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Modeling coupled transcription, translation and degradation and miRNA-based regulation of this process

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The translation-transcription process with the description of the most basic "elementary" processes consists in: 1) production of mRNA molecules, 2) initiation of these molecules by circularization with help of initiation factors, 3) initiation of translation, recruiting the small ribosomal subunit, 4) assembly of full ribosomes, 5) elongation, i.e. movement of ribosomes along mRNA with production of protein, 6) termination of translation, 7) degradation of mRNA molecules. A certain complexity in the mathematical formulation of this process arises when one tries to take into account the phenomenon of polysome first, when several ribosomes are producing peptides on a single mRNA at the same time. This leads to multiplicity of possible states of mRNA with various numbers of ribosomes with potentially different dynamics, interaction between ribosomes and other difficulties. In this preprint we provide 1) detailed mechanistic description of the translation process with explicit representation of every state of translating mRNA, followed by 2) deriving the simplest and basic ODE model of coupled transcription, translation and degradation, and 3) developing a model suitable for describing all known mechanisms of miRNA action on translation. The basic model is constructed by correct lumping of the detailed model states and by separating the description of ribosomal turnover. It remains linear under assumption of that the translation is not limited by availability of ribosomal subunits or initiation factors. The only serious limitation of this type of translation modeling is in that it does not take into account possible interactions between ribosomes. The latter might lead to more complex phenomena which can be taken into account in simulatory models of the detailed representation of translation at the cost of more difficult analytical analysis of the model.

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