NON-EQUILIBRIUM RESPONSE RELATIONS: INSIGHTS FOR BIOLOGICAL INFORMATION PROCESSING

Ruicheng Bao^{1,2}, Shiling Liang^{2,3,4*}

¹ Department of Physics, Graduate School of Science, 7-3-1, The University of Tokyo, Hongo, Bunkyo-ku, Tokyo 113-0033, Japan

² Center for Systems Biology Dresden, 01307 Dresden, Germany

³ Max Planck Institute for the Physics of Complex Systems, 01187 Dresden, Germany

⁴ Max Planck Institute of Molecular Cell Biology and Genetics, 01307 Dresden, Germany

*shiling@pks.mpg.de

ABSTRACT

We uncover fundamental physical constraints on information processing in nonequilibrium networks through rigorous analysis of response relations of Markov chains. Our work establishes two key principles: a universal precision bound of 1/2 for state observable responses to single edge/vertex perturbation that cannot be overcome by increasing network complexity of the unperturbed parts, and exact identities and bounds describing system responses to strong perturbations. These results provide physical insights into why simple network architectures - as illustrated with a push-pull motif - can be optimal despite evolutionary pressure for precision. By bridging statistical physics and information theory, our framework reveals how thermodynamic and structural constraints shape the design of nonequilibrium markov networks, with implications for biological sensing and information processing systems.

Keywords: Markov Chain, Response Theory, Information Processing, Nonequilibrium Thermodynamics, Stochastic Thermodynamics *Physics and Astronomy Classification Scheme*: 02.50.Ga

REFERENCES

 R. Bao and S. Liang, "Nonequilibrium Response Theory: From Precision Limits to Strong Perturbation," arXiv preprint arXiv:2412.19602 (2024).