**Data**

We sought to characterize H3K36me3 dynamics in a large number of genes in three biological conditions: after light activation of Set2 (writer add), and after dark inactivation of Set2 with and without the presence of Rpd3 (writer loss and writer eraser loss, respectively). H3K36me3 levels were measured through ChIP-seq across four timepoints for each condition (0/20/40/60 min for writer add and 0/30/60/90 min for the loss conditions) for 5,368 genes. Sequence data was measured from three sample replicates for each condition across the timepoints. Within each replicate, H3K36me3 levels for a gene and condition were scaled to the proportion of maximum H3K36me3 level observed (for said replicate, gene, and condition), resulting in a common scale across all replicates, genes, and conditions.

**Statistical model**

Though the H3K36me3 data are large and well-balanced, with the vast majority of genes having complete measurements of three replicates from each condition across four timepoints, they possess challenging features from a statistical modeling perspective. Namely, the statistical model should accommodate the proportional scale of the H3K36me3 data, which will violate the assumptions of traditional models of normally distributed variables, as well as the time course, *i.e.* longitudinal, nature of measurements within a replicate. This broad range of features can be flexibly handled using Bayesian inference (Gelman & Hill 2006).

The Stan statistical platform (Carpenter et al. 2017) is one such computational tool for fitting complex Bayesian hierarchical models. We used the brms software package (Bürkner 2017), which acts as a wrapper of Stan for the R statistical programming language (R Core Team 2019).

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