Currently, the number of reported transmission of avian flu to humans is small and subsequent human-to-human transitions are of limited virulence. The avian virus’ ability to infect humans is dependent on whether it can bind to one specific shape of receptor on the surface of human respiratory cells [1]. How these viruses evolve to infect humans is not adequately explained by current research. We are creating a basic algorithm supplemented by an option in which two different viral strains can infect the same cell and recombine randomly and the overall fitness of the recombined viruses will be taken into consideration. The algorithm will start with a flu genome (all 8 segments) and will generate random mutations according to a mutation rate. Sequences will be selected based on some fitness function and the process will be repeated. After analyzing the mutated sequences, we can make comparisons and predict how the evolution of the avian virus is capable of infecting humans.