

Self-consistent theory of transcriptional control in complex regulatory architectures

Jasper Landman^{1,2} and Willem Kegel¹

¹*Van 't Hoff Laboratory for Physical & Colloid Chemistry, Universiteit Utrecht, Utrecht, the Netherlands, and* ²*European Synchrotron Radiation Facility, Grenoble, France*

In living cells, the proteins associated with gene regulation, the so-called transcription factors, are often shared between multiple pathways simultaneously. Genes therefore have to compete for transcription factors whose availability may fluctuate. Moreover, multiple copies of identical genes may exist in cells. We have developed a self-consistent model for gene regulation suitable for complex regulatory architectures and shared transcription-factors [1]. It will be shown that the competitive effects of the regulatory environment can be isolated into a single effective concentration, allowing the accurate description of a collection of gene expression data from diverse regulatory situations.

[1] F.M. Weinert et al., *Phys Rev. Lett.* 113:258101 (2014).