

Binomial regression

Bert van der Veen

Department of Mathematical Sciences, NTNU

Outline

- ▶ Binomial regression
- ▶ Model comparison
- ▶ P-values
- ▶ R^2
- ▶ Q & A

Questions about yesterday?



Makes sure that the mean is on the right scale (e.g., positive only, or between 0 and 1)



Binomial GLM use

- ▶ When a linear regression is not appropriate :)
- ▶ For binary data or counts of successes/failures

In ecology

- ▶ Predicting species' distributions
- ▶ Number of germinated plant seeds
- ▶ Prevalence of disease in a population
- ▶ Probability of observing a behavior
- ▶ Proportion of orchids 🙄

Is binomial regression really a GLM?

$$\mathcal{L}(y_i; \Theta) = \exp \left\{ \log \binom{N}{r} + \frac{\frac{r}{N} \log(\frac{\pi_i}{1-\pi_i}) + \log(1-\pi_i)}{1/N} \right\} \quad (2)$$

All GLMs can be formulated as:

$$\mathcal{L}(y_i; \Theta) = \exp\left\{\frac{y_i \eta_i - b(\eta_i)}{a(\phi)} + c(y_i, \phi)\right\} \quad (3)$$

- ▶ for some known functions $a(\cdot)$, $b(\cdot)$ and $c(\cdot)$
- ▶ for binomial distribution: $\eta_i = \log(\frac{\pi_i}{1-\pi_i})$, $a(\phi) = 1/N$,
 $b(\eta_i) = -\log(1 - \pi_i)$, $c(y_i, \phi) = \log \binom{N}{r}$
- ▶ canonical link

Bernoulli

- ▶ $r \in \{0, 1\}$: Bernoulli (presence-absence)
- ▶ $N = 1$

$$\mathcal{L}(y_i; \Theta) = \exp \left\{ \log(1) + \frac{r \log\left(\frac{\pi_i}{1-\pi_i}\right) + \log(1 - \pi_i)}{1} \right\} \quad (4)$$

All GLMs can be formulated as:

$$\mathcal{L}(y_i; \Theta) = \exp \left\{ \frac{y_i \eta_i - b(\eta_i)}{a(\phi)} + c(y_i, \phi) \right\} \quad (5)$$

- ▶ for some known functions $a(\cdot)$, $b(\cdot)$ and $c(\cdot)$
- ▶ for Bernoulli distribution: $\eta_i = \log\left(\frac{\pi_i}{1-\pi_i}\right)$, $a(\phi) = 1$,
 $b(\eta_i) = -\log(1 - \pi_i)$, $c(y_i, \phi) = \log(1) = 0$
- ▶ canonical link

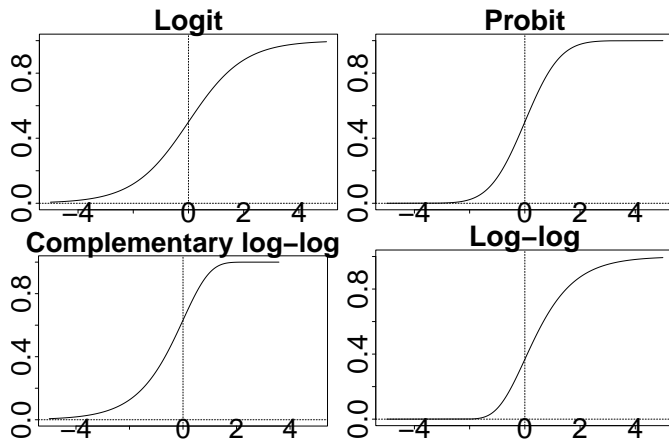
The binomial GLM

Link functions:

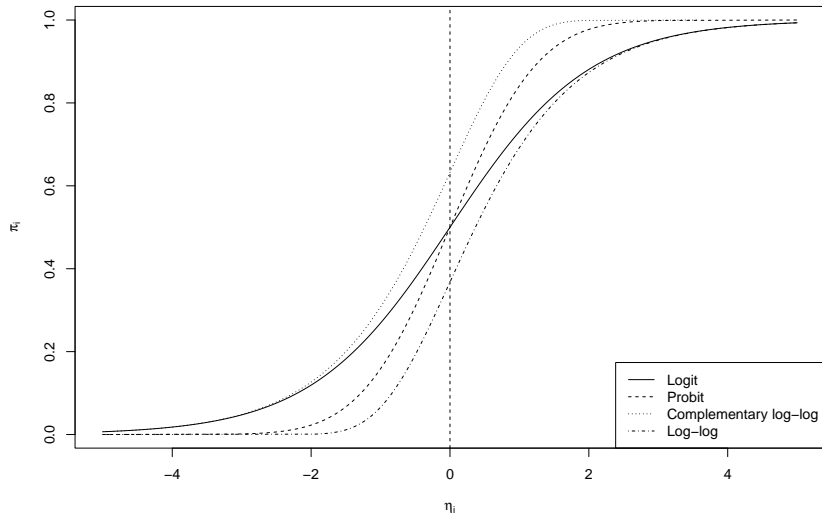
- ▶ Logit: $\log\left(\frac{\pi_i}{1-\pi_i}\right)$ and inverse $\frac{\exp(\eta_i)}{1+\exp(\eta_i)}$ - *the canonical link*
- ▶ Probit: $\Phi^{-1}(\pi_i)$ and inverse $\Phi(\eta_i)$
- ▶ Complementary log-log: $\log(-\log(1 - \pi_i))$ and inverse $1 - \exp(-\exp(\eta_i))$
- ▶ Log-log
- ▶ Logit is canonical and easier to interpret
- ▶ Probit is sometimes easier mathematically than Logit
- ▶ Complementary log-log for counts

Binomial link functions

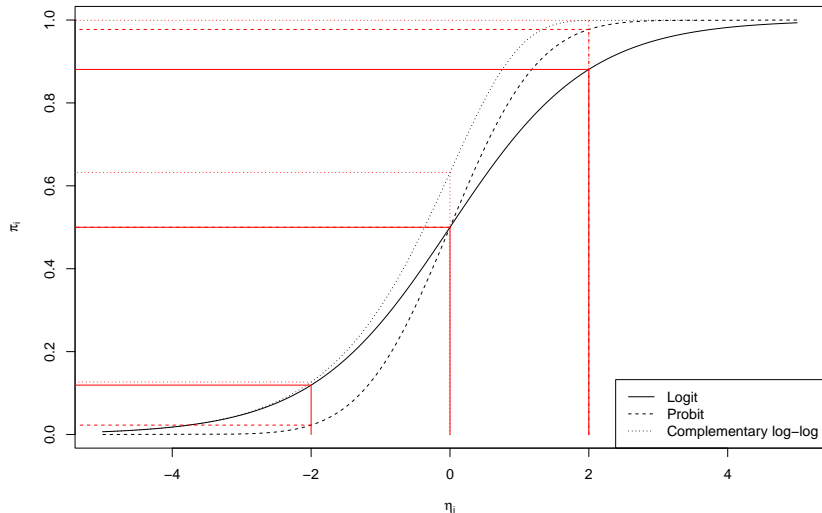
Each is a little different, but all translate from $(0, 1)$ to $(-\infty, \infty)$



Binomial link functions (2)



Binomial link functions (2)



Binomial link functions: logit

$$\begin{aligned} \text{pr}(y_i = 1) &= \pi_i = \frac{\exp(\eta_i)}{1 + \exp(\eta_i)} \\ \log\left(\frac{\pi_i}{1 - \pi_i}\right) &= \eta_i = \mathbf{x}_i\boldsymbol{\beta} \end{aligned} \tag{6}$$

- ▶ η is the log odds
- ▶ Odds ratio: $\frac{\pi_i}{1 - \pi_i} = \exp(\eta_i)$
 - ▶ E.g., horse races: 10:1 (for every 1 dollar spent, you get 10 if won)
 - ▶ I.e., you think that horse 1 is 10 times more likely to win than horse 2
- ▶ $\text{pr}(y_i = 0) = 1 - \pi$

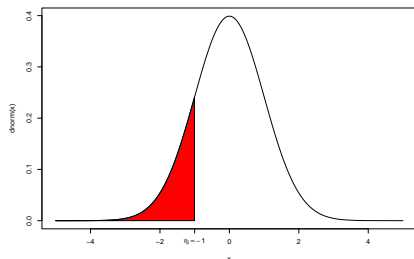
Binomial link functions: probit

$$\pi_i = \Phi(\eta_i)$$

$$\eta_i = \mathbf{x}_i \boldsymbol{\beta}$$
(7)

$$\eta_i^* = \mathbf{x}_i \boldsymbol{\beta} + \epsilon_i \sim \mathcal{N}(0, 1)$$

$$y_i = \begin{cases} 1, & \text{if } \eta_i^* > 0 \\ 0, & \text{otherwise} \end{cases}$$
(8)



if η_i^* is positive, we have 1 and 0 if it is negative

Binomial: Logit LVM

$$\pi_i = \frac{\exp(\eta_i)}{1 + \exp(\eta_i)} \quad (9)$$

$$\eta_i = \mathbf{x}_i \boldsymbol{\beta}$$

$$\eta_i^* = \mathbf{x}_i \boldsymbol{\beta} + \epsilon_i \sim \mathcal{Logistic}(0, 1)$$

$$y_i = \begin{cases} 1, & \text{if } \eta_i^* > 0 \\ 0, & \text{otherwise} \end{cases} \quad (10)$$

Binomial link functions: complementary log-log

$$\begin{aligned}
 \log(\lambda_i) &= \log(-\log(1 - \pi_i)) \\
 \lambda_i &= -\log(1 - \pi_i) = \exp(\eta_i)
 \end{aligned}
 \tag{11}$$

- ▶ Has a link to count data
 - ▶ Just look at the Poisson likelihood! **Thursday**
- ▶ When binary data are really counts
- ▶ Probability to get a count larger than 0
- ▶ Can also be interpreted as LVM (reverse extreme value distribution)

Cumulative link

Suppose you have ordered data:

Braun-Blanquet scale	Range of cover
r	< 5 %; very few individuals
+	< 5 %; few individuals
1	< 5%; numerous individuals
2	5 – 25 %
3	25 – 50 %
4	50 – 75 %
5	75 – 100 %

Cumulative link functions facilitate this kind of response by introducing **order**. **More on Thursday.**

Example: Lizard habitat preference

- ▶ Data originally by Schoener (1970)
- ▶ Counts of two species of lizard in Jamaica



Figure 2: wikipedia.org: grahami



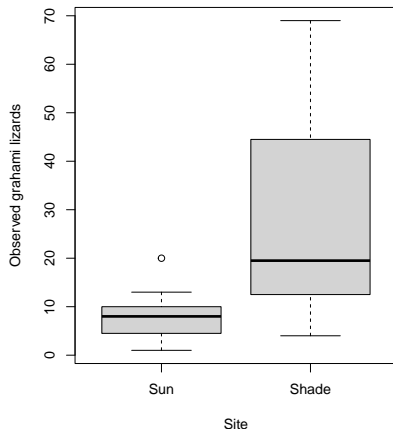
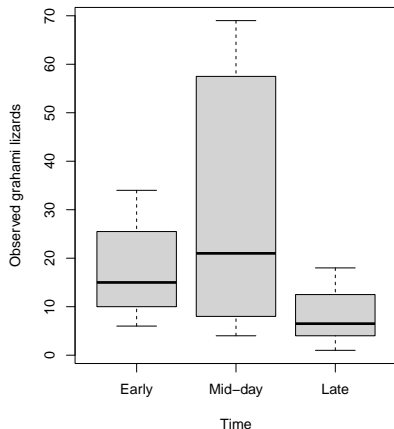
Figure 3: wikipedia.org: opalinus

Lizards: the data

Dataset also covered in McCullagh and Nelder (1989)

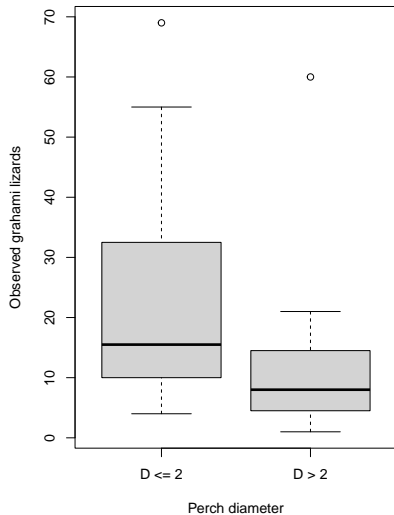
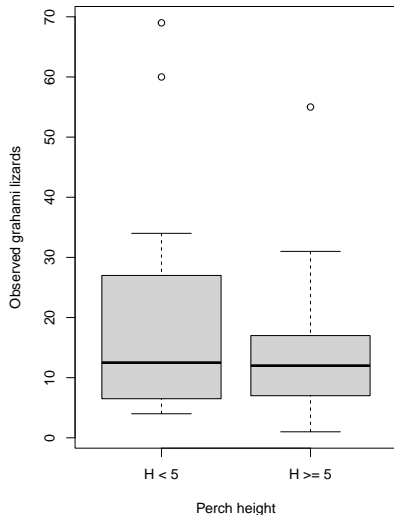
	Site	Diameter	Height	Time	grahami	opalinus
1	Sun	D ≤ 2	H < 5	Early	20	2
2	Sun	D ≤ 2	H < 5	Mid-day	8	1
3	Sun	D ≤ 2	H < 5	Late	4	4
4	Sun	D ≤ 2	H ≥ 5	Early	13	0
5	Sun	D ≤ 2	H ≥ 5	Mid-day	8	0
6	Sun	D ≤ 2	H ≥ 5	Late	12	0
7	Sun	D > 2	H < 5	Early	8	3
8	Sun	D > 2	H < 5	Mid-day	4	1
9	Sun	D > 2	H < 5	Late	5	3
10	Sun	D > 2	H ≥ 5	Early	6	0
12	Sun	D > 2	H ≥ 5	Late	1	1
13	Shade	D ≤ 2	H < 5	Early	34	11
14	Shade	D ≤ 2	H < 5	Mid-day	69	20
15	Shade	D ≤ 2	H < 5	Late	18	10
16	Shade	D ≤ 2	H ≥ 5	Early	31	5
17	Shade	D ≤ 2	H ≥ 5	Mid-day	55	4
18	Shade	D ≤ 2	H ≥ 5	Late	13	3
19	Shade	D > 2	H < 5	Early	17	15
20	Shade	D > 2	H < 5	Mid-day	60	32
21	Shade	D > 2	H < 5	Late	8	8
22	Shade	D > 2	H ≥ 5	Early	12	1

Lizards: visually inspect the data

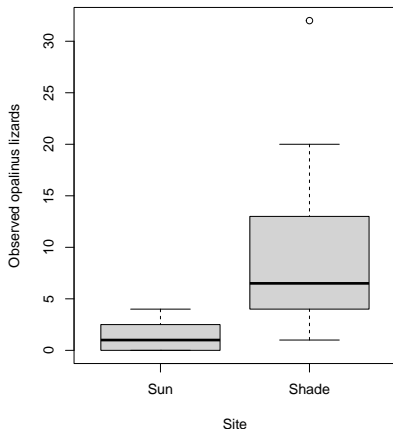
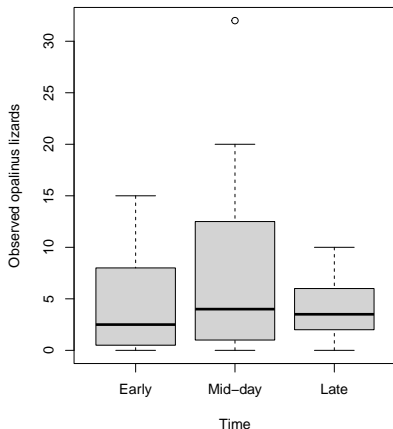


What can we tell about grahami lizards in Sunny or Shady sites?

Lizards: visually inspect the data



Lizards: visually inspect the data



What can we tell about opalinus lizards in Sunny or Shady sites?

Lizards: fit the model

```
model <- glm(cbind(ghahami, opalinus)~Time+Diameter+Height+Site,
             data = lizards, family="binomial")
```

- ▶ cbind: combines two vectors as columns
- ▶ N_i is the row sum (total lizards per site)
- ▶ Canonical link is used by default

Lizards: interpreting parameters

##		Estimate	Std. Error	z value	Pr(> z)
##	(Intercept)	1.90	0.34	5.70	1.2e-08
##	TimeMid-day	0.23	0.25	0.91	3.6e-01
##	TimeLate	-0.74	0.30	-2.50	1.4e-02
##	DiameterD > 2	-0.76	0.21	-3.60	3.1e-04
##	HeightH >= 5	1.10	0.26	4.40	1.1e-05
##	SiteShade	-0.85	0.32	-2.60	8.6e-03

- ▶ (Intercept) = Early, small diameter low perches
- ▶ Change in odds for observing grahami lizards mid-day:
 $\exp(0.23) = 1.26$
- ▶ Down for late-day: $\exp(-0.74) = 0.48$
- ▶ What else?

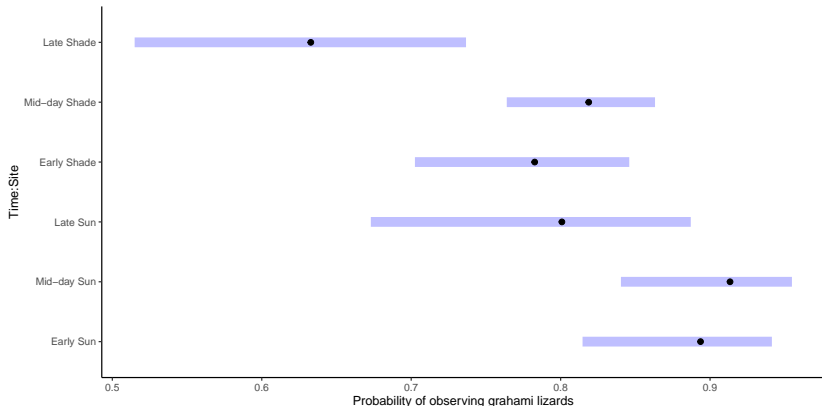
Lizards: inspecting the groups

```
emmeans::emmeans(model, ~Time+Site, type = "response")
```

```
##   Time      Site   prob      SE   df asymp.LCL asymp.UCL
##   Early    Sun   0.894 0.0314 Inf      0.815      0.941
##   Mid-day  Sun   0.913 0.0280 Inf      0.840      0.955
##   Late     Sun   0.801 0.0545 Inf      0.673      0.887
##   Early    Shade 0.783 0.0366 Inf      0.702      0.846
##   Mid-day  Shade 0.819 0.0253 Inf      0.764      0.863
##   Late     Shade 0.633 0.0574 Inf      0.515      0.737
##
## Results are averaged over the levels of: Diameter, Height
## Confidence level used: 0.95
## Intervals are back-transformed from the logit scale
```

Lizards: inspecting the groups visually

```
plot(emmeans::emmeans(model, ~Time+Site, type = "response"))+ggplot2::theme_classic()+ggplot2::xlab("Probability of observing grahmi lizards")
```



Lizards: parameter estimates with different link functions

##		logit	probit	cloglog
##	(Intercept)	1.90	1.20	0.78
##	TimeMid-day	0.23	0.13	0.12
##	TimeLate	-0.74	-0.44	-0.42
##	DiameterD > 2	-0.76	-0.45	-0.41
##	HeightH >= 5	1.10	0.65	0.58
##	SiteShade	-0.85	-0.51	-0.49

Lizards: group estimates with different link functions

##		logit	probit	cloglog
##	Early Sun	0.89	0.90	0.91
##	Mid-day Sun	0.91	0.92	0.93
##	Late Sun	0.80	0.80	0.79
##	Early Shade	0.78	0.78	0.77
##	Mid-day Shade	0.82	0.82	0.81
##	Late Shade	0.63	0.63	0.62

Overdispersion

In a binomial glm we (amongst others) assume:

- ▶ Independent Bernoulli trials
- ▶ $\text{var}(y_i) = N_i \pi_i (1 - \pi_i)$

If these are violated, we can have overdispersion. And due to omitted covariates.

Methods for diagnosing:

- ▶ Residual diagnostics
- ▶ Overdispersion factor
- ▶ Overdispersion test

Ignoring overdispersion is likely to cause inflated type I error.

This will come back for Poisson responses.
It is not possible to detect overdispersion in binary responses.

Lizards: checking overdispersion

```
deviance(model)/df.residual(model)
```

```
## [1] 0.7103637
```

```
sum(residuals(model, "pearson")^2)/df.residual(model)
```

```
## [1] 0.6431694
```

- ▶ Deviance is (approx.) χ^2 -distributed
- ▶ Can do a test for overdispersion

Lizards: checking overdispersion

```
performance::check_overdispersion(model)
```

```
## # Overdispersion test
##
## dispersion ratio = 0.994
## p-value = 0.92
```

```
## No overdispersion detected.
```


Accounting for overdispersion

- ▶ Beta-binomial GLM
- ▶ Quasibinomial GLM
- ▶ Mixed-effects model See [GLMM workshop by Physalia](#)

Perfect separation

Warning message: glm.fit: fitted probabilities numerically 0 or 1 occurred

Complete separation occurs whenever a linear function of x_i can generate perfect predictions of y_i

In essence: MLE is on the boundary of valid parameter space. We perfectly classify the response.

Solution:

- ▶ Sometimes it happens
- ▶ Change model (simplify)
- ▶ Collapse categories in covariates
- ▶ Penalised regression
- ▶ Other

Perfect separation: example

```
x <- seq(-3, 3, by=0.1)
y <- x > 0
model <- glm(y ~ x, family=binomial)
```

```
## Warning: glm.fit: algorithm did not converge
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

Perfect separation (2)

```
summary(model)
```

```
##
## Call:
## glm(formula = y ~ x, family = binomial)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -17.89     4642.58  -0.004    0.997
## x             357.72     65657.28   0.005    0.996
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 8.4548e+01  on 60  degrees of freedom
## Residual deviance: 6.8270e-08  on 59  degrees of freedom
## AIC: 4
##
```

Perfect separation: example (3)

```
cbind(y, signif(predict(model, type = "response"),2))
```

```
##      y
## 1  0 2.2e-16
## 2  0 2.2e-16
## 3  0 2.2e-16
## 4  0 2.2e-16
## 5  0 2.2e-16
## 6  0 2.2e-16
## 7  0 2.2e-16
## 8  0 2.2e-16
## 9  0 2.2e-16
## 10 0 2.2e-16
## 11 0 2.2e-16
## 12 0 2.2e-16
## 13 0 2.2e-16
## 14 0 2.2e-16
```

Choosing the wrong link

Summary

- ▶ Binomial GLMs for binary of count (succeses/failures) responses
- ▶ Four potential link functions: logit, probit, cloglog, loglog
- ▶ Fixed dispersion: can exhibit overdispersion issues
- ▶ Perfect separation