

Chunlin Wang

CONTACT INFORMATION

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RESEARCH INTERESTS

Metagenomics, sequence analysis on next-generation sequencing platform, comparative genomics, graph theory for protein interaction network and gene regulatory network, molecular evolution, machine-learning methods for modeling functional motifs, parallel computing.

EDUCATION

University of Alabama at Birmingham, Birmingham, Alabama USA
Department of Microbiology

Ph.D. August 2005

- Dissertation Topic: "Molecular Evolution and Genomic Analysis of Poxviruses"
- Advisor: Dr. Elliot J. Lefkowitz

Shanghai Institute of Biochemistry, Academia Sinica, Shanghai, P.R. China

Ph.D. Candidate, Molecular Biology, September 1996 (drop out on May 2000)

- Dissertation Topic: "Exploration of Hepatitis C Virus E2 Protein as Vaccine Candidate"
- Advisor: Professor Guangdi Li

Nanjing University, Nanjing, P.R. China

Department for Intensive Instruction of Fundamental Sciences

B.S., Biochemistry, July 1996

ACADEMIC EXPERIENCE

Stanford University, Stanford, California USA

Research Associate

October, 2007 - Present

Metagenomics; computational and statistical methods on analyzing next-generation sequencing data; computational analysis viral metagenomic data; genome sequencing microbes for biofuel production, molecular evolution on viruses.

Stanford University, Stanford, California USA

Postdoctoral Researcher

October, 2006 - October, 2007

Computational and statistical methods on analyzing pyrosequencing data; computational methods detecting similarity between distantly related sequences; molecular evolution on viruses.

Lawrence Berkeley National Laboratory, Berkeley, California USA

Computational Scientist Postdoctoral Research Fellow

November, 2005 - October, 2006

Graph theory (transitivity closure and clique finding) modeling protein interaction complex; machine-learning techniques for predicting functional motifs in prokaryotic and eukaryotic genome sequences, including small function RNA genes, regulatory motifs for gene expression and splice site.

University of Alabama at Birmingham, Birmingham, Alabama USA

Postdoctoral Research Fellow

August 2005 - November 2005

Research in molecular evolution and covariant sites in RNA virus genome sequences

University of Alabama at Birmingham, Birmingham, Alabama USA

Graduate Student

August 2000 - August 2005

PUBLICATIONS

Margeridon-Thermet S, Shulman NS, Ahmed A, Shahriar R, Liu T, **Wang C**, Holmes SP, Babrzadeh F, Gharizadeh B, Hanczaruk B, Simen BB, Egholm M, Shafer RW. Ultra-deep pyrosequencing of hepatitis B virus quasispecies from nucleoside and nucleotide reverse-transcriptase inhibitor (NRTI)-treated patients and NRTI-naive patients. *J Infect Dis.* 2009 May 1;199(9):1275-85.

Victoria JG, Kapoor A, Li L, Blinkova O, Slikas B, **Wang C**, Naeem A, Zaidi S, Delwart E. Metagenomic analyses of viruses in stool samples from children with acute flaccid paralysis. *J Virol.* 2009 May;83(9):4642-51.

Kapoor A, Victoria J, Simmonds P, Slikas E, Chieochansin T, Naeem A, Shaikat S, Sharif S, Alam MM, Angez M, **Wang C**, Shafer RW, Zaidi S, Delwart E: A highly prevalent and genetically diversified Picornaviridae genus in South Asian children. *Proc Natl Acad Sci USA.* 2008 Nov 25. [Epub ahead of print]

Mitsuya Y, Varghese V, **Wang C**, Liu TF, Holmes SP, Jayakumar R, Gharizadeh B, Ronaghi M, Klein D, Fessel WJ, Shafer RW: Minority HIV-1 Variants in Antiretroviral Naive Persons with Reverse Transcriptase Codon 215 Revertant Mutations. *Journal of Virology* 2008 Aug 20. [Epub ahead of print]

Rubins KH, Hensley LE, Bell GW, **Wang C**, Lefkowitz EJ, Brown PO, Relman DA: Comparative analysis of viral gene expression programs during poxvirus infection: a transcriptional map of the vaccinia and monkeypox genomes. *PLoS ONE.* 2008 Jul 9;3(7):e2628.

Eriksson N, Pachter L, Mitsuya Y, Rhee SY, **Wang C**, Gharizadeh B, Ronaghi M, Shafer RW, Beerenwinkel N: Viral population estimation using pyrosequencing. *PLoS Comput Biol.* 2008 Apr 25;4(4):e1000074.

Kapoor A, Victoria J, Simmonds P, **Wang C**, Shafer RW, Nims R, Nielsen O, Delwart E: A highly divergent picornavirus in a marine mammal. *Journal of Virology* 2008, 82(1): 311-320.

Wang C, Ding C, Yang Q, Holbrook SR: Consistent dissection of the protein interaction network by combining global and local metrics. *Genome Biology* 2007 8(12): R271.

Wang C, Mitsuya Y, Gharizadeh B, Ronaghi M, Shafer RW. Characterization of mutation spectra with ultra-deep pyrosequencing: application to HIV-1 drug resistance. *Genome Research* 2007, 17(8):1195-1201.

Wang C, Meraz RF, He X, Ding CHQ, and Holbrook SR. PSol: a positive sample only learning algorithm for finding non-coding RNA genes. *Bioinformatics* 2006, 22(21):2590-6.

Lefkowitz EJ, **Wang C** and Upton C: Poxviruses: past, present and future. *Virus Research* 2006, 117(1):105-118.

Wang C and Lefkowitz EJ: Refinement of genomic sequence multiple alignments using a genetic algorithm. *BMC Bioinformatics.* 2005, 6:200.

Chen N, Li G, Liszewski MK, Atkinson JP, Jahrling PB, Feng Z, Schriewer J, Buck C, **Wang C**, Lefkowitz EJ, Esposito JJ, Harms T, Damon IK, Roper RL, Upton C and Buller RM: Virulence differences between monkeypox virus isolates from West Africa and the Congo basin. *Virology.* 2005, 340(1):46-63.

Wang C and Lefkowitz EJ: SS-Wrapper: A package of wrapper applications for similarity searches

on Linux clusters. BMC Bioinformatics 2004, 5(1):171.

Zhu LX, Liu J, Xie YH, Kong YY, Ye Y, **Wang CL**, Li GD, and Wang Y: Expression of hepatitis C virus envelope protein 2 induces apoptosis in cultured mammalian cells. World Journal of Gastroenterology 2004, 10(20):2972-2978.

Harvey SC, **Wang C**, Teletchea S, Lavery R: Motifs in nucleic acids: molecular mechanics restraints for base pairing and base stacking. Journal of Computational Chemistry 2003, 24(1):1-9.

Chen N, Danila MI, Feng Z, Buller RM, **Wang C**, Han X, Lefkowitz EJ, Upton C: The genomic sequence of ectromelia virus, the causative agent of mousepox. Virology 2003, 317(1):165-186.

Zhu J, **Wang C**, Zhu LX, Kong YY, Wang Y, Li GD: DNA immunization with recombinant HCV E2 expression plasmids. Acta Biochimica et Biophysica Sinica 2002, 34(4): 445-451.

Wang C, Zhu LX, Liu J, Zhang ZC, Wang Y, Li GD: Expression and characterization of hepatitis C Virus E2 glycoprotein fused to hepatitis B virus preS1(21-47) fragment in CHO cells. Acta Biochimica et Biophysica Sinica 2002,34(4): 400-404

Yang L, **Wang C**, Wang Y, Li GD: Expression and characterization of hepatitis C virus core protein fused to hepatitis B virus core protein. Science in China (series C) 1999, 42(3):286-292.

PATENT
APPLICATION

Wang C, Gharizadeh B and Ronaghi M: Enrichment of target sequences with conserved sequence motif probes and probe design algorithm (Stanford Docket Number = S08-086)

Wang C, Gharizadeh B, Babrzadeh F and Ronaghi M: Targeting sequences sequencing (Stanford Docket Number = S08-102)

PAPERS IN
PREPARATION

Wang C, Babrzadeh F, Jalili R, Stambuk B, Shafer R, Ronaghi M, Davis RW, Gharizadeh B: Diploid genome sequencing and comparative analysis of a fuel-ethanol fermentative saccharomyces cerevisiae strain CAT-1

Wang C, Ding CHQ, and Holbrook SR. Dissecting Protein Interaction Networks With A Robust Algorithm.

Wang C, Sanders M. C., Yang Q., Schroeder H., Wang E., Babrzadeh F., Gharizadeh B., Davis R., Myers R., Hudson J., Han J. High throughput sequencing reveals a complex pattern of dynamic interrelationships among human T cell subsets (Submitted to Nature).

Gottlieb B., Alvarado C., **Wang C**, Gharizadeh B., Babrazadeh F., Basik M., Beitel L., Trifiro M. Quantifying Human Genetic Variation: Use of Ultra-Deep Pyrosequencing to Measure Genetic Heterogeneity (submitted to Science).

CONFERENCE
PRESENTATIONS

Wang C, Sanders C., Yang Q., Wang E, Gharizadeh B., Han J. Immunorepertoire Analysis by Multiplex PCR Amplification and High-Throughput Sequencing. The 96th Annual Meeting of The American Association of Immunologists, Seattle, Washington, May 8-12 2009.

Wang C and Lefkowitz EJ., Reductive evolution as a controlling event in poxvirus speciation and biology. The XIIIth International Congress of Virology, San Francisco, July 23-28 2005.

Wang C and Lefkowitz EJ., Poxvirus gene prediction with the poxvirus genome annotation system (PGAS). The XIIIth International Congress of Virology, San Francisco, July 23-28 2005.

Wang C and Lefkowitz EJ., Detection of Vaccinia Virus Promoters Using Interpolated Context Models. The 13th Annual International conference on Intelligent Systems for Molecular Biology (ISMB 2005), Detroit, Michigan, June 25-29, 2005

Wang C and Lefkowitz EJ., Refinement of Genomic Sequence Multiple Alignments using a Genetic Algorithm. The ASM Conference on Functional Genomics and Bioinformatics Approaches to Infectious Disease Research, Portland, Oregon, October 6-9, 2004.

Wang C and Lefkowitz EJ., Bioinformatic Analysis of Poxvirus Promoters. The XVth International Poxvirus and Iridovirus Conference, Keble College, Oxford, England September 3-8, 2004.

Wang C and Lefkowitz EJ., Bioinformatic Analysis of Poxvirus Promoters: Biological Differences between Viruses May Be Influenced by Alternative Gene Expression Profiles. The ASM Biodefense meeting, Baltimore, Maryland, March 7-10, 2004.

PROFESSIONAL
EXPERIENCE

Consultant on poxvirus genome annotation **May, 2005 - November, 2005**
Carried out consultant project on annotating two vaccine strains of poxvirus genomes for Therion Biologics Corporation. <http://www.therionbio.com/>

Consultant on ultra-deep sequencing detect drug-resistant **June, 2008 - August, 2008**
Analyzed 454 sequence data for HCV, HIV drug-resistant mutations for Monogram Biosciences, Inc. <http://www.monogrambio.com/>

COMPUTER SKILLS

- Languages: C/C++, Java, Perl, Python, Matlab, Unix shell scripts, some experience with statistical package like R, extensive use of MPI library, Java JFC/Swing library.
- Applications: Extensive experience with many Bioinformatics tools (BLAST, HMMer, PAUP, Clustalw, Vienna RNA package, phylip phylogenies package, GCG package), L^AT_EX, database, Microsoft office package, Adobe graphics tools, gnuplot.
- Algorithms: Experience programming hidden markov model, interpolated context model, support vector machines, genetic algorithms. Familiar with most artificial intelligence algorithms.
- Operating Systems: Unix/Linux, Windows, MAC OS X, Linux cluster

Accomplishments

- Developed a generic wrapper application optimizing most sequence database searching applications using Linux clusters (C/C++, parallel programming).
- Developed a genetic algorithm in parallel mode to improve the quality of multiple alignments of genome sequences (PERL, BioPerl, parallel programming).
- Developed genome sequence comparison viewer displaying comparison information of multiple genomes of varying phylogenetic distances, in various scales (JAVA GUI application).
- Developed interpolated context models (ICMs) to predict functional DNA motifs (Implemented in PERL).
- Developed an accurate, integrated poxvirus-specific gene prediction and genome comparison platform (including a JAVA GUI application).
- Unveiled the reductive process behind poxvirus evolution using comparative genomics approach.
- Developed the PSoL application to predict functional sequence motifs (Implemented in Python)
- Developed the BCD algorithm to decompose protein interaction network (Implemented in Python)
- Developed the Milu algorithm to decompose protein interaction network (Implemented in Python)
- Developed a set of computational and statistical tools to analyze pyrosequencing data.
- Developed a novel statistical platform combining weak BLAST hits to predict new viral sequences.
- Familiar with HPC (High Performance Computing) with hands-on experiences on software development, hardware installation.