

**Invitation to M.Tech. Thesis Defense of Khushal Sharma: May 30, 2022 (Monday): 02:45 PM-03.30 PM IST**

In Partial Fulfilment of the Requirements for the Degree of

**M.Tech. CB**

**Khushal Sharma (MT20210)**

Will defend his thesis

**Title: “Genome-based in silico models to predict infectious strains of Influenza A and Rotavirus A Khushal Sharma”**

IIIT-D Faculty and Students are invited

**Date: May 30, 2022 (Monday)  
Time:** **02.45 PM-03.30 PM IST**

**Venue: Room No: A-320 (Meeting Room), R & D Building**

**Examiner: Internal:   Jaspreet Kaur Dhanjal**

**External/~~Internal~~: Manish Kumar (University of Delhi)**

**Advisor: G P S Raghava**

**Co-Advisor NA**

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

**Abstract**

The transmission of pathogens or infectious agents from animals to humans, i.e. zoonosis, is of global concern. Outbreaks pertaining to zoonosis have been the one of the major causes of fatalities worldwide. Both Influenza A, a viral disease that infects the lungs, and Rotavirus A, an enteric disease in humans and livestock, are zoonotic. Furthermore, recent outbreaks such as Ebolavirus, Zikavirus, Coronavirus are all examples of viruses of zoonotic origin, increasing in frequency due to globalization. This is where host reservoir prediction becomes essential as a preventive measure in order to curb a potential outbreak. In this study, we have made insilico machine learning based models for the prediction of host reservoir of Influenza A and Rotavirus A, whether the strain has the chances of being infectious to humans or not. This analysis would aid to the preventive measures healthcare authorities can take in order to control and mitigate possible outbreaks. We achieved 0.979 accuracy as well as area under the curve (AUC) on Influenza A based models for the training dataset. The accuracy and area under the curve (AUC) for the validation dataset is 0.98. Similarly, for Rotavirus A based models, training accuracy and area under the curve (AUC) is 0.986, validation accuracy is 0.953, and area under the curve (AUC) is 0.915. We have provided webservers FluSPred(https://webs.iiitd.edu.in/raghava/fluspred/), for Influenza A, and RotaVPred(https://webs.iiitd.edu.in/raghava/rotavpred/), for Rotavirus A, which have been made open source for the scientific community.