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Stochastic discrete-state simulation of cell population growth in different environments MERZU K. BELETE, University of Houston & MD Anderson Cancer Center, RHYS M. ADMAS, GABOR BALAZSI, MD Anderson Cancer Center — Living cells possess low copies of many molecular components like DNA and proteins which cause stochastic fluctuations in gene expression. Gene expression affects cell phenotypes as a function of the environment.[1] Among all encoded phenotypes, fitness measures how well the organism survives in its environment. A number of experimental gene expression measurements confirmed that gene expression is a determinant factor for cellular fitness in various environments[2]. Yet, gene expression is a stochastic process better described by its probability distribution rather than its first moment. For bimodal gene expression, the individual cell gene expression is quite different from population average gene expression and it involves stochastic transitions between cellular states. Therefore, cell fitness is noisy and fluctuates randomly according to noisy gene expression. To address fitness in noise, we develop a stochastic model accounting different environments (combinations of drug and inducer). We found that the population fitness is nontrivial dependence on drug and inducer in agreement with our lab.[3]

[1] Jacob F, Monod J. J Mol Biol **3**, 318-356 (1961)
[2] Dekel E, Alon U. Nature **436**: 588-592 (2005)
[3] Nevozhay et al., PLoS Comp Bio (2012)

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