

Miten Jain

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RESEARCH INTERESTS:

Computer Science: machine learning, neural networks and deep learning, big data, genomics, computational biology, mobile apps.

Life Sciences: nanopore technology, DNA, RNA, and protein sequencing, long reads, *de novo* assembly, DNA modifications, epigenetics, solving complex biological questions.

EDUCATION:

Ph.D., Bioinformatics and Biomolecular Engineering, 2017, UC Santa Cruz	GPA: 3.91/4.0
M.S. Bioinformatics, 2013, University of California, Santa Cruz	GPA: 3.91/4.0
M.S. Biotechnology, 2008, University at Buffalo, New York	GPA: 3.77/4.0
B.E. Biotechnology Engineering, 2006, University of Rajasthan, India	GPA: 81% Honors

RESEARCH/WORK EXPERIENCE:

- **Assistant Research Scientist, UC Santa Cruz, CA [December 2018 – present]**
Current projects include: 1) developing tools for analyzing genomics data; 2) developing wet-lab methods for long read sequencing of DNA and RNA; 3) developing wet-lab methods and software for resolving homopolymers and base modifications; 4) developing the nanopore MinION and PromethION sequencing platforms; 5) developing methods for sequencing and analysis of different classes of RNA (mRNA, rRNA, tRNA, non-coding RNA); 6) interfacing with a host of collaborations within UCSC and outside, including international consortiums and NASA, on nanopore sequencing applications.
- **Postdoctoral Scholar, Nanopore Group, UC Santa Cruz, CA [August 2017 – December 2018]**
Projects include: 1) developing analysis tools for genomics data; 2) developing methods for long read DNA sequencing; 3) developing methods and software for resolving base modifications; 4) developing the nanopore MinION and PromethION sequencing platforms; 5) interfacing with a host of collaborations within UCSC and outside, with international consortiums, and with NASA, on nanopore sequencing applications.
- **PhD Candidate, Nanopore Group, UC Santa Cruz, CA [June 2012 – June 2017]**
Projects include: 1) developing bioinformatics for computational analysis of nanopore data (single-channel and MinION); 2) developing wet-lab methods for the MinION to facilitate long reads and resolve homopolymers and base modifications; 2) direct RNA sequencing; 4) developing machine learning algorithms (HMMs, dynamic time warping, recurrent neural networks) for nanopore data (DNA, RNA, and protein); and 5) analyzing bacterial and human epigenomes.
Previous projects include: classification and pattern analysis of human centromere sequences; developing metagenome assembly pipelines.
- **Research Assistant, Nanopores Inc., Yaphank, NY [Dec. 2009 – July 2011]**
Worked on R&D of biomedical imaging and therapeutic applications of metal nanoparticles.

- **Teaching Assistant; Student Assistant, University at Buffalo, New York**
 - **Dept. of Biotechnical and Clinical Laboratory Sciences [Aug. 2007 – May 2008]**
Taught undergraduate and graduate labs; graded and corrected papers.
 - **Center for Excellence in Data Analysis and Recognition [May – Aug. 2007]**
CEDAR work involved verifying machine read data from United States Postal Service.
 - **Dept. of Physiology and Biophysics [Dec. 2006 – Aug. 2007]**
Prepared and maintained *Drosophila* lines used in research for Huntington disease.
- **Intern, Ranbaxy Research Laboratories Ltd. Gurgaon, India [Feb. – June 2006]**
Performed research and development of novel drug candidates.
- **Intern, Cadila Pharmaceuticals Limited, Ahmedabad, India [Summer 2005]**
Analyzing and writing a summary report on the company's various divisions.
- **Research Intern at Birla Institute of Scientific Research, Jaipur, India [Summer 2004]**
Worked with medicinal *proteases* producing bacteria from soil.

BIOINFORMATICS TECHNICAL SKILLS:

Proficient: **Python, MATLAB, R, Bash, Cython, Mac OSX, Linux, Windows, HTML**
Familiar: **Statistical Package for Social Sciences (SPSS), C, C++, DBMS (Oracle).**

LIFE SCIENCES TECHNICAL SKILLS:

Proficient: DNA sequencing, Molecular and cell biology techniques, handling analytical instruments, microbiology techniques, Laboratory animals' certification program.

PATENTS:

2018

- **Miten Jain, Andrew M. Smith. 2018. Methods of Producing Ribosomal Ribonucleic Acid Complexes (PCT).**

2016

- **Miten Jain, Hugh E. Olsen, Mark Akeson. 2016. Methods for Determining Base Locations in a Polynucleotide (PCT).**

PUBLICATIONS:

- **Total Citations – 1389**
- **Independent citations –**
- **First authored publications – 10/18**
- **Total number of articles in Nature group of journals - 5**

2019

- **Miten Jain**. Bioinformatic Analysis (Book Chapter). Nanopore Sequencing – An Introduction. 2019.

2018

- **Miten Jain***, Rachael E Workman*, Alison Tang*, Paul S Tang*, John R Tyson*, Philip C Zuzarte, Timothy Gilpatrick, Roham Razaghi, Joshua Quick, Norah Sadowski, Nadine Holmes, Jaqueline Goes de Jesus, Karen Jones, Terrance P Snutch, Nicholas James Loman, Benedict Paten, Matthew W Loose, Jared T Simpson, Hugh E. Olsen, Angela N Brooks, Mark Akeson, Winston Timp. Nanopore native RNA sequencing of a human poly(A) transcriptome. *BioRxiv*. 2018.
- Natalie Ring, Jonathan Abrahams, **Miten Jain**, Hugh Olsen, Andrew Preston, Stefan Bagby. Resolving the complex Bordetella pertussis genome using barcoded nanopore sequencing. *Microbial Genomics*. 2018.
- **Miten Jain***, Sergey Koren*, Josh Quick*, Arthur C Rand*, Thomas A Sasani*, John R Tyson*, Andrew D Beggs, Alexander T Dilthey, Ian T Fiddes, Sunir Malla, Hannah Marriott, Karen H Miga, Tom Nieto, Justin O'Grady, Hugh E Olsen, Brent S Pedersen, Arang Rhie, Hollian Richardson, Aaron Quinlan, Terrance P Snutch, Louise Tee, Benedict Paten, Adam M. Phillippy, Jared T Simpson, Nicholas James Loman, Matthew Loose. Nanopore sequencing and assembly of a human genome with ultra-long reads. *Nature Biotechnology*. 2018 (36), 338-345. **Citations – 220**
- **Miten Jain***, Hugh E. Olsen*, Daniel J. Turner, David Stoddart, Kira V. Bulazel, Benedict Paten, David Haussler, Huntington F. Willard, Mark Akeson, and Karen H. Miga. Linear Assembly of a Human Y Centromere using Nanopore Long Reads. *Nature Biotechnology*. 2018 (36), 321-323. **Citations – 20**

2017

- **Miten Jain***, Arthur C. Rand*, Jordan Eizenga*, Audrey Musselman-Brown, Hugh E. Olsen, Mark Akeson, Benedict Paten. Mapping DNA methylation with high-throughput nanopore sequencing. *Nature Methods*. 2017 Apr;14 (4):411-413. **Citations – 83**
- Ashley Byrne, Anna E. Beaudin, Hugh E. Olsen, **Miten Jain**, Charles Cole, Theron Palmer, Rebecca M. DuBois, E. Camilla Forsberg, Mark Akeson & Christopher Vollmers. Nanopore Long-Read RNAseq Reveals Widespread Transcriptional Variation Among the Surface Receptors of Individual B cells. *Nature Communications*. 2017 Jul 19;8:16027. **Citations – 60**
- **Miten Jain***, John R Tyson*, Nigel J O'Neil*, Hugh E Olsen, Philip Hieter, Terrance P Snutch. MinION-based long-read sequencing and assembly extends the *Caenorhabditis elegans* reference genome (2017). *Genome Research*, gr. 221184.117. **Citations – 32**
- **Miten Jain***, John R. Tyson*, Matthew Loose*, Camilla L.C. Ip*, David A. Eccles, Justin O'Grady, Sunir Malla, Richard M. Leggett, Ola Wallerman, Hans J. Jansen, Vadim Zalunin, Ewan Birney*, Bonnie L. Brown*, Terrance P. Snutch*, Hugh E. Olsen*, MinION Analysis and Reference Consortium. MinION Analysis and Reference Consortium: Phase 2 data release and analysis of R9.0 chemistry (2017). *F1000Research*. **Citations – 23**
- Andrew M Smith, **Miten Jain**, Logan Mulroney, Daniel R Garalde, Mark Akeson. Reading canonical and modified nucleotides in 16S ribosomal RNA using nanopore direct RNA sequencing (2017). *bioRxiv* (<http://www.biorxiv.org/content/early/2017/04/29/132274>). **Citations – 10**

2016

- **Miten Jain**, Hugh E. Olsen, Benedict Paten, Mark Akeson (2016). The Oxford Nanopore MinION: delivery of nanopore sequencing to the genomics community. *Genome Biology* 2016, **17**:239. **Citations – 195**

2015

- **Miten Jain**, Ian T. Fiddes, Karen H. Miga, Hugh E. Olsen, Benedict Paten and Mark Akeson. Improved data analysis for the MinION nanopore sequencer. *Nature Methods*, 2015, 12:351–356. **Citations – 355**
- **Miten Jain**^{*}, Camilla L.C. Ip^{*}, Matthew Loose^{*}, John R. Tyson^{*}, Mariateresa de Cesare^{*}, Bonnie L. Brown^{*}, Richard M. Leggett^{*} et al. MinION Analysis and Reference Consortium: Phase 1 data release and analysis. *F1000Research* 2015, **4**:1075. **Citations – 140**

2014

- Karen H. Miga, Yulia Newton, **Miten Jain**, Nicolas F. Altemose, Huntington F. Willard and W. James Kent. Centromere reference models for human chromosomes X and Y satellite arrays. *Genome Research*, 2014, 24:697-707. **Citations – 87**

2012

- Michelle M. Maalouf, **Miten Jain**, Paolo Actis, Nader Pourmand. Single-cell manipulation using Nanopipettes. *Nanotech*, 2012, 2:384–7.

2011

- Jamie Heimburg-Molinaro, Michelle Lum, Geraldine Vijay, **Miten Jain**, Adel Almogren, Kate Rittenhouse-Olson. Cancer vaccines and carbohydrate epitopes. *Vaccine*, 2011, 48:8802-26. **Citations – 165**
- Vishwas N. Joshi, **Miten Jain**, Frederic R. Furuya, Richard D. Powell, James F. Hainfeld, Marc C. Llaguno, and Donald W. Hilgemann. HaloTag® Protein-Mediated Live Cell Imaging with Bigger FluoroNanogold™. *Microscopy and Microanalysis*, 2011, 17:150-1.
- Vishwas N. Joshi, **Miten Jain**, Frederic R. Furuya, Richard D. Powell, J. F. Hainfeld, Johanna Nelson, Chris Jacobsen, James Quinn, Aaron M. Neiman. Combined Texas Red and 1.8 nm FluoroNanogold™ for Multimodal Imaging. *Microscopy and Microanalysis*, 2011, 17:152-3.

* *Equal Contributions*

THESES:

- **Miten Jain**. High-Coverage Long Read DNA Sequencing with the Oxford Nanopore MinION. Doctor of Philosophy Dissertation, University of California, Santa Cruz, CA, 2017.
- **Miten Jain**. Cloning of a sialyltransferase gene to analyze surface sialic acid effects on metastasis. M.S. Thesis, State University of New York at Buffalo, 2008.

Evidence for implementation of research work in scientific community:

- **Nature Biotechnology** - [link](#)

This article covered the state-of-the-art tools for nanopore sequencing and data analysis. I was considered due to my experience in the field and provided suggestions and feedback regarding the tools that were included in the blog.

- **Science** - [link](#)

I was quoted in the article as I was one of the authors on the RNA manuscript (under review) in 2016 from UCSC. I got contacted for this due to my experience with nanopore sequencing of DNA and RNA. This article covers the broad applications of nanopore sequencing to healthcare and genomics.

- **Nature Methods** - [link](#)

This article covered developments in nanopore sequencing and I was in the picture that was used to demonstrate the MinION.

- **Santa Cruz Sentinel** - [link](#)

This article covered the work I presented on nanopore DNA sequencing and technology developments at the Research Review Day at UC Santa Cruz in 2015.

- **Blog** - [link](#)

This article covers the work I have been involved in doing over the past few years and covers the applications of nanopore sequencing technology to the genomics community.

- **Science** - [link](#)

Nanopore sequencing was included among the Top 10 scientific developments or advancements by the magazine when choosing their 2016 “Breakthrough of the Year”.

- **Oxford Nanopore Technologies** - [link](#) and [link](#)

This video covers how we are using the PromethION sequencer at UCSC, and I was involved in the filming as an advanced nanopore expert and user.

CODE REPOSITORIES CONTRIBUTED TO:

These tools help with data analysis using a variety of algorithms and visualization methods. marginAlign software allows for better estimation of errors in nanopore data by using machine learning and posterior probabilities. Additionally, it also provides measurement of statistics from data analysis. signalAlign software can model the ionic current signal data from nanopore sequencing of RNA and DNA which allows for learning different types of base modification. Nanopore software allows for analysis of sequence data and performs a suite of analyses that can help characterize the properties of the data. tRNApore and protpore software use hidden Markov models (HMMs) to help analyze nanopore ionic current signal data corresponding to tRNA and protein molecules respectively.

- <https://github.com/benedictpaten/marginAlign>
- <https://github.com/mitenjain/signalAlign>
- <https://github.com/mitenjain/nanopore>
- <https://github.com/mitenjain/tRNApore>
- <https://github.com/mitenjain/protpore>

ORAL PRESENTATIONS: (National and international meetings)

2018

- Generating high-quality reference human genomes using PromethION nanopore sequencing. **GIAB/GRC Meeting, ASHG 2018, San Diego, USA.**
- Native RNA sequencing using nanopore technology. **Invited Talk, IUPUI, USA.**
- RNA is the future. **BME Department Talk, UC Santa Cruz, Santa Cruz, CA, USA.**
- A reference human transcriptome based on native RNA sequencing. **Selected Talk, Biophysical Society 2018, Santa Cruz, USA.**
- A reference human transcriptome based on native RNA sequencing. **Sponsored Talk, RNA Society 2018, Berkeley, USA.**
- Resolving complex genomic regions using 100 kb+ nanopore long reads. **Plenary Talk, Long-Read Sequencing Workshop, The Jackson Laboratory for Genomic Medicine Farmington, CT, USA.**
- Nanopore sequencing - changing how we solve biological questions. **Lightning Talk, UCSC Postdoc Symposium, Santa Cruz, CA, USA.**
- Disruptive genomics using nanopore sequencing. **BME Department Talk, UC Santa Cruz, Santa Cruz, CA, USA.**

2017

- Direct RNA and cDNA sequencing of the human transcriptome. **Plenary Talk, Nanopore Community Meeting, Metropolitan Pavilion, New York, USA.**
- Resolving complex nucleic acid molecules using nanopore technology. **Plenary Talk, Nanopore Meeting, Utrecht, The Netherlands.**
- Nanopore sequencing. **Lightning Talk, PBSE Retreat, UC Santa Cruz, Santa Cruz, CA, USA.**
- Recent progress at UCSC: long reads, DNA, and RNA sequencing. **Breakout Talk, London Calling, Old Billingsgate, London, UK.**
- Long reads and library preparation. **Plenary Workshop Talk, London Calling, Old Billingsgate, London, UK.**

2016

- Recent developments in MinION sequencing. **Breakout Talk, Nanopore Community Meeting, Metropolitan Pavilion, New York, USA.**
- DNA sequencing with the MinION. **BME Department Talk, UC Santa Cruz, Santa Cruz, CA, USA.**
- Long Reads and MinION Software Development. **Breakout Talk, London Calling, Old Billingsgate, London, UK.**

2015

- Long reads and base modifications using the MinION. **Breakout Talk, MinION Community Meeting, New York Genome Center, New York, USA.**
- Nanopore sequencing of DNA comes of age. **Plenary talk, IEEE SFBA Nanomimetics Symposium, Santa Clara, CA, USA.**
- DNA sequencing with the Oxford Nanopore MinION. **Research Review Day, University of California, Santa Cruz, CA, USA.**

- Nanopore sequencing: canonical bases and beyond. **Breakout Talk, London Calling, Millbank Tower, London, UK.**
- DNA sequencing with the MinION. **Platform talk, Genomes10K, Santa Cruz, CA, USA.**

2014

- DNA sequencing comes of age. **Plenary talk, Oxford Nanopore Meeting, American Society of Human Genetics (ASHG), San Diego, CA, USA.**

REVIEWER EXPERIENCE / EXPERIENCE AS REVIEWER FOR OTHER SCIENTIFIC WORK

- **Total of manuscripts reviewed – 16**
- **Reviewer for following journals – Nature Biotechnology, Nature Communications, Genome Research, Nucleic Acids Research, Genome Biology, Briefings in Bioinformatics, Bioinformatics, Journal of Experimental Botany**
- **Sessions chaired in conference/symposium – 1 (Chaired a Rapid Fire Session at the UC Bioengineering Symposium 2015 held at UC Santa Cruz, Santa Cruz, CA, USA)**

FUNDING/PROFESSIONAL HONORS

- **Keck/QB3 Fellow (Keck Foundation, QB3 Fellow, 2011 and 2012)**
- **Regents Fellow (UC Santa Cruz, Regents Fellow, 2011)**
- **Mark Diamond Research Fund**

LEADERSHIP AND MANAGEMENT EXPERIENCE:

- **Secretary and Webmaster, Graduate Student Association (GSA), UC Santa Cruz, 2015-2016.**
- **Internal Vice-President, GSA, UC Santa Cruz, 2013-2014.**
- **Keck/QB3 fellow at UC Santa Cruz, 2011.**
- **Department Representative, GSA, UC Santa Cruz, 2011-2017.**
- **Mark Diamond Research Fund Grantee for M.S. research at University at Buffalo (UB), 2008.**
- **Founder and President, Biotechnology Graduate Student Association at UB, NY, 2007-2008.**
- **Vice-President, Graduate Indian Student Association at University at Buffalo, NY, 2007-2008.**
- **President, Tantraa, an intercultural club at UB, NY, 2007-2008.**
- **Consistently ranked amongst top 3 in co-curricular activities at school and college levels.**

TEACHING EXPERIENCE:

- **Guest lecturer, Harvard University**
 - **FRSEMR 250 - Building a Living Cell One Brick at a Time, Fall 2016.**
- **Teaching Assistant, University at Buffalo**

- Clinical Chemistry
- Methods of Analysis
- Technical Communication for Scientific Professionals
- Statistics Methods for Oral Science

Link to Google Scholar Citations: <https://scholar.google.com/citations?user=WvaMAEcAAAAJ&hl=en>

Permanent Residency Category – EB-1B Outstanding Researcher

Or

EB-1A Alien of Extraordinary Ability