

Abstract Submitted  
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**Population-level control of gene expression**<sup>1</sup> DMITRY NEVOZHAY, RHYS ADAMS, Department of Systems Biology, UT M. D. Anderson Cancer Center, ELIZABETH VAN ITALLIE, MATTHEW BENNETT, Department of Biochemistry and Cell Biology and Institute of Biosciences and Bioengineering, Rice University, GABOR BALAZSI, Department of Systems Biology, UT M. D. Anderson Cancer Center — Gene expression is the process that translates genetic information into proteins, that determine the way cells live, function and even die. It was demonstrated that cells with identical genomes exposed to the same environment can differ in their protein composition and therefore phenotypes. Protein levels can vary between cells due to the stochastic nature of intracellular biochemical events, indicating that the genotype-phenotype connection is not deterministic at the cellular level. We asked whether genomes could encode isogenic cell populations more reliably than single cells. To address this question, we built two gene circuits to control three cell population-level characteristics: gene expression mean, coefficient of variation and non-genetic memory of previous expression states. Indeed, we found that these population-level characteristics were more predictable than the gene expression of single cells in a well-controlled environment.

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