

STATISTICS COLLOQUIUM

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TALK: 4:00 PM — SCIENCE CENTER RM. 309

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“Modeling Influenza Epidemics: Challenges and Opportunities”

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ABSTRACT

In spite of the natural shortcomings common to most modeling efforts in the field of population biology, particularly as they interphase with human social dynamics, a lack of self-criticism of modeling patterns seems to remain. Modeling communities carrying out research, driven by prediction and forecasting demands (not a bad thing at all), tend to generate results without providing a systematic critical assessment of the modeling frameworks used; the limitations in existing data; and the lack of ability to properly define or measure key modeling parameters. The emergence and/or reemergence of diseases have played a critical role in promoting change (HIV, TB, SARS, Dengue, Influenza and others). The SARS outbreaks, nearly a decade ago, generated tremendous interest in extending the theory for single outbreak deterministic models, a significant event in a field that had been primarily dominated by the study of long-term disease dynamic patterns (asymptotic behavior). Embedded concepts like contact are finally being dissected because, for example, what constitutes a “contact” between individuals (leading to transmission) is still poorly defined. Similarly, the dominant role of the basic reproduction number, a concept that has undergone transitions and revisions over the past decades, is also being questioned. This level of scrutiny will lead to changes and shifts in the paradigms and frameworks used to model disease dynamics. In this lecture, I will explore some of the history behind these shifts. The discussion will be carried out in the context of “slow” diseases like HIV or TB and “fast” diseases like influenza.