Abstract Submitted
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Statistical Physics of Vaccine Design MICHAEL DEEM, Rice University — I will define a new parameter to quantify the antigenic distance between two H3N2 influenza strains. I will use this parameter to measure antigenic distance between circulating H3N2 strains and the closest vaccine component of the influenza vaccine. For the data between 1971 and 2004, the measure of antigenic distance correlates better with efficacy in humans of the H3N2 influenza A annual vaccine than do current state of the art measures of antigenic distance such as phylogenetic sequence analysis or ferret antisera inhibition assays. I suggest that this measure of antigenic distance can be used to guide the design of the annual flu vaccine. I will describe combining this measure of antigenic distance with a multiple-strain avian influenza transmission model to study the threat of simultaneous introduction of multiple avian influenza strains. For H3N2 influenza, the model is validated against observed viral fixation rates and epidemic progression rates from the World Health Organization FluNet - Global Influenza Surveillance Network. I find that a multiple-component avian influenza vaccine is helpful to control a simultaneous multiple introduction of bird-flu strains. I introduce Population at Risk (PaR) to quantify the risk of a flu pandemic, and calculate by this metric the improvement that a multiple vaccine offers.

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