

Introduction to binomial models in glmmTMB

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This video covers

- basics of binomial data
- survival example
 - using `cbind` for the response
 - using $I(^2)$ for a quadratic term
- presence/absence salamanders
 - non-default link `cloglog`

Basics

- N trials with k successes
- binary, Bernoulli, same as binomial $N = 1$
- probability of success $p = g^{-1}(X\beta)$
- mean = pN
- variance = $p(1 - p)N$
- default `binomial(link = "logit")`

Link functions

- logit
- probit
- cloglog

Ex: Density-dependent larvae survival (Reilly & Hajek 2008)

- suggested $S \sim \text{Binom}(p = \beta_0 + \beta_1 D^{\beta_2}, N)$,
- can't get that shape with glmmTMB
- for demonstration purposes $I(D^2)$

see `code_binomial.R`

Ex: Salamander presence/ absence (Price et al. 2016)

- Salamanders in streams affected by mining
- ignoring pseudoreplication (Hurlbert 1984)
- `family=binomial(link="cloglog")`

see `code_presence_absence.R`

Recap

- `cbind(k, N-k)` for response (if $N > 1$)
- binary response, single column