Dev Patel

US Citizen

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Education

University of North Dakota	**May 2024**
Doctorate of Science in Bioinformatics/Data Science	*Location, USA*

- − Best Paper Award at academic conference, Essay Winner, Best Thesis Presenter Award

University of North Dakota	**December 2018**
Bachelor of Science in Biochemistry	*Location, USA*

Skills

Languages: Python, JavaScript, TypeScript, SQL, R, Java, Power BI, Data Analysis, Predictive Modeling
Frameworks/Technologies: React, Node.js, Docker, Flask, AWS, Terraform, TensorFlow
Developer Tools: Git, GitLab CI/CD, Jenkins, Jest, Selenium, Linux, Jira, LaTeX

Experience

Aethero	**Aug 2024 – Present**
Data Scientist I	*USA*

- − Developed predictive models integrating IoT and biological datasets; improved accuracy of environmental/bioinformatics forecasts by 20%.
- − Designed and deployed machine learning workflows (Python, R, TensorFlow, scikit-learn) for large-scale data analysis.
- − Built automated data pipelines on AWS using Terraform and Docker, reducing end-to-end processing time by 25%.
- − Created interactive dashboards (React, Flask) for real-time visualization of model outputs and multi-omics datasets.

University of North Dakota	**Jan 2022 – Aug 2024**
Graduate Research Assistant	*USA*

- − Developed real-time environmental analytics pipeline in Python, integrating AWS + IoT data streams; improved HAB forecasts by 98%.
- − Built interactive visualization dashboards (React, Flask) to support research collaboration.
- − Published peer-reviewed papers on predictive analytics in environmental informatics.
- − Mentored undergraduate assistants in data science workflows and statistical modeling.

Dakota Venture Group	**Sep 2022 – Feb 2024**
Managing Associate – Business Intelligence	*USA*

- − Designed interactive dashboards (React.js, D3.js) to track metrics and inform investment decisions.
- − Automated reporting pipelines, saving 15+ hours per month.
- − Presented quarterly analyses that contributed to a 20% portfolio increase.

Projects

Genomics Data Processing Pipeline | *Python, Nextflow, Docker, R* — **2023**

- − Designed and deployed an automated pipeline for RNA-Seq and metagenomic datasets using Nextflow and Docker, ensuring reproducibility across HPC and cloud environments.
- − Implemented quality control, read alignment, and differential expression analysis workflows; reduced processing time by 30%.
- − Integrated downstream analysis in R/Bioconductor, producing interpretable reports for biological collaborators.
- − Optimized resource allocation across HPC clusters, lowering computational costs by 15%.

Multi-Omics Analytics Dashboard | *Python, Flask, React, R, SQL* — **2022 – 2024**

- − Developed an interactive dashboard for visualization of transcriptomics, proteomics, and environmental datasets, enabling cross-disciplinary collaboration.
- − Integrated predictive modeling (random forest, ARIMAX) with real-time data ingestion from SQL and IoT sensors.
- − Delivered cross-platform web interface with responsive design, used by research teams for decision-making.
- − Implemented user authentication and role-based access controls, ensuring data security and integrity.