

# Additional Aspects of Generalised Linear Models

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## Exponential Family

$$\ln[\mathbf{y}; \boldsymbol{\eta}] = \frac{\mathbf{y}\boldsymbol{\eta} - \mathbf{b}(\boldsymbol{\eta})}{\phi} + c(\mathbf{y}, \phi)$$

$\boldsymbol{\eta} = g(\boldsymbol{\mu})$ , where  $\boldsymbol{\mu} = E(\mathbf{y})$ .

$\boldsymbol{\eta}$  known as the **canonical parameter**.

$g$  known as the **(canonical) link function**.

$\phi$  known as the **dispersion** parameter.

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## Generalised Linear Models

- Very large topic – could easily fill up a course.
- Still relatively young – started in early 1970s.
- Lots of methodology options.
- Quite a bit of jargon.
- Diagnostics more delicate.

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## Exponential Family Examples

name	canonical link	$b(\boldsymbol{\eta})$	$c(\mathbf{y}, \phi)$	$\phi$
Bernoulli	$\boldsymbol{\eta} = \text{logit}(\boldsymbol{\mu})$	$\log(1 + e^\boldsymbol{\eta})$	0	1
Poisson	$\boldsymbol{\eta} = \ln(\boldsymbol{\mu})$	$e^\boldsymbol{\eta}$	$-\ln(\mathbf{y}!)$	1
$N(\boldsymbol{\mu}, \sigma^2)$	$\boldsymbol{\eta} = \boldsymbol{\mu}$	$\boldsymbol{\eta}^2/2$	$(\mathbf{y}^2/\sigma^2 - \ln(2\pi\sigma^2))/2$	$\sigma^2$

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## Connections Involving the $b$ Function

$$\boldsymbol{\mu} = \mathbf{E}(\mathbf{y}) = \mathbf{b}'(\boldsymbol{\eta})$$

$$\text{Var}(\mathbf{y}) = \phi \mathbf{b}''(\boldsymbol{\eta})$$

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## $\hat{\boldsymbol{\eta}}$ and $\hat{\boldsymbol{\mu}}$ Vectors

Convenient notation is

$$\hat{\boldsymbol{\eta}} = \mathbf{X}\hat{\boldsymbol{\beta}} = \text{vector of fitted values on the link scale}$$

and

$$\hat{\boldsymbol{\mu}} = \mathbf{g}^{-1}(\mathbf{X}\hat{\boldsymbol{\beta}}) = \text{vector of fitted values on the response scale}$$

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## General GLM Fitting with Canonical Link

The log-likelihood is

$$\ell(\boldsymbol{\beta}) = \{\mathbf{y}^T \mathbf{X}\boldsymbol{\beta} - \mathbf{1}^T \mathbf{b}(\mathbf{X}\boldsymbol{\beta})\} / \phi + \text{const.}$$

So need maximise  $S(\boldsymbol{\beta}) = \mathbf{y}^T \mathbf{X}\boldsymbol{\beta} - \mathbf{1}^T \mathbf{b}(\mathbf{X}\boldsymbol{\beta})$ .

Newton-Raphson reduces to iteratively reweighted least squares.

$$\hat{\boldsymbol{\beta}} = \text{estimate of } \boldsymbol{\beta}$$

$$\widehat{\text{se}}(\hat{\boldsymbol{\beta}}) = \sqrt{\text{diagonal entries of } [\mathbf{X}^T \text{diag}\{\mathbf{b}''(\mathbf{X}\hat{\boldsymbol{\beta}}) / \phi\} \mathbf{X}]^{-1}}$$

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## Deviance

Write the log-likelihood  $\ell(\boldsymbol{\beta})$  as a function of  $\boldsymbol{\mu} = \mathbf{g}^{-1}(\mathbf{X}\boldsymbol{\beta})$ .

e.g. in Bernoulli case

$$\begin{aligned} \ell(\boldsymbol{\beta}) &= \mathbf{y}^T \mathbf{X}\boldsymbol{\beta} - \mathbf{1}^T \ln(1 + e^{\mathbf{X}\boldsymbol{\beta}}) \\ &= \mathbf{y}^T \ln(\boldsymbol{\mu}) + (\mathbf{1} - \mathbf{y})^T \ln(1 - \boldsymbol{\mu}) = \ell_{\boldsymbol{\mu}}(\boldsymbol{\mu}), \quad (\text{say}) \end{aligned}$$

The deviance is:

$$D = 2\phi\{\ell_{\boldsymbol{\mu}}(\mathbf{y}) - \ell_{\boldsymbol{\mu}}(\hat{\boldsymbol{\mu}})\}$$

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## Examples of Deviance Expressions

Normal:  $D = (\mathbf{y} - \hat{\boldsymbol{\mu}})^T(\mathbf{y} - \hat{\boldsymbol{\mu}})$

Bernoulli:  $D = 2[\mathbf{y}^T \ln(\mathbf{y}/\hat{\boldsymbol{\mu}}) + (1 - \mathbf{y})^T \ln\{((1 - \mathbf{y})/(1 - \hat{\boldsymbol{\mu}}))\}]$

Poisson:  $D = 2\{\mathbf{y}^T \ln(\mathbf{y}/\hat{\boldsymbol{\mu}}) - \mathbf{1}^T(\mathbf{y} - \hat{\boldsymbol{\mu}})\}$

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## Overfitting Caveat

Can achieve

zero deviance

just by fitting with very high degree polynomials.

Need to trade-off against parsimony.

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## Interpretation of Deviance

The

smaller the deviance

the

better the model fits the data.

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## AIC

This is short for Akaike's Information Criterion

$$\text{AIC} = \text{Deviance} + 2 \times \text{no. of parameters} + \text{const}(\mathbf{y}).$$

(Generalises Mallows's  $C_p$  from linear regression.)

AIC is often used for model selection in GLM.

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## Galapagos Turtle Example

- Species the number of species of tortoise found on the island
- Area the area of the island (km<sup>2</sup>)
- Elevation the highest elevation of the island (m)
- Nearest the distance from the nearest island (km)
- Scruz the distance from Santa Cruz island (km)
- Adjacent the area of the adjacent island (square km)

Zoological interesting in modelling Species in terms of predictors.

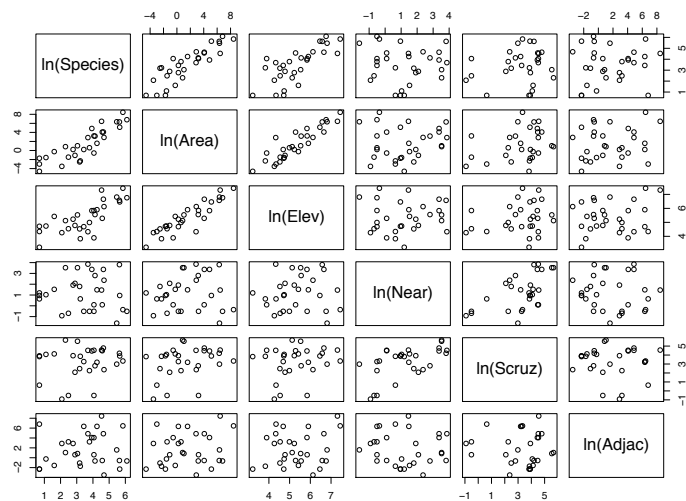
## Initial Model

Since response variable Species is a count we try the model:

$$\text{Species}_i \sim \text{Poisson}(\exp(\beta_0 + \beta_1 \text{Area}_i + \beta_2 \text{Elevation}_i + \beta_3 \text{Scruz}_i + \beta_4 \text{Adjacent}_i))$$

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```
glm(formula = Species ~ ., family = poisson, data = galapagos)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-8.2752	-4.4966	-0.9443	1.9168	10.1849

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	3.155e+00	5.175e-02	60.963	< 2e-16 ***
Area	-5.799e-04	2.627e-05	-22.074	< 2e-16 ***
Elevation	3.541e-03	8.741e-05	40.507	< 2e-16 ***
Nearest	8.826e-03	1.821e-03	4.846	1.26e-06 ***
Scruz	-5.709e-03	6.256e-04	-9.126	< 2e-16 ***
Adjacent	-6.630e-04	2.933e-05	-22.608	< 2e-16 ***

---

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```

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

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 3510.73  on 29  degrees of freedom
Residual deviance:  716.85  on 24  degrees of freedom
AIC: 889.68

```

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## Model Checking Essential!

For most scientific purposes we

**CANNOT STOP HERE**

We now have to conduct **diagnostic checks** on the model.

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## Diagnostic Checks

These are required to check:

- Linearity assumption.
- Leverage and influence.
- Distributional assumptions  
(e.g. Poisson versus overdispersed).

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## GLM Residuals

$i$ th Pearson residual:  $r_i^P = (y_i - \hat{\mu}_i) / \sqrt{\phi b''(\hat{\eta}_i)}$

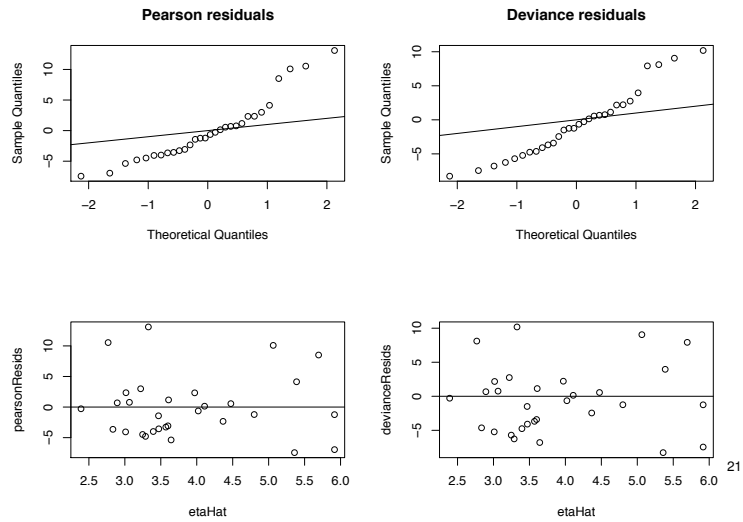
$i$ th Deviance residual:  $r_i^D = \text{sign}(y_i - \hat{\mu}_i) \sqrt{d_i}$

where  $D = \sum_{i=1}^n d_i$

If model is correct then these should each behave approximately like a

$N(0, 1)$  sample.

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## Comments on Previous Slide

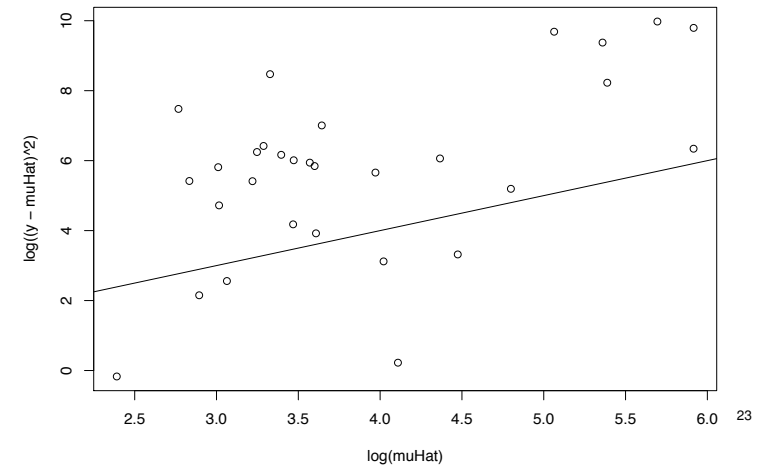
### Upper Panels

These are normal Q-Q plots with a 1:1 line added.

Both Pearson and deviance residuals are much more dispersed (large spread) than  $N(0,1)$  data indicating strong violation of Poisson assumption.

### Lower Panels

These are the residuals against  $\hat{\eta}_i$  values (with zero line added). These show no strong patterns.



## Comments on Previous Slide

This is a plot of

$$\ln\{(y_i - \hat{\mu}_i)^2\} \text{ versus } \ln(\hat{\mu}_i)$$

with a 1:1 line added. The fact that the most points are well above the line indicates an overdispersion problem.



This indicates incompatibility with the Poisson distribution.  
The data are (mildly) overdispersed.

```
Call:
glm(formula = Species ~ ., family = quasipoisson, data = galapagos)
```

```
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-8.2752  -4.4966  -0.9443   1.9168  10.1849
```

```
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  3.1548079  0.2915901  10.819 1.03e-10 ***
Area         -0.0005799  0.0001480  -3.918 0.000649 ***
Elevation    0.0035406  0.0004925   7.189 1.98e-07 ***
Nearest      0.0088256  0.0102622   0.860 0.398292
Scruz       -0.0057094  0.0035251  -1.620 0.118380
Adjacent    -0.0006630  0.0001653  -4.012 0.000511 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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## Quasi-likelihood

A remedy is **quasi-likelihood** where the Poisson log-likelihood

$$\ell(\beta) = \mathbf{y}^T \mathbf{X}\beta - \mathbf{1}^T e^{\mathbf{X}\beta}$$

is replaced by

$$q\ell(\beta) = \frac{\mathbf{y}^T \mathbf{X}\beta - \mathbf{1}^T e^{\mathbf{X}\beta}}{\phi}$$

where  $\phi$  is estimated from the data. Note that  $q\ell$  does not correspond to a 'proper' probability distribution (hence the **quasi** label).

```
(Dispersion parameter for quasipoisson family taken to be 31.74921)
```

```
Null deviance: 3510.73 on 29 degrees of freedom
Residual deviance: 716.85 on 24 degrees of freedom
AIC: NA
```

```
Number of Fisher Scoring iterations: 5
```

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## Comment on Previous Output

The over-dispersion parameter is estimated as 31.74921

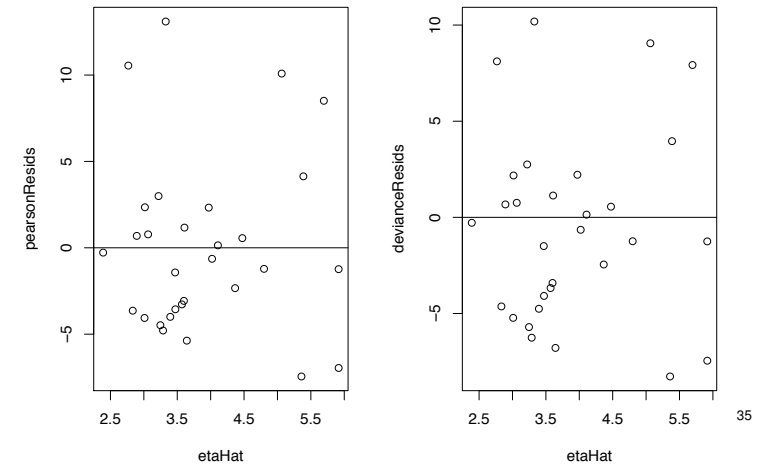
The coefficient estimates haven't changed much

**BUT**

the **standard errors** have changed enormously!

This can have a big effect on statist. significance.

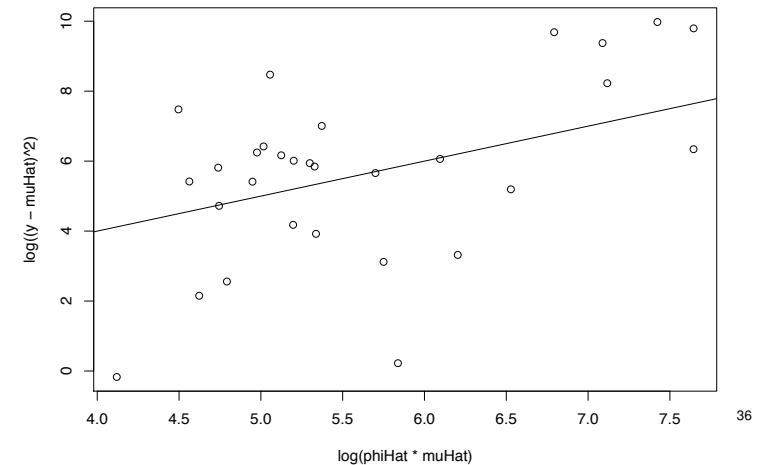
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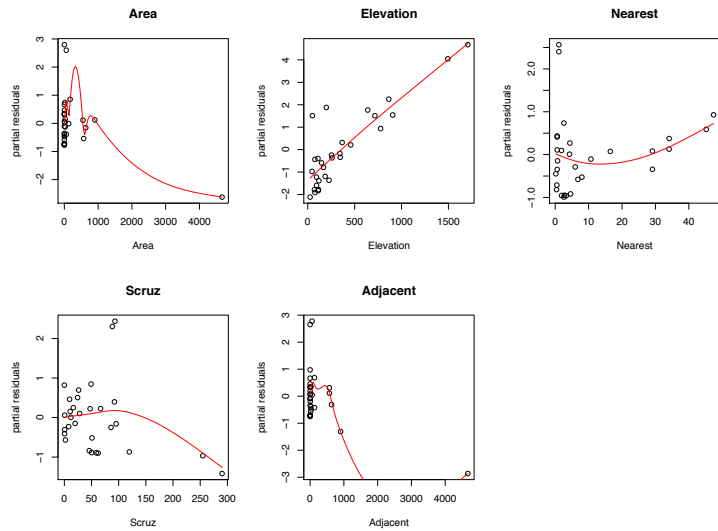
## Diagnosis of New Model

The following figures show residual plots for the quasi-likelihood extension:

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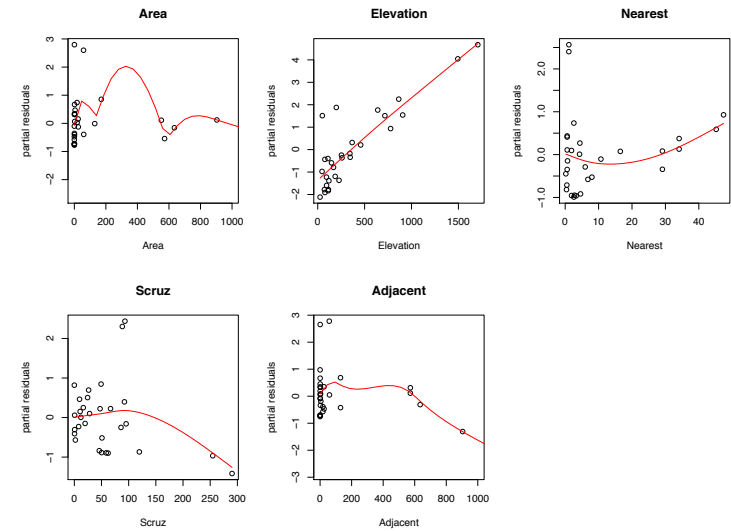


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Two of the panels in the previous slide are distorted by a single high value on the  $x$ -axis.

We will re-do these plots with a restricted range.

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## Comment on Previous Graphic

These are **partial residual plots** for each predictor.

Linearity of the **red curve** indicates that the linearity assumption is reasonable.

e.g. **Elevation** looks fine, but **Adjacent** appears to have non-linear a effect.

( **Nearest** and **Scruz** also look non-linear; but are not significant).

Even though the red curve for **Area** looks weird, the points are reasonably well-behaved (on a straight line).

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Later in this course we will look at ways to address the non-linear effects.

- Models that include **offsets**.

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## Other GLMs

With the aim of fitting data better, several other GLMs have emerged. These include:

- **Negative binomial** regression models for count data.
- Quasi-likelihood models with **variance modelling**.

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## Model Selection

AIC-based strategies for 'automatic' selection of a model are now available.

In R the relevant function is `step()`.

(Assignment 6 illustrates `step()`)

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## Further reading

Faraway, J.J. (2006). *Extending the Linear Model with R*, Chapman & Hall/CRC.

McCullagh, P., and Nelder, J.A. (1989). *Generalized Linear Models (Second Edition)*. London: Chapman and Hall.

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## Practical GLM Beyond Advanced Data Analysis

Recommendation if you have to do lots of GLM analyses in a future role (e.g. job, thesis research):

- Spend \$100 on the Faraway book.
- Work through its GLM examples.

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