# FluVaxAI: A Novel AI-Inspired Regional Flu Vaccine Formulation

Sharma, Cameron (School: Mills E. Godwin High School)

Influenza virus causes an estimated 9.0-35.6 million severe illnesses and 850,000 deaths worldwide annually. Aided by its error-prone, open-ended RNA genome, the virus mutates rampantly to evade the host immune system. The annual quadrivalent flu vaccine has two components each of Type A and Type B lineages. Type A strains cause majority of the flu related morbidity and mortality because they have zoonotic hosts. WHO/CDC announce a single global flu vaccine annually. This one-vaccine-fits-all-worldwide model has limited effectiveness (mean: 40%, range: 10%-60%). In this experiment, the global and regional vaccines were the levels of independent variable. Efficacy of the vaccine was the dependent variable. It was hypothesized that the vaccines tailored to the regions around the globe would be more effective. FluVaxAI presented here is a novel methodology for computing antiviral vaccines. Nucleotide and protein sequences of the hemagglutinin segments of the influenza virus were downloaded from the IVR and GISAID data repositories. Mutations in individual amino acids in the segments were tracked over the study period of 2005 to 2020. A long short-term memory model was fitted to the mutational history of the amino acids to project their future course. The vaccines were then assembled from the resulting amino acids. The process was repeated for each region. The computed regional vaccines were distinct and showed efficacy in their respective regions, proving the hypothesis. The results for Africa and Asia need further investigation. The future work could include refinement of the model and field testing. There were no safety issues.

**Awards Won:**