





The conference is supported by the National Laboratory for Health Security project RRF-2.3.1-21-2022-00006

Persistence and stability of generalized ribosome flow models

Gábor Szederkényi

Pázmány Péter Catholic University, Hungary szederkenyi@itk.ppke.hu

In this contribution the qualitative dynamical properties of generalized ribosome flow models are presented using a compartmental modeling approach. Compartmental models are used to describe and analyze the transport between different containers, called compartments in various natural and technological systems. The modeled objects (molecules, people, vehicles, etc.) can move between compartments obeying the given constraints such as limits of directions, flow rates, or capacities. The dynamical modeling of the mRNA translation process has been in the focus of research since the second half of the 20th century. The first large scale analysis of gene translation through the so-called ribosome flow model (RFM) was presented in [1], where the applied second order nonnegative compartmental model based on the principle of totally asymmetric exclusion was able to capture the most important dynamical features of the translation process. We generalize the original RFM model class having a tubular or ring-like structure in two ways. Firstly, we assume arbitrary directed graph structure between the compartments and secondly, we allow general time-varying rate functions describing the compartmental transitions. Persistence of the dynamics is shown using the kinetic and the corresponding Petri net representation of the system by efficiently characterizing all siphons in the network. Further, we show the stability of different compartmental structures including strongly connected ones with an entropy-like logarithmic Lyapunov function. The L^1 contractivity of solutions is also studied in the case of periodic reaction rates having the same period. Additionally, it is shown that different Lyapunov functions may be assigned to the same model depending on the factorization of the transition rates. Finally, a so-called port-Hamiltonian representation of the system is constructed both in the original and in the reduced state spaces with clear connection between the structure matrices and the compartmental graph topology.

- S. REUVENI, I. MEILIJSON, M. KUPIEC, E. RUPPIN, T. TULLER, Genome-scale analysis of translation elongation with a ribosome flow model, *PLoS Comput. Biol.*, 7(2011), No. 9, 1002127.
- [2] G. SZEDERKÉNYI, B. ÁCS, G. LIPTÁK, M. A. VÁGHY, Persistence and stability of a class of kinetic compartmental models, J. Math. Chem., 60(2022), No. 6, 1001–1020.
- [3] G. SZEDERKÉNYI, M. A. VÁGHY, Persistence and stability of generalized ribosome flow models with time-varying transition rates, 2022, arXiv:2211.10653 [math.DS].