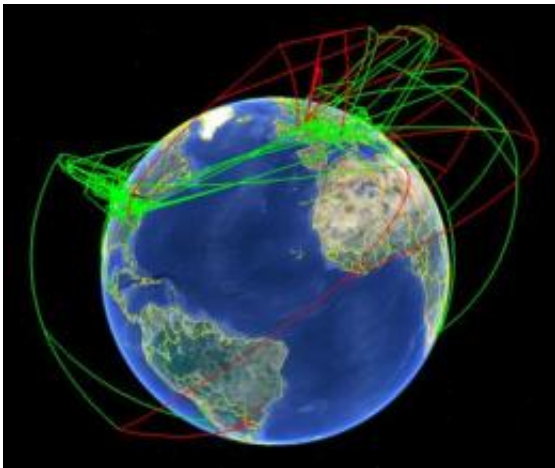


Researchers take virus-tracking software worldwide

May 22 2012



Associate Professor Daniel Janies, Ph.D., an expert in computational genomics at the Wexner Medical Center at The Ohio State University, is working with software engineers at the Ohio Supercomputer Center to expand the reach of SUPRAMAP, a web-based application that synthesizes large, diverse datasets and displays them in geospatial browsers. This is a screenshot of the spread of H7 influenza as produced by SUPRAMAP and visualized by Google Earth™. This view illustrates the historical spread of high pathogenic lineages (high-altitude red lines) and the recent local evolution of high pathogenicity (low-altitude red lines). Credit: Daniel Janies

A biomedical informatics researcher who tracks dangerous viruses as they spread around the globe has restructured his innovative tracking software to promote even wider use of the program around the world.

Associate Professor Daniel Janies, Ph.D., an expert in computational genomics at the Wexner Medical Center at The Ohio State University (OSU), is working with [software engineers](#) at the [Ohio Supercomputer Center](#) (OSC) to expand the reach of SUPRAMAP ([supramap.org](#)), a web-based application that synthesizes large, diverse datasets so that researchers can better understand the spread of [infectious diseases](#) across hosts and geography. By separating SUPRAMAP's client application from the underlying server [software](#), the goal is to reconfigure the server in a way that researchers and public safety officials can develop other front-end applications that draw on the logic and [computing resources](#) of SUPRAMAP.

Janies and his colleagues at Ohio State, the [American Museum of Natural History](#) (AMNH) and OSC developed SUPRAMAP in 2007 to track the spread and evolution of pandemic (H1N1) and avian influenza (H5N1).

"Using SUPRAMAP, we initially developed maps that illustrated the spread of drug-resistant influenza and host shifts in H1N1 and H5N1 influenza and in coronaviruses, such as SARS," said Janies.

"SUPRAMAP allows the user to track strains carrying key mutations in a geospatial browser such as [Google Earth](#)™. Our software allows public health scientists to update and view maps on the evolution and spread of pathogens."

The original implementation of SUPRAMAP was built with a single client that was tightly coupled to the server software.

"We now have decoupled the server from the original client to provide a modular [web service](#) for POY, ([poyws.org](#)) an open-source, freely available phylogenetic analysis program developed at AMNH. The web service can be used by other researchers with new ideas, data, and clients to create novel applications," said Ward Wheeler, curator-in-charge of

scientific computing at AMNH and a coauthor with Janies and others on a recent article about the project in the journal *Cladistics*.

"To demonstrate the POY web service, we have produced a new client software application, GEOGENES (www.geogenes.org)," said Wheeler.

"Unlike in SUPRAMAP, in which the user is required to create and upload data files, in GEOGENES the user works from a graphical interface to query a curated dataset, thus freeing the user from managing files."

Currently this service is hosted on large shared systems at OSC, the center's flagship HP Intel Xeon Oakley Cluster, their IBM Opteron Glenn Cluster and on a smaller dedicated cluster at Ohio State's Wexner Medical Center.

"Decoupling the client from the server provides another advantage in that the implementation of the server can change to take advantage of advances in computing technology," noted Thomas Bitterman, a senior software engineer at OSC and co-author of the journal article. "For example, the recent addition of the Oakley Cluster at OSC has made available a large set of GPUs that could result in performance improvements."

To give their new software implementation a proper road test, the researchers examined groups of key mutations in a pathogen they hadn't tracked before – the H7 avian influenza virus. Infection of humans by the H7 virus is rare, but it has occurred among people who have direct contact with infected poultry.

"H7 influenza, like H5N1 is largely an avian virus, but infects humans periodically, and therefore we wanted to see how it evolves," said Janies.

"We have shown that pathogenicity of the H7 influenza is highly labile on a molecular evolutionary level and has occurred independently in

many places around the world. Now that the H5N1 papers detailing transmission among mammals have been published, we can next pinpoint the natural geographic distribution of key sets of mutations that could lead to human-to-human transmission. Our maps will allow scientists to better deploy public health resources to protect citizens and forces in the field."

Provided by Ohio Supercomputer Center

Citation: Researchers take virus-tracking software worldwide (2012, May 22) retrieved 18 May 2024 from <https://phys.org/news/2012-05-virus-tracking-software-worldwide.html>

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