

Julianna Lamm

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Reproductive computational biologist with 5 years of experience applying statistical modeling, machine learning, and advanced clustering to identify phenotypic responses in multi-omics, flow cytometry, and high-content imaging datasets.

EDUCATION

University of California, Berkeley | *B.A Molecular and Cell Biology*

May 2020

Fordham University | *M.S Computer Science* | GPA 3.94

May 2025

WORK EXPERIENCE

Translational Data Science Consultant - ExSeed Health - Remote (freelance)

Jun 2025 - Present

- Applied statistical modeling and unsupervised learning (PCA, UMAP, Gaussian Mixture Models, k-means) to integrate multivariate features from high-dimensional time-series datasets, identifying distinct phenotypic subtypes and functional states.
- Designed interactive Python dashboards enabling clinical, R&D, and manufacturing teams to explore population shifts across treatments in real time, supporting data-driven stratification and evaluation.
- Developed end-to-end computational pipelines for data cleaning, QC, clustering, and visualization, scalable to >80,000 tracked trajectories and 400 patients.

Zhou Lab - Computer Vision Graduate Student Researcher - New York, NY

Aug 2023 - May 2025

- Built deep learning pipelines for segmentation and morphological quantification of neural tissue from high-resolution microscopy datasets, supporting large-scale 3D reconstruction and circuit mapping.

Dewpoint Therapeutics -Data Science Research Associate II & I, - Boston, MA

May 2021 - Mar 2023

- Developed image processing algorithms and statistical scoring methods to objectively rank compound efficacy, eliminating subjective bias in lead compound identification for drug discovery programs
- Performed cell painting assays and tissue-based immunofluorescence (IF) to assess phenotypic responses to compound libraries in a drug discovery setting.
- Automated high-throughput microscopy analysis for drug screening campaigns, acquiring and processing thousands of IF images weekly using confocal, high content imaging systems and automated microscopy platforms (Opera Phenix, CellProfiler)
- Designed and conducted experimental data workflows for novel target deconvolution platform including biochemical assays to validate molecular targets (qPCR, RNA-seq, protein purification, click-chemistry bioconjugation)
- Performed primary and immortalized neuron culture under sterile conditions for use in downstream assays and phenotypic screens

Ohana Biosciences - Research Associate - Cambridge, MA

Jun 2020 - Apr 2021

- Extracted quantitative phenotypic metrics from high-dimensional single-cell data to inform diagnostic development and assay optimization
- Advanced early diagnostics for male fertility as part of the foundational research team dedicated to building the industry's first sperm biology platform
- Performed sperm DNA fragmentation, surface marker profiling, and immunofluorescence (IF) assays, and flow cytometry-based cell surface characterization assays to evaluate sperm quality and identify phenotypic biomarkers.

Research Assistant - Lishko Lab, UC Berkeley, CA

Sept 2019 - Jun 2020

- Independently developed Python-based Computer Assisted Sperm Analysis (CASA) system from scratch, building computer vision algorithms to extract kinematic parameters (velocity, path curvature, motility patterns) from brightfield microscopy videos.
- Designed end-to-end image processing and time-series tracking pipeline for automated sperm analysis, forming technical foundation for subsequent deep learning applications in reproductive biology

ADDITIONAL PROJECTS

Interactive Bioinformatics Data Dashboard: Built a web-based, story-driven platform to visualize clustering results from microscopy-based motion tracking. Combined narrative structure with interactive charts to translate complex computational results into accessible insights for cross-disciplinary teams.

Automated Motility Classification App: Developed a standalone computer vision application for automated classification of motility patterns from microscopy videos. Enabled biological subtype labeling (e.g., progressive, non-progressive, hyperactivated) without the need for specialized equipment, allowing standardized analysis across laboratories.

Deep Learning Model Optimization for Sperm Detection: Enhanced YOLOv8 architecture for microscopy-based object detection and motion classification. Improved performance from a 0.22 mAP baseline to .412 mAP (**87% improvement**), optimizing for biological noise, occlusion, and video artifacts across 29,000+ frames.

PUBLICATIONS

Mitochondrial uncouplers impair human sperm motility without altering ATP content. *Biology of Reproduction*, 2023.

SKILLS

Languages: Python, SQL, JavaScript, HTML/CSS **Cloud & Infra:** AWS S3, Google Cloud, Git, Streamlit, Jupyter, CometML **Data and ML:** Pandas, NumPy, Matplotlib, Scikit-learn, PyTorch, Model Optimization **Web & Visualization:** React, D3.js, Dash, [Next.js](#) **Wet-lab:** RNA-seq, flow cytometry, immunofluorescence, hiPSC maintenance, stem-cell differentiation, mammalian/neural cell culture, high-throughput screening, qPCR, biochemical assays