Nishant Joshi

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PERSONAL SUMMARY

Machine learning engineer and computational scientist with deep expertise in multi-modal biological data integration, scalable ML and DL pipelines, and FAIR-compliant research software development. Proven track record processing large-scale, high-dimensional datasets (3.6B+ data points), designing reproducible AI workflows, and implementing production-grade tools on HPC infrastructure. Passionate about bridging computational innovation and biological discovery to accelerate impact across life sciences domains, with particular interest in multi-omics data analysis and translational applications.

SKILLS

Machine Learning & Statistical Methods	Python (NumPy, SciPy, scikit-learn)	PyTorch, TensorFlow, Keras	Supervised & unsupervised learning, Dimensionality reduction (manifold learning, PCA, t-SNE), Clustering algorithms , Statistical hypothesis testing & multiple comparison correction	Time-series analysis , Generative models (GANs)
Data Integration & Analysis	Multi-modal data fusion	High-dimensional data analysis	FAIR data principles	Biostatistics	Signal processing	Feature engineering and extraction
Software Engineering & High-Performance Computing	Version control (Git)	Containerization (Docker, Kubernetes)	CI/CD pipelines	HPC infrastructure (SLURM, CUDA, Horovod, GPU optimization)	Linux	Reproducible code practices & testing	Code documentation
Secondary Tools & Languages	MATLAB, R, C++ (ROS, MORSE), LaTeX

RESEARCH EXPERIENCE

PhD Candidate (Thesis approved)   05/2021 — 10/2025
Donders Institute for Brain, Cognition and Behavior | Radboud University, NL
Prof. Dr. Tansu Celikel *(Georgia Tech, USA)* and **Dr. Fleur Zeldenrust** *(Radboud, NL)*   *Nijmegen, Netherlands*

- Designed and deployed a scalable end-to-end data analysis pipeline (Python/ML) to process large-scale, high-dimensional biological data (3.6+ billion data points from 1200+ electrophysiological recordings) for multi-modal feature extraction, integration, data driven phenomenological neuron models and statistical modeling.
- Applied Siamese networks and manifold learning to extract biological signatures from high-dimensional time-series data.
- Spearheaded collaborations with the Netherlands eScience center. Applying FAIR compliant data management methods and advance machine learning techniques to single-cell data.
- Collaborated with Gent University on developing novel methods and architectures to study the effect of heterogeneity on biological networks.
- Actively participated in scientific dissemination through conference posters and abstracts. Also, designed course material for the dutch brain bee and carried out outreach activities.

MSCA Visiting Researcher   02/2024 — 04/2024
Prof. Dr. Panayiota Poirazi *(IMBB Forth, GR)*   *Iraklion, Greece*

- As a part of the MSCA ITN, I developed a pipeline for fitting Generalized Leaky Integrate-and-Fire models to single unit electrophysiological data.
- Developed analysis workflows to incorporate the passive features extracted from the model into unsupervised clustering results.

Research Software Engineer (MSCA Secondment)   02/2023 — 05/2023
Netherlands eScience Center   *Amsterdam, Netherlands*

- Designed scalable unsupervised clustering pipelines for high-dimensional biological data, emphasizing reproducibility best practices: version control (Git), containerization (Docker), CI/CD pipelines, and FAIR data principles.

- Led collaboration between eScience Center and Donders Center for Neuroscience (DCN), resulting in 2 peer-reviewed publications and multiple conference presentations. Mentored junior developers on software engineering best practices.
- Translated research innovations into production-grade tools suitable for collaborative and clinical use.

Research Assistant   **02/2020 — 04/2021**
Prof. Dr. Abigail Morrison (INM6/IAS6 – Forschunszentrum Jülich, DE)   *Jülich, Germany*

- Developed scalable pipelines for designing, training and extracting the dynamical scaffolding of more than 100 RNNs and SNNs using GPU nodes on JURECA HPC infrastructure.
- Performed Multi-dimensional scaling and SV-CCA to study representational similarity of RNNs on 3 bit Flip-Flop task.
- Designed study material on GANs for a seminar course.

EDUCATION

PhD – Computational Neuroscience (thesis accepted; defense expected June 2026)   **05/2021 — 10/2025**
Radboud University, Nijmegen, NL

Master of Science – Computer Science and Engineering (Dual Degree)   **10/2018 — 11/2020**
KTH Royal Institute of Technology, Stockholm, SE & TU Berlin, Berlin, DE

Bachelor of Engineering – Mechanical/Industrial Engineering   **08/2013 — 05/2017**
R.V. College of Engineering, Bangalore, IN

OUTREACH AND TEACHING ACTIVITIES

- Presented my research in the form of posters at 4 international conferences
- Supervised 4 students (2 bachelor and 2 master)
- Designed Course Material for Dutch Brain Bee and TA for Mathematics for Biology
- Presented my methods at AI for Science symposium (Radboud University)

ACHIEVEMENTS

- Marie Skłodowska Curie ITN fellowship   2021 — 2024
- EIT Digital excellence scholarship   2018 — 2020
- Best thesis in the department of Industrial Engineering   2017

PUBLICATIONS

- **Joshi N**, van Der Burg S, Celikel T, Zeldenrust F (2025) Neuronal identity is not static: An input-driven perspective. PLoS Comput Biol 21(12): e1013821. https://doi.org/10.1371/journal.pcbi.1013821

In preparation

- **Joshi N**, van Der Burg S, Celikel T, Zeldenrust F. Neuromodulatory Control of Cortical Function: Cell-Type Specific Reshaping of Neuronal Information Transfer
- Iacob[†] S, **Joshi[†] N**, Dambre J, Zeldenrust F. Timescale Heterogeneity in Reservoir Computing

Posters

- Iacob, S.[†], **Joshi, N.[†]**, Dambre, J., Zeldenrust, F. (2024) Co-evolved structural and temporal network heterogeneity. Bernstein Conference 2024. https://doi.org/10.12751/nncn.bc2024.309
- **Joshi, N.**, Celikel, T., Zeldenrust, F. (2023) High dimensional clustering reveals heterogeneity in excitatory and inhibitory cells in the neocortex. Bernstein Conference 2023. https://doi.org/10.12751/nncn.bc2023.095