



Figure S2: **Training error of SA-inferred gene circuits.** Boxplots show root mean square (RMS) error of gene circuits inferred from 100 synthetic datasets using SA. For each combination of the number of genes  $G$ , the number of trajectories  $N$ , and the number of timepoints  $N_t$ , synthetic datasets corresponding to 100 random parameter sets were generated. SA was used to infer 5 replicate gene circuits from each dataset. The replicate with the lowest RMS is included in the plot. The box lines are the first quartile, median, and the third quartile. The whiskers extend to the most extreme values lying within 1.5 times the interquartile range, and any datapoints outside the whiskers are shown as dots.