

# IEICE Proceeding Series

Predicting antigenic changes of influenza viruses through data assimilation

Kimihito Ito

Vol. 2 pp. 448-448

Publication Date: 2014/03/18

Online ISSN: 2188-5079

Downloaded from [www.proceeding.ieice.org](http://www.proceeding.ieice.org)

## Predicting antigenic changes of influenza viruses through data assimilation

Kimihito Ito<sup>†</sup>

<sup>†</sup>Research Center for Zoonosis Control, Hokkaido University  
Kita 20 Nishi 10, Kita-ku, Sapporo, Hokkaido 001-0020, Japan  
Email: itok@czc.hokudai.ac.jp

### Abstract—

The hemagglutinin (HA) molecule of influenza A viruses is the prime target of antibodies that neutralize viral infectivity. The strong immune pressure against HA in the human population selects a new variant every 2-5 years. Thus influenza A viruses undergo antigenic changes with gradual accumulation of amino acid substitutions on HA. This antigenic change is one of the primary reasons why vaccination is not a perfect measure to control seasonal influenza. Influenza vaccine often requires replacement to avoid antigenic mismatch between vaccine and epidemic strains. The decision of vaccine replacement must be made several months before a minor strain become dominant strain. Therefore the prediction of antigenic change of influenza A virus has been one of the major public health goals [1].

To establish a practical method enabling us to predict the future direction of the viral evolution, the timing when the dominant epidemic strains were replaced by other strains, and the magnitude of outbreaks of seasonal influenza, we developed a new prediction method based on a framework of data assimilation.

Data assimilation is a statistical method by which actual observations are integrated into computer simulations. So far data assimilation techniques have been applied in many scientific fields, including geosciences, life science, and engineering. Significant improvements in prediction accuracy have been reported, especially in weather forecast and hydrology [2].

In this presentation, I will introduce the newly developed data-assimilation-based system for the prediction of influenza virus evolution. We constructed a mathematical model of viral population, infection, and host immunity. Based on the developed model, actual viral evolution observed in past 42 years was analyzed by a sequential Bayesian inference method called particle filters. Currently available results showed the data assimilation could have better potential to predict future amino acid substitutions on HA than our previous method [3].

### References

- [1] W.G. Laver, G.M. Air and R.G. Webster, “Mechanism of antigenic drift in influenza virus : Amino acid sequence changes in an antigenically active region of Hong-Kong (H3N2) influenza virus hemagglutinin,” *J Mol Biol*, **145**, 339-361, (1981)
- [2] J.L. Anderson, “An ensemble adjustment Kalman filter for data assimilation,” *Mon Weather Rev*, **129**, 2884-2093, (2001)
- [3] K. Ito et.al, “Gnarled-Trunk Evolutionary Model of Influenza A Virus Hemagglutinin,” *PLoS ONE*, **6:10**, e25953, (2011).