

Nikhil Nageshwar Inturi

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SUMMARY:

Data Scientist with 7+ years of experience in ML, AI, and Bioinformatics, specializing in building predictive models, optimizing ETL pipelines, and deploying scalable AI solutions in cloud environments (AWS, Azure). Proficient in data visualization (Plotly, Bokeh), containerization (Docker, Kubernetes), and CI/CD workflows.

EXPERIENCE:

Data Scientist, The University of Texas at Dallas

Feb 2023 – Present

- Built ensemble learning models (XGBoost, LightGBM) for rat jaw-size prediction, achieving 93% accuracy and improving predictive performance in VNS simulation experiments.
- Developed clustering models, processing 70M+ reads across ~4900 features, using shared nearest neighbor clustering to identify pain-related biomarkers.
- Developed image segmentation models (Detectron2, YoloV11) to detect neurons, increasing detection accuracy by 15% and reducing processing time by 95%.
- Developed a GPT-powered RAG pipeline (LangChain) for literature review and dataset integration at CAPS, reducing research and analysis time by 40% for the Center for Advanced Pain Studies.
- Automated statistical analysis using a CI/CD pipeline, enabling rapid mRNA-ribosome association analysis in TRAP sequencing.
- Streamlined computational pipelines in collaboration with researchers at McGill (CAN) and University of Queensland (AUS).

Data Scientist, Aganitha Cognitive Solutions

Jun 2022 – Nov 2022

- Developed clustering models(K-means, GMM) to identify AAV capsid sequence identification that cross the blood-brain-barrier, resulting in a 99.96% reduction in required in-vivo experiments.
- Built an interactive analysis tool to process 30M+ records for AAV Capsid Engineering, integrating Python, Cromwell, Bash, R, and RESTful APIs for data visualization workflows.
- Fine-tuned a deep learning model (Splice-AI - spliceai5) to improve novel splice junction detection in humans, leading to a ~30% reduction in false positives and improving downstream biomarker identification.
- Enhanced genome search efficiency by developing advanced search algorithms for AutoBLAST, achieving 2x faster performance compared to the traditional BLAST search.

Data Scientist, Infosys Ltd

Sep 2018 – Jun 2022

- Built 40+ database connectors (SQL, NoSQL, Cloud) in Python, improving data accessibility for ML pipelines.
- Integrated ML classification and clustering algorithms (Scikit-learn, LightGBM, CatBoost, H2O, AutoML, Keras) into Infosys Data Science Platform (IDSMLP), enhancing model automation and predictive capabilities of the tool.
- Implemented ML-based predictive models (LightGBM, CatBoost, XGBoost) to optimize financial analytics the CFIN team.
- Automated data ingestion & processing pipelines using Pandas, PySpark, and Airflow, reducing data preparation time by 30% while ensuring data quality, traceability, and 100% code coverage with robust testing.
- Automated SAP CFIN (S/4 HANA) reporting in Python, eliminating manual data extraction inefficiencies and reducing report generation time by 40% through cross-functional collaboration.
- Implemented Containerization strategies using docker for AutoML platform to streamline deployments.

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 | GPA: 3.9

Jan 2023 – Dec 2024

Purdue Global – Simplilearn, Post Graduate Program in AI and Machine Learning

| GPA: 10

Oct 2020 - Nov 2021

Ramaiah Institute of Technology, Bachelor of Engineering in Mechanical Engineering

| GPA: 7.8

Aug 2014 - June 2018

SKILLS:

Programming: Python(NumPy, Pandas, SciPy), R, SQL, Shell Scripting, Java, Workflow languages (Cromwell and NextFlow), DQL
Machine Learning and AI: Supervised and Unsupervised Learning, Statistical and Predictive Modeling, Deep Learning(Keras and PyTorch), NLP(RNN, LSTM, Transformers), Hugging Face, Generative AI(LlamaIndex, LangChain)
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

CERTIFICATIONS:

- Databricks GenAI Fundamentals
- Graduate Certificate in Applied Machine Learning
- Post Graduate Program in AI and Machine Learning
- Amazon Cloud Computing Practitioner
- Microsoft Certified: Azure AI/Data Fundamentals

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 transcriptomes 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 transcriptomes 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.