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Some physics problems in biological networks

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Most of the interesting things that happen in living organisms require interactions among many components, and it is convenient to think of these as a "network" of interactions. We use this language at the level of single molecules (the network of interactions among amino acids that determine protein structure), single cells (the network of protein-DNA interactions responsible for the regulation of gene expression) and complex multicellular organisms (the networks of neurons in our brain). In this talk I'll try to look at two very different kinds of theoretical physics problems that arise in thinking about such networks. The first problems are phenomenological: Given what our experimentalists friends can measure, can we generate a global view of network function and dynamics? I'll argue that maximum entropy methods can be useful here, and show how such methods have been used in very recent work on networks of neurons, enzymes, genes and (in disguise) amino acids. In this line of reasoning there are of course interesting connections to statistical mechanics, and we'll see that natural statistical mechanics questions about the underlying models actually teach us something about how the real biological system works, in ways that will be tested through new experiments. In the second half of the talk I'll ask if there are principles from which we might actually be able to predict the structure and dynamics of biological networks. I'll focus on optimization principles, in particular the optimization of information flow in transcriptional regulation. Even setting up these arguments forces us to think critically about our understanding of the signals, specificity and noise in these systems, all current topics of research. Although we don't know if we have the right principles, trying to work out the consequences of such optimization again suggests new experiments.