The general linear model:

$$y_i \sim Normal(\mu_i, \sigma)$$
$$\mu_i = \beta_o + x_i \beta_1$$

Simulate from the model and draw x from a standard normal distribution:

$$y_i \sim Normal(\mu_i, \sigma)$$
$$\mu_i = \beta_o + x_i \beta_1$$
$$\beta_0 = 0.5$$
$$\beta_1 = 0.5$$
$$\sigma = 0.75$$

Generalized linear models have:

1. A response distribution
2. A linear function trying to predict the response from the predictors
3. A link function that maps the linear prediction to a parameter in the response distribution.

If we call the link function $g()$, the general linear model looks like:

$$y_i \sim Normal(\mu_i, \sigma)$$
$$g(\mu_i) = \beta_0 + x_i \beta_1$$

In this case we use the identity link function (think just multiplying by 1). So the general linear model is a *generalized* linear model with a normal response distribution and an identity link.

How do we bring Allie's lizard example into the linear model framework since it doesn't have normal residuals? We could use a binomial response distribution and the logit link function:

$$y_i \sim Binomial(1, p_i)$$
$$logit(p) = \beta_0$$

What is a logit? First turn probability into odds:

$$odds = \frac{p}{1-p}$$

Next we take the log of the odds and get the logit:

$$logit(p) = log\left(\frac{p}{1-p}\right)$$

Allies lizard example with size.

$$dive_i \sim Binomial(1, p_i)$$
$$logit(p_i) = \beta_0 + size_i \beta_1$$

The model for germination as a function of area:

$$germ_i \sim Binomial(1, p_i)$$
$$logit(p_i) = \beta_0 + area_i\beta_1$$

Let's add in the crosses now. This works by indexing the intercept so that there is a unique intercept for each cross.

$$germ_i \sim Binomial(1, p_i)$$
$$logit(p_i) = \beta_{0[cross_i]} + area_i\beta_1$$