Anoushka Joglekar

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Education_

Weill Cornell Medicine New York, NY

PHD COMPUTATIONAL BIOLOGY AND MEDICINE

2017 - 2022

- Thesis: A cell-type centric view of alternative splicing in the mammalian brain
- Advisor: Dr. Hagen Tilgner
- · Committee: Dr. M. Elizabeth Ross, Dr. Jonathan Victor, Dr. Davide Risso, Dr. Iman Hajirasouliha

The Ohio State University

Columbus OH

2013 - 2017

- **BS Applied Mathematics** Focus: Mathematical Biology
- Magna Cum Laude

The Ohio State University

Columbus OH

- **BS ENGLISH** 2013 - 2017
- Honor's thesis: From the Atom to the Grain of Sand: Ascending the Stoppardian Ladder
- Advisor: Dr. Sebastian Knowles
- Magna Cum Laude

Academic and Research Interests _____

- Neuroscience
- Alternative splicing
- Computational biology

- · Long-read sequencing
- Neurogenetics
- · Single-cell transcriptomics

In the past decade, there have been increasingly concerted efforts to piece together a holistic picture of how the brain functions under normal and diseased conditions. One trajectory involves looking at neuronal structure and function at a single cell level. In the Tilgner lab, I have worked on elucidating the molecular architecture of the brain, particularly the alternative splicing landscape at a single cell level. Examining differential splicing within the brain could shed light on a multitude of neurological conditions, especially since aberrant splicing is associated with brain disorders, but has remained unexplored due to technological limitations. Keeping with the idea that creativity and necessity are at the heart of scientific progress, I am excited about developing new tools that can uncover information that lies just beyond our collective reach.

Past Research Experiences

Dept. of Neuroscience, Weill Cornell Medicine

New York, NY

2018 - 2022

GRADUATE STUDENT. PI: HAGEN TILGNER

Developing new techniques to study splicing patterns at the single-cell level in mammalian tissues, including but not limited to single-cell long read sequencing for fresh cells from model organisms, single-nuclei long-read sequencing for frozen tissue types, resolving isoform expression at the spatial level, computational methods for transcript assignment, quantification, differential analysis.

Dept. of Bioengineering, Cornell University

Ithaca, NY

ROTATION STUDENT, PI: IWIJN DE VLAMINCK

Oct - Dec 2017

Using cell-free DNA (cfDNA) from liquid biopsy samples of post-transplantation patients, I developed code to trace back tissue of origin for the cfDNA using methylation status of tissue of origin as a reference.

Dept. of Neuroscience, Cornell University

Ithaca, NY

ROTATION STUDENT, PI: THOMAS CLELAND

July - Sept 2017

Expanded a pre-existing model of the mouse olfactory bulb to include a more extensive network of biophysically constrained glomeruli, mitral cells, and piriform cells to study network dynamics in discerning odors of interest in the presence of competitive odors.

Dept. of Biomedical Informatics, The Ohio State University

Columbus, OH

RESEARCH ASSISTANT, PI: KEVIN COOMBES

2016 - 2017

Worked as a research assistant in a transcriptomics lab. Drove a project on developing algorithms for outlier detection of aberrantly expressed genes in small sample sizes using publicly available lung cancer datasets.

Dept. of Mathematics, The Ohio State University

Columbus, OH

RESEARCH ASSISTANT, PI: DAVID TERMAN

2014 - 2016

Worked as a research assistant in a dynamical systems labs. Helped model a 2 dimensional biophysically constrained network of neurons and astrocytes in order to investigate the role of gap junctions between astrocytes during ischemic stroke

Publications —

PUBLISHED

- Prjibelski AD, Mikheenko A, **Joglekar A**, Smetanin A, Jarroux J, Lapidus A, Tilgner HU. Accurate isoform discovery with Iso-Quant using long reads. In press, *Nat Biotechnol*
- Stein AN, **Joglekar A**, Poon CL, Tilgner HU. ScisorWiz: Visualizing Differential Isoform Expression in Single-Cell Long-Read Data. *Bioinformatics*. 2022 May 23. doi: 10.1093/bioinformatics/btac340. PMID: 35604081.
- Hardwick S*, Hu W*, **Joglekar A***, Fan L, Collier PG, Foord C, Balacco J, Lanjewar S, Sampson MM, Koopmans F, Prjibelski A, Mikheenko A, Belchikov N, Jarroux J, Palkovits M, Luo W, Milner TA, Ndhlovu LC, Smit AB, Trojanowski JQ, Lee VMY, Fedrigo O, Sloan SA, Tombácz D, Ross ME, Jarvis E, Boldogkői Z, Gan L, Tilgner HU. Single-nuclei isoform RNA sequencing unlocks barcoded exon connectivity in frozen brain tissue. *Nat Biotechnol*. 2022 Mar 7. doi: 10.1038/s41587-022-01231-3. Epub ahead of print. PMID: 35256815
- Mikheenko A, Prjibelski AD, **Joglekar A**, Tilger HU. Sequencing of individual barcoded cDNAs using Pacific Biosciences and Oxford Nanopore Technologies reveals platform-specific error patterns. *Genome Res.* 2022 Apr;32(4):726-737. doi: 10.1101/gr.276405.121. Epub 2022 Mar 17. PMID: 35301264.
- Joglekar A, Prjibelski A, Mahfouz A, Collier P, Lin S, Schlusche AK, Marrocco J, Williams SR, Haase B, Hayes A, Chew JG, Weisenfeld NI, Wong MY, Stein AN, Hardwick SA, Hunt T, Wang Q, Dieterich C, Bent Z, Fedrigo O, Sloan SA, Risso D, Jarvis ED, Flicek P, Luo W, Pitt GS, Frankish A, Smit AB, Ross ME, Tilgner HU. A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. *Nat Commun.* 2021 Jan 19;12(1):463. doi: 10.1038/s41467-020-20343-5. PMID: 33469025; PMCID: PMC7815907.
- Hardwick SA, **Joglekar A**, Flicek P, Frankish A, Tilgner HU. Getting the Entire Message: Progress in Isoform Sequencing. *Front Genet*. 2019;10:709. PubMed Central PMCID: PMC6706457.
- Gupta I, Collier PG, Haase B, Mahfouz A, **Joglekar A**, Floyd T, Koopmans F, Barres B, Smit AB, Sloan SA, Luo W, Fedrigo O, Ross ME, Tilgner HU. Single-cell isoform RNA sequencing characterizes isoforms in thousands of cerebellar cells. *Nat Biotechnol*. 2018 Oct 15; PubMed PMID: 30320766.
- Huguet G, **Joglekar A**, Messi LM, Buckalew R, Wong S, Terman D. Neuroprotective Role of Gap Junctions in a Neuron Astrocyte Network Model. *Biophys J.* 2016 Jul 26;111(2):452-462. doi: 10.1016/j.bpj.2016.05.051. PMID: 27463146; PMCID: PMC4968398.

In Review

Belchikov N*, Hu W*, Fan L*, **Joglekar A**, ... Gan L, Tilgner HU. A single-cell long-read isoform resolved case-control study of frontotemporal dementia reveals cell-type specific and broad splicing dysregulation in post-mortem human brain.

IN PREP

Joglekar A, Hu W, Zhang B, Stein A, Ross ME, Tilger HU. A compendium of cell-type specific isoform patterns across spatiotemporal axes of the mouse brain

- Hsu J*, Jarroux J*, Joglekar A, Romero JP, Nemec C, Reyes D, Royall A, He Y, Belchikov N, Leo K, Taylor SEB, Tilgner HU. A single molecule comparison of 10X single-cell sequencing platforms
- Abrams ZB, Joglekar A, Gershkowitz GR, Sinicropi-yao S, Asiaee A, Carbone DP, Coombes KR. Personalized Transcriptomics: Selecting Drugs Based on Gene Expression Profiles.

Awards and Fellowships _____

- Second place, Oral presentation, Vincent DuVigneaud Research Symposium 2022
- 2021 Graduate Student Fellowship, Weill Cornell Medicine
- 2019 Scholarship, JTech CSHL Biological Data Science
- 2018 David O. Frantz Thesis Award, Dept. of English, The Ohio State University
- Dean's List, The Ohio State University 2013-18
 - STEP Study Abroad Fellowship, The Ohio State University 2015

Presentations_

INVITED TALKS

- Sept 2022. ScisorWiz: Methods for visualizing isoform expression between conditions. Invited talk, PacBio IsoSeq Social Club, Virtual.
- Sept 2022. Single-nuclei isoform sequencing unlocks barcoded exon connectivity in frozen tissue. Guest speaker, DNA After Hours, Unwind with Agilent, New York, NY
- May 2022. A cell-type centric view of isoform expression reveals combination patterns of transcript elements in the brain. Guest presenter, group meeting. Single Cell Genomics Team, CNAG, Barcelona
- April 2022. A cell-type centric view of isoform expression reveals combination patterns of transcript elements in the brain. Featured speaker PacBio Discoveries Roadshow, New York, NY
- January 2022. Building towards a brain region and cell-type specific isoform atlas of the mouse brain Guest speaker, Dept. of Mathematics Seminar Series, Fatima Jinnah Women University
- July 2022. A computational framework for quantifying alternative splicing at a single-cell resolution. Guest speaker Instituto de Medicina Molecular, University of Lisbon
- June 2021. A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. Speaker PacBio SMRT Journal Club. Virtual
- February 2021. Cell-type, single-cell, and spatial signatures of brain-region specific splicing in postnatal development. Invited talk, Tri-I CBM Recruitment, Weill Cornell Medicine
- February 2020. Neuronal cell type heterogeneity through the lens of alternative splicing. Invited talk, Tri-I CBM Recruitment, Weill Cornell Medicine

CONTRIBUTED PRESENTATIONS

- July 2022. A cell-type centric view of isoform expression reveals combination patterns of transcript elements across spatiotemporal axes of the brain. Oral Presentation. iRNA COSI, Intelligent Systems for Molecular Biology (ISMB), Madison WI
- April 2022. A cell-type centric view of isoform expression reveals combination patterns of transcript elements across brain regions and development. Oral presentation, Vincent DuVigneaud Research Symposium, Weill Cornell Medicine
- March 2022. Single-nuclei isoform sequencing unlocks barcoded exon connectivity in frozen tissue. Poster presenter, Single Cell Symposium, Center for Genomic Regulation, Barcelona
- July 2021. Building towards a brain region and cell type-specific isoform atlas of the postnatal mouse brain. Speaker. ACCESS Research Seminar, Weill Cornell Medicine
- November 2020. Cell-type signatures of brain-region specific splicing in postnatal development. Poster presenter, Biological Data Science, Cold Spring Harbor Laboratories
- April 2020. Neuronal cell type heterogeneity through the lens of alternative splicing. Presenter, Bench to Bedside Seminar Series, Feil Family Brain and Mind Institute, Weill Cornell Medicine

November 2019. Enhanced interpretation of ScISOr-Seq reveals distinct programs of alternative splicing. Lightning talk, Genome Informatics, Cold Spring Harbor Laboratories

November 2019. Variety is the splice of life. Finalist, Three Minute Thesis Competition, Weill Cornell Medicine

Teaching Experience _____

Fall 2016 College Algebra, Teaching Assistant

Spring 2016 Calculus III, Tutor Fall 2015 Calculus I-II, Tutor

Mentoring_

PhD students: Designed and helped set up rotation, guided and supervised their analysis, and met with them one-on-one frequently based on individual needs. Once in lab, brainstormed project ideas, met weekly/biweekly to supervise particular projects, and edited writing for grants and papers.

- 2018 Suniyya Waraich, Hui Xian Poh
- 2019 George Zakusilo
- 2020 Natan Belchikov⁺, Careen Foord⁺, Eduardo Munoz
- 2021 Deirdre O'Sullivan, Divya Koyyalagunta, Justine Hsu⁺, Kirby Leo
- 2022 Jake Qiu, Berk Mankaliye

Master's students: Brainstormed project ideas, met frequently to help set up the analysis, and guided throughout their time in the lab.

2020-22 Chi Lam Poon

Summer intern / Research assistant: Set up mini projects depending on duration of commitment, met frequently to familiarize them with software and analysis methods, supervised projects.

2019-22 Alexander Stein

2021-22 Shaun Pollard

Leadership and Outreach _____

2020-22	Social Justice and A	Anti-Racism	Tasktorce,	Sate space	(SOS) R	epresentative
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2020-22 **Social Justice and Anti-Racism Taskforce**, Social Media Liaison

2020-21 **Tri-Institutional Biotechnology Club**, Director of Internal Affairs

2020-22 **Computational Biology Summer Internship Program, MSKCC**, Admissions Committee

2020-22 Tri-I Computational Biology and Medicine, Social Median Liaison

2020-21 NIH Graduate Student Fair, Representative: Tri-I CBM

2018-21 **Skype a Scientist**, Scientist

2019 Annual Biomedical Research Conference for Minority Students (ABRCMS), Representative

2018-19 **Tri-I Computational Biology and Medicine**, Research in Progress Representative

2018 Vincent DuVigneaud Memorial Research Symposium, Publicity Committee

2017-18 Tri-I Computational Biology and Medicine, Social Chair

⁺ Joined lab