**Nikhil Nageshwar Inturi**

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**SUMMARY:**

Data Scientist with 7+ years of experience in Generative AI, Applied Machine Learning, Statistical and Predictive Analysis, and Bioinformatics. Proven track record of developing innovative tools for Neuron Detection and bioinformatic analysis pipelines, contributing to multiple research publications. Proficient in Python, R, Shell Scripting, SQL, NoSQL Databases, and Cloud Computing (AWS, Azure), with expertise in Data Visualization (Bokeh, Plotly, Panel dashboards, IPython widgets) and Containerization (Docker, Podman, Kubernetes). Experience with LLMs (fine-tuning LlaMA 3) for research applications.

**EXPERIENCE:**

**Data Scientist, The University of Texas at Dallas** Feb 2023 – Present

* Developed an image segmentation model (Detectron2, YoloV11, FastAI, SAM) to generate barcodes for hDRG neuronal images, improving neuron detection by 15% and processing speed by 40% for the [Visium workflow](https://github.com/utdal/Visium-NextFlow-Pipeline), a seq-based spatial profiling technology.
* Developed and optimized NextFlow pipelines for comprehensive analysis of 50-60 million multi-omics records including Single-cell, [Bulk RNA-seq](https://github.com/utdal/Bulk-RNA-Seq-Nextflow-Pipeline), [Visium (spatial)](https://github.com/utdal/visium10x-spatial-transcriptomics-pipeline), [ATAC-seq](https://github.com/utdal/ATACSeq-NextFlow-Pipeline), and Xenium, enhancing reproducibility and faster biomarker detection by 60%.
* Implemented [containerized bioinformatics workflows](https://hub.docker.com/r/utdpaincenter/bulk_rna_sequencing_nextflow_pipeline), using docker and Podman, increasing the analytical efficiency by 60% in indentifying differentially expressed genes and biomarkers.
* Designed and implemented a CI/CD pipeline to automate statistical analysis similar to DESeq2, enabling investigation of cell-specific mRNA-ribosome associations from [Translating Ribosome Affinity Purification](https://github.com/utdal/TRAP-Analysis) (TRAP) sequencing.
* Developed an ensemble learning predictive model(XGBoost, LightGBM) for detecting rat jaw-size (Pre & Post-VNS) achieving 93% accuracy in VNS simulation data analysis.
* Implemented AI-driven RAG pipelines leveraging LangChain, improving search accuracy on research papers at Center for Advanced Pain Studies, significantly reducing literature review time. This significantly accelerated the ideation-to-data phase of research.
* Collaborated with cross-functional teams from multiple research labs including McGill and University of Queensland, to streamline computational pipelines using workflow management tools and containers for improved efficiency.

**Data Scientist, Aganitha Cognitive Solutions** Jun 2022 – Nov 2022

* Developed and deployed clustering models to identify optimal AAV capsid sequences ("golden templates") for crossing the blood-brain barrier in the AAV Capsid Engineering Project, resulting in a 99.96% reduction in required in-vivo experiments.
* Developed an interactive Midstream and Downstream Analysis tool for AAV Capsid Engineering Project using Python, Cromwell, Bash, and R, providing RESTful APIs for data integration and visualization workflows.
* Integrated midstream sequencing data into Snowflake DB, enabling efficient tracking of AAV capsid sequences and TM-scores across multiple runs, streamlining data management for the AAV Capsid Engineering Project.
* Fine-tuned a [Splice-AI](https://github.com/Illumina/SpliceAI) model(spliceai5) to improve the efficiency of novel splice junction detection in humans, leading to a ~30% reduction in false positives and improving downstream biomarker identification.
* Developed and implemented novel search-based algorithms for the AutoBLAST, a genome browser, doubling efficiency compared to the [Basic Local Alignment Search Tool.](https://github.com/unikill066/BLAST-Search)

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

* Developed 40 database connectors for ICETS-Infosys, integrating SQL databases (MySQL, MSSQL, MariaDB, PostgreSQL, Snowflake, Redshift, Informix, DB2) and NoSQL/document databases (Azure Cosmos DB, AWS Dynamo DB, Cassandra, Elasticsearch, MongoDB) with Python, contributing to valuable internal intellectual property.
* Integrated classification and clustering algorithms from scikit-learn, LightGBM, CatBoost, H2O, AutoML and Keras, significantly expanding the capabilities of the Infosys Data Science and Machine Learning Platform (IDSMLP).
* Reduced deployment times by 75% and significantly boosted operational efficiency by implementing a CI/CD pipeline with Docker for the ICETS-Infosys Data Science and Machine Learning Platform.
* Enhanced IDSMLP tool interface with advanced data visualization techniques, incorporating interactive univariate, bivariate, and multivariate charts using [Bokeh](https://bokeh.org/) and [Plotly](https://plotly.github.io/plotly.py-docs/). Implemented [Nginx load balancing](https://docs.bokeh.org/en/3.1.0/docs/user_guide/server/deploy.html) to improve availability.
* Developed a user-friendly interface for the CFIN tool using Python, enhancing report-generation with the Infosys SAP Team using python(RESTAPIs) and java-script.

**Data Science Project**, PURDUE University Nov 2020 – Oct 2021

* The project enhances stock market prediction using Deep Reinforcement Learning (DRL), Natural Language Processing (NLP), and LSTM to analyze historical data and sentiment from news/social media.
* The model achieves 96.8% accuracy in sentiment analysis, improves stock price prediction by 80%, and outperforms traditional strategies with a Sharpe ratio of 3.0 and ARR of 1.1.

**EDUCATION:**

**The University of Texas at Dallas,** *Master’s in Business Analytics & Artificial Intelligence* Jan 2023 – Dec 2024

**Purdue Global – Simplilearn,** *Post Graduate Program in AI and Machine Learning* Oct 2020 - Nov 2021

**Ramaiah Institute of Technology,** *Bachelor of Engineering in Mechanical Engineering* Aug 2014 - June 2018

**SKILLS:**

**Programming:** Python(Pandas, Numpy, Scipy), R, SQL, Shell Scripting, Java, Workflow languages (Cromwell and Nextflow)

**Bioinformatics:** NGS Data Analytics (scRNA-seq, Bulk RNA-seq, ATAC-seq, Visium and Xenium), Deconvolution

**Machine Learning and AI:** Statistical Modelling, Predictive Analytics, Deep Learning(Keras and PyTorch), NLP(RNN, LSTM, Transformers), Deep Learning(Tensorflow, PyTorch & Keras), Hugging Face, Generative AI(LlamaIndex, LangChain)

**Data Visualization & Reporting:** Power BI, Streamlit, Bokeh, Plotly, RShiny, Matplotlib, Seaborn, Enhanced Volcano Plots

**Databases and Cloud Tools:** MySQL, MSSQL, MariaDB, Informix DB, IBM DB2, Redis, PostgreSQL, Snowflake, Redshift, Azure Cosmos DB, AWS DynamoDB, Cassandra, Elasticsearch, MongoDB, and **AWS** (*certified*) and **Azure** (*certified*)

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

**Web server:** Tornado (Restful API), Django, Flask, xPlore (indexing), and Nginx (high-availability nginx load-balancing)

**CERTIFICATIONS:**

1. [Post Graduate Program in AI and Machine Learning](https://success.simplilearn.com/3477eb04-5e46-4fab-9c3d-78b185a8a842#gs.33finl) Oct 2021
2. [Microsoft Certified: Azure AI Fundamentals](https://www.credly.com/badges/69697008-59c5-44b7-95f5-9f81185cf3fc?source=linked_in_profile) Jul 2021
3. [Microsoft Certified: Azure Data Fundamentals](https://www.credly.com/badges/5fccd0ea-623d-4459-b0e2-45b907ebb7e5?source=linked_in_profile) Jul 2021
4. [Microsoft Certified: Azure Fundamentals](https://www.credly.com/badges/878ac772-4cd4-4e17-a627-379ffeb9b47a?source=linked_in_profile) Jun 2021
5. [Amazon Cloud Computing Practitioner](https://www.credly.com/badges/6be88838-1016-4c6a-9eec-f9c508fd6d8c/public_url) May 2024
6. [Graduate Certificate in Applied Machine Learning](https://www.michaelsutter.com/ediploma?fn=diplomastatuscheck&key=020000007d6e5e48b9f67b8258cbc63d8f541c24a43c9d0dbb90dc754f7c045f1dcd9976e4b70bb0d51c336b6c994e6051bc174fee2b2d685f889067a08feb1f6d7ca818) Jun 2024

**PUBLICATIONS:**

1. [Exploring the Single-Cell Transcriptome Landscape of the Human Dorsal Root Ganglion in Diabetic Peripheral Neuropathy](https://www.jpain.org/article/S1526-5900(24)00135-4/abstract)

*[ Ishwarya Sankaranarayanan, Juliet M Mwirigi,* ***Nikhil Nageshwar Inturi****, Diana Tavares-Ferreira, Theodore J Price ]*

This study used single-nucleus RNA sequencing to analyze dorsal root ganglion (DRG) tissues from diabetic peripheral neuropathy (DPN) patients and healthy donors. The research revealed significant changes in neuronal and non-neuronal cell populations in DPN, providing insights into the condition's molecular mechanisms and potential therapeutic targets.

1. [Epigenomic landscape of the human dorsal root ganglion: sex differences and transcriptional regulation of nociceptive genes](https://pubmed.ncbi.nlm.nih.gov/38586055/)

*[ Úrzula Franco-Enzástiga,* ***Nikhil N Inturi****, Keerthana Natarajan, Juliet M Mwirigi, Khadja Mazhar, Johannes C M Schlachetzki, Mark Schumacher, Theodore J Price ]*

This study used bulk and spatial ATAC-seq to investigate chromatin accessibility in human dorsal root ganglion (hDRG), revealing significant epigenomic sex differences. The findings showed distinct patterns of differentially accessible chromatin regions and transcription factor binding motifs between males and females, suggesting these differences may underlie sex-specific transcriptional responses and pain mechanisms.

1. [Persistent changes in nociceptor translatomes govern hyperalgesic priming in mouse models](https://pubmed.ncbi.nlm.nih.gov/39149295/)

*[ Ishwarya Sankaranarayanan, Moeno Kume, Ayaan Mohammed, Juliet M. Mwirigi****, Nikhil Nageshwar Inturi****, Gordon Munro, K. A. Petersen, Diana Tavares-Ferreira, Theodore J. Price ]*

Hyperalgesic priming, a model of nociceptor plasticity, was studied using paclitaxel treatment and translating ribosome affinity purification (TRAP) to measure changes in mRNA translation in Nav1.8+ nociceptors. The study identified 161 genes with altered translation in the primed state, including upregulated Gpr88 and downregulated Metrn, demonstrating that altered nociceptor translatomes contribute to hyperalgesic priming.

1. [Deciphering the Molecular Landscape of Human Peripheral Nerves: Implications for Diabetic Peripheral Neuropathy. 2024. *Manuscript in Preparation*](https://pmc.ncbi.nlm.nih.gov/articles/PMC11195245/)

*[ Diana Tavares Ferreira, Breanna Q Shen, Juliet M Mwirigi, Stephanie Shiers, Ishwarya Sankaranarayanan, Miriam Kotamarti,* ***Nikhil N Inturi****, Khadijah Mazhar, Eroboghene E Ubogu, Geneva Thomas, Trapper Lalli, Dane Wukich, Theodore J ]*

This study used bulk and spatial RNA sequencing on tibial and sural nerves from diabetic patients to investigate diabetic peripheral neuropathy (DPN) mechanisms. The research revealed key pathway differences between nerve types, shifts in endothelial and immune cells associated with axonal loss, and evidence of perturbed RNA transport in sensory axons, highlighting the importance of axonal mRNA localization in DPN pathogenesis.

1. [Translational control in the spinal cord regulates gene expression and pain hypersensitivity in the chronic phase of neuropathic pain](https://elifesciences.org/reviewed-preprints/100451)

*[ Kevin C. Lister, Calvin Wong, Sonali Uttam, Marc Parisien, Patricia Stecum, Nicole Brown, Weihua Cai, Mehdi Hooshmandi, Ning Gu, Mehdi Amiri, Francis Beaudry, Seyed Mehdi Jafarnejad, Diana Tavares-Ferreira,* ***Nikhil Nageshwar Inturi****, Khadijah Mazhar, Hien T. Zhao, Bethany Fitzsimmons, Christos G. Gkogkas, Nahum Sonenberg, Theodore J. Price, Luda Diatchenko, Jeffrey S. Mogil and Arkady Khoutorsky ]*

Recent research shows that changes in gene expression during chronic neuropathic pain are primarily regulated at the translational level in the spinal cord, particularly in inhibitory neurons. Manipulating translation in inhibitory neurons, especially parvalbumin-positive interneurons, significantly affects pain hypersensitivity, highlighting the crucial role of translational control mechanisms in mediating neuropathic pain.

1. [Molecular architecture of human dermal sleeping nociceptors](https://www.biorxiv.org/content/10.1101/2024.12.20.629638v1)

*[ Jannis Körner, Derek Howard, Hans Jürgen Solinski, Marisol Mancilla Moreno, Natja Haag, Andrea Fiebig, Idil Toklucu, Raya Bott, Ishwarya Sankaranarayanan, Diana Tavares-Ferreira,* ***Nikhil N. Inturi****, Anna Maxion, Lisa Ernst, Ingo Kurth, Theodore Price, Martin Schmelz, Barbara Namer, Shreejoy Tripathy, Angelika Lampert ]*

This study identified oncostatin-M-receptor (OSMR) and somatostatin (SST) as molecular markers for mechano-insensitive C-fibers (CMis) in human skin, which are associated with neuropathic pain. The research combined single-cell transcriptomics, electrophysiology, and human volunteer experiments to characterize these "sleeping nociceptors," providing new insights into neuropathic pain mechanisms and potential therapeutic targets.