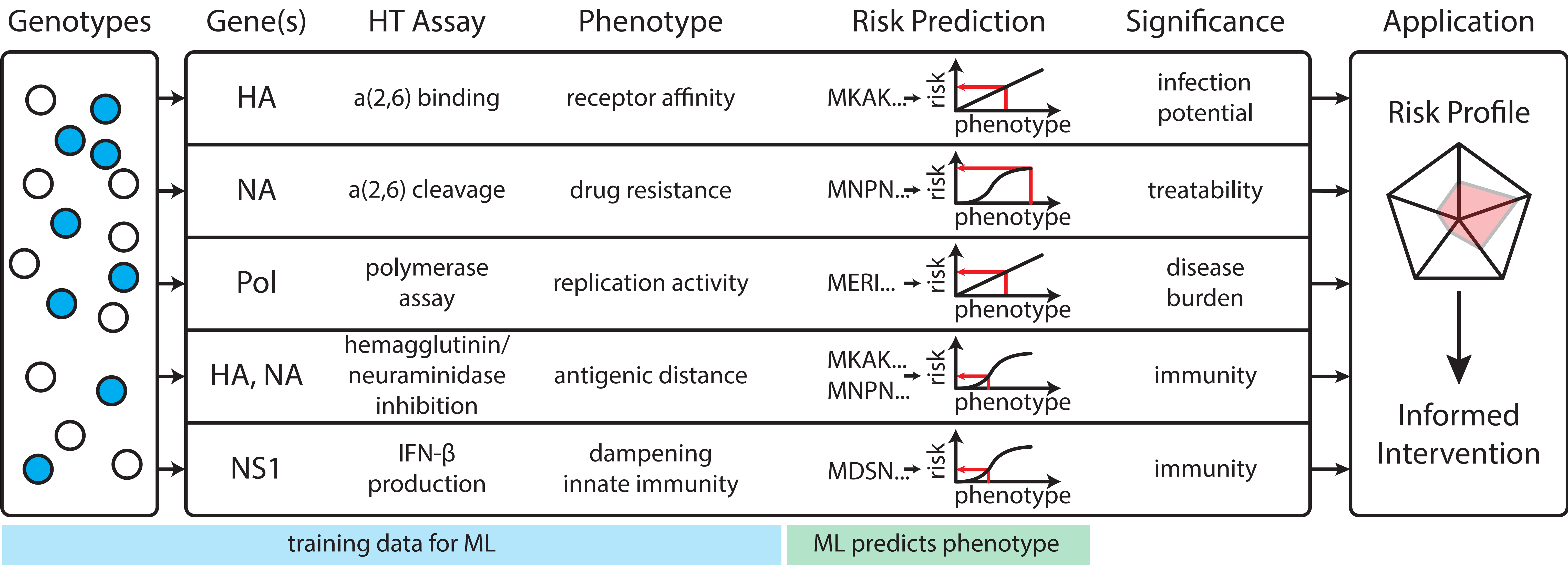


# A real-time surveillance dashboard for monitoring viral phenotype from sequence

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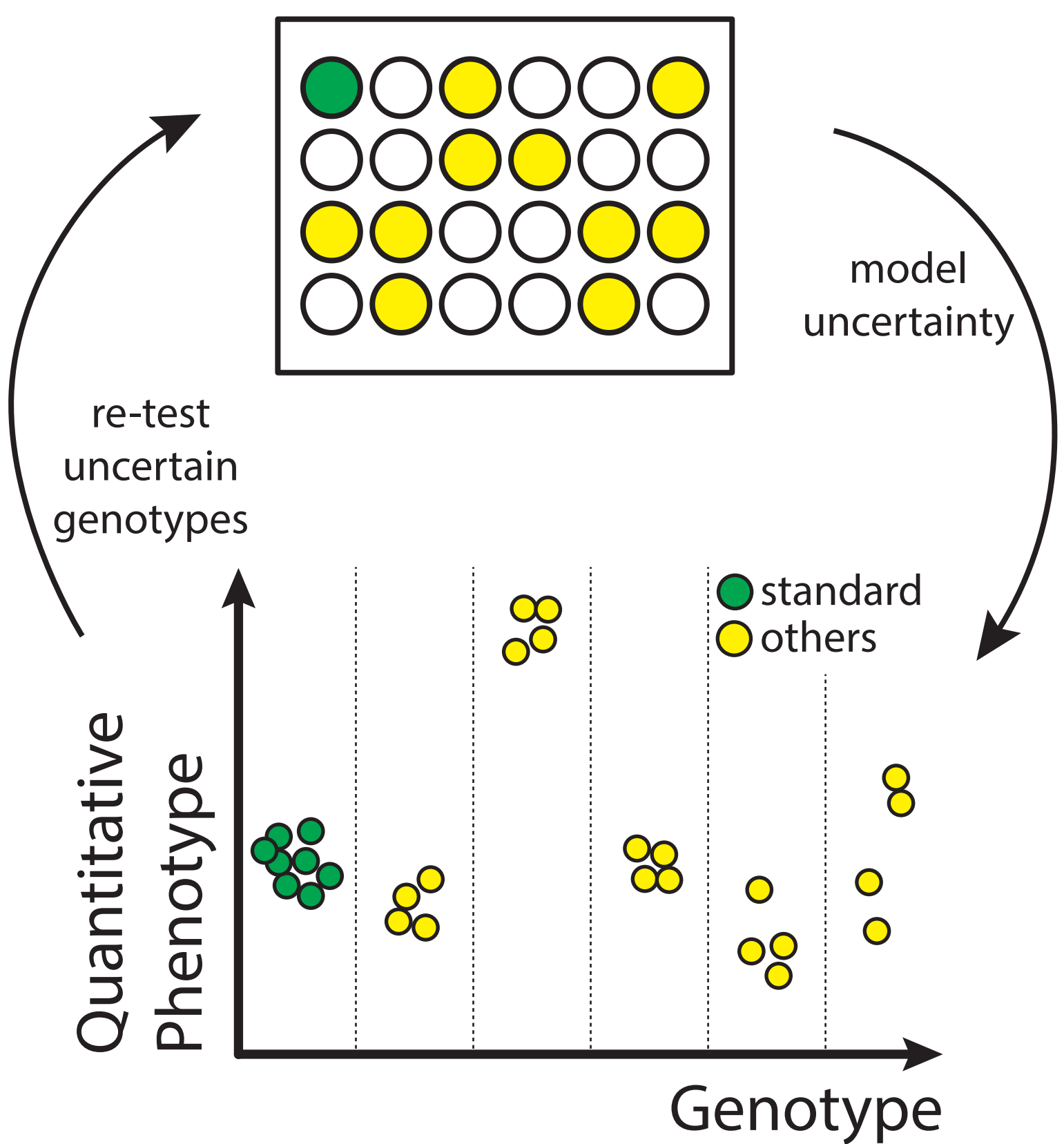
<sup>1</sup>Department of Biological Engineering and <sup>2</sup>Division of Comparative Medicine, MIT

## Dashboard Vision



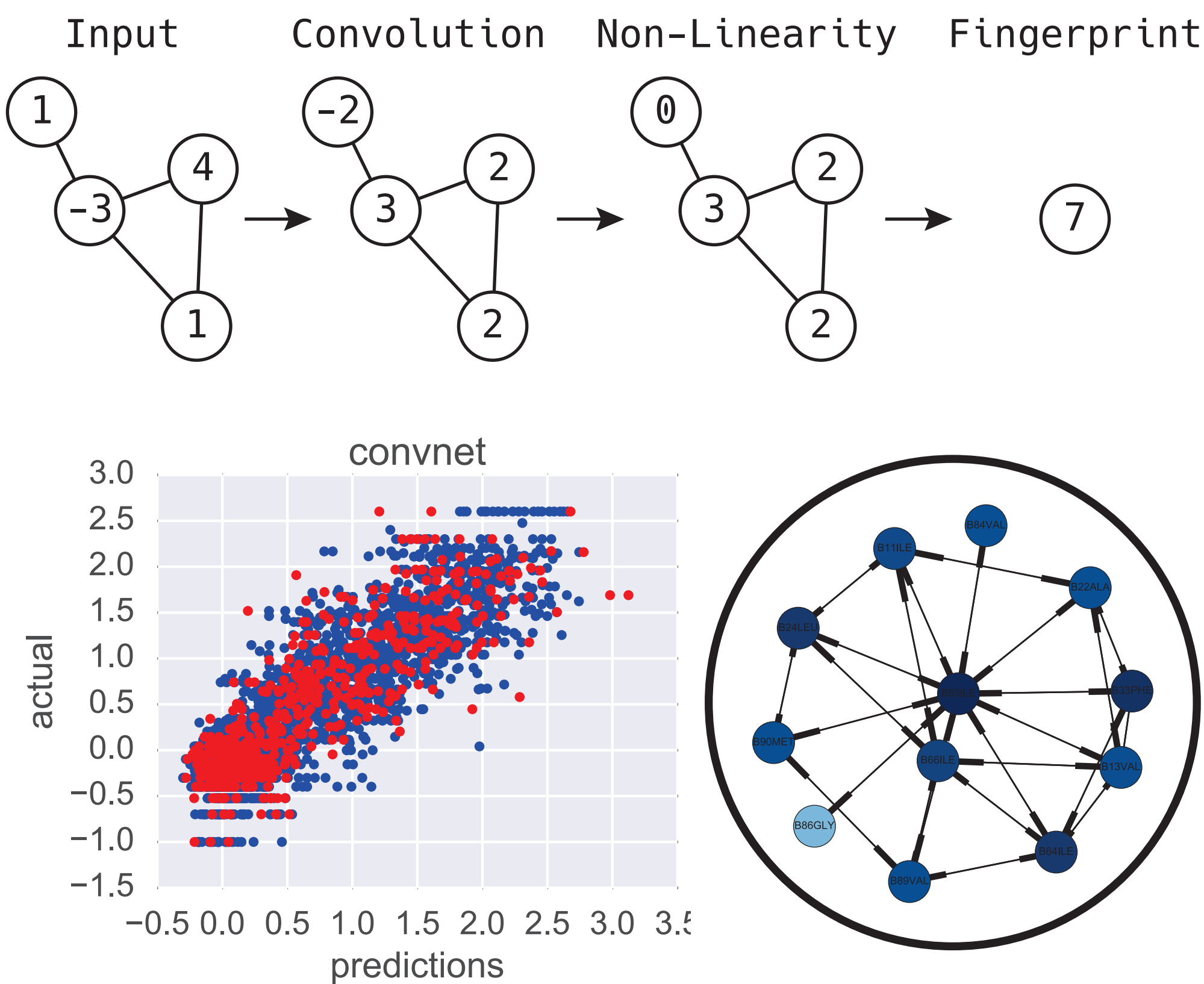
We envision building a real-time phenotypic interpretation system for viral genomic data. The goal is to predict, with associated uncertainty, quantitative and epidemiologically-relevant phenotype from genotype. Below we outline the technical foundations for this vision.

## Iterative Phenotyping



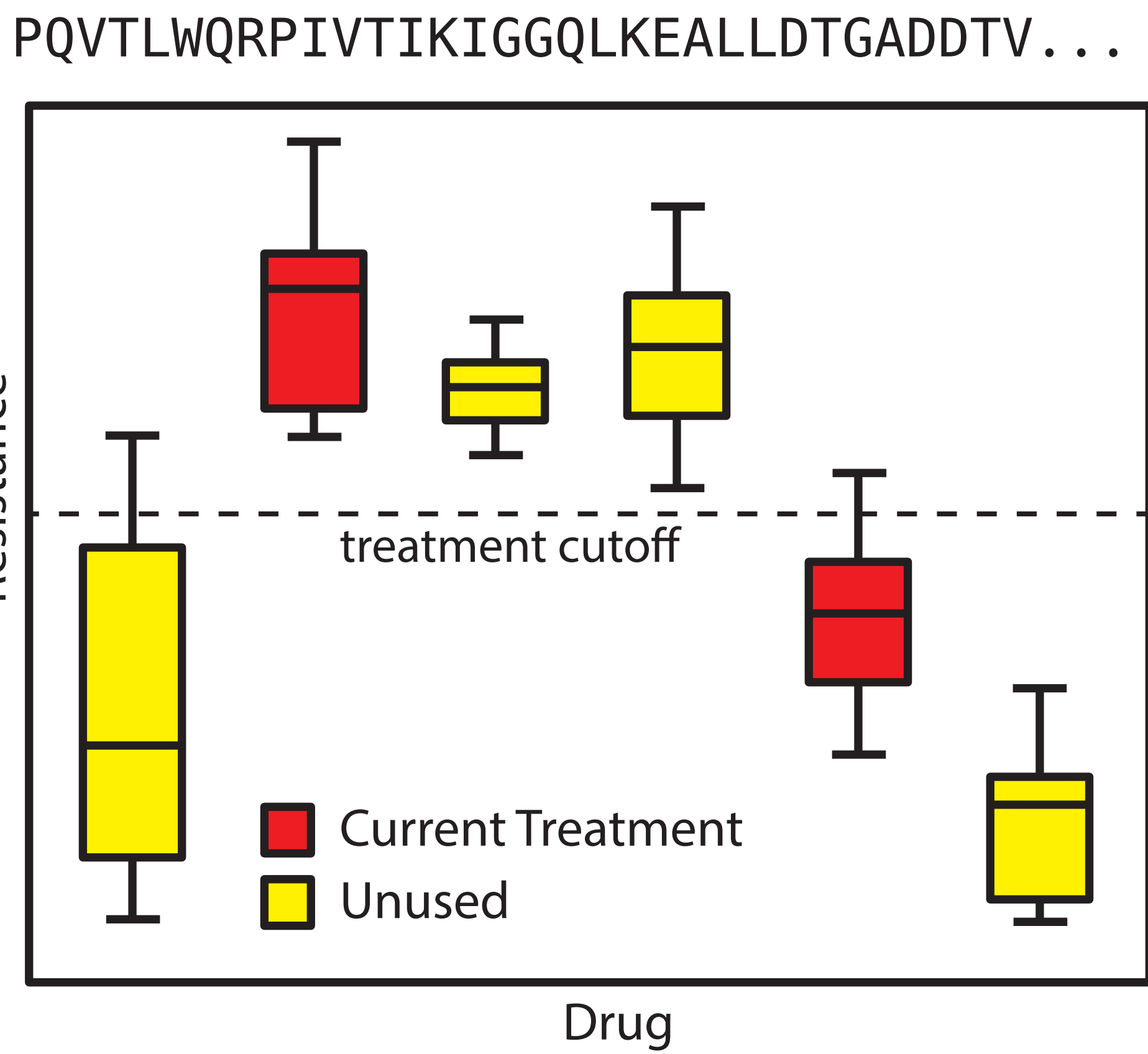
By explicitly modelling uncertainty in phenotype measurements, we can re-test genotypes that have high measurement variance, iteratively improving precision.

## Bayesian ConvNets on Protein Structure



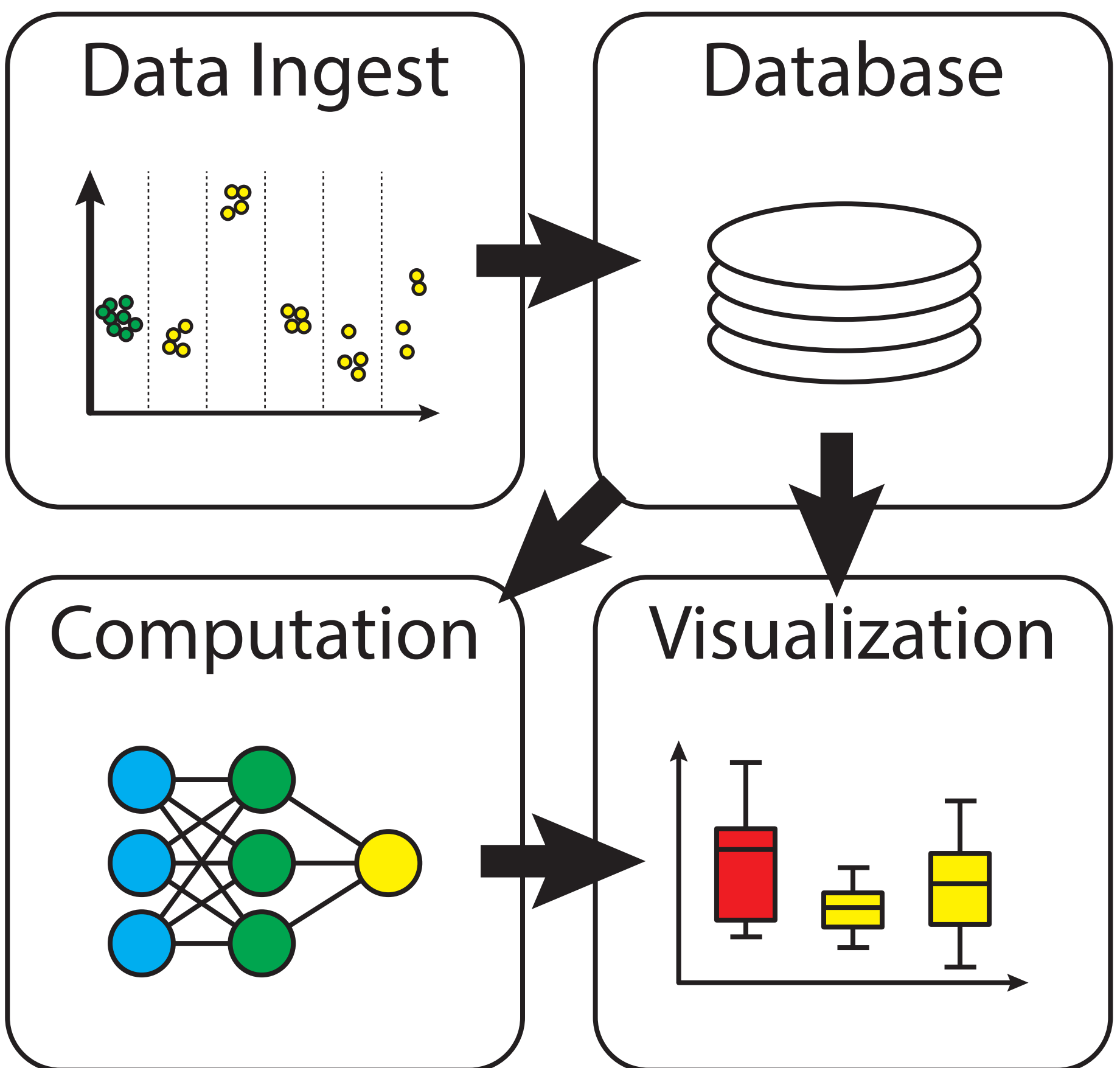
Using convolutional neural networks that take protein structures as inputs allows us to accurately and interpretably learn features predictive of phenotype.

## Predictions with Uncertainty



From the convolutional neural network, we will produce predictions with uncertainty, a step up from point estimates, allowing for more rational decision making.

## Microservices Architecture



Adopting a microservices architecture increases modularity, making the phenotypic interpretation system easier to maintain and resilient against failures.

## Open Source Software



We use open source software for scientific reproducibility and transparency. All work is conducted openly on GitHub.  
[ericmjl/genomic-surveillance-dashboard](https://github.com/ericmjl/genomic-surveillance-dashboard)  
[ericmjl/protein-systematic-characterization](https://github.com/ericmjl/protein-systematic-characterization)

## Thoughts & Suggestions