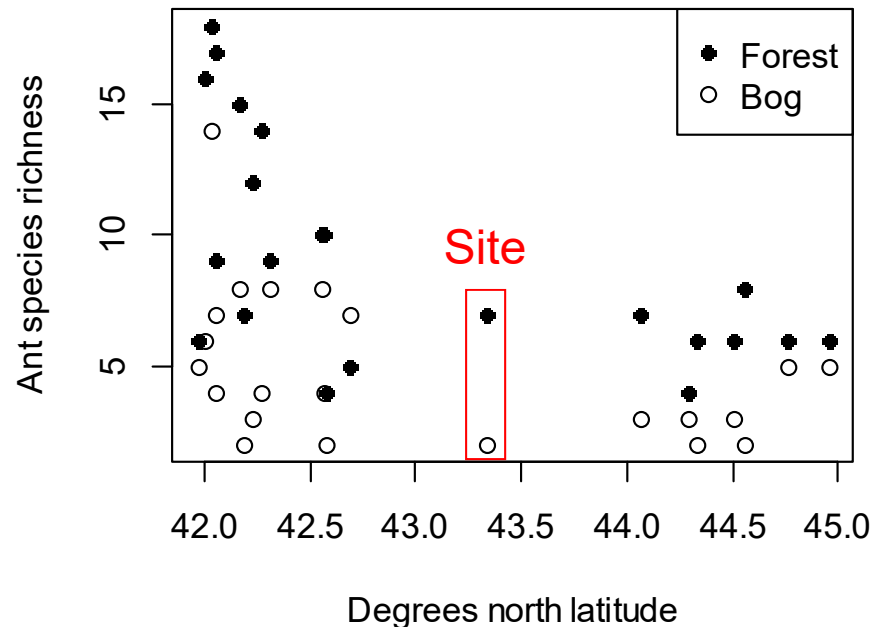


Ants multilevel model

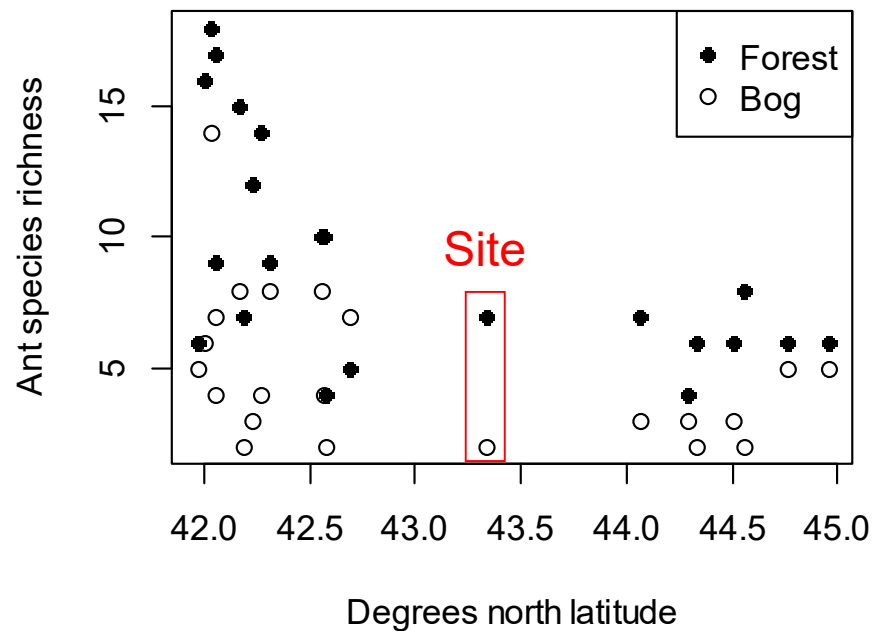
- Sketch study design (how data structured)
- Math equations (2 ways: nested, additive)
- Linear model syntax



Poisson
Log link

Ants multilevel model

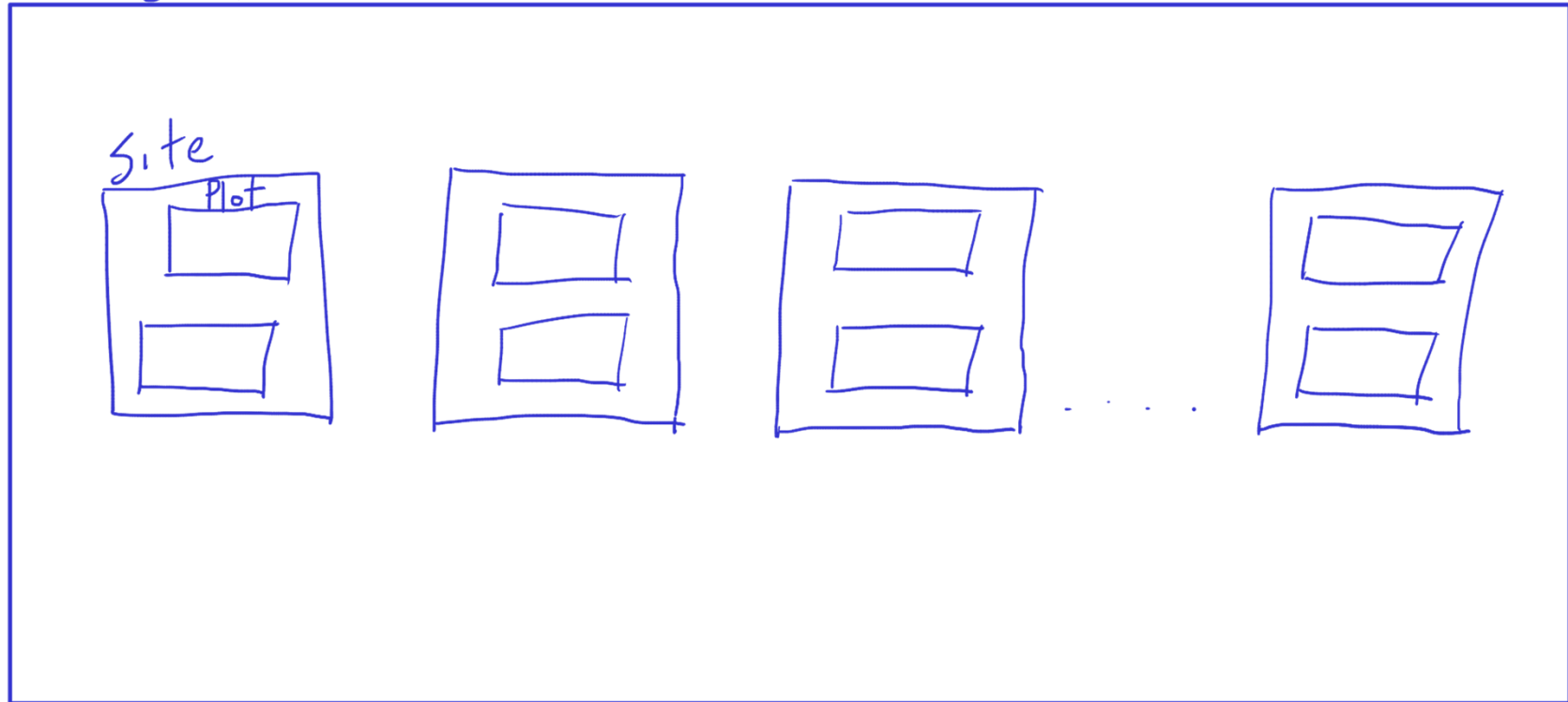
- Sketch study design (how data structured)



- 1) extent (largest scale)
- 2) study units (smallest scale)
- 3) groups (eg spatial scales)
- 4) predictors (different scales)

Ants: sketch study design

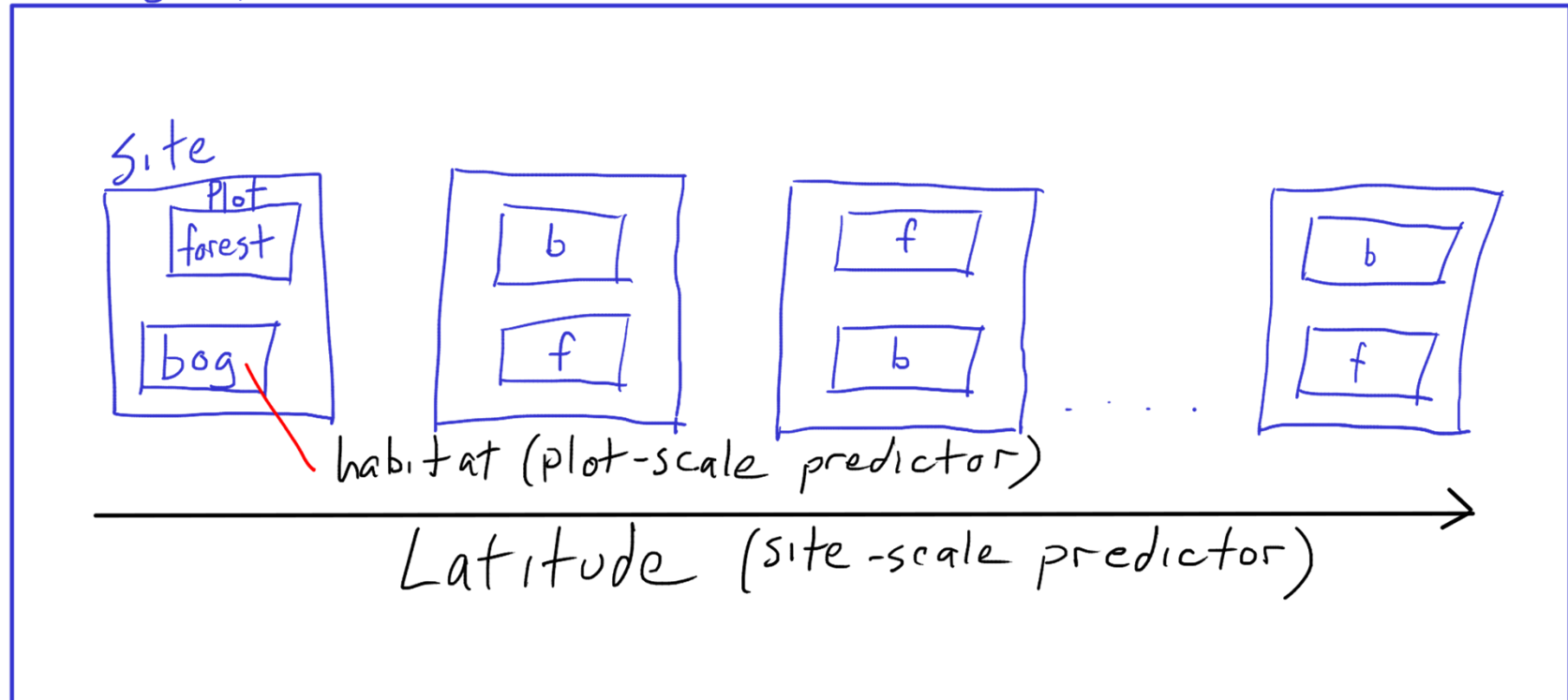
Study extent



Grouping structure at different scales

Ants: sketch study design

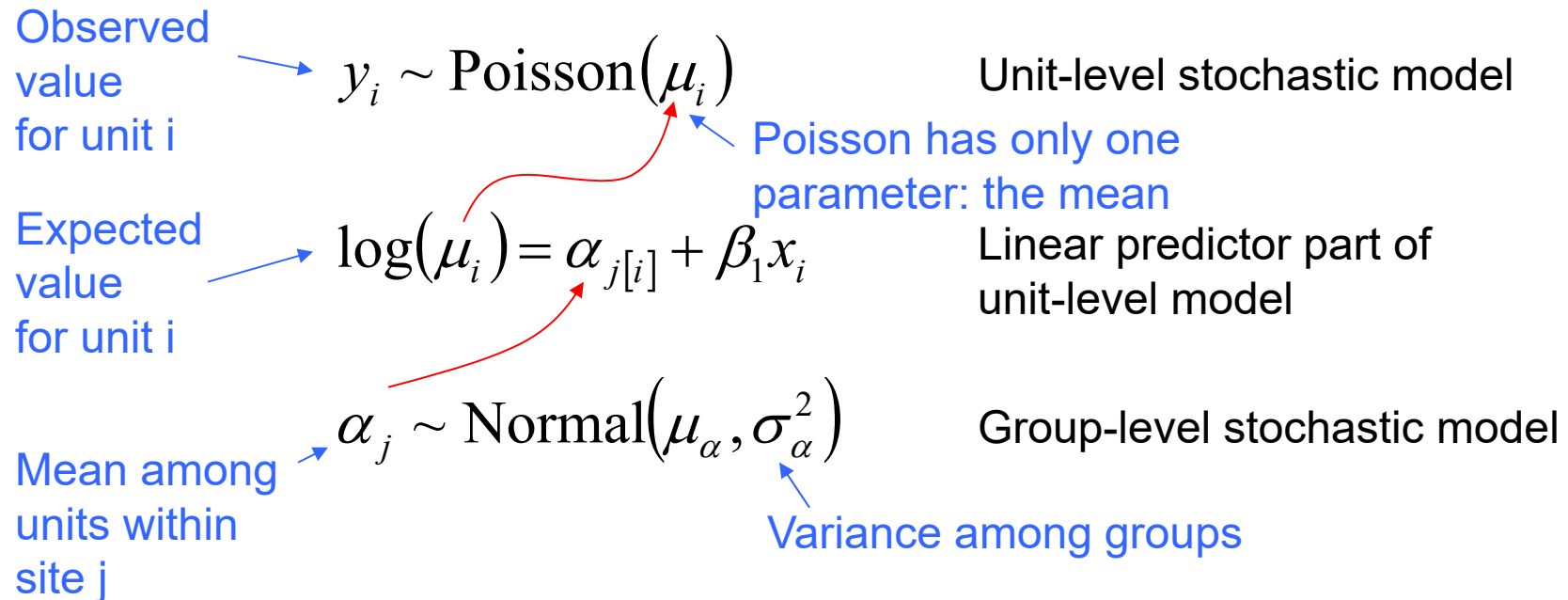
Study extent



Mapping predictors to different scales

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

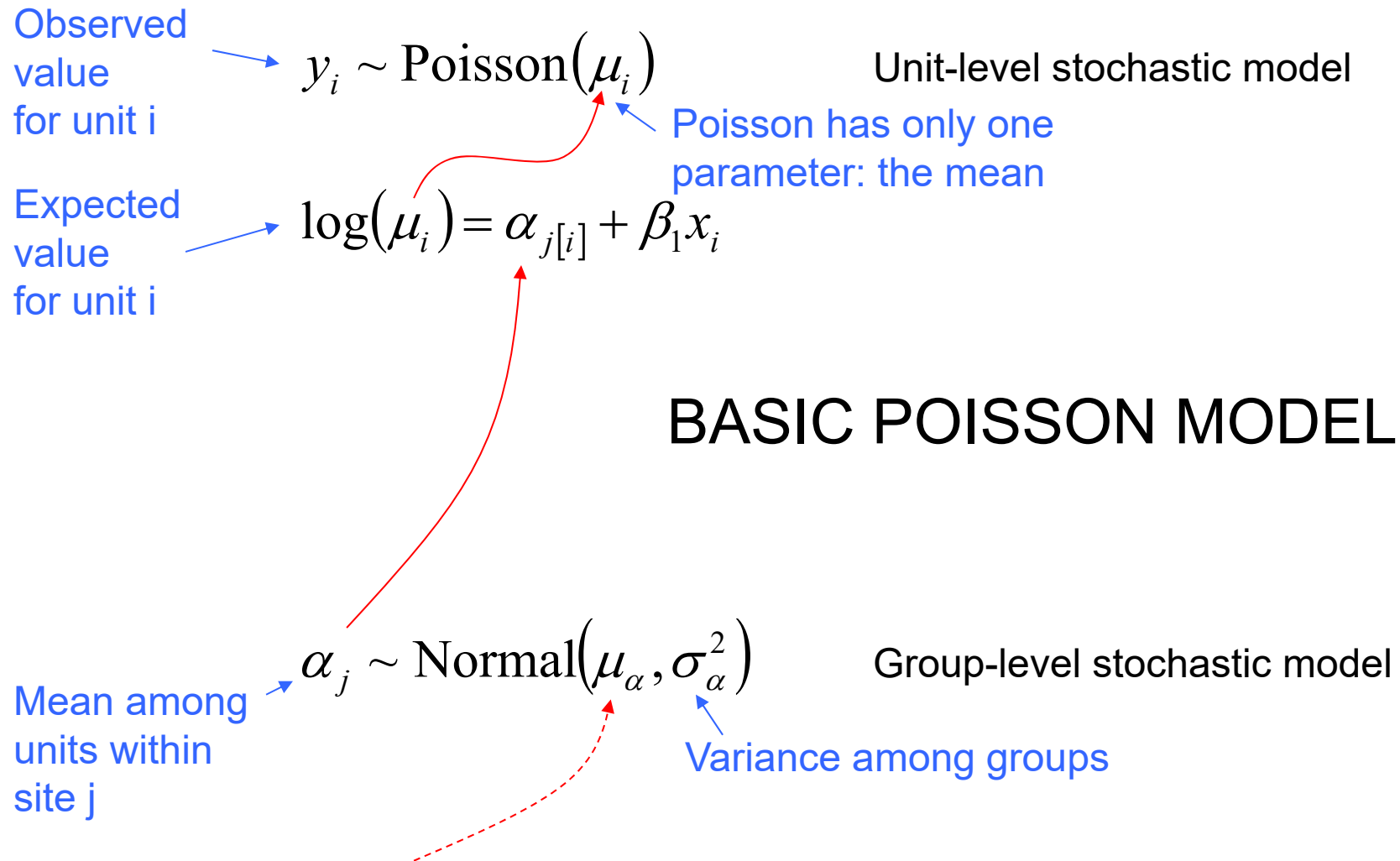
- 13_4_ants_multilevel.Rmd
- 13_4_ants_multilevel.md

GLMM with overdispersion

Allow for extra variation at unit (data) scale

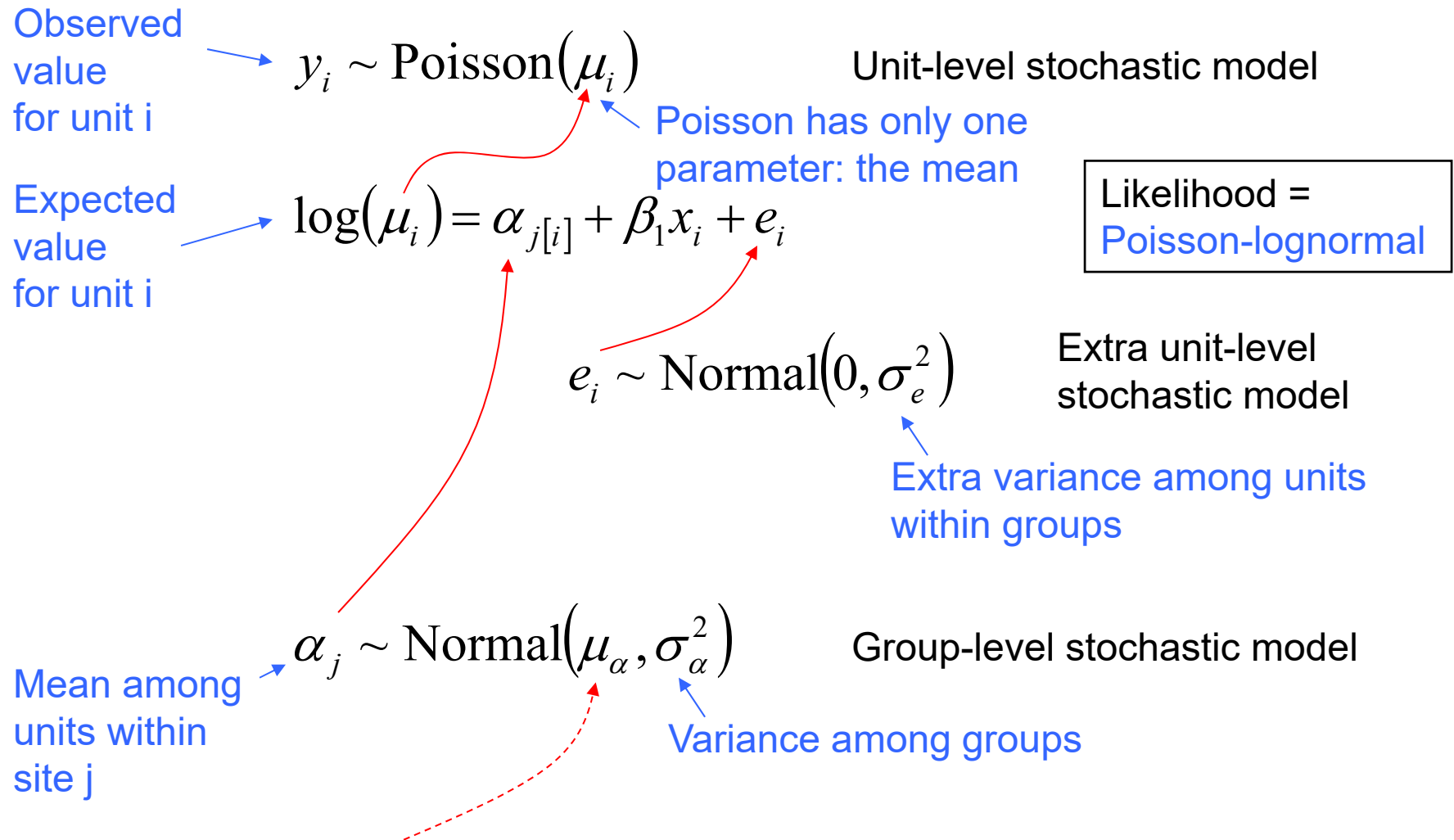
GLMM with overdispersion

Allow for extra variation at unit (data) scale



GLMM with overdispersion

Allow for extra variation at unit (data) scale



GLMM with overdispersion

Set up in R:

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

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

Then:

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

Other common 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

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

latitude

Extra plot-level
stochastic model

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

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

GLMM: Ants + overdispersion

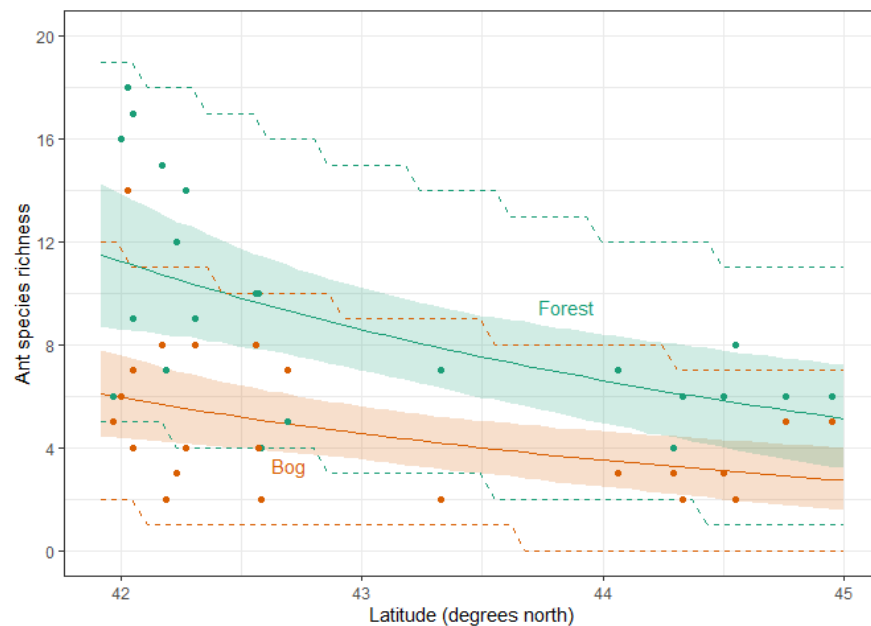
$$y_i \sim \text{Poisson}(\mu_i)$$

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

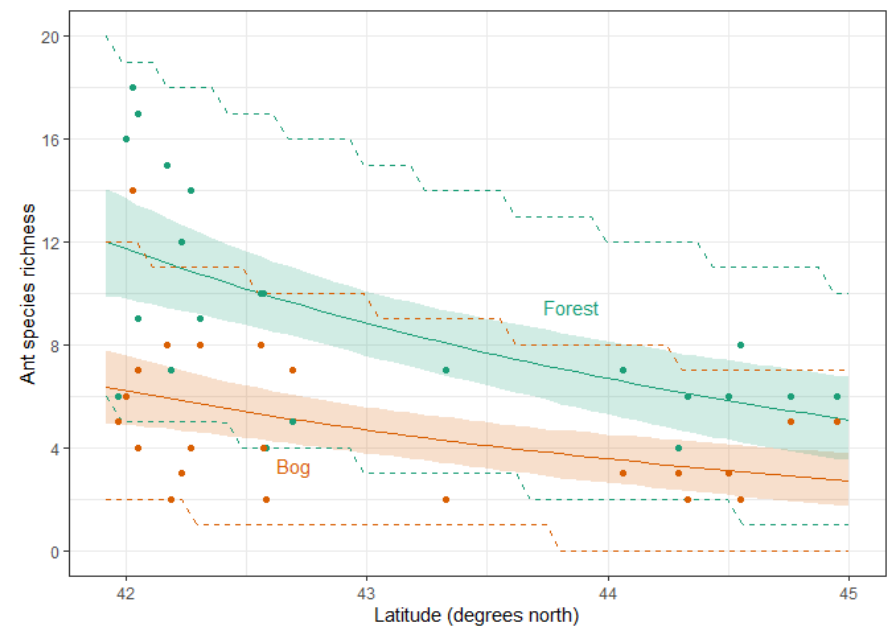
$$s_j \sim \text{Normal}(0, \sigma_s^2)$$

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

With site-scale and
unit-scale (overdispersion)
random effects

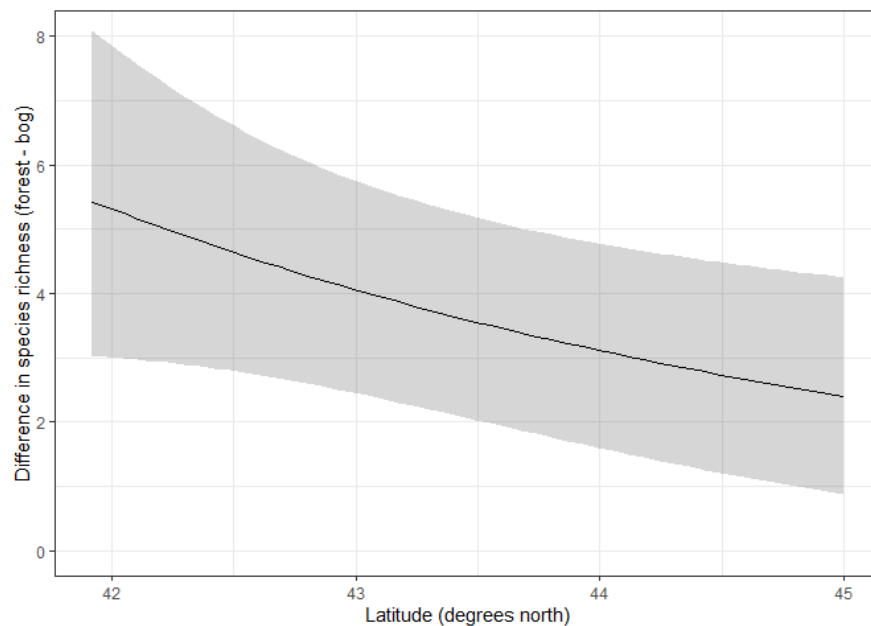


Without random effects

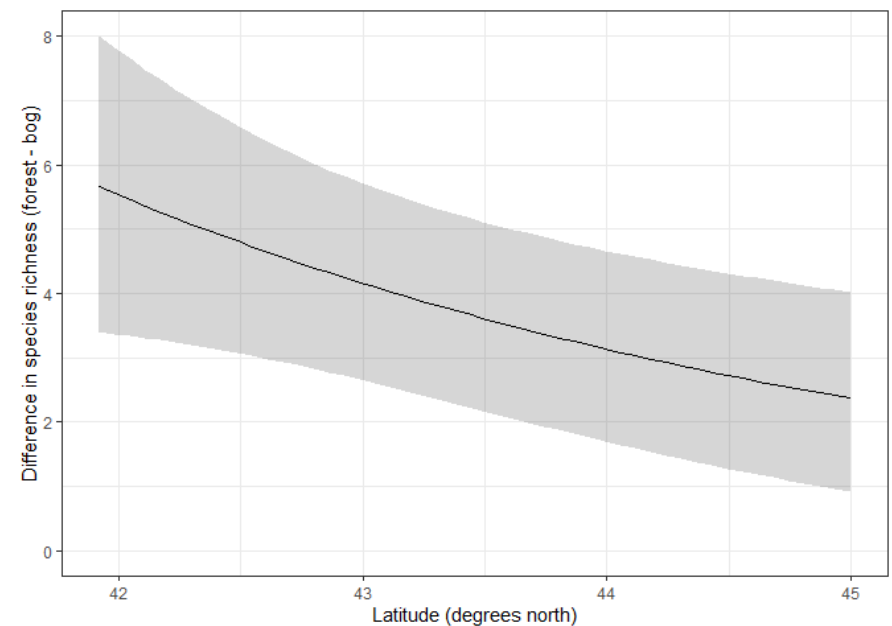


Intervals are **wider** because
less independence and more
variation than Poisson. Also,
slightly less-steep relationship.

With site-scale and
unit-scale (overdispersion)
random effects



Without random effects



Intervals are **wider** because
less independence and more
variation than Poisson. Also,
slightly less-steep relationship.