Workshop on the Systems Biology of Infectious Diseases - August 2007

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Biological Physicists have become key players in the reshaping of modern Biology into a quantitative science in which mathematical and computational approaches are used hand in hand with molecular and cell biology, biochemistry, biophysics experiments to solve problems at the forefront of life-science research. Apart from their scientific expertise, physicists have brought a more integrative approach to these problems, addressing the integration of different scales, from the structural aspects of the various components (proteins) and the mechanisms governing the behavior of the molecular motors involved to bio-molecular signaling and genetic pathways, to the behavior of the system as a whole. The systems biology of infectious diseases offers a unique opportunity for physicists who want to make a fundamental contribution to life-science driven interdisciplinary research.

Of all the global environmental problems facing humanity, none is more urgent, or more likely to cause large-scale human suffering, than the changing epidemiological environment. New diseases, like AIDS and SARS, are emerging, while old diseases, like tuberculosis and influenza, are rebounding or evolving into new forms. The situation will not get better in the short run. Whether or not the current H5N1 avian influenza will be the source of the next human influenza pandemic is uncertain, but there is little disagreement among experts that another pandemic will occur, with many millions of deaths, and likely in the not-too-distant future. Furthermore, the recent outbreaks of novel diseases, especially those that jump from animals to humans (zoonoses), are likely to become an ever-increasing problem as barriers to travel and the exchange of materials diminish. Bio-terrorism exacerbates these risks, and mandates greater attention to what we can do to prevent, contain and cope with outbreaks. Bacterial infections are a threat of increasing importance, not only because of the bioterror potential of agents like anthrax, but more urgently because of the dramatic rise in antibiotic resistance among the pathogens, and the consequent loss of effectiveness of our most reliable antibiotics.

More than virtually any other contemporary problems, dealing with the epidemiological environment poses multidisciplinary, and indeed interdisciplinary, challenges of great magnitude, and great potential. Molecular biology lies at the core, as we seek new vaccines and antibiotics, while mathematical and computer modeling is playing an increasingly important role in molecular design, data integration and rational strategies for identifying, selecting and testing combinations of potential vaccine components. In addition, the contribution of mathematical and physical scientists who understand complex dynamical systems is especially important since the dynamics of diseases is at its heart ecological and epidemiological, tied closely to human demography and to the dynamics of animal reservoirs and vectors. Consequently modeling host parasite interactions at the level of individuals and populations is becoming an established part of infectious disease research. Climate change will also affect the distribution of non-human sources of disease, making paramount a coupling of climate prediction models with mathematical models of epidemic spread, for diseases ranging from cholera to dengue to influenza.

Mathematical approaches to these problems have been central to management and control for a century, with emphasis on how the potential for outbreaks (essentially, phase transitions) depend upon key parameters, and optimization of vaccination and other control measures. More recently, high-speed computation has led to the development of large-scale, agent-based models that track individual behaviors. As with any such models, questions arise about dimensionality, parameter estimation and robustness, and about how statistical mechanical and other methods can be used to coarse grain these models. Advances in immunological studies, including modeling, introduce the need to cross scales from the cellular to population. Climate change takes these studies to broader scales, and to the interface with global circulation models. Finally, optimization and game-theoretic methods will be needed to help guide policy decisions, and expertise in international negotiation will be needed to implement solutions, even for such seemingly straightforward challenges as surveillance and honest reporting.

The problems raised in the study of diseases are urgent and novel, and yet familiar and similar in their structure to other problems in physics. The time is perfect for assembling a group ranging from medical practitioners to epidemiological modelers to physicists and mathematicians to confront the novel problems that are being faced.

The proposed workshop brings together leading biologists, population geneticists, computational and mathematical biologists, and biological physicists interested in the various aspects of infectious diseases.

Roy Anderson Tim Buchman Don Burke Carl Bergstrom Jay Berzofsky Stefan Bornhold Anne De Groot Joe DeRisi Jonathan Dushoff David Earn Vince Emery Neil Ferguson Don Ganem Julia Gog Bryan Grenfell Mark Klempner Bette Korber Bruce Levin Simon Levin

Marc Lipsitch Robert May Martin Nowak Evgeny Nudler Mercedes Pascual Alan Perelson Josh Plotkin Alex Sette Burt Singer

Interested physicists:

Gyan Bhanot Bill Bialek Robijn Bruinsma Harmen Bussemaker Terry Hwa Stan Leibler Herbert Levine Nikolaus Rajewsky Harlan Robbins Andrei Ruckenstein Eric Siggia Anrivan Sengupta Boris Shraiman Gustavo Stolovitzky Yuhai Tu Chris Wiggins Ned Wingreen