Future-proof Countermeasures

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sequence database (NCBI,GISAID)

Immunological and structural information

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

Infer dependencies across mutations and genomic variations

Mechanistic Knowledge + Novel Machine Learning

$Pr(x \to y)$

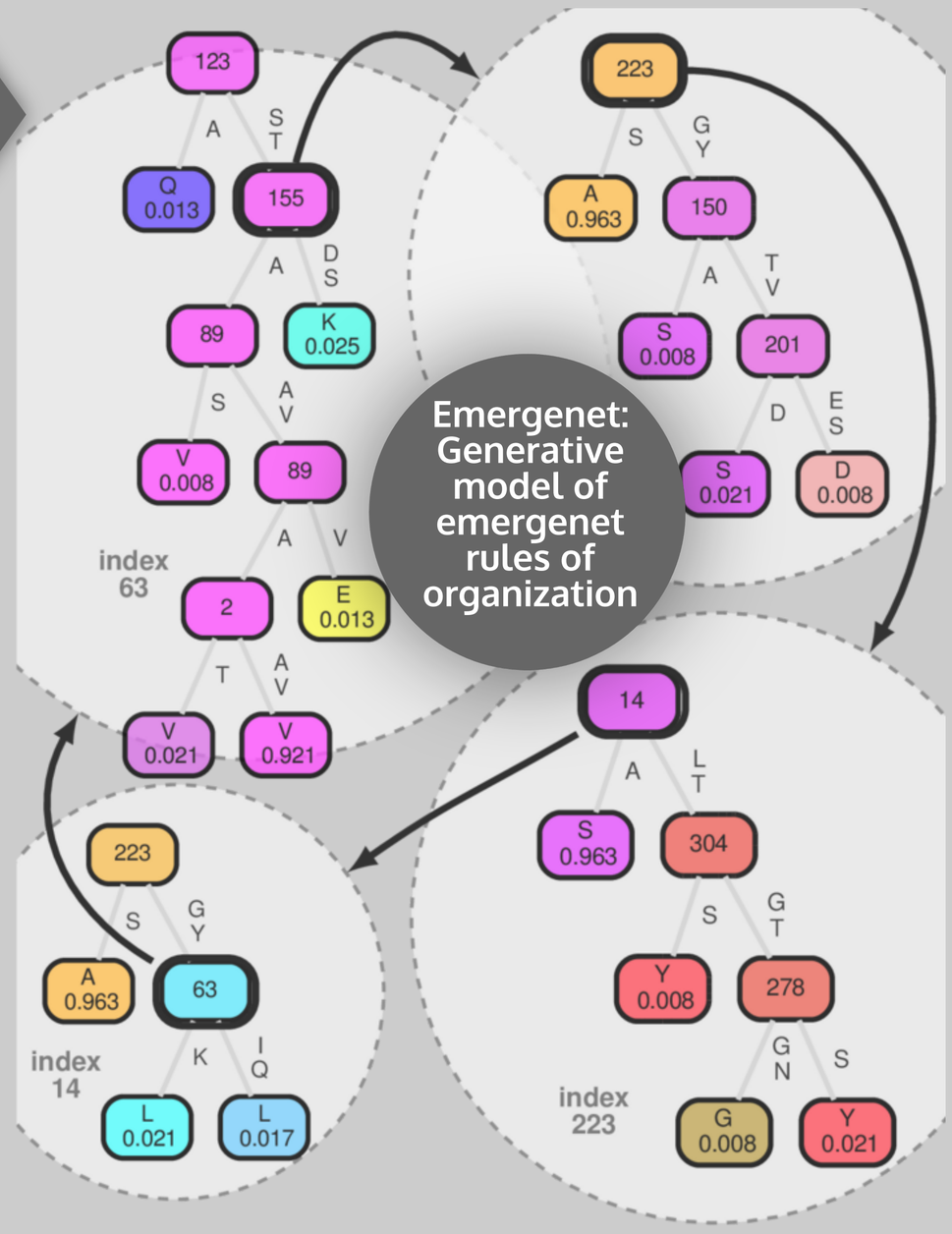
x y

Emergenet

What are we trying to do?

Develop future-proof vaccines and countermeasures, escape-resistant to emergence of variants and zoonosis

Emergenet: Generative model of emergenet rules of organization

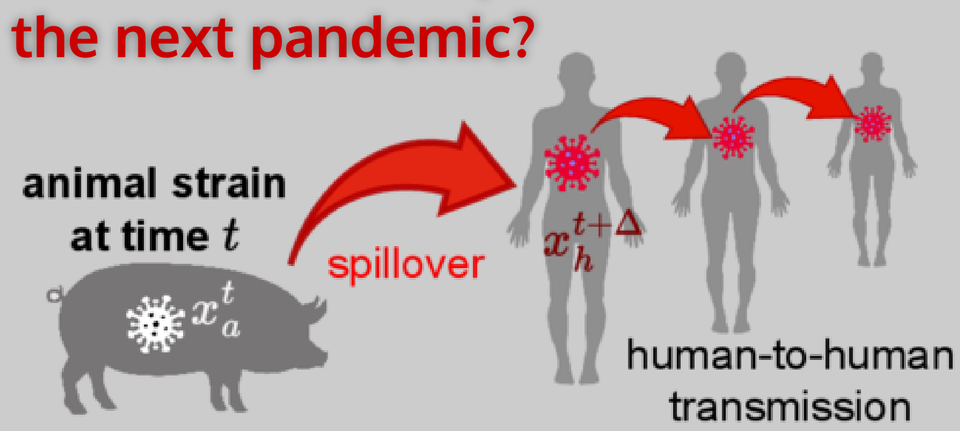


What is the new approach?

Learn deep generative models of emergent dependencies acoss non-colocated residue variations, which induce a biology aware metric

Can we predict future mutations? Can we define the "edge of emergence"?

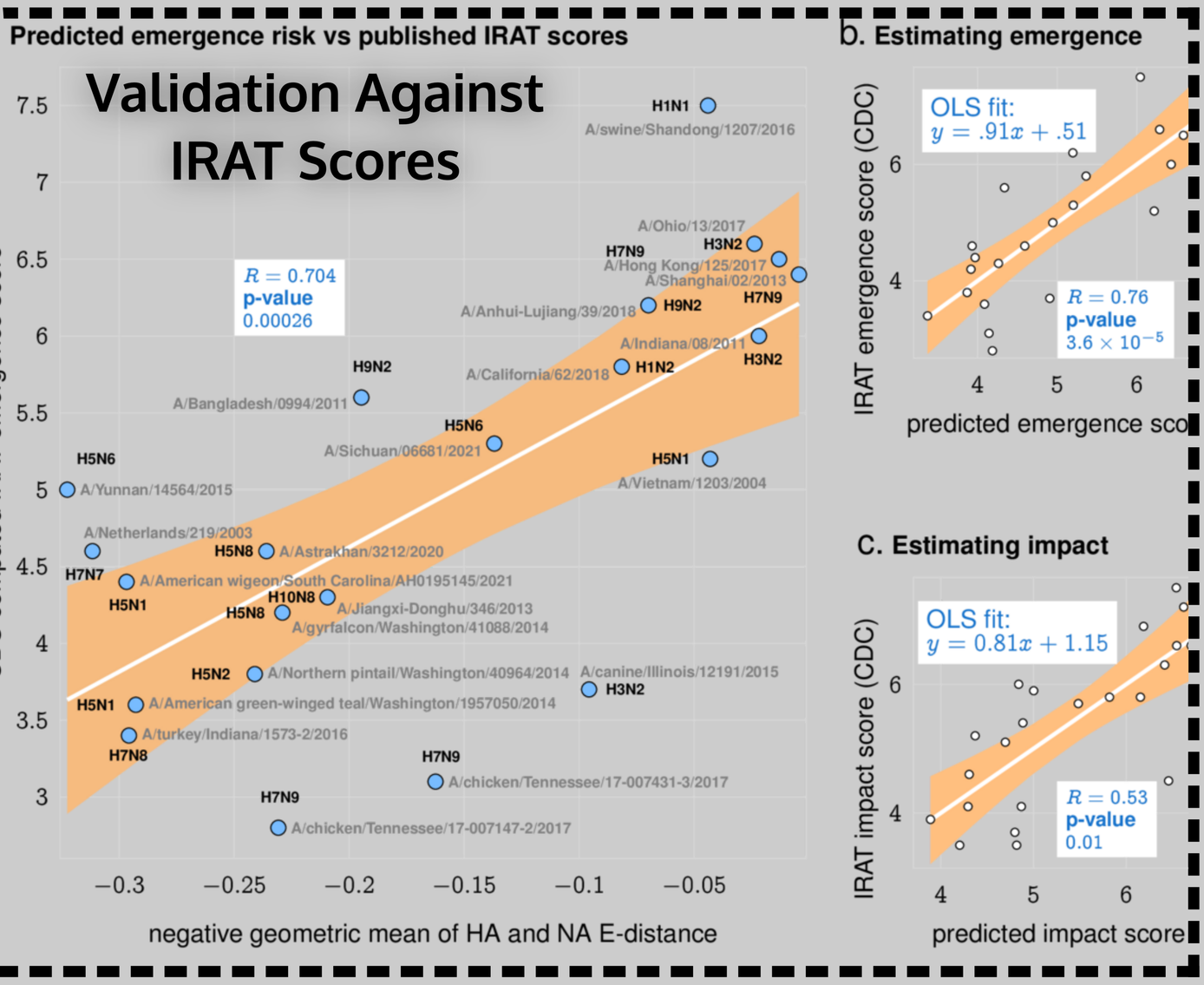
Problem: Can we predict the next pandemic?

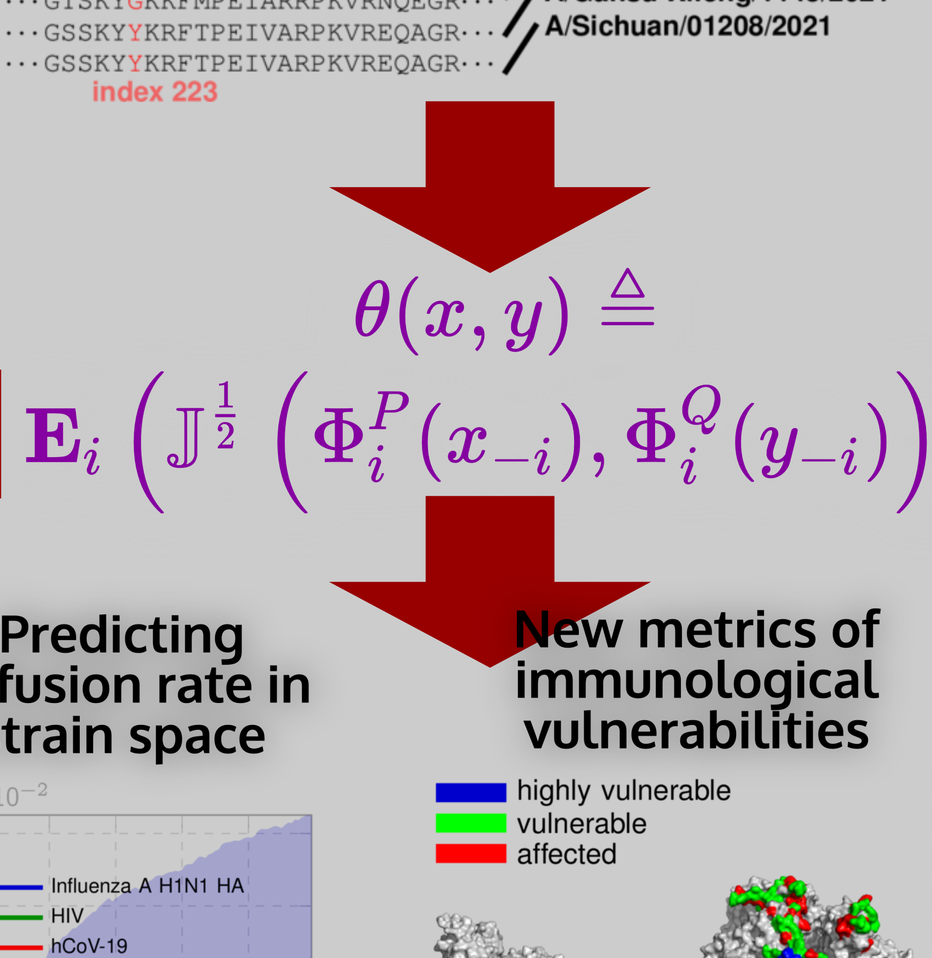


Who Cares?

Allows rapid reliable prediction of future mutations, variants and rank orders strains by their pandemic risk. Can target viruses BEFORE the first human infection

Validation Against IRAT Scores





$$\theta(x,y) \triangleq \mathbf{E}_i\left(\mathbb{J}^{\frac{1}{2}}\left(\Phi_i^P(x_{-i}), \Phi_i^Q(y_{-i})\right)\right)$$

Predicting diffusion rate in strain space

b. Diffusion plotted against time measured in replication intervals

New metrics of immunological vulnerabilities

Bio_NORAD

Chattopadhyay, Ishanu, Kevin Wu, Jin Li, and Aaron Esser-Kahn. "Emergenet: Fast Scalable Pandemic Risk Assessment of Influenza A Strains Circulating In Non-Human Hosts," December 23, 2022. https://doi.org/10.21203/rs.3.rs-2336091/v1.