

## A geometric analysis of fast-slow models for stochastic gene expression

*Nikola Popovic*

*School of Mathematics, University of Edinburgh,*

*Edinburgh, United Kingdom*

*Nikola.Popovic@ed.ac.uk*

**Abstract:** Stochastic models for gene expression frequently exhibit dynamics on different time-scales. One potential scale separation is due to significant differences in the lifetimes of mRNA and the protein it synthesises, which allows for the application of perturbation techniques [1, 2].

Here [3], we develop a dynamical systems framework for the analysis of a family of "fast-slow" models for gene expression that is based on geometric singular perturbation theory [4]. We illustrate our approach by giving a complete characterisation of a standard two-stage model which assumes transcription, translation, and degradation to be first-order reactions. In particular, we develop a systematic expansion procedure for the resulting propagator probabilities that can in principle be taken to any order in the perturbation parameter. We verify our asymptotics by numerical simulation, and we explore its practical applicability, as well as the effects of a variation in the system parameters and the scale separation. Finally, we discuss the generalisation of our geometric framework to models for regulated gene expression that involve additional stages, which is a subject of ongoing research.

[1] V. Shahrezaei and P.S. Swain, "Analytical distributions for stochastic gene expression", *Proc. Natl. Acad. Sci USA* 105.45(2008), 17256-17261

[2] P. Bokes, J.R. King, A.T.A. Wood, and M. Loose, "Multiscale stochastic modelling of gene expression", *J. Math. Biol.* 65.3(2012), 493-520

[3] N. Popovic, C. Marr, and P.S. Swain, "A geometric analysis of fast-slow models for stochastic gene expression", *J. Math. Biol.* 72.1(2016), 87-122

[4] C.K.R.T. Jones, "Geometric singular perturbation theory", in *Dynamical Systems (Montecatini Terme, 1994)*, *Lecture Notes in Math.* 1609(1995), 44-118, Springer-Verlag, Berlin