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Transcriptional Regulation by the Numbers HERNAN GARCIA, California Institute of Technology, LACRAMIOARA BINTU, JANE' KONDEV, Brandeis University, ROB PHILLIPS, California Institute of Technology — The study of gene regulation and expression is becoming ever more quantitative. In particular, with increasing regularity the expression of genes is characterized quantitatively with respect to how much, when and where. The key argument of the present work is that such quantitative data demands quantitative models. We examine a class of models ("thermodynamic models") which exploit the tools of statistical mechanics to compute the probability that RNA polymerase will be found at the appropriate promoter. Recent arguments have suggested that in some instances, the action of activators can be thought of strictly as agents of recruitment which increase the probability that RNA polymerase will be found at the promoter of interest. We develop an allied mathematical framework which describes the interactions of repressors, activators, helper molecules and RNA polymerase and culminates in an expression for the probability of RNA polymerase binding at the promoter of interest as a function of the concentrations of all of these regulatory agents. These ideas are applied to several case studies which illuminate the general formalism and shed light on the role of DNA looping.

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