



BioMedical AI Laboratory @NTOU

指導老師：Kuan Y. Chang (張光遠) kchang@ntou.edu.tw

Tsung-Hsien Lin (林宗憲), Yen-Guang Chen (陳彥光), Po-Yu Tsai (蔡博宇)

Zhi-Jian Cheng (程治堅), Roy Yang (楊皓宇)

實驗室網址：<https://sites.google.com/view/kchang>

Influenza Research 流行性感冒研究

Motivation

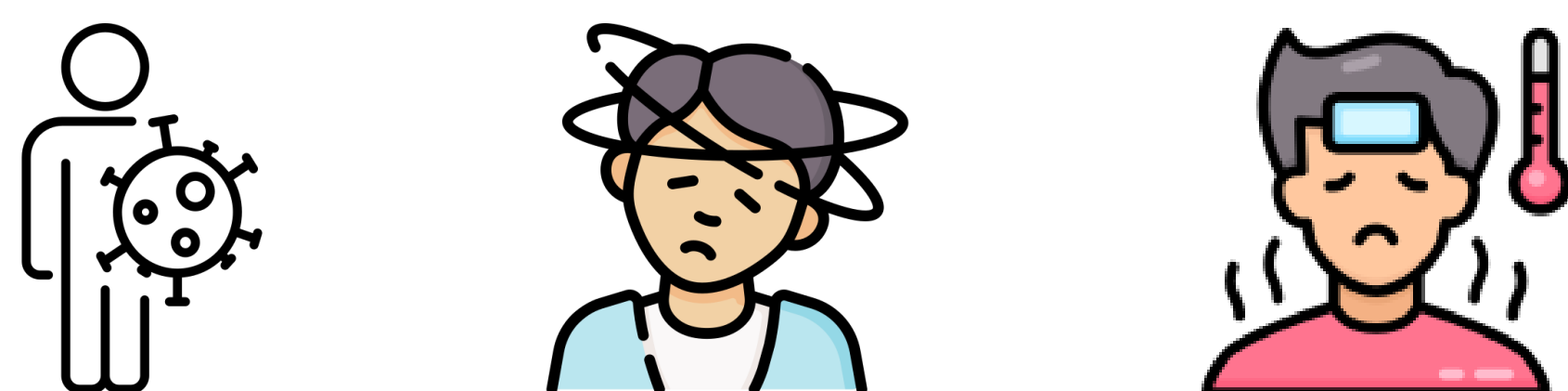
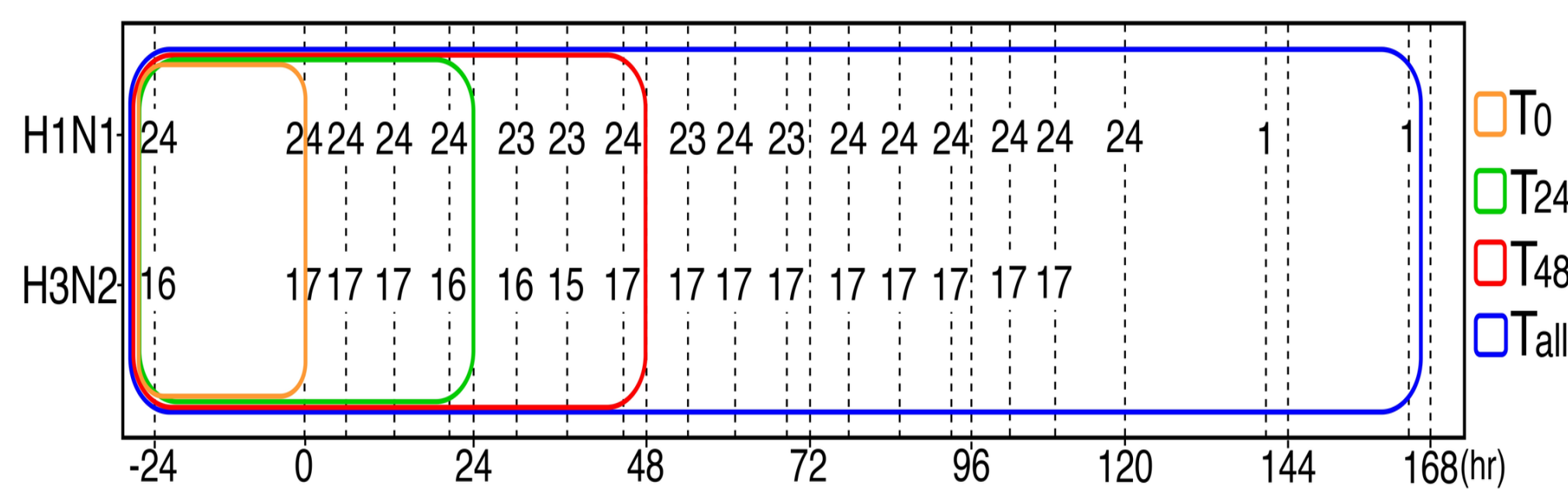
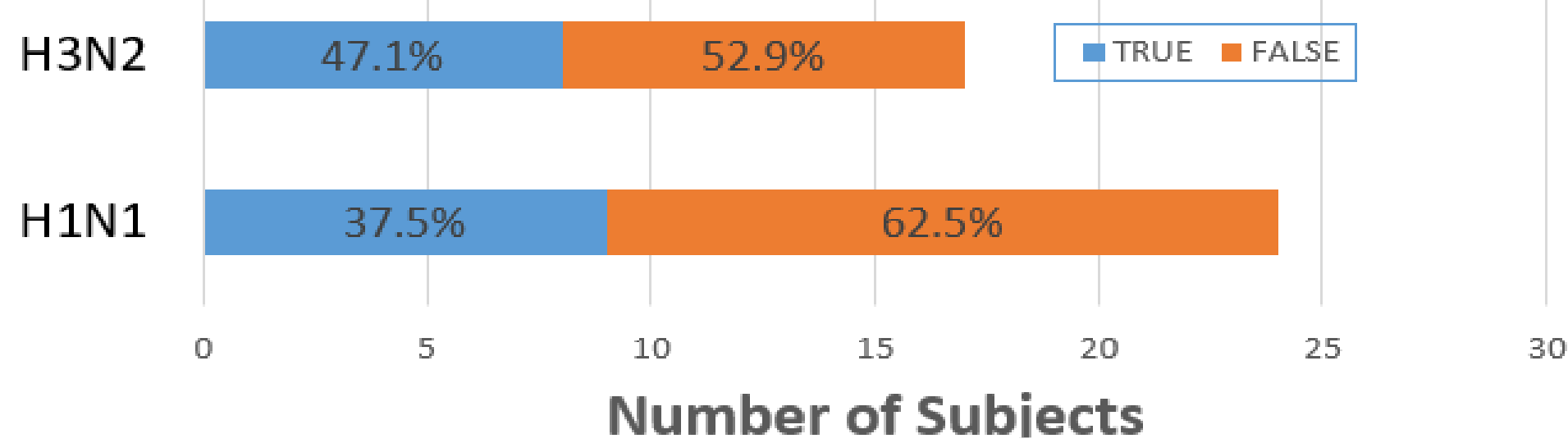
- Not everyone gets sick after an exposure to Influenza A Viruses (IAV).
- It was unclear whether forecasting who would get the flu based on pre-exposure host gene expression could work.
- It was also unclear whether Deep Learning could work on this problem with relatively small-scale data.

Background

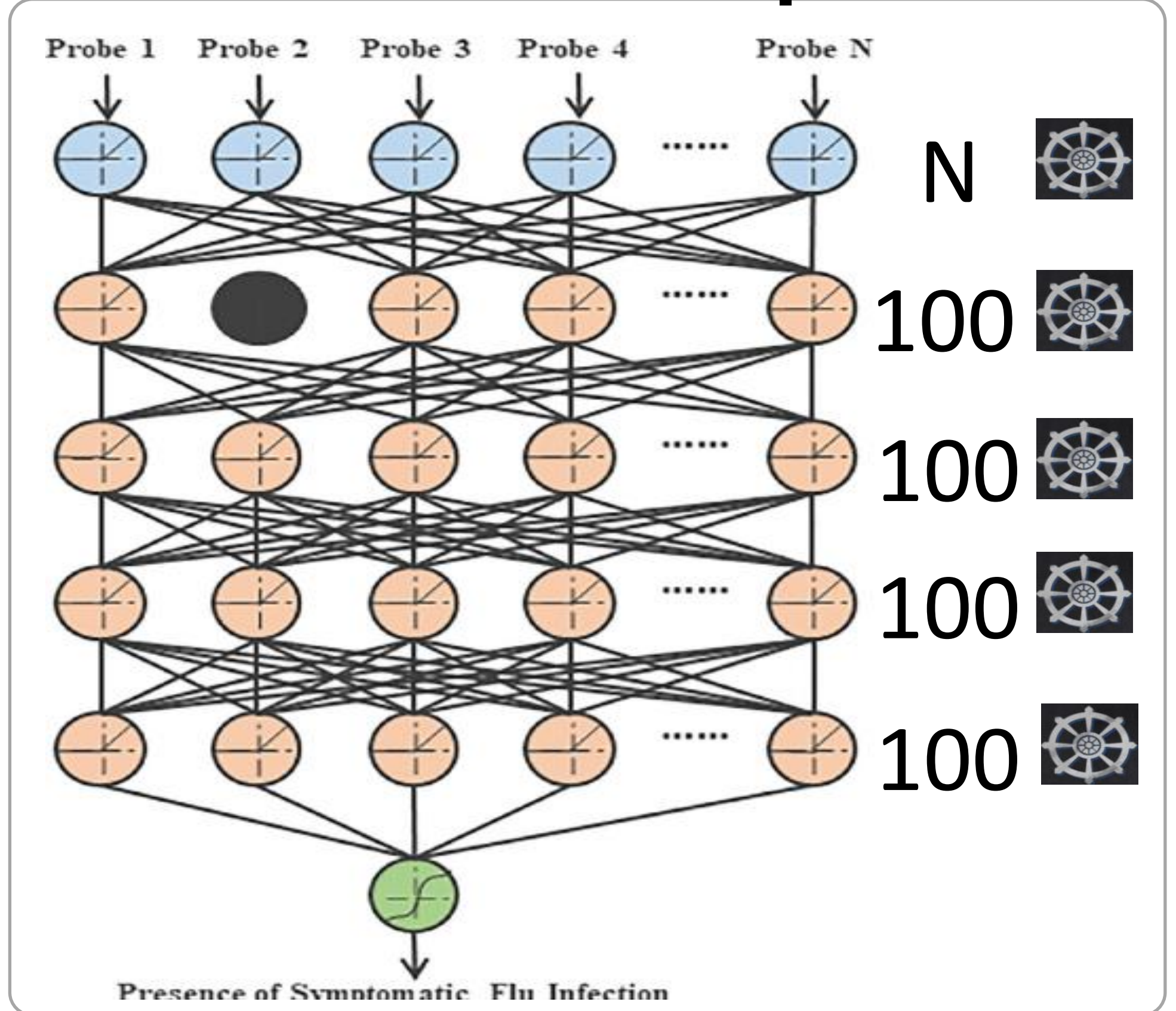
- Post IAV infection can be identified by the expressions of
 - ✓ Either Top 50 genes derived from a latent factor regression analysis
 - ✓ Or only 11 genes derived from a multi-cohort analysis
- Forecasting susceptibility to respiratory syncytial virus (RSV) works by
 - ✓ An epsilon support vector regression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

Materials

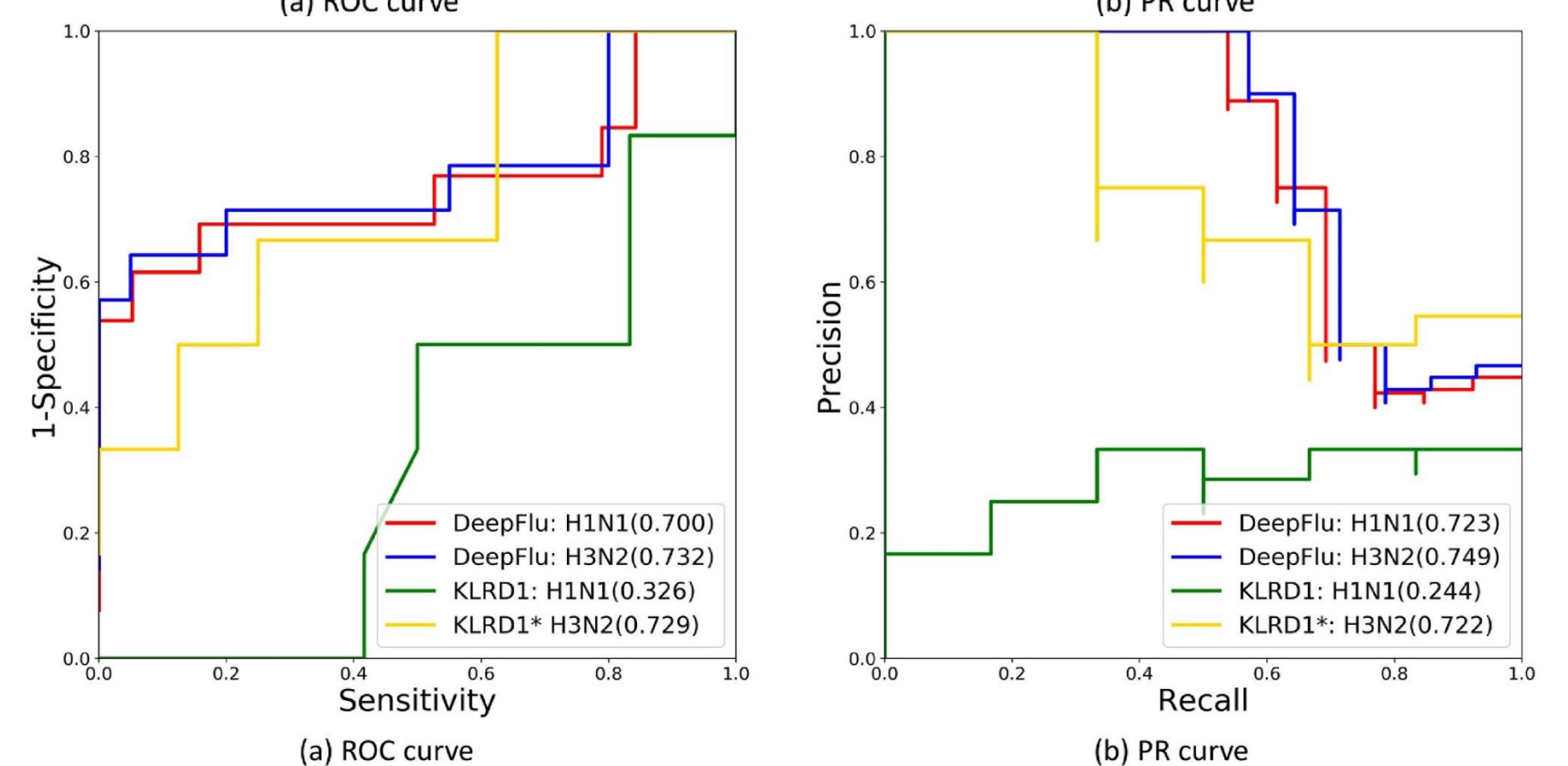
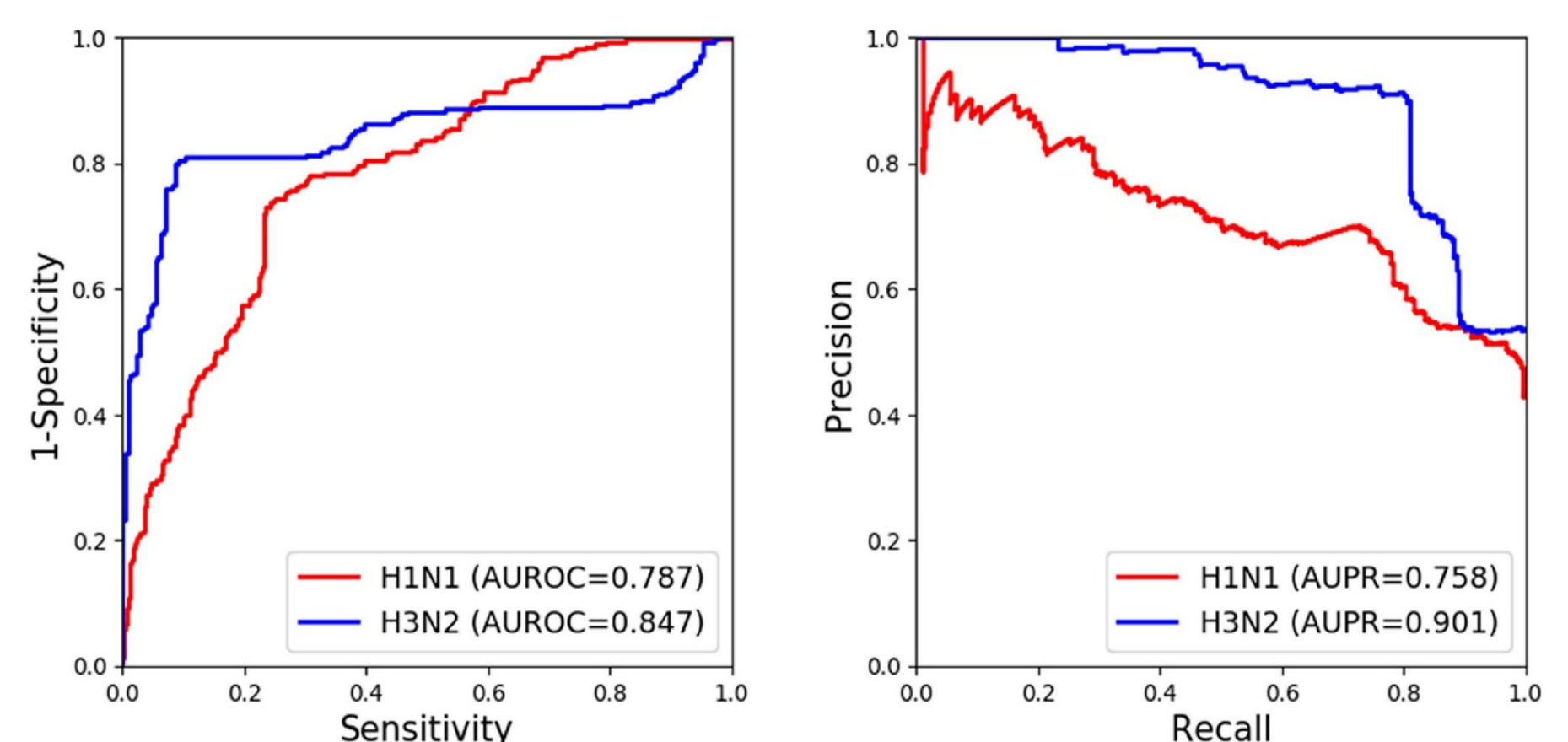
Infection



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.