

Vedrana Ivezić

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Ph.D student in Medical Informatics at UCLA with experience developing representation learning models for multimodal biomedical data, including cytology, ultrasound, and wearables. Demonstrated expertise in Python, PyTorch, and large-scale self-supervised learning. Proven track record in building scalable AI systems for healthcare applications, with a focus on improving model generalization and robustness in low-resource clinical settings. Proven track record of publications in top venues such as CVPR, MICCAI, and JAMIA.

EDUCATION

University of California, Los Angeles, CA

PhD student in Medical Informatics

Sept. 2022 - May 2027

(*expected*)

Princeton University, Princeton, NJ

B.A. Computer Science

Sept. 2018 - May 2022

GPA 3.74

Minor in Quantitative and Computational Biology

Magna cum laude

PUBLICATIONS

**Co-first authors. Please see more on [Google Scholar](#).*

EXPERIENCE

Medical Informatics PhD Student - UCLA

Sept 2022 - Present

Biomedical AI Research Lab, University of California, Los Angeles

- Developing an automated thyroid cancer diagnostic pipeline using radiology and cytology image analysis
- Improving thyroid cancer risk stratification from cytological biopsy images with deep learning techniques
- Building a Fitbit foundation model by integrating temporal patterns with large language models
- Performing statistical analysis and predictive modeling on a private heart failure Fitbit dataset

Undergraduate Researcher

Sept. 2020 - May 2022

Troyanskaya Lab, Princeton University

- Developed cell type-specific functional gene networks through Bayesian data integration to enhance gene prediction accuracy
- Leveraged machine learning to prioritize candidate genes relevant to kidney disease mechanisms
- Benchmarked cell type prediction methods across single-cell and single-nucleus RNA-seq datasets
- Analyzed differential gene expression to identify molecular changes across diseased kidney cell types

Research Intern

June 2021 - April 2022

Jarosz Lab, Stanford University

- Analyzed FASTQ sequencing data from yeast strains to identify gene essentiality and construct gene interaction networks
- Applied statistical and computational methods to evaluate gene correlations associated with prion phenotypes

Research Intern

June 2019 - Aug. 2019

Tolić Group, Insitute Ruder Bošković, Zagreb, Croatia

- Imaged and analyzed mitotic spindles during pro-metaphase and metaphase to study spindle dynamics.
- Utilized transfection, cell splitting, and protein tagging methods to analyze PRC1 in pro-metaphase

Research Intern

Intellectual Ventures Laboratory - Bellevue, WA

• Co-Inventor: “Methods and System for Concentration of Samples for Lateral Flow Assays”

• Developed diagnostic assays to enable rapid and accurate identification of tuberculosis infection

June 2017 - Aug. 2017

PROJECTS

Robust cytological image representation learning

Feb. 2025 - present

• Developed the first cytology foundation model using self-supervised learning

• Curated the largest cytology dataset of 1.4 million images using public and private datasets

• Outperformed natural image and histopathology foundation models on 2 out of 3 tasks

Wearable device adherence in heart failure patients

Feb. 2023 - Sept. 2024

• Led data processing and statistical analysis for a randomized controlled trial

• Evaluated digital monitoring adherence in heart failure patients

• Identified signal patterns and adherence trends from Fitbit and symptom-tracking survey data

SKILLS

Deep learning

Self-supervised training, contrastive learning, multi-modal learning, transformers, CNNs

Technical

Python, Pytorch, pandas, SQL, C, numpy, Scipy, scikit-learn, git, openCV, OpenSlide, Hugging Face, Weights & Biases

Last updated: October 22, 2025