Stochasticity and universal dynamics in communicating cellular populations JAVAD NOORBAKHSH, PANKAJ MEHTA, Boston University, ALLYSON SGRO COLLABORATION, DAVID SCHWAB COLLABORATION, TROY MESTLER COLLABORATION, THOMAS GREGOR COLLABORATION — A fundamental problem in biology is to understand how biochemical networks within individual cells coordinate and control population-level behaviors. Our knowledge of these biochemical networks is often incomplete, with little known about the underlying kinetic parameters. Here, we present a general modeling approach for overcoming these challenges based on universality. We apply our approach to study the emergence of collective oscillations of the signaling molecule cAMP in populations of the social amoebae *Dictyostelium discoideum* and show that a simple two-dimensional dynamical system can reproduce signaling dynamics of single cells and successfully predict novel population-level behaviors. We reduce all the important parameters of our model to only two and will study its behavior through a phase diagram. This phase diagram determines conditions under which cells are quiet or oscillating either coherently or incoherently. Furthermore it allows us to study the effect of different model components such as stochasticity, multicellularity and signal preprocessing. A central finding of our model is that *Dictyostelium* exploit stochasticity within biochemical networks to control population level behaviors.

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