



Yinghua Wu

Senior Research Investigator

3610 Hamilton Walk
Philadelphia, PA 19104
☎ (610) 572-2436
✉ yinghua@upenn.edu
 [wuyinghua](#)
 [yhwu](#)

Summary

- I have made fundamental contributions in quantum dynamics research. I have strong mathematical abilities and keen intuition.
- I have developed statistical analysis methods for cancer research and bioinformatics pipeline for CART19 trial. I have strong coding and project management skills.
- My next career objective is to develop predictive algorithms through deep learning and build self updating platforms to constantly improve them.

Skill sets

| | |
|----------------|---|
| Computer | Comprehensive: R, C++, C, SQL, MPI, pThread, PERL, Fortran Functional: Python, PHP |
| Bioinformatics | Full stack |
| Biostatistics | Advanced |
| Math | Advanced |
| Linux/HPC | System administration |
| Miscellaneous | Windows, Office, Mathematica, Bioconductor |

Education

- 1999 – 2004 **PHD**, *Yale University*, Theoretical Physical Chemistry, Adviser: Victor S. Batista.
- 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.

Experience

- Oct 2014 – Present **Senior Research Investigator**, *University of Pennsylvania*, Dept. of Microbiology, Bushman Lab.
- Implemented N-mixture model to estimate number of integrated cells in gene therapy cancer treatments.
 - Developed an efficient clustering algorithm to classify vector integrated cells.
 - Developed a highly efficient analysis pipeline based on next generation sequencing for the CART19 gene therapy trial.

- Jun 2011 – Sep 2014 **Postdoctoral Research Fellow**, *University of Pennsylvania*, Dept. of Biostatistics, Hongzhe 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 a 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 – May 2011 **Programmer analyst**, *Collaborative Center for Statistics in Science*, New Haven, CT.
- Developed a coherent sampling algorithm for genotype/phenotype simulations that retains linkage disequilibrium structures for all variants including rare ones.
 - Developed an imputation method for rare variants based on associations for whole genome studies.
- May 2007 – Dec 2008 **Postdoctoral Research Associate**, *Georgia Institute of Technology*, Dept. of Chemistry, Bredas Lab.
- Derived a closed form expression for the auto-correlation function for large organic molecules under Duschinsky rotation effect.
 - Derived a closed form expression for the photo emission spectrum for large organic LED molecules based on Feynman path integral theory.
- Jun 2004 – May 2007 **Postdoctoral Research Associate**, *Tulane University*, Dept. of Chemistry, Adviser: Michael F. Herman.
- 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.

Languages

English Professional
Chinese Native