# JOSHUA WANG

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## E D U C A T I O N

**NYU SCHOOL OF MEDICINE**, New York, NY
Expected May 2025
MD/PhD Candidate, Computational Biomedicine, 4.0/4.0

**BROWN UNIVERSITY**, Providence, RI
May 2017
Bachelor of Science, Biology (Computer Science track), 3.9/4.0

## E X P E R I E N C E

**Merck**, San Francisco, CA
June 2022 – August 2022
**Digital Pathology Summer Intern**
- Trained U-Net models on immunohistochemistry (IHC) images to quantify tumor associated antigens (TAAs).
- Compared stain deconvolution methods and transfer learning approaches to improve segmentation performance.
- Applied multiple-instance learning to identify histology features predictive of MSI-H in colorectal cancer.

**Fenyo Lab – NYU School of Medicine**, New York, NY
March 2020 – Current
**Graduate Student**
- Develop machine learning models to infer clinical and molecular signatures directly from histopathology images and harness the power of omics research with the feasibility of image-based diagnosis.
- Train multi-resolution convolutional neural networks with Keras on imaging data from 1,600 patients to predict clinical annotations, histology outcomes, and critical mutations with AUCs exceeding clinical standards.
- Implement saliency mapping, activation maximization, and gradient class activation with Tensorflow to visually explain uncharacterized histology features of high predictive value and ensure that the model's decision-making process parallels medical intuition.
- Refine statistical techniques to correlate latent image features with proteogenomic expression datasets to identify pathway-level signatures driving tissue morphology changes and uncover biological insights conserved across multiple layers of the central dogma.
- Built linear regression and XGBoost trees to study biomarkers predictive of worsening COVID-19 severity.
- Quantified "fast-track" publication speeds across 200 journals from >150K PubMed records, and summarized collated results in R Shiny app for other scientific researchers: http://time2pub.josh.wang
- NCI F30 fellowship, impact score: 20, percentile: 10 (pending FY2023 payline determination).

**Bennett Lab – Brown University**, Providence, RI
January 2014 – May 2017
**Undergraduate Student Researcher**
- Designed and developed Python scripts to identify genomic regions with mutation patterns violating inheritance by descent in *Candida albicans*. Created a data genome viewer: http://snpmap.asc.ohio-state.edu
- Developed and deployed a R library to perform Gene Ontology enrichment for C. albicans research. Uses Selenium to request, pull and web scrape results from a canonical database lacking API access.
- Led a systematic investigation of RNA-Seq data to annotate novel untranslated regions and construct gene expression networks using weighted gene correlation network analysis.
- Established centralized computational server and wrote Bash, Python, and R pipelines to support lab efforts.

**Regeneron Pharmaceuticals,** Tarrytown, NY
June 2015 – August 2015
**Bioinformatics Intern**
- Applied unsupervised clustering techniques to identify marker genes for proprietary disease conditions.
- Created a visualization platform to analyze single-cell transcriptome data: http://scap.josh.wang
- Presented internship project to Senior VP of Research as one of four interns selected out of 175.

## P U B L I C A T I O N S

- **Wang JM\***, Hong R\*, Lazar AJ, Demicco EG, Tan J, Moreira AL, Razavian N, Schraink T, Gillette MA, Omenn G, An E, Rodriguez H, Tsirigos A, Ruggles KV, Ding L, Robles AI, Mani DR, Rodland KD, Liu W, Fenyö D. Deep-Learning Integrates Histopathology and Proteogenomics at a Pan-cancer Level. In-Revision. *Cell*. October 2022.
- […] **Wang JM\*** […]. Proteogenomic Characterization of the Tumor Immune Microenvironment. In-Preparation. *Cell Immunity*. October 2022.
- **Wang JM,** Liu W, Chen X, McRae MP, McDevitt JT, Fenyö D. "Predictive modeling of morbidity and mortality in COVID-19 hospitalized patients and its clinical implications." *J Med Internet Res.* May 2021. doi: 10.2196/29514.
- **Wang JM\***, Woodruff AL\*, Dunn MJ, Bennett RJ, Anderson MZ. "Intra-species transcriptional profiling reveals key regulators of Candida albicans pathogenic traits." *mBio*. April 2021. doi:10.1128/mBio.00586-21
- Full list available at http://science.josh.wang

## EXTRACURRICULAR

**Machine Learning – NYU School of Medicine,** New York, NY                                     September 2021 – Current
  **Graduate Teaching Assistant**
- Wrote Python and R assignments to implement linear regression using analytic and numeric gradients, and code Principal Component Analysis by finding the eigenvalues and vectors from covariance matrix.
- Assisted in teaching different functions for activation, loss, optimization, weights initialization, and L1/L2 regularization to explore drawbacks including exploding gradients, weight decay, and overfitting.
- Held weekly office hours to review lecture materials and graded student submissions.

**NYU Grossman School of Medicine,** New York, NY                                     September 2019 - Current
*Student Interviewer*
- Interview MD/PhD applicants for the 2020-2021 cycle and write evaluations assessing social competency, personality fit, and research potential.
- Conduct MMI interviews for 2019-2020 cycle and score MD applicants based on verbal and behavioral responses.
- Contribute to question bank and debrief on applicant files to standardize notes across different interviewers.

**Business and Economics in Medicine,** New York, NY                                     December 2018 – December 2019
*Co-President*
- Hosted a career panel of industry physicians attended by 75+ medical students.
- Organized seminars addressing the financial determinants of health and teaching how health insurance works.

**Brown University – Department of Computer Science,** Providence, RI                                     January 2017 – May 2017
*Teaching Assistant for CSCI 0040 (Introduction to Scientific Computing)*
- Held open office hours to help students review concepts taught in lecture.
- Wrote weekly problem sets, developed semester projects, and graded student submissions.