Theoretical physics meets experimental biology

This is a special time for physicists interested in the phenomena of life: almost every area of modern biology, from molecular genetics to neuroscience, is being revolutionized by large scale, quantitative experiments. At the same time, developments in statistical mechanics and dynamical systems have prepared the physics community to address theoretical questions posed by more complex systems. Each subfield of experimental investigation poses interesting and important challenges in modelling and data analysis, but behind these problems lies the grand challenge of providing a proper theoretical framework for the emergence of functionality in biological systems. The goal of this seminar series is to give all of these problems sharper formulations. Topics will include:

Statistical information. From DNA sequences to neural spike trains to language, living systems represent information in code. How do we characterize the order and complexity of such a data stream? What do we mean by saying that the data can be segmented into elementary symbols or "words"? Are symbols and features that are significant in the statistical structure of the sequence itself in fact "meaningful" in the biological context? How complex are the rules that we need to learn in order to interpret these data, and what are the limits on what can be learned from examples? Can an analysis of learning as a statistical problem inform our exploration of learning by humans and animals?

Dynamics and dimensionality. Even the simplest of biological systems has hundreds of degrees of freedom, often without obvious separations of time scales or other hints for dimensionality reduction. Can we identify stable functional states of biological networks—from cell types in development to memories in the brain—with attractors of the relevant network dynamics? What features of network topology are essential for stability and robustness of these attractors? Faced with data of high dimensionality, how do we recognize the relevant low dimensional features? Is our own perception of the world (in part) the problem of discovering these low dimensional features in sensory data?

Fluctuations and noise. Much of cellular biochemistry, from the regulation of gene expression to the stabilization of memories at a synapse, operates in a regime where the crucial molecules are present in just a handful of copies. Do we understand how to describe cellular dynamics in this noise dominated regime? Does the nonequilibrium nature of the system introduce qualitatively new features in the noise? How do robust behaviors emerge from so few molecules? Are there cases where fluctuations change the average behavior of the system, perhaps even qualitatively? Why do cells operate in this limit?

Because the goal is to identify and sharpen our theoretical questions, the seminar will be more like a journal club with informal discussion than the usual series of talks on completed work. The assumption is that the audience is composed of theoretical physicists; we assume mathematical maturity but will pause for biological background.

Participating faculty will include (at various times): W. Bialek, C. G. Callan, J. J. Hopfield, D. W. Tank, and S. Tavazoie.

Organizational meeting: Monday 17 September 2001, 4 PM in *** Jadwin. For more information contact W. Bialek (360 Jadwin, wbialek@princeton.edu).