Urminder Singh, PhD

Staff Bioinformatics Scientist, Illumina
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PROFESSIONAL SUMMARY

● Bioinformatician and Computer Scientist with over 10 years of experience working with NGS and multi-omics data.
● Skilled collaborator and leader, fostering cross-functional teamwork across diverse teams to drive results.
● Product development experience in a fast-paced, rapidly evolving industry, showcasing agility and adaptability.
● Proficient knowledge in Data structures and Algorithms, Statistics, Optimization, Mathematics, and Analytics.
● Experienced programmer and software engineer with experience in managing software teams and projects.
● Solid publication record with multiple first-author publications in high-impact peer-reviewed journals.
● Confident and articulate speaker adept at presenting scientific ideas to diverse audiences.

TECHNICAL SKILLS

Bioinformatics Analysis: Multiomics analysis, NGS assay development, DNA/RNA Variant analysis, Algorithm development, Neoantigen prediction
Machine Learning and Data Analysis: TensorFlow, Keras, NumPy, Pandas, Scikit, Tidyverse
Software Engineering: Object oriented design, Software testing and validation, SCRUM, CI/CD, Git
Programming Language: Python, Java, R, C, C++
Database: Data modelling, MySql, MongoDB
Workflow Management and Scaling: NextFlow, Snakemake, Anaconda, Docker, HPC, AWS

PROFESSIONAL EXPERIENCE

Staff Bioinformatics Scientist, Illumina   **May 2024-Present**
● Assumed a leadership role within the team, managing one direct report and mentoring team members to drive efforts aligned with organizational goals. Effectively strategized projects, delegated tasks, provided feedback, and fostered collaborations to ensure deliverables.
● Led the bioinformatics team in the development of the next version of Illumina's TruSight Oncology (TSO) NGS panel for comprehensive genomic profiling, resulting in a faster assay with higher variant detection sensitivity, lower false positive rate, and improved coverage in difficult genomic regions.
● Advanced Illumina's DRAGEN HLA genotyper by making it comprehensive to cover all HLA genes and implementing algorithms in C++ to achieve industry-leading accuracy in HLA genotyping. Collaborated closely with a team of software engineers to ensure the incorporation of best practices in testing and deployment.
● Engaged in collaborator- and customer-facing interactions as bioinformatics expert for clients seeking support or guidance on diverse bioinformatics topics while fostering positive relationships with customers and collaborators.

Sr. Bioinformatics Scientist, Illumina   **Oct 2022-April 2024**
● Bioinformatics Lead on Illumina's TruSight Oncology (TSO) NGS panels product development. Led a team of bioinformatics scientists and collaborated with cross-functional teams ensuring the improved quality and accuracy of Illumina's oncology NGS panels and bioinformatics analysis software, aligned with customer needs, and industry standards.
● Bioinformatics Lead and Subject Matter Expert (SME) for Illumina's DRAGEN HLA Genotyper. Spearheaded the development, enhancement, and implementation of HLA calling algorithm in C++ and python.
● Conducted an extensive study into the application of liquid biopsy to significantly expand actionable neo-antigen prediction for cancer immunotherapy. Built an end-to-end data analysis pipeline, disseminated research findings across multiple teams and published scientific discoveries.
● Participated in strategic external research collaborations with pharma partners to assess feasibility, and advance the development of companion diagnostic (CDx) assays.

Bioinformatics Scientist, Illumina   **August 2021-Sept 2022**
- Developed infrastructure to automate data processing, analysis, visualization, and report generation for Design Verification Testing studies, using Python, Streamlit, Jenkins, and Nextflow.
- Supported the assay, software, and biostats team to plan, support and execute clinical and internal studies.
- Member of hiring committee to hire Bioinformatics Scientists in the Bioinformatics department.

Bioinformatics Graduate Researcher, Iowa State University   **August 2017-August 2021**
- Collaborated with international research teams COV-IRT and COVID-19 Consortium in accelerating COVID-19 research
- Designed and executed computational workflows for automated and reproducible analysis of >30,000 bulk and single-cell RNA-Seq datasets (250 terabytes) from GTEx, TCGA, and SRA
- Formulated computational pipelines for annotating novel protein-coding biomarkers in diseases like cancer and COVID
- Developed and published efficient, open-source computational tools in python, Java, and R for big data statistical analysis and interactive visualization with emphasis on reproducibility
- Worked on a deep generative model for RNA-Seq normalization and batch-correction

Bioinformatician Researcher, School of Computational and Integrative Sciences   **Nov. 2015-July 2016**
- Developed a novel machine learning method, PlncPRO, for accurate identification of long non-coding RNAs

Graduate Student Researcher, School of Computational and Integrative Sciences   **August 2013-June 2015**
- Formulated novel machine learning, deep learning, and information theory-based methods for prokaryotic whole-genome sequence analysis
- Developed ORIS, a Java tool for interactive exploratory data analysis and visualization of genomic data

EDUCATION

Iowa State University (ISU), Ames, IA   **August 2016-July 2021**
PhD Bioinformatics and Computational Biology (Minor in Statistics)

Jawaharlal Nehru University, New Delhi   **August 2013-June 2015**
M. Tech. Computational and Systems Biology

South Asian University, New Delhi   **Sept. 2010-June 2013**
MS Computer Science

University of Delhi, Delhi   **August 2007-June 2010**
BS Applied Physical Sciences

SELECT PUBLICATIONS
- **Singh, Urminder et al.** "Tumor neoantigen prioritization from liquid biopsy whole exome sequencing for selected tumor-infiltrating lymphocyte therapy." ***BMJ Specialist Journals*** **(2023)**
- **Singh, Urminder et al.** "MetaOmGraph: a workbench for interactive exploratory data analysis of large expression datasets." ***Nucleic acids research*** **(2020)**

SELECT HONORS/GRANTS (3 of 13 honors/grants)
- Illumina spot bonus award nominated by the Director of Bioinformatics   **Nov 2021**
- COVID-19 Exceptional Effort Graduate Student Research Impact Award, ISU   **Jan 2021**
- Wendell Miller Trust Graduate Fellowship and Presidential Scholarship, ISU   **August 2016**