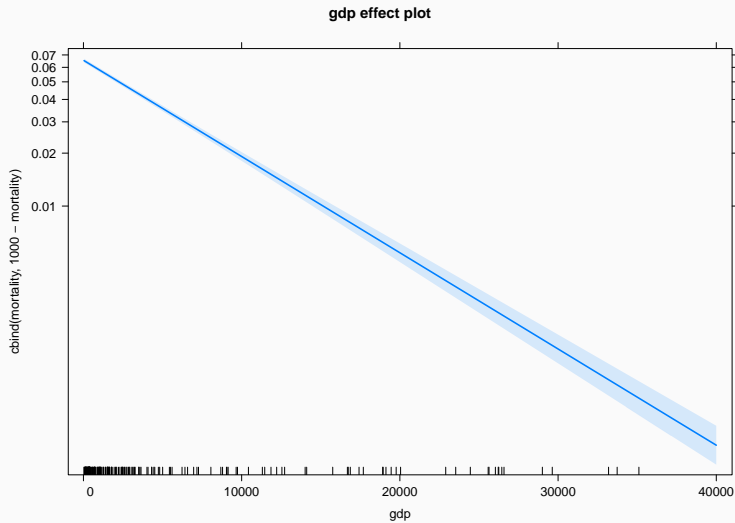
```
model: cbind(mortality, 1000 - mortality) ~ gdp
```

```
gdp effect
```

```
gdp
```

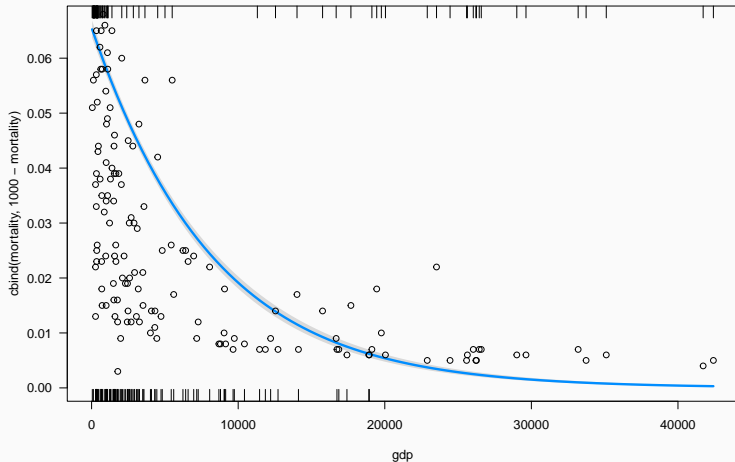
	40	10000	20000	30000	40000
	0.0652177296	0.0191438829	0.0054028095	0.0015096074	0.0004206154

Effects plot



Plot model using visreg:

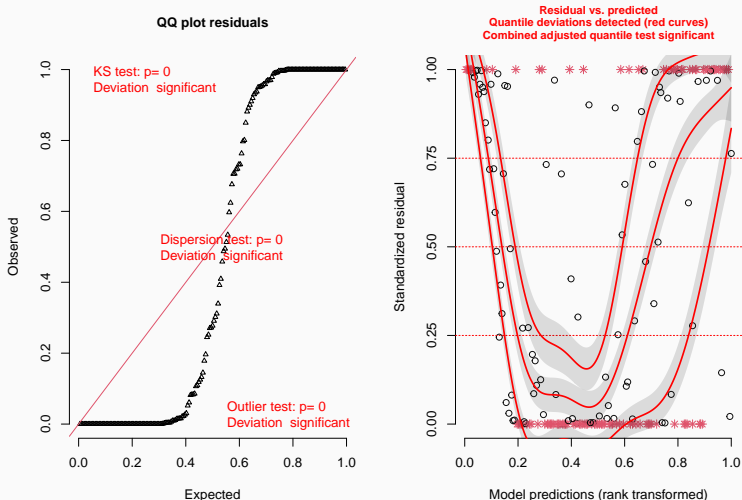
```
visreg(gdp.glm, scale = "response")  
points(mortality/1000 ~ gdp, data = gdp)
```



Residuals diagnostics with DHARMA

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

DHARMA residual diagnostics



Overdispersion

Overdispersion:

more variation in the data than assumed by statistical model

$$\text{Var}(y) = np(1 - p)$$

Testing for overdispersion (DHARMA)

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

DHARMA nonparametric dispersion test via mean deviance residuals
vs. simulated-refitted

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

`quasibinomial` allows us to model overdispersed binomial data

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 = quasibinomial,  
    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 20.7947)

Null deviance: 6430.2 on 192 degrees of freedom
Residual deviance: 3530.2 on 191 degrees of freedom

Mean estimates do not change after accounting for overdispersion

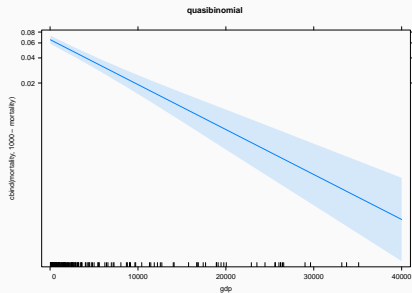
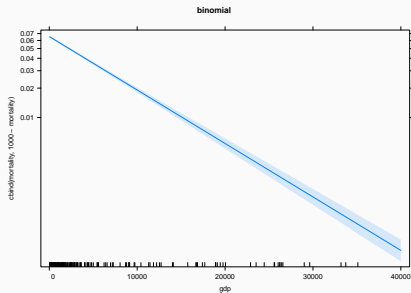
```
coef(gdp.overdisp)
```

(Intercept)	gdp
-2.6574663734	-0.0001278976

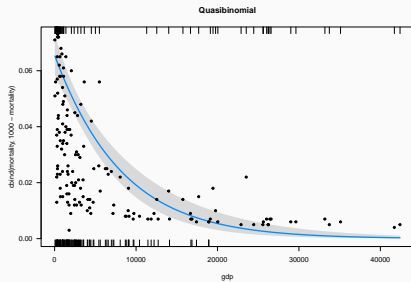
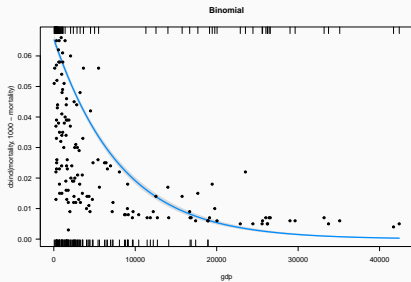
```
coef(gdp.glm)
```

(Intercept)	gdp
-2.6574663734	-0.0001278976

But standard errors (uncertainty) do!



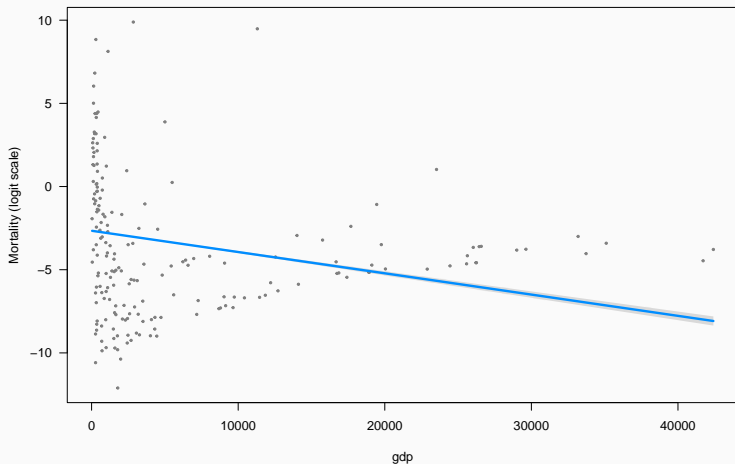
Plot model and data



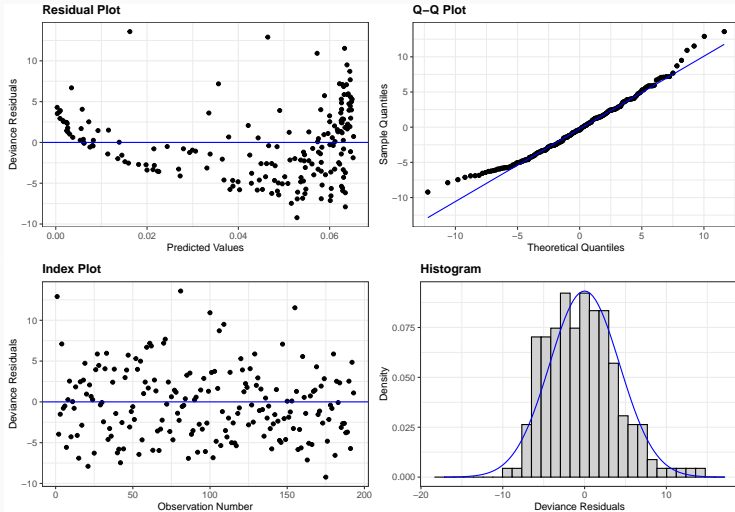
Think about the shape of
relationships

Think about the shape of relationships

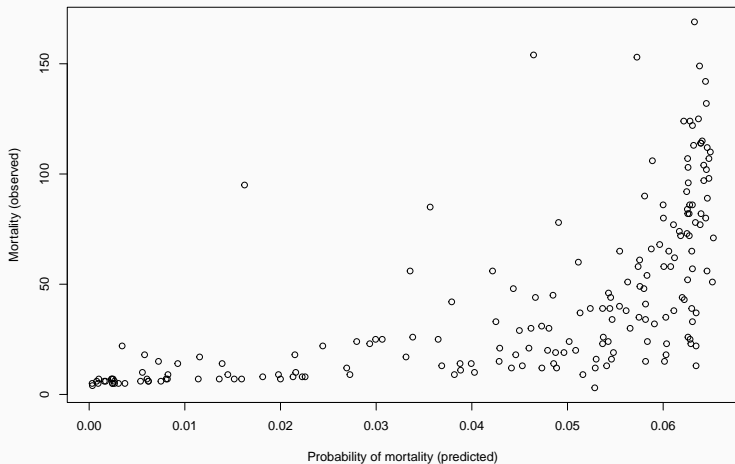
Not everything has to be linear...



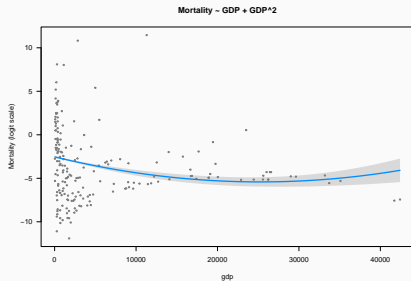
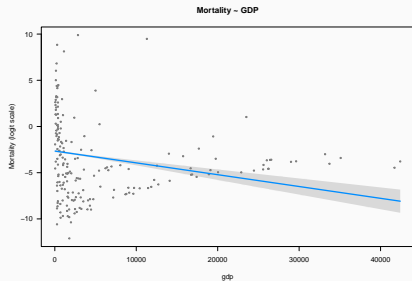
Residuals show non-linear pattern



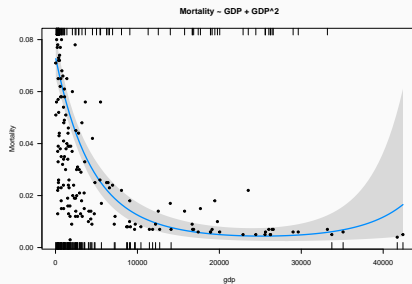
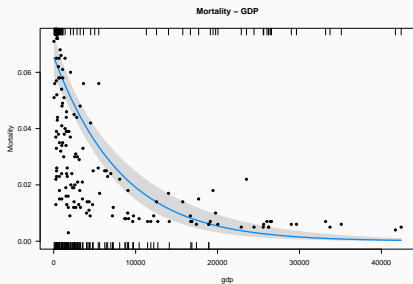
Calibration plot shows non-linear pattern



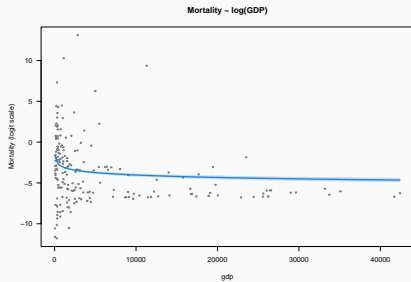
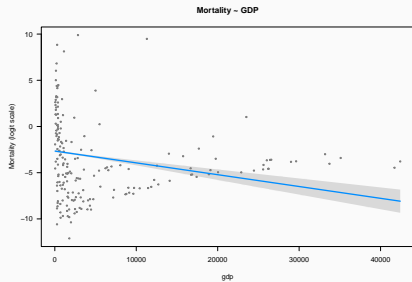
Trying polynomial predictor (GDP + GDP²)



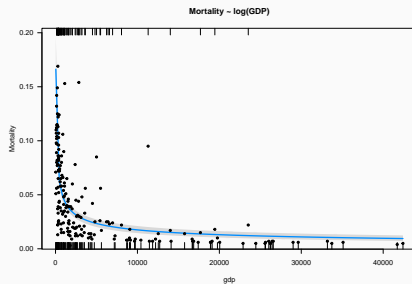
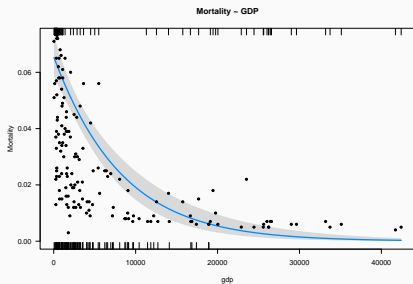
Think about the shape of relationships



Trying log(GDP)



Trying $\log(\text{GDP})$



More examples

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

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- `seedset.csv`: Comparing seed set among plants (Data from [Harder et al. 2011](#))
- `moth.csv`: Probability of moth predation on trunk trees depending on morph (light/dark) and distance to Liverpool ([Bishop 1972](#))

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- `moth.csv`: Probability of moth predation on trunk trees depending on morph (light/dark) and distance to Liverpool ([Bishop 1972](#))
- `soccer.csv`: Probability of scoring penalty depending on goalkeeper's team being ahead, behind or tied ([Roskes et al 2011](#))

Probability of scoring penalty

Data on penalty shots

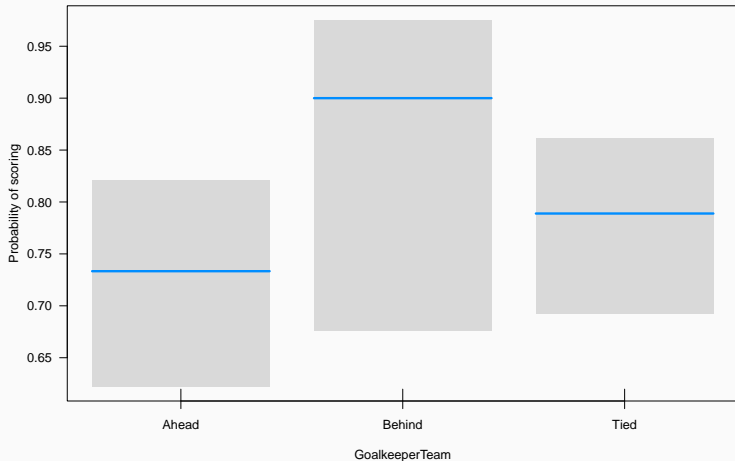
```
soccer <- read.csv("data/soccer.csv")  
soccer
```

	GoalkeeperTeam	Nshots	Scored
1	Behind	20	18
2	Tied	90	71
3	Ahead	75	55

Does probability of scoring penalty depends on match situation?

<https://pollev.com/franciscorod726>

Probability of scoring depending on match situation



Seed set among plants

Seed set among plants



Seed set among plants

```
# 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

Questions:

<https://pollev.com/franciscorod726>

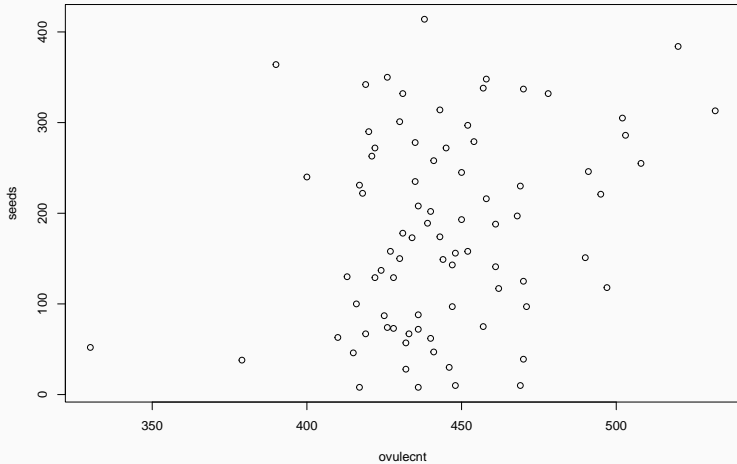
- Is seed set related to proportion of outcross pollen (pcmass)?

Questions:

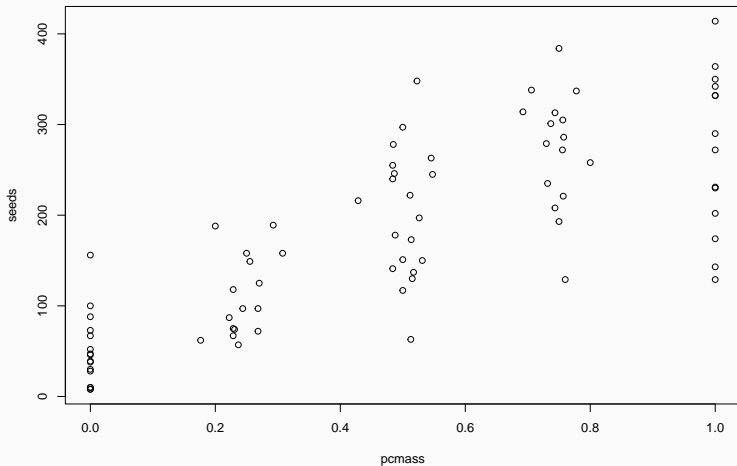
<https://pollev.com/franciscorod726>

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

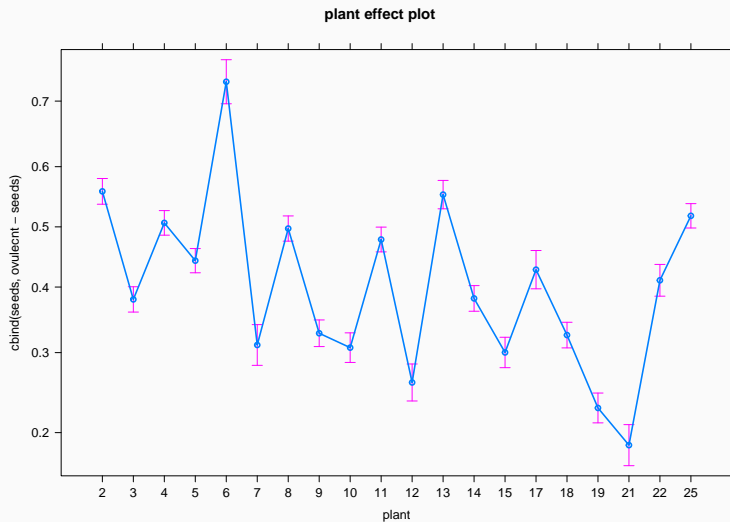
Number of seeds vs Number of ovules



Number of seeds vs Proportion outcross pollen



Seed set across plants



Seed set ~ outcross pollen

