

mixed models: introduction

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Overview

Acknowledgements

- shoulders of giants
- especially
 - Doug Bates, Martin Mächler, Steve Walker (`lme4`)
 - Kasper Kristensen, Mollie Brooks (`glmmTMB`)
- the R community, `r-sig-mixed-models` denizens, bug reporters ...
- McMaster, NSERC, Univ Florida, US NSF, BIRS

Mixed models

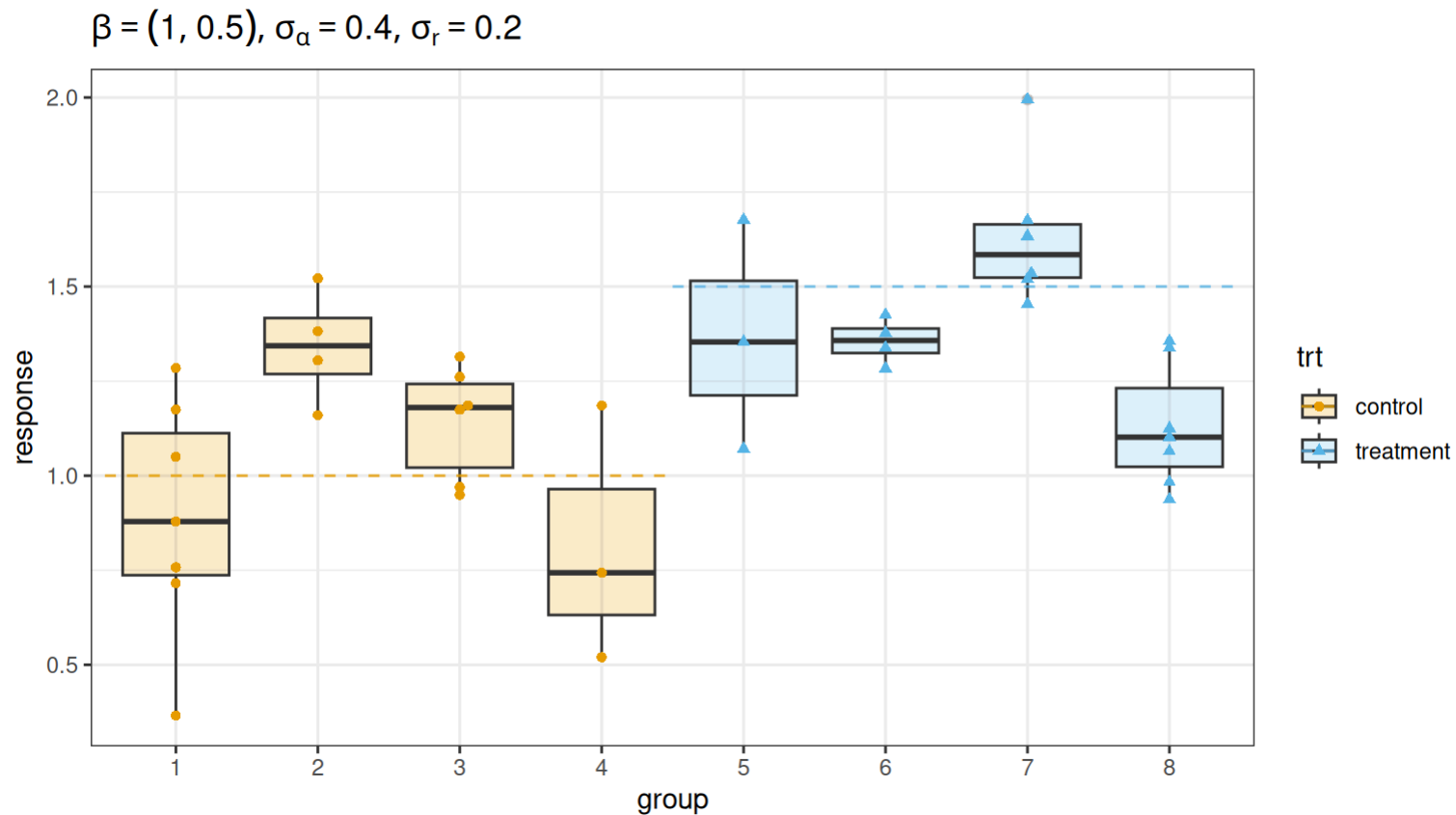
- *tabular* data (row = observation, column = variable)
- *regression* models
 - continuous and categorical *predictor* variables
 - single (univariate) numeric *response* variable
- with one or more *grouping variables* ('blocks', 'clusters', ...)
- for prediction or inference
- typically for 'medium-sized' data (e.g. 10^6 rows, 10^3 clusters, 10-20 predictors)

Mixed models (easy version)

- take a standard linear-type model (e.g. $y_i = a + bx_i + \epsilon_i$)
- ... but observations fall in *groups*
- breaks assumption of independence (*pseudoreplication*)
- add *between-group* (random) variation:

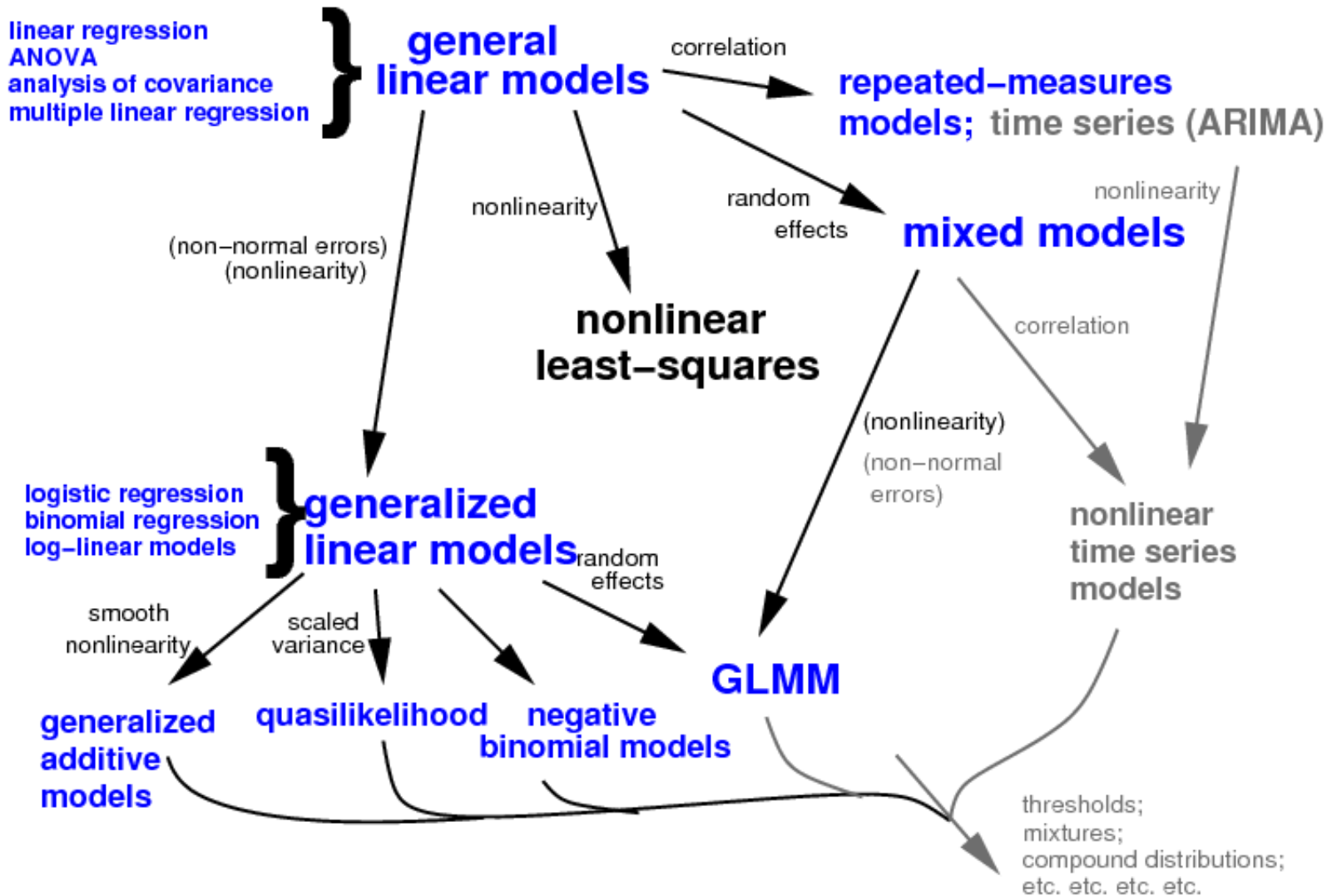
$$y_{ij} = a + bx_{ij} + \alpha_i + \epsilon_{ij}$$

single group, categorical predictor (= one-way ANOVA)



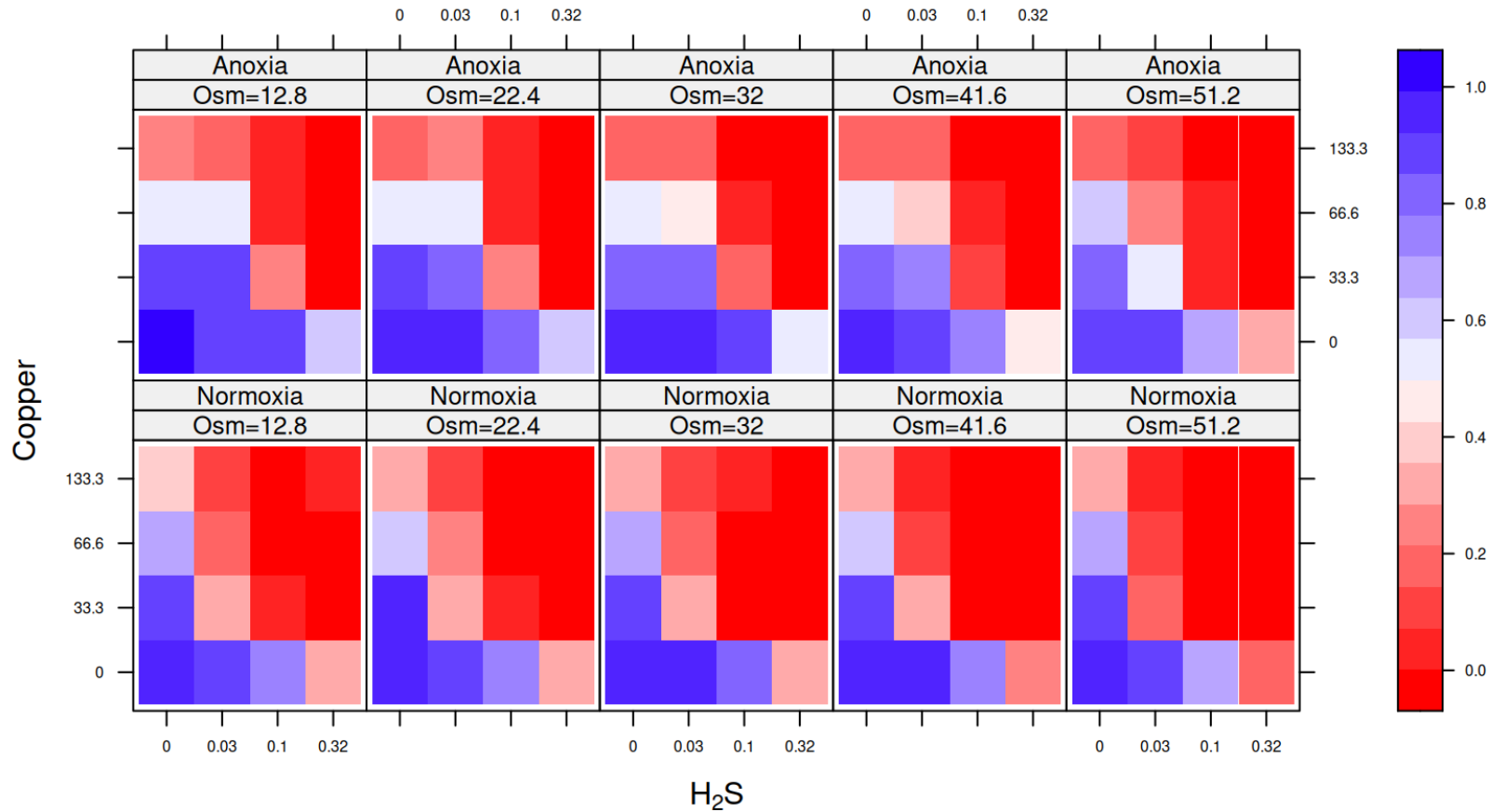
The mixed model universe

- more complex *fixed effects* components (multivariate regression, multiway ANOVA, ANCOVA, ...)
- multiple grouping variables (random effects *terms*); multiple effects per group ("*random slopes*")
- interesting *conditional distributions*
 - exponential dispersion family (à la GLMs): binomial/Poisson/etc.
 - weirder: Tweedie, t distribution, Beta, ...
- nonlinearity: *link functions* (log, logit, etc.)
- structured covariances: autoregressive, compound symmetry, regression splines ...



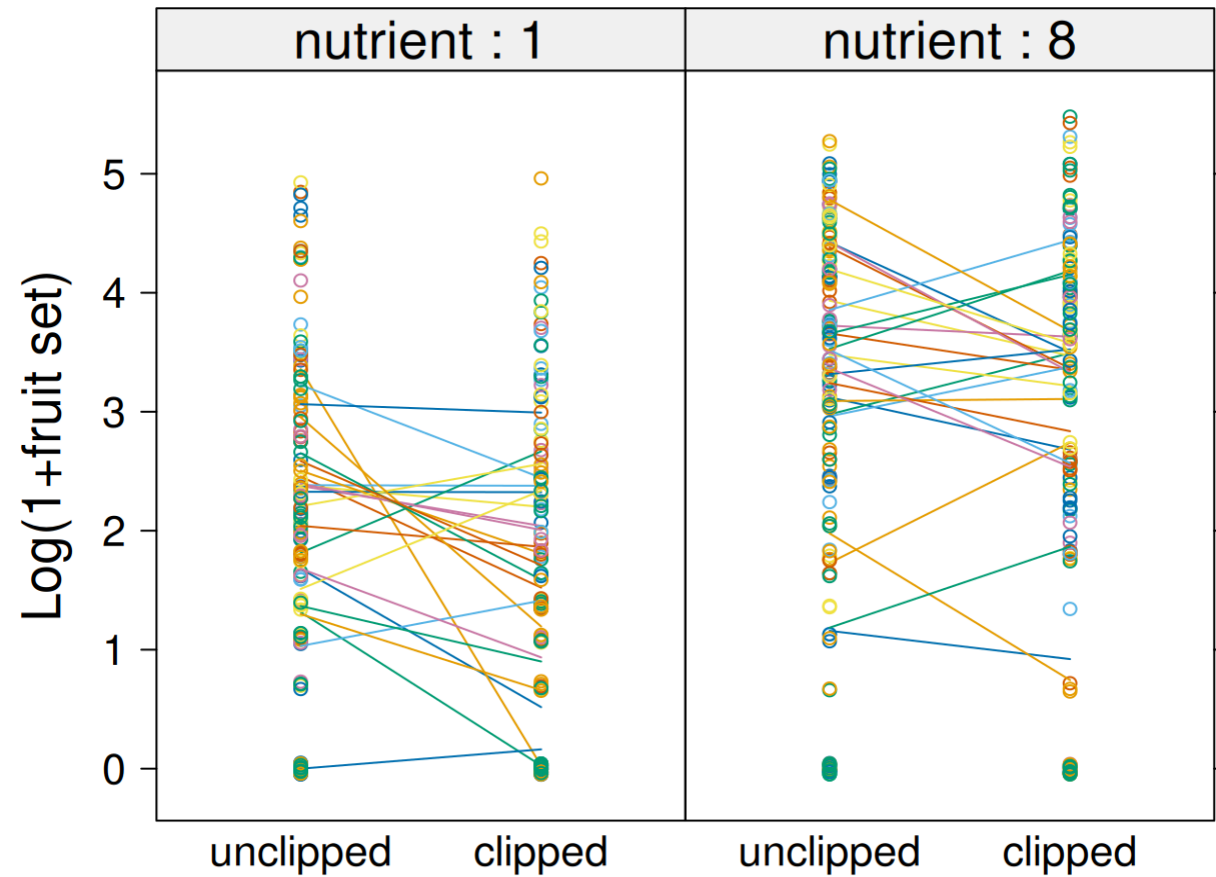
Examples

Experimental: bloodworm cell survival



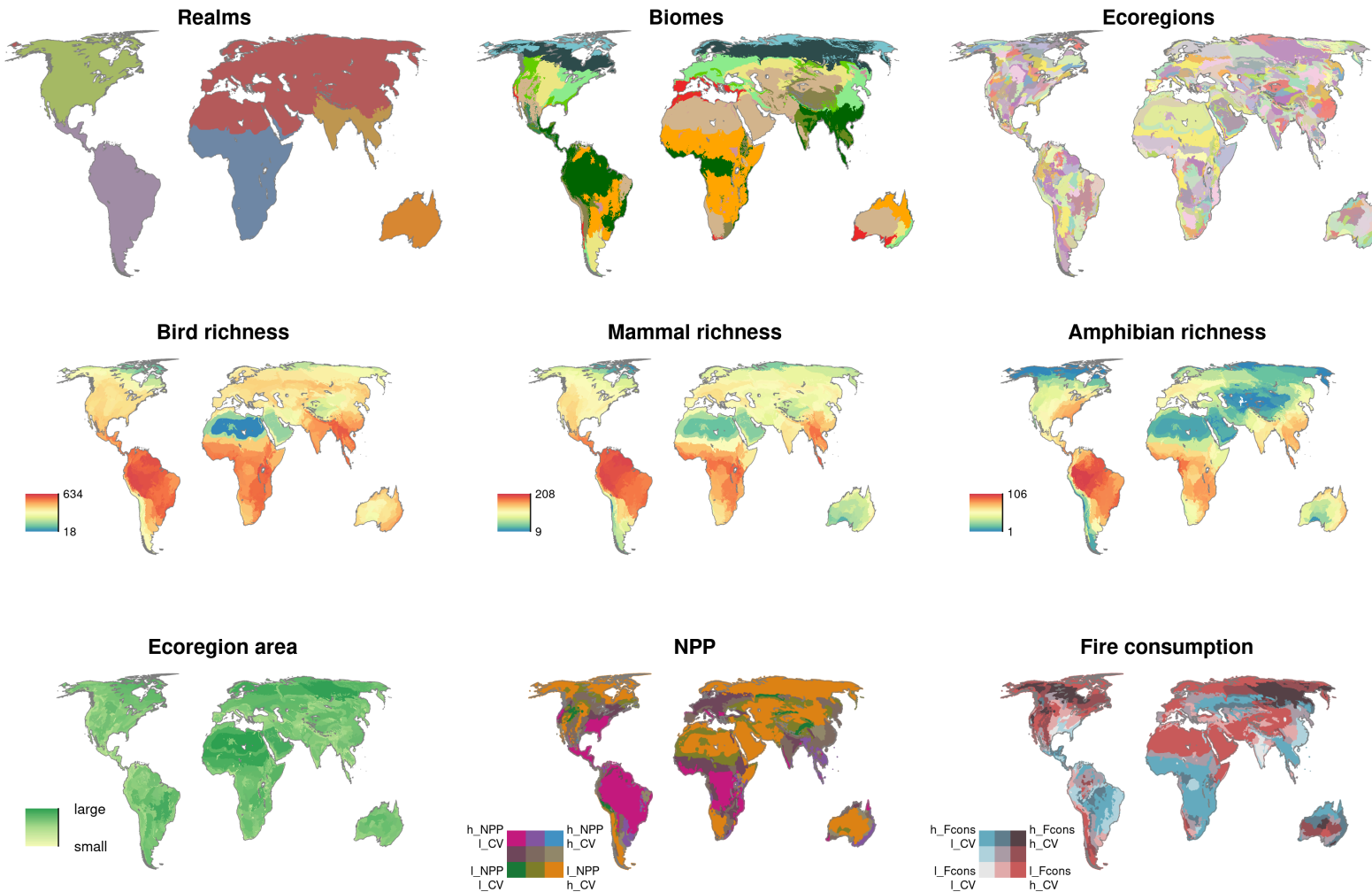
D. Julian, unpublished data

Arabidopsis: fertilization & herbivory



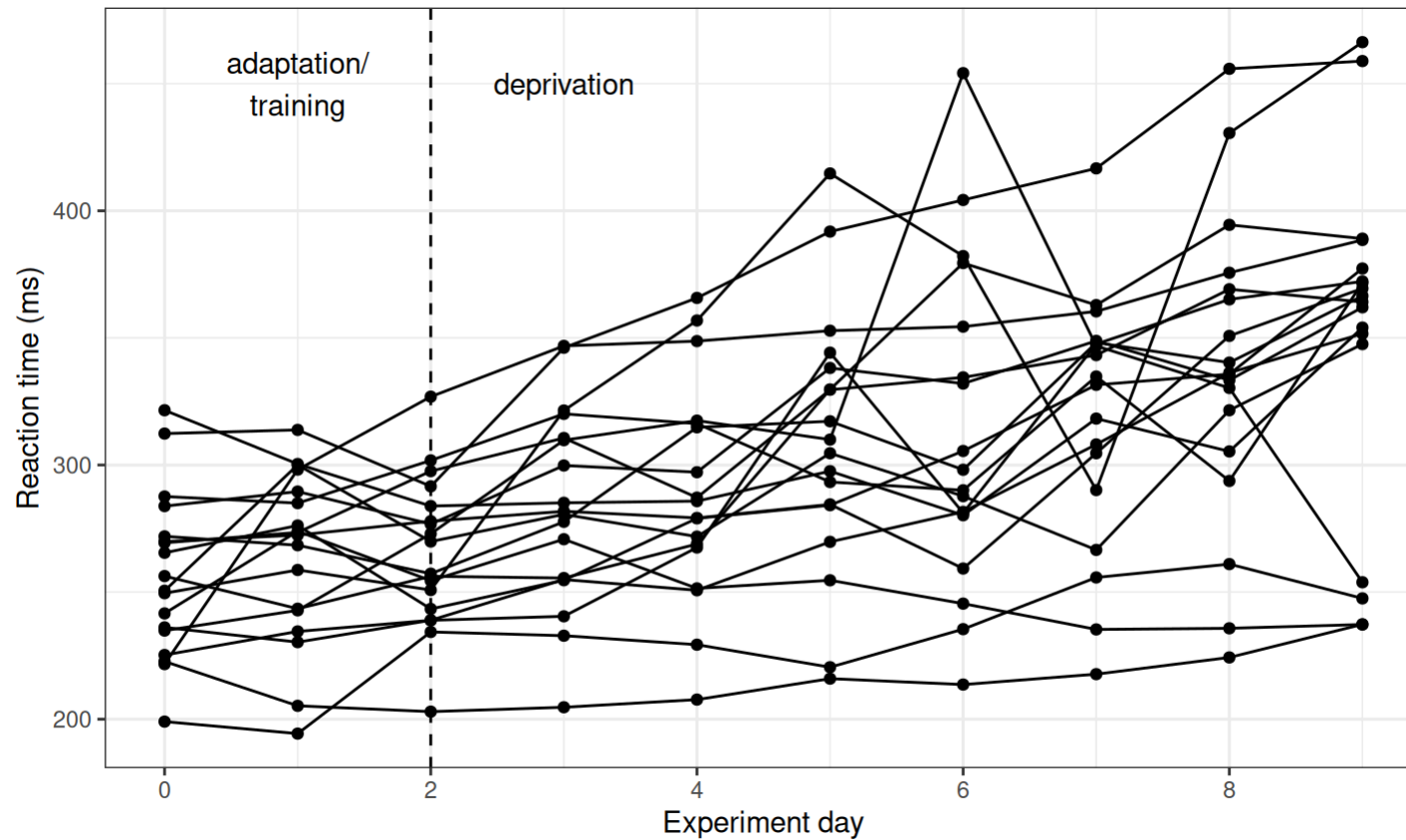
Banta et al. 2010

Wildfire/diversity (Moritz et al. 2023)



Sleep deprivation study

Belenky et al. (2003)



Definitions and descriptions

Simple mixed models

(scalar, intercept-only)

$$\begin{aligned}y_{ij} &= \beta_0 + \beta_1 x_{ij} + \epsilon_{0,ij} + \epsilon_{1,j} \\ &= (\beta_0 + \epsilon_{1,j}) + \beta_1 x_{ij} + \epsilon_{1,j}\end{aligned}$$

$$\epsilon_{0,ij} \sim \text{Normal}(0, \sigma_0^2)$$

$$\epsilon_{1,j} \sim \text{Normal}(0, \sigma_1^2)$$

- Could have multiple, nested levels of random effects (genotype within population within region ...), or *crossed* REs

Random-slopes model

$$\begin{aligned}y_{ij} &= \beta_0 + \beta_1 x_{ij} + \epsilon_{0,ij} + \epsilon_{1,j} + \epsilon_{2,j} x_{ij} \\&= (\beta_0 + \epsilon_{1,j}) + (\beta_1 + \epsilon_{2,j}) x_{ij} \\ \epsilon_{0,ij} &\sim \text{Normal}(0, \sigma_0^2) \\ \{\epsilon_{1,j}, \epsilon_{2,j}\} &\sim \text{MVN}(0, \Sigma)\end{aligned}$$

- variation in the *effect* of a treatment or covariate across groups
- correlated variation in intercepts/slopes

Terminology

- **grouping variables** define sets of clusters (e.g. school, year, country ...)
- **varying effects**: predictors whose effects vary across clusters (e.g. intercept, herbivory, time)
- random effects **term**: the combination of a clustering variable and a set of varying effects
- **conditional mode** ("BLUP"): the predicted value of the *difference* of a cluster effect from the population mean
- **conditional distribution**: distribution of the data (Gaussian, Poisson, binomial, Beta, Tweedie, ...)

General definition

$$\underbrace{Y_i}_{\text{response}} \sim \overbrace{\text{Distr}}^{\text{conditional distribution}} \left(\underbrace{g^{-1}(\eta_i)}_{\substack{\text{inverse} \\ \text{link} \\ \text{function}}}, \underbrace{\phi}_{\substack{\text{scale} \\ \text{parameter}}} \right)$$
$$\underbrace{\eta}_{\substack{\text{linear} \\ \text{predictor}}} = \underbrace{\mathbf{X}\boldsymbol{\beta}}_{\substack{\text{fixed} \\ \text{effects}}} + \underbrace{\mathbf{Z}\mathbf{b}}_{\substack{\text{random} \\ \text{effects}}}$$
$$\underbrace{\mathbf{b}}_{\substack{\text{conditional} \\ \text{modes}}} \sim \text{MVN}(\mathbf{0}, \underbrace{\Sigma(\boldsymbol{\theta})}_{\substack{\text{variance-} \\ \text{covariance} \\ \text{matrix}}})$$

What are random effects?

A method for ...

- accounting for among-individual variation, within-cluster correlation
- compromising between
complete pooling (no among-cluster variance)
and *fixed effects* (large among-cluster variance)
- handling levels selected at random from a larger population
- sharing information among clusters (*shrinkage estimation*)
- estimating among-cluster variability
- allowing predictions for unobserved clusters
- modeling **exchangeable** groups

Random-effect myths

- clusters must always be sampled at random
- a complete sample cannot be treated as a random effect
- random effects are always a *nuisance variable*
- nothing can be said about the predictions of a random effect
- you should always use a random effect no matter how few clusters you have

Reasons for random effects (inferential/philosophical)

- **don't** want to
 - test hypotheses about differences between responses at particular levels of the grouping variable;
- **do** want to
 - quantify variation among groups
 - make predictions about unobserved groups
- have levels that are randomly sampled from/representative of a larger population (*exchangeable*)

Reasons for random effects (practical)

- want to combine information across groups
- have variation in information per level (number of samples or noise level)
- have a categorical predictor that is a nuisance variable (i.e., not of direct interest, but needs to be controlled for)
- have more than 5-10 levels¹ (Clarke 2008; Austin et al. 2018)

See also Crawley (2002); Gelman (2005)

¹• Economists say 30-50

Avoiding mixed models

- average: for *nested* (balanced) LMMs (Murtaugh 2007)
- use fixed effects (or *two-stage models*) instead of random effects when there are
 - many observations per cluster (shrinkage unimportant)
 - few clusters (little advantage in # parameters; bad variance estimates)

Model setup

Formulas

- random effects specified with | ("pipe"/"bar")
as $(1+a|g1) + (1+b|g2) + \dots$
- right-hand side ($g1, g2$) is the *grouping variable* (always treated as categorical, usually a factor)
- left-hand side describes the *varying terms* (1 [intercept], a, b)
- $+$ separates independent terms
- formulas: empower but conceal details (McElreath 2015)

Formula definitions

equation

$$\beta_0 + \beta_1 X_i + e_{si}$$

$$(\beta_0 + b_{S,0s}) + \beta_1 X_i + e_{si}$$

$$(\beta_0 + b_{S,0s}) + (\beta_1 + b_{S,1s}) X_i + e_{si}$$

$$(\beta_0 + b_{S,0s} + b_{I,0i}) + (\beta_1 + b_{S,1s}) X_i + e_{si}$$

As above, but S_{0s}, S_{1s} independent

$$(\beta_0 + b_{S,0s} + b_{I,0i}) + \beta_1 X_i + e_{si}$$

$$(\beta_0 + b_{I,0i}) + (\beta_1 + b_{S,1s}) X_i + e_{si}$$

formula

n/a (Not a mixed-effects model)

~ X + (1|Subject)

~ X + (1 + X|Subject)

~ X + (1 + X|Subject) + (1|Item)

~ X + (1||Subject) + (1|Item)

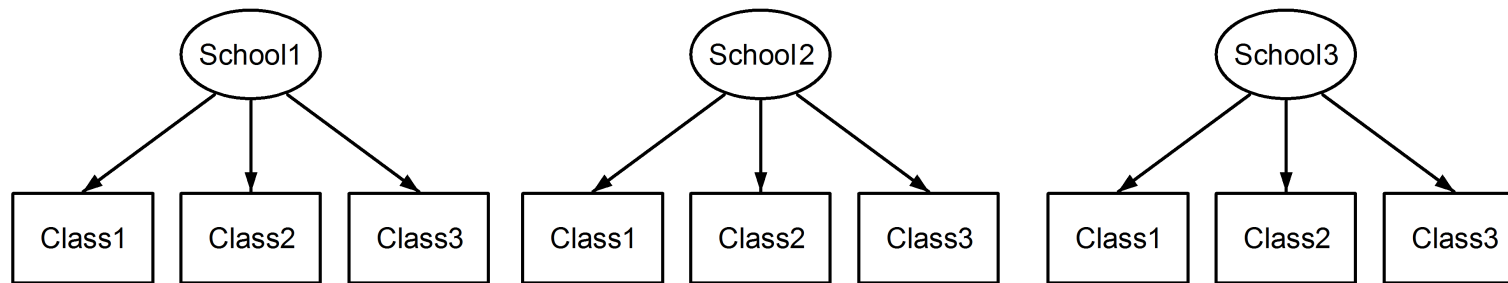
~ X + (1|Subject) + (1|Item)

~ X + (0 + X|Subject) + (1|Item)

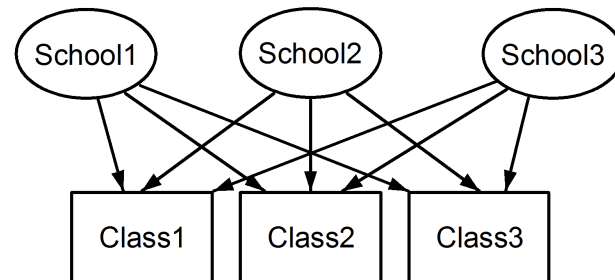
Modified from: <http://stats.stackexchange.com/questions/13166/rs-lmer-cheat-sheet?lq=1> (Livius). Subscripts $\{S, I\}$ refer to Subject vs Item effects. Lower-case $\{s, i\}$ indicate particular subjects/items. $\{0, 1\}$ refer to intercept vs slope effects.

Nesting vs crossing

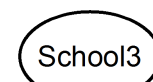
Nested: sub-unit IDs only measured within a single larger unit. e.g.: Class1 in School1 independent of Class1 in School2



Crossed: sub-unit IDs can be measured in multiple larger units. e.g.



Unique coding: removes ambiguity



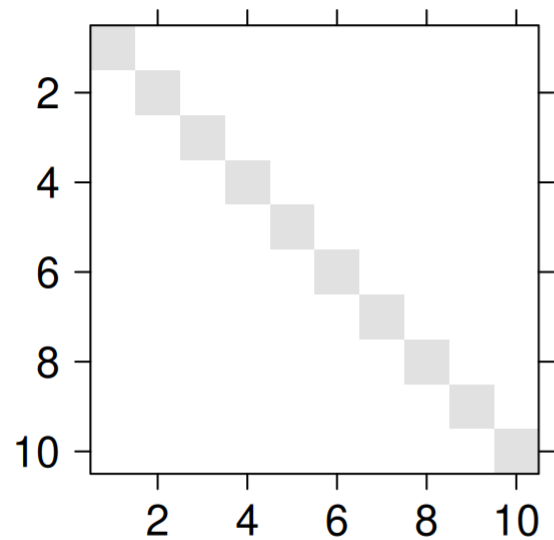
Formulas, interactions, nesting etc.

- Nested: $(1|f/g) \equiv (1|f) + (1|f:g)$. Subplots vary within plots, no commonality across plots
- Crossed: $(1|f) + (1|g)$. Years vary; plots vary independently
- Crossed+: $(1|f*g) \equiv (1|f) + (1|g) + (1|f:g)$. Years vary, plots vary independently, plots vary within years (need >1 observation per plot/year combination).

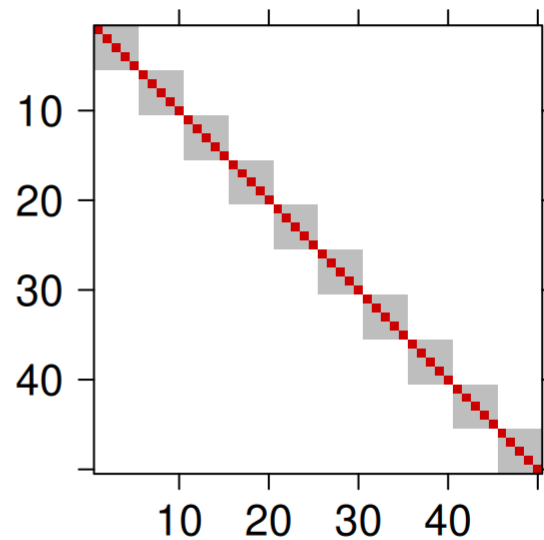
Don't need explicit nesting if sub-groups are uniquely labeled (i.e. A1, A2, ..., B1, B2, ...)

example covariance matrices

- 10 groups, 5 obs/group, intercept RE



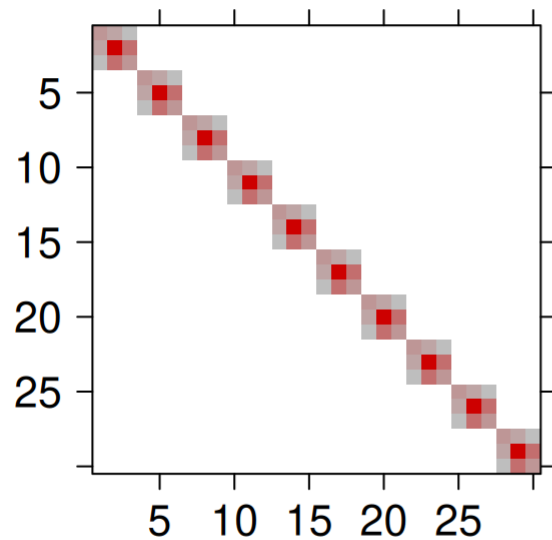
random effects Σ



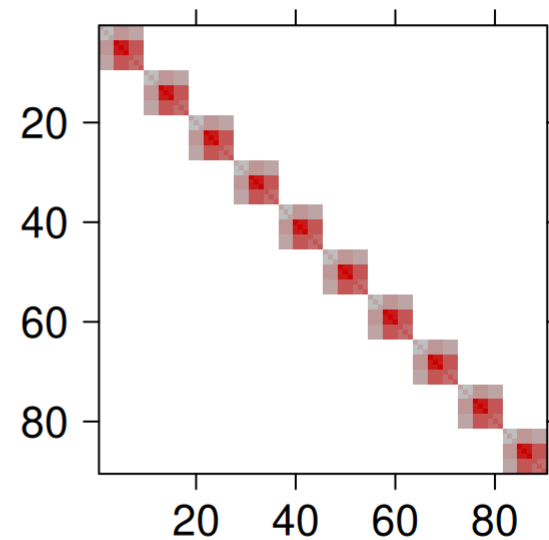
observation Σ

example covariance matrices

- 10 groups, 5 obs/group, 3 effects/group



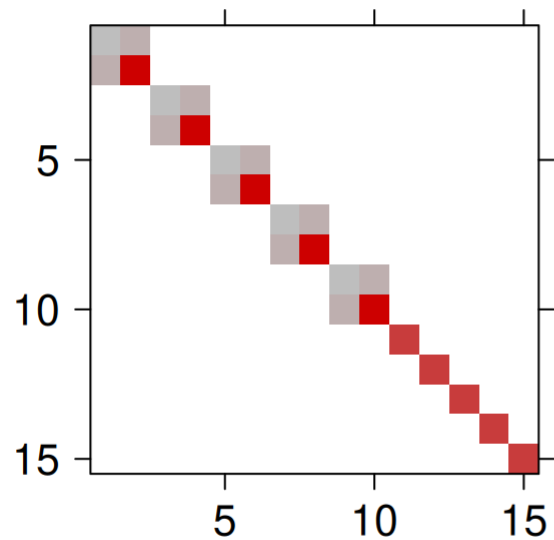
random effects Σ



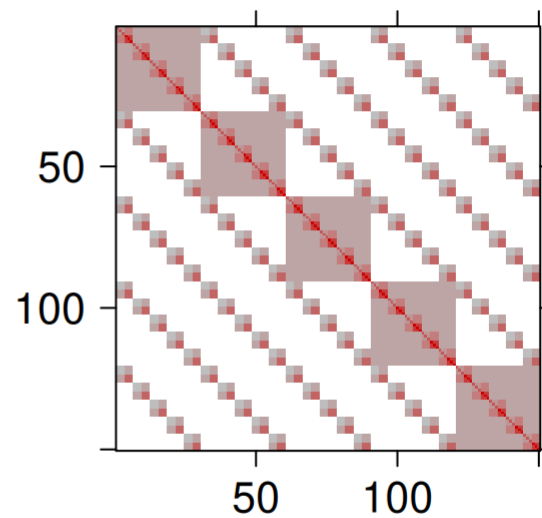
observation Σ

example covariance matrices

- 5 groups, 2 effects (v1) \times 5 groups, 1 effect (v1)



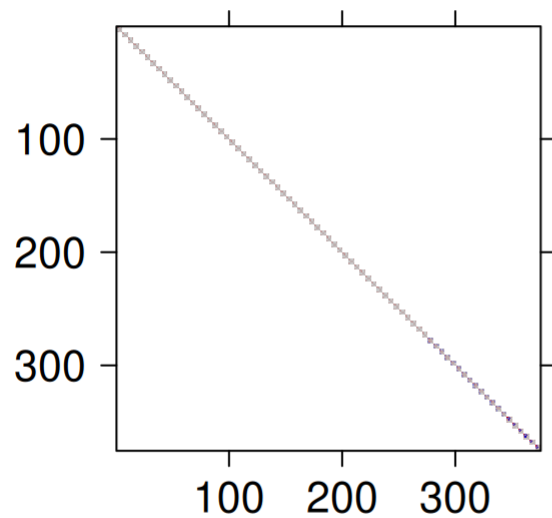
random effects Σ



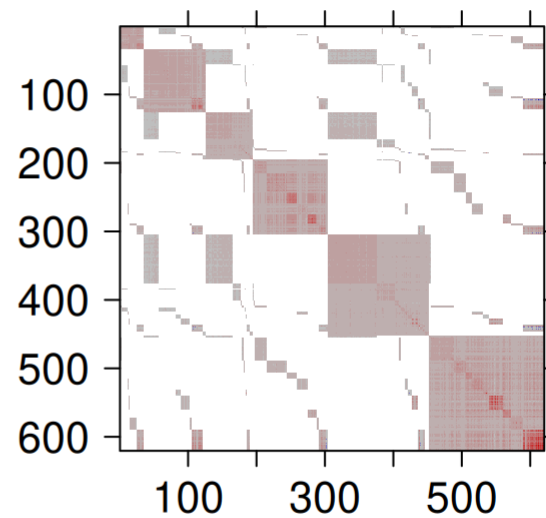
observation Σ

example covariance matrices

Moritz et al. (2023) (fire/diversity; blocks are geographic regions)



random effects Σ



observation Σ

Factors varying across groups

Can generate large variance-covariance matrices. For a four-level factor, we have β_0 (intercept), β_1 (level 2 - level 1), β_2 (level 3 - level 1), β_3 (level 4 - level 1).

$$\Sigma = \begin{bmatrix} \sigma_{\{b|1\}}^2 & \cdot & \cdot & \cdot \\ \sigma_{\{b|1\},\{b|a_{21}\}} & \sigma_{\{b|a_{21}\}}^2 & \cdot & \cdot \\ \sigma_{\{b|1\},\{b|a_{31}\}} & \sigma_{\{b|a_{21}\},\{b|a_{31}\}} & \sigma_{\{b|a_{31}\}}^2 & \cdot \\ \sigma_{\{b|1\},\{b|a_{41}\}} & \sigma_{\{b|a_{21}\},\{b|a_{41}\}} & \sigma_{\{b|a_{31}\},\{b|a_{41}\}} & \sigma_{\{b|a_{41}\}}^2 \end{bmatrix}$$

What is the maximal model?

- Which effects vary *within* which groups?
- If effects don't vary within groups, then we *can't* estimate among-group variation in the effect
 - e.g. in typical clinical trials each patient gets only one treatment (placebo or drug)
 - convenient
 - maybe less powerful (among-group variation is lumped into residual variation)
 - can't evaluate variation in effects

Maximal model is often impractical

- for a RE where n effects vary across clusters we need to estimate $p = n(n + 1)/2$ covariance parameters
- e.g. bloodworm example: 5×4×4×2 factorial design (160 combinations), all measured in each of 10 individuals.
 - Treating covariates as numeric, allow all interactions:
16 effects → $p = 136$
 - Categorical predictors, no interactions:
12 effects → $p = 78$
 - Numeric predictors, no interactions: 4 effects → $p = 10$
- **BUT** ignoring within-cluster effects is also dangerous (Schielzeth et al. 2009; Heisig et al. 2019; Oberauer 2022)


Estimation

Maximum likelihood estimation

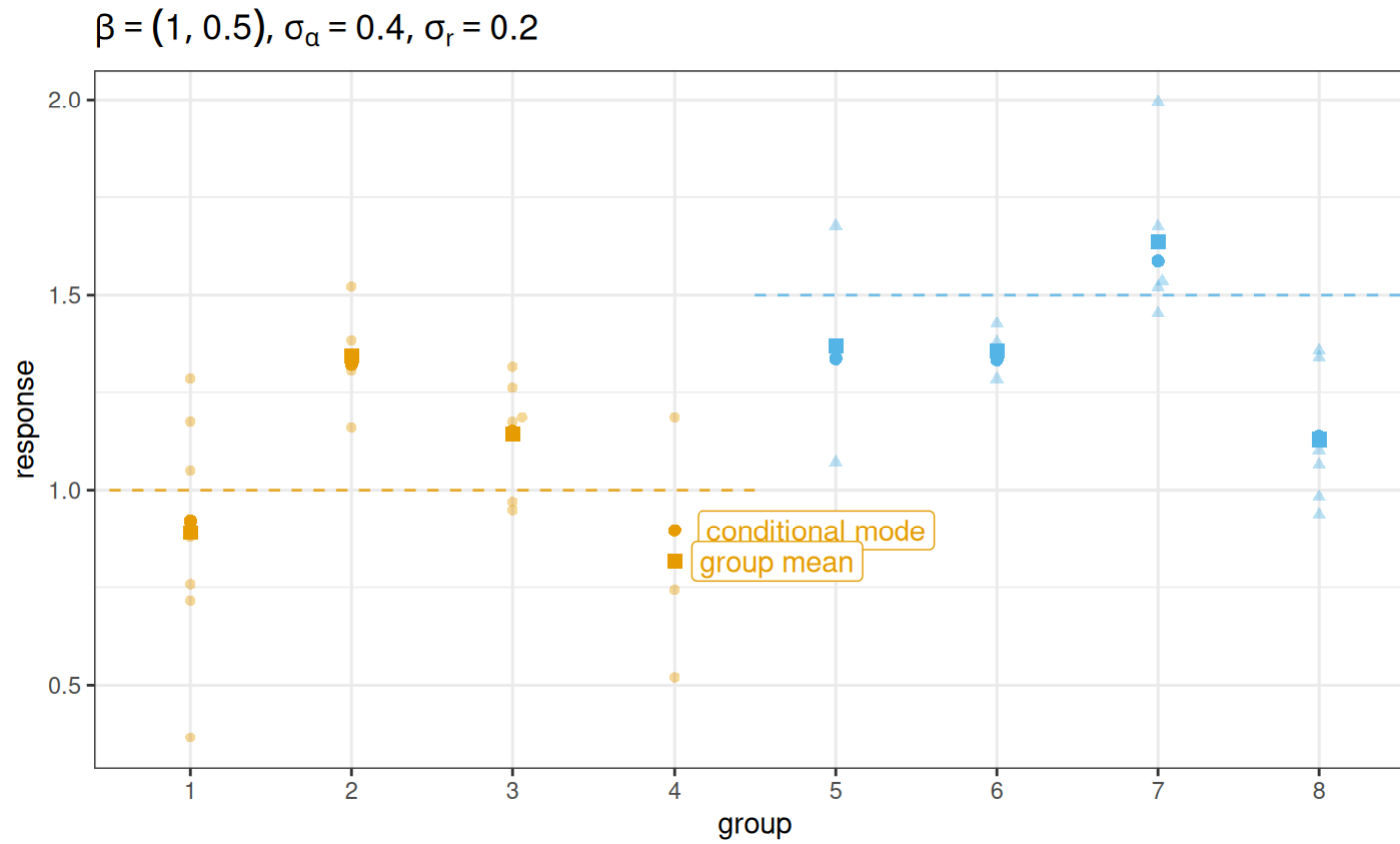
- Best fit is a compromise between
 - consistency of data with fixed effects + conditional modes
 - consistency of random effect with RE distribution
- Goodness-of-fit *integrates* over the RE distribution

$$\mathcal{L}(x|\beta, \theta) = \iint \mathcal{L}(x|\beta, \mathbf{b}) \cdot \mathcal{L}(\mathbf{b}|\Sigma(\theta)) d\mathbf{b}$$

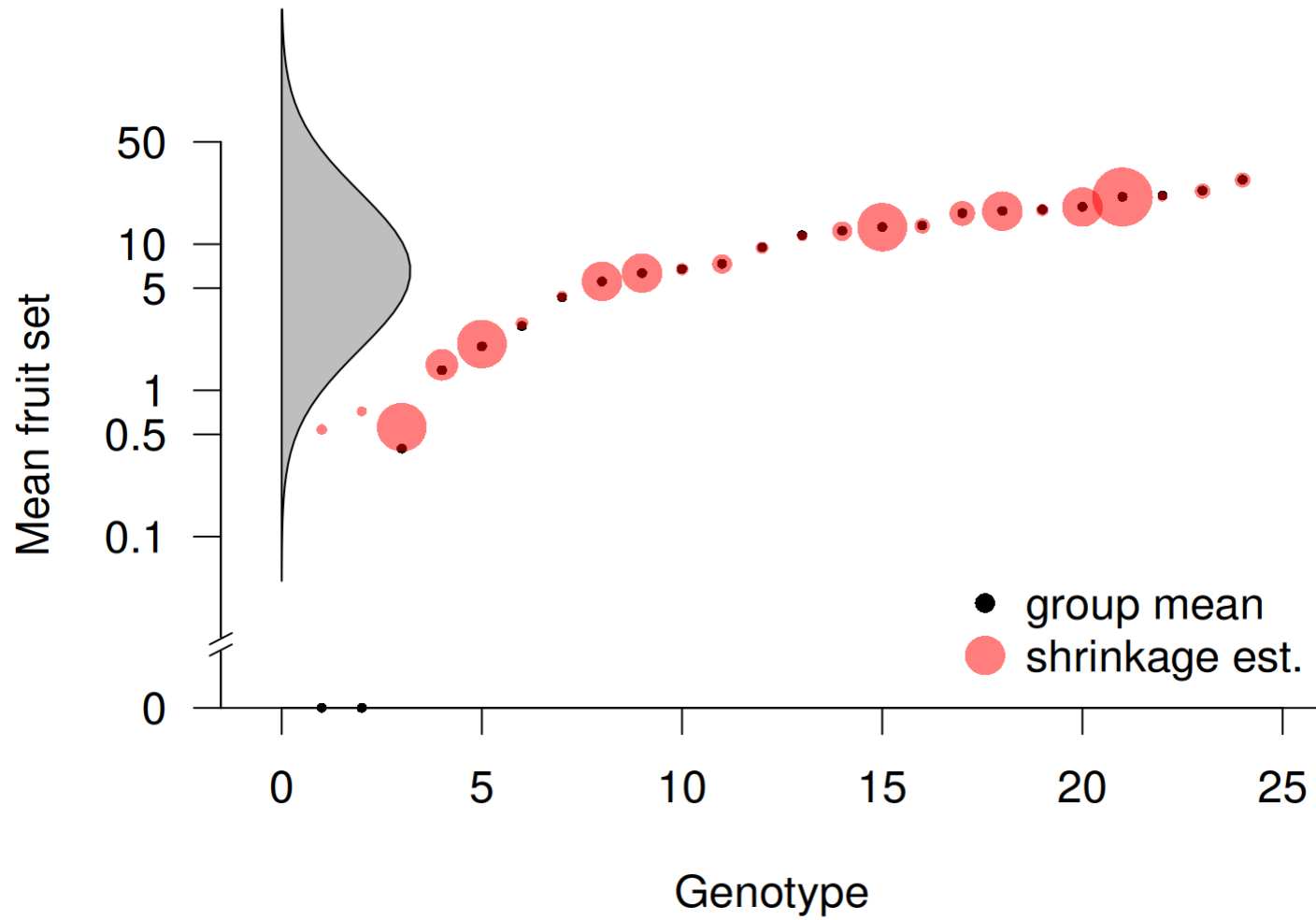
Restricted maximum likelihood (REML)

- factor out fixed effects when estimating variances
- analogous to estimating $s^2 = \frac{SSQ}{n-1}$ rather than $\frac{SSQ}{n}$
- typically better variance estimates (unbiased in simple cases)
- defaults differ across packages
- **never** compare models with differing fixed effects fitted by REML 

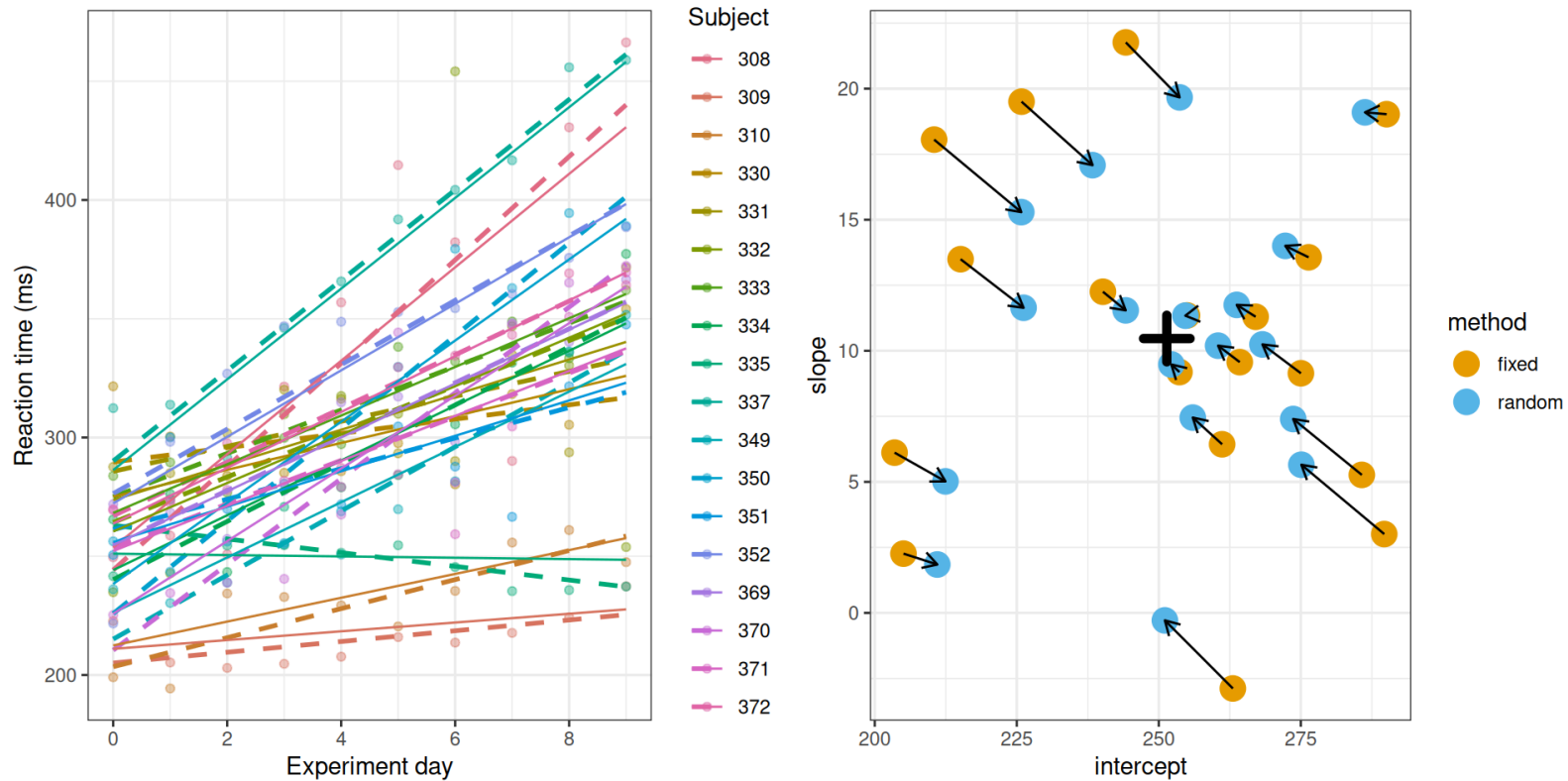
Shrinkage



Arabidopsis shrinkage



Shrinkage in the sleep-study model



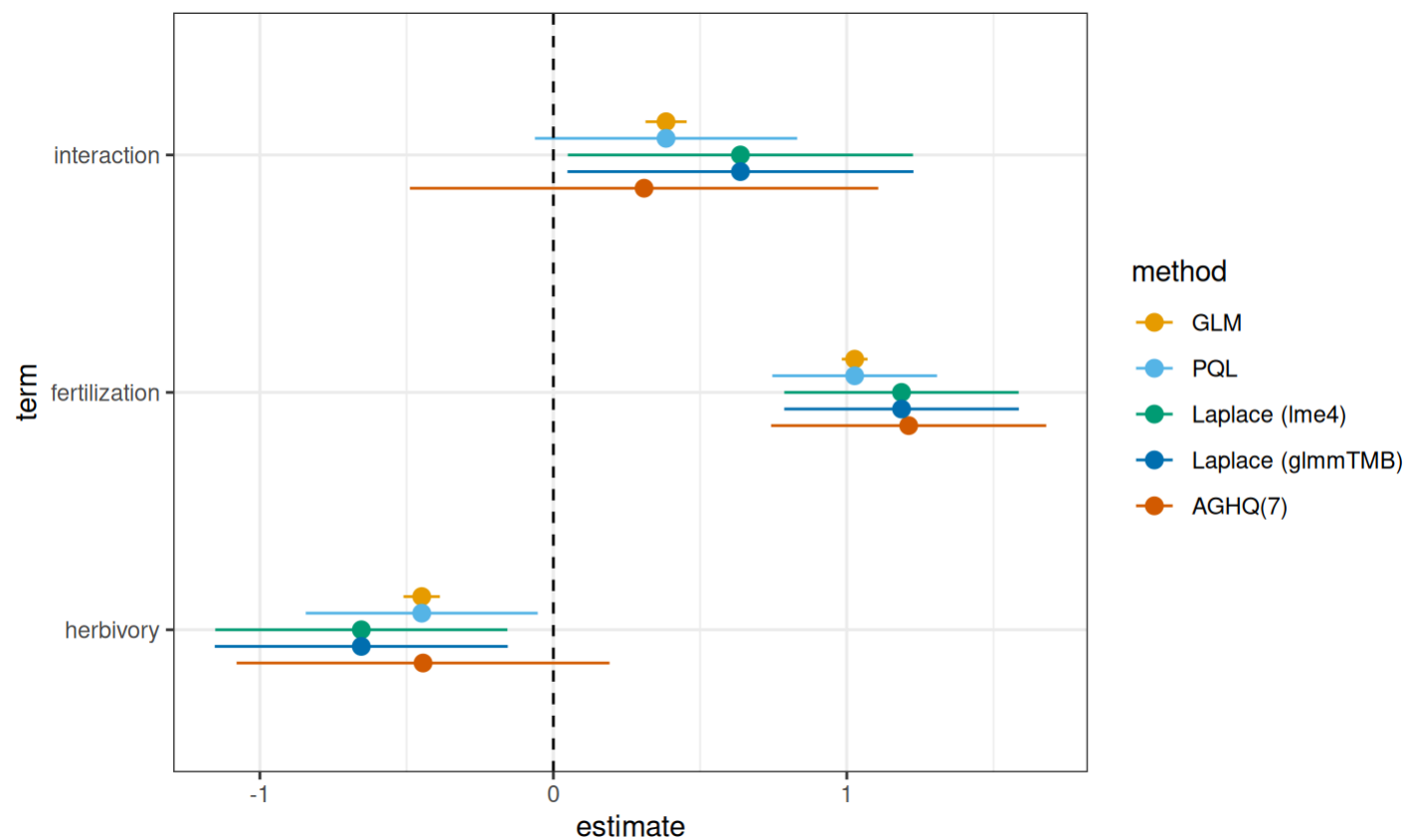
Methods

Estimation methods

Integrating the likelihood is hard (for GLMMs)

- **deterministic**
 - penalized quasi-likelihood (Breslow 2004), Laplace, Gauss-Hermite quadrature, ... (Biswas 2015; Bilodeau et al. 2024)
 - need best methods for small clusters (binary, small # of observations)
 - available methods depend on problem structure
 - accuracy (GHQ) vs. flexibility and speed (PQL, Laplace)
- **stochastic** (Monte Carlo): mostly Bayesian, some frequentist
 - Booth et al. (1999); Gelman et al. (2006); Sung et al. (2007); Ponciano et al. (2009); McElreath (2015)
 - much slower, but flexible and accurate

Estimation: *Arabidopsis*



Inference/post-fitting

Diagnostics

- make sure model is working OK (**singular fits** etc.)
- check model assumptions
 - generalizations of linear/GLM diagnostics: residuals vs fitted, scale-location, etc.
 - conditional modes should be Normally distributed
 - simulation-based residuals (**DHARMA**)

Parameter/model interpretation

- fixed effects: same as linear models (population level trends/effects)
- conditional modes/group-level effects
 - deviations from population-level effects
 - can get *conditional standard deviations*, but can't test significance!
- interpreting random effects
 - standard deviations (on same scale as corresponding fixed effects)
 - variances (for population geneticists)

references

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