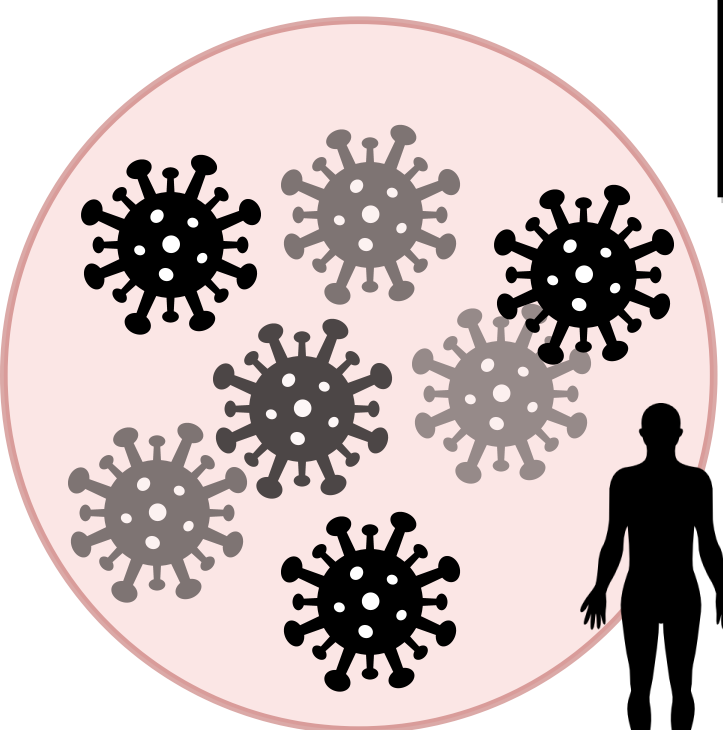
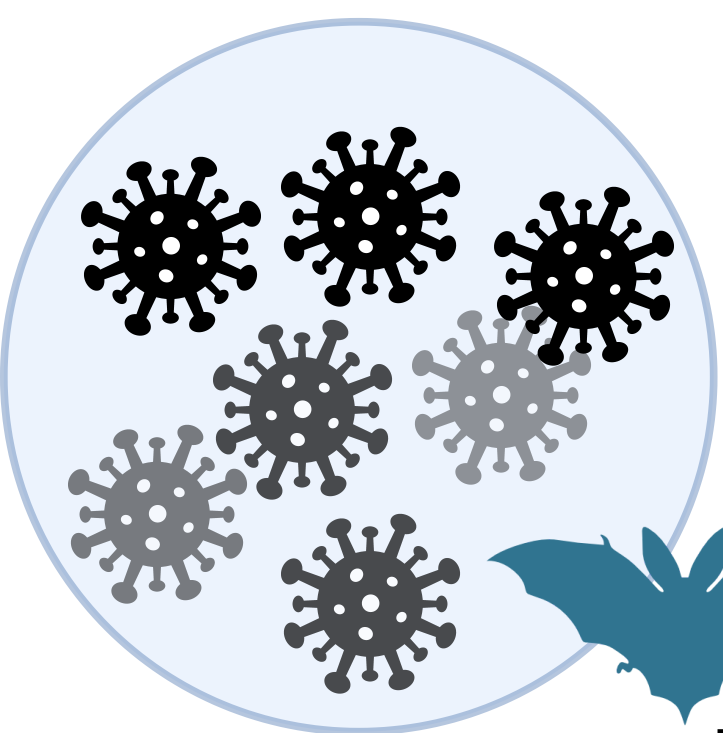


sequence  
databases  
(NCBI+GISAID)



machine learning

infer mutational  
dependencies & motifs

Q-net  
+  
q-distance

evolutionary  
theory

Fine-tune  
prediction algorithm

Aim 1

Estimate  
species jump  
probability

Aim 2

Strain  
divergence:  
predict future  
mutations &  
timeline

Aim 3

Forecast  
Escape  
mutants from  
current  
vaccines

Aim 4

Estimate  
pathogenicity and  
h2h transmission  
probability

outcomes

Rank  
order  
strains at  
scale

Predict  
future  
variants &  
timeline

Predict  
escape  
mutants

Escape  
resistant  
vaccine  
design

