# Probabilistic Graphical Modeling of Gene Expression Modulation by CRISPR Perturbation

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# **EEGGO:**

### Estimation of Enhancer-Gene Guide Outcomes



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#### Model Intuition & Formulation

We rely on empirically-derived statistics from **Control Samples**, to predict gene expression and beta coefficients proportional to the gene's level of inhibition by CRISPR.

**Goal:** Estimate gene expression values, and infer beta coefficients for each gene-enhancer pair given the following model:

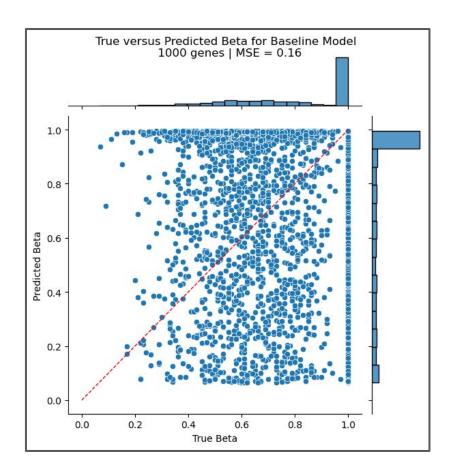
$$X_{ ext{experiment}} \sim eta_{ ext{gene-enhancer}} imes \mu_{ ext{control}}$$

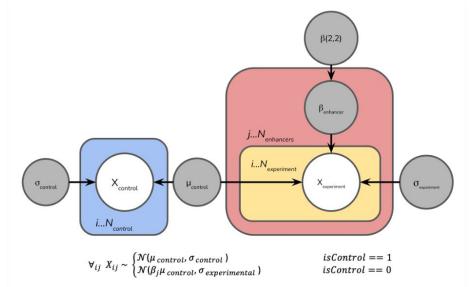
$$eta_{ ext{gene-enhancer}} = rac{\mu_{ ext{experiment}}}{\mu_{ ext{control}}}$$

With this formulation, expression is only modulated with a beta coefficient if it is an experimental sample.

We did not scale or otherwise transform the input data.

## **Baseline**: Control-Aware Normally Distributed Expression



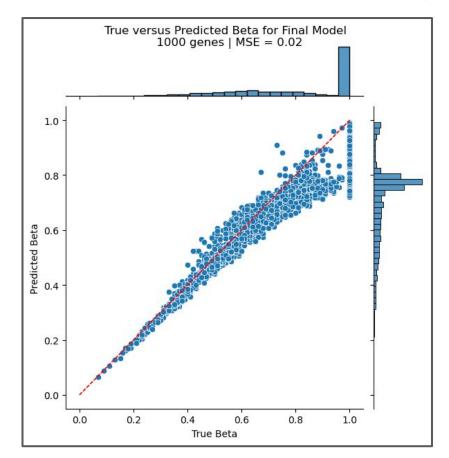


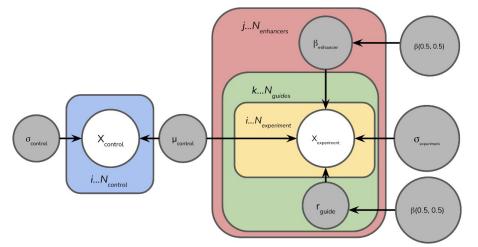
- This control-aware model infers the beta value only in cases where the the observation is not a control.
- Expression values,  $X_i$ , and  $\mu_{control}$ ,  $\sigma_{control}$  are observed, and control statistics are defined **globally** across all 1,000 genes
- This model ignores guideIDs.

Performance (Beta Coefficients):

Mean Squared Error (MSE): 0.16402

# **Final Model**: Control-Aware Mixture Model for Guide Potency





$$X_{ijk} \sim (r_{jk}) N(\beta_j \mu_{j control}, \sigma_{j experimental}) + (1 - r_{jk}) N(\mu_{control}, \sigma_{j control})$$

We introduce the latent mixture proportion,  $r_{\rm d}$ , with a  $\beta$  (0.5, 0.5) prior to our formulation, which is meant to account for GuidelD functionality

Assumption: Not all GuideIDs are functional

Performance (Beta Coefficients):

Mean Squared Error (MSE): 0.02228