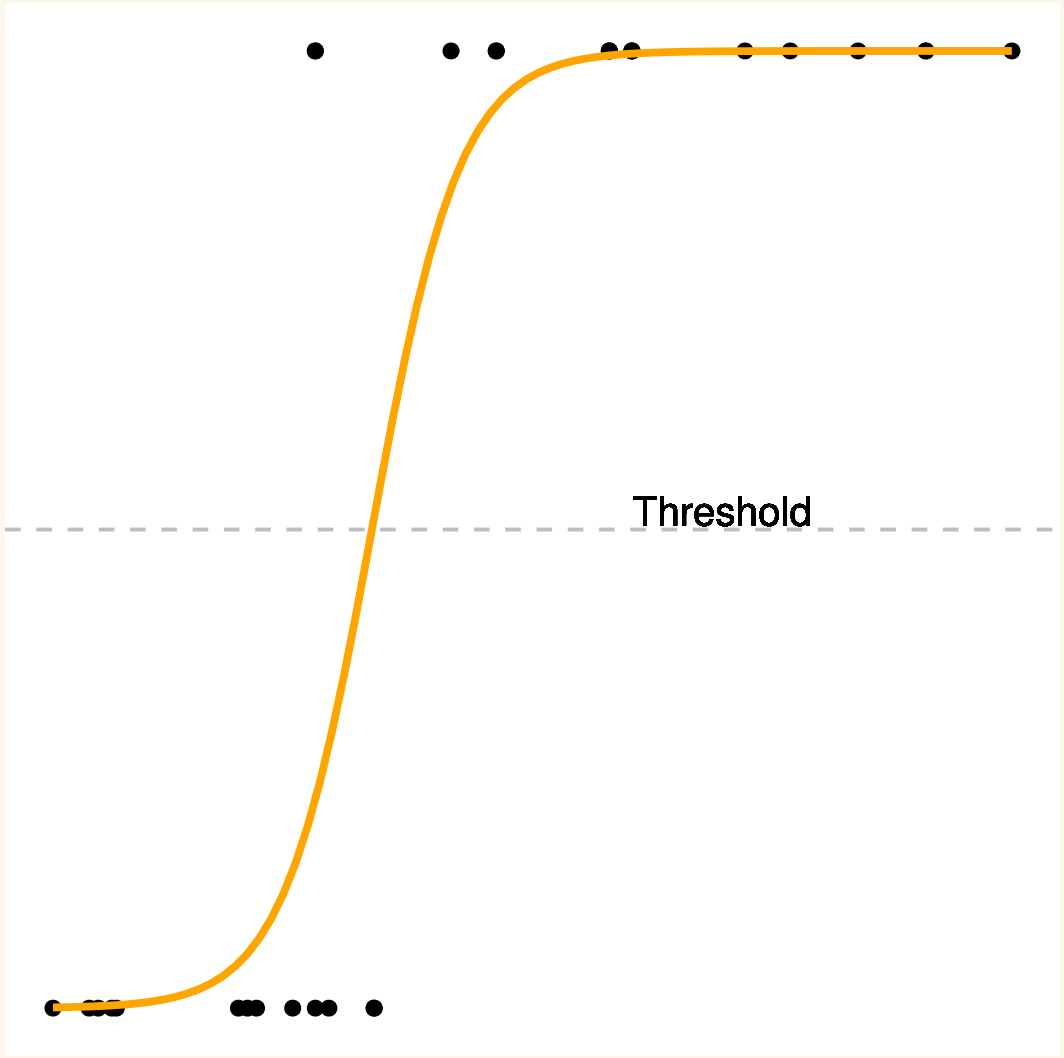
Binomial Logistic regression: deviance

Stat 230

May 22 2022

Overview



Today:

Deviance

Assumptions

Residuals and case influence

Review: A Logistic Regression Model for Binomial Count Data

For all $i = 1, \ldots, n$,

$$y_i \sim \text{binomial}(m_i, \pi_i),$$

where m_i is a known number of trials for observation i,

$$\pi_i = \frac{\exp\left(\boldsymbol{x}_i'\boldsymbol{\beta}\right)}{1 + \exp\left(\boldsymbol{x}_i'\boldsymbol{\beta}\right)},$$

and $y_1, \ldots, y_n$ are independent.

Overview: Binomial Distribution

Recall that for $y_i \sim \text{binomial}(m_i, \pi_i)$, the probability mass function of y_i is

$$P(y_i = y) = \begin{cases} \binom{m_i}{y} \pi_i^y (1-\pi_i)^{m_i - y} & \text{for } y \in \{0, \ldots, m_i\} \\ 0 & \text{otherwise} \end{cases}$$

$$E(y_i) = m_i \pi_i, \quad \text{and } \text{Var}(y_i) = m_i \pi_i (1-\pi_i).$$

The binomial log likelihood function is

$$\ell(\boldsymbol{\beta} \mid \boldsymbol{y}) = \sum_{i=1}^{n} \left[y_i \log\left(\frac{\pi_i}{1-\pi_i}\right) + m_i \log(1-\pi_i) \right] + \text{constant}$$

Deviance for Binomial responses

- With Binomial responses, the likelihood function is

$$L(\beta) = \prod_{i=1}^{n} \binom{m_i}{y_i} \pi(X_i)^{y_i} (1 - \pi(X_i))^{m_i - y_i}$$

- and the deviance is

$$\begin{aligned} G^2 &= 2[\ln L(\bar{\pi}) - \ln L(\hat{\pi}(X))] \\ &= 2 \sum_{i=1}^{n} \left[y_i \ln \left(\frac{y_i}{m_i \hat{\pi}(X_i)} \right) + (m_i - y_i) \ln \left(\frac{m_i - y_i}{m_i - m_i \hat{\pi}(X_i)} \right) \right] \end{aligned}$$

- $L(\hat{\pi}(X))$: likelihood of the data that plugs in estimates $\hat{\pi}(X_i)$ from the logistic model.
- $L(\bar{\pi})$: likelihood of the data that plugs in estimates $\bar{\pi}_i = y_i / m_i$

$$L(\bar{\pi}) \geq L(\hat{\pi}(X))$$

Logistic Regression Model vs Saturated model

Logistic Regression Model

- $y_i \sim \text{binomial}(m_i, \pi_i)$
- $y_1, \ldots, y_n$ independent

$$\pi_i = \frac{\exp\left(\boldsymbol{x}_i'\boldsymbol{\beta}\right)}{1 + \exp\left(\boldsymbol{x}_i'\boldsymbol{\beta}\right)}$$

- $p + 1$ β parameters
- MLE: $\hat{\pi}_i = \frac{\exp\left(\boldsymbol{x}_i'\hat{\boldsymbol{\beta}}\right)}{1+\exp\left(\boldsymbol{x}_i'\hat{\boldsymbol{\beta}}\right)}$

Saturated Model

- $y_i \sim \text{binomial}(m_i, \pi_i)$
- $y_1, \ldots, y_n$ independent
- $\pi_i \in [0, 1]$ for $i = 1, \ldots, n$ with no other restrictions
- n parameters
- MLE: y_i/m_i

Deviance for Binomial responses

Deviance for binomial models can be used for two types of hypothesis tests:

1. **Drop-in-deviance:** Used to compare two models, just like in binary logistic models.
2. **Goodness-of-fit:** Used to test binomial response model adequacy.

Goodness-of-fit test

Our hypotheses for the GOF test are:

$$H_0: \text{ logistic model}$$
$$H_A: \text{ saturated model}$$

$H_0 : Y_i \mid X_i \sim \text{Binom}(m_i, \pi(X_i))$

- $\pi(X_i)$ equals the logistic function of the p predictor terms.

H_A : the saturated "model"

- uses the n empirical proportion of successes $\bar{\pi} = y_i/m_i$ for each case as the probability of success for all m_i trials.

Goodness-of-fit test

- The test statistic is the residual deviance of the logistic model

$$G^2 = 2[\ln L(\bar{\pi}) - \ln L(\hat{\pi}(X))]$$

- If the "fit" (likelihood) of the logistic model is "close" then G^2 is "close" to 0 and we can claim that the logistic model is adequate.
- If H_0 is true and m_i 's are large, G^2 will have an approximate chi-square distribution with $n-(p+1)$ (model) degrees of freedom. The **p-value** is the probability of getting residual deviance values larger than the observed value:

$$p- \text{ value } = 1 - P\left(\chi^2 > G^2\right) = 1 - \text{pchisq}\left(G^2, df = n-(p+1)\right)$$

The suggested rule of thumb for "large m " is that we want most m_i 's to be at least 5 .

Goodness-of-fit test conclusions

Do not reject the null: (large p-value)

- Your logistic model is adequate.
- You don't have a large enough sample size n to have the power to detect inadequacies in your model.

Reject the null: (small p-value)

- You have outlier(s) that are inflating the residual deviance.
- Your logistic model is inadequate.

Goodness-of-fit test conclusions

Why might a model be inadequate?

- Your log-odds model is inadequate, it is ill-fitting and transformations are needed
- Extra-binomial variation: your response counts aren't well modeled by a Binomial model*.

*This could mean:

- trials are not **independent** for each case
- probability of success is **not** constant across trials for each case
- your choice of predictors **isn't** sufficient (i.e. you are missing key explanatory variables)

Case study 21.1: Krunnit Island

- **GOF** test hypotheses are

$$H_0 : \log(\text{odds}) = \beta_0 + \beta_1 \log(\text{area})$$
$$H_A : \log(\text{odds}) = \alpha_i(\text{saturated model})$$

We can conduct a GOF test because all our m_i's (AtRisk), are above 5

```
island <- case2101
island$AtRisk
```

```
 [1] 75 67 66 51 28 20 43 31 28 32 30 20 31 16 15 33 40  6
```

Case study 21.1: Krunnit Island

Test stat: residual deviance of $G^2 = 12.062$

```
krunnit_glm <- glm(Extinct/AtRisk ~ log(Area), family="binomial", weights=AtRisk, data = island)
summary(krunnit_glm)

Call:
glm(formula = Extinct/AtRisk ~ log(Area), family = "binomial",
    data = island, weights = AtRisk)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-1.71726  -0.67722   0.09726   0.48365   1.49545

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.19620    0.11845 -10.099  < 2e-16 ***
log(Area)   -0.29710    0.05485  -5.416 6.08e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 45.338  on 17  degrees of freedom
Residual deviance: 12.062  on 16  degrees of freedom
AIC: 75.394

Number of Fisher Scoring iterations: 4
```

Case study 21.1: Krunnit Island

- **p-value:** Using $18 - 2 = 16$ degrees of freedom

$$p\text{-value } = 1 - P\left(\chi^2 > 12.062\right) = 1 - pchisq(12.062, df = 16) = 0.7397$$

- The **large** p-value means that we **do not reject** the null hypothesis.
- Our model for the probability of extinction given log-area looks to be adequate.

Case study 21.1: Krunnit Island

```
krunnit_glm_nolog <- glm(Extinct/AtRisk ~ Area, family="binomial", weights=AtRisk, data = is
summary(krunnit_glm_nolog)

Call:
glm(formula = Extinct/AtRisk ~ Area, family = "binomial", data = island,
    weights = AtRisk)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.6526  -1.0661  -0.1877   1.0038   2.1860

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.305957   0.117339 -11.130  < 2e-16 ***
Area        -0.010121   0.002684  -3.771 0.000163 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 45.338  on 17  degrees of freedom
Residual deviance: 24.661  on 16  degrees of freedom
AIC: 87.993

Number of Fisher Scoring iterations: 4
```

Case study 21.1: Krunnit Island

- Regression of extinction on area (not logged) has residual deviance of 24.661.
- The GOF p-value for this model is 0.076, which suggests that this model may not be adequate
  - agrees with our EDA for the log-odds suggests

```
1-pchisq(24.661, df=16)
```

```
[1] 0.07602884
```

Checking Assumptions

Binomial logistic model as the **same assumptions** as binary models:

- **Independence** of cases takes an understanding of how the data was collected.
- Log-odds **linearity** can be checked with an empirical log-odds plot against quantitative predictors and residual plots.

A third assumption is that the counts of successes Y_i has a **binomial distribution**:

- the m_i trials are independent events, and a success or failure for one trial doesn't affect the outcome of another trial, and
- the probability of success $\pi(X_i)$ is the same for all m_i trials.

Checking Assumptions

- If one, or both, of these assumptions is violated, then it often induces extra-binomial variation (a.k.a. **over dispersion**):
- the actual variation $SD\left(Y \mid X_i\right)$ is larger than the binomial SD of $\sqrt{m_i \pi\left(X_i\right)\left(1-\pi\left(X_i\right)\right)}$
- making our reported standard errors larger and p-values too small
- **Check:** use the goodness-of-fit test, when m_i are large enough, to check our binomial distribution assumption.

Checking Assumptions

If we do find evidence of lack-of-fit in our binomial model, then you should

- Check deviance residuals as case influence stats to see if an outlier(s) is affecting GOF results.
- Check the log odds form, change model structure, see if transformations of quantitative predictors are needed

If outliers and transformations aren't a concern, then consider an alternative model:

- binary logistic model if trial-level predictors are available
- quasi-binomial logistic model
- a model that allows for correlated trials (like a mixed-effects logistic model)

Case study 21.1: Krunnit Island

How might the Krunnit Island extinction counts violate the binomial counts model assumptions?

Independence:

- This assumption implies that the extinction, or not, of all at risk species on an island are independent events.
- This could be violated if the extinction of one species makes the extinction of a second more likely.

Case study 21.1: Krunnit Island

Probability:

- This assumption implies that the probability $\pi\left(area_i\right)$ of extinction on island i is the same for all at risk species on island i.
- This could be violated if, for example, species living primarily on the interior of the island had a lower chance of extinction than species living on the coastal region.

Residuals

Pearson residuals are basically response residuals standardized based on the binomial SD:

$$pr_i = \frac{y_i - m_i\hat{\pi}\left(X_i\right)}{\sqrt{m_i\hat{\pi}\left(X_i\right)\left(1-\hat{\pi}\left(X_i\right)\right)}}$$

- `resid(my_glm, type = "pearson")`
- `augment(my_glm, type.residuals = "pearson")`

Residuals

Deviance residuals are each case's contribution to the residual deviance, with a $\pm$ based on whether we over- or under-estimate a case's response (the $\pm$ is denoted by $\text{sign}(y_i - m_i\hat{\pi}(X_i))$) :

$$\text{Dres}_i = \text{sign}(y_i - m_i\hat{\pi}(X_i))\sqrt{2\left[y_i \ln\left(\frac{y_i}{m_i\hat{\pi}(X_i)}\right) + (m_i - y_i)\ln\left(\frac{m_i - y_i}{m_i - m_i\hat{\pi}(X_i)}\right)\right]}$$

- `resid(my_glm, type = "deviance")`
- `augment(my_glm, type.residuals = "deviance")`

Residuals

- Pearson residuals are "easy" to interpret
- Deviance residuals are good to check if you find significant results in a GOF test.
- When m_i 's are large (at least 5), both types of residuals should be similar in value and have a $N(0,1)$ distribution (approximately).
- Regardless of size of m_i, we should plot residuals vs. quantitative predictors to assess linearity of the log odds.

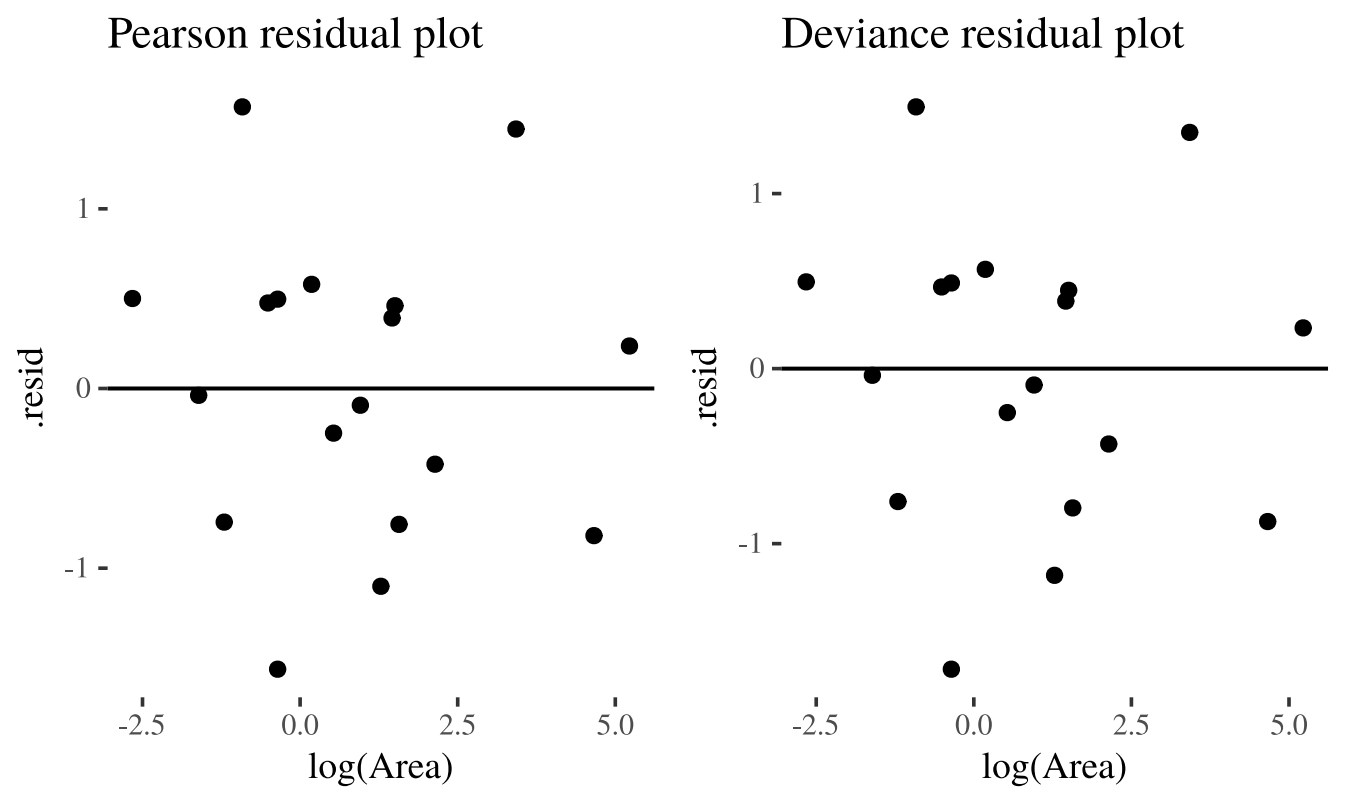
Case study 21.1: Krunnit Island

- use the `augment` command to get both sets of residuals

```
island_aug <- augment(krunnit_glm, type.residual="pearson")

plotA <- ggplot(island_aug, aes(x=`log(Area)`, y=.resid)) +
 geom_point() +
 geom_hline(yintercept = 0) +
 labs(title="Pearson residual plot")

island_aug <- augment(krunnit_glm, type.residual="deviance")

plotB <- ggplot(island_aug, aes(x=`log(Area)`, y=.resid)) +
 geom_point() +
 geom_hline(yintercept = 0) +
 labs(title="Deviance residual plot")
```

Case study 21.1: Krunnit Island

```
library(gridExtra)
grid.arrange(plotA, plotB, ncol=2)
```



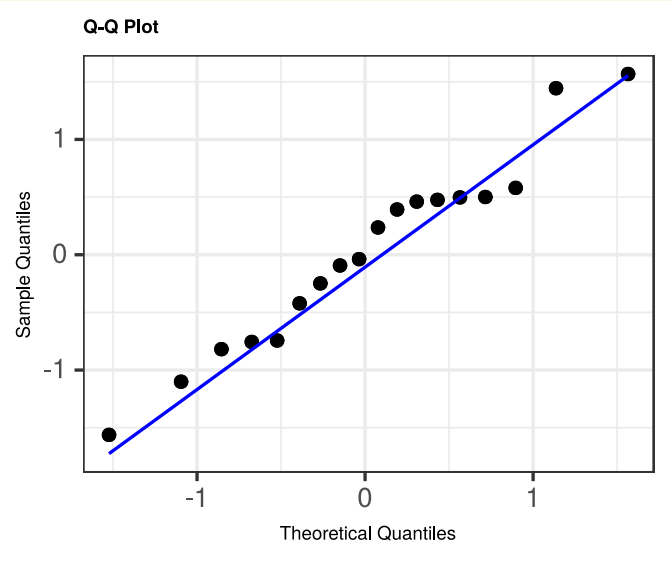
Residuals using `ggResidpanel`

- `resid_xpanel(my_glm, type = )`: where type could be pearson or deviance (or response)
- `resid_panel(my_glm, plots = "qq", type = )`: qq plot of residuals given by type

Case study 21.1: Krunnit Island

At risk counts m_i are rather large (all cases are 6 or larger) so residuals should be approximately $N(0, 1)$.

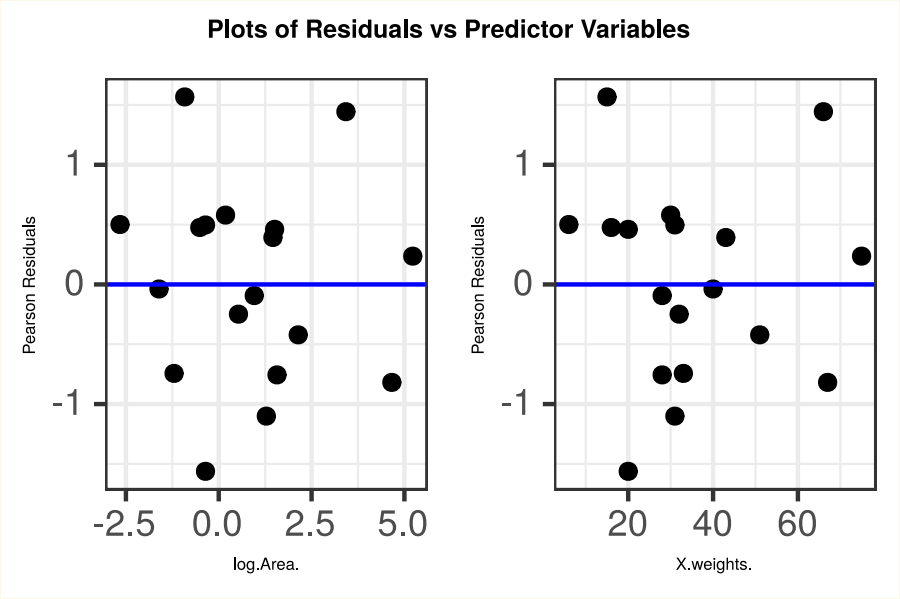
```
resid_panel(krunnit_glm, plots = "qq", type = "pearson", axis.text.size = 6, title.text.size = 6)
```



Case study 21.1: Krunnit Island

at risk counts m_i are the `X.weights` variable (we don't want residual values to depend on m_i)

```
resid_xpanel(krunnit_glm, type = "pearson", axis.text.size = 4, title.text.size = 6)
```



Case influence stats

In a GLM, leverage measures

- both a cases's "extremeness" in terms of it's predictor values and
- the size of a case's weight m_i

- cases with high values of m_i are given more weight, and hence higher leverage, in the fitted model
- Cook's distance also takes into account a cases leverage (measured both by predictor values and by m_i size) and a case's residual value.

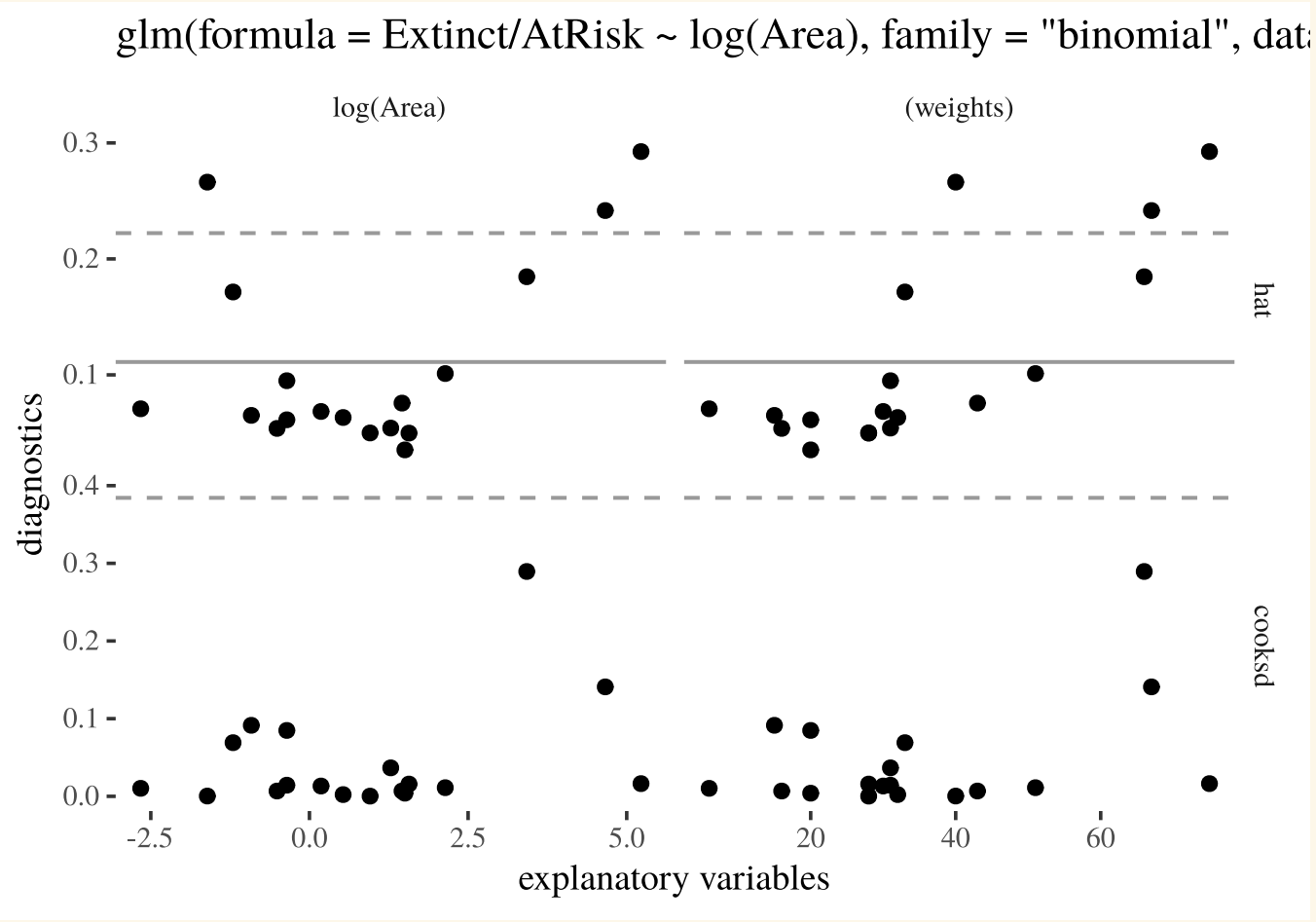
Case study 21.1: Krunnit Island

```
plot(krunnit_glm, which=5, id.n=18)
```

- rows 1,2 and 17 have largest leverage while case 3 looks to have the highest Cook's distance value.

Case study 21.1: Krunnit Island

```
library(GGally)
ggnostic(krunnit_glm, columnsY = c(".hat",".cooksd"))
```

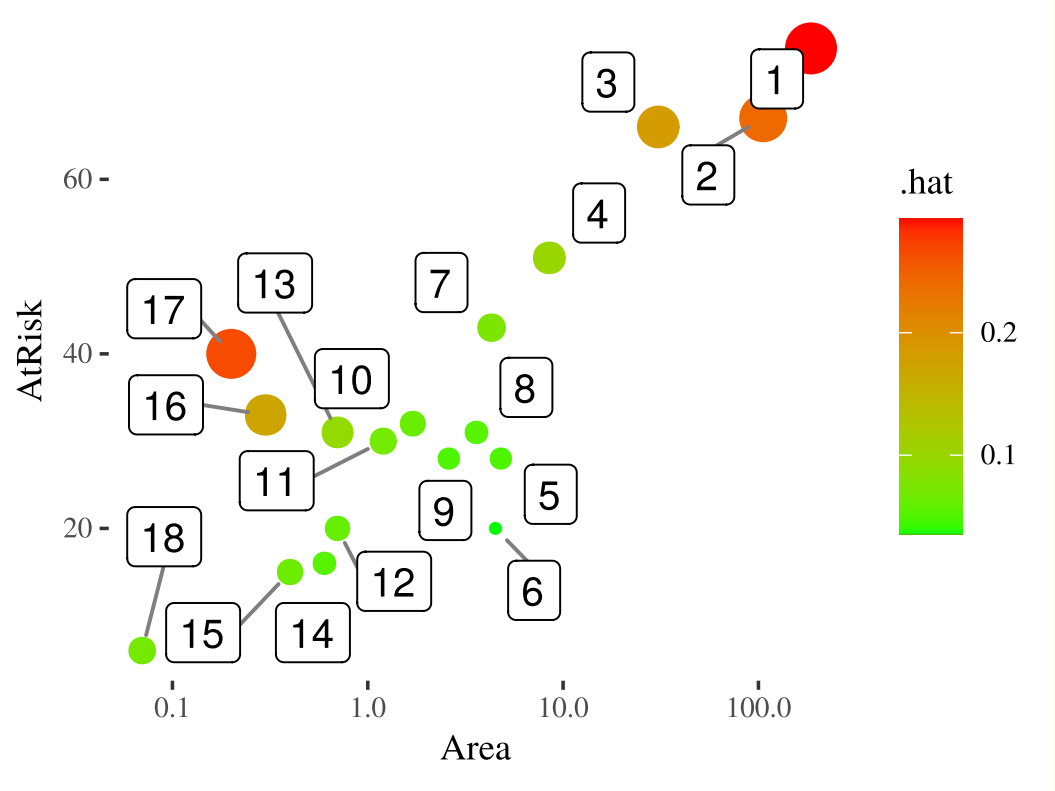


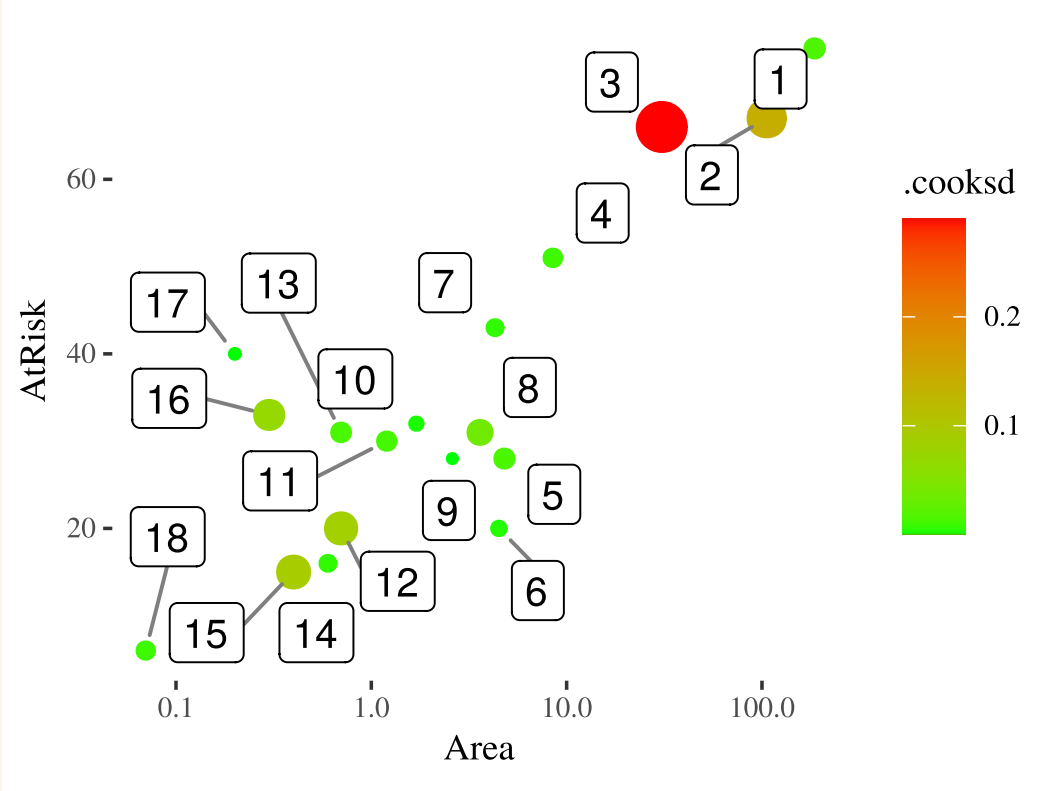
Case study 21.1: Krunnit Island

```
island_aug <- augment(krunnit_glm, data=island, type.predict = "response")
island_aug <- island_aug %>% mutate(ID = row_number())
island_aug %>% slice(1,2,3,17) %>% select(-.sigma)
# A tibble: 4 × 10
  Island       Area AtRisk Extinct .fitted  .resid .std.resid  .hat .cooksd    ID
  <fct>       <dbl>  <int>   <int>   <dbl>   <dbl>      <dbl> <dbl>   <dbl> <int>
1 Ulkokrunni 186.      75       5  0.0602  0.233       0.277  0.293 1.63e-2     1
2 Maakrunni  106.      67       3  0.0704 -0.874      -1.00   0.242 1.41e-1     2
3 Ristikari   30.7     66      10  0.0985  1.35        1.49   0.185 2.89e-1     3
4 Tiirakari    0.2     40      13  0.328  -0.0381    -0.0445 0.266 3.59e-4    17
```

```
summary(select(island_aug, Area, AtRisk))
      Area              AtRisk
 Min.   :  0.070   Min.   : 6.00
 1st Qu.:  0.625   1st Qu.:22.00
 Median :  2.150   Median :31.00
 Mean   : 19.804   Mean   :35.11
 3rd Qu.:  4.725   3rd Qu.:42.25
 Max.   :185.800   Max.   :75.00
```

Case study 21.1: Krunnit Island



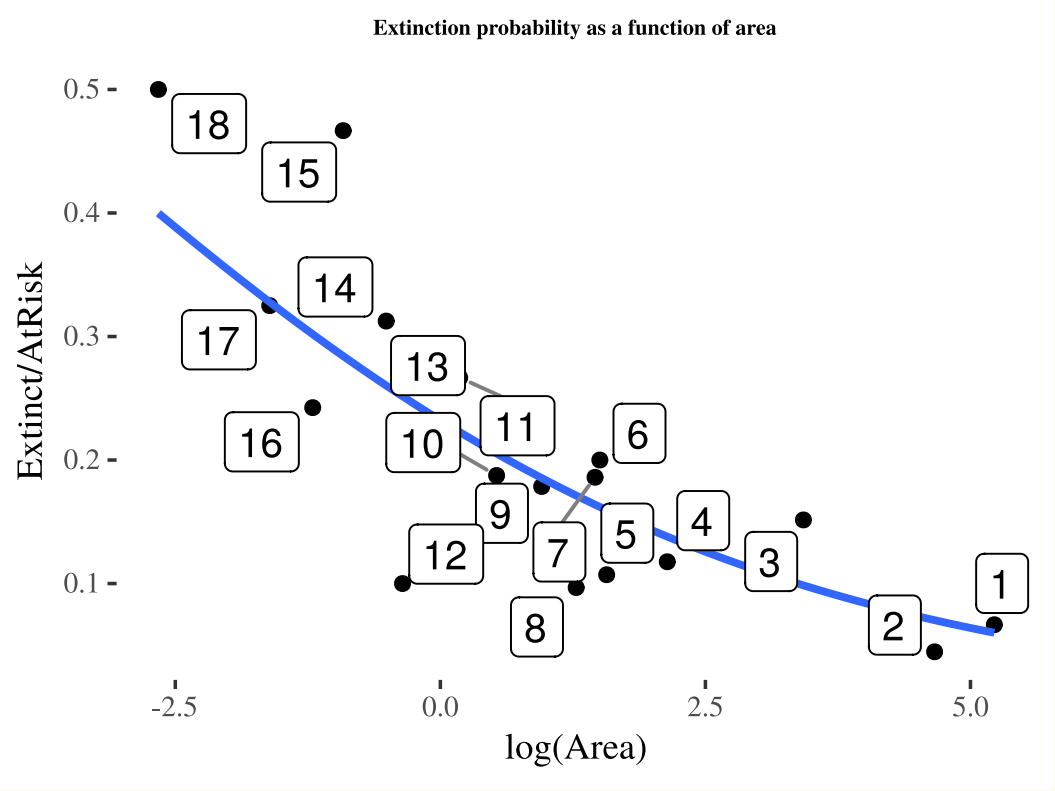


Case study 21.1: Krunnit Island

Case 1 (Ulkokrunni):

- largest area and the largest number at risk m_i.
- has largest leverage but it doesn't have an large residual value so it doesn't have high Cook's distance.

```
library(ggrepel)
island <- island %>% mutate(ID = row_number())
plot <- ggplot(island, aes(x=log(Area),
                           y = Extinct/AtRisk,
                           weight = AtRisk)) +
 geom_point() +
 geom_smooth(method="glm", se=FALSE,
 method.args = list(family="binomial")) +
 labs(title="Extinction probability as a functi
 theme(plot.title = element_text(hjust=0.5, siz
                                 face='bold'))

plot +  geom_label_repel(aes(label = ID),
                  box.padding   = 0.15,
                  point.padding = 0.3,
                  segment.color = 'grey50')
```



Case study 21.1: Krunnit Island

Case 17 (Tiirakari)

- second smallest area but a large number of at risk species given its small size.
- has larger leverage than case 18 which has the smallest area but smaller number at risk.
- has a small residual and low Cook's distance.

Case 3 (Ristikari)

- third largest area (30.7) but it's number at risk (66) is only one smaller than case 2 (Maakrunni) which is the second largest area (106).
- has a much larger residual than case 2, which results in it having the highest Cook's distance value in the data set.

- None of these cases is overly influential in the model it and removal of case 3 , the highest Cook's distance, changes the estimate of β_1 from 0.30 to 0.33 and it's significance doesn't change.