Stanford-South Africa Biomedical Informatics Program

Betty Cheng

Program Mission

The Stanford-South Africa Biomedical Informatics (SSABMI) Training Program expands teaching, training, and research opportunities for individuals interested in the application of informatics technologies to problems in biomedical research in South Africa. The program goal is to train the next generation of BMI faculty in South Africa. The program is a partnership between the University of the Western Cape (UWC), the University of Cape Town (UCT), the National Institute of Communicable Diseases (NICD), and Stanford University. The SSABMI program is part of the Fogarty International Center's Informatics Training for Global Health (ITGH) initiative to develop informatics research capacity around the world.

Who we are

Russ B. Altman, PI, Stanford University
Win Hide, Co-PI, UWC, SANBI
Vlad Bajic,UWC, SANBI
Cathal Seioghe, UCT
Betty Cheng, Prog. Dir., Stanford Univ.
Patricia Josias, Prog. Admin., UWC
Adele Kruger, Student representative, South Africa
Sarah Aerni, Student representative, Stanford

What we do

The SSABMI program has offered 7 short courses in biomedical informatics taught in Cape Town, funds graduate students in BMI at UWC and UCT and supports research visits for South African researchers at Stanford and other Bay Area institutions.

Current SSABMI Students

Adele Kruger

Cancer is the leading cause of death worldwide and was responsible for 13% of all deaths in 2005. The origin of cancer is unknown but It has been theorized that cancers arise from a small population of stem cells. Cancer is known to be a disease originating from a sequence of mutations that results in a deregulation of the normal pathways of terminal differentiation. It is thought that cells generally do not live long enough to enable the accumulation of these sequential mutations. A subset of cancer cells have been identified that, when cultured, are multipotent and can regenerate a tumor. These cancer cells share similarities with normal long-term, self-renewing stem cells and are therefore known as cancer stem cells. These cells are thought to accumulate cancer-forming mutations and are the origin of tumors. Our goal is to understand stem cell regulation which may lead to understanding of cancerous stem cells.

Cameron MacPherson

Neurological diseases are socially disabling and often mortal. To even begin to combat these diseases, a deep understanding of cellular processes, function and anatomy is required. However, differential regulation of genes across anatomy is poorly understood. This study utilized large-scale gene expression data to define the gene expression profile of the hippocampus to which a large degree of neurological disease pathologies may be associated. Furthermore, we specifically aimed to: identify key regulatory transcription factors (TF) responsible for observed gene expression patterns, reconstruct transcription regulatory networks and prioritize likely TFs responsible for anatomically restricted gene expression. We restricted most of our analysis to the CA3 sub-region of ammon's horn within the hippocampus. We identified expressed core genes and predict corresponding TF binding site (TFBS) distributions. We demonstrate the validity of the predictions by re-clustering genes based on TFBS distributions and found that genes tend to be correctly assigned to groups of co-expressing genes with sensitivity of 67.74% and positive predictive value of 100%. This study represents one of the first to merge anatomical architecture, expression profiles and transcription regulatory potential on such a large scale in hippocampal sub-anatomy.

Nobubelo Ngandu

Although multiple HIV therapeutic drugs have been developed the development of a vaccine remains the best hope of controlling the global HIV epidemic. In order to develop an effective vaccine against HIV, there is a need to (i) identify highly conserved and immuno-dominant epitopes in the virus, (ii) characterize immune responses of the population to be vaccinated and (iii) understand viral sequence evolution constraints within host. My PhD research aims are (A) to investigate the impact of host humoral and cytotoxic immune responses on HIV-1 diversity and evolution in distinct human population and (B) to carry out a detailed investigation of selection acting on synonymous sites in HIV protein-coding genes.

Sumir Panji

There are numerous contributing causative factors leading to cancer. All of these factors result in a common denominator, the aberrant expression of a diploid cell's genomic complement. Aberrant gene expression during oncogenesis is exemplified by a subset of human genes known as the Cancer/Testis (CT) genes. The CT genes are a heterogeneous collation of human genes expressed primarily in the testis and a wide variety of cancer types. From a biomedical standpoint, the CT genes represent a novel route in the prophylaxis of cancer as a subset of CT genes, known as Cancer / Testis Antigens (CTA), elicit immune responses against CTA expressing neoplasms. Due to the heterogeneity of the CT genes, defining what core characteristics constitute a CT gene is problematic. Theoretically, any gene whose expression is restricted to the testis and cancer can be termed a CT gene. To identify CT genes, I search for conserved elements close to known CT genes. The identification of conserved elements will elucidate CT regulatory networks and assist with the identification of CT gene function.

Events Spring Qtr 2008

The SSABMI graduate students will travel to Stanford for research visits intended to add breadth or depth to their graduate experience. Stanford faculty will host each student for a short research project and students will participate in classes in biomedical informatics.

You are invited to attend the Stanford-South Africa Seminar Series. We will videoconference with students and faculty in South Africa to present the SSABMI students' work in progress.

For more information, see http://southafrica.stanford.edu or email betty.cheng@stanford.edu

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