

Note: The following news release is being issued by the Ohio Superconductor Center. It describes the expansion of virus-tracking software that was developed by researchers and engineers at the American Museum of Natural History, The Ohio State University, and the Ohio Superconductor Center.



AMERICAN MUSEUM OF NATURAL HISTORY

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RESEARCHERS TAKE VIRUS-TRACKING SOFTWARE WORLDWIDE PROJECT ALLOWS NEW FORMS OF CLIENT SOFTWARE TO JOIN GENETIC SURVEILLANCE

COLUMBUS, Ohio — 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, 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](http://supramap.org) (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](http://poyws.org), (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](http://www.geogenes.org) (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.”

Grant funding through the U.S. Army Research Laboratory and Office supports this [Innovation Group on Global Infectious Disease Research](http://gidr.osu.edu) (gidr.osu.edu) project. Support for the computational requirements of the project comes from AMNH and OSC. Ohio State’s Wexner Medical Center, Department of Biomedical Informatics and offices of Academic Affairs and Research provide additional support.

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Editor’s Note: Hi-res versions of the images in this release are available at:

<http://www.osc.edu/press/releases/2012/Janies.shtml>.

The **Ohio Supercomputer Center** (OSC), a member of the Ohio Technology Consortium of the Ohio Board of Regents, addresses the rising computational demands of academic and industrial research communities by providing a robust shared infrastructure and proven expertise in advanced modeling, simulation and analysis. OSC empowers scientists with the vital resources essential to make extraordinary discoveries and innovations, partners with businesses and industry to leverage computational science as a competitive force in the global knowledge economy, and leads efforts to equip the workforce with the key technology skills required to secure 21st century jobs. For more, visit www.osc.edu.

The **Department of Biomedical Informatics** at the Wexner Medical Center at The Ohio State University is a cross-disciplinary department, focusing on scientific data integration, imaging and simulation, medical informatics, computational biology and bioinformatics. The BMI staff leads the advancement of health and biomedicine through the development, application and dissemination of

novel biomedical informatics theories and methods capable of driving biological discovery, generating and translating knowledge and advancing personalized healthcare. For more, visit biomed.osu.edu/bmi.

The **American Museum of Natural History**, founded in 1869, is one of the world's preeminent scientific, educational, and cultural institutions. The Museum encompasses 45 permanent exhibition halls, including the Rose Center for Earth and Space and the Hayden Planetarium, as well as galleries for temporary exhibitions. Five active research divisions and three cross-disciplinary centers support 200 scientists, whose work draws on a world-class permanent collection of more than 32 million specimens and artifacts, including specialized collections for frozen tissue and genomic and astrophysical data, as well as one of the largest natural history libraries in the Western Hemisphere. **The Science Computer Cluster Facility** is a major resource used by museum research scientists, postdoctoral fellows, and graduate and undergraduate students for high-end capability computing in the areas of biology, genomics, astrophysics, paleontology and anthropology. For more, visit research.amnh.org/scicomp/.

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No. 49