

# PROPERTIES OF GENE EXPRESSION AND CHROMATIN STRUCTURE WITH MECHANICALLY REGULATED TRANSCRIPTION

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**Short Abstract** — The mechanical properties of transcription have emerged as central elements in our understanding of gene expression. Recent work has been done introducing a simple description of the basic physical properties of transcription. Here we generalize this framework to accommodate the behavior of many RNAPs operating on multiple genes on a shared piece of DNA. The resulting framework offers a preliminary explanation a number of previously unexplained unrelated phenomena in gene expression and DNA organization.

**Keywords** — Gene Expression, Transcription, Chromatin, Mechanics

## I. PURPOSE

IT has long been recognized that during transcription a elongation a combination of RNA polymerase (RNAP) rotation and DNA twist would have to occur. This simple fact has the potential to effect many aspects of transcription and gene expression [1]. However, only recently has a physical model of this process been developed.

Recent work has been done introducing a simple description of the basic physical elements of transcription where RNA elongation, RNA polymerase (RNAP) rotation and DNA super-coiling are coupled [2]. Here we generalize this framework to accommodate the behavior of many RNAPs operating on multiple genes on a shared piece of DNA. The resulting framework is combined with well-established stochastic processes of transcription resulting in a model which characterizes the impact of the mechanical properties of transcription on gene expression and DNA structure. Transcriptional bursting readily emerges as a common phenomenon with origins in the geometric nature of the genetic system and results in the bounding of gene expression statistics. Properties of a multiple gene system are examined with special attention paid to role that genome composition (gene orientation, size, and intergenic distance) plays in the ability of genes to transcribe. The role of transcription in shaping DNA structure is examined and the possibility of transcription driven domain formation is discussed [3].

## REFERENCES

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