Investigating the predictive power of machine learning algorithms for antigenic novelty of influenza H3 viruses

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General overview

HI assay data

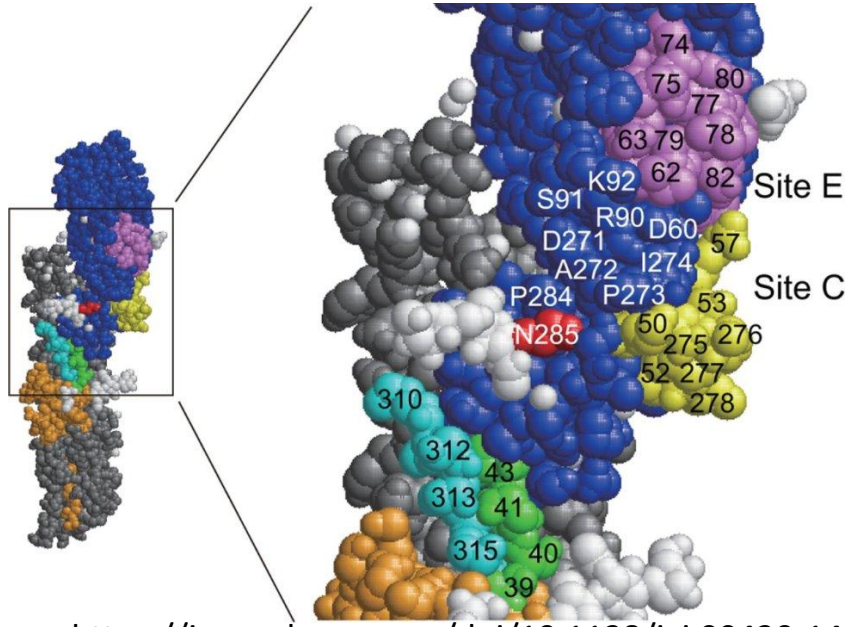
Genetic sequences

Amino acid physicochemical properties

Feature engineering

Genotype to phenotype and antigenic cartography mapping

Genotype to phenotype mapping 1 year ahead



https://journals.asm.org/doi/10.1128/jvi.00420-14

- Property differences
- 3D smoothing methods
  - distance/proximity weight matrices
  - relative solvent accessibility (RSA)
- Epitope weighting
- Positional difference ratios
- Protein language model embeddings

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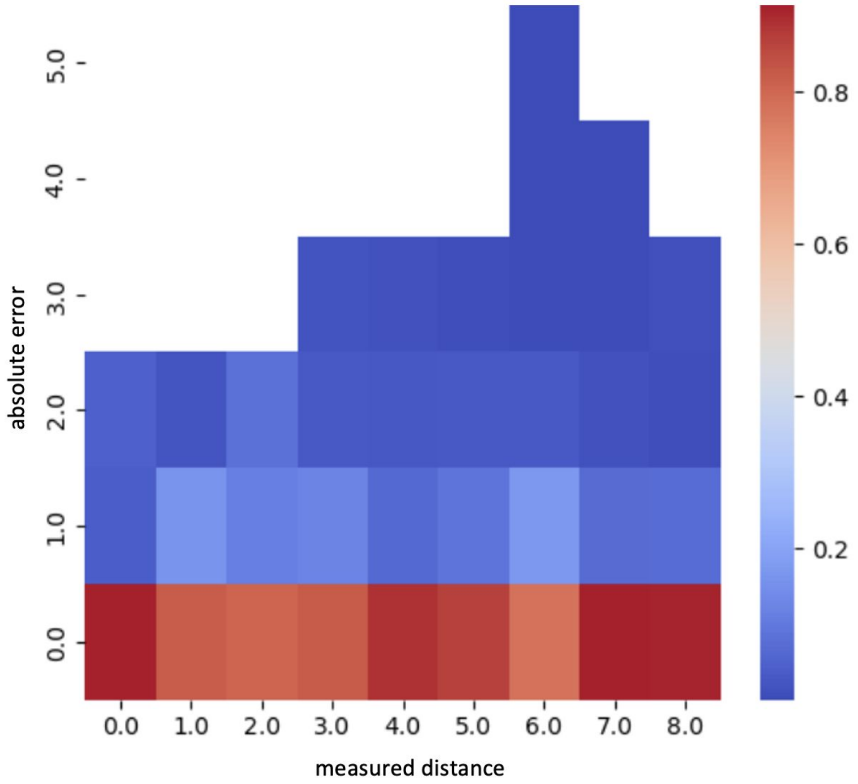
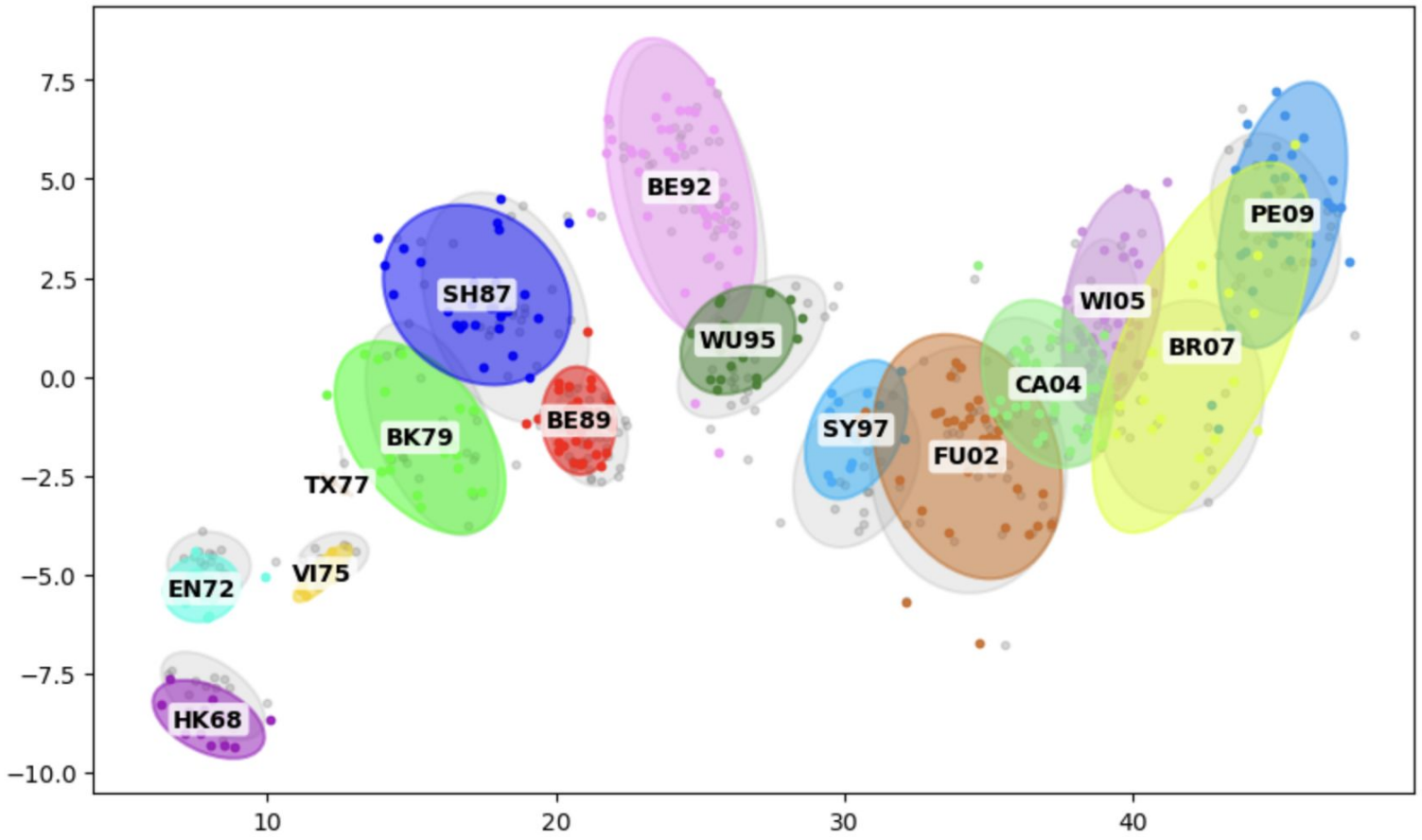
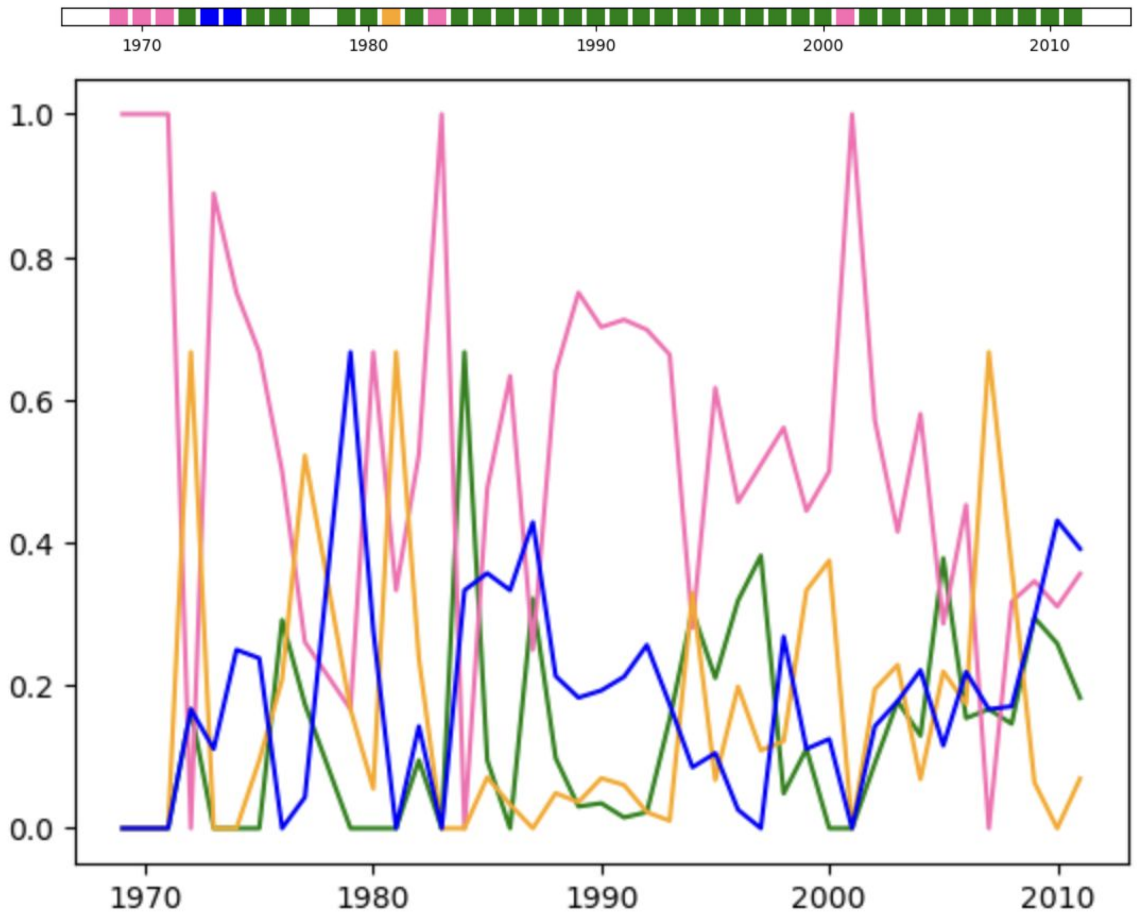
Genotype to phenotype mapping – GP mapping



95.6% within 1 antigenic unit
85.8% exact predictions



GP map – real time implementation



50 positions, context-driven, stochastic gradient descent

Vaccine change threshold set at 4 antigenic units.

Aim: predict when a change in vaccine strain might be needed

PREDICTED DISTANCE

MEASURED DISTANCE

No change predicted or required	Change predicted but not required
Change required but not predicted	Change predicted and required

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Conclusions and next steps

Conclusions

- A GP map informed on physiochemical property differences can predict antigenic distances between any two viral sequences with a very high degree of certainty.
  - 95.6% within 1 antigenic unit
- Blinded one year ahead predictions indicate good match between measured and predicted distances across contiguous antigenic clusters
- Simulation of real-time implementation as an antigenic novelty detection tool is in the process of being updated

Next steps

- Evolution model and structure identification
- Incorporation into transmission model

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