Han Fang

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RESEARCH INTERESTS

Computational Genomics, Statistical Learning, Algorithm Development, Human Genetics

EDUCATION

Stony Brook University (SBU) — **Stony Brook, NY**
Ph.D in Applied Mathematics & Statistics (AMS) — *2014–present*
M.S. in Applied Mathematics & Statistics — *2011–2013*

Sun Yat-sen University (SYSU) — **Guangzhou, China**
B.S. in Optical Informatics — *2007–2011*

SKILLS

Proficient: Python, C++, R, Shell

Familiar: SQL, LaTeX, SAS, HTML, UNIX/LINUX, Git/SVN, SGE/HPC

Language: English, Mandarin, Cantonese, Teochew

EXPERIENCE

Cold Spring Harbor Laboratory (CSHL) — **Cold Spring Harbor, NY**
PhD student - Research Assistant, Simons Center for Quantitative Biology — *2014–Present*

- Supervisors: Dr. Micheal C. Schatz, Dr. Gholson J. Lyon

Cold Spring Harbor Laboratory (CSHL) — **Cold Spring Harbor, NY**
Computational Science Developer, Stanley Institute for Cognitive Genomics — *2013–2014*

- Supervisor: Dr. Gholson J. Lyon

Stony Brook University — **Stony Brook, NY**
Teaching Assistant, Department of AMS — *Fall 2012*

- AMS 315 - Data Analysis, upper-level course for applied math undergraduate

AWARDS

Travel Awards:

- Research Access Project Award - Stony Brook University 2012
- Graduate Travel Grant - Stony Brook University 2012

Student Scholarship:

- Scholarship - Summer Institute in Statistics for Big Data at University of Washington 2015
- Tuition Scholarship - Stony Brook University 2014
- Outstanding Scholarship - Sun Yat-sen University 2010

PUBLICATIONS

Peer-reviwed Journal Publications:

- **Fang H**, Wu Y, Narzisi G, O'Rawe JA, Jimenez Barron LT, Rosenbaum J, Ronemus M, Iossifov I, Schatz MC*, Lyon GJ*, "Reducing INDEL calling errors in whole genome and exome sequencing data.", *Genome Medicine* (2014) doi:10.1186/s13073-014-0089-z
- Narzisi G*, O'Rawe JA, Iossifov I, **Fang H**, Lee Y, Wang Z, Wu Y, Lyon GJ, Wigler M, Schatz MC, "Accurate detection of de novo and transmitted INDELs within exome-capture data using micro-assembly.", *Nature Methods* (2014) doi:10.1038/nmeth.3069

- O'Rawe JA, **Fang H**, Rynearson S, Robison R, Kiruluta ES, Higgins G, Eilbeck K, Reese MG, Lyon GJ*, "Integrating precision medicine in the study and clinical treatment of a severely mentally ill person.", *PeerJ* (2014) doi: 10.7717/peerj.177. 2013

Manuscripts in Preparation:

- **Fang H**, Grabowska EA, Arora K, Vacic V, Zody M, Iossifov I, O'Rawe JA, Lyon GJ, Wigler M, Schatz MC, Narzisi G, "De novo and somatic indel variant analysis of whole genome and exome capture sequencing experiments with Scalpel", *In preparation* (2015)
- **Fang H**, Wu, Y, Jimenez Barron LT, O'Rawe, JA, Highman, G, Mittleman, D, Lyon, GJ*, "Challenges and strategies for advancing precision medicine by integrating whole genome sequencing and human phenotype ontology". *Under review* (2015)
- Jimenez Barron LT, O'Rawe, JA, Wu Y, Ivan I, Yoon M, **Fang H**, Wu, Y, Lyon, GJ*, "Genome Wide Variant Analysis of Simplex Autism Families with an Integrative Clinical-Bioinformatics Pipeline". *Under review* (2015)
- O'Rawe JA, Wu Y, Rope A, Jimenez Barron LT, Swensen J, **Fang H**, Mittelmann D, Highnam G, Robison R, Wang K, Lyon GJ*, "Comprehensive whole genome sequencing of a three generation pedigree: Genetic components of a new syndrome with severe developmental delay and dysmorphic features". (2015)

CONFERENCE ABSTRACTS

Platform Talk Presentations:

- *Reducing INDEL calling errors in whole genome and exome sequencing data.*
  CSHL Biological Data Science Meeting, Cold Spring Harbor, NY 2014

Posters Presentations:

- *Reducing INDEL calling errors in whole genome and exome sequencing data.*
  CSHL Personal Genomes Meeting, Cold Spring Harbor, NY 2014
- *Whole genome analysis of a pedigree with Prader-Willi syndrome, hereditary hemochromatosis, and dysautonomia.*
  CSHL Personal Genomes Meeting, Cold Spring Harbor, NY 2014
- *Reducing INDEL calling errors in whole genome and exome sequencing data.*
  American Society of Human Genetics Annual Meeting, San Diego, CA 2014
- *Complexities of INDEL detection based on micro-assembly methods; WGS and WES comparisons.*
  CSHL Biology of Genome Meeting, Cold Spring Harbor, NY 2014
- *Whole genome sequencing analysis of a family with familial dysautonomia and neuropsychiatric symptoms.*
  CSHL Personal Genomes Meeting, Cold Spring Harbor, NY 2013

SEMINARS

Cold Spring Harbor Laboratory:

- *Reducing INDEL calling errors in whole genome and exome sequencing data.*
  CSHL Quantitative Biology Seminar, Cold Spring Harbor, NY 2014
- *Complexities of INDEL detection based on micro-assembly methods; WGS & WES comparisons.*
  CSHL Genome Center Seminar, Cold Spring Harbor, NY 2014