

# Information Entropy of Single-Gene Expression Responses during Genome Wide Perturbations <sup>†</sup>

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Transcription factors (TF) are known to drive gene-to-gene interaction dynamics under optimal growth conditions, but lesser is known about how much they affect the dynamics of gene regulatory networks (GRN) at the global level, due to the contribution of many other variables.

We investigate how TF interactions of the GRN of *E. coli* affects the global entropy of single-genes response dynamics, during a genome-wide perturbation caused by a shift in RNA polymerase (RNAP) concentrations.

For this, we classified genes based on their number of (known) input TFs. Also, we assigned a value to each TF input (−1 for repression and +1 for activation) and classified genes based on the sum of its input interactions. For both classification schemes, we estimated the information entropy of the single-gene input interactions of each class.

Next, we measured by RNA-seq the fold changes of each gene due to weak, medium, and strong perturbations of RNAP concentration, from which we quantified the information entropy of single-gene responses of each class.

We found that the information entropy of the fold changes of the classes of genes increases (non-linearly) with the magnitude of the perturbation, in a manner that is consistent with the information entropy of the sum of the input interactions of individual genes, rather than their number of inputs.

Overall, we argue that, in the event of genome wide perturbations, asymmetries in input functions of TFs partially control the propagation of information between genes of the GRN of *E. coli*.



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