

International Conference on
PHARMACEUTICAL CHEMISTRY &
International Conference on
SYNTHETIC BIOLOGY

July 16-17, 2018 | Paris, France



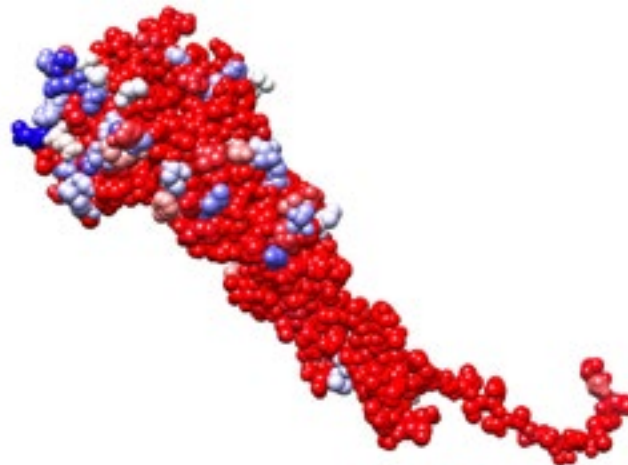
Eva k Lee

Georgia Institute of technology, Georgia

Predicting antigenicity of human influenza virus A (H₃N₂) using deep learning

The rapid and large-scale pathogenesis of influenza virus requires constant monitoring, and frequent vaccine development to protect the world population not only from seasonal influenza but also from novel influenza A viruses that could trigger a pandemic. Seasonal Influenza is an acute viral infection and is estimated to cause 3 to 5 million cases of severe illness and around 250,000 to 500,000 deaths worldwide¹. Among the three subtypes, type A is the only one known to cause pandemics. Previously developed models utilize a wide range of predictive algorithms to model the antigenic distance of influenza A viruses and achieved great success. However, these models only measure the contribution of chosen amino acids as individuals, which lacks the context that changes of amino acids in Hemagglutinin may have composite effects since they form a 3D structure in space. Besides reporting point mutations with their association of influenza epidemic, they also involve only a limited number of amino acid properties⁴. Understanding the combination effect of point mutations of influenza A and expanding the number of amino acids in the analysis may better unveil the relationship between HA sequence and its antigenicity. In this study, we design a convoluted neural network (CNN) to model the patterns of HA protein sequence to analyze the patterns introduced by individual mutations and their associated and combination effect. Furthermore, we

systematically analyze all available amino acid properties for the predictability of H3N2 antigenicity. Particle swarm optimization algorithm is used to construct the structure of CNN. This approach produces good results with 10-fold cross validation of over 94% unbiased estimate, and blind prediction of 100% accuracy.



Biography

Eva Lee is Virginia C. and Joseph C. Mello Chair and Professor in the H. Milton Stewart School of Industrial and Systems Engineering at Georgia Institute of Technology, and Director of the Center for Operations Research in Medicine and HealthCare, a center established through funds from the National Science Foundation and the Whitaker Foundation. The center focuses on biomedicine, public health, and defense, advancing domains from basic science to translational medical research; intelligent, quality, and cost-effective delivery; and medical preparedness and protection of critical infrastructures. She is a Distinguished Scholar in Health Systems, Health System Institute at Georgia Tech and Emory University. She is also the Co-Director of the Center for Organization Transformation, an NSF Industry/University Cooperative Research Center.

eva.lee@gatech.edu