GISAID-ISIRV-WHO Workshop on
'Genetic Analyses of Influenza Viruses'
29th August 2016 (8am-5pm)
<u>Weinberg Computer Laboratory, Northwestern University, Chicago</u>

The purpose of the training workshop is to instruct participants in the use of GISAID's new EpiFlu™ 2.0 database (which is used to share influenza genetic sequence data and related metadata among laboratories of the WHO Global Influenza Surveillance and Response System) and its novel features and advanced analysis tools. The skills obtained will enable laboratories to contribute to and benefit from the extensive genetic and related data on influenza viruses, in relation to understanding the epidemiology of influenza, the evolution of the viruses and the emergence and spread of novel genetic and antigenic variants. A phylogenetic Tree Tool, which includes annotation with amino acid changes, allows non-experts to easily conduct detailed genetic analyses of viruses in their region and understand changes in relation to evolution globally, while FluSurver assists the interpretation of mutations underlying the evolution and antigenic variation of human and animal influenza viruses, and the emergence of antiviral resistance. Enhanced capability to analyse and understand the relationships among influenza viruses is also aimed at stimulating increased interaction among institutions involved in human and animal influenza surveillance and research.

0800 am – 0830 am	**Registration**
0830 am – 0915 am	**Introduction to GISAID 2.0** Catherine Smith, CDC, USA
0915 am – 1000 am	**Browsing, Retrieving and Downloading Data** Naomi Komadina, VIDRL, Australia
1000 am – 1015 am	**Coffee/Tea Break - Method Atrium**
1015 am – 1100 am	**Uploading Data to GISAID** Rebecca Garten, CDC, USA
1100 am – 1130 am	**Data Curation** Annotation and Post-Processing of Data Anne Pohlmann, FLI, Germany

1130 am –0100 pm	**Lunch Break – Ryan Family Atrium**
0100 pm - 0130 pm	**Creating and Sharing Worksets** Catherine Smith, CDC, USA
0130 pm - 0215 pm	**FluSurver Tool** Sebastian Mauer-Stroh, Bioinformatics Institute, A*STAR, Singapore
0215 pm – 0300 pm	**NextFlu Tree tool** Richard Neher, Max Planck Institute for Developmental Biology, Germany
0300 pm – 0315 pm	**Coffee/Tea Break - Method Atrium**
0315 pm – 0430 pm	**Hands-On Practice of Tools** Question/Answer Period
0430 pm – 0500 pm	**Roundtable Discussion** Workshop Conclusion

<u>Instruction will be provided by:</u>

Roxana Cintron, CDC, Atlanta, USA

Rebecca Garten (GISAID DTG), WHO Collaborating Centre, CDC, Atlanta, USA

Naomi Komadina (GISAID DTG), VIDRL, Melbourne, Australia

*Sebastian Maurer-Stroh (GISAID DTG), Bioinformatics Institute, A*STAR, Singapore*

Alan Hay, The Francis Crick Institute, London, UK

Richard Neher, Max Planck Institute for Developmental Biology, Tubingen, Germany

Anne Pohlmann, Friedrich-Loeffler-Institut, Greifswald - Insel Riems, Germany

Catherine Smith, (GISAID DTG), WHO Collaborating Centre, CDC, Atlanta, USA