



TITLE: Bayesian dose–response mixed modeling: application to perturbation screening data

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ABSTRACT: Dose–response (DR) analyses struggle to jointly model fixed effects (conditions/perturbations) and random effects (plate, batch, run, donor), especially when DR data are combined with CRISPR screening. We use an interpretable four-parameter logistic (4PL) model familiar to biologists and extend it to capture biological signal and technical noise, incorporating gene knockout (gKO) effects directly within the full DR curve.

We analyzed raw CRISPR DR data with a Bayesian mixed effects 4PL model. gKO effects are estimated on the full curve (bottom, top, EC50, slope), and plate within biological replicate is modeled as nested random intercepts, correcting technical offsets in-curve and propagating uncertainty. Each gKO has one curve with partial pooling across replicates, and contrasts for EC50, bottom, and top versus neutral controls are reported with 95% credible intervals and posterior hit probabilities. The joint model recovered hits missed under early viability loss and reduced false positives by shrinking isolated high-dose wells toward curve-supported values with appropriately wider intervals.

A Bayesian mixed-effects DR model recovers actives from incomplete or early signal-loss curves and yields more robust, less outlier-driven calls. It adjusts technical noise within the curve and enables hit decisions with transparent, uncertainty-aware summaries.