Virginia Tech

VIRGINIA POLYTECHNIC INSTITUTE
AND STATE UNIVERSITY

Center for Molecular Medicine and Infectious Diseases
Virginia-Maryland Regional College of Veterinary Medicine

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Dr. Yves Brun
Systems Biology/Microbiology Faculty Search
Department of Biology
Indiana University
Jordan Hall 142
1001 E 3rd Street
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Members of the Recruiting Committee:

I wish to be considered for the faculty positions on systems biology/microbiology, as listed in the Science Magazine issue of September 2, 2005. Enclosed please find my *curriculum vitae* (including four referees), statements of research and teaching interests and three representative publications.

I have received training and further performed independent research in a variety of fields (microbiology, infectious diseases, genomics, bioinformatics, systems biology modeling and simulation, genetics, biochemistry, molecular biology, toxicology, plant science and computer science).

In 1990, I finished my M.S. degree of Microbiology. In this work, I was the first person in the world who transferred *Bacillus thuringenesis* insecticidal gene into rice protoplasts and regenerated transgenic plants for insect control.

In 1998, I received my Ph.D. degree of Biochemistry and Molecular Biology on genomics and molecular mechanisms of multiple drug resistance determinants of infectious *Escherichia coli* isolates. A portion of research results was published in Journal of Biological Chemistry, Molecular Microbiology, and FEMS Microbiology Letters, *etc.*

Later, I held faculty/professional appointments at different institutions and directed a few academic and industrial teams on toxicogenomics, biomedical and health care projects.

From 2000 to 2001, I held graduate faculty appointments at Bar Harbor, Maine based NIEHS Biomedical Center, Mount Desert Island Biological Laboratory, and the University of Maine. I directed the initiation and operation of the new bioinformatics center. Duties included quotations and purchases of hardware and software, recruiting new staff, grant application and a comparative toxicogenomics database design and implementation. Owing to family reasons (for example, allergy to local environment), however, I left Maine in 2001.

From 2001 to 2004, I had been a Bioinformatics Scientist / Computational Biologist and Medical Modeler at Virginia Bioinformatics Institute. In this post, I carried out research on anti-bioterrorism and biodefense projects on by then all available genomic data of infectious bacteria and viruses pathogens with IBM Bio-Dictionary Annotation system and many other bioinformatics and genomics resources and analysis tools. Meanwhile, I also built mathematical models to simulate systems biology dynamics of anti-HIV drugs.

While at US Environmental Protection Agency in the fall of 2004, I found out that chimpanzees have a truncated inactive arsenic methyltransferase, which is well conserved in other animal species. This discovery puts arsenic methyltransferase to the catalogue with only 53 different proteins between humans and chimpanzees.

Currently, as a Research Scientist at the Center for Molecular Medicine and Infectious Diseases at Virginia Tech, I am combining my skills on genomics, bioinformatics, and bench experiments to identify and characterize virulent factors of *F. tularensis* and *B. mallei* in order to develop efficient vaccines to counter these category A and B bugs.

During recent years, I have been invited as reviewer for Journal of Biological Chemistry, Bioinformatics, and Genomics. In 2003, the Gerson Lehrman Group Company invited me to be a Council Advisor to provide consultation to international clients with knowledge and insights in public health care and agriculture industries.

I have developed wide contacts with experts in the fields of microbiology, infectious diseases, biochemistry, genomics, bioinformatics, and systems biology. Those people are certainly potential collaborators in my future research.

I have actively participated several pre-award grant applications and have gained considerable post-award funding administration experience.

In my career in the future, I will focus on genome analysis and computational modeling field to address molecular mechanisms of gene/protein networks, evolution and pathogenesis dynamics. I believe that I am a mature candidate with all the qualifications, rigorous critical thinking, and interest in establishing collaborations. I very much look forward to hearing from you.

Sincerely yours,

Jiaxin Li, Ph.D.
Research Scientist

Research Interests

Dr. Jiaxin Li

After training and independent research in a variety of fields (microbiology, infectious diseases, genomics, bioinformatics, systems biology modeling and simulation, genetics, biochemistry, molecular biology, toxicology, and computer engineering/science) at various institutions, I am now searching for an academic position that would allow me to establish a unique research group with the following interests:

1) Protein-coding sequences and structural genomics of *Francisella tularensis* and *Burkholderia mallei*: I will use the combination of heuristic and *ab initio* approaches to predict the higher-order structures of all the genome-wide predicted peptides of *F. tularensis* and *B. mallei*. I have the experience of predicting the 3-D structure of rat arsenic (+3)-methyltransferase (Toxicol. Appl. Pharmacol. 204, 164-169, 2005).

2) Building mathematical models to simulate the complex dynamics, biofilm and pathogenesis of pathogen-host interactions. I recently built AZT metabolism models in different cell types (*Biochem.J.* Accepted and in press, 2005).

3) Designing and implementing a knowledge database of vaccines against infectious diseases and diagnostic tests for virulent pathogens. I have eight years experience in developing various bioinformatics and genomics databases.

4) Based on AZT modeling expertise (*Biochem.J.* In press, 2005), continuing to develop computational models for pharmacogenomics, pharmacokinetics, and pharmacodynamics of antiviral, antibacterial, and counter-cancer drugs such as anti-HIV regimens, antibiotics, xenobiotics and chemotherapeutic agents.

5) Molecular microbial evolution of pathogenesis genes in different subspecies of *F. tularensis* and *B. mallei*, using approaches such as synonymous substitution rates (K_S) and non-synonymous substitution rates (K_A). Actually, this will be extending my current work.

6) Molecular evolution of toxicology genes in eukaryotic species, especially, human and chimpanzee. Toxicology genes are ideal targets to study environment-host-pathogen triangle interactions. Marine species are completely and directly exposed to various toxins in the ocean. It is of great interest to carry out comparative genomics study among human, great ape, mouse, rat, and fish species by calculating and comparing K_S and K_A. My recent work of comparative and structural genomics on arsenic (+3)-methyltransferase between human and chimpanzee (Toxicol. Appl. Pharmacol. 204, 164-169, 2005) is such a pilot example.

7) Molecular mechanism for various genome sequence divergence rates. Genetic variations along genome are not evenly distributed. That is, there exist mutational hot spots in genomes. For example, exons are more conserved than introns in eukaryotic species. I have spent more than five years to think about it and have recently proposed a hypothetical mechanism to interpret the regional mutation differences of genome sequences. I will continue the work and prove my hypothesis.

8) Modifying the computational model of mitochondrial DNA replication (*Biochem.J.* In press, 2005) to simulate plant chloroplast DNA replication and senescence. This will be a unique and unprecedented project.

Teaching Interests

Jiaxin Li

While a Ph.D. candidate, I was a Teaching Assistant from 1994-1997. As a TA, I gave numerous lectures in both General Biochemistry and question-answering classes. While working for my Ph.D. thesis and later holding advanced appointments in other institutions and industrial companies, I supervised more than 30 high school summer students, rotation Ph.D. students, technicians, and professionals. As an assistant professor, I gave lectures of genomics and bioinformatics at the University of Maine. During recent years, I have given tens of invited presentations. If I were offered the faculty position in your institution, I would be willing and able to offer one or more of the following courses:

1) Bioinformatics and Genomics
2) Computational Modeling and Simulation of Complex Dynamics of Pathogenesis
3) Mathematical Modeling and Simulation of Pharmacogenomics, Pharmacokinetics, and Pharmacodynamics
4) Computer languages (C/C++, PERL, JAVA), operating systems (Unix, Linux), modeling tools (MatLab, Mathematica), database systems (MySQL, Oracle, Access)
5) General Microbiology
6) Microbial Genetics
7) Microbial Physiology
8) Microbial Evolution
9) Pathology of Emerging and Reemerging Infectious Diseases
10) General / Microbial Biochemistry
11) Medical Microbiology
12) Environmental Microbiology
13) Toxicology and Pharmacology
14) Prokaryotic Molecular Biology
15) Eukaryotic Molecular Biology
16) Protein Structure and Function and the Relevant Bioinformatics Tools