Grid-based International Network for Flu Observation

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Molecular epidemiology plays a very important role in human efforts to deal with dangerous infectious diseases such as avian influenza or H1N1 influenza. One of the most basic and popular methods of molecular epidemiology is phylogeny.

Therefore, some public data sources about influenza such as NCBI or BioHealthBase often offer phylogenetic tools to allow epidemiologists easy access and analyze on their influenza database. However, these tools are limited on the results number and also the data is taken from one source only.

Project “Global Surveillance Network for Influenza A” is developed on EGEE’s infrastructure with the goal is a new complete and update virus data source together with molecular tools. This paper will present a phylogenetic workflow build on this surveillance network that provides a whole process from searching to building phylogenetic trees. Applying grid’s approach assures the availability and allows epidemiologists to analyze on multiple resources and get more results.