

ANDREW X. YANG

yang.andrew@mayo.edu

RESEARCH FOCUS

I am an MD-MS student interested in the nuances of clinician-patient conversations. I apply computational methods to measure aspects of care in videotaped clinical encounters. I am particularly interested in natural language processing and computer vision as scalable approaches to characterize both verbal and nonverbal communication.

EDUCATION

Mayo Clinic Graduate School of Biomedical Sciences	<i>Jul. 2021 – Present</i>
M.S. Candidate in Artificial Intelligence in Healthcare	Rochester, MN
Mayo Clinic Alix School of Medicine	<i>Jul. 2019 – Present</i>
M.D. Candidate	Rochester, MN
Carleton College	<i>Sep. 2011 – Jun. 2016</i>
B.A. in Computer Science	Northfield, MN

RESEARCH EXPERIENCE

Health AI Partnership (Duke-Mayo Clinic-UC Berkeley)	<i>Jan. 2022 – Present</i>
Regulatory Research Assistant	Rochester, MN
<ul style="list-style-type: none">Collaborate with diverse team of AI experts across technical, legal, and ethical domains to devise training and best practices in health AI software procurement and integration.Synthesize literature and white papers on regulatory issues in the Software as a Medical Device space.Summarize key findings from interviews with stakeholders in health AI.	
Mayo Clinic Department of Artificial Intelligence and Informatics	<i>Oct. 2021 – Present</i>
Graduate Student Researcher	Rochester, MN
<ul style="list-style-type: none">Build NLP model using BERT and other transformer architectures for content classification of patient portal messages.Characterize visual gaze in clinician-patient encounters through object detection and attention target detection models.	
Mayo Clinic Knowledge and Evaluation of Research Unit	<i>Jun. 2020 – Present</i>
Medical Student Researcher	Rochester, MN
<ul style="list-style-type: none">Lead a secondary analysis of SDM4Afib clinical trial, investigating timing and rationales of clinician recommendations for whether and how to anticoagulate.Examine relationship between recommendation styles and various shared decision making metrics.Contributed to study design and abstract review in systematic review of video-based observation studies in outpatient settings.	
Broad Institute of MIT and Harvard (Connectivity Map)	<i>Nov. 2017 – Jun. 2019</i>
Associate Computational Biologist	Cambridge, MA
<ul style="list-style-type: none">Developed pipelines and metrics assessing compound bioactivity in group's entire gene expression library comprising millions of gene signatures.Analyzed gene signature connectivity and developed mechanistic hypotheses for novel compounds in collaborations with various pharmaceutical and biotechnology companies.	
South University of Science and Technology	<i>Dec. 2016 – Oct. 2017</i>
Fulbright Research Fellow	Shenzhen, China
<ul style="list-style-type: none">Assessed performance of single molecule sequencing platform and compared accuracy of various alignment algorithms.	
Mayo Clinic (Nelson Lab)	<i>Jun. 2015 – Aug. 2015</i>
IMPACT Research Intern	Rochester, MN
<ul style="list-style-type: none">Tested award-winning hypothesis for genetic etiology of hypoplastic left heart syndrome by analyzing whole genome sequencing variants in probands and parent/sibling controls.	
National Institutes of Health (Levin Lab)	<i>Jun. 2013 – Aug. 2013</i>
Summer Research Intern	Bethesda, MD
<ul style="list-style-type: none">Aligned deep sequencing data to examine patterns of transposon integration in relation to nucleosome occupancy and protein binding in fission yeast.	

PUBLICATIONS

Voller VK, Olirus Owilli A, **Yang AX**, Finnegan AC, Westerhaus M. Evaluating the Impact of a Social Medicine Course Delivered in a Local-Global Context: A 10-Year Multi-Site Analysis. *World Medical & Health Policy*. 2022.

Zhao L, Deng L, Li G, Jin H, Cai J, Shang H, Li Y, Wu H, Xu W, Zeng L, Zhang R, Zhao H, Wu P, Zhou Z, Zheng J, Ezanno P, **Yang AX**, Yan Q, Deem MW, He J. Single molecule sequencing of the M13 virus genome without amplification. *PLoS One*. 2017.

Hickey A, Esnault C, Majumdar A, Chatterjee AG, Iben JR, McQueen PG, **Yang AX**, Mizuguchi T, Grewal SIS, Levin HL. Single Nucleotide Specific Targeting of the Tf1 Retrotransposon Promoted by the DNA-Binding Protein Sap1 of *Schizosaccharomyces pombe*. *Genetics*. 2015.

ABSTRACTS

Way G, Natoli T, Adeboye A, Litichevskiy L, **Yang A**, Lu X, Caicedo J, Cimini B, Karhohs K, Logan D, Rohban M, Kost-Alimova M, Hartland K, Bornholdt M, Chandrasekaran N, Haghighi M, Singh S, Subramanian A, Carpenter A. Morphology and Gene Expression Profiling Provide Complementary Information for Mapping Cell State. In: *International Society for Computational Biology: Rocky Bioinformatics Conference 2021*. 2021 Dec 2-Dec 4. Aspen/Snowmass, CO.

Huang C, **Yang AX**, Natoli T, Litichevskiy L, Vaillancourt F, Rolfe A, Xiao Y, Subramanian A, Yu L. Heme-CMap: Generation and characterization of 20K L1000 profiles across 11 hematologic malignant lines. In: *Proceedings of the American Association for Cancer Research Annual Meeting 2019*. 2019 Mar 29-Apr 3. Atlanta, GA.

HONORS AND AWARDS

Fulbright Research Grant: China	<i>December 2016 – October 2017</i>
Fulbright Program	

Critical Language Enhancement Award: Mandarin	<i>September 2016 – December 2016</i>
Fulbright Program	

Multicultural Alumni Network Scholar	<i>May 2015</i>
Carleton College	

Gold Medal, IMPACT Program	<i>February 2015</i>
Mayo Clinic	

Exemplary Writing Portfolio	<i>July 2013</i>
Carleton College	