

## [Nikhil Nageshwar Inturi](#)

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### SUMMARY:

**Computational Data Scientist and Neuroinformatician** with **7+ years** of experience in **drug discovery** and **pharmaceutical research**, specializing in **NGS data analysis**, **multi-omics integration**, and **biomarker discovery**. Proven track record of improving **data processing efficiency by 50%+** using **docker** and contributing to **10+ research papers**. Proficient in **Python, R, Unix/Linux, Bash, Nextflow**, and **cloud computing**, with expertise in **data visualization** (Bokeh, Plotly, Ipython-widgets, RShiny, Gradio), **workflow automation** and **containerization (Docker)**. Experience with **LLMs (LlamaIndex and LangChain)** for research applications. Published in leading journals including **Nature** and **The Journal of the International Association for the Study of Pain**. Certified in **Cloud Computing (Azure, AWS)**. Passionate about translating complex biological data into actionable insights and leading cross-functional teams to solve challenging problems in **computational biology**.

### SKILLS:

Programming: Python, R, SQL, Shell Scripting, Java, HTML, CSS, Workflow languages (Cromwell and Nextflow)

Data Analytics: Data Science, Machine Learning, Natural Language Processing, Deep Learning(Keras and PyTorch), Object Detection

AI/ML and Cloud Tools: Hugging Face, LlamaIndex, LangChain, **AWS (certified)** and **Azure (certified)**

SQL Databases: MySQL, MSSQL, MariaDB, PostgreSQL, Snowflake, Redshift, Informix, and DB2

NoSQL Databases: Azure CosmosDB, AWS Dynamo DB, Cassandra, Elasticsearch, and MongoDB

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

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

### EXPERIENCE:

#### Data Scientist and Neuroinformatician

Feb 2023 – Present

Center for Advanced Pain Studies, The University of Texas at Dallas, Richardson, Texas

1. Developed **image classification** and **segmentation** models (**Detectron2**, **YoloV11**, **FastAI**, **SAM**) to generate barcodes for **hDRG neuronal images**, improving barcode detection by 15% for the **Visium workflow**.
2. Developed and optimized **NextFlow pipelines** for comprehensive analysis of multi-omics datasets including **Single-cell**, **Bulk RNA-seq**, **Visium (spatial)**, **ATAC-seq**, and **Xenium**.
3. Implemented **containerized workflows**, resulting in a 60% increase in analytical efficiency in identification of *differentially expressed genes* and *biomarkers*, using **docker** and **podman**.
4. Developed **predictive models** of **rat jaw-size** (Pre & Post-VNS) using **classification** and **ensemble learning** techniques (bagging, boosting). Decoded complex neural patterns, achieving 80% accuracy in predicting key biomarkers.
5. Developed and deployed an **AI agent**, fine-tuning **Meta's Llama3** model, automating *scientific literature review and genomic dataset* analysis. This significantly accelerated the *ideation-to-data phase of research*.

#### Data Scientist

Jun 2022 – Nov 2022

Aganitha Cognitive Solutions, Hyderabad, India

1. 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*.
2. 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**.
3. 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*.
4. **Fine-tuned a Splice-AI 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*.
5. Developed and implemented **novel search-based algorithms** for the **AutoBLAST**, a genome browser, doubling efficiency compared to the **Basic Local Alignment Search Tool**.

#### Technology Analyst

Sep 2018 – Jun 2022

Infosys Ltd, Hyderabad, India

1. 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.
2. 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)**.
3. **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**.
4. Enhanced IDSMLP tool interface with **advanced data visualization techniques**, incorporating interactive **univariate, bivariate, and multivariate charts** using **Bokeh** and **Plotly**. Implemented **Nginx load balancing** to improve **availability**.
5. 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**.

## EDUCATION:

The University of Texas at Dallas, *Master's in Business Analytics & Artificial Intelligence*

Jan 2023 - Present

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

## CERTIFICATIONS:

1. [Post Graduate Program in AI and Machine Learning](#) Oct 2021
2. [Microsoft Certified: Azure AI Fundamentals](#) Jul 2021
3. [Microsoft Certified: Azure Data Fundamentals](#) Jul 2021
4. [Microsoft Certified: Azure Fundamentals](#) Jun 2021
5. [Amazon Cloud Computing Practitioner](#) May 2024
6. [Graduate Certificate in Applied Machine Learning](#) Jun 2024

## PUBLICATIONS:

1. [Exploring the Single-Cell Transcriptome Landscape of the Human Dorsal Root Ganglion in Diabetic Peripheral Neuropathy](#)  
[ 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
2. [Epigenomic landscape of the human dorsal root ganglion: sex differences and transcriptional regulation of nociceptive genes](#)  
[ 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
3. [Persistent changes in nociceptor translomes govern hyperalgesic priming in mouse models](#)  
[ 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 translomes contribute to hyperalgesic priming.
4. [Deciphering the Molecular Landscape of Human Peripheral Nerves: Implications for Diabetic Peripheral Neuropathy. 2024.](#)  
[Manuscript in Preparation](#)  
[ 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
5. [Translational control in the spinal cord regulates gene expression and pain hypersensitivity in the chronic phase of neuropathic pain](#)  
[ 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.
6. [Molecular architecture of human dermal sleeping nociceptors](#)  
[ 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.