

Panel Discussion Proposal for SC09 (<http://sc09.supercomputing.org/?pg=panels.html>);  
November 18, Wednesday, 2009; 1:30 PM – 3:00 PM, R# 252), Portland, Oregon

Title: **CYBERINFRASTRUCTURE IN HEALTHCARE MANAGEMENT**

**List of Panelists:**

Arun K. Datta (Moderator), National University

Terry Boyd, Center for Disease Control (CDC)

Stanley J. Watowich, University of Texas Medical Branch at Galveston (UTMB)

Wilfred Li, San Diego Supercomputing Center (SDSC)

Fang-Pang Lin, NCHC (Taiwan)

**Abstract** (150 words; topic and questions to be addressed)

This panel will discuss the impact of cyberinfrastructure in healthcare management. The recent outbreak of Flu by Swine virus in US and other parts of the Globe will be discussed as a case study. Swine Flu virus causes Influenza in pigs similar to the outbreak of human influenza virus that affects the US population every winter. However, it infected human and the recent outbreak is caused by swine virus type H1N1, which has some sequence similarity with avian virus and human influenza virus. The panel will share how the informatics took an important role in controlling this pandemic flu. In this context, this panel will also share the role of PRAGMA in controlling SARS outbreak that occurred in 2003. Dengue viral management using World Community Grid will also be discussed. In addition, the panel will discuss the possible impact of sharing genomic information in Electronic Health Record of an individual.

**Target Audience:**

The target audience is allied health professionals, nurses, clinicians, Health IT personnel, researchers, CTO of health organizations and general audience because of the nature of the topics that touches everybody's life.

**STATEMENT OF INTERESTS**

This panel will discuss the impact of *cyberinfrastructure* in healthcare management.

**Panel member, Terry Boyd, Director, Division of Informatics and Shared Services, National Center for Public Health Informatics, Centers for Disease Control and Prevention,** will discuss on the recent outbreak of H1N1 in US and other parts of the Globe. In US alone, at the time of writing this statement, 141 people from nineteen states have been infected and one

child already died in Texas. This outbreak is caused by Swine Flu virus, which causes Influenza in pigs similar to the outbreak of human influenza virus that affects the US population every winter. Serological tests indicated that this swine virus is of type H1N1. There are four different serotypes for Swine Flu: H1N1, H1N2, H3N2, and H3N1. Any of these serotypes alone or in combination can cause influenza in pigs. Moreover, pigs can be infected by avian influenza and human influenza viruses as well as these swine influenza viruses. Incidentally, when influenza viruses from different species infect pigs, the viruses can reassort/swap genes and new viruses that are a mixture of swine, human and/or avian influenza viruses can emerge. This panel member will discuss the genetic makeup of this new virus that has caused this pandemic flu. CDC continues to take aggressive action to respond to an expanding outbreak caused by H1N1. CDC's response goals are to reduce transmission and illness severity, and provide information to help health care providers, public health officials and the public address the challenges posed by this emergency.

H1N1 (2009) has already infected people in dozens of countries including Mexico, Canada, Austria, Britain, Germany, Israel, the Netherlands, Spain, Switzerland, besides the United States. It has already claimed 16 deaths, all from Mexico (one Mexican toddler died in Houston). It has sickened nearly 350 people in Mexico, and about 250 others from New York to New Zealand, including children, teens, adults, students and tourists. It has rattled the world's financial markets, pushed oil prices down, caused a run on surgical masks and hand sanitizers, closed schools and churches, postponed sporting events, prompted travel bans, rerouted cruise ships. The World Health Organization has already issued a level 6 warning. The directors of the HHS and CDC have also issued a similar warning in US. This panel member will discuss how the informatics took an important role in coordinating the efforts of the CDC for controlling this flu.

**Wilfred Li, Executive Director of the National Biomedical Computation Resource, and a senior fellow at the San Diego Supercomputer Center, at the University of California, San Diego,** will discuss about a similar outbreak of SARS (severe acute respiratory syndrome), which occurred in 2003 and resulted in more than 8,000 cases and 810 deaths in 29 countries, according to estimates by the World Health Organization. This deadly acute respiratory disease in humans was caused by the SARS coronavirus (SARS-CoV). Within a matter of weeks in early 2003, SARS spread from the Guangdong province of China to rapidly infect individuals in some 37 countries around the world including Taiwan. When the medical staffs of several key hospitals in Taiwan were quarantined by the SARS epidemic, threatening to make a critical situation even worse, PRAGMA—the Pacific Rim Applications and Grid Middleware Assembly—showed how relationships and expertise developed to tackle computational research could help thousands of SARS patients in Taiwan.

PRAGMA, an international collaboration consisting of fourteen founding institutions, is funded by the National Science Foundation. This program develops grid-enabled applications and deploys high-tech infrastructure throughout the Pacific Region, with the goal of sharing member institutions' data, computing power, and other resources. In this case, the resource to be shared was PRAGMA's expertise in network-based, high-performance teleconferencing. Dr. Li's collaborator, **Dr. Fang-Pang Lin, who is the director of the Grid Computing Division of Taiwan's National Center for High-Performance Computing (NCHC)** that is responsible for the national grid project of Taiwan, will share his experience with this audience how PRAGMA partners and other institutions around the world offered assistance within a remarkable short time.

These institutions included the Computer Network Information Center (CNIC) of the Chinese Academy of Sciences, the National Institute of Advanced Industrial Science and Technology (AIST), the Korea Institute for Science and Technology Information (KISTI), Indiana University and the NSF-funded TransPac project, the San Diego Supercomputer Center (SDSC), the National Center for Microscopy and Imaging Research, as well as the National Biomedical Computation Resource of UCSD, the National Center for Supercomputing Applications (NCSA), Queensland University of Technology, AARnet, Argonne National Laboratory and inSORS (now IOCOM), and the California Institute of Telecommunications and Information Technology [Cal-IT]2]. That was possible because of the grid infrastructure developed under PRAGMA.

**Stanley J. Watowich, Professor, Department of Biochemistry & Molecular Biology, University of Texas Medical Branch at Galveston, the another panel member,** will discuss how the grid infrastructure is helping his drug discovery research. His lab is working to discover novel drugs and drug targets to combat infectious diseases, such as, dengue virus. Dengue is caused by four closely related virus serotypes of the genus *Flavivirus* (family *Flaviviridae*) which is transmitted to humans by the mosquito, *Aedes aegypti* or more rarely the *Aedes albopictus*. *Flaviviridae* can be responsible for causing multiple major diseases including Hepatitis C, Yellow fever, West Nile fever, besides Dengue. His drug discovery program involves screening of thousands of small molecules before discovering the 'hit'. This screening is facilitated by World Community Grid of IBM, which is a virtual supercomputer that uses the extensive computing power of hundreds and thousands of private computers to tackle projects that benefit humanity. Prof. Watowich's project aims to identify new drug-like molecules that stop the replication of viruses from the *Flaviridae* family, which pose significant health threats throughout the developing and developed world. According to WHO, dengue fever is a serious and growing public health problem affecting millions of people and there are no drugs to treat it. His lab has now been involved working on H1N1 with similar approach.

**Arun Datta, Director (Technology R & D), NU Community Research Institute and a Senior Faculty member at the National University (San Diego),** will discuss how information sharing, particularly on genomic information, through a patient's Electronic Health Record is important. Electronic Health Record of an individual is now becoming a useful software tool for recording physical condition of an individual. More than 30 vendors market such tool. However, none of these provides relevant information, particularly on genomic information that often is helpful to the clinicians and even to the patients. In case of infectious diseases, such as, Flu and dengue, the biological samples from the patients are analyzed for the confirmation of the disease condition. Often, DNA from those samples is used for sequencing and comparative genomics. However, in most of the cases, such genomic information remains with the sequencing lab, because the EHR does not provide the feature to include such vital information. National Institute of Health is now interested to include genome information in EHR of an individual. This panel member will discuss how such information may impact the personalized healthcare management.