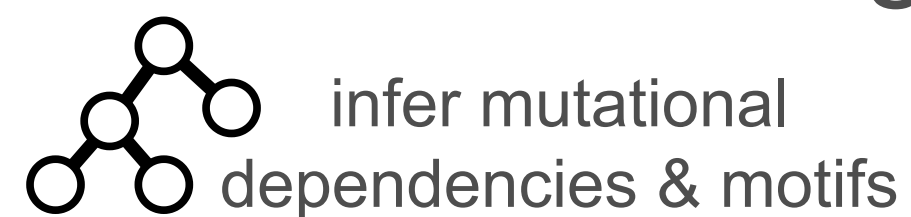
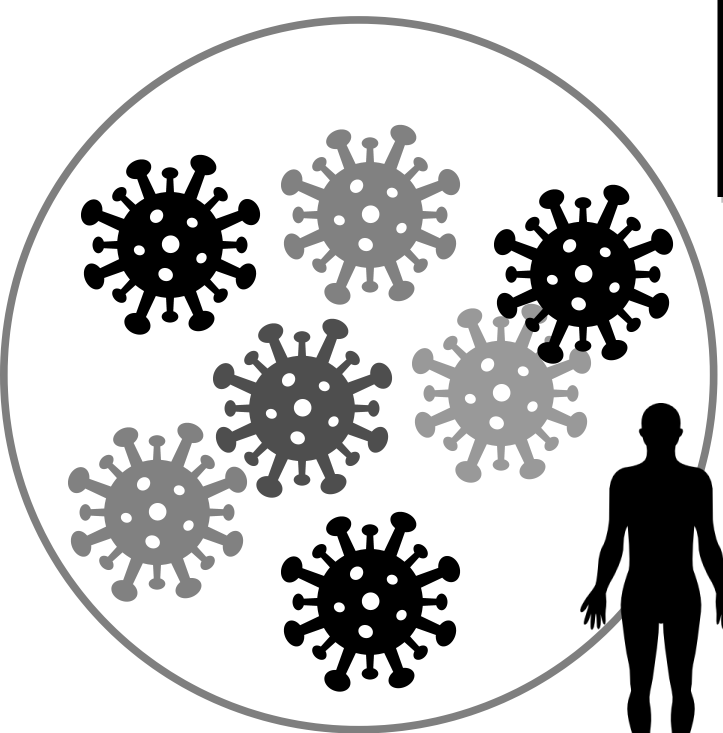
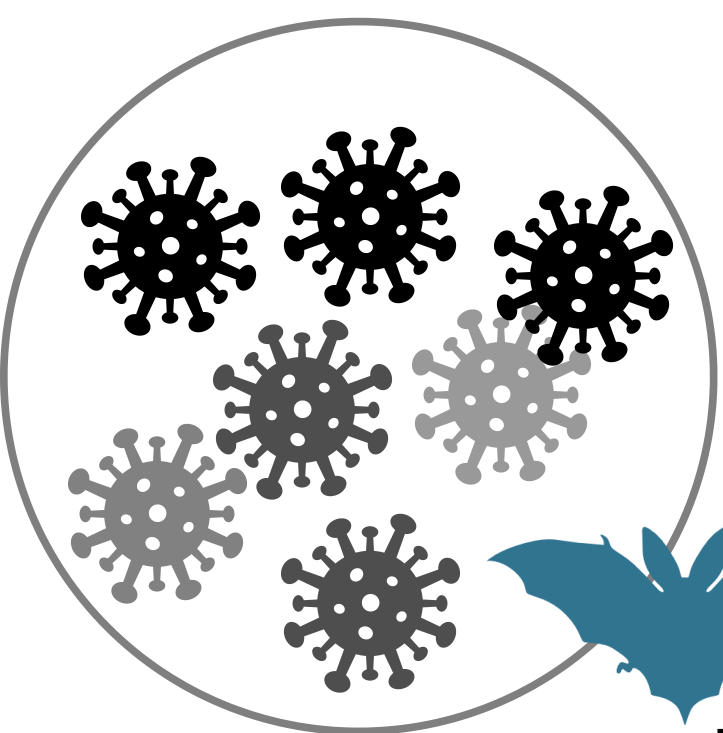


**sequence
databases
(NCBI+GISAID)**



evolutionary
theory

**Q-net
+
q-distance**

machine learning

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

