Generalized linear mixed models for biologists

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McMaster University

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Outline

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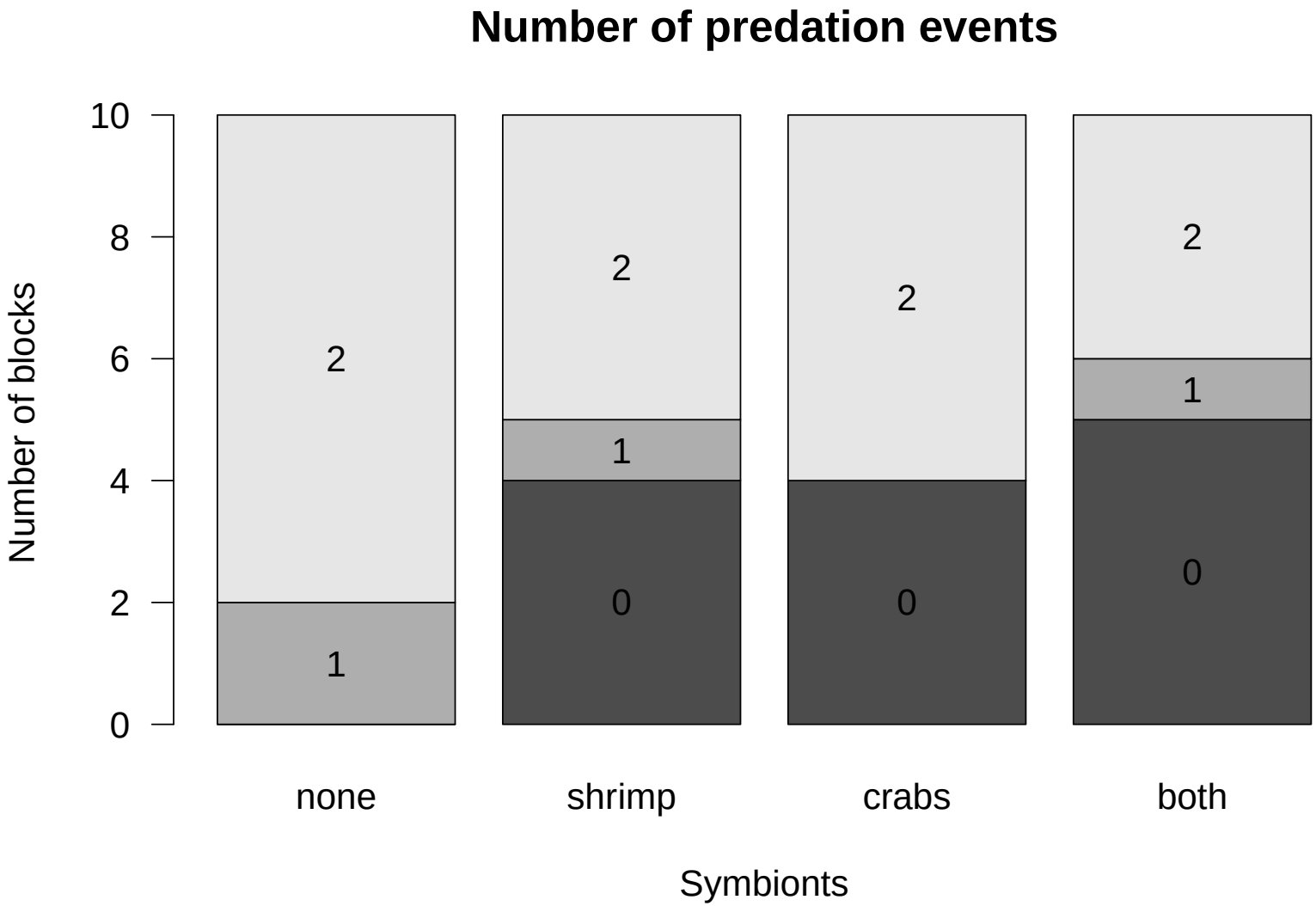
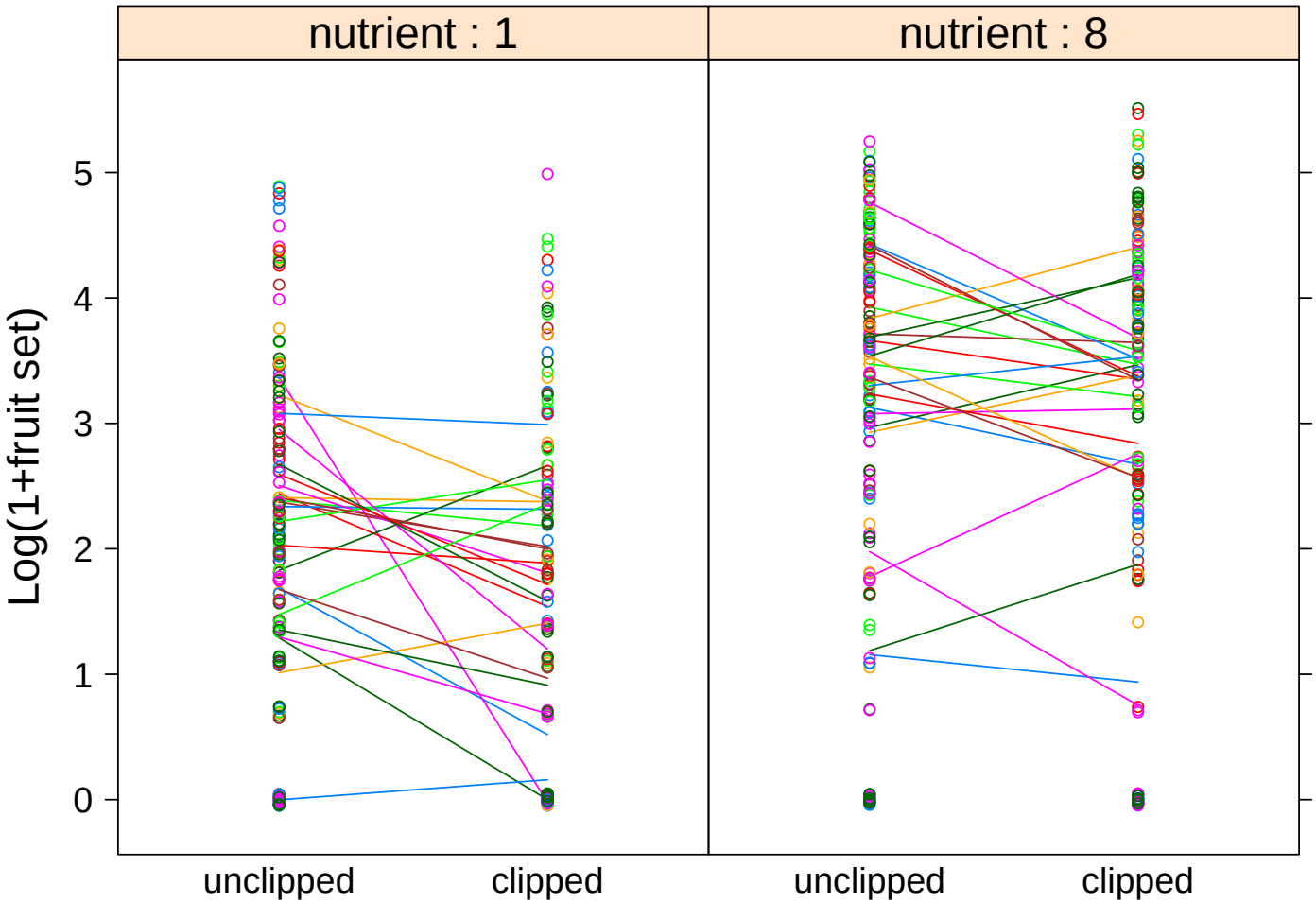
Coral protection by symbionts

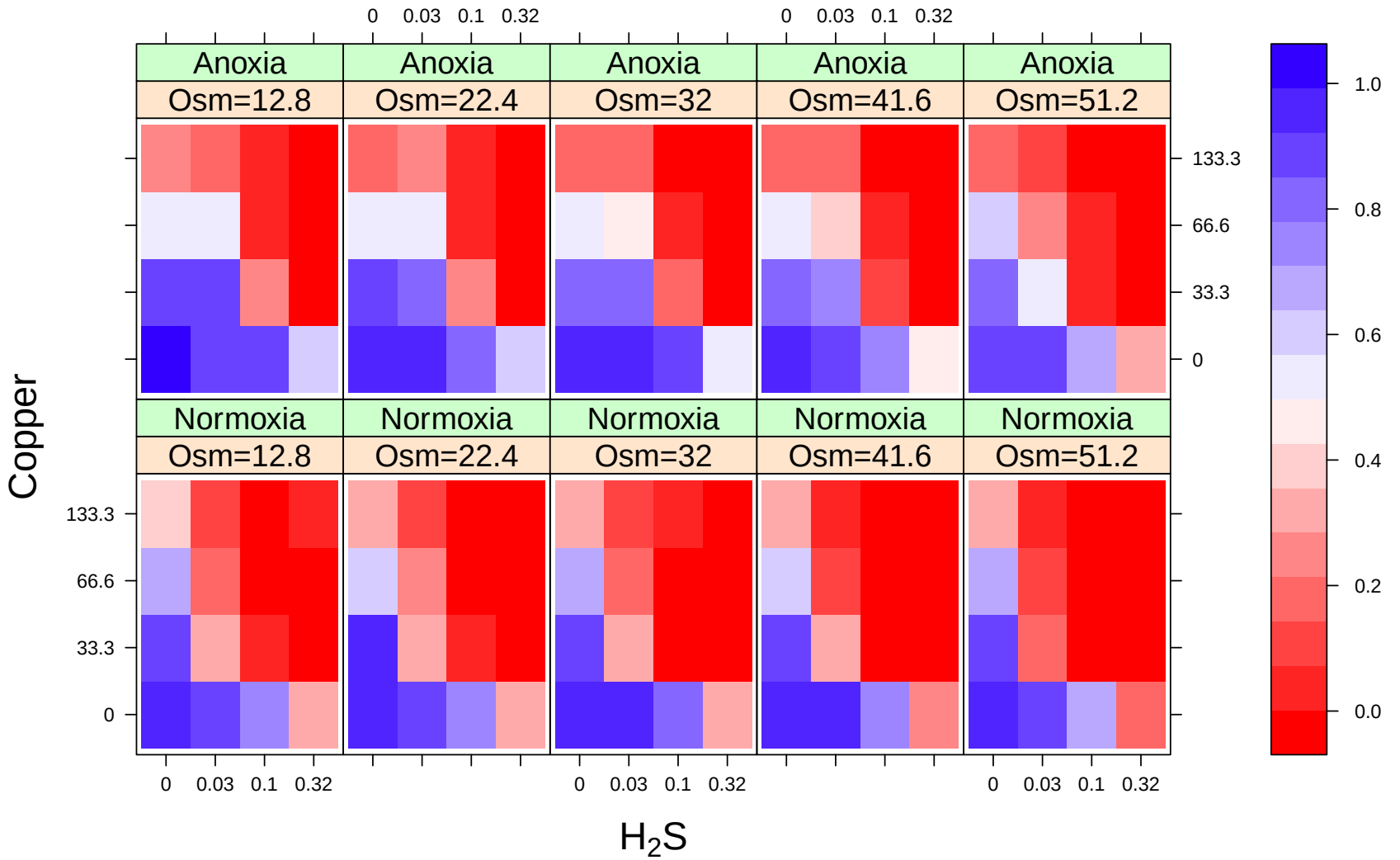


Arabidopsis response to fertilization & clipping

panel: nutrient, color: genotype



Environmental stress: *Glycera* cell survival



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Generalized linear models (GLMs)

- non-normal data, (some) nonlinear relationships; modeling via **linear predictor**
  - presence/absence, alive/dead (binomial)
  - count data (Poisson, negative binomial)
- typical applications: **logistic regression** (binomial/logistic), **Poisson regression** (Poisson/exponential)

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Random effects (RE)

- examples: experimental or observational "blocks" (temporal, spatial); species or genera; individuals; genotypes
- inference on **population** of units rather than individual units
- (units randomly selected from all possible units)
- (reasonably large number of units)

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Mixed models: classical approach

- Partition sums of squares, calculate null expectations if fixed effect is 0 (all coefficients $\beta_i = 0$) or RE variance=0
- Figure out numerator (model) & denominator (residual) sums of squares and degrees of freedom
  - **Model SSQ, df**: variability explained by the "effect" (difference between model with and without the effect) and number of parameters used
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Classical LMM cont.

- Robust, practical
- OK if
  - data are **Normal**
  - design is (nearly) **balanced**
  - design not too complicated (single RE, or nested REs) (**crossed** REs: e.g. year effects that apply across all spatial blocks)

Mixed models: modern approach

- Construct a **likelihood** for the data (Prob(observing data|parameters)) — in mixed models, requires integrating over possible values of REs (**marginal likelihood**)
- e.g.:
  - likelihood of i^{th} obs. in block j is $L_{\text{Normal}}(x_{ij}|\theta_i, \sigma_w^2)$
  - likelihood of a particular block mean θ_j is $L_{\text{Normal}}(\theta_j|0, \sigma_b^2)$
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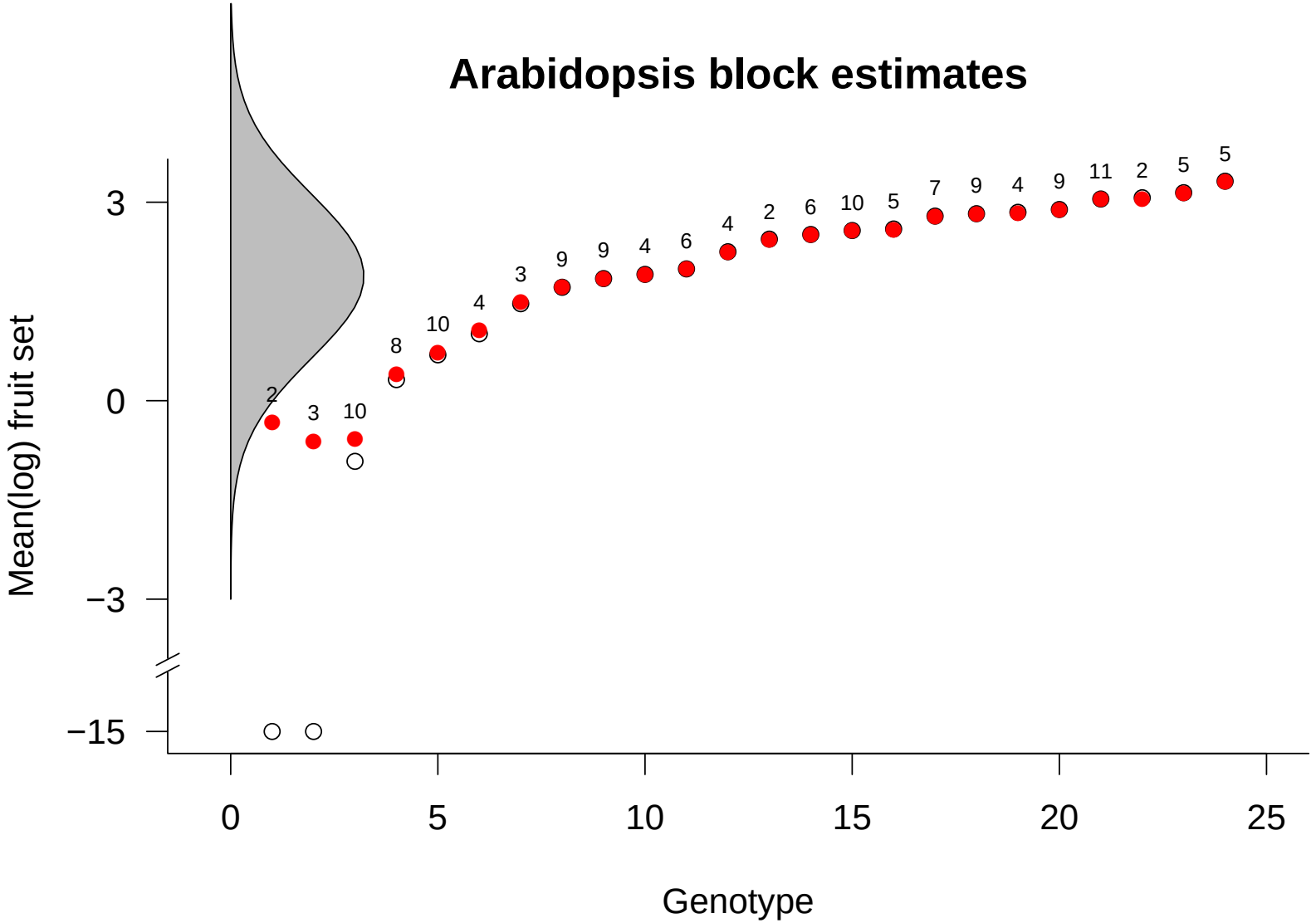
Shrinkage


Arabidopsis block estimates
Mean(log) fruit set
3
0
−3
−15
0
5
10
15
20
25
Genotype
2 3 10 8 10 4 3 9 9 4 6 4 2 6 10 5 7 9 4 9 11 2 5 5

RE examples

- Coral symbionts: simple experimental blocks, RE affects intercept (overall probability of predation in block)
- *Glycera*: applied to cells from 10 individuals, RE again affects intercept (cell survival prob.)
- *Arabidopsis*: region (3 levels, treated as fixed) / population / genotype: affects intercept (overall fruit set) as well as treatment effects (nutrients, herbivory, interaction)

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Penalized quasi-likelihood (PQL)

- alternate steps of estimating GLM given known block variances; estimate LMMs given GLM fit
- flexible (allows spatial/temporal correlations, crossed REs)
- **biased** for small unit samples (e.g. counts < 5, binary or low-survival data) (Breslow, 2004)
- nevertheless, **widely** used: SAS `PROC GLIMMIX`, R `glmmPQL`: in $\approx 90\%$ of small-unit-sample cases

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Better methods

- **Laplace approximation**
  - approximate marginal likelihood
  - considerably more accurate than PQL
  - reasonably fast and flexible
- **adaptive Gauss-Hermite quadrature** (AGQ)
  - compute additional terms in the integral
  - most accurate
  - slowest, hence not flexible (2–3 RE at most, maybe only 1)

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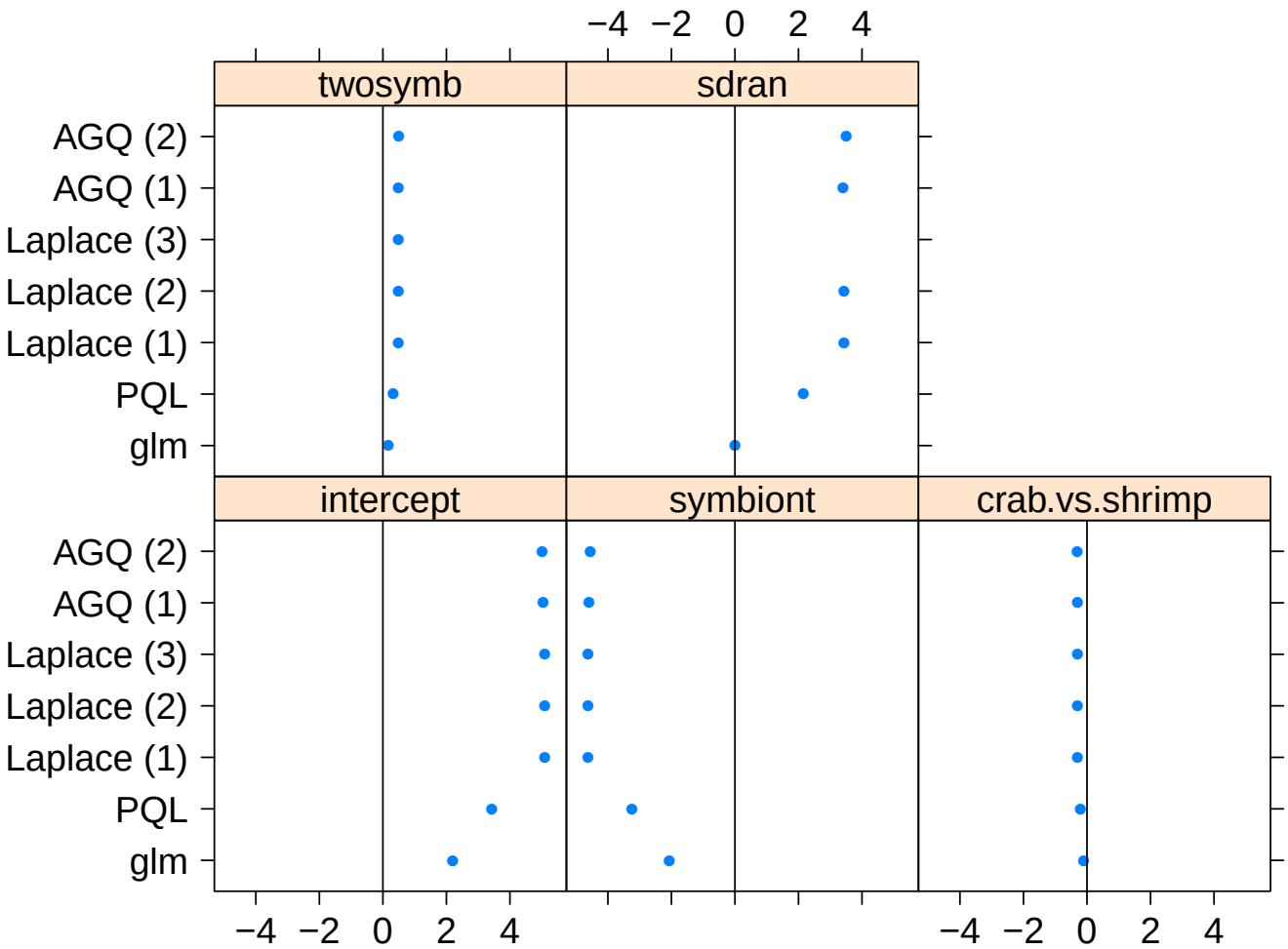
Comparison of coral symbiont results



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General issues: testing RE significance

- Counting "model" df for REs
  - how many parameters does a RE require? Somewhere between 1 and n . . . Hard to compute, and depends on the **level of focus** (Vaida and Blanchard, 2005)
- Boundary effects for RE testing
  - most tests depend on null hypothesis being **within** the parameter's feasible range (Molenberghs and Verbeke, 2007): **violated** by $H_0 : \sigma^2 = 0$
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General issues: finite-sample issues (!)

How far are we from "asymptopia"?

- Many standard procedures are **asymptotic**
- "Sample size" may refer the number of RE **units** — often far more restricted than total number of data points
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Specific procedures

- Likelihood Ratio Test:
  need large sample size (= large # of RE units!)
- Wald (Z, χ^2, t or F) tests
  - crude approximation
  - asymptotic (for non-overdispersed data?) or ...
  - ...how do we count residual df?
  - don't know if null distributions are correct
- AIC
  - asymptotic (properties unknown)
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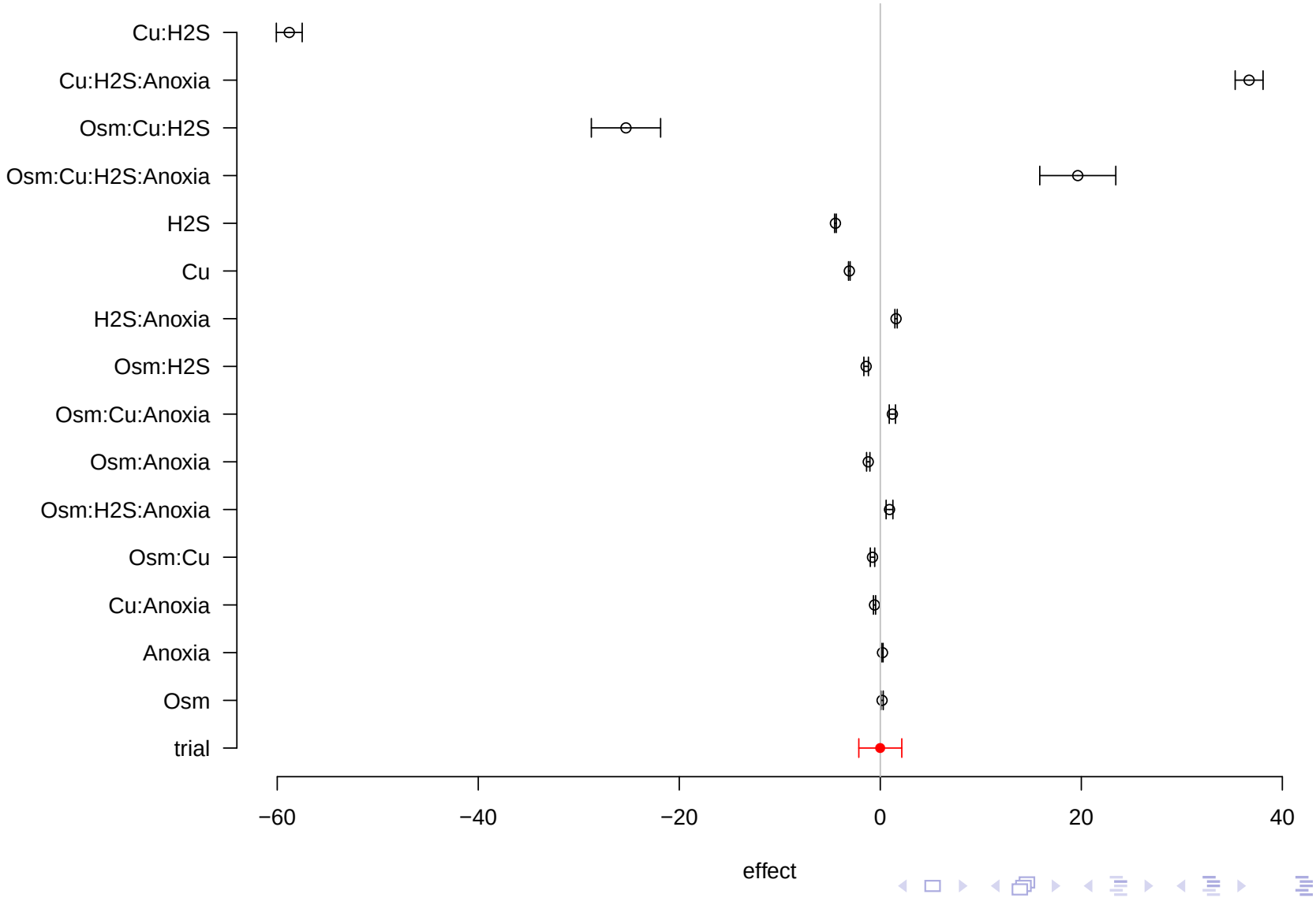
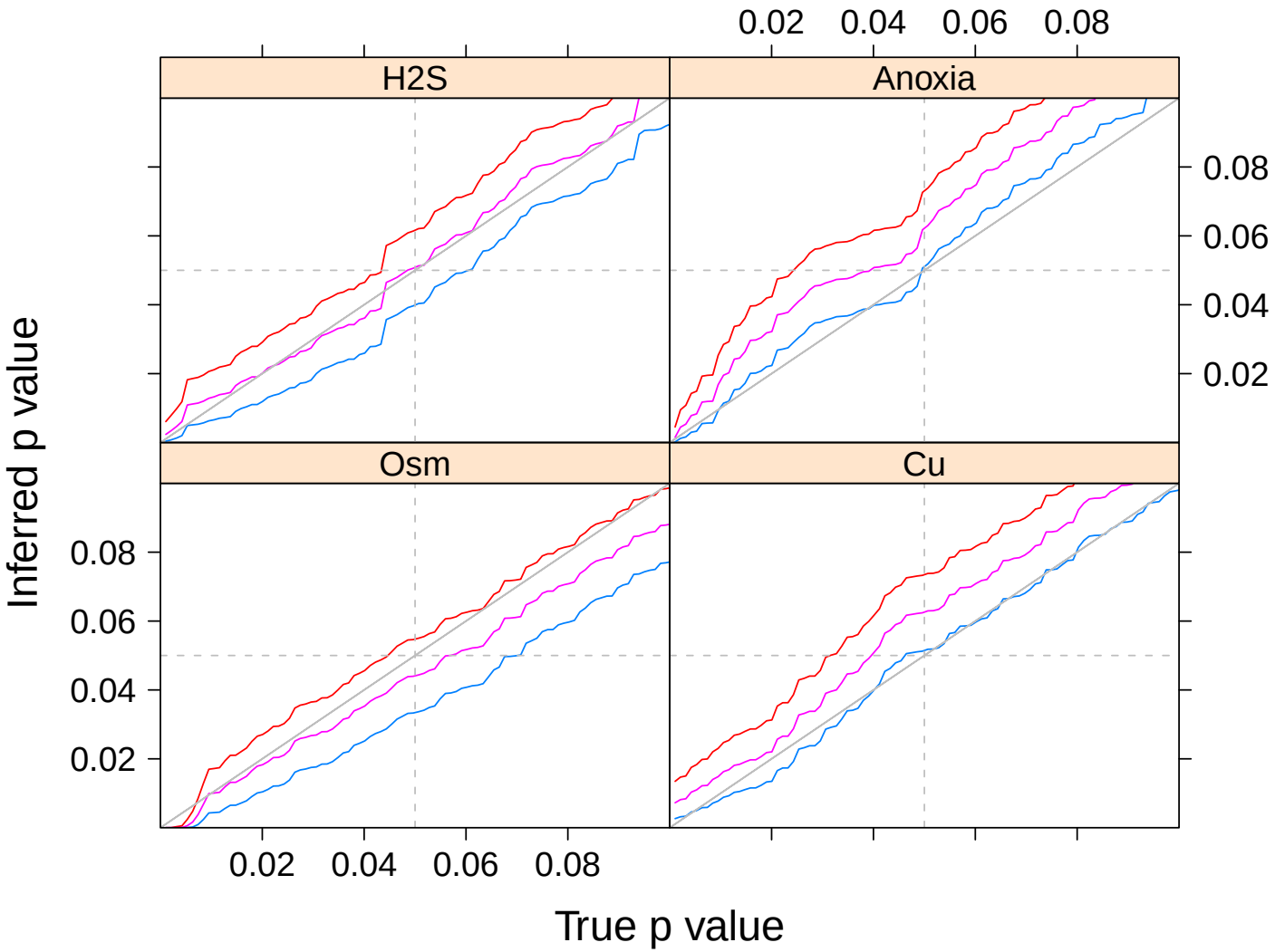
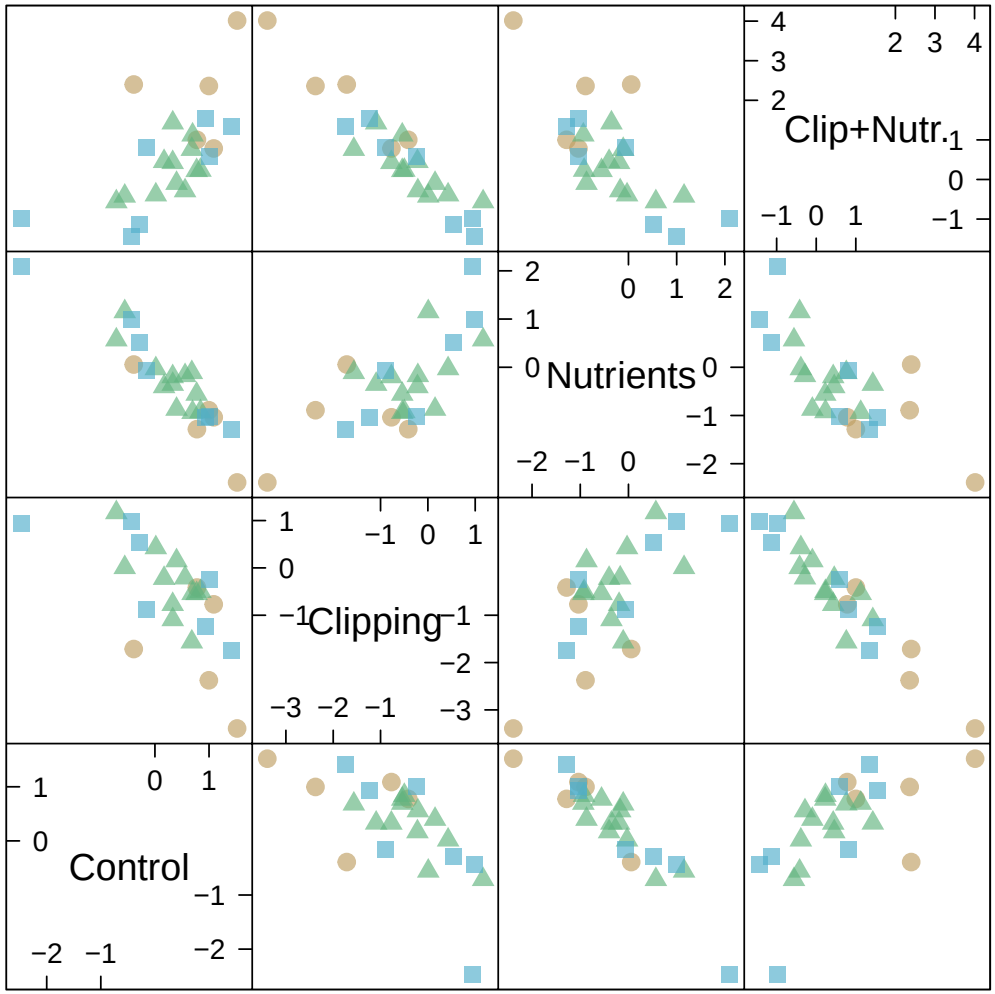
Glycera results



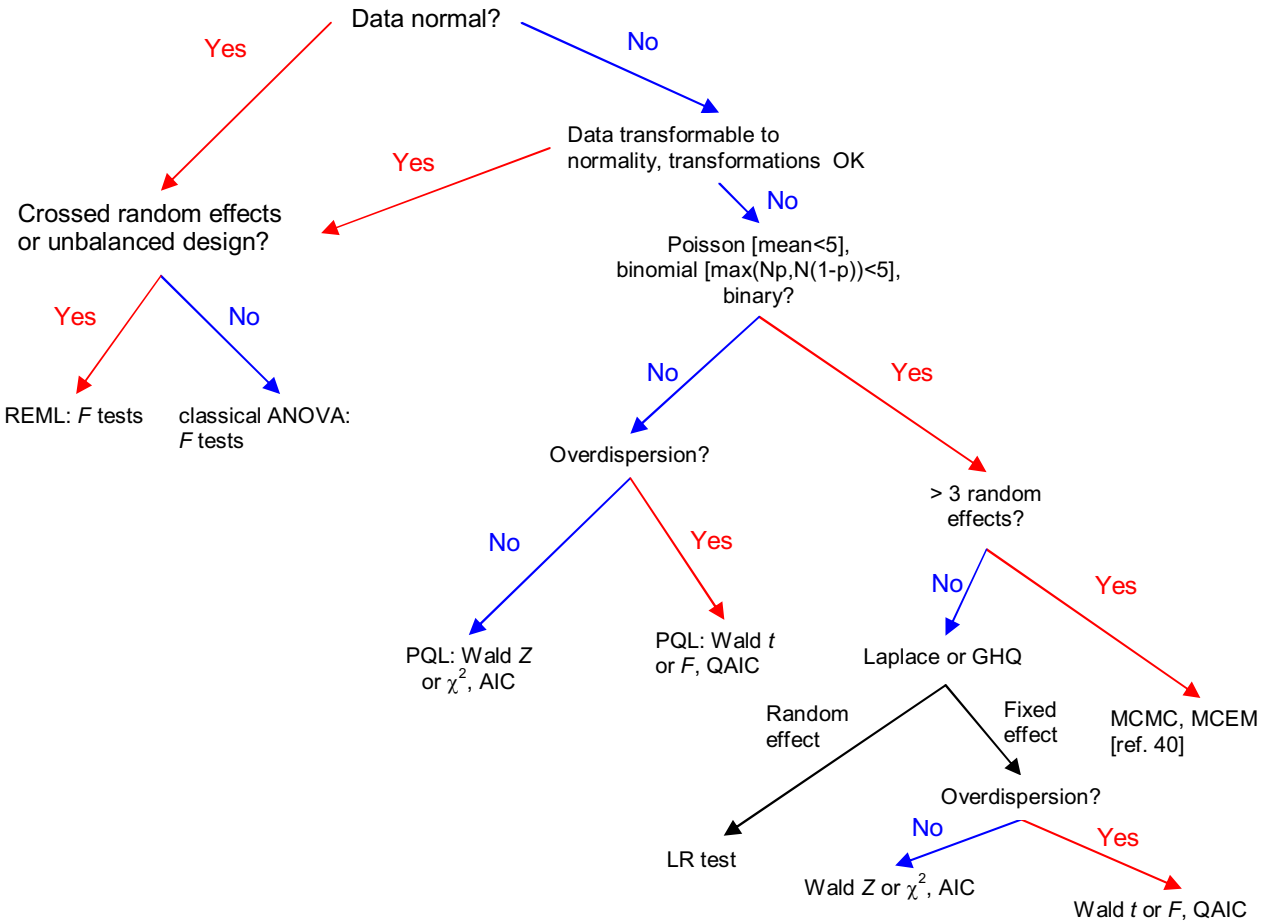
Testing assumptions



Arabidopsis genotype effects



Where are we?


Data normal?
Yes
No
Data transformable to normality, transformations OK
Yes
No
Crossed random effects or unbalanced design?
Poisson [mean<5], binomial [max(Np,N(1-p))<5], binary?
Yes
No
No
Yes
REML: F tests
classical ANOVA: F tests
Overdispersion?
> 3 random effects?
No
Yes
No
Yes
PQL: Wald Z or χ^2, AIC
PQL: Wald t or F, QAIC
Laplace or GHQ
MCMC, MCEM [ref. 40]
Random effect
Fixed effect
Overdispersion?
LR test
No
Yes
Wald Z or χ^2, AIC
Wald t or F, QAIC

Now what?

- MCMC (finicky, slow, dangerous, we have to "go Bayesian": specialized procedures for GLMMs, or WinBUGS translators? (`glmmBUGS`, `MCMCglmm`)
- quasi-Bayes `mcmcsamp` in `lme4` (unfinished!)
- parametric bootstrapping:
  - fit null model to data
  - simulate "data" from null model
  - fit null and working model, compute likelihood diff.
  - repeat to estimate null distribution
  - ? analogue for confidence intervals?
- challenges depend on data: total size, # REs, # RE units, overdispersion, design complexity ...

More info: `glmm.wikidot.com`

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Acknowledgements

- Data: Josh Banta and Massimo Pigliucci (*Arabidopsis*); Adrian Stier and Sea McKeon (coral symbionts); Courtney Kagan, Jocelynn Ortega, David Julian (*Glycera*);
- Co-authors: Mollie Brooks, Connie Clark, Shane Geange, John Poulsen, Hank Stevens, Jada White

References

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