計算生物學實驗室

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Influenza Research 流行性感冒研究

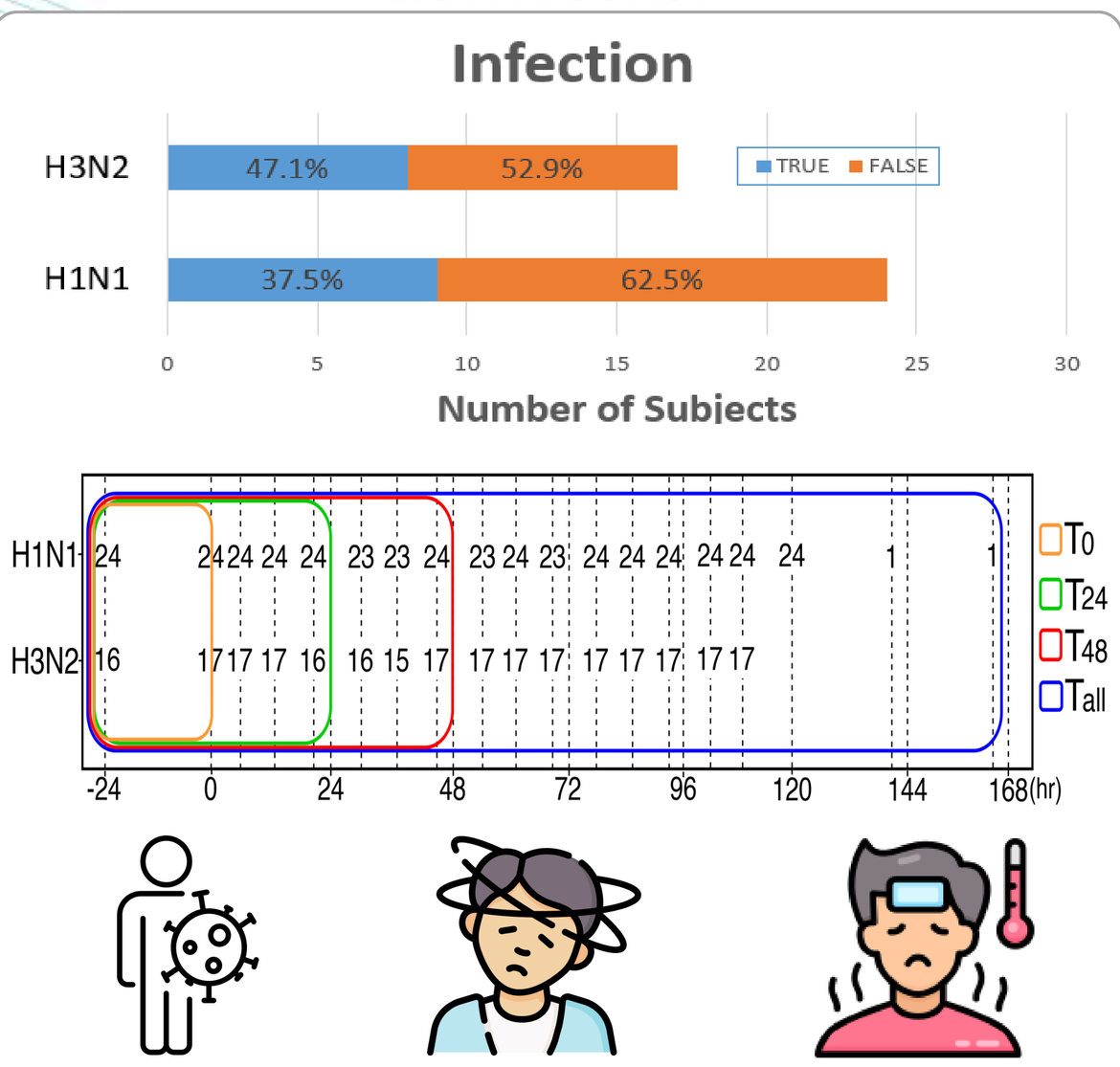
Motivation

- Not everyone gets sick after an exposure to Influenza A Viruses (IAV).
- It was unclear whether forecasting who would get the flu based on pre-exposure host gene expression could work.
- It was also unclear whether Deep Learning could work on this problem with relatively small-scale data.

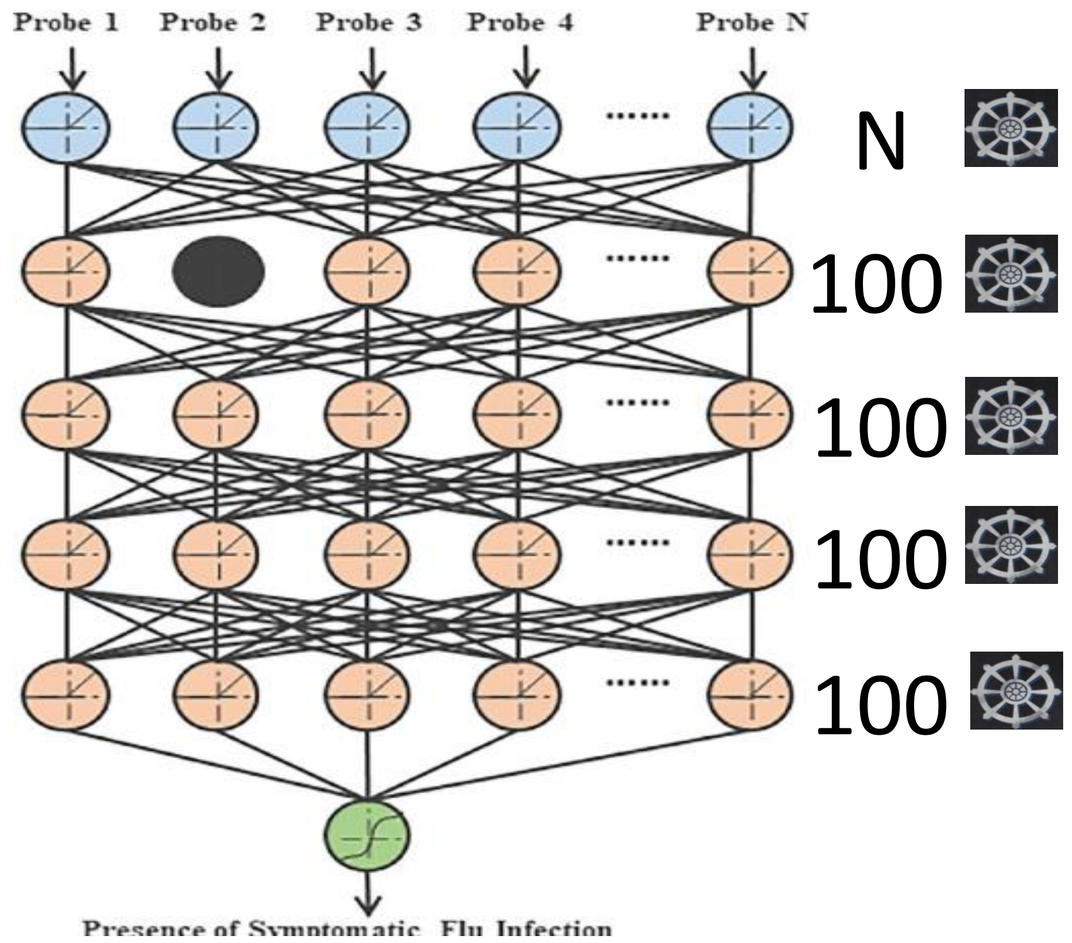
Background

- Post IAV infection can be identified by the expressions of
  - ✓ Either Top **50** genes derived from a latent factor regression analysis
  - ✓ Or only **11** genes derived from a multi-cohort analysis
- Forecasting susceptibility to respiratory syncytial virus (RSV) works by
  - ✓ An epsilon support vector regression model
  - ✓ A LASSO regularized regression model

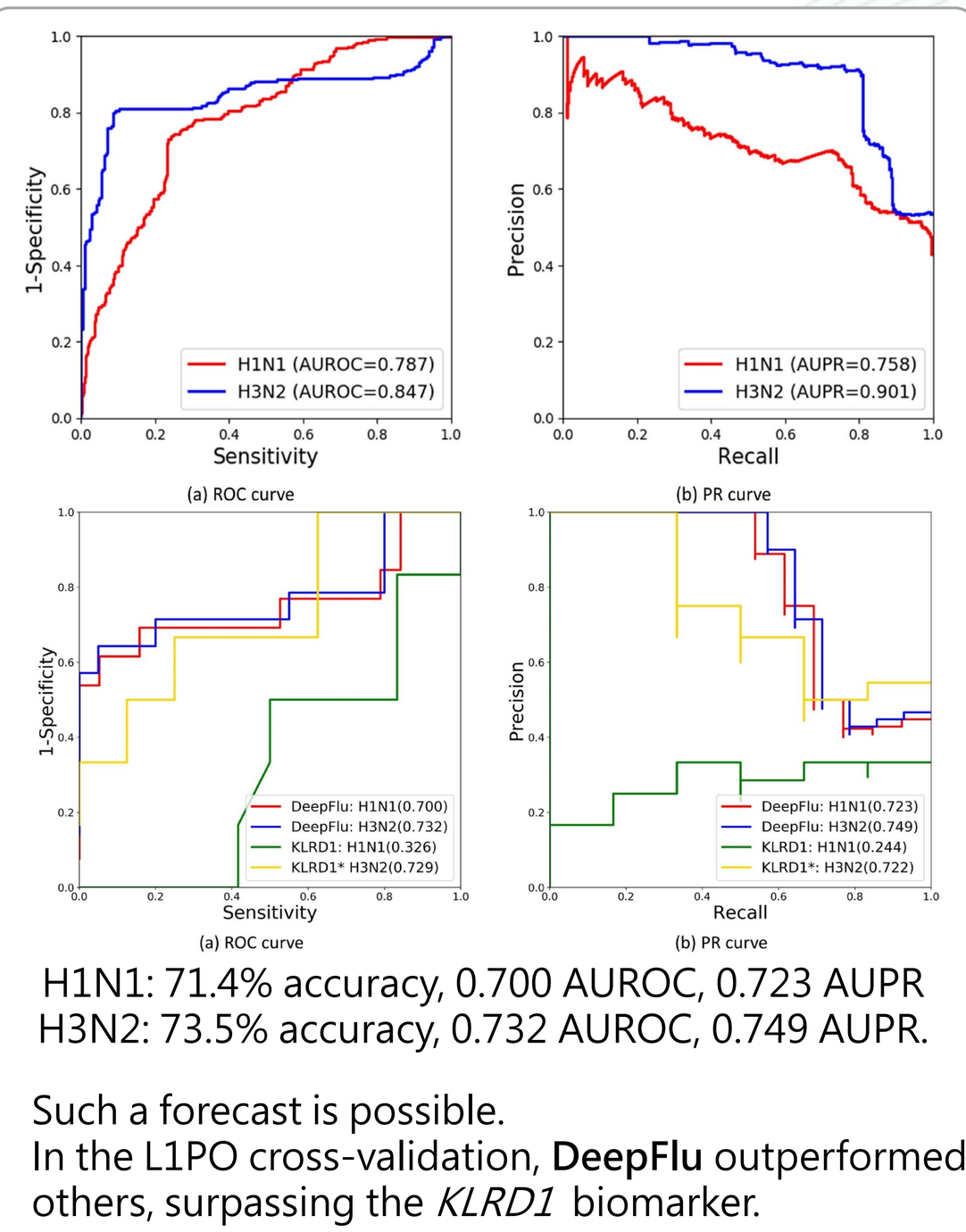
Materials



Method: DeepFlu



Results



H1N1: 71.4% accuracy, 0.700 AUROC, 0.723 AUPR
H3N2: 73.5% accuracy, 0.732 AUROC, 0.749 AUPR.

Such a forecast is possible.
In the L1PO cross-validation, **DeepFlu** outperformed others, surpassing the *KLRD1* biomarker.

MOST 科技部 Ministry of Science and Technology ROC MOST 110-2221-E-019-060

Computer Methods and Programs in Biomedicine, 213, 106495, 2022