On the Distribution of Transcription Times

Marc R. Roussel
Alberta RNA Research and Training Institute,
Department of Chemistry and Biochemistry, University of Lethbridge
roussel@uleth.ca

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We have developed a detailed model of transcription in prokaryotes [1]. For the case where the polymerases interact rarely (i.e. when the initiation rate is sufficiently low that, on average, polymerases are well spaced), we can analytically derive expressions for the moments of the distribution of transcription times. In some cases, we are also able to obtain the distribution itself semi-numerically. For small transcription units, this distribution can be strongly non-Gaussian, displaying both a large skewness and a large excess kurtosis (i.e. a slowly decaying tail, albeit one that decays exponentially). Multi-polymerase effects are also studied by simulation. We find that the analytic model generally predicts the behavior of the multi-polymerase simulations, often quantitatively, provided termination is not rate-limiting.

References

[1] M. R. Roussel and R. Zhu, *Stochastic kinetics description of a simple transcription model*, Bull. Math. Biol. **68** 1681–1713.