

Teaching Statement

There is an ancient Chinese saying “If you give a man a fish, you feed him for a day, but, if you teach a man how to fish, you feed him for life”. This serves as the basis of my teaching philosophy.

A teacher’s role is more than the mere dissemination of knowledge. When teaching a course my goals are threefold: we should help students (1) develop their own ways of learning and gain relevant skills, (2) know how to apply their newly-acquired knowledge to solve practical problems and feel a sense of accomplishment in the learning process, and (3) get a clear picture about current accomplishments and issues in the field concerned. When I was a teacher in graduate level course Mathematical Biology and MATLAB programming at Zhongshan University, I found that the example-based teaching way is usually very effective.

I like to teach undergraduate or graduate courses such as Bioinformatics, Biostatistics, Computing techniques for chips, Mathematical Biology, MATLAB programming. I am also interested in developing an advanced seminar course, for example, Structural Biology and Drug Design. In addition, I am also very interested in another aspect of teaching: advising graduate students. I have already co-supervised one PhD student at Hong Kong University, I am glad to report that our co-authored papers (about 10 papers) have been published in peer-reviewed journals.

Bioinformatics is a very comprehensive discipline, which involves biology, mathematics, statistics and computer science. I believe teaching students bioinformatics requires a different approach than standard approaches in biology teaching alone or mathematics teaching alone. I like to start with a specific example to show how bioinformatics works: understanding biological background of the question, designing new algorithm using mathematical and statistical skills, and finally implementing in the computer. Success in bioinformatics teaching means the realization of the following goals: (1) The students should be equipped with enough biological background, (2) The students should be familiar with common computational tools and databases, (3) The students should be trained well in using different sets of skills (mathematics, statistics and computer techniques).

Research Statement

Main research interests

Bioinformatics

Statistical analysis of microarray and proteomics data The new challenge in human disease diagnosis is to find a method for detecting unique biomarkers from thousands of elements (genes or proteins). Applying mathematical and statistical techniques, such as ANOVA (Analysis of Variance), ANN (Artificial Neural Network), GA (Genetic Algorithms), SVD/PCA (Singular Value Decomposition/Principal Component Analysis), ICA (Independent Component Analysis), PLS (Partial Least Square), etc., to analyze transcriptome and proteomics data with the aim at identifying disease-related biomarkers and defining the diagnostic rules for clinical use.

Cancer diagnosis and biomarkers identification The precise diagnosis of human cancer type is of particular importance and is also a challenging task. We design new pattern recognition procedures to diagnose human cancers, such as colon cancer, prostate cancer, lung cancer, etc. In particular, we discovered highly conserved transcription factor binding motifs in lung cancer marker genes, suggesting new interesting candidate of cancer targets for therapeutic intervention of lung adenocarcinomas.

Structure-based drug design A major goal of modern drug design is to develop new ligands with high affinity of binding to a given protein receptor. Using molecular modelling techniques to conduct the 3D structural analysis of SARS coronavirus proteinase and spike protein, to understand their interactions with small molecule ligands and define the essential structure features for the binding of potent inhibitors to the targets (pharmacophore), hence to provide important information for virtual screening and structure-based drug design.

Epitope-based vaccine design The recognition of antigenic epitopes by the immune system is the key molecular event at the heart of the immune response to pathogens. Working on systematic in silico identification of T-cell epitopes for SARS coronavirus S, M and N proteins, to perform the structural analysis of peptide-MHC-TCR complex for improvement of binding affinity, hence to optimize epitope-based vaccine design and develop new immunotherapy strategy.

Mathematical Medicine: Dynamics for HIV, T cells (CD4+ and CD8+) and drug therapy

The requirements for the eradication of HIV in infected individuals are unknown. HIV-specific CD8+ T lymphocytes play a crucial role in control of HIV replication in vivo. A new five-dimensional deterministic model was developed to describe the interactions between HIV, CD4+ T-cells and CD8+ T-cells. The model reveals

that anti-HIV CTL action is insufficient to eradicate HIV, even in the presence of 100% effective intermittent HAART (highly active anti-retroviral therapy) and IL-2 therapy. However, HIV eradication is feasible in the absence of virus reservoir or in the presence of an anti-HIV vaccine.

Mathematical Cell Biology: Cell cycle kinetics of blood cells

The molecular machinery that regulates cell division is still unknown. Mathematical model can help us to better understand the kinetics of complex system and to bridge the gap between mechanisms and physiology.

The cell cycle kinetics of primitive hematopoietic cells was investigated. The mean fractions of quiescent, dividing and apoptotic primitive hematopoietic cells were estimated by using a simple stochastic branching model. This information is useful in gene therapy/bone marrow transplantation.