

Enes Senel

Senior Scientist · Machine Learning & Computational Biology

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PROFILE

Senior computational biologist and machine-learning scientist with 10+ years designing, leading, and shipping ML systems for high-stakes biomedical decisions. Technical lead for single-cell multi-omics in oncology and immunology at Johnson & Johnson Innovative Medicine — setting analytical strategy, mentoring scientists, and translating computational results into clinical and CMC decisions. PhD on machine learning for spatial transcriptomics (Max Delbrück Center), with open-source tools used in academia and industry. Earlier career spans real-time computer vision for image-guided medical robotics, deep learning for pharmaceutical QC, and multi-omics integration in computational neuroscience — a computer-science foundation that travels well across applied ML domains.

CORE EXPERTISE

Leadership & strategy: technical leadership, scientific strategy, mentorship, cross-functional alignment with discovery, clinical, and CMC; managing external consultants and CROs.

Computational biology: single-cell & spatial multi-omics (scRNA-seq, CITE-seq, ATAC, spatial), biomarker discovery, cell-therapy analytics, optimal-transport tissue reconstruction.

Machine learning: deep learning, computer vision, transformers and protein language models (ProtBERT), domain adaptation, multi-modal integration, reproducible benchmarking.

Engineering: Python, R, C++, CUDA, PyTorch, TensorFlow, Nextflow, Docker, SQL, Git; production-grade pipelines, reproducibility tooling, regulatory-grade documentation.

Adjacent domains: medical robotics & image-guided systems, pharmaceutical QC, computational neuroscience.

SELECTED EXPERIENCE

Senior Scientist, Computational Biology

Johnson & Johnson Innovative Medicine · Berlin · Aug 2025 — Present

- Technical lead for single-cell multi-omics in oncology & immunology; set analytical strategy across multiple parallel discovery and translational programs.
- Mentor junior scientists and direct external consultants; raise the bar on rigor, reproducibility, and code quality across the group.
- Partner with wet-lab, clinical, and CMC stakeholders to translate ML outputs into target-selection, mechanism-of-action, and go/no-go decisions on assets in development.

Data Scientist, Computational Biology

Johnson & Johnson Innovative Medicine · Berlin · Oct 2023 — Jul 2025

- Architected and shipped automated Nextflow/Python pipelines for scRNA-seq, CITE-seq, and multi-modal analyses — turned week-long manual workflows into reproducible, audited runs.
- Led single-cell analyses underpinning biomarker discovery for a clinical-stage CAR-T program (CARTITUDE) and CMC process characterization, contributing to regulatory-grade documentation.
- Established team conventions for reproducibility (containerization, version-controlled pipelines, QC standards) adopted as the default for new projects.

Doctoral Researcher — Computational Biology & Machine Learning

Max Delbrück Center for Molecular Medicine · Humboldt University of Berlin · Oct 2019 — Sep 2023

- Designed and led **Optocoder**, an ML pipeline decoding barcoded transcripts from imaging-based spatial transcriptomics — published in NAR Genomics & Bioinformatics; adopted by external labs.
- Re-architected **novoSpaRc** (optimal-transport reconstruction of tissue architecture from scRNA-seq) for scalability to whole-tissue datasets; co-author on Nature Protocols paper.
- Co-inventor on US patent for 3D spatial gene-expression reconstruction. Owned full lifecycle: problem framing, method, benchmarking, open-source release, user support.

Visiting Scientist — Protein Language Models

The Hebrew University of Jerusalem · Rehovot · Feb 2023 — Apr 2023

- Independent short-term project applying ProtBERT to discover novel anti-insecticidal proteins from raw sequence data — combined transfer learning with biological priors to guide experimental validation.

Earlier — Applied ML across Robotics, Pharma & Neuroscience

Coriolis Pharma · Max Planck Institute for Brain Research · Ozyegin Robotics Lab · 2014 — 2019

- **Coriolis Pharma (2019):** shipped an end-to-end deep-learning system (PyTorch/TensorFlow) for automated particle detection in pharmaceutical QC; handed off as a self-serve internal tool.
- **Max Planck (2018–2019):** multi-omics ML integration bridging proteomic and transcriptomic datasets — early work in cross-modality reasoning later applied at industry scale.
- **Ozyegin Robotics Lab (2014–2016):** real-time needle-tip localization and tracking from ultrasound for image-guided biopsy robots; C++/CUDA coupling vision with robot control. Four peer-reviewed publications (ICRA, ICAR, Mechatronics).

EDUCATION

Ph.D. Computational Biology — Humboldt University of Berlin · Max Delbrück Center · 2019 — 2026 (expected)

M.Sc. Computer Science — Technical University of Munich · 2016 — 2019 · DAAD MSc Scholarship

B.Sc. Computer Science — Ozyegin University, Istanbul · 2012 — 2016

SELECTED OUTPUTS

Patent: US20240257914A1 — Method and system for 3D reconstruction of tissue gene-expression data (2022).

Open source: Optocoder (lead author) · novoSpaRc (core contributor) — ML tools used by academic labs and industry for spatial transcriptomics.

Selected publications: Blood Cancer Discovery (CARTITUDE-1 biomarkers, 2025) · NAR Genomics & Bioinformatics (Optocoder, 2022) · Nature Protocols (novoSpaRc, 2021) · Cytotherapy (2021) · Mechatronics (2019) · ICRA (2016, 2017).

Service: Helmholtz Juniors — elected representative for ~8,000 PhD students (2022–2023). MDC PhD Representatives — awareness team (2020–2023).

Languages: English (fluent) · German (advanced) · Turkish (native).

OPEN-SOURCE PROJECTS

Optocoder — ML pipeline for decoding spatially indexed barcoded bead arrays in imaging-based spatial transcriptomics. Lead author and maintainer. Adopted by external labs; published in NAR Genomics & Bioinformatics.

novoSpaRc — Optimal-transport reconstruction of tissue architecture from dissociated single-cell RNA-seq. Core contributor; re-architected for scalability to whole-tissue datasets. Nature Protocols (2021).

ProtBERT for agricultural biotech — Independent visiting project applying protein language models to discover novel anti-insecticidal proteins from raw sequence data (Hebrew University).

Image-guided biopsy robotics — Real-time ultrasound needle-tip tracking with C++/CUDA; coupled vision with robot control loop. Four peer-reviewed publications (ICRA, ICAR, Mechatronics).

WHAT I BRING TO A TEAM

- **Translates strategy into systems.** I take ambiguous biological or product questions and turn them into reproducible analytical frameworks teams can rely on.
- **Builds production from research.** Comfortable bridging exploratory analysis and engineered pipelines — Nextflow, containers, version-controlled workflows, regulatory-grade documentation.
- **Grows people and standards.** Mentor scientists, run code reviews, and establish team-wide conventions that compound across projects.
- **Moves across domains.** Computer-science training, ML method development, biology, and hardware-adjacent computer vision — I learn new domains quickly and ship in them.