Project Title: The Establishment of Influenza Virus Bioinformatics System
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Executing Institute: Bioinformatics Research Center, National Yang Ming University
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Abstract:

Bioinformatics Analysis is the cornerstone of in silico-based methodologies that are used to understand biological systems and processes across species. In order to provide the infrastructure required to sustain current influenza virus research, especially in projects that are addressing the needs of bioinformatics analysis, the "Influenza Virus Bioinformatics System" (IVBS) has established a potal of computational support for biologically related influenza virus research disciplines. This core facility is set up to increase both the analysis efficiency and the work quality when a large-scale research project is initiated not only here in Taiwan but also in many countries around the world. The prupose of this bioinformatics core facility is to serve the needs of other related projects. For the first year, this influenza information core facility collected all the available influenza data and information and provided them to the other team projects after integrating with the RSS technology. In the second year, this core facility analyzed the viral biological characteristics such as antigene, drug resistance, HI titer, virus recombination and genetic reassorment etc., to further expand the knowledge base. The core also seeks for the capacity of processing large dataset and forming pipeline and quality control for data analysis. As for the third year, according to the request of other related projects, the influenza A virus genotype prediction tool and personal working set database have been added. By using bioinformatics techniques, we have developed tools to predict trend of influenza virus evolution and facilitated the prediction of vaccine targets.

In summary, in the third year, we have accomplished the following:

1. Automatic update of influenza virus sequence

2. Use sequence logo to show the conserved region of similar influenza protein sequences

3. Influenza A virus genotype database and prediction tool

4. Personal workingset database for saving and analysing personal sequence data

5. B-cell epitope prediction tool

    a. Simialrity analysis of B-cell epitope nucleotide sequences

    b. Investigation of available tools for B-cell epitope predtion

    c. Development of in-house B-cell epitope predtion tools

Keywords: influenza information core facility, genotyping, Personal workingset database, epitope prediction tool