

# Han Fang

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## EDUCATION

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### Stony Brook University (SBU)

*Ph.D in Applied Mathematics and Statistics (AMS)*

*M.S. in Applied Mathematics and Statistics*

**Stony Brook, NY**

2014 - 2017

2011 - 2013

### Sun Yat-sen University (SYSU)

*B.S. in Optical Informatics*

**Guangzhou, China**

2007 - 2011

## EXPERIENCE

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### Facebook

*Data Scientist*

**Menlo Park, CA**

July 2017 - Present

- Developed machine learning models on geo-spatial data to solve connectivity problems at a global scale

### Facebook

*Data Scientist Intern*

**Menlo Park, CA**

Jun 2016 - Aug 2016

- Built machine learning models to predict user engagement with extremely high precision recall on billions of users and find effective strategies for product & infrastructure problems using big data techniques.
- Applied statistical modeling methods and developed automated pipelines in production to analyze large-scale web/mobile data; identified patterns and provided actionable recommendations.
- Developed optimization models on global geo-spatial data and solved problems which benefit 30 countries.

### Cold Spring Harbor Laboratory (CSHL)

*Research Assistant*

**Cold Spring Harbor, NY**

Aug 2014 - Jun 2017

- Machine learning methods for large-scale genomics data
  - Developed Scikit-ribo, a statistical framework for analyzing large-scale genomics data in Python
    - Achieved 98% classification accuracy on millions of sequences using random forest and recursive feature selection.
    - Implemented a module using negative binomial mixture modeling to identify peaks from over-dispersed data.
    - Built a generalized linear model (GLM) with ridge penalty to robustly estimate thousands of parameters.
  - Maintaining glmnet for python ([github.com/bbalasub1/glmnet\\_python](https://github.com/bbalasub1/glmnet_python))
    - Efficiently fits lasso, ridge, and elastic-net regularized GLM via penalized maximum likelihood for linear, logistic, multinomial, and Poisson regression
    - Supports outcome prediction, cross-validation, sparse scipy matrix, and range constraints on coefficients
  - Led a group in a data science hackathon and built classifiers to predict cancer cell types
    - Performed dimension reduction with sparse PCA, identified samples groups using hierarchical clustering.
    - Built classifiers to predict cancer types at 89% accuracy using Logistic regression with Elastic net regularization.
  - Led statistical analyses of four major studies to identify candidates of interest from massive omics data.
- Graphical algorithms for analyzing genomics data
  - Developed Topsorter for graphical assessment of structural variants ([github.com/hanfang/Topsorter](https://github.com/hanfang/Topsorter))
    - Traverses & finds the longest path with topological sorting of a weighted directed acyclic graph (DAG).
  - Developed Forceps, a program for comparing & choosing optimal sequences ([github.com/hanfang/forceps](https://github.com/hanfang/forceps))

### Cold Spring Harbor Laboratory

*Computational Science Developer*

**Cold Spring Harbor, NY**

June 2013 - June 2014

- Computational methods for next-generation sequencing data analysis
  - Developed Scalpel, a C++ software to detect genomic mutations ([scalpel.sourceforge.net](http://scalpel.sourceforge.net))
    - Built modules, reviewed and optimized codes for de Bruijn graph assembly of millions sequences.
    - Deployed a Google cloud pipeline for analyzing and visualizing results ([github.com/hanfang/scalpel-protocol](https://github.com/hanfang/scalpel-protocol)).

## SKILLS

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**Proficient:** Python, SQL, R, C/C++, UNIX, Hive, Shell. **Familiar:** HPC, Hadoop, Spark, Java

## Awards and fellowship

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- 2017 President's Award to Distinguished Doctoral Students @ SBU (5 out of 449)
- 2017 The Woo-Jong Kim Dissertation Award @ AMS (1 out of 34)
- 2017 Excellence in Research Award @ AMS (5 out of 34)
- 2016 Research Access Project @ SBU
- 2016 Department Travel Grant @ AMS
- 2015 Reviewers' Choice @ The American Society of Human Genetics (Top 10%)
- 2015 Summer Institute in Statistics for Big Data Scholarship @ University of Washington
- 2014 Research Assistant Fellowship @ CSHL
- 2013 Research Access Project @ SBU
- 2013 Department Travel Grant @ AMS
- 2010 Outstanding Student Scholarship @ SYSU (Top 10%)

## PUBLICATIONS

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### Under review:

- Sedlazeck, Rescheneder, Smolka, **Fang**, Nattestad, Haeseler, Schatz, "[Accurate detection of complex structural variations using single molecule sequencing](#)", *Under review* (2017)
- Nattestad, Goodwin, Ng, Baslan, Sedlazeck, Rescheneder, Garvin, **Fang**, Gurtowski, Hutton, Tseng, Chin, Beck, Sundaravadanam, Kramer, Antoniou, McPherson, Hicks, McCombie, Schatz, "[Complex rearrangements and oncogene amplifications revealed by long-read DNA and RNA sequencing of a breast cancer cell line](#)", *Under review* (2017)
- Yang, Chen, Lima, **Fang**, Jimenez, Li, Lyon, He, Wang, "PennCNV-Hadoop: Accurate Detection of Copy Number Variation from Whole Genome Sequencing Data", *Under review* (2017)

### Peer-reviewed:

- **Fang**, Huang, Radhakrishnan, Siepel, Lyon, Schatz, "[Scikit-ribo Enables Accurate Estimation and Robust Modeling of Translation Dynamics at Codon Resolution](#)", *Cell Systems* (2017)
- Vurture, Sedlazeck, Nattestad, Underwood, **Fang**, Gurtowski, Schatz, "[GenomeScope: Fast reference-free genome profiling from short reads](#)", *Bioinformatics* (2017)
- **Fang**, Wu, Yoon, Jiménez-Barrón, Mittelman, Robison, Wang, Lyon, "[Whole genome sequencing of one complex pedigree illustrates challenges with genomic medicine](#)", *BMC Medical Genomics* (2017)
- **Fang**, Bergmann, Arora, Vacic, Zody, Iossifov, O'Rawe, Wu, Jimenez Barron, Rosenbaum, Ronemus, Lee, Wang, Dikoglu, Jobanputra, Lyon, Wigler, Schatz, Narzisi, "[Indel variant analysis of short-read sequencing data with Scalpel](#)", *Nature Protocols* (2016)
- Doerfel, **Fang**, Crain, Klingener, Weiser, Lyon, "[Proteomic and genomic characterization of a yeast model for Ogden syndrome](#)", *Yeast* (2016)
- O'Rawe, Wu, Doerfel, Rope, Billie Au, Parboosingh, Moon, Kousi, Kosma, Smith, Tzetis, Schuette, Hufnagel, Prada, Martinez, Orellana, Crain, Caro-Llopis, Oltra, Monfort, Jiménez-Barrón, Swensen, Ellingwood, Smith, **Fang**, Ospina, Stegmann, Den Hollander, Mittelman, Highnam, Robison, Yang, Faivre, Roubertie, Rivière, Monaghan, Wang, Davis, Katsanis, Kalscheuer, Wang, Metcalfe, Kleefstra, Innes, Kitsiou-Tzeli, Rosello, Keegan, Lyon, "[TAF1 Variants Are Associated with Dysmorphic Features, Intellectual Disability, and Neurological Manifestations](#)", *American Journal of Human Genetics* (2015)
- Jimenez-Barron, O'Rawe, Wu, Yoon, **Fang**, Iossifov, Lyon, "[Genome Wide Variant Analysis of Simplex Autism Families with an Integrative Clinical-Bioinformatics Pipeline](#)". *Molecular Case Studies* (2015)
- Narzisi, O'Rawe, Iossifov, **Fang**, Lee, Wang, Wu, Lyon, Wigler, Schatz, "[Accurate detection of de novo and transmitted INDELS within exome-capture data using micro-assembly](#)", *Nature Methods* (2014)
- **Fang**, Wu, Narzisi, O'Rawe, Jimenez Barron, Rosenbaum, Ronemus, Iossifov, Schatz, Lyon, "[Reducing INDEL calling errors in whole genome and exome sequencing data](#)", *Genome Medicine* (2014)
- O'Rawe, **Fang**, Rynearson, Robison, Kiruluta, Higgins, Eilbeck, Reese, Lyon, "[Integrating precision medicine in the study and clinical treatment of a severely mentally ill person](#)", *PeerJ* (2014)

### Dissertation:

- **Fang**, "Graphical and machine learning algorithms for large-scale genomics data" (2017)

## CONFERENCE

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### Platform Talk Presentations:

- *Facebook Infrastructure Data Science*  
The Data Science Conference, Chigaco, IL 2018
- *Scikit-ribo reveals precise codon-level translational control by dissecting ribosome pausing and codon elongation.*  
Biological Data Science Meeting, Cold Spring Harbor, NY 2016
- *Scikit-ribo reveals precise codon-level translational control by dissecting ribosome pausing and codon elongation.*  
Advances in Genome Biology and Technology(AGBT) Meeting, Orlando, FL 2016
- *Scikit-ribo: Accurate A-site prediction and robust modeling of translation control from Riboseq & RNAseq data.*  
Genome Informatics Meeting, Cold Spring Harbor, NY 2015
- *Reducing INDEL calling errors in whole genome and exome sequencing data.*  
Biological Data Science Meeting, Cold Spring Harbor, NY 2014

### First-author Poster Presentations:

- *Scikit-ribo: Accurate estimation and robust modelling of translation dynamics at codon resolution*  
Biology of Genome Meeting, Cold Spring Harbor, NY 2017
- *Scikit-ribo reveals precise codon-level translational control by dissecting ribosome pausing and codon elongation.*  
Advances in Genome Biology and Technology(AGBT) Meeting, Hollywood, FL 2017
- *Scikit-ribo reveals precise codon-level translational control by dissecting ribosome pausing and codon elongation.*  
Genome Informatics Meeting, Cambridge, UK 2016
- *Scikit-ribo reveals precise codon-level translational control by dissecting ribosome pausing and codon elongation.*  
Translational control Meeting, Cold Spring Harbor, NY 2016
- *Scikit-ribo: Accurate A-site prediction and robust modeling of translation control from Riboseq & RNAseq data.*  
Probabilistic Modeling in Genomics Meeting, Cold Spring Harbor, NY 2015
- *Indel variant analysis of short-read sequencing data with Scalpel. (Reviewers' Choice)*  
American Society of Human Genetics Annual Meeting, Baltimore, MD 2015
- *Reducing INDEL calling errors in whole genome and exome sequencing data.*  
Personal Genomes Meeting, Cold Spring Harbor, NY 2014
- *Whole genome analysis of a pedigree with Prader-Willi syndrome, hereditary hemochromatosis, and dysautonomia.*  
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.*  
Biology of Genome Meeting, Cold Spring Harbor, NY 2014
- *Whole genome sequencing analysis of a family with familial dysautonomia and neuropsychiatric symptoms.*  
Personal Genomes Meeting, Cold Spring Harbor, NY 2013
- *The statistical properties of longitudinal phenotypes determined by trajectory models in linkage analysis*  
Genetics Analysis Workshop 18, Stevenson, WA 2012

### Seminars:

- *Methods for analyzing Riboseq and 10X Genomics data*  
Quantitative Biology Seminar, Cold Spring Harbor, NY 2017
- *Scikit-ribo reveals precise codon-level translational control by dissecting ribosome pausing and codon elongation.*  
Quantitative Biology Seminar, Cold Spring Harbor, NY 2016
- *Reducing INDEL calling errors in whole genome and exome sequencing data.*  
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

## Journal Reviewing

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Nucleic Acids Research, RECOMB, WABI, MCBIOS