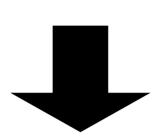
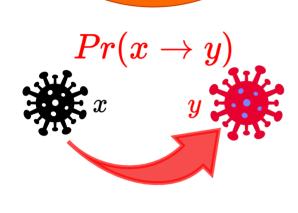
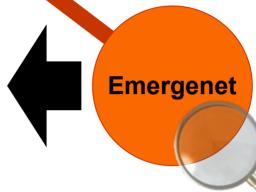
sequence database (NCBI,GISAID)

- Quantify probability of specific mutations in the wild
- Implicitly factor in functional constraints and selection pressures

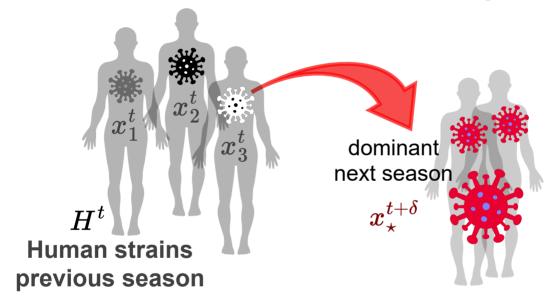
Infer dependencies across mutations and genomic variations





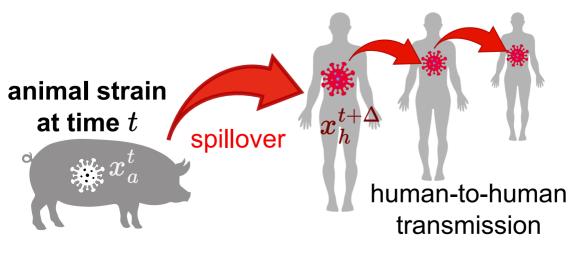


Application 1: Forecast dominant strain(s) in upcoming season



$$x_{\star}^{t+\delta} = \mathop{argmax}\limits_{x} \prod_{x^t \in H^t} Pr(x^t o x)$$

Application 2: Estimate pandemic potential of animal strains



$$ext{risk}(x_a^t) \propto \langle \log Pr(x_a^t
ightarrow x_h^{t+\Delta})
angle$$