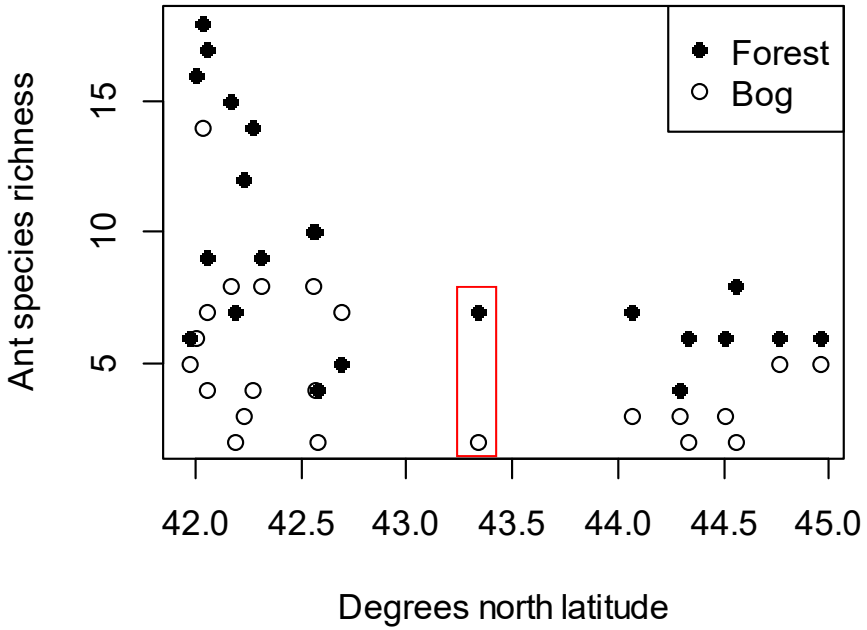
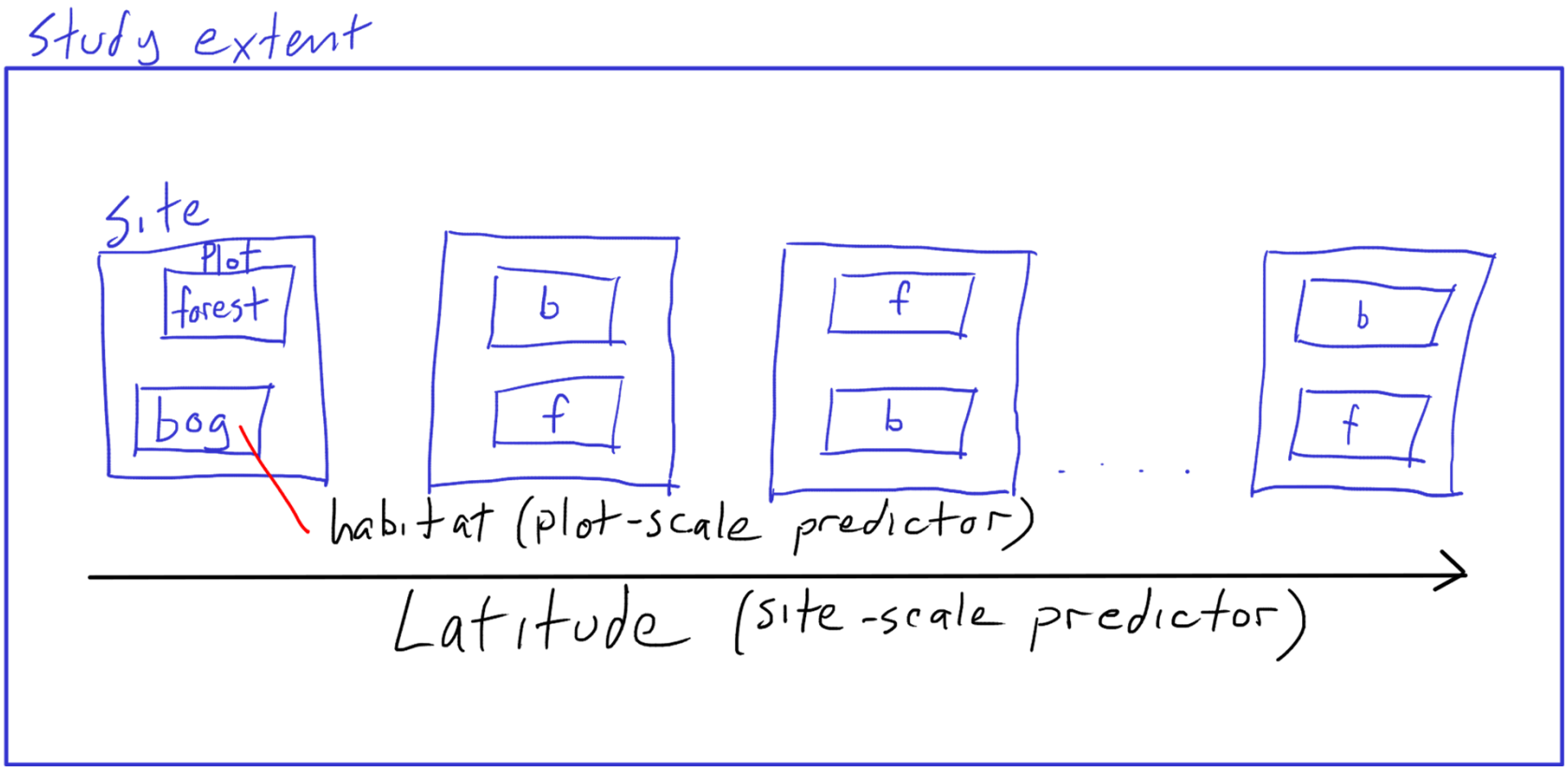
Ants multilevel model

- Sketch data design
- Math equations (2 ways: nested, additive)
- Linear model syntax



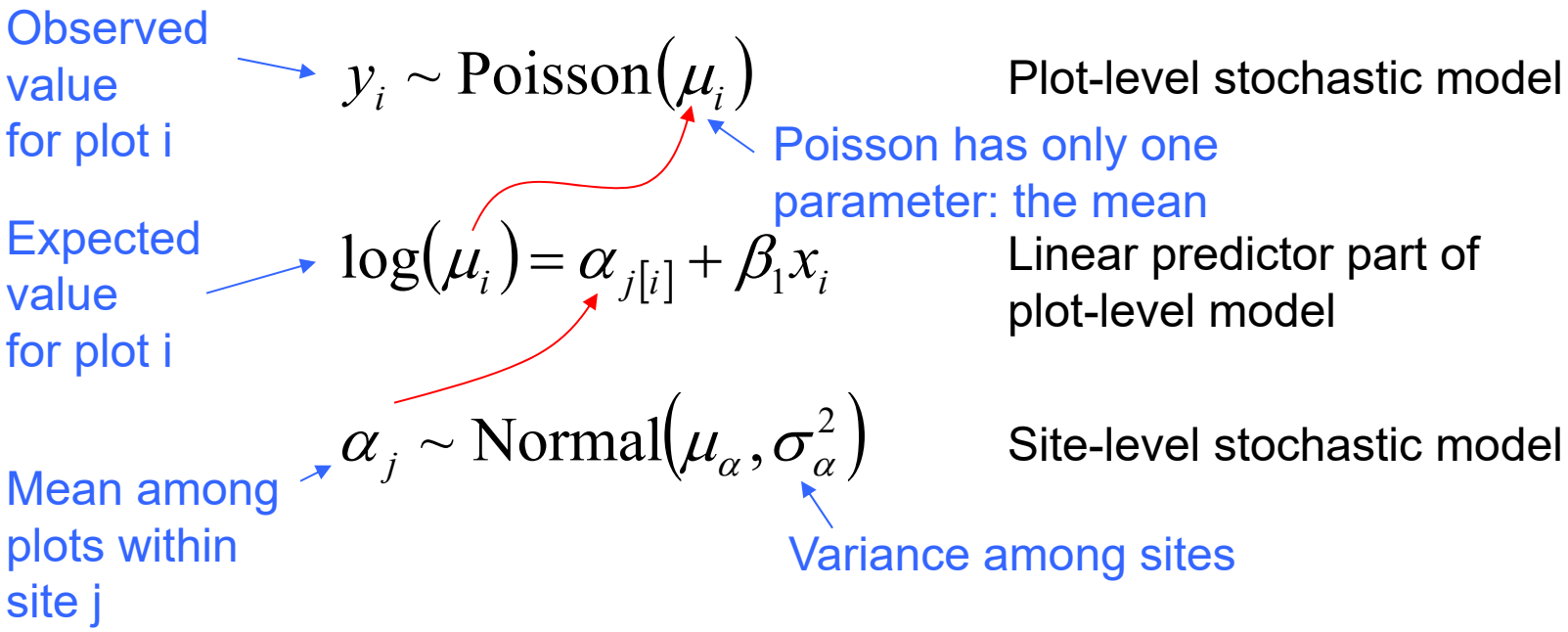
Poisson
Log link

Ants: sketch data structure



GLMM

Poisson with log link (aka Poisson regression)



GLMM - Ants

Two variables with an interaction.
Where does the interaction go? Lowest component

$$y_i \sim \text{Poisson}(\mu_i)$$ Plot-level stochastic model

$$\ln(\mu_i) = \alpha_{j[i]} + \beta_1 x_{1,i} + \beta_3 x_{1,i} x_{2,j[i]}$$

forest (habitat)

$$\alpha_j \sim \text{Normal}(\mu_\alpha, \sigma_\alpha^2)$$ Site-level stochastic model

$$\mu_\alpha = \beta_0 + \beta_2 \, x_{2,j}$$

latitude

x_2 is a vector with only the site-level latitude in it – i.e. not by plot

Ants – additive decomposition

$$y_i \sim \text{Poisson}(\mu_i)$$

$$\ln(\mu_i) = \beta_0 + \beta_1 x_{1,i} + \beta_2 x_{2,i} + \beta_3 x_{1,i} x_{2,i} + s_{j[i]}$$

$$s_j \sim \text{Normal}(0, \sigma_s^2)$$

What is the inverse link model?

$$\mu_i = e^{\beta_0} e^{\beta_1 x_{1,i}} e^{\beta_2 x_{2,i}} e^{\beta_3 x_{1,i} x_{2,i}} e^{s_{j[i]}}$$

Syntax

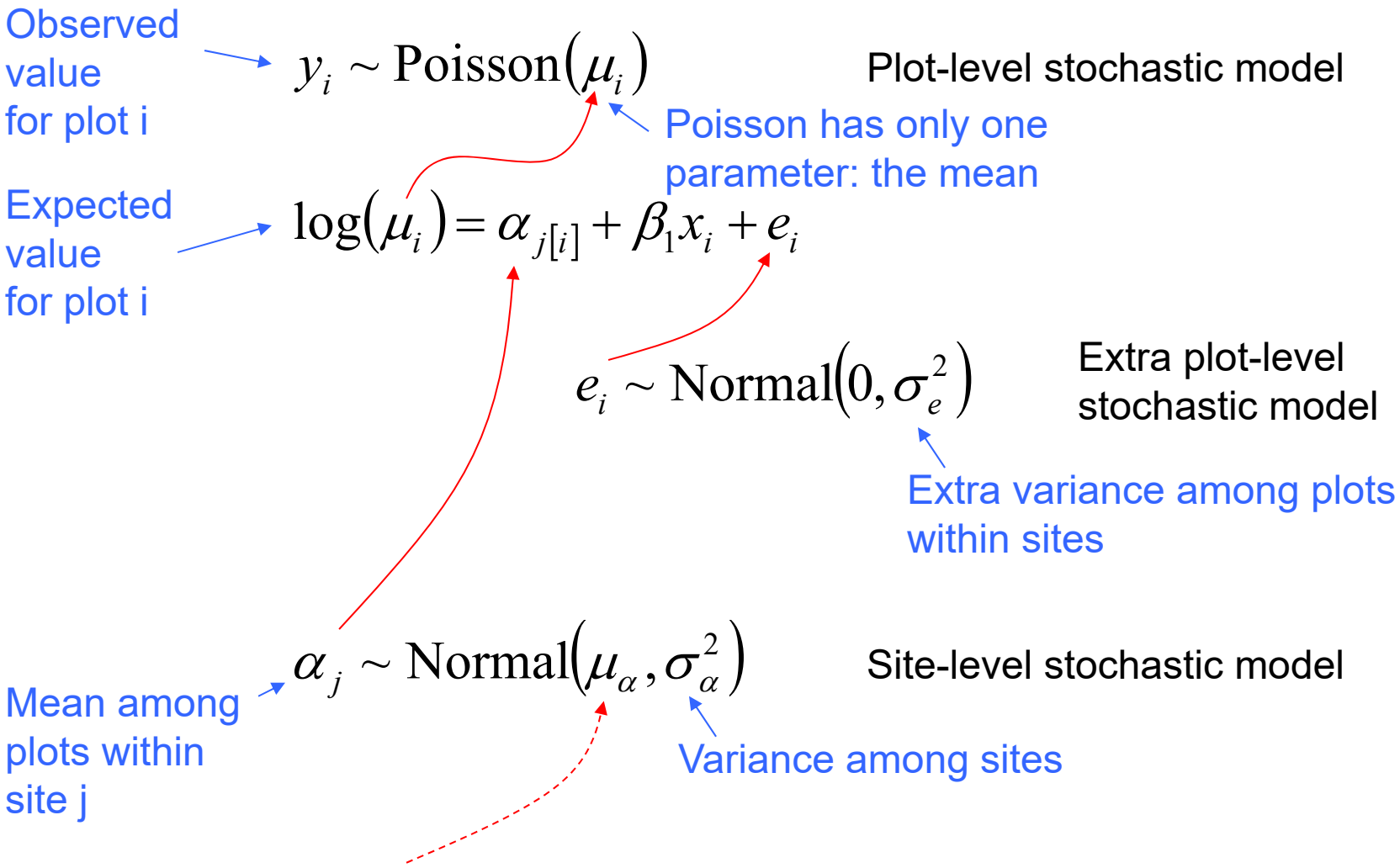
```
glmer(y ~ habitat*latitude + (1|site),
      family=poisson, data=df)
```

Code - ants

- 12_4_ants_multilevel.R
- 12_4_ants_multilevel.md

GLMM with overdispersion

Allow for extra variation at data scale



GLMM with overdispersion

Set up in R:

First make a data-level identifier, e.g.

```
df$plot <- 1:nrow(df)
```

Then:

```
glmer(y ~ x + (1|site) + (1|plot),
      family=poisson, data=df)
```

Other approaches

- quasi-Poisson family: `family=quasipoisson`
- negative binomial (= Poisson-gamma)

GLMM: Ants + overdispersion

$$y_i \sim \text{Poisson}(\mu_i)$$

Plot-level stochastic model

$$\ln(\mu_i) = \alpha_{j[i]} + \beta_1 x_{1,i} + \beta_3 x_{1,i} x_{2,j[i]} + e_i$$

forest (habitat)

$$\alpha_j \sim \text{Normal}(\mu_\alpha, \sigma_\alpha^2)$$

Site-level stochastic model

Extra plot-level stochastic model

$$e_i \sim \text{Normal}(0, \sigma_e^2)$$

$$\mu_\alpha = \beta_0 + \beta_2 x_{2,j}$$

latitude

x_2 is a vector with only the site-level latitude in it – i.e. not by plot

GLMM: Ants + overdispersion

$$y_i \sim \text{Poisson}(\mu_i)$$

$$\ln(\mu_i) = \beta_0 + \beta_1 x_{1,i} + \beta_2 x_{2,i} + \beta_3 x_{1,i} x_{2,i} + s_{j[i]} + e_i$$

$$s_j \sim \text{Normal}(0, \sigma_s^2)$$

$$e_i \sim \text{Normal}(0, \sigma_e^2)$$