Week 6: Further GLM Topics

MATH-516 Applied Statistics

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Section 1

Logistic vs. Log-linear Model

Logistic vs. Log-linear Model

If Y is binary, then there is a certain equivalence between logistic and log-linear models:

- let $Z = (Z_1, \ldots, Z_p)^\top$ be all other variables
- the logistic model `Y~Z` is equivalent to the log-linear model `freq~Y*Z+(Z)^p`
  - `Y*Z` are interactions between Y and all $Z_1, \ldots, Z_p$
  - `(Z)^p` denotes the full interaction term between all $Z_1, \ldots, Z_p$
- coefficients of the logistic model are exactly those corresponsing to `Y*Z` in the log-linear model
  - including standard errors and everything else ... this is because the extra parameters of the log-linear model are fitting counts and they can be shown asymptotically independent of those that fit probabilities
- logistic regression pushes frequencies out of consideration, it does not care about the distribution of Z's or their relationship
  - which we also often do not care about, so using logistic can be the simpler way to go

Logistic vs. Log-linear Model

- interpretation is the same in terms of probabilities (odds and odds ratios), but interpretation of the whole model is slightly different - the difference between the two types of asymptotics
  - what can we predict?
- when Y wouldn't be binary, the log-linear model `freq~Y*Z+(Z)^p` would be equivalent to the *proportional odds model* (a multi-class generalization of logistic regression)
  - and including three-way interactions including Y in the log-linear model would lead to a more general model (with non-proportional odds)

Example: Premier League Data

```
Call:
glm(formula = score ~ (home_flag * covid)^2, family = poisson,
    data = Data)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.7509  -1.5890  -0.2788   0.5635   4.4586

Coefficients:
                 Estimate Std. Error z value Pr(>|z|)
(Intercept)       0.23309    0.03518   6.626 3.45e-11 ***
home_flag         0.19401    0.04751   4.084 4.43e-05 ***
covid1            0.06115    0.05655   1.081   0.2796
covid2            0.03331    0.05704   0.584   0.5592
home_flag:covid1 -0.18620    0.07851  -2.372   0.0177 *
home_flag:covid2 -0.04622    0.07754  -0.596   0.5511
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for poisson family taken to be 1)

    Null deviance: 3624.8  on 2799  degrees of freedom
Residual deviance: 3600.9  on 2794  degrees of freedom
AIC: 8597.7

Number of Fisher Scoring iterations: 5
```

```
Call:
glm(formula = home_flag ~ covid, family = binomial, data = Data2)

Deviance Residuals:
   Min      1Q  Median      3Q     Max
-1.261  -1.241   1.096   1.115   1.174

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.19401    0.04751   4.084 4.43e-05 ***
covid1      -0.18620    0.07851  -2.372   0.0177 *
covid2      -0.04622    0.07754  -0.596   0.5511
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 5367.5  on 3883  degrees of freedom
Residual deviance: 5361.8  on 3881  degrees of freedom
AIC: 5367.8

Number of Fisher Scoring iterations: 3
```

What the models predict:

- Poisson (a.k.a. log-linear): how many goals will be scored in a given match
- binomial (a.k.a. logistic): was a given goal scored at home or away

Example: Premier League Data

- the log-linear model targets goal frequencies
  - the intercept and the two `covid`-related coefs estimate expected baseline (away and before covid) goals
  - the other three coefficients show how the expected goals change when we move home or into/past covid
    - $e^{0.19} \approx 1.21$ is the proportional change in the expected number of goals when a team plays at home as opposed to playing away ... frequency interpretation
    - $e^{0.19} \approx 1.21$ is the odds of scoring at home against scoring away before covid ... probability interpretation
- the logistic model targets probabilities of goal being scored away/home
  - the intercept provides the baseline (before covid) probability of a goal being scored at home
    - $e^{0.19} \approx 1.21$ is the odds of success (scoring at home) against failure (scoring away) before covid ... the only and arguably a bit weird interpretation
  - the `covid`-related coefs show how the probability of a goal being scored at home changes when we move into/past covid

Section 2

Uncertainty Quantification in GLMs

Confidence Interval

- $\sqrt{N}(\widehat{\beta} - \beta) \to \mathcal{N}_p(0, I^{-1}(\theta))$ [Wald]
  - the Fisher information matrix can be consistently estimated, then...
  - easy to obtain CIs for any β_j
  - easy to obtain CI for $c^\top \beta$ for any $c \in \mathbb{R}^p$
- $2[\ell(\widehat{\beta}) - \ell(\beta)] \to \chi^2_p$ [LR]
  - invert numerically to obtain confidence region for the whole beta β
  - similarly invert the model-submodel test to obtain confidence regions for some entries of β

Question: How to build prediction intervals for GLMs?

Graph of GLM

$$\begin{tikzcd} & \mu_n \arrow[dr, bend left, "g"] & \\ \theta_n \arrow[ur, bend left, "b'"] \arrow[rr, phantom, "\underset{\text{for } g \text{ canonical}}{=}"] & & \eta_n = X_n^\top \beta \end{tikzcd}$$

- asymptotic Gaussianity for β and hence for η_n
  - on the linear predictor scale, things are roughly Gaussian
- unless g is identity (which makes sense only for the Gaussian linear model), no Gaussianity for the modelled mean μ_n
  - no Gaussianity on the response scale

Prediction Interval

- new observation $(Y_\star, X_\star)^\top$ with $Y_\star$ unknown
- goal: construct interval $(L_{Y_\star}, U_{Y_\star})$ depending on the fitted GLM and $X_\star$ such that $P\big(Y_\star \in (L_{Y_\star}, U_{Y_\star})\big) = 1 - \alpha$
- [Wald] provides $(L_{\eta_\star}, U_{\eta_\star})$ such that $P(\eta_\star \in (L_{\eta_\star}, U_{\eta_\star})) = 1 - \alpha$
- $\Rightarrow P(\mu_\star \in (g^{-1}(L_{\eta_\star}), g^{-1}(U_{\eta_\star}))) = 1 - \alpha$
- if $Y_\star$ is distributed according to a certain distribution, the prediction interval is given by quantiles of that distribution
- $\Rightarrow$ run $(g^{-1}(L_{\eta_\star}), g^{-1}(U_{\eta_\star}))$ through the quantile function (of the response distribution estimated by the GLM) and report the minimum and maximum value as the prediction interval $(L_{Y_\star}, U_{Y_\star})$
  - this is conservative, but it is not easy to do better because, unlike Gaussian linear models, other GLMs do not have distribution of the "error" independent of that of $\widehat{\eta}_n$
    - also, we should take $1 - \alpha/4$ quantiles for both distributions to apply Bonferroni correction
  - replace this step by Monte Carlo?
- prediction intervals are fairly useless for binary data, there CI for $\eta_\star$ or for $\mu_\star$ (obtained by the Delta method) is enough

Sources of Uncertainty in Prediction

1. uncertainty in the model
2. uncertainty in the model parameters
3. uncertainty in the new observation

- we try to remove source 1 by careful model building and diagnostics
  - we act like if we have succeeded
- sources 2 and 3 are independent for Gaussian linear model, but not for other GLMs
  - and we don't know what the form of the dependence is, so we conservatively take the worst case
- Monte Carlo simulation?
  - often people simulate only from the fitted model (i.e. parametric bootstrap), but that ignores source 2 of uncertainty
  - simulating for given $X_\star$ the whole $\beta \mapsto \eta_\star \mapsto \mu_{star} \mapsto$ "new sample" path by starting from the asymptotic distribution of β is better for moderate/low sample sizes

Section 3

GLMs for Positive Response

Main Areas for GLM

There are three exemplary situations where a (Gaussian) linear model is inadequate:

- binary response
  - Bernoulli distribution is the only viable one
  - but still, the GLM can be wrong, e.g. due to overdispersion
- frequency (count) response
  - Poisson distribution is arguably the most natural one
  - negative binomial distribution is another option
    - related to overdispersed Poisson
    - has a quadratic variance function
- continuous positive response
  - many options for the response distribution here...

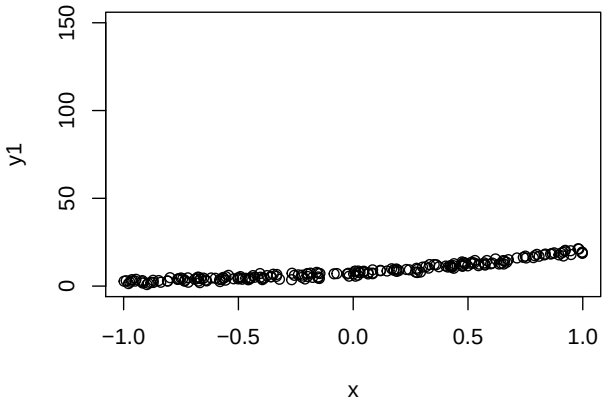
Positive Response

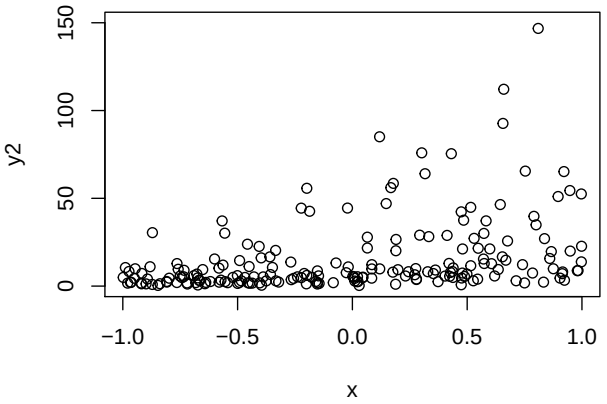
Several exponential family options for the response distribution:

1. Gaussian modelled as a GLM with a log-link
   - here the response can be technically negative
2. log-normal
   - take a logarithm of the response and model it as Gaussian
3. Gamma
4. inverse-Gaussian

Gaussian with a log-link vs. log-normal

```
N <- 200; set.seed(517)
x <- runif(N,-1,1)
beta0 <- 2; beta1 <- 1 #intercept and slope
y1 <- rnorm(N) + exp(beta0+beta1*x)
y2 <- exp(rnorm(N)+beta0+beta1*x)
plot(x,y1,ylim=c(0,150)); plot(x,y2,ylim=c(0,150))
```





Some Fun on Stack Exchange

How to specify a lognormal distribution in the glm family argument in R?

Asked 11 years ago Modified 1 year, 5 months ago Viewed 50k times

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Simple question: How to specify a lognormal distribution in the GLM family argument in R? I could not find how this can be achieved. Why is lognormal [redacted] not an option in the family argument?

[redacted]

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Lognormal is not an option because the log-normal distribution is not in the exponential family of distributions. Generalized linear models can only fit distributions from the exponential family.

I'm less clear why exponential is not an option, as the exponential distribution *is* in the exponential family (as you might hope). [redacted]

11 The lognormal is in the exponential family - it even says so in the very link you gave! See the second sentence here, and see this table, right above "Inverse Gaussian", [redacted]

Do you have a reference for the statement that "Generalized linear models can only fit distributions from the exponential family"? – Henrik May 13, 2018 at 11:20

I would think that the people who wrote `glm` would have checked the validity of this before including the option `family=gaussian(link=log)`. – abalter Mar 5, 2020 at 19:28

@abalter `family=gaussian(link=log)` is not the same as lognormal regression. This is using the link function on the mean value as the log. Not to be confused with a log transformation of the response. – Therkel Dec 13, 2021 at 10:06

Distribution of a Positive Response

Recall that in exponential family: $\mathrm{var}(Y) = \varphi V(\mathbb{E}Y)$

- $V(\cdot)$ is the variance function

Gaussian with a log-link	log-normal	Gamma	inverse-Gaussian
$Y \sim \mathcal{N}(\cdot,\cdot)$	$\log(Y) \sim \mathcal{N}(\cdot,\cdot)$	$Y \sim \Gamma(\cdot,\cdot)$	$Y \sim IG(\cdot,\cdot)$
$\log(\mathbb{E}Y) = X^\top\beta$	$\mathbb{E}\log(Y) = X^\top\beta$	$\mathbb{E}Y = \frac{1}{X^\top\beta}$	$\mathbb{E}Y = \frac{1}{\sqrt{X^\top\beta}}$
$V(\mathbb{E}y) = 1$	$V(\mathbb{E}Y) = \mathbb{E}Y$	$V(\mathbb{E}Y) = (\mathbb{E}Y)^2$	$V(\mathbb{E}Y) = (\mathbb{E}Y)^3$

Example: Permeability of Building Materials

- permeabilty (time needed for water particles to get through a material) of 81 sheets produced on 3 different machines over 9 days measured
- 2 factors as regressors (day and machine)
  - does permeability differ for the different machines?
  - does day matter?
- we will use log-links for all the model to facilitate the same interpretation

```
library(GLMsData)
data(perm)
perm$Day <- as.factor(perm$Day)
fit1_loglink <- glm(Perm ~ Mach * Day, data=perm,
                    family=gaussian(link="log"))
fit2_lognormal <- lm(log(Perm) ~ Mach * Day, data=perm)
fit3_gamma <- glm(Perm ~ Mach * Day, data=perm,
                  family=Gamma(link="log"))
fit4_igauss <- glm(Perm ~ Mach * Day, data=perm,
                   family=inverse.gaussian(link="log"))
```

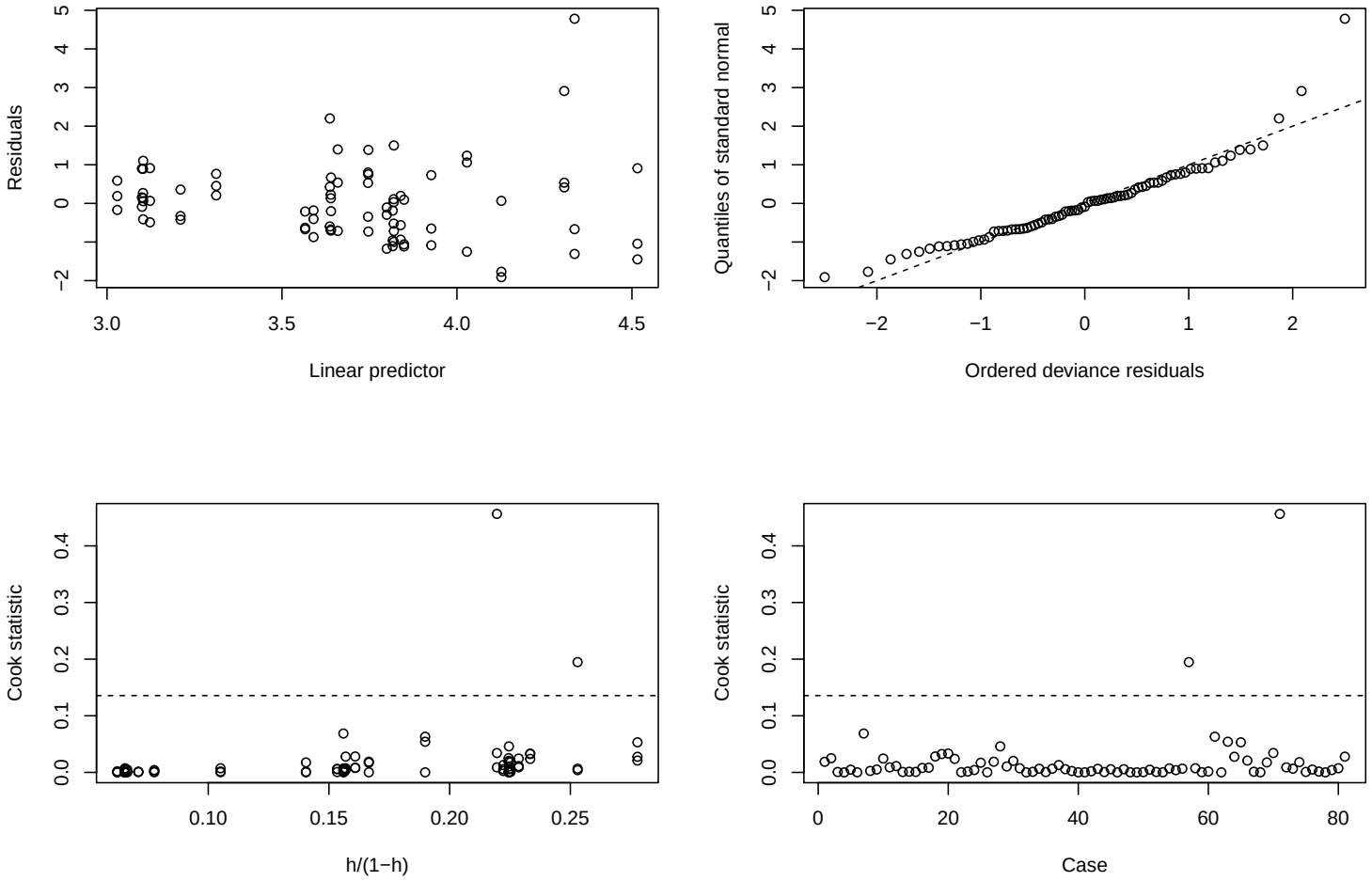
Example: Permeability of Building Materials

- aiming for simplicity, model-submodel tests lead us to the following models:
  - notice how day matters in only two of them

```
fit1_loglink <- glm(Perm ~ Mach + Day, data=perm,
                    family=gaussian(link="log"))
fit2_lognormal <- lm(log(Perm) ~ Mach, data=perm)
fit3_gamma <- glm(Perm ~ Mach + Day, data=perm,
                  family=Gamma(link="log"))
fit4_igauss <- glm(Perm ~ Mach, data=perm,
                   family=inverse.gaussian(link="log"))
```

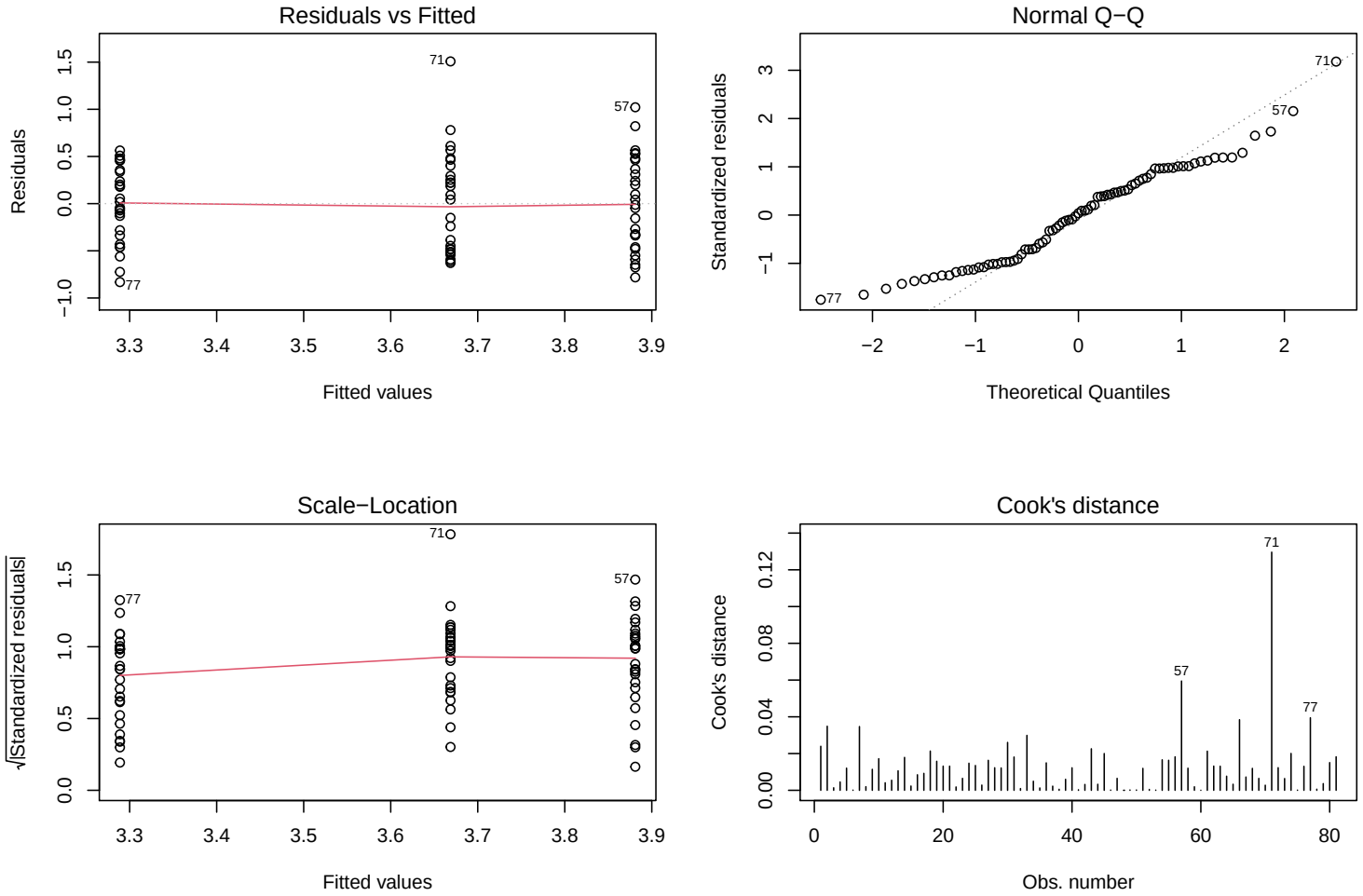
Example: Permeability of Building Materials

```
library(boot)
glm.diag.plots(fit1_loglink)
```



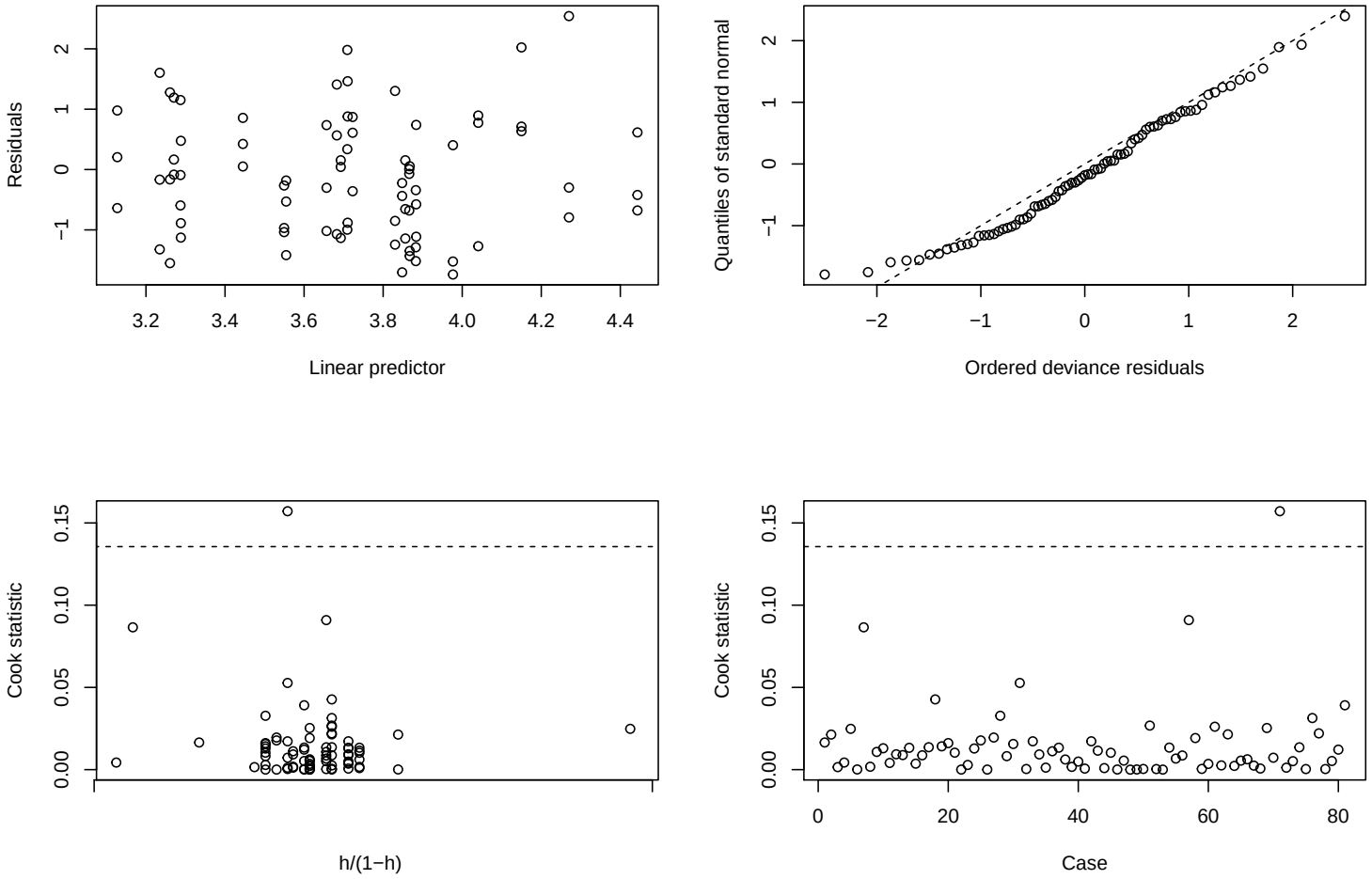
Example: Permeability of Building Materials

```
par(mfrow=c(2,2))
plot(fit2_lognormal,1:4)
```



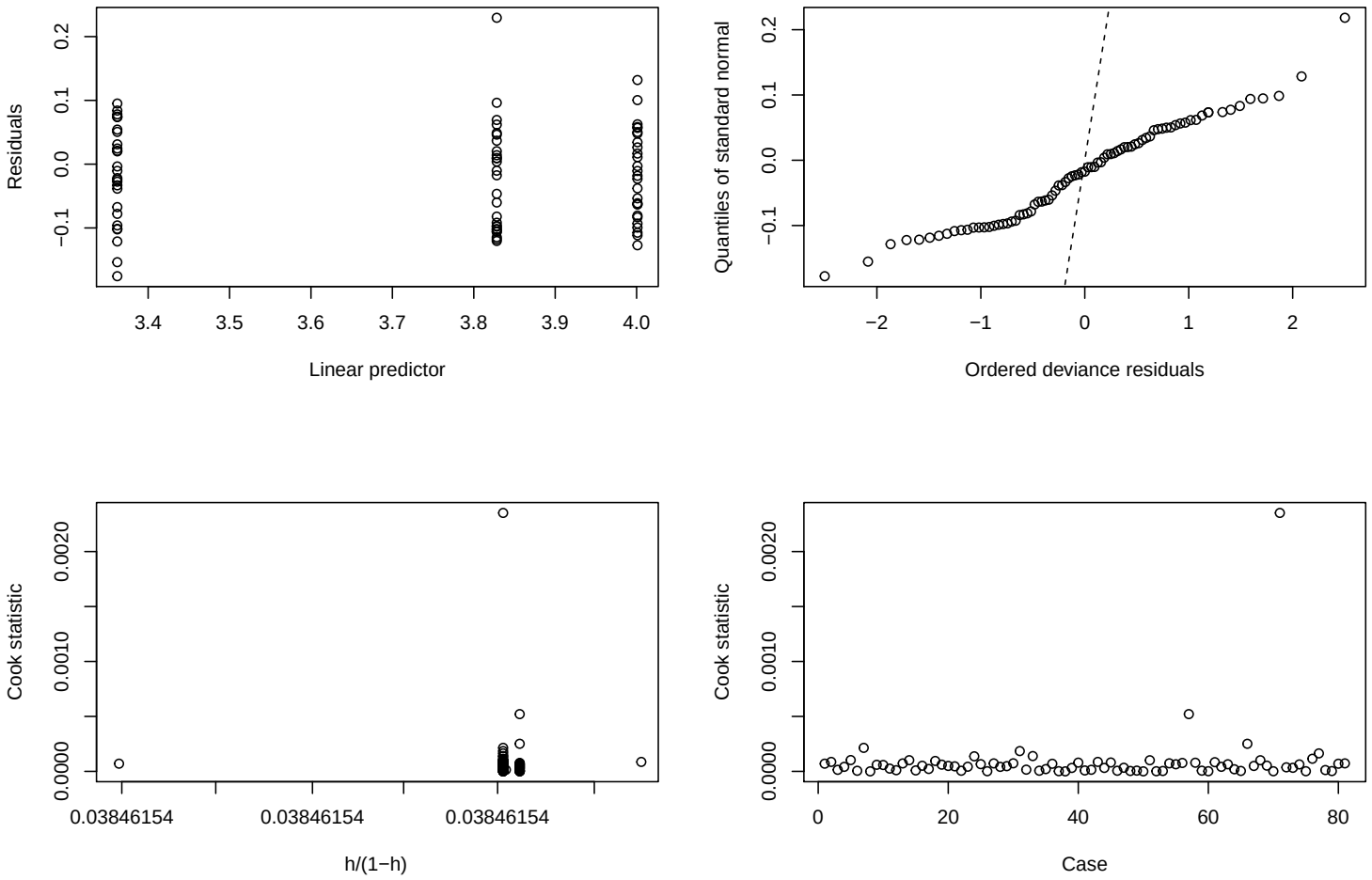
Example: Permeability of Building Materials

```
glm.diag.plots(fit3_gamma)
```



Example: Permeability of Building Materials

```
glm.diag.plots(fit4_igauss)
```




```
hist(residuals(fit4_igauss))
```

Example: Permeability of Building Materials

- Gaussian model with a log-link is clearly wrong
- log-normal model is not that problematic, but the residual plots are not great
- Gamma and inverse Gaussian models are both alright
  - the inverse Gaussian QQ plot shows that the axes are flipped in `boot`'s implementation of diagnostic plots, otherwise that plot does not display a problematic behavior!
- how do we choose between Gamma and inverse Gaussian?
  - Gaussian distribution describes a Brownian motion's level at a fixed time, which is why the hitting-time (the time it takes the Brownian motion - with a drift - to reach a fixed level) distribution is called inverse Gaussian
  - hence inverse Gaussian is likely a good model for permeability (since Brownian motion is the most common model for random movement of particles over time, so assuming a uniform material with microscopic pores... otherwise Gamma distribution as the hitting time of a Poisson process might be more appropriate for a coarse-grained material, where particles travel by jumping from grain to grain with an exponential waiting time)