Applied Statistical Regression
AS 2013 – Week 12

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ETH Zürich, December 2, 2013

Extending the Linear Model

What is the problem?

→ **So far, we exclusively considered continuous response variables. Now, we wish to extend this to binary and categorical response, proportions or counts!**

- This does not fit within the current framework
- Counterexamples: → see next slides

We need some additional techniques which can deal with these types of situations. Depending on how the response variable is, there are several different approaches.

Extending...: Example 1

Logistic Regression, i.e. 0/1 response:

In human medicine, we are often interested in the question for how much „dose“ of a medication we have an effect, i.e. a reduction in pain or symptoms.

Data:

Patients, where each one obtains some „dose“ and as a response, either has a reduction (1), or not (0).

There may be some further predictors such as age, sex, … that contribute towards predicting the response.

Extending...: Example 1

Logistic Regression, i.e. 0/1 response:

- A statistical model for this example takes into account that for a given “dose” resp. predictor configuration, we will only have an effect on some of the subjects, but not on all of them.

- We thus need to model the relation between the binary response and a number of predictors.

The perhaps ***simplest, but faulty approach*** is:

$$P(y_i = 1 \mid X) = \beta_0 + \beta_1 x_{i1} + \ldots + \beta x_{ip}$$

→ **This will ultimately lead to probabilities beyond [0,1]**.

Extending...: Example 1

- We obtain a better model if we transform the response variable to a scale that ranges from minus to plus infinity.

- Usual choice is the so-called ***logit transformation***:

$$p \mapsto \log(p/(1-p))$$

We obtain the ***logistic regression model***:

$$\log\left(\frac{P(y_i=1|X)}{1-P(y_i=1|X)}\right)=\beta_0+\beta_1 x_{i1}+\ldots+\beta x_{ip}$$

→ **all fitted values are within [0,1]**.

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Extending...: Example 2

Poisson Regression

What are predictors for the locations of starfish?

→ analyze the number of starfish at several locations, for which we also have some covariates such as water temperature, ...

→ the response variable is a count. The simplest model for this assumes a Poisson as the conditional distribution.

We assume that the parameter λ_i at location *i* depends in a linear way on the covariates:

$$y_i \mid X \sim Pois(\lambda_i), \text{ where } \log(\lambda_i) = \beta_0 + \beta_1 x_{i1} + \ldots + \beta_p x_{ip}$$

Extending...: Example 3

Log-Linear-Models

Question:

Prediction of a nominal response variable

Example:

Which party does a person favor, depending on covariates such as education, age, sex, region, …

→ such data can be summarized with contingency tables

→ and they can be modeled using log-linear models

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Generalized Linear Models

What is it?

- General framework for regression type modeling
- Many different response types are allowed
- Notion: the responses' conditional expectation has a monotone relation to a linear combination of the predictors.

$$E[Y_i \mid X] = g(\beta_0 + \beta_1 x_{i1} + ... + \beta_p x_{ip})$$

- Some further requirements on variance and density of Y

→ **may seem complicated, but is very powerful!**

Binary Logistic Regression

What is it?

- Response $Y_i \in \{0,1\}$

What do we need to take care of?

- Formulation of the model
- Estimation
- Inference
- Model diagnostics
- Model choice

Example

Premature Birth, by Hubbard (1986)

$y_i \in \{0,1\}$ survival (1) / death (0) after premature birth.

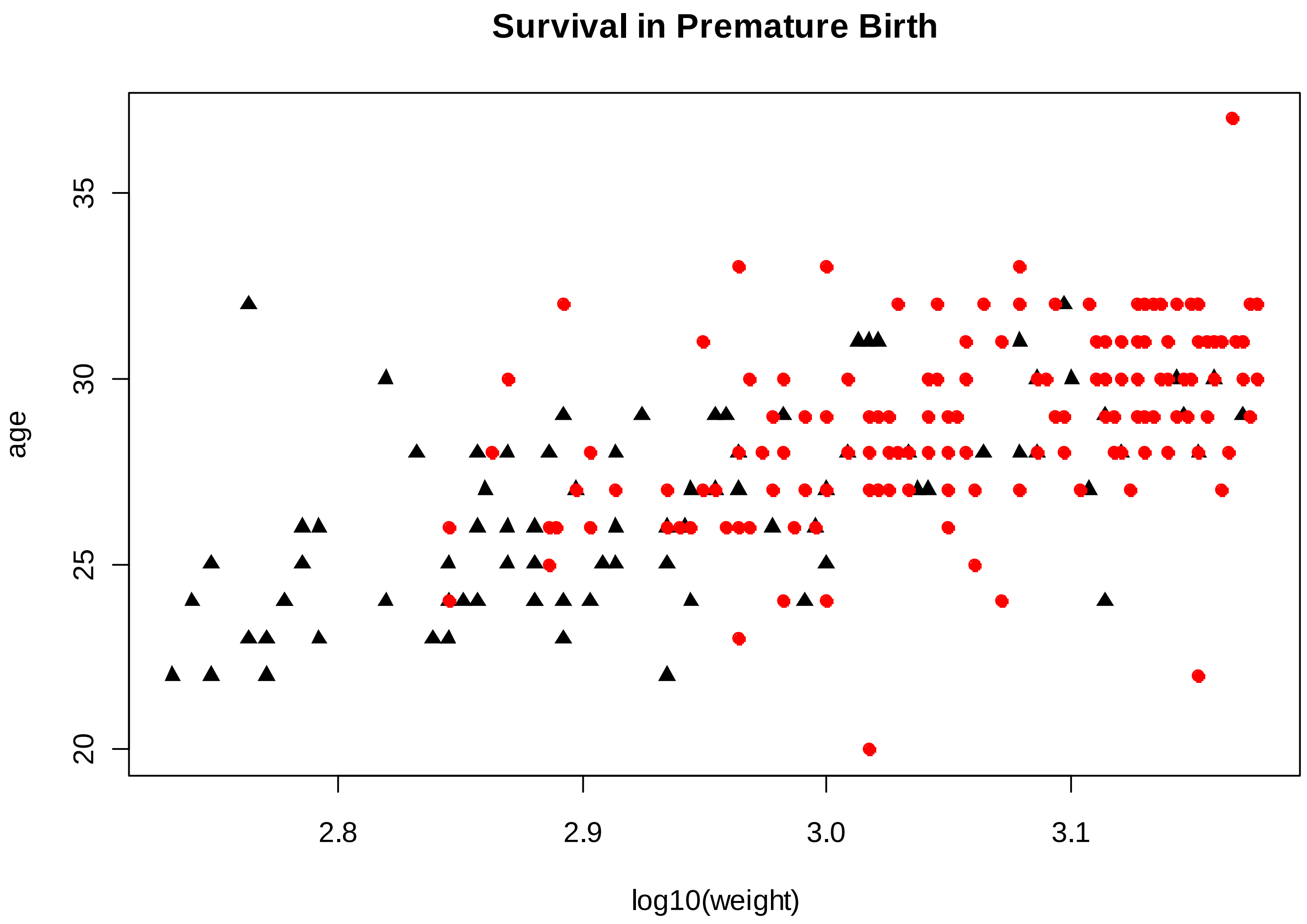
Predictors:

- weight (in grams) at birth
- age at birth (in weeks of pregnancy)
- apgar scores (vital function after 1 and 5 min)
- pH-value of the blood (breathing)

Observations:

- there are 247 instances

Example


Survival in Premature Birth
age
20
25
30
35
2.8
2.9
3.0
3.1
log10(weight)

Logistic Regression Model

- $y_i \in \{0,1\}$ has a Bernoulli distribution.
- The parameter of this distribution is p_i, the success rate

Now please note that:

$$p_i = P(y_i = 1 | X) = E[y_i | X]$$

→ the most powerful notion of the logistic regression model is to see it as a model where we try to find a relation between the conditional expected value of y_i and the predictors!

Important: $P(y_i = 1) = \beta_0 + \beta_1 x_{i1} + ... + \beta x_{ip}$ is no good here!

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Logit Transformation

Goal: mapping from $[0,1] \mapsto (-\infty, +\infty)$

Logit transformation: $g(p) = \log\left(\dfrac{p}{1-p}\right)$

Interpretation: probabilities are mapped to logged odds ("Wettverhältnisse") which can then be modeled linearly.

$$\log\left(\frac{P(y_i = 1 \mid X)}{1 - P(y_i = 1 \mid X)}\right) = \beta_0 + \beta_1 x_{i1} + \ldots + \beta x_{ip}$$

→ where is the error term?

...

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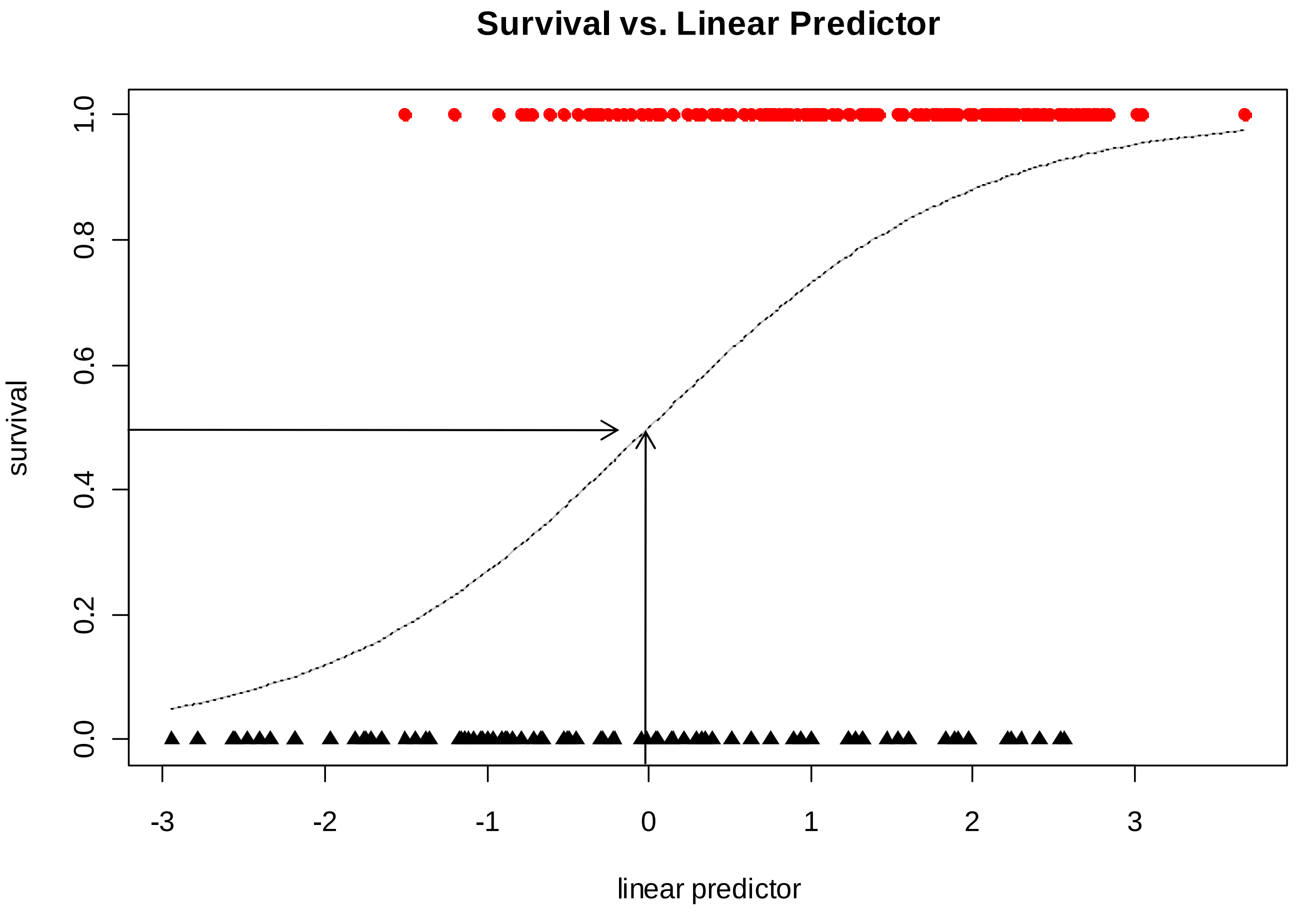
Some Remarks

- For estimating the regression coefficients, we require the observations to be independent.
- There is no restriction for the predictors. They can be continuous, categorical, transformed, interactions, …
- $\eta_i = \beta_0 + \beta_1 x_{i1} + ... + \beta_p x_{ip}$ is called the linear predictor
- $g(\cdot)$ is the link function, mapping from $E[y_i \mid X]$ to η_i
- **There are other (less important) link functions:**
  - *probit link*
  - *c-log-log link*

Survival vs. Linear Predictor

- $g\left(P(y=1 \mid \log_{10}(weight), age)\right) = -33.97 + 10.17 \cdot \log_{10}(weight) + 0.14 \cdot age$



Estimation

Multiple linear regression:

→ *minimize sum of squared residuals!*

can be solved in closed form

Logistic regression:

→ *maximum likelihood approach!*

leads to a non-linear equation system that needs to be solved with an iterative approach by weighted multiple linear regressions.

Important:

→ seems like a very different paradigm, but is it?

Interpretation of the Coefficients

→ see blackboard…

Summary Output from R

```
> summary(glm(survival ~ I(log10(weight)) + age,
              family  = "binomial", data = baby)

Deviance Residuals: ...

Coefficients:     Estimate Std. Error z value Pr(>|z|)
(Intercept)      -33.97108    4.98983  -6.808 9.89e-12 ***
I(log10(weight))  10.16846    1.88160   5.404 6.51e-08 ***
age                0.14742    0.07427   1.985   0.0472 *
---
Null deviance: 319.28  on 246  degrees of freedom
Residual deviance: 235.94  on 244  degrees of freedom
AIC: 241.94
```

Inference: Individual Parameter Tests

Multiple Linear Regression:

Gaussian errors → $\hat{\beta}_j$ are normally distributed

Logistic Regression:

There are no errors, variability arises from Bernoulli distribution

The regression coefficients $\hat{\beta}_j$ are only approximately normally distributed with a covariance matrix V that can be derived from the coefficients.

Hence: $Z = \dfrac{\hat{\beta}_j - \beta_j}{\sqrt{\hat{V}_{jj}}} \sim N(0,1)$

Inference: Global Tests with GLMs

There are three tests, two can be done with logistic regression:

- **Goodness-of-fit test**
  - based on comparing against the saturated model
  - not suitable for non-grouped, binary data
- **Comparing two hierarchical models**
  - likelihood ratio test leads to deviance differences
  - test statistics has an asymptotic Chi-Square distribution
- **Global test**
  - comparing versus an empty model with only an intercept
  - this is a nested model, take the null deviance

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Goodness-of-Fit

Multiple Linear Regression:

Sum of Squared Residuals

Logistic Regression:

Residual Deviance

$$D(y, \hat{p}) = -2\sum_i (y_i \log(\hat{p}_i) + (1-y_i)\log(1-\hat{p}_i))$$

- based on the log-likelihood
- in principle: comparison against fully saturated model
- for logistic regression, there is no formal test here

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Comparing Hierarchical Models

Model 1: small model S, with q parameters

Model 2: big model B, with p parameters

Null hypothesis and test statistic:

$$H_0 : \beta_{q+1} = \beta_{q+2} = ... = \beta_p = 0$$

$$2\left(ll^{(B)} - ll^{(S)}\right) = D\left(y, \hat{p}^{(S)}\right) - D\left(y, \hat{p}^{(B)}\right)$$

Distribution of the test statistic:

$$D^{(S)} - D^{(B)} \sim \chi^2_{p-q}$$

Example with drop1()

```
> drop1(fit, test="Chisq")
Single term deletions
Model: survival ~ I(log10(weight)) + age
                 Df Deviance    AIC    LRT   Pr(Chi)
<none>                235.94 241.94
I(log10(weight))  1   270.19 274.19 34.247 4.855e-09 ***
age               1   239.89 243.89  3.948   0.04694 *
```

Question:

- where is the difference to the summary output?
- it exists, though it‘s not obvious and asymptotically vanishes

AIC and Variable Selection

General remark:

All comparison between models of different size can also be done using the AIC criterion. Not only in logistic regression, but also here.

The criterion:

$$AIC = D(y_i, \hat{p}) + 2p$$

Variable selection:

- stepwise approaches as with multiple linear regression
- factor variables need to be treated the right way!

Null Deviance

Smallest model:

- The smallest model is without predictors, only with intercept
- Fitted values will all be equal to $\hat{\pi}_0$
- Our best fit (F) and the smallest model (0) are nested

A global test:

$$2\left(ll^{(F)} - ll^{(0)}\right) = D\left(y, \hat{p}^{(0)}\right) - D\left(y, \hat{p}^{(F)}\right)$$

Example and "Quick Check": → see blackboard...

```
Null deviance: 319.28  on 246  degrees of freedom
Residual deviance: 235.94  on 244  degrees of freedom
```

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Model Diagnostics

Diagnostics are:

- in principle as important with logistic regression as they are with multiple linear regression models
- again based on differences between fitted & observed values

→ we now have to take into account that the variances are not equal for the different instances.

→ we have to come up with novel types of residuals:

Pearson and **Deviance residuals**

Pearson Residuals

Take the difference between observed and fitted value and divides by an estimate of the standard deviation:

$$R_i = \frac{y_i - \hat{p}_i}{\sqrt{\hat{p}_i(1-\hat{p}_i)}}$$

→ R_i^2 is the contribution of the *ith* observation to the Pearson statistic for model comparison.

→ It is important to note that Pearson residuals exceeding a value of two in absolute value warrant a closer look

Deviance Residuals

Take the contribution of the i*th* observation to the log-likelihood, i.e. the chi-square statistic for model comparison.

$$d_i = \left(y_i \cdot \log(\hat{p}_i) + (1-y_i) \cdot \log(1-\hat{p}_i) \right)$$

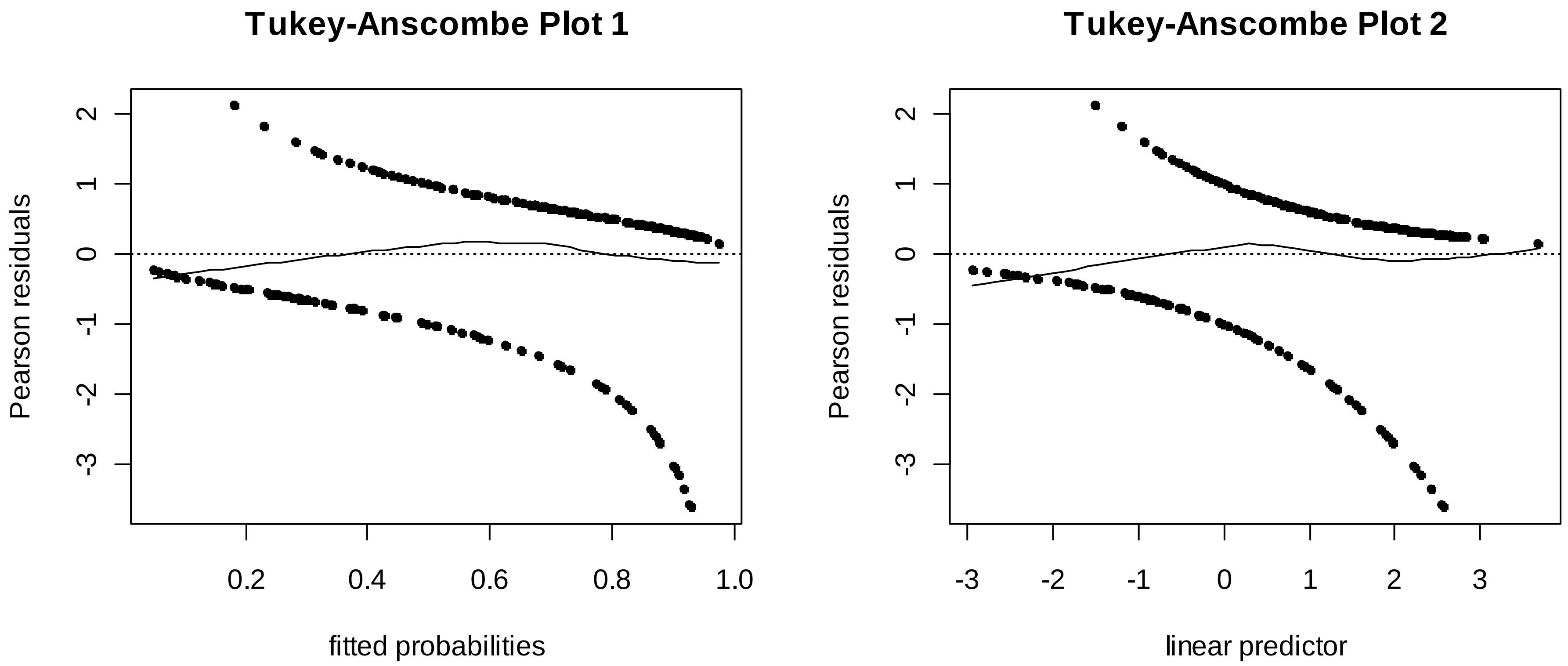
For obtaining a well interpretable residual, we take the square root and the sign of the difference between true and fitted value:

$$D_i = sign(y_i - \hat{\pi}_i) \cdot \sqrt{d_i}$$

→ - *deviance residuals > 2 warrant a closer look*.
- *the distribution of the deviance residuals is not known*.

Tukey-Anscombe Plot

Remark: sometimes studentized residuals are used!



Tukey-Anscombe Plot

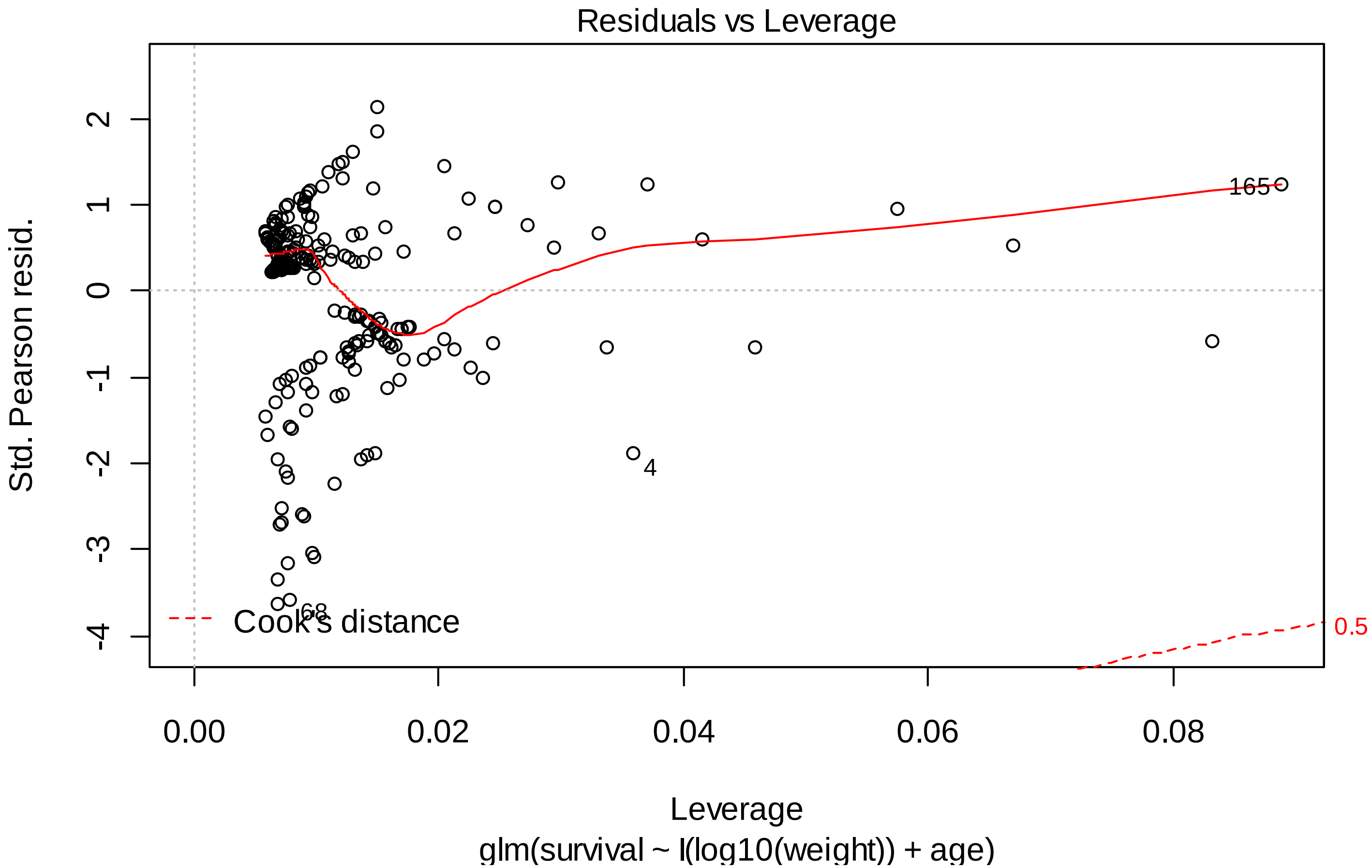
The Tukey-Anscombe plots in R are not perfect. Better use:

```
xx <- predict(fit, type="response")
yy <- residuals(fit, type="pearson")
loess.smooth(xx, yy, family="gaussian", pch=20)
abline(h=0, lty=3)
```

Reasons:

- using a non-robust smoother is a must
- different types of residuals can be used
- on the x-axis: probs or linear predictor

More Diagnostics



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Binomial Regression Models

Concentration in log of mg/l	Number of insects n_i	Number of killed insects y_i
0.96	50	6
1.33	48	16
1.63	46	24
2.04	49	42
2.32	50	44

→ for the number of killed insects, we have $y_i \sim Bin(n_i, p_i)$

→ we are mainly interested in the proportion of insects surviving

→ these are grouped data: there is more than 1 observation for a given predictor setting

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Model and Estimation

The goal is to find a relation:

$$p_i = P(y_i = 1 | X) \sim \eta_i = \beta_0 + \beta_1 x_{i1} + \ldots + \beta_p x_{ip}$$

We will again use the logit link function such that $\eta_i = g(p_i)$

$$\log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + \beta_1 x_{i1} + \ldots + \beta_p x_{ip}$$

Here, p_i is the expected value $E[y_i / n_i]$, and thus, also this model here fits within the GLM framework. The log-likelihood is:

$$l(\beta) = \sum_{i=1}^{k} \left[\log\binom{n_i}{y_i} + n_i y_i \log(p_i) + n_i (1-y_i) \log(1-p_i) \right]$$

Fitting with R

We need to generate a two-column matrix where the first contains the “successes” and the second contains the “failures”

```
> killsurv
     killed surviv
[1,]      6     44
[2,]     16     32
[3,]     24     22
[4,]     42      7
[5,]     44      6
```

```
> fit <- glm(killsurv~conc, family="binomial")
```

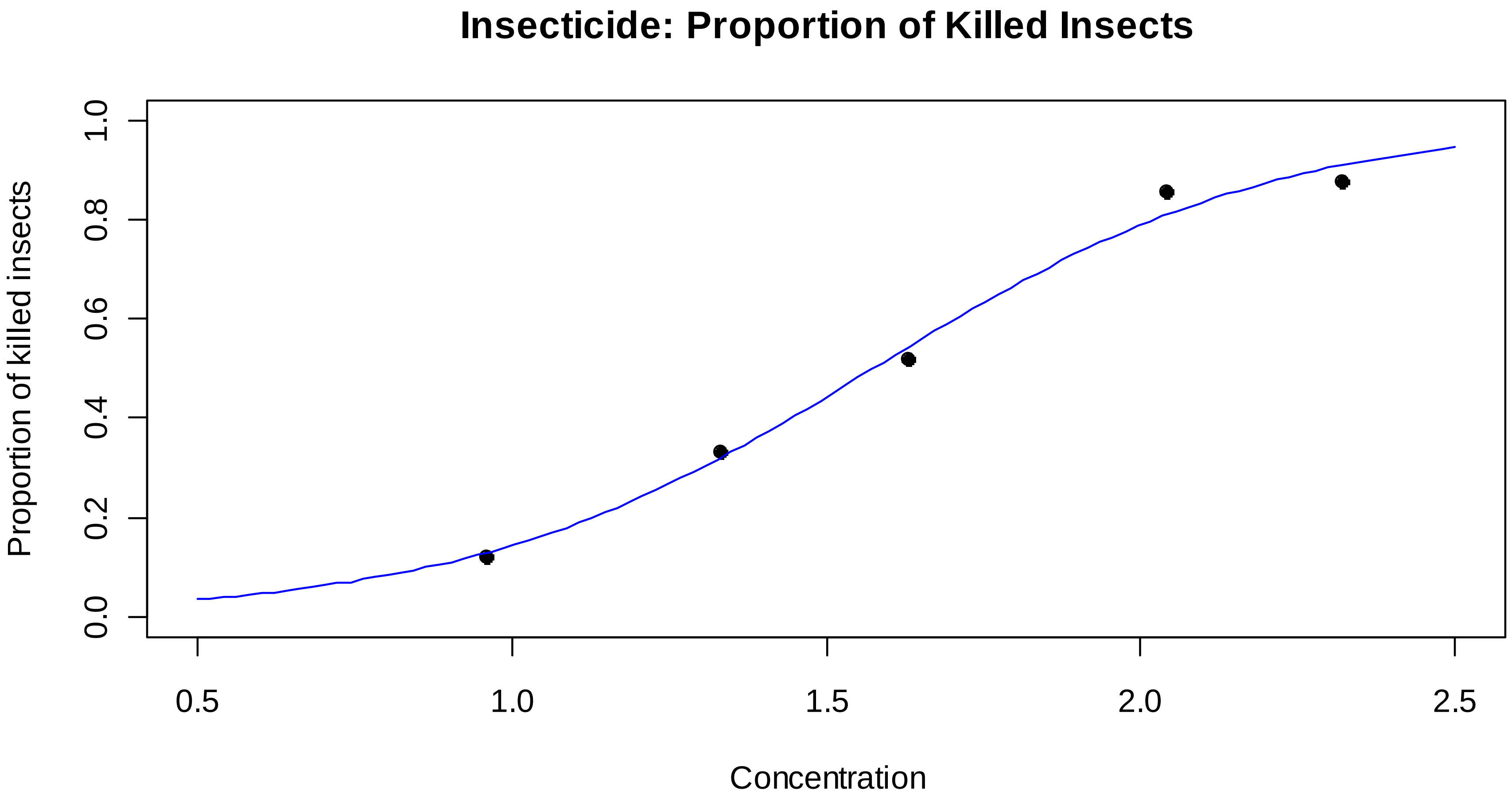
Summary Output

The result for the insecticide example is:

```
> summary(glm(killsurv ~ conc, family = "binomial")

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -4.8923     0.6426  -7.613 2.67e-14 ***
conc          3.1088     0.3879   8.015 1.11e-15 ***
---
Null deviance: 96.6881  on 4  degrees of freedom
Residual deviance:  1.4542  on 3  degrees of freedom
AIC: 24.675
```

Proportion of Killed Insects



Global Tests for Binomial Regression

For GLMs there are three tests that can be done:

- **Goodness-of-fit test**
  - based on comparing against the saturated model
  - not suitable for non-grouped, binary data
- **Comparing two hierarchical models**
  - likelihood ratio test leads to deviance differences
  - test statistics has an asymptotic Chi-Square distribution
- **Global test**
  - comparing versus an empty model with only an intercept
  - this is a nested model, take the null deviance

Goodness-of-Fit Test

→ **the residual deviance will be our goodness-of-fit measure!**

Paradigm: take twice the difference between the log-likelihood for our current model and the saturated one, which fits the proportions perfectly, i.e. $\hat{p}_i = y_i / n_i$

$$D(y,\hat{p}) = 2\sum_{i=1}^{k}\left[y_i \log\left(\frac{y_i}{\hat{y}_i}\right) + (n_i - y_i)\log\left(\frac{(n_i - y_i)}{(n_i - \hat{y}_i)}\right)\right]$$

Because the saturated model fits as well as any model can fit, the deviance measures how close our model comes to perfection.

Evaluation of the Test

Asymptotics:

If Y_i is truly binomial and the n_i are large, the deviance is approximately χ^2 distributed. The degrees of freedom is:

$$k - (\#\ of\ \ predictors) - 1$$

```
> pchisq(deviance(fit), df.residual(fit), lower=FALSE)
[1] 0.69287
```

Quick and dirty:

$Deviance \gg df$: → model is not worth much.
More exactly: check $df \pm 2\sqrt{df}$

→ only apply this test if at least all $n_i \geq 5$

Overdispersion

What if $Deviance \gg df$ **???**

1) Check the structural form of the model

- model diagnostics
- predictor transformations, interactions, …

2) Outliers

- should be apparent from the diagnostic plots

3) IID assumption for p_i **within a group**

- unrecorded predictors or inhomogeneous population
- subjects influence other subjects under study

Overdispersion: a Remedy

We can deal with overdispersion by estimating:

$$\hat{\phi} = \frac{X^2}{n-p} = \frac{1}{n-p} \cdot \sum_{i=1}^{n} \frac{(y_i - n_i \hat{p}_i)^2}{n_i \hat{p}_i (1-\hat{p}_i)}$$

This is the sum of squared Pearson residuals divided with the df

Implications:

- regression coefficients remain unchanged
- standard errors will be different: inference!
- need to use an F-test for comparing nested models

Results when Correcting Overdispersion

```
> phi <- sum(resid(fit)^2)/df.residual(fit)
> phi
[1] 0.4847485
> summary(fit, dispersion=phi)
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -4.8923     0.4474  -10.94   <2e-16 ***
conc          3.1088     0.2701   11.51   <2e-16 ***
---
(Dispersion parameter taken to be 0.4847485)
Null deviance: 96.6881  on 4  degrees of freedom
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AIC: 24.675
```

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Testing Hierarchical Models / Global Test

For binomial regression, these two tests are conceptually equal to the ones we already discussed in binary logistic regression.

→ *We refer to our discussion there and do not go into further detail here at this place!*

Null hypothesis and test statistic:

$$H_0 : \beta_{q+1} = \beta_{q+2} = \ldots = \beta_p = 0$$

$$2\left(ll^{(B)} - ll^{(S)}\right) = D\left(y, \hat{p}^{(S)}\right) - D\left(y, \hat{p}^{(B)}\right)$$

Distribution of the test statistic:

$$D^{(S)} - D^{(B)} \sim \chi^2_{p-q}$$