Abstract Submitted
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On the Analysis of Time-Dependent Biochemical Systems Via the Utilization of Ising Mean Field Parameters[1] CURTIS PETERSON, Department of Physics and School of Mathematical and Statistical Sciences, Arizona State University, Tempe, Arizona 85287, USA, TOMMY BYRD, Department of Physics and Astronomy, Purdue University, West Lafayette, Indiana 47907, USA, ROBERT VOGEL, IBM T. J. Watson Research Center, Yorktown Heights, New York 10598, USA, AMIR EREZ, Immunodynamics Group, Cancer and Inflammation Program, National Cancer Institute, National Institutes of Health, Bethesda, Maryland 20814, USA, ANDREW MUGLER, Department of Physics and Astronomy, Purdue University, West Lafayette, Indiana 47907, USA — Cell behaviors are governed by non-equilibrium systems of interacting molecules. Often, these systems exhibit qualitative transitions in their parameter space, e.g. from one to two stable states. These transitions are reminiscent of critical transitions in equilibrium systems from many-body physics. A particular class of non-equilibrium biochemical systems with feedback has been shown to exhibit the critical scaling properties of the Ising universality class in the mean-field limit, and this prediction is supported by measurements of doubly phosphorylated ppERK in T cells. We extend upon the analysis by studying time-dependent data of ppERK abundance as the system transitions from two stable states to one. Our analysis reveals that T cells experience critical slowing down in their response to drugs. Our approach is broadly applicable to the investigation of critical dynamics in biological systems.

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