1163-65-1104   **Kee-Myoung Nam*** (`kmnam@g.harvard.edu`). *Robustness and parameter geography in post-translational modification systems.*

Biological systems are often acknowledged to be robust to perturbations, but a rigorous understanding of this has been elusive. In a mathematical model, perturbations often exert their effect through parameters, so sizes and shapes of parametric regions offer an integrated, global view of robustness. Here, we explore this "parameter geography" for the property of bistability in post-translational modification (PTM) systems. In particular, we exploit two recent mathematical advances: first, we use the "linear framework" for timescale separation to describe the steady-state of a two-site PTM system as the solutions of two polynomial equations in two variables, with eight non-dimensional parameters. Importantly, this approach allows us to accommodate arbitrarily complex enzyme mechanisms, beyond the conventional Michaelis-Menten scheme, which unrealistically forbids product rebinding. Furthermore, we use the numerical algebraic geometry tools Bertini, Paramotopy, and alphaCertified to compute and statistically assess the solutions to these equations at billions of parameter points. Combining these developments in theory and software, we are able to uncover mathematical conjectures and questions regarding parameter geography through a high-dimensional, data-centric analysis. (Received September 14, 2020)