## Satya Nandivada

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#### **SUMMARY**

Deep Learning Systems Engineer with expertise in distributed GPU training, model optimization, and scalable ML pipeline architecture.

#### TECHNICAL SKILLS

**Deep Learning Frameworks:** PyTorch, HuggingFace, TensorRT, TorchDynamo, Triton, CUDA, CUTLASS **Optimization Techniques:** Pruning, Quantization, Sparsity, Mixed Precision, Tensor Parallelism, Model Sharding

Programming & Systems: Python, C++, Docker, Kubernetes, AWS, GCP, Nextflow

Profiling & Performance Tools: Nsight Systems, PyTorch Profiler, CUDA Graphs, Torch Compile Stack

Other: Graph Neural Networks, Diffusion Models, ODE Solvers, Large Language Models

#### **EXPERIENCE**

# DeepOMAP L.L.C, Portland, Maine

Founding Engineer | Computational Biologist

March 2025 - Present

- Designed and maintained ETL pipelines for high-throughput multi-omics datasets using Nextflow, Apache Arrow, and Parquet, enabling efficient data ingestion, transformation, and cross-cloud integration.
- Researched and implemented advanced **deep learning** architectures (MLP, GAT, Transformer) for cross-modal genomic data mapping, leveraging **multi-head attention** and complex embedding optimization.
- Engineered GPU-aware memory management for large-scale ML systems, including dynamic device selection, mixed-precision training, asynchronous data loading, and CPU fallback mechanisms.
- Optimized model performance through resource-aware scheduling, data-parallel/distributed training (DDP), and TensorRT-based inference acceleration, balancing computational complexity with infrastructure constraints.

### Vanaja Systems Biology lab, Northeastern University

Computational Biology Research Assistant/ Fall-Coop (2024)

March 2023 – Present

- Experienced in developing various Deep Learning models (GAT, Variation Encoder, Transforer Encoders) for sequential gene expression analysis, achieving accurate AML subtype classification and measurable improvements in relapse prediction accuracy.
- Build end-to-end single-cell omics pipelines from 10x Genomics preprocessing through Scanpy/Seurat workflows with Harmony/scVI integration seamlessly combining RNA-seq, ATAC-seq, and CITE-seq modalities
- Constructed mechanistic ordinary differential equation (**ODE**) models to simulate protein-protein interaction networks and elucidate dose-dependent signaling pathway dynamics under drug perturbation conditions.

#### GAME L.L.C. Remote

Software Engineer

July 2025 – Present

- Designed and deployed a PostgreSQL full-text search microservice with synonym expansion, ranked retrieval, and safe parameterization; scaled to millions of records for LLM-augmented semantic querying.
- Built backend systems in **NestJS** with modular architecture, connection pooling, structured logging, and MLOps support for large-scale **data ingestion pipelines**.
- Diagnosed and resolved cross-platform **Firebase/Flutter initialization crashes**, reducing critical setup failures to zero. Worked with distributed, microservice-oriented architecture, ensuring performance and compliance

# Conduent Inc, Hyderabad, India

Application Developer-1, Full-Time

*July 2021 – December 2022* 

- Built large-scale React.js, Node.js, and Spring Boot microservices with **Apache Kafka** for real-time streaming, reducing latency and enabling reliable distributed communication.
- Built Spark and Hadoop-based data pipelines and containerized them on Kubernetes for fault-tolerant, scalable batch analytics and deployment

## **EDUCATION**

Northeastern University *Electrical and Computer engineering*Gitam University *Electronics and Communication engineering* 

Jan 2023 - May 2025

March 2017 - April 2021

# **CONFERENCES**

**Poster and Flash Talk Presentation:** A complete mathematical model of the MAPK pathway predicts mechanisms of resistance to BRAF inhibition in BRAF V600E-driven tumors. International Conference of Systems Biology (ICSB 2024), IIT Mumbai, India. December 2024.