Genetic Reporter Systems for Understanding the *mar* operon in *Escherichia coli*

Nicholas A. Rossi, Mary J. Dunlop

Keywords: Genetic Networks, Stochasticity, Signal Processing

Over the past decade, there has been increasing interest in bacterial individuality arising in clonal populations[1]. This emergent behavior often arises from stochasticity at the transcriptional level and is modulated by elements of the greater genetic network[2]. We seek to understand the role that interlocking negative and positive feedback loops within the multiple antibiotic resistance (mar) regulon of *Escherichia coli* serve to maximize population fitness while maintaining phenotypic heterogeneity in individuals. To do this, we have developed a series of plasmid-based dynamic reporters to measure expression of transcription factors *marA* and *marR* in real time. It is important to note that the dynamics of the genes must be normalized to basal fluctuations in total transcription – so-called extrinsic noise. Therefore these reporter systems have the capacity to filter out unwanted variation through cross-correlative analysis with constitutively expressed genes. This platform allows us to gather quantitative, single-cell data on the dynamics of various proteins in the *mar* network as a result of transcriptional stochasticity and genetic network architecture. By combining the reporter systems with iterative deletions in the surrounding genetic architecture, we can further our understanding of how each of the network components contributes to emergent phenomena in the genetic network.

1. Davidson, C. J. & Surette, M. G. Individuality in Bacteria. *http://dx.doi.org/10.1146/annurev.genet.42.110807.091601* (2008). doi:10.1146/annurev.genet.42.110807.091601
2. Sanchez, A. & Golding, I. Genetic Determinants and Cellular Constraints in Noisy Gene Expression. *Science* **342,** 1188–1193 (2013).