

Exploring host specificity of Influenza A virus

USING MACHINE LEARNING

ANGEL AUSMUS
ABHIRUPA GHOSH

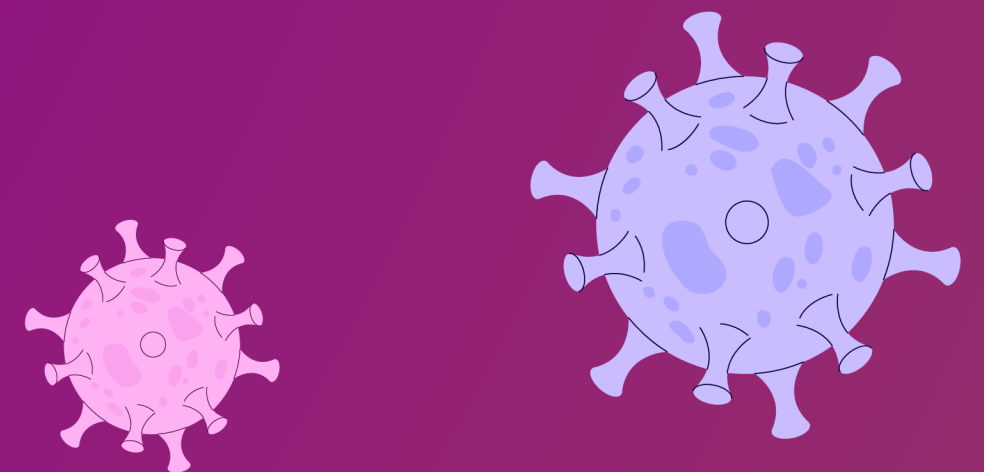
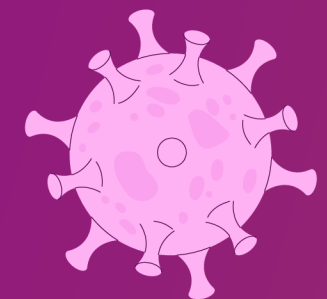
JRAVI LAB

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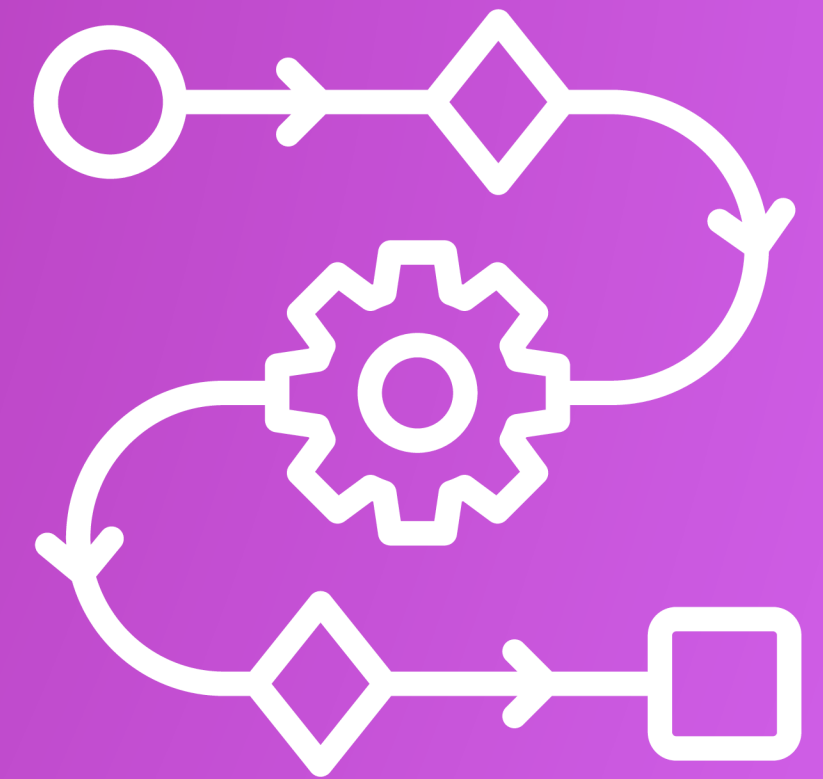
Influenza A (IAV)

- single-stranded RNA genome consisting of 8 separate segments
- possesses 2 major proteins important for viral entry:
 - hemagglutinin (H)
 - neuraminidase (N)
- particularly susceptible to zoonosis:
 - **antigenic drift:** RNA genomes lack proofreading during replication and accumulate point mutations at a higher rate
 - **antigenic shift:** different IAV subtypes may swap gene segments during coinfection



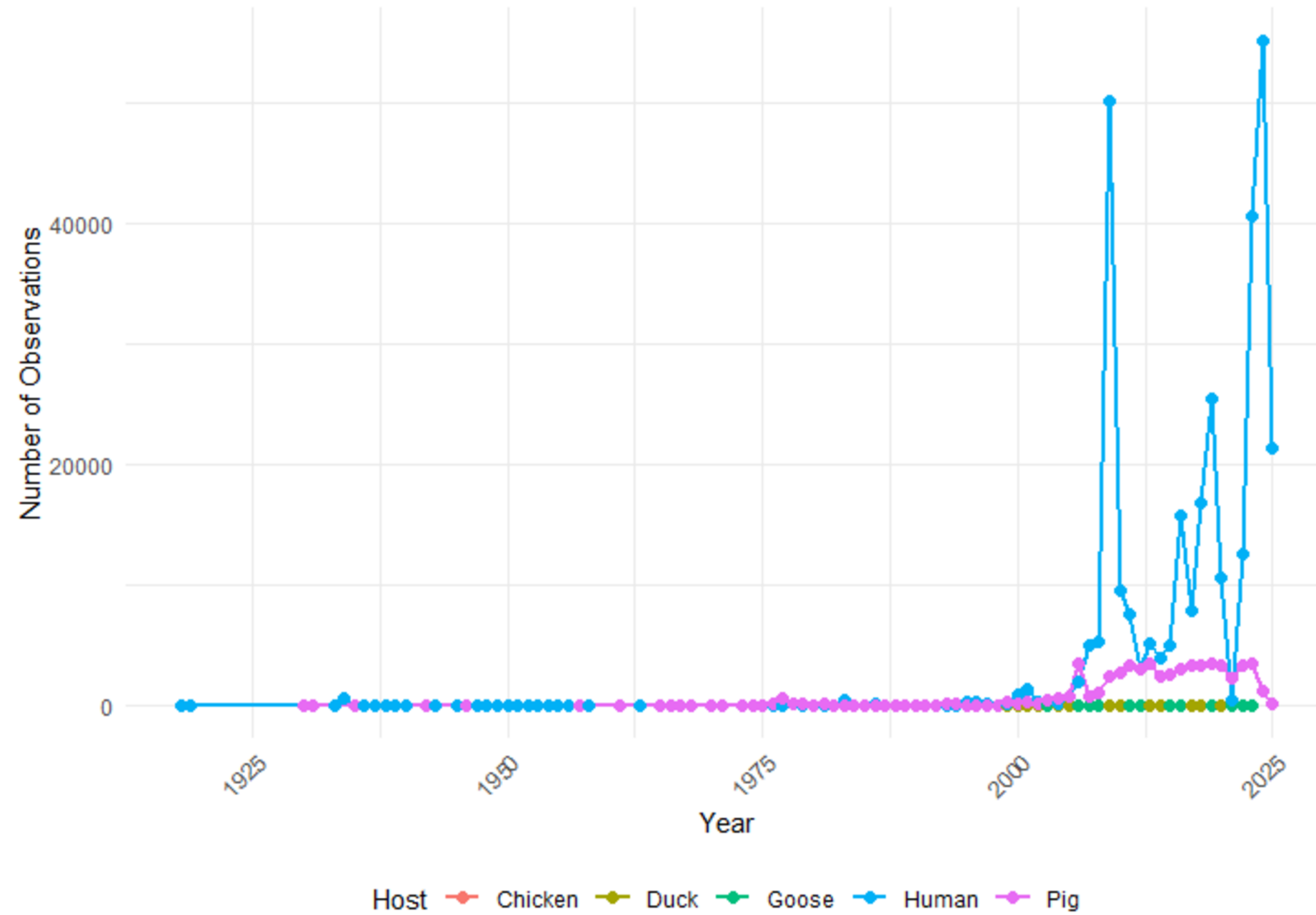
preliminary goal

**develop machine learning model
that identifies which viral
sequences classify viral genome
host specificity**

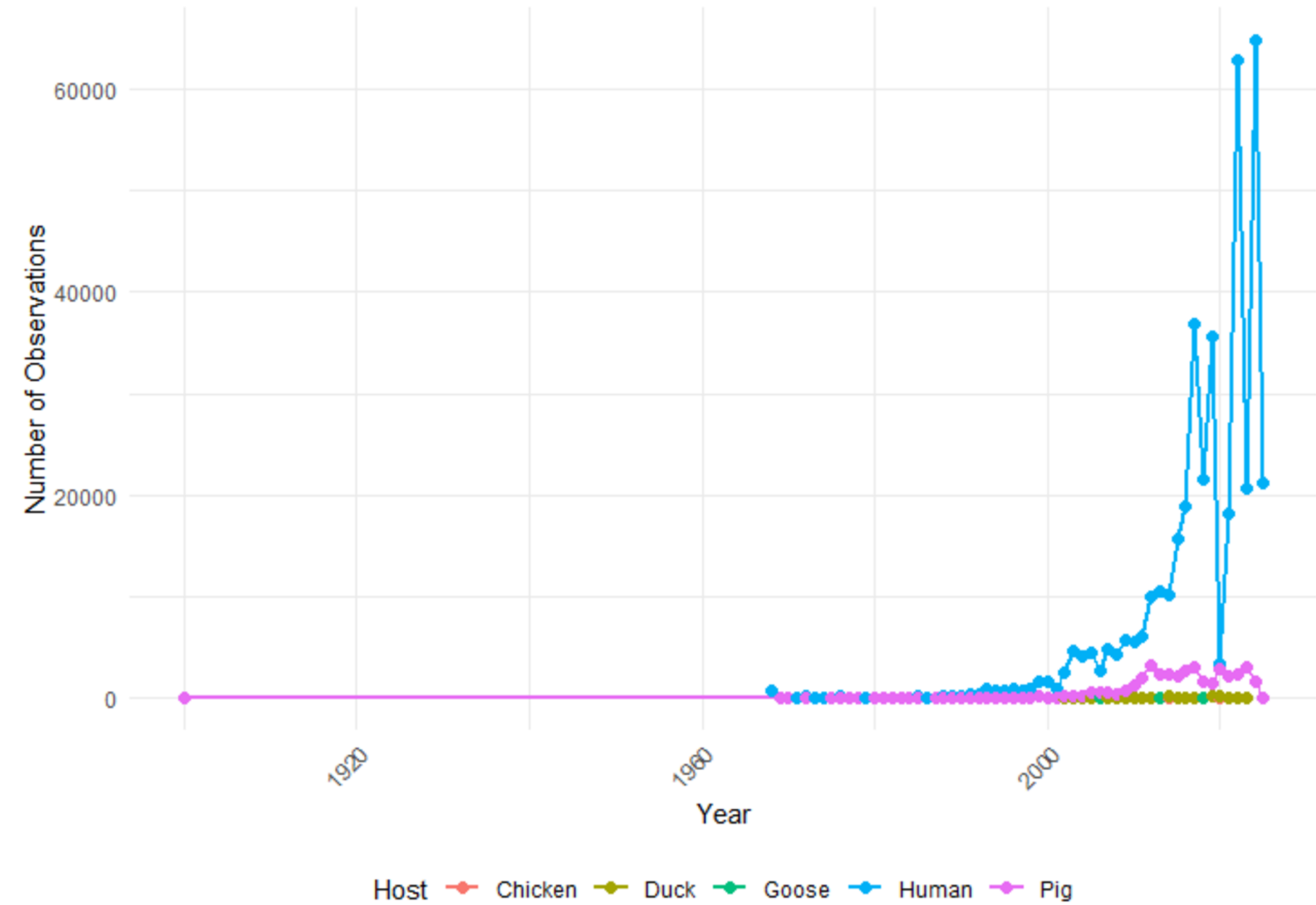


in service of the ultimate goal of predicting when viruses have jumped the species barrier

Temporal Distribution of H1N1



Temporal Distribution of H3N2

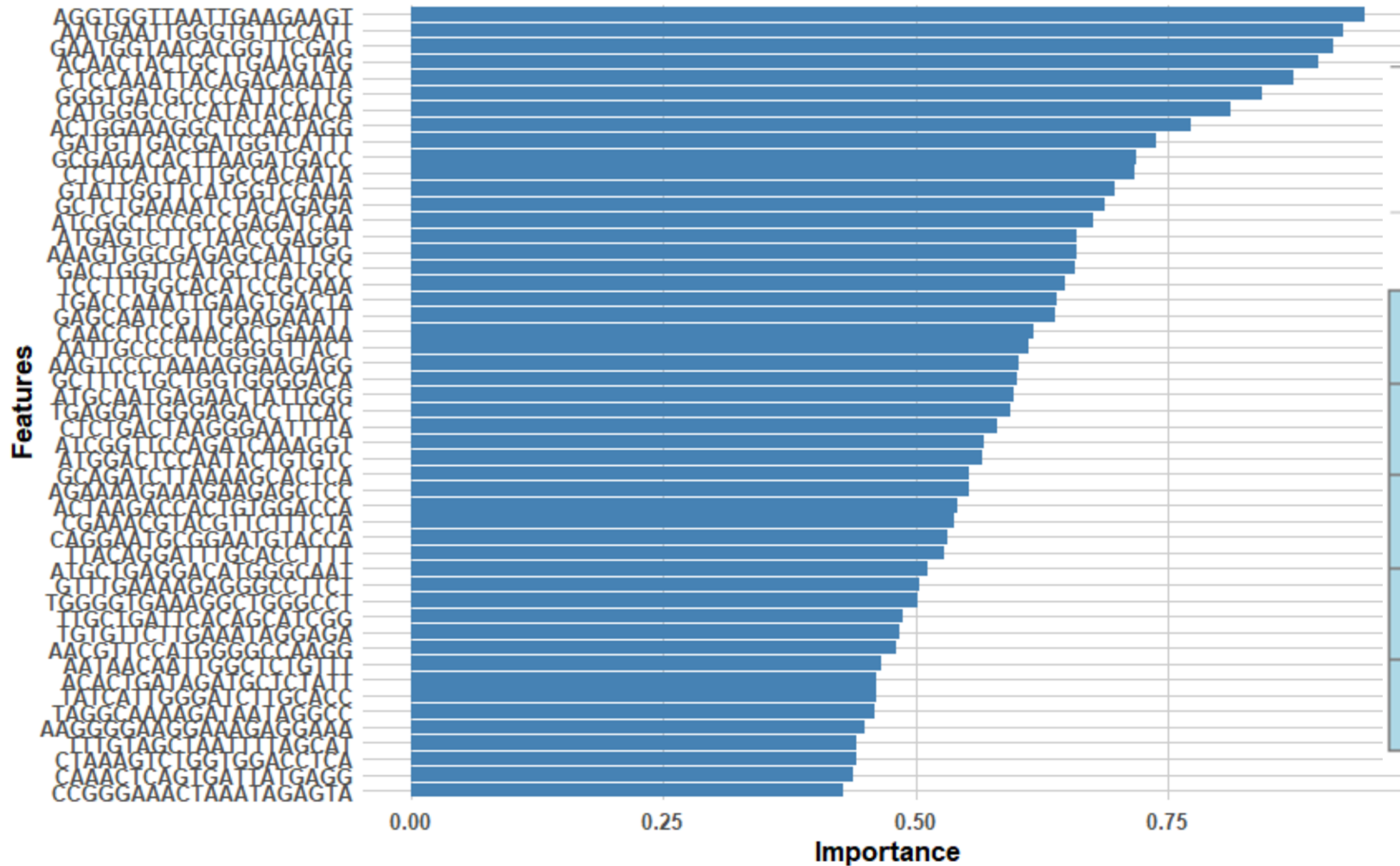


determining subtypes of interest through plotting influenza A subtype data in R

Machine Learning Model Development in R

- create k-mer matrix of influenza A genomes from BV-BRC filtered by:
 - Pig & Human Hosts
 - 2010-2015 collection year
 - USA isolation country
 - complete genomes
- using the k-mer matrix → train using 5 fold cross validation and testing where 75% is training and 25% testing

Top 50 kmers that classifies viral genomes originating in pig or human ho



Cross-Validation Results

Metrics for Each Fold

Fold ID	Accuracy	Sensitivity	Specificity	F1_score	ROC AUC
Fold1	1.000	1.000	1.000	1.000	1.000
Fold2	0.969	1.000	0.947	0.963	1.000
Fold3	0.938	1.000	0.857	0.947	1.000
Fold4	0.968	1.000	0.933	0.970	1.000
Fold5	0.968	1.000	0.929	0.971	0.987

machine learning model

Cultural Exchange

- where we've lived and gone to school
- preferences on weather and places to live
- differences in the education systems between the US and India
- house cleaning preferences



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