

Attempts to describe real biological systems usually lead to a forest of parameters, and sometimes “theory” seems to be little more than fitting these many parameters to experimental results. If we want to have theories of biological systems in the sense that we are familiar with from the rest of physics, then we need a way around all these parameters. I will present two approaches. One view is that simplification occurs as it does in condensed matter physics, where the microscopic properties of materials can be complicated but the macroscopic behaviors are described by simpler effective theories. I’ll illustrate this approach by analyzing data on a real network of neurons, using methods inspired by the renormalization group. We will see evidence of scaling and convergence to fixed distributions of coarse grained variables, hinting at a nontrivial fixed point. A different view starts with the observation that the mechanisms of life are extraordinarily precise: our visual system counts single photons, signaling systems are limited by the random arrivals of individual molecules, and more. I’ll show how these observations of performance near the relevant physical limits can be turned into optimization principles, using the early events of embryonic development as an example. We will see that it is possible to predict detailed, quantitative relationships among different sets of measurements, avoiding all free parameters; these predictions are in strikingly good agreement with the data. I’ll conclude with some perspectives on where we are going in the larger effort to build a theoretical physics of biological systems.