

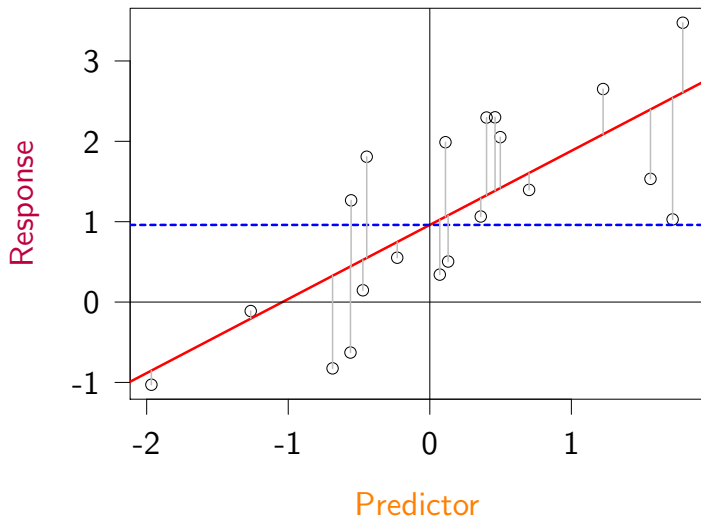
Generalized Linear Models (GLMs)

May 17, 2018

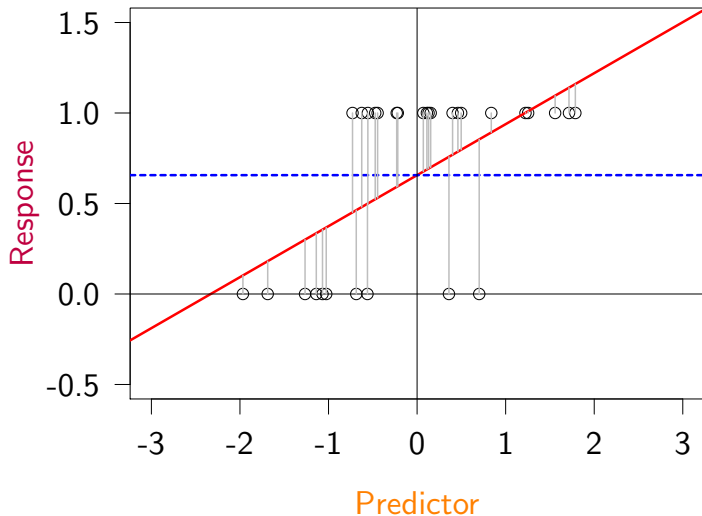
1 Linear model, reminder

A simple linear model

$$\text{Response} = \text{Intercept} + \text{Slope} \times \text{Predictor} + \text{Error}$$



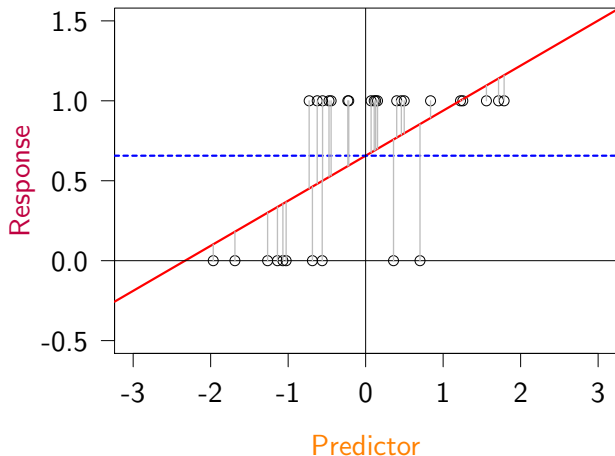
A simple linear model failure: binary data



Linear model basic assumptions

- Linear combination of parameters (including transformation, polynoms, interactions. . .)
Risk: biologically meaningless
- Predictor not perfectly correlated
Risk: Model won't run, unstable convergence, or huge SE
- Little error in predictors
Risk: bias estimates (underestimate with Gaussian error)
- Gaussian error distribution
Risk: Poor predictions
- Homoscedasticity (constant error variance)
Risk: Over-optimistic uncertainty, unreliable predictions
- Independence of error
Risk: Bias and over-optimistic uncertainty

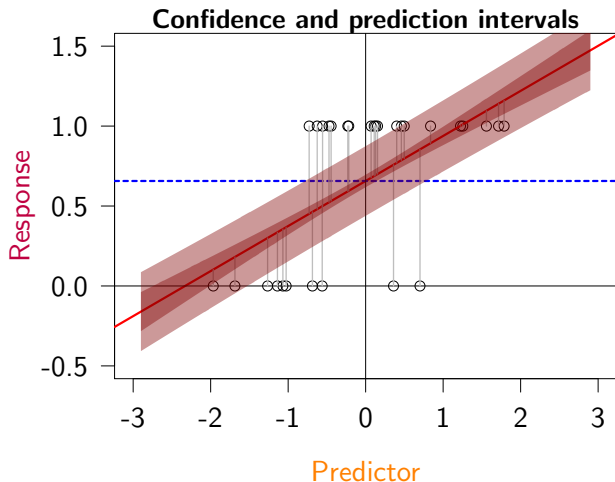
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Assumptions violated:

Non-Gaussian errors, non-constant error variance, correlated errors

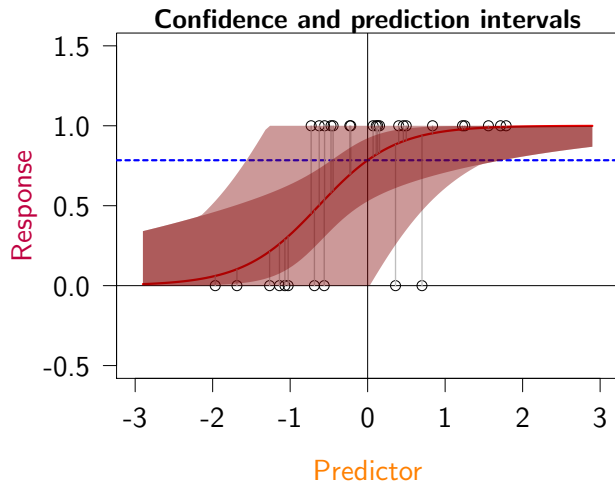
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Practical consequences:

Non-sensical predictions, wrong confidence-interval and p-value, extrapolation
ALWAYS fails

What we want our model to do



Good features:

Never out of $[0,1]$, variable uncertainty, non-linear trend, close fit

That is what a Generalized Linear Model does

Vocabulary warning

- General Linear Model (=linear model with several responses, multivariate)
- **Generalized Linear Model (=non-normal errors, and uncertainty dependent on the mean)**

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What a GLM is:

- 1 A linear function ($y = \mu + \beta x \dots$)
- 2 A probability distribution (Bernoulli, Binomial, Poisson...)
- 3 A "link function" to convert between the scale of the linear function ($-\infty$ to $+\infty$) and the scale of the data and the probability distribution (often positive integer: 0, 1, 2, 3...)

A GLM fits a continuous expected response; we observe discrete realizations

Logistic regression

- Binary or proportion data (survival, presence/absence. . .)
- Binomial probability distribution (= Bernouilly if binary data)
- Link function often logit: $y = \log\left(\frac{\text{probability}}{1-\text{probability}}\right)$
- Back-transformation inverse-logit: $\text{probability} = \frac{1}{1+\exp(-y)}$
- Linear function $y = \text{intercept} + \text{slope}_1\text{predictor}_1 + \text{slope}_2\text{predictor}_2 + \dots$

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Binomial (and Bernouilli distribution in R):

```
bernouilli_random_sample <- rbinom(n = 10000, size = 1, prob = 0.3)
hist(bernouilli_random_sample)
mean(bernouilli_random_sample); 0.3
var(bernouilli_random_sample); 0.3*(1-0.3)
```

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```

Logistic regression in R:

```
glm(formula = obs ~ 1 + x, family = "binomial", data=data)
```

Exercise

- 1 Load `survivalsize.csv`
- 2 Plot survival data. What kind of distribution is it?
- 3 Fit a linear model and a logistic model with intercept only. How to interpret the estimate?
- 4 Fit a linear regression and a logistic regression of survival on relative size, compare the output
- 5 Check the diagnostic plots for both models. Should you be worried?
- 6 Extract and visualize a model prediction from both models (use the function `predict`, and/or do it by hand to practice link-function back-transformation)

Logistic regression: trivia

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- logit and inverse-logit functions in boot and mixtools packages
- $\exp(\text{slope})$ is an odd-ratio
- GLMs on binary data are more (or equally) powerful than proportion data

Poisson regression

- Count data
- Poisson distribution
- Link function: logarithm
- Inverse link function: exponential
- Linear function $y = \textit{intercept} + \textit{slope}_1 \textit{predictor}_1 + \textit{slope}_2 \textit{predictor}_2 + \dots$

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Poisson distribution in R:

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poisson_random_sample <- rpois(n = 10000, lambda = 4)
hist(poisson_random_sample)
mean(poisson_random_sample)
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Poisson regression in R:

```
glm(formula = obs ~ 1 + x, family = "poisson", data = data)
```

Poisson regression

Exercise

- 1 Load the data reproduction.csv
- 2 Plot reproduction data, calculate the mean and variance.
- 3 Overlay a Gaussian distribution of same mean and variance, does it fit?
- 4 Fit and compare a lm and a Poisson glm of reproduction on size
- 5 Check the diagnostic plots for both models. Should you be worried?
- 6 Extract and visualize a model prediction from both models (use the function predict, and/or do it by hand to practice link-function back-transformation)
- 7 Before GLMs, researchers used to log-transform the data and fit linear models. What are the problems with this approach?

Poisson regression: over-dispersion

Sadly, simple Poisson models are almost always wrong in natura

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 - ▶ Quasi-Poisson (multiplicative over-dispersion)

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- **You should NEVER use `glm(family = poisson)` again!**

Poisson regression: over-dispersion demonstrated

```
set.seed(123) # random seed
x <- rnorm(100) # predictor with no effect
y <- exp(-1 + rnorm(100, 0, 2)) # variation of unknown origin
obs <- sapply(y, FUN = function(y){
  rpois(n = 1, lambda = y)}) # generate Poisson data

#plot(x, obs) # visualize data
glm2 <- glm(obs ~ x, family = "poisson") #fit Poisson regression
sglm2 <- summary(glm2) #look at the summary
sglm2$coefficients[2,4] # the p-value
```

```
[1] 1.25526e-49
```

```
glm2q <- glm(obs ~ x, family = "quasipoisson") #quasiPoisson regression
sglm2q <- summary(glm2q) #summary
sglm2q$coefficients[2,4] # p-value
```

```
[1] 0.09476039
```

Poisson regression: over-dispersion demonstrated

Maybe just bad luck?

Exercise

Write a for loop to look at the distribution of p-values

```
set.seed( )  
poisson_pvalues <- vector(length = 1000)  
quasipoisson_pvalues <-  
for(i in )  
{  
  simulation + poisson and quasipoisson GLMs  
}  
hist( )  
mean( <0.05)
```

If time allows:

- Jensen inequality
- Poisson model in MCMCglmm