Area of Excellence
CONTROL OF PANDEMIC AND INTER-PANDEMIC INFLUENZA

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jointly present the following seminar

Machine Learning for Predicting Vaccine Immunity

by

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Abstract

The ability to better predict how different individuals will respond to vaccination and to understand what best protects individuals from infection greatly facilitates developing next-generation vaccines. It facilitates both the rapid design and evaluation of new and emerging vaccines as well as identifies individuals unlikely to be protected by vaccine. We describe a general-purpose machine learning framework, DAMIP, for discovering gene signatures that can predict vaccine immunity and efficacy. DAMIP is a multi-group 'concurrent' classifier that offers unique features not present in other models: a nonlinear data transformation to manage the curse of dimensionality and noise; a reserved-judgment region that handles fuzzy entities; and constraints on the allowed percentage of misclassifications.

Using DAMIP, implemented results for yellow fever demonstrated that, for the first time, a vaccine's ability to immunize a patient could be successfully predicted (with > 90% accuracy) within one week after vaccination. A gene identified by DAMIP decrypted a seven-decade-old mystery of vaccination. Results for flu vaccine demonstrated DAMIP's applicability to both live-attenuated and inactivated vaccines. Results in a Malaria study enabled targeted delivery to individual patients.

Our project's methods and findings permit highlighting and probabilistically prioritizing hypothesis design to enhance biological discovery. Moreover, they guide the rapid development of better vaccines to fight emerging infections, and improve monitoring for poor responses in the elderly, infants, or others with weakened immune systems. In addition, the project's work should help with universal flu-vaccine design.

This work is joint with the Centers for Disease Control and Prevention and the Emory Vaccine Center.

ALL ARE WELCOME