Paramita Chatterjee

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LinkedIn Profile: LinkedIn Profile GitHub Profile: GitHub Profile

SUMMARY

Accomplished Molecular Biology and Bioinformatics professional with over eight years of progressive experience in both academic and hybrid genomics research environments. Recently earned a Ph.D. from the Georgia Institute of Technology, specializing in the generation, analysis, and interpretation of large datasets from single-cell RNA and multi-omics platforms. I am highly skilled in project management and deeply committed to advancing the field of cell and gene therapy. My expertise encompasses stem cell characterization, therapeutic genomics, and proficiency in R, Linux, Unix, and Python. I am actively seeking a collaborative role in genomics research that demands leadership, analytical prowess, and the ability to oversee complex projects.

EXPERIENCE

GEORGIA INSTITUTE OF TECHNOLOGY
Atlanta, GA
Research Scientist I, The Marcus Center for Cell Characterization and Manufacturing
2017 - Present

• Lead Bioinformatician spearheading the analysis, interpretation, and visualization of transcriptomics and proteomics data from clinical trials and cell therapy projects. Utilized R, Python, Bash, and Linux within a High-Performance Computing (HPC) environment to deploy large-scale analytical pipelines efficiently.

• Executed comprehensive single-cell and genomic sequencing projects using 10x Genomics Chromium and Connect platforms, including scRNA-seq, scATAC-seq, and CITE-seq. Expertly performed WGS, WGBS, and miRNA-seq, utilizing both Illumina platforms and sophisticated in-house library preparation protocols, resulting in robust, large-scale datasets.

• Managed the commercialization aspects of clinical therapy cells by coordinating with external clinics and companies for cellular characterization. Facilitated operational logistics and established strategic partnerships to enhance service delivery and scientific outcomes.

• Led and established NGS projects in the lab in 2017, enhancing the mainstream integration and automation of NGS and Single-cell genomics. Task lead for all Genomics work for any incoming project internal and external. Use 10x Genomics and Illumina platforms heavily for data generation.

• Spearheaded big data generation, analysis, and management in the domain of therapeutic genomics and single-cell genomics research. This resulted in getting funded $1.8 Million for MILES clinical trial characterization project in 2019 and NIH-IDCCH grant of $1.7 Million in 2022.

• Awarded Technologist of the year by one of the largest cells and gene therapy conference, ISCT (International Society of Cell and Gene Therapy) in 2023.

• Played a pivotal role in clinical data management, ensuring adherence to compliance standards and data security protocols.

• Collaborated with NIH and RTI, offering consultancy in genomics data analytics pipelines, experimental support, and troubleshooting.

• Assisted in GMP lab setup and instrument selection, ensuring quality control in alignment with industry standards.

• Leveraged MBA knowledge for efficient project administration, budgeting, cost analysis, and priority management.

Research Scientist, Georgia Institute of Technology
2015-2017

• Established NGS (WGS, WGBS) in-house SOP to generate quality libraries from different tissue sources from different species like Human, Chimp, Macaque, Sparrow, Wasp and Honey bees.

• Worked extensively with collaborators ensuring lab safety regulation management and protocol registration.

• Managed multiple projects, ensuring timely deliverables and coordination with collaborators and graduate students.

• Established in-house methods for Epigenetics evaluation through whole-genome sequencing (WGS) and Chromatin accessibility assay (ATACseq), resulting in the publication of over 8 research articles.

Research Technician, School of Biology, Georgia Institute of Technology
2011-2013

• Designed and executed experiments, ensuring data integrity and relevance. • Managed lab safety and operations, ensuring compliance with institutional guidelines. • Authored protocols and manuscripts, advancing the field's understanding and practices.

EDUCATION

- **Georgia Institute of Technology** **Atlanta, Georgia, USA**
  Ph.D., Bioinformatics 2024

- **MS Ramaiah Institute of Management** **Bangalore, Madurai Kamaraj University, India**
  MBA, Industry Integrated 2010

- **Periyar University** **Tamilnadu, India**
  M.S. Applied Microbiology 2008

SKILLS/PRESENTATIONS

Skills: Proficient in R, Python, Linux, Bash, HPC, JMP, and SQL database queries. Expertise in NGS data analysis, single-cell RNA data interpretation, and bioinformatics tools. Experienced in clinical trial data management, storage, and transportation.

Presentations: Contributed to various academic and management meetings including ISCT, AWSOM, CMAT, and SESAR Workshop. Published numerous research articles and abstracts in leading journals and conferences.

AWARDS/CERTIFICATIONS

- ISCT Technologist Abstract Award (2023)
- Advanced Transcriptomics Data Analysis (NIH, 2019)

PUBLICATIONS

Publications:

Published:

1. Dr Michael Gottschalk, **Paramita Chatterjee**, et al (2023). Cell based versus corticosteroid injections for knee pain in osteoarthritis: a randomized phase 3 trial.
2. Keenum MC, **Chatterjee P**, et al. (2023). Single-cell epitope-transcriptomics reveal lung stromal and immune cell response kinetics to nanoparticle-delivered RIG-I and TLR4 agonists. Biomaterials.
3. Vantucci CE, **Chatterjee P**, et al. (2022). Systemic Immune Modulation Alters Local Bone Regeneration in a Delayed Treatment Composite Model of Non-Union Extremity Trauma. Front. Surg.
4. Medrano-Trochez C, **Chatterjee P**, et al. (2021). Single-cell RNA-seq of out-of-thaw mesenchymal stromal cells shows tissue-of-origin differences and inter-donor cell-cycle variations. Stem Cell Res Ther.
5. Jeong H, **Chatterjee P**, et al. (2021). Evolution of DNA methylation in the human brain. Nature Communications.
6. Sun D, **Chatterjee P**, et al. (2021). Genome-wide variation in DNA methylation linked to developmental stage and chromosomal suppression of recombination in white-throated sparrows. Molecular Ecology.
7. Wu X, **Chatterjee P**, et al. (2020). Lineage and parent-of-origin effects in DNA methylation of honey bees (Apis mellifera) revealed by reciprocal crosses and whole-genome bisulfite sequencing. Genome Biology and Evolution.
8. Wu X, **Chatterjee P**, et al. (2020). Distinct epigenomic and transcriptomic reprogramming associated with Wolbachia-mediated asexuality. PLOS Pathogens.
9. Berto S, **Chatterjee P**, et al. (2019). Accelerated evolution of oligodendrocytes in human brain. PNAS.
10. Sun D, **Chatterjee P**, et al. (2019). Regional epigenetic differentiation of the Z Chromosome between sexes in a female-heterogametic system. Genome Research.
11. Mendizabal I, **Chatterjee P**, et al. (2019). Cell-type specific epigenetic links to schizophrenia risk in brain. Genome Biology.
12. Lee KS, **Chatterjee P**, et al. (2018). Selection on the regulation of sympathetic nervous activity in humans and chimpanzees. PLOS Genetics.

Abstracts:

1. **Chatterjee P**, Kippner L, et al., Single cell omics comparison of cell therapeutics in osteoarthritis
2. **Chatterjee P**, Stevens H, et al., High-dimensional multi-omics comparison of cells in bone marrow revealed alterations to immune cells in osteoarthritis

Preprint/Submitted:

1. **Chatterjee P**, Hazel Y. Stevens, et al., Single-cell transcriptome and crosstalk analysis reveal systemic alteration of immune cell phenotype and key pathways in the bone marrow of patients with knee osteoarthritis; Cell Reports Medicine

1. Cummins KD, **Chatterjee P**, et al., G-CSF mobilized apheresis as an alternative source of CAR T-cells; Molecular Therapy
2. Pradhan P, **Chatterjee P**, et al., Single-Cell Transcriptomic Attributes and Unbiased Computational Modeling for the Prediction of Immunomodulatory Potency of Mesenchymal Stromal Cells; bioRxiv

3. Anderson SE, **Chatterjee P**, et al., Fibro-Adipogenic Progenitor Heterogeneity and Implications in Volumetric Muscle Loss-Induced Fibrosis.