Figure S3: **Inference of h_g and kinetic parameters from synthetic data.** Continued on following page.

Figure S3: **Inference of h_g and kinetic parameters from synthetic data.** The discrepancy between inferred and theoretical values of h_g, R_g, and λ_g from 100 random parameter sets is shown as boxplots. Note that each boxplot is constructed from $100G$ parameter values since each random parameters set contains G values of h_g, R_g, and λ_g, where G is the number of genes. 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 crosses. **A–E**. Number of trajectories $N = 100$ and number of timepoints $N_t = 21$. The number of genes G was varied between 2 and 50 for FIGR and 2 and 20 for SA. **F,G**. Number of trajectories $N = 100$ and number of genes $G = 20$. The number of timepoints N_t was varied between 41 (panel F) and 11 (panel G). **H–J**. Number of genes $G = 20$ and number of timepoints $N_t = 21$. The number of trajectories N_t was varied between 10 and 50. SA was not run for $G = 50$ since it was impractical.