Decoupling cellular memory from other gene expression characteristics[1] GABOR BALAZSI, RHYS ADAMS, DMITRY NEVOZHAY, Dept. of Systems Biology - Unit 950, The University of Texas M. D. Anderson Cancer Center, Houston, TX — Non-conventional population level gene expression characteristics (such as the noise, cellular memory, skewness, modality, etc.) can have phenotypic impact and can affect cell population fitness independently of the gene expression mean. To study the phenotypic impact of gene expression characteristics other than the mean, they must be decoupled from the mean, and possibly from each other, i.e., two cell populations have to be established with similar means, but different non canonical gene expression characteristics. We study by experiment and mathematical modeling how positive feedback regulation can be used to decouple and adjust the cellular memory independently of the noise and the mean. We describe a state of "population dynamic bistability" where the cell population has bistable expression while individual cell lineages do not. Our results have implications for modeling gene expression bimodality and controlling cellular memory in cell populations.

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