

g-INFO Portal

In this paper, we present a flexible workflow to monitor the evolution of the avian flu virus. Indeed, avian flu remains a major threat to public health worldwide if it acquires the capacity for human to human transmission. The Grid-based International Network for Flu Observation project (<http://g-info.healthgrid.org/>) aims at running and connecting various bioinformatics programs, recognized for their accuracy and speed, to continuously reconstruct a robust phylogenetic tree from a set of sequences publicly available and daily updated. The sequences, extracted from existing data sources populated by the scientific community, are processed dynamically based on Service Oriented Architecture principles (SOA) and Grid technologies. Analysis of the virus genome and particularly of some key regions related to its pathogenicity and capacity for human-to-human transmission is of utmost importance for preparedness and evaluation of pandemics risk. For this purpose, a dynamic bioinformatics workflow was implemented in g-INFO. The workflow is considered dynamic because it is configurable so that an expert can choose which components he wants as well as the order of the components in the workflow for its specific analysis.

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