**Nikhil Nageshwar Inturi**

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**SUMMARY:**

Computational biologist with 8 years of combined industry and academic experience translating next‑generation sequencing (NGS) and multi‑omic datastreams into actionable hypotheses for drug discovery. Expert in Python and R, Linux HPC, and AWS; hands‑on with single‑cell & spatial RNA‑seq, WGS/WES/panel‑seq, and public reference cohorts (TCGA, DepMap, GTEx). Track record of integrating and curating heterogeneous datasets, uncovering novel immune‑cell states, and partnering with discovery teams to prioritize high‑confidence targets.

**SKILLS:**

**Core:** Molecular subtype discovery for immune‑mediated diseases, Curating TCGA, GTEx, DepMap & other public resources, NGS data analysis (scRNA/Bulk rna-seq, ATAC-seq, spatial-omics – visium/xenium, Variant calling and annotation

**Bioinformatics Tools:**BWA‑MEM, STAR, GATK, Mutect2, Strelka2, Manta, CNVkit, SpliceAI, VCFtools, SAMtools, stringtie, htseq

**Programming:** Python(anndata, scanpy, squidpy, PyVCF, pysam), R, SQL, Shell Scripting, Java, Cromwell and NextFlow

**Machine Learning and AI:** Deep Learning(Keras and PyTorch), NLP(RNN, LSTM, Transformers), Generative AI(LlamaIndex, LangChain)

**Containerization and Deployment CI/CD:** Git, Docker, Singularity, Podman, Kubernetes, Jenkins, GitLab CI, and Docker Swarm

**Databases and Cloud Tools:** Redis, PostgreSQL, Snowflake, Redshift, Azure Cosmos DB, AWS DynamoDB, MongoDB, AWS and Azure

**EXPERIENCE:**

**Bioinformatician and Sr. Data Scientist, The University of Texas at Dallas** Feb 2023 – Present

* Integrated bulk & single‑cell RNA‑seq (scRNA‑seq) and spatial transcriptomics from GTEx controls, TCGA tumours, and internal cohorts to map immune‑cell infiltrates driving chronic neuro‑inflammation; identified three myeloid subclusters linked to cytokine IL‑23 signalling, informing a new therapeutic programme.
* Curated >200 TB of public multi‑omic data (TCGA, DepMap) into a Snowflake warehouse with harmonised metadata; enabled one‑click comparative analyses across disease indications, reducing ad‑hoc ETL time by >70 %.
* Developed a Bayesian latent factor model in Python/scanpy + scvi‑tools that stratified patient biopsies into four transcriptional endotypes; manuscript under review at Genome Medicine.
* Architected and maintained a containerized NextFlow pipeline for bulk & single‑cell RNA‑seq (STAR → RSEM → DESeq2) and ATAC‑seq (BWA → MACS2 → DiffBind) across 50 + clinical datasets; reduced compute cost 42 % on AWS Batch.
* Built an neuron‑detection pipeline using image segmentation (Detectron2 | YOLOv11 | FastAI | SAM) that raised F1‑score 0.78 → 0.89 (+15%) while slashing processing time 95%.
* Developed a GPT‑powered RAG chatbot (LangChain) that unifies scRNA‑seq, ATAC-seq, Bulk RNA-seq, Visium / Xenium spatial data related publications-cutting knowledge‑retrieval time 70‑90%.
* Led weekly cross‑functional stand‑ups summarizing analytic findings to clinicians and product managers; recognized for clear, non‑jargon communication.

**Full-stack Data Scientist, Aganitha Cognitive Solutions** Jun 2022 – Nov 2022

* Implemented AWS‑native NextFlow deployment for AAV capsid sequencing; automated raw FASTQ, annotated VCF in < 90 min/sample (4 × acceleration).
* Built clustering & GMM‑based analysis in Python (scikit‑learn) to select optimal capsids crossing blood‑brain barrier; enabled 99.9 % reduction in in‑vivo screens.
* Containerized entire workflow in Docker/Singularity with reproducible Conda environments; fulfilled strict pharma audit requirements.

**Data Scientist, Infosys Ltd** Sep 2018 – Jun 2022

* Developed 40 + universal DB connectors and Python ETL scripts for the Infosys ML Platform; decreased data‑wrangling time 30 % and ensured full unit‑test coverage.
* Containerized IDSMLP with Docker, CI/CD, and Nginx load balancing, reducing deployment cycles 75% & pushing platform uptime to 99.9%.
* Integrated AutoML pipelines (LightGBM, CatBoost) and deployed via Kubernetes & CI/CD, boosting delivery speed by 70 %.
* Championed adoption of Git branching strategy, code review, and automated documentation (Sphinx), raising team code quality metrics by >25 %.
* Automated ingestion & prep pipelines with Pandas, PySpark, and Airflow, cutting data‑wrangling time 30% while maintaining 100% unit‑test coverage and full lineage.
* Built REST‑based SAP CFIN reporting tool (Python+JavaScript) that ended manual data pulls & slashed generation time 40%.

**EDUCATION:**

**The University of Texas at Dallas,** *Master’s in Business Analytics & Artificial Intelligence* | GPA: 3.9 Dec 2024

**Purdue Global – Simplilearn,** *Post Graduate Program in AI and Machine Learning* | GPA: 10 Nov 2021

**Ramaiah Institute of Technology,** *Bachelor of Engineering in Mechanical Engineering* | GPA: 9.8 June 2018

**CERTIFICATIONS:**

* Databricks GenAI Fundamentals (2025)
* Graduate Certificate in Applied Machine Learning (2024)
* Post Graduate Program in AI and Machine Learning(2021)
* Amazon Cloud Computing Practitioner(2024)
* Microsoft Certified: Azure AI/Data Fundamentals (2021)
* Microsoft Certified Azure Fundamentals (2021)

**PUBLICATIONS**:

* Ishwarya Sankaranarayanan. et al., Exploring the Single-Cell Transcriptome Landscape of the Human Dorsal Root Ganglion in Diabetic Peripheral Neuropathy
* Úrzula Franco-Enzástiga. et al., Epigenomic landscape of the human dorsal root ganglion: sex differences and transcriptional regulation of nociceptive genes
* Ishwarya Sankaranarayanan. et al., Persistent changes in the dorsal root ganglion nociceptor translatome governs hyperalgesic priming in mice: roles of GPR88 and Meteorin
* Kevin C Lister. et al., Translational control in the spinal cord regulates gene expression and pain hypersensitivity in the chronic phase of neuropathic pain
* Diana Tavares Ferreira. et al., Deciphering the molecular landscape of human peripheral nerves: implications for diabetic peripheral neuropathy
* Jannis Koerner. et al., Molecular architecture of human dermal sleeping nociceptors
* Juliet M Mwirigi. et al., Expansion of OSMR expression and signaling in the human dorsal root ganglion links OSM to neuropathic pain
* Asta Arendt-Tranholm. et al., Single-cell characterization of the human C2 dorsal root ganglion recovered from C1-2 arthrodesis surgery: implications for neck pain