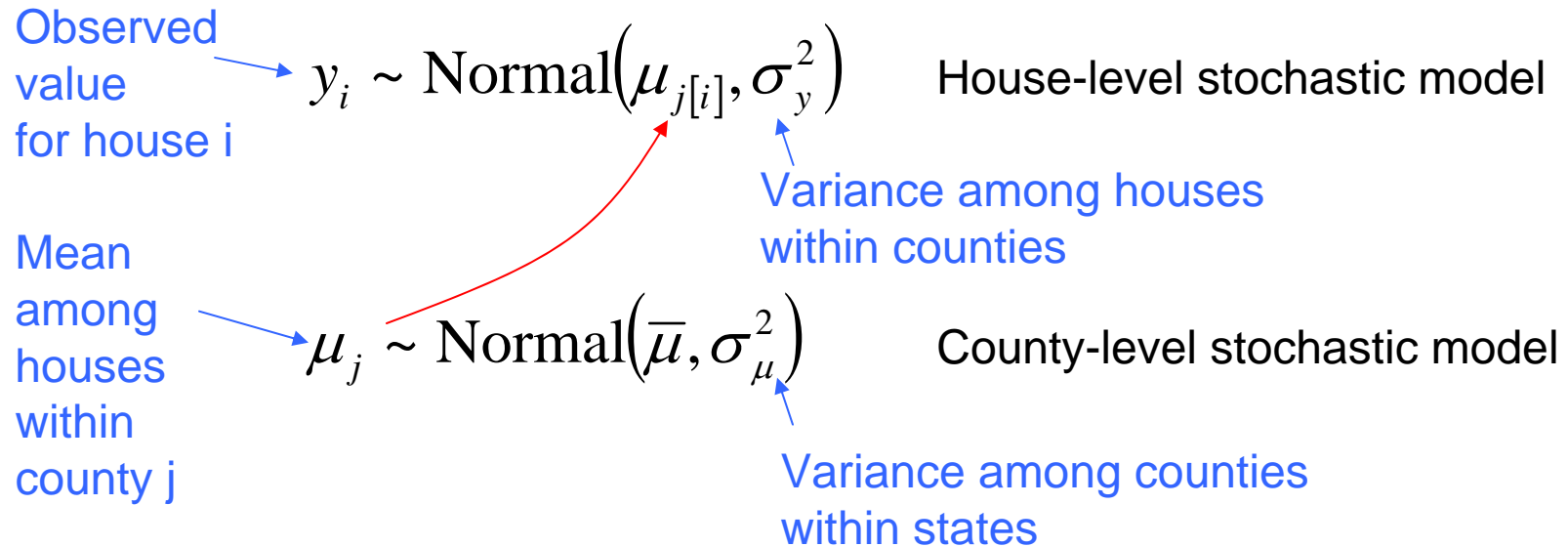


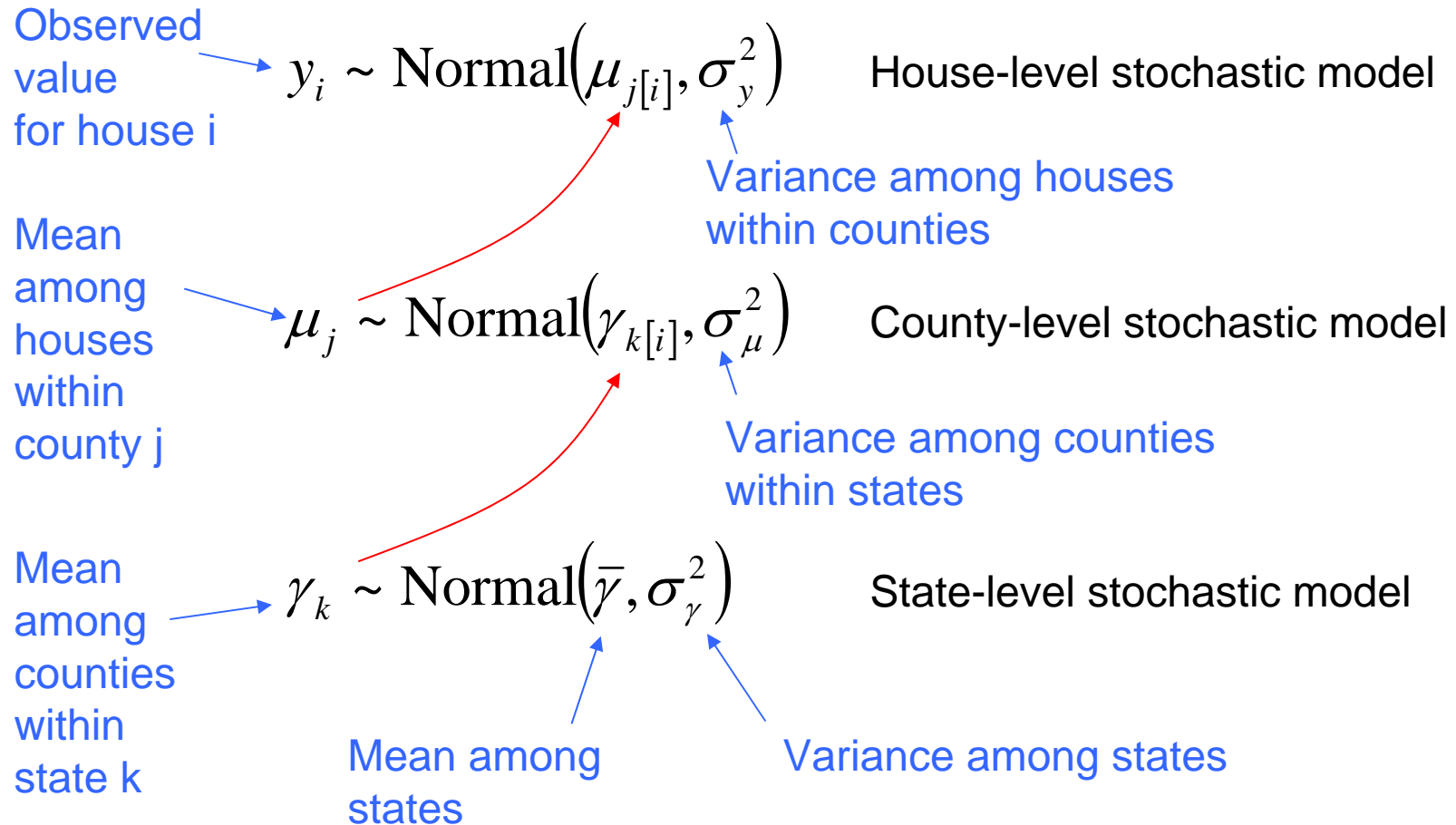
Multiple nested scales

Multilevel model, with Gnested levels



Multiple nested scales

Multilevel model, with 3 nested levels



Multiple nested scales

Alternative parameterization

$$y_i = \beta_0 + s_{k[i]} + c_{j[i]} + e_i$$

Residual: deviation of house i from county j mean

Overall mean among states

Deviation of state k mean from overall mean

Deviation of county j mean from state k mean

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

Variance among states

$$c_j \sim \text{Normal}(0, \sigma_c^2)$$

Variance among counties within states

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

Variance among houses within counties

Multiple nested scales

Linear model syntax for lmer

If states and counties uniquely identified in data:

$$y \sim 1 + (1 | \text{state}) + (1 | \text{county})$$

Otherwise you can form unique identifiers with the nested operator:

$$y \sim 1 + (1 | \text{state}/\text{county})$$

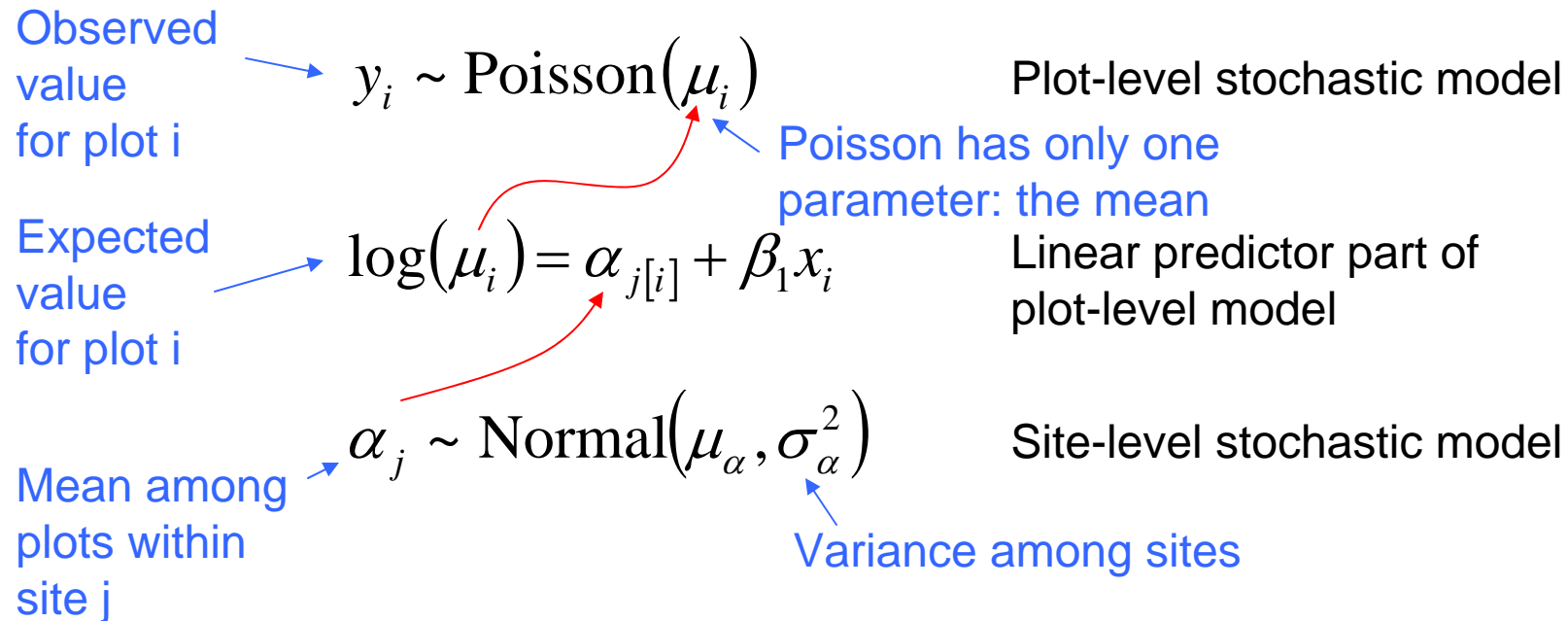
which expands to (you can also use this):

$$y \sim 1 + (1 | \text{state}) + (1 | \text{state}:\text{county})$$

thus, the interaction `state:county` uniquely identifies all counties in the dataset

GLMMs

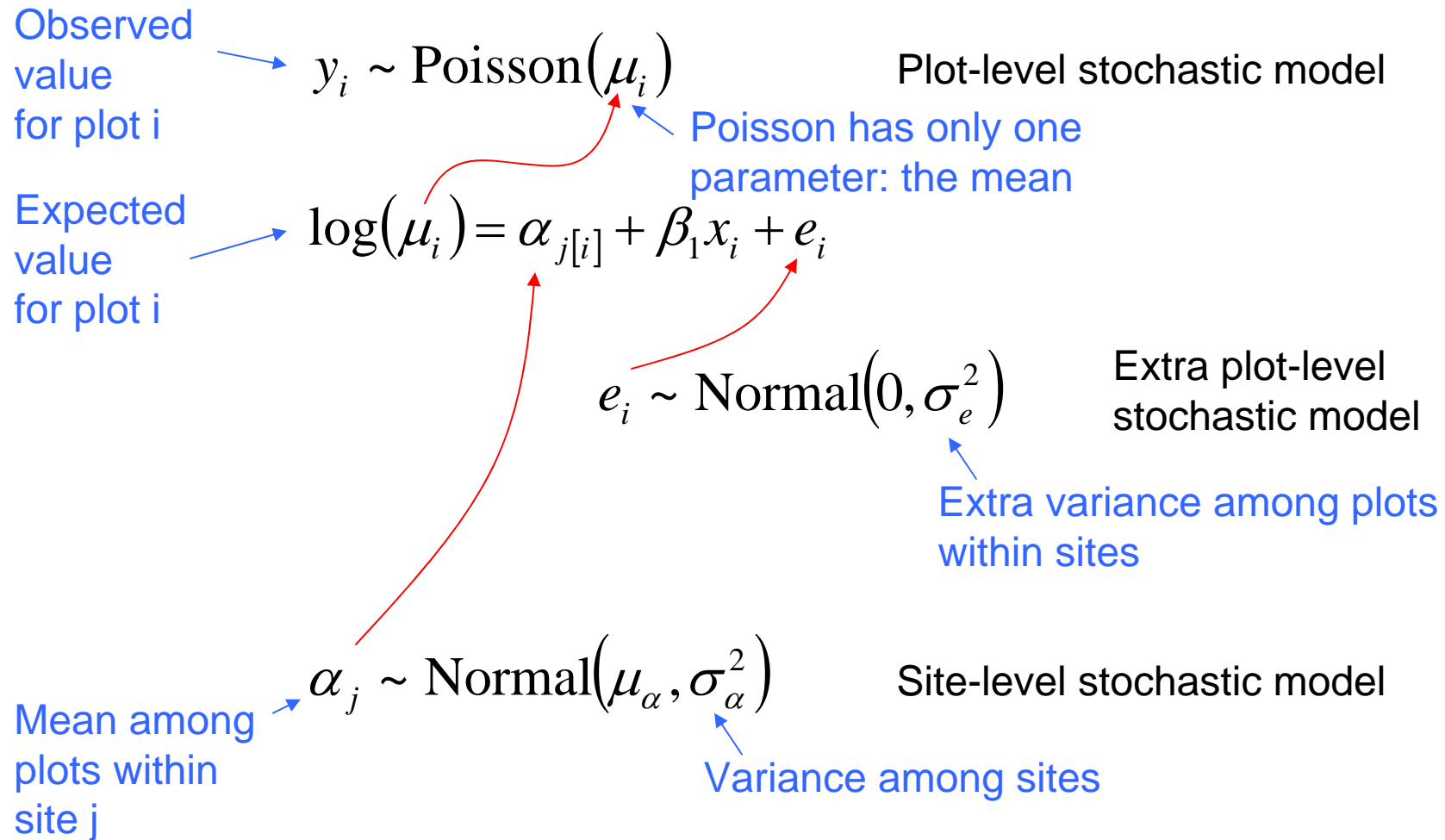
For example: Poisson regression (e.g. ants dataset)



In GLMMs, the data level can have a different distribution, such as Poisson or binomial, but the upper levels are all Normal

GLMMs - overdispersion

Allow for extra variation at data scale



GLMMs - overdispersion

Set up in R:

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

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

Then:

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

Other approaches

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