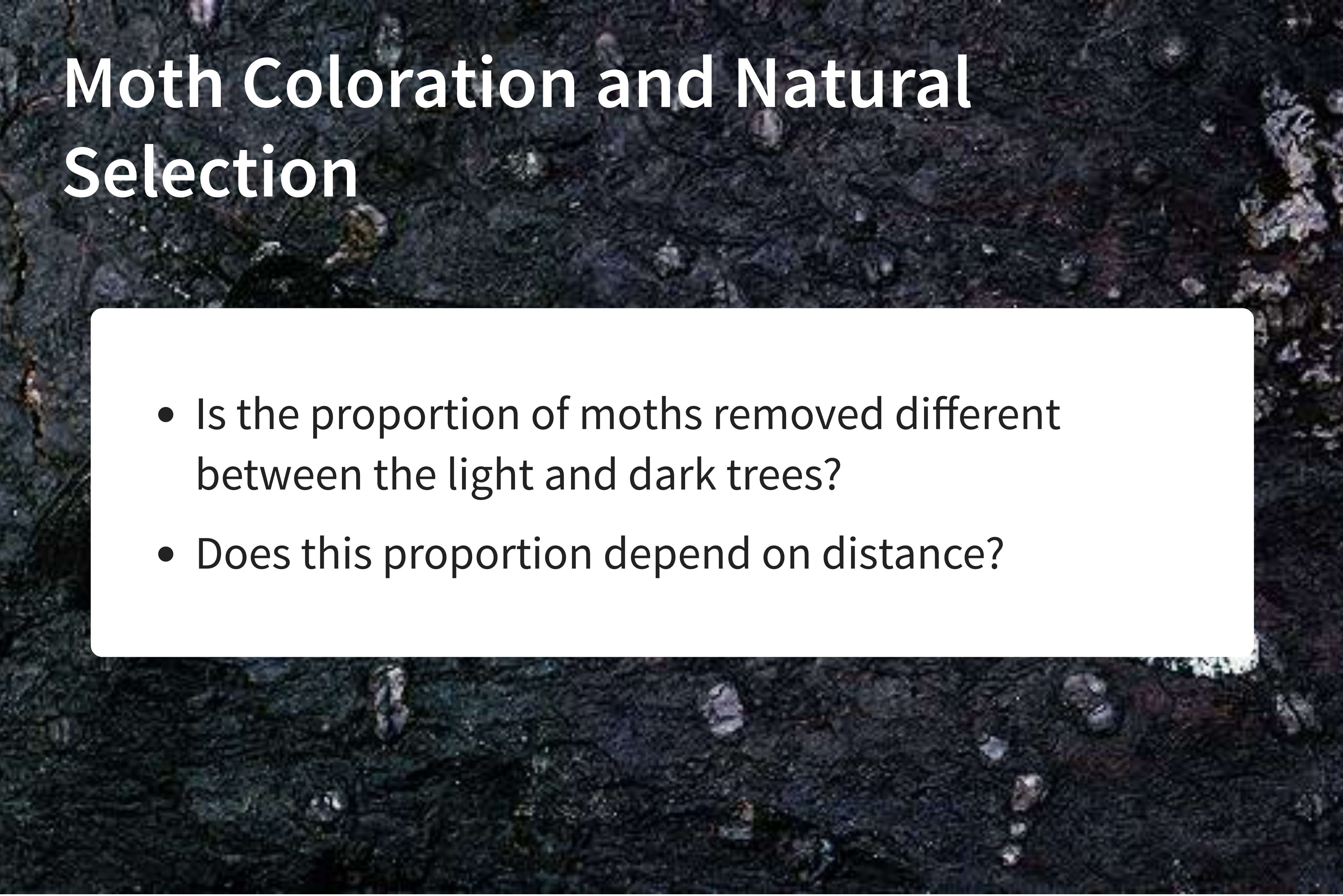
Modeling Binomial Counts

Logistic regression – Stat 230

Moth coloration data

- J. A. Bishop studied how natural selection worked on moths in England. Trees near Liverpool England were blackened by air pollution from the mills (1970's).
- 7 locations chosen, progressively farther from Liverpool
- At each location, 8 trees were chosen at random and equal number of light and dark moths were glued on the trees
- After 24 hours, the number of moths taken (presumably by birds) were counted for each morph

Morph	Distance	Placed	Removed
light	0.0	56	17
dark	0.0	56	14
light	7.2	80	28
dark	7.2	80	20



Moth Coloration and Natural Selection

- Is the proportion of moths removed different between the light and dark trees?
- Does this proportion depend on distance?

Binomial response

- Y_i = the number of moths removed (i.e. successes) on each tree, in each morph

- Y_i = sum of n_i success/failure (Bernoulli) trials

- We will **assume** that these trials are independent

Binomial distribution

The sum of independent and identically distributed success/failure trials follows a Binomial(n, p) distribution.

Binomial logistic regression

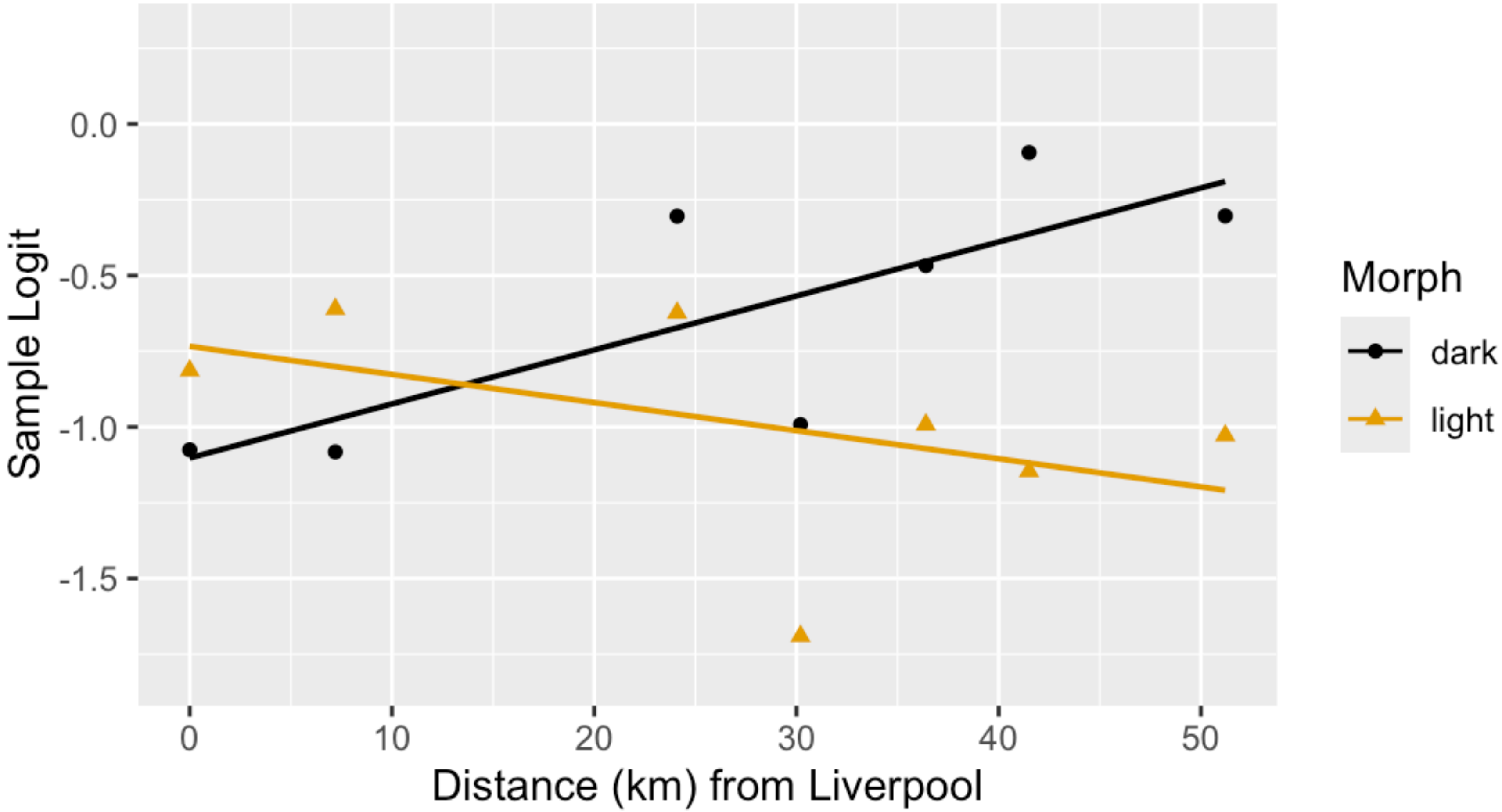
Goal: Model $\pi_i = \text{P}(\text{success} | x_{1i}, x_{2i}, \ldots, x_{pi})$

$$\text{logit}(\pi_i) = \log\left(\frac{\pi_i}{1-\pi_i}\right) = \beta_0 + \beta_1 x_{1i} + \cdots + \beta_p x_{pi} = \eta_i$$

$$\pi_i = \frac{e^{\eta_i}}{1+e^{\eta_i}} = \frac{e^{\beta_0+\beta_1 x_{1i}+\beta_2 x_{2i}+\cdots+\beta_p x_{pi}}}{1+e^{\beta_0+\beta_1 x_{1i}+\beta_2 x_{2i}+\cdots+\beta_p x_{pi}}}$$

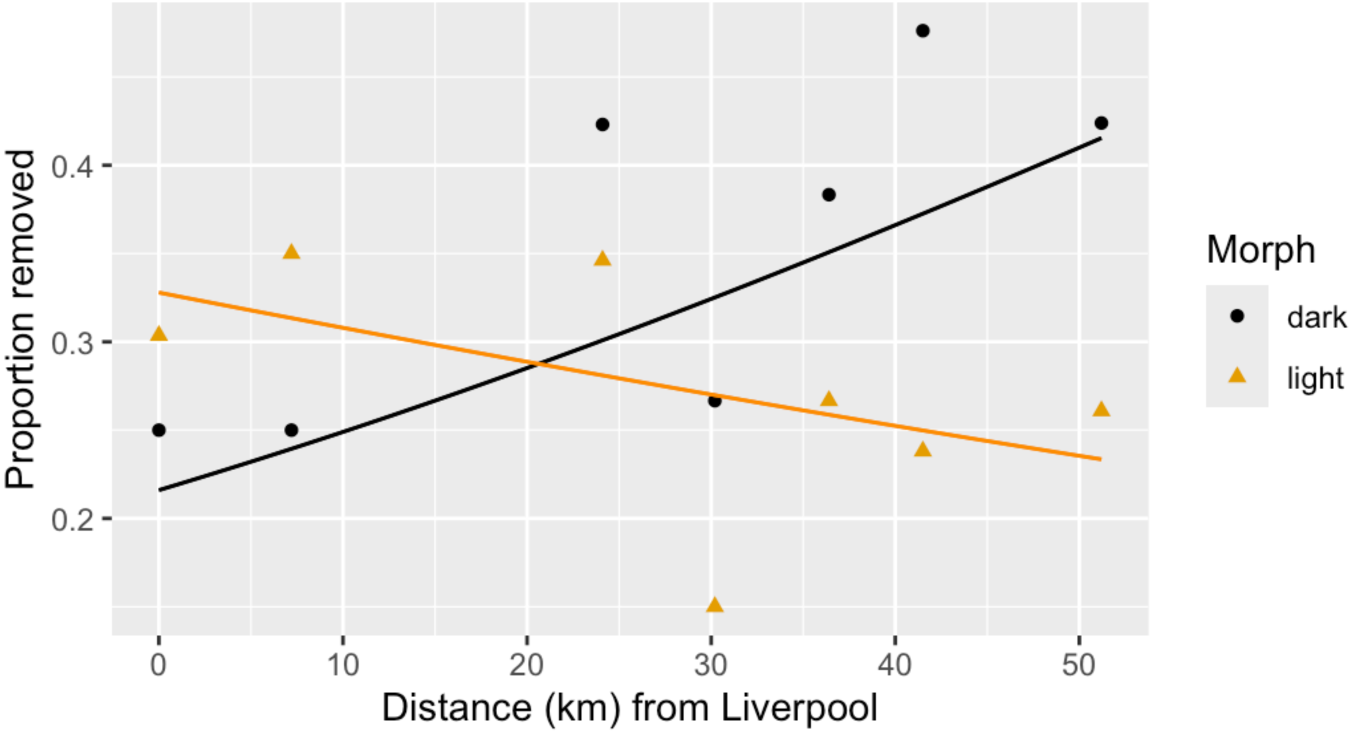
EDA before modeling

The binomial logistic regression model **assumes** that the **logit is linearly related to the predictors**



Fitted model

$$\log\left(\frac{\widehat{\pi}_i}{1-\widehat{\pi}_i}\right) = -1.289 + 0.0185\texttt{distance}_i + 0.415\texttt{morph}_i \\ -0.0277\texttt{distance}_i \times \texttt{morph}_i$$


Proportion removed
0.2
0.3
0.4
0
10
20
30
40
50
Distance (km) from Liverpool
Morph
● dark
▲ light

Interpretations

We interpret the fitted model just like we did in binary logistic regression!

$$\log\left(\frac{\hat{\pi}_i}{1-\hat{\pi}_i}\right) = -1.289 + 0.0185\texttt{distance}_i + 0.415\texttt{morph}_i$$
$$-0.0277\texttt{distance}_i \times \texttt{morph}_i$$

For dark moths, a 1 km increase in the distance from Liverpool is associated with about a 2% increase ($e^{0.0185} \approx 1.02$ factor increase) in the odds of being taken.

Inference

We conduct inference for binomial logistic regression using the same tools as for binary logistic regression!

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	-1.129	0.198	-5.705	0.000	-1.527	-0.750
Distance	0.019	0.006	3.277	0.001	0.008	0.030
Morphlight	0.411	0.274	1.498	0.134	-0.126	0.952
Distance:Morphlight	-0.028	0.008	-3.437	0.001	-0.044	-0.012

- Wald tests and intervals for individual regression coefficients

- Drop-in deviance tests for sets of regression coefficients

Model assumptions

- **Binomial counts**
- **Independence**: observations are independent
- **Linearity**: the log odds is a linear function of the predictors
- **Variance structure**: the variance of a binomial random variable is $n\pi(1 - \pi)$

  $\implies$ so the variance of Y_i is $n_i\pi_i(1 - \pi_i)$ (not constant!)

Pearson residuals

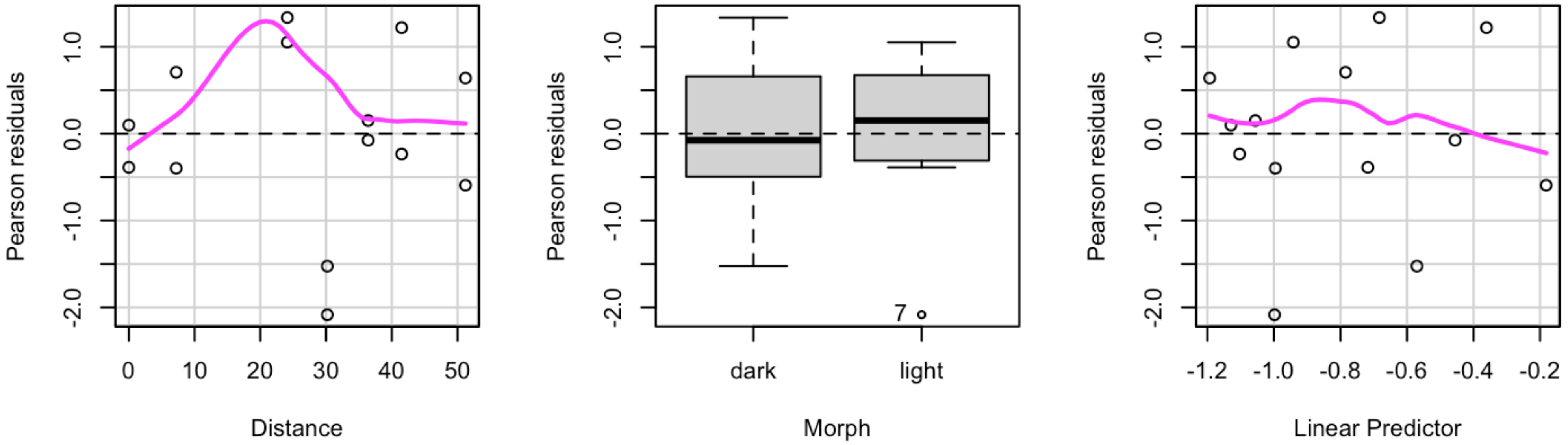
$$\text{Pres}_i = \frac{Y_i - n_i\hat{\pi}_i}{\sqrt{n_i\hat{\pi}_i(1-\hat{\pi}_i)}}$$

For large enough n_i, Pearson residuals tend to behave like they come from $N(0,1)$

How to use?

- Plot against fitted values, predictors
- Check for curvature, outliers

Pearson residuals



- Evidence of a nonlinear relationship between the log odds and distance
- No obvious outliers

Deviance residuals

$$\text{Dres}_i = \text{sign}(Y_i - n_i\hat{\pi}_i)\sqrt{2\left[Y_i \log\left(\frac{Y_i}{n_i\hat{\pi}_i}\right) + (n_i - Y_i)\log\left(\frac{n_i - Y_i}{n_i - n_i\hat{\pi}_i}\right)\right]}$$

For large enough n_i, deviance residuals tend to behave like they come from $N(0, 1)$

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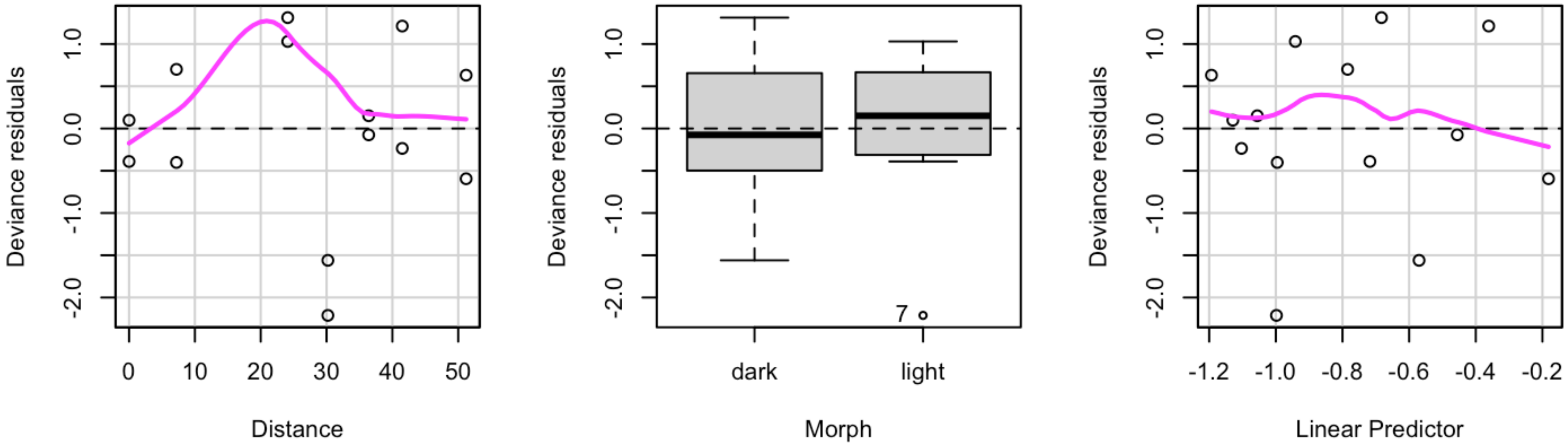
Deviance residuals



- Evidence of a nonlinear relationship between the log odds and distance
- No obvious outliers

Drop-in deviance test

Do we need a quadratic term for distance?

$$
\begin{aligned}
\mathrm{H}_0 \ &: \mathrm{logit}(\pi_i) = \beta_0 + \beta_1 \texttt{dist} + \beta_2 \texttt{morph} + \beta_3 \texttt{dist} \times \texttt{morph} \\
\mathrm{H}_\mathrm{a} \ &: \mathrm{logit}(\pi_i) = \beta_0 + \beta_1 \texttt{dist} + \beta_2 \texttt{morph} + \beta_3 \texttt{dist} \times \texttt{morph} \\
&\qquad + \beta_4 \texttt{dist}^2 + \beta_4 5\texttt{dist}^2 \times \texttt{morph}
\end{aligned}
$$

Reduced model deviance = 13.2299

Full model deviance = 12.7283

```r
1 - pchisq(0.5016, df = 2)
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[1] 0.778178
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