Supplementary File- 1

A systems view of the protein expression process

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Table contains some details of mathematical models included in the review. Modeling approach states whether the model is deterministic or stochastic, discrete or continuous, and analyzed at steady state or the kinetics is studied. The output column lists the major finding of the study.

Process	Model	Modeling approach	Processes considered	Output
Chromatin remodeling and histone modification	Blossey and Schiessel 2008	Deterministic/ Continuous/ Steady state	Histone tail modification	A quantitative model to test the role of histone tail modification in kinetic proofreading of gene activation
	Kuli and Schiessel 2003	Deterministic/ Discrete/ Equilibrium	Nucleosome sliding	Estimation of mobility of nucleosomes as function of thermal motion of DNA and underlying base pair sequence
	Chou 2007	Stochastic/ Discrete/ Kinetic	Hisone sliding and unwrapping	Calculation of mean histone detachment time and mean detachment distance as a function of remodeler motor speed
	Boeger, Griesenbeck et al. 2008	Stochastic/ Discrete/ Kinetic	Nucleosome sliding	Identification of nucleosome disassembly to be a rate limiting step, particularly for PHO5 promoter
	Raj, Peskin et al. 2006	Stochastic/ Discrete/ Kinetic	Gene activation and inactivation	Statistical properties of transcriptional burst and effect of gene activation kinetics of burst size and frequency
	Kim H. D and O'Shea E.K 2008	Deterministic/ Continuous/ Kinetic	Nucleosome association, dissociation and gene activation PHO5 gene	Relationship between transcription factor affinity for DNA and gene expression
	Luca Mariani 2010	Stochastic/ Discrete/ Kinetic	Gene opening and closing for il4 gene	Study of cell to cell variability as a result of stochastic gene opening and closing events
	Narula J., Smith A. M. et al. 2010	Deterministic/ Continuous/ Kinetic	Enhancement in gene expression particularly for Scl-Gata2-Fli1 triad network module	Study of steady state and transient of components in the triad, effect of mutation in the regulatory region on the components of this network module
	Sedighi M. and Sengupta A. M 2008	Stochastic/ Continuous/ Steady state	Positive feedback by chromatin remodeling proteins	Study of effect of change in chromatin silencing on stability of chromatin state
Transcription	Young, Ramirez et al. 1997	Deterministic/ Continuous/ Kinetic	mRNA synthesis	Prediction of optimal conditions for in vitro mRNA synthesis, in terms of NTP and Mg ion concentration
	Arnold, Siemann et al. 2001	Deterministic/ Continuous/ Kinetic	Initiation and elongation	Study of effect of RNA polymerase, promoter and nucleotide concentration on mRNA synthesis rate
	Bai, Shundrovsky et al. 2004	Deterministic/ Discrete/ Equilibrium	Elongation	Prediction of back-tracking and pauses during transcription depending upon the sequence information
	Höfer and Malte 2005	Stochastic/ Discrete/ Steady state	Initiation	Study of effect of kinetics of PIC assembly on mRNA noise
	Yamada and Peskin 2009	Deterministic/ Discrete/ Kinetic	Elongation with look-ahead feature of polymerase	Estimation of window size for RNA polymerase
	Roussel and Zhu 2006	Stochastic/ Discrete/ Kinetic	Elongation	Identification of probability distribution of transcriptional delay and elongation rate
	Voliotis, Cohen et al. 2008	Stochastic/ Discrete/ Steady state	Initiation and elongation	Analytical expression for transcription time
	Tripathi and Chowdhury 2008b, a	Stochastic/ Discrete/ Kinetic	Elongation with RNA polymerase traffic	Identification of mRNA synthesis rate and RNA polymerase average density

	von Hippel and Yager 1991	Deterministic/Continuous/Equilibrium	Elongation and termination	Prediction of elongation and termination phases during transcription depending upon sequence information
	von Hippel and Yager 1992	Deterministic/Continuous/Equilibrium	Elongation and termination	Prediction of elongation, back-tracking and termination efficiency
	von Hippel 1998	Deterministic/Continuous/Equilibrium	Elongation, termination and editing	Prediction of control at any template site and error correction
	Guajardo and Sousa 1997	Deterministic/Continuous/Equilibrium	Elongation	Identification of force generation by polymerase translocation as a function of energy available from NTP binding
	Vasisht 2006	Stochastic/Continuous/Equilibrium	Elongation	Prediction of polymerase pause and back-tracking
	Konishi 2005	Deterministic/Continuous/Equilibrium	mRNA synthesis and degradation	General relation between transcript level produced by sequence specific interaction between DNA and protein factors
	Kugel and Goodrich 2000	Deterministic/Continuous/Kinetic	Initiation specific at AdMLP	Identification of promoter escape to be a rate limiting step in transcription initiation
	Samuel Bernard 2006	Deterministic/Continuous/Kinetic	Transcription regulation with feedback for Hes1 transcription factor	Mathematical model transcriptional regulation by feedback loop, which shows oscillations in Hes1 expression
	Rajala T., Hakkinen A. et al. 2010	Stochastic/Discrete/Kinetic	Initiation, elongation with pausing, editing, termination	Relation between RNA polymerase pausing and transcriptional dynamics in terms of interval between successive mRNA production
RNA processing and degradation	Singh, Yang et al. 2007	Deterministic/Continuous/Kinetic	Transcription, pre-mRNA splicing, pre-mRNA turnover and mRNA degradation	Quantitative model with identification of reaction rate parameters for steps in RNA processing
	Ciocchetta, Hillston et al. 2008	Stochastic/Discrete/Kinetic	Co-transcriptional cleavage and alternate splicing	Determination of relative frequency of alternate splicing pathways
	Cao and Parker 2001	Deterministic/Continuous/Kinetic	mRNA synthesis and degradation	Study of effect of degradation reaction rate parameters on mRNA level
	Carrier and Keasling 1997	Stochastic/Discrete/Kinetic	Degradation by endonuclease and protection by ribosomes	Study of effect of 3 different mechanisms of degradation in relation to ribosome loading and translation rate
	Khanin and Higham 2007	Deterministic/Continuous/Steady state	miRNA mediated post transcriptional regulation	Study of effect of presence of miRNA on target mRNA level
	Levine, Ben Jacob et al. 2007	Deterministic/Continuous/Steady state	sRNA mediated post transcriptional regulation	Study of effect of presence of sRNA on target protein level
	Aguda, Kim et al. 2008	Deterministic/Continuous/Kinetic	miRNA mediated post transcriptional regulation in feedback	Occurrence of oscillations in target protein level due to presence of negative feedback
Translation	von Heijne, Nilsson et al. 1978	Deterministic/Continuous/Kinetic	Initiation, Elongation and Termination	Study of effect of the ribosome movement and RNA secondary structure on the elongation rate.
	Bergmann and Lodish 1979	Deterministic/Continuous/Steady state	Initiation, Elongation and Termination	Relationship between polysome size and protein synthesis.
	Heinrich and Rapoport 1980	Deterministic/Continuous/Kinetic	Initiation, Elongation, Termination	Identification of elongation to be an important regulatory step in translation; effect of ribosome concentration on mRNA
	Dimelow and Wilkinson 2009	Deterministic/Continuous/Steady state	Initiation	Distribution of the rate parameters in initiation.
	You, Coghill et al. 2010	Deterministic and stochastic/Continuous/Steady state	Initiation	Effect on initiation factor concentration on protein synthesis rate and variation of protein synthesis rate in population
	Skjondal-Bar and Morris 2007	Deterministic/Continuous/Kinetic	Initiation and elongation	Relationship between amino acids, tRNA and other factors. Ribosomal density on RNA.

	Gilchrist and Wagner 2006	Stochastic/ Discrete and Continuous/ Kinetic	Initiation, Elongation, Termination	Study of effect of nonsense errors at any codon on capability of ribosome recycling
	Drew 2001	Stochastic/ Discrete/ Steady state	Initiation, elongation and termination	Study of effect of binding of regulator to DNA on protein synthesis
	Heyd and Drew 2003	Stochastic/ Discrete/ Steady state	Elongation	Study of effect of concentration of amino acids and elongation factors on elongation rate
	Nayak S. , Siddiqui J.K. et al. 2011	Deterministic/ Continuous/ Kinetic	Initiation	Detailed model of translation initiation; effect of regulation at translation initiation on protein output
	Zouridis and Hatzimanikatis 2007	Deterministic/ Continuous/ Steady state	Initiation ,Elongation(in detail),Termination	Study of effect of polysome size and distribution of ribosome along mRNA on protein synthesis rate
	Bar N.S. 2009	Deterministic/ Continuous/ Dynamic	Initiation	Study of effect of regulation by eIF2 on translation initiation rate
	De Silvaa E., Krishnana J. et al. 2010	Deterministic/ Continuous/ Steady state	Termination	Mathematical model of feedback regulation of translation termination by termination factors; the effect of premature stop codon on termination regulation
Protein degradation	Holzhütter and Kloetzel 2000	Deterministic/ Continuous/ Kinetic	Protein degradation	Protein fragment pattern by proteasomal cleavage
	Peters, Janek et al. 2002	Deterministic/ Continuous/ Kinetic	Proteasome mediated degradation	Dynamics of protein fragment generation
	Luciani, Kesmir et al. 2005	Deterministic/ Continuous/ Kinetic	Proteasome mediated degradation	Study of effect of proteosomal gate size on protein degradation.
	Lee J., Choi K. et al. 2010	Deterministic/ Continuous/ Kinetic	Ubiquitination of NF-κB	Study of effect of ubiquitination of NF-kB activation; effect of mutant NF-kB on ubiquitination