# ZEYU CHANG

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#### Personal Statement

Data scientist with 3 years of research and clinical AI experience, including FDA trials and peer-reviewed publications in reproductive technology. I develop machine learning models and tools for embryo grading, ovarian stimulation, and genotype analysis. I am interested in combining machine learning, causal inference, and biomedical informatics to improve healthcare outcomes and decision.

#### **EDUCATION**

**Tufts University**MS in Data Science
Medford, MA
08/2020 - 12/2022

MS in Innovation and Management

Ohio State University

Columbus, OH

BS in Theoretical Mathematics, Magna Cum Laude

## 08/2016 - 05/2020

#### **Publications**

#### **Pending**

Barash O.O., Miller K.A., Wozniak M., Kaskar K., Sessions B.R., Abeyta M.J., Bhakta S.A., Baker M., Gangrade B., **Chang Z.**, Fanton M., Suraj V., VerMilyea M. *Evaluation of artificial intelligence for embryo selection during IVF: a prospective, randomized controlled trial*. Target journal: *Lancet Digital Health*.

#### **Journal**

Canon C., Leibner L., Fanton M., **Chang Z.**, Suraj V., Lee J.A., Loewke K., Hoffman D. *Optimizing oocyte yield utilizing a machine learning model for dose and trigger decisions: a multi-center, prospective study. Scientific Reports* **14**, 18721 (2024).

#### Conference

Barash O.O., Miller K.A., Wozniak M., Kaskar K., Sessions B.R., Abeyta M.J., Bhakta S.A., Baker M., Gangrade B., **Chang Z.**, Fanton M., Suraj V., VerMilyea M. *Evaluation of the effect on ongoing pregnancy rate of using artificial intelligence for embryo prioritization: an interim analysis of a prospective randomized controlled trial. Fertility and Sterility* **122**, e347 (2024). Presented at ASRM Scientific Congress, 2024.

Fanton M., **Chang Z.**, Suraj V., Miller B. *Post-market analysis of an AI-powered clinical decision support tool for ovarian stimulation. Human Reproduction* **39** Suppl. 1, deae108.095 (2024). Presented at ESHRE Scientific Congress, 2024.

VerMilyea T., Fanton M., **Chang Z.**, Sadek S. *An artificial intelligence model to predict upcoming patient oocyte collections to help optimize efficiency and safety in the embryology laboratory. Human Reproduction* **39** Suppl. 1, deae108.1076 (2024). Presented at ESHRE Scientific Congress, 2024.

**Chang Z.**, Cho J.H., Sakkas D., Miller K.A., VerMilyea M., Barash O.O., Loewke K.E. *Automated morphology grading of blastocyst stage embryos from a single image using deep learning. Fertility and Sterility* **120**, e110 (2023). Presented at ASRM Scientific Congress, 2023.

Alife Health

Data Scientist

San Francisco, CA

06/2022 - 05/2025

- FDA Clinical Trial on IVF AI System. Participated in the world's first FDA clinical trial comparing an AI embryo ranking model with human embryologists, achieving non-inferiority. Led study dataset analysis and contributed to the FDA report and the manuscript targeting *Lancet Digital Health*. The interim analysis was presented at 2024 ASRM Annual Meeting. The original model was published on Fertility and Sterility
- Prospective Clinical Trial on AI-Guided Ovarian Stimulation. Contributed to a prospective clinical study evaluating
  the impact of an AI platform on optimizing FSH starting dose and trigger timing in IVF treatment. Led comparative
  outcome analysis between AI-assisted treatment cycles and propensity matched historical controls, showing trends
  toward increased mature oocyte (MII) yield and reduced total FSH use. Results suggest AI-assisted protocols are safe
  and may improve stimulation efficiency; findings are published in *Scientific Reports*. The original model was published
  on *Fertility and Sterility*
- Deep Learning Model for Embryo Grading. Developed a deep learning model to predict Gardner embryo grades, achieving human-level and highly consistent performance in retrospective studies. Designed the training pipeline on AWS EC2. Presented the work at the 2023 ASRM Annual Meeting, highlighting its potential for embryologist training, performance assessment, and morphology grading standardization.
- Reproduction and Generalization of Oocytes and Dose Prediction Models. Reproduced and analyzed internal
  models predicting mature oocyte (MII) counts and initial FSH doses by learning from similar historical patient profiles.
   Led efforts to evaluate generalizability across populations, retraining the models with European patient data and
  developing a localized decision support tool. Comparative results will be presented at ESHRE 2025.

#### Visual Analytics Lab at Tufts

Medford, MA

Research Assistant

06/2020 - 05/2022

- **Interactive Platform for Genotype Data Analysis.** Designed a web-based interface for genotype data visualization using JavaScript and containerized the application with Docker, reducing development time by 30%. Built backend functionality to allow biologists to run and tune random forest models directly through the interface. Implemented Taylor diagrams in Python to monitor model performance; the team's predictions ranked in the top 5 in the *NSF NEON Challenge* 2021.
- Interactive Visualization and Analysis System for GNNs. Built an interactive visual analytics platform for exploring Graph Neural Networks on large-scale co-purchasing data from Amazon (500K+ nodes, 6M+ edges). Developed an ETL pipeline to transform raw transactional data into a co-purchase network and implemented tools for visualizing BFS/DFS traversal from arbitrary or user-defined nodes. Enabled no-code GNN model prototyping for users with limited technical backgrounds.

Xsphera Bioscience Boston, MA

Data Scientist Intern

06/2021 - 12/2021

- Gene Feature Selection and Visualization for Treatment Response. Applied logistic regression on high-dimensional gene expression data (1000+ genes) to identify key predictors of treatment response, classifying patients into responders and nonresponders. Successfully identified the top 20 genes with the most influential coefficients. Developed an interactive visualization (Plotly/Dash) to display gene fold change patterns across cohorts, revealing clear biological separation; the tool increased clinician engagement time by 20%.
- CNN-Based Microscopy Image Classifier for Collagen Collapse Detection. Developed a convolutional neural network
  to detect collagen collapse in cancer drug microscopy images, overcoming small and imbalanced datasets using data
  augmentation, resampling, and transfer learning. Achieved 0.91 accuracy and 0.97 AUC. Visualized model decision
  regions to validate key features learned by the model. This fully automated classifier became a core tool for sample
  selection in the experimental pipeline.

## TECHNICAL OWNERSHIP OF PUBLISHED WORK

While not involved in the original studies, I later became the product owner for several published models. I re-implemented core algorithms, led in-depth validation and generalization analyses, and enhanced performance for clinical deployment based on the following publications.

Loewke K., Cho J.H., Brumar C.D., Maeder-York P., Barash O., Malmsten J.E., Zaninovic N., Sakkas D., Miller K.A., Levy M., VerMilyea M.D. *Characterization of an artificial intelligence model for ranking static images of blastocyst stage embryos*. *Fertility and Sterility* **117**, 528–535 (2022).

Fanton M., Nutting V., Rothman A., Maeder-York P., Hariton E., Barash O., Weckstein L., Sakkas D., Copperman A.B., Loewke K. *An interpretable machine learning model for individualized gonadotrophin starting dose selection during ovarian stimulation. Reprod Biomed Online* **45**, 1152–1159 (2022).

Fanton M., Nutting V., Solano F., Maeder-York P., Hariton E., Barash O., Weckstein L., Sakkas D., Copperman A.B., Loewke K. *An interpretable machine learning model for predicting the optimal day of trigger during ovarian stimulation. Fertility and Sterility* **118**, 101–108 (2022).

## TECHNICAL SKILL

**Programming Language:** Python, C/C++, R, SAS

Frameworks & Tools: PyTorch, TensorFlow, OpenCV, AWS, CUDA, LATEX, SQL, Git