NATIONAL UNIVERSITY OF SINGAPORE

School of Computing

C S S E M I N A R

Title: **Deciphering Cancer using Big Data**

Speaker: Dr Anders Jacobsen Skanderup
              Genome Institute of Singapore

Date/Time: 19 August 2015, Wednesday, 02:00 PM to 03:30 PM

Venue: Executive Classroom, COM2-04-02

Chaired by: Dr Wong Lim Soon, KITHCT Chair Professor, School of Computing
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Abstract:

The advent of DNA sequencing technologies is currently generating a paradigm shift in medical research. Cancer research has traditionally been a laborious effort of testing individual hypothesis in the laboratory. However, it is now also evolving into a Big Data domain where disease etiology can be analyzed directly from rich molecular and genetic profiles of cancer patients. Here, I will present ongoing work that uses data-intensive computational approaches to identify the regions of our genome that are critical for development of cancer. Our approach leverages complete genome sequence data from over 2000 cancer patients, which comprise over 1 petabyte of data. We use state-of-the-art DNA sequence analysis tools in a distributed computing environment to effectively summarize and reduce dimensionality of the data. This data is then analyzed using a statistical learning and inference approach to infer the genomic regions displaying features indicative of cancer involvement. Finally, we will discuss the computational challenges in scaling up this type of analysis to ten thousands of genomes, which is needed in order to catalogue all cancer causing genes and events. This will ultimately enable us to leverage the entire human genome for next-generation cancer precision medicine.

Biodata:

Anders Jacobsen Skanderup is a principal investigator at the Genome Institute of Singapore. He is interested in developing computational and quantitative data-intensive approaches to decipher the genetic and molecular basis of human disease. Dr. Skanderup received his B.S. in computer science from University of Copenhagen, Denmark. He later earned a M.Sc. and Ph.D. in Bioinformatics under supervision of Prof. Anders Krogh, University of Copenhagen. He completed postdoctoral training at Memorial Sloan-Kettering Cancer Center in New York with Chris Sander, where he focused on developing and applying computational methods to study non-coding DNA and RNA in cancer.