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Work Experiences

(1) 2003-

Research Assistant Professor, Hong Kong University-Pasteur Research Centre, Hong Kong, China

(2) 2001- 2002

Postdoctoral Researcher, UCLA(University of California, Los Angeles), USA

(3) 2000- 2001

Postdoctoral Researcher, University of Manitoba, Winnipeg, Canada

(4) 1999- 2000

Postdoctoral Researcher, UBC(University of British Columbia), Vancouver, Canada

(5) 1998- 1999

Postdoctoral Researcher, University of Hong Kong, Hong Kong

(6) 1993-1998

Associate Professor (since 1995), Food Engineering Research Center of State Education Ministry, Zhongshan University ,China

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.

Publications in International Journals (since 1996)

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[34] **Zhang X.W**., Yap YL, Altmeyer R Generation of predictive pharmacophore model for SARS-Coronavirus main proteinase. **European Journal of Medicinal Chemistry** 2005 40: 57-62.

[33**] Zhang X.W.**, Yap YL, Danchin A Testing the hypothesis of a recombinant origin of the SARS-associated coronavirus. **Archieves of Virology** 2005 150: 1-20.

[32] Yap, Y., **Zhang, X.W**., Ling, M.T., Wang, X., Wong, Y.C., Danchin, A. Class prediction between tumor and normal tissues based on the pair-wise gene expression ratio. **BMC Cancer** 2004 4: 72-88.

[31] **Zhang X.W**., Yap YL, Putative structure and function of ORF3 in SARS coronavirus. **Journal of Molecular Structure (THEOCHEM)** 2004 715: 55-58.

[30] **Zhang X.W.**, Yap YL. The 3D structure analysis of SARS-CoV S1 protein reveals a link to influenza virus neuraminidase and implications for drug and antibody discovery. **Journal of Molecular Structure (THEOCHEM)** 2004 681: 137-141.

[29] **Zhang X.W.**, Yap YL. Old drugs as lead compounds for a new disease? Binding analysis of SARS coronavirus main proteinase with HIV, psychotic and parasite drugs. **Bioorganic & Medicinal Chemistry** 2004 12: 2517-21.

[28] **Zhang, X.W.**, Yap, Y.L. Structural similarity between HIV-1 gp41 and SARS-CoV S2 proteins suggests an analogous membrane fusion mechanism. **Journal of Molecular Structure (THEOCHEM)** 2004 677: 73-76

[27] **Zhang, X.W**., Yap, Y.L. Exploring the binding mechanism of the main proteinase in SARS-associated coronavirus and its implication to anti-SARS drug design. **Bioorganic & Medicinal Chemistry** 2004 12: 2219-2223.

[26] Yap, Y.L., **Zhang, X W**, and Danchin, Antoine Relationship of SARS-CoV to other pathogenic RNA viruses explored by tetranucleotide usage profiling. **BMC Bioinformatics** 2003 4: 43-59.

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[24] **Zhang,X.W**.,Audet,J.,Piret,J.M., Li,Y.X. Cell cycle distribution of primitive haematopoietic cells stimulated in vitro and in vivo. **Cell Proliferation**, 2001,34,321-330.

[23] Shi,X.M.,**Zhang,X.W**.,Chen,F. Heterotrophic production of biomass and lutein by Chlorella protothecoides on various nitrogen sources. **Enzyme and Microbial Technology**,2000,27,312-318.

[22] Ren,G.X.,**Zhang,X.W**.,Chen,F. Predicting Color Kinetics During Red Asian Ginseng (Panax ginseng) preparation. **Pharmazie**, 2000, 55(4), 300-302.

[21] **Zhang,X.W**.,Chen,F.,Johns,M.R. Kinetic models for heterotrophic growth of Chlamydomonas reinhardtii in batch and fed-batch cultures. **Process Biochemistry**,1999,35,385-389.

[20] **Zhang,X.W**.,Gong,X.D.,Chen,F. Dynamics and stability analysis of the growth and astaxanthin production system of haematococcus pluvialis. **Journal of Industrial Microbiology and Biotechnology**, 1999, 23, 133-137.

[19] **Zhang,X.W**.,Sun,T.,Zeng,X.Y.,Liu,X.,Gu,D.X. Expression of recombinant tumor necrosis factor-alpha in baculovirus expression system. **Bioresource Technology**,1999,70,299-301.

[18] **Zhang,X.W**., Sun,T., Zhou,X.F., Liu,X., Gu,D.X., Huang, X.N. Expression of human interleukin-6 (IL-6)in insect system. **Bioresource Technology**,1999,68(2),201-203.

[17] **Zhang,X.W**., Sun,T., Huang,X.N., Liu,X., Gu,D.X., Tang,Z.Q. Recombinant streptokinase production by fed-batch cultivation of Escherichia coli. **Enzyme and Microbial Technology**, 1999, 24, 647-650.

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fermentation of secretory recombinant Escherichia coli . **Process Biochemistry**,1999,34,55-58.

[15] Shi,X.M., Liu,H.J., **Zhang,X.W**., Chen,F. Heterotrophic growth of Chlorella protothecoides and its formation of lutein on various concentrations of glucose. **Process Biochemistry**,1999,34,341-347.

[14] **Zhang,X.W**.,Shi,X.M.,Chen,F. A kinetic model for lutein production by the green microalga Chlorella protothecoides in heterotrophic culture.**Journal of Industrial Microbiology and Biotechnology**, 1999, 23, 503-507.

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[21] **Xue-Wu Zhang** et al. Time-dependent kinetic models for citric acid fermentation. ***Journal of Chinese Food Science and Technology, 1998,2(3): 27-32.***

[20] **Xue-Wu Zhang** et al. A kinetic model for protein hydrolysis. ***Journal of Chinese Food Science and Technology, 1998,2(2): 1-6.***

[19] Zhou Qiang, **Xue-Wu Zhang** et al. Predation of Multi-predators on rice planthoppers. ***Plant Protection,1997,23(2):3-6.***

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[17] **Xue-Wu Zhang** et al.The spatial distribution and life table of natural population for Aonidiella aurantii(Maskell). ***Entomological Knowledge,1996,33(1):25-28.***

[16] **Xue-Wu Zhang** et al.Dispersal pattern of Aonidiella aurantii and its population dynamics modeling. ***Journal of Sun Yatsen University,1996,2:35-41.***

[15] **Xue-Wu Zhang** et al. Molecular technique to promote food security. ***Food Science,1996, 17(8):14-18.***

[14] **Xue-Wu Zhang** et al. Supercritical fluid extrusion processing technique. ***Food Industrial Technology, 1995, 5:18-21.***

[13] **Xue-Wu Zhang** et al.The introduction and biology of Aphytis melinus. ***Journal of Sun Yatsen University,1995,2:1-7.***

[12] **Xue-Wu Zhang** et al.The dynamics studies of Aonidiella aurantii and its three parasites system in citrus trees. ***Journal of Sun Yatsen University,1995,2:47-54.***

[11] **Xue-Wu Zhang** et al.Parasitism of three parasites on Aonidiella aurantii. ***Chinese Journal of Applied Ecology,1995,6(supp.):79-82.***

[10] **Xue-Wu Zhang** et al.Oviposition distribution of Aphytis sp.,a parasite of Hemiberlesia pitysophila Takagi. ***Entomological Knowledge,1995,32(3):156-158.***

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[8] **Xue-Wu Zhang** et al.Experimental release of Aphytis melinus to control Aonidiella aurantii in citrus orchard in Guangdong. ***Chinese Journal of Biological Control,1994,10(3):103-105.***

[7] **Xue-Wu Zhang** et al.Study on the competitions among three parasites of Aonidiella aurantii. ***Ecological Science,1994,1:94-99.***

[6] **Xue-Wu Zhang** et al.Studies on parasitism and host-feeding of Aphytis sp.,a parasite of Hemiberlesia pitysophila Takagi. ***Acta Ecologica Sinica,1993,13(2):135-138.***

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[4] **Xue-Wu Zhang** et al.Researches on the growth and development of Aphytis melinus. ***Chinese Journal of Biological Control,1992,8(1):45-48.***

[3] **Xue-Wu Zhang** et al.Investigations of logevity and oviposition of Aphytis sp.,a parasite of Hemiberlesia pitysophila Takagi. ***Ecological Science,1991,1:62-65***.

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Educational Background

(1) 1990-1993

Ph.D. in Mathematical Biology, Zhongshan University, China

(2) 1987-1990

M.Sc. in Mathematical Biology,Zhongshan University ,China

(3) 1979-1983

B.Sc. in Mathematics, Hunan Normal University, China.

Teaching Experiences

Taught Mathematical Biology to graduate students

Taught Professional English in Biology to undergraduate students

Awards

Guanghua Foundation Award (1991)

Zeng Xianzi Foundation Award (1992)

South-China Excellent Graduate Student Award (1993)

Personal data

Gender M Birth 1963.5. in Hunan Marital status Married

Nationality Chinese (Canadian Permanent Resident)