

Zero-Eigenvalue Turing Instability in General Chemical Reaction Networks

Maya Mincheva¹, Gheorghe Craciun²

¹ Northern Illinois University

mincheva@math.niu.edu

² University of Wisconsin-Madison

craciun@@math.wisc.edu

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Biochemical reaction networks with diffusion are usually modeled by reaction-diffusion systems of equations and are studied in connection with pattern formation in biology. We say that Turing instability occurs if a spatially homogeneous equilibrium is asymptotically stable as a solution of the ordinary differential equation system and unstable as a solution of the corresponding reaction-diffusion systems of equations. We describe a necessary condition for zero-eigenvalue Turing instability, i.e., Turing instability arising from a real eigenvalue changing sign from negative to positive, for general chemical reaction networks with any number of species, modeled with mass-action kinetics. The reaction mechanisms are represented by the species-reaction graph (SR graph) which is an undirected bipartite graph. If the SR graph satisfies certain conditions, similar to the conditions for ruling out multiple equilibria in spatially homogeneous differential equations systems, then the corresponding mass-action reaction-diffusion system cannot exhibit zero-eigenvalue Turing instability for any parameter values, rate constants and diffusion coefficients.

References

- [1] M. Mincheva, G. Craciun *Zero-Eigenvalue Turing Instability in General Chemical Reaction Networks*, Math. Biosc. and Eng. (to appear)