Yinghua Wu

Senior Research Investigator

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Summary

- I have made fundamental contributions in quantum dynamics research. I have strong mathematical abilities and keen intuition.
- I have developed statistical analysis methods and pipelines for various cancer treatment studies and gene therapy trials. I have strong numerical and project management skills.
- My next career objective is to develop predicting algorithms through deep learning and build self updating platforms to constantly improve them.

Experience

Present Lab.

Oct 2014 - Senior Research Investigator, University of Pennsylvania, Dept. of Microbiology, Bushman

- o Implemented N-mixture model to estimate number of integrated cells in gene therapy cancer treatments.
- Developed efficient clustering algorithm to classify vector integrated cells.
- Developed highly efficient analysis pipeline based on next generation sequencing for gene therapy trials including Was-Lenti, beta-Thal, SCID1, SCID2, and most recently, CART19 trials.
- Developed analysis pipeline for Dam-ID protocol for HIV genome integration.

Jun 2011 - Sep Postdoctoral Research Fellow, University of Pennsylvania, Dept. of Biostatistics, Hongzhe 2014 Lee's Lab.

- Developed an algorithm to evaluate parent of origin effect based on maximum likelihood ratio test and haplotype frequencies.
- Developed robust segment identification method based on negative binomial transformation for copy number variation detection.
- Developed a copy number variation detection algorithm based on CIGAR string, edit distance, and abnormal pair length.
- Developed permutation method to control batch effect for RNAseq gene expression studies.
- Performed genome-wide association studies for eye diseases and identified rare coding SNPs that might be causal factors for long/short sightedness.

Aug 2010 - Programmer analyst, Collaborative Center for Statistics in Science, New Haven, CT.

- May 2011 Developed a coherent sampling algorithm for genotype/phenotype simulations that retains linkage disequilibrium structures for all variants including rare ones.
 - Developed imputation method for rare variants based on associations for whole genome studies.

May 2007 - Postdoctoral Research Associate, Georgia Institute of Technology, Dept. of Chemistry, Dec 2008 Bredas Lab.

- Derived a closed form expression for the auto-correlation function for large organic molecules under Duschinsky rotation effect.
- o Derived a closed form expression for the photo emission spectrum for large organic LED molecules based on Feynman path integral theory.

Jun 2004 - Postdoctoral Research Associate, Tulane University, Dept. of Chemistry, Herman Lab.

- May 2007 Developed and theoretically proved the time-dependent semi-classical two-state surface hopping method, which is accurate to the first order of the Planck constant.
 - Proved mathematical lemma that the stationary phase approximation to the Feynman path integral is accurate to the first order of the Planck constant or the small number.

Education

1999 – 2004 PHD, Yale University, Theoretical Physical Chemistry.

- Developed a two-state quantum dynamical propagator for multi-dimensional systems.
- Developed the matching pursuit split operator Fourier transform method for multi-dimensional quantum dynamical wave function evolution.

1993 – 1998 BS, University of Science and Technology of China, Chemistry.

Languages

English Professional

Chinese Native

Skill sets

Computer Comprehensive: C, C++, Fortran, PERL, R, SQL

Functional: Python, PHP

Bioinformatics Full stack

Biostatistics Advanced

Math Advanced

Unix/Linux System administration

Miscellaneous Windows, Office, HPC, Mathematica