

Paarth Parekh

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PROFESSIONAL SUMMARY

Bioinformatics & Computational Scientist with over four years of experience integrating multi-omics data to support therapeutic target discovery and mechanistic modeling. Skilled in developing generalizable analysis pipelines, network-based inference, and scalable computational platforms to support cross-functional teams in translational research. Proven success in modeling disease phenotypes, simulating PK/PD dynamics, and extracting biological insights from large-scale NGS data. Proficient in Python, R, and tools (AWS, Docker, Git), with a track record of cross collaboration across disciplines.

EXPERIENCE

Javelin Biotech | Woburn, MA

Bioinformatics & Computational Scientist II

06/21 – Present

- Developed and generalized modular multi-omics analysis pipelines, enabling reproducibility and scalability across multiple therapeutic areas.
- Integrated transcriptomic, proteomic, and clinical data for metabolic disease characterization and biomarker discovery
- Applied network inference and pathway-level analytics to interpret omics signatures and elucidate mechanisms of action for metabolic and hepatic diseases.
- Developed a transcriptomic metric integrating clinical and in vitro data, supporting model development and validation to improve pre-clinical to clinical translation by ensuring the presence of relevant hallmarks.
- Collaborated with wet lab scientists and project stakeholders to plan, prioritize, and troubleshoot analyses, proactively resolving data pipeline issues tied to lab and computational processes.
- Designed and deployed machine learning and ODE-based models for pharmacokinetics and IVIVC applications on organ-on-a-chip platform.
- Assisted in the development of standardized SOPs and experimental workflows to ensure consistent, reproducible data generation and downstream analysis.
- As a project manager, collaborated with external teams to develop a client-facing software product that analyzes Liver Chip Data using predictive algorithms for hepatic metabolism, streamlining data analysis and decision-making processes.
- Presented project findings and platform innovations to stakeholders, effectively translating technical insights into strategic direction for data-driven R&D.
- Supported grant-seeking efforts by conducting literature reviews, contributing to research proposals, and collaborating with different CROs to optimize grant application processes, budgets, and timelines.

GlaxoSmithKline | Rockville, Maryland

Bioinformatics Scientist, Pre-Clinical Vaccines Lab

06/20 – 12/20

- Conducted single-cell transcriptomic analysis to identify immunological biomarkers from vaccine response data, identifying key immune-response biomarkers.
- Processed and interpreted long-read NGS data (PacBio) to characterize mRNA constructs, applying tools like Minimap2 and SAMtools in a Linux-based analysis environment.
- Applied network and pathway inference tools to connect transcriptomic signals with biological pathways and response phenotypes.
- Collaborated with immunologists, molecular biologists, and biostatisticians to integrate computational insights with experimental validation.

Georgia Institute of Technology | Atlanta, Georgia

Graduate Teaching Assistant, Experiment Design and Statistics

01/21 – 05/21

- Trained students to use R and R studio to perform basic statistical analysis.
- Organized class presentations, office hours and participated in grading of assignments for a class of 130 students.

Graduate Research Assistant, Storici Lab

05/19 – 05/20

- Developed and optimized an ETL pipeline to analyze the ribonucleotide incorporation in *Saccharomyces cerevisiae* DNA, enabling comprehensive downstream analysis.
- Built a machine learning model leveraging the transformed dataset to predict the firing times of autonomously replicating sites (ARS), providing novel insights into DNA replication processes.

TECHNICAL SKILLS

- **Programming:** Python, R, Bash, SQL, Java
- **Tools:** NextFlow, AWS, Git, Docker, Jupyter, RStudio, VSCode
- **Bioinformatics & Modeling:** NGS data analysis, multi-omics integration, product development, scRNA-seq, RNA-seq, proteomics, systems biology, GSEA, ODE-based PK/PD modeling, GEMs, machine learning frameworks, ChIP-seq, variant calling, epigenomics
- **Web & Software Development:** Dash, R-Shiny, HTML, CSS, React.js, PostgreSQL
- **Operating Systems:** Linux, Unix, Windows

EDUCATION

Georgia Institute of Technology, Atlanta, GA

M.S. in Bioinformatics (GPA: 4.0/4.0)

University of Mumbai, Mumbai, India

B.E. in Biomedical Engineering

SELECTED PUBLICATIONS

- Sherfey J, Rajan S.A.P., Nichols L., **Parekh P.**, Cirit M. A novel multi-organ tissue chip for Clinical pharmacokinetics applications. * (In-works)
- **Parekh P**, Sherfey J, Alaybeyoglu B, Cirit M. Pathway-Based Similarity Measurement to Quantify Transcriptomics Similarity Between Human Tissues and Preclinical Models. Clin Pharmacol Ther. October 8, 2024.
- Ohri S, **Parekh P**, Nichols L, Rajan SAP, Cirit M. Utilization of a Human Liver Tissue Chip for Drug-Metabolizing Enzyme Induction Studies of Perpetrator and Victim Drugs. Drug Metab Dispos. September 30, 2024.
- Rajan S. A. P., Sherfey J., Ohri S., Nichols L., **Parekh P.**, Cirit, M. A novel Milli-fluidic liver tissue chip with continuous recirculation for predictive pharmacokinetics applications AAPS J. 2023;25(6):102. Oct 27, 2023.