Ting "Helen" He

Education and Current Work

Johns Hopkins University School of Medicine	Baltimore, MD
PhD Student, Biomedical Informatics and Data Sciences	Aug. 2020 – Present
Columbia University Medical Center	New York, NY
Research Associate, Biomedical Informatics	Sep. 2019 – Aug. 2020
Johns Hopkins University School of Medicine	Baltimore, MD
Master of Science, Health Science Informatics with Health Economics certificate	Jul. 2017 – Aug. 2019
University of Calgary School of Medicine	Calgary, Canada
Visiting Student, Bioinformatics	Jun. 2016 – Dec. 2016
 Dalian University of Technology School of Life and Sciences Bachelor of Science, Bioinformatics Award: China National Scholarship among 0.2% colleges 	Dalian, China Jun. 2013 - Aug. 2017

Research Experience

Decision Support for Breast Cancer Chemoprevention	Advisor: Rita Kukafka
Research Associate, Columbia University Department of Biomedical Informatics	Sep. 2019 - Present
• Goal : to increase the wellness of preventing breast cancer for high-risk pa patient-centered and provider-centered decision support tools	tients by integrating
• Obtain, clean and analyze aggregated data from EHR to identify women's risks (breast cancer and facilitate clinical trials recruitment	BCSC model & Gail model) for
$\circ~$ Analyze survey data to evaluate the influence of decision support tools (work in ${\bf j}$	progress)
• Implement a data pipeline using Fast Healthcare Interoperability Resource (FHII systems (Epic, Cerner, Allscripts) and stream them into patient-centered decision	/ 1
Mining Adverse Drug Events in Biomedical Abstract Graduate Researcher, Johns Hopkins Division of Health Science Informatics	Advisor: Taxiarchis Botsis Jan. 2019 - Aug. 2019
• Goal : to determine whether SemRep might efficiently support the retrieva information from biomedical abstracts	al of adverse drug event
• Detected drug and symptom entities and predicted aliskiren related drug-sympto abstracts through SemRep	m relationship from 1,203 PubMee
$\circ~$ Analyzed XML based drug-symptom outcomes by finding entities linked to term adverse drug event	of interest and inferring potential
 Quantified the semantic relatedness between two entities by using prediction-base progress) 	ed semantic indexing (work in
Clustering Analysis of Comorbidity in eMERGE Cohorts Adv Graduate Researcher, Johns Hopkins Division of Health Science Informatics	isor: Casey Overby Taylor Apr. 2019 - Aug. 2019
• Goal : to stratify the risk of various comorbidities in eMERGE cohorts by cluster	understanding the comorbidity
$\circ~$ Conducted literature review in comorbidity index (Charlson Cormorbidity index comorbidity cluster	& Johns Hopkins ACG indices) an
 Identified and described the biological patterns of comorbidities in a range of clin hierarchical and spectral clustering methods 	ical conditions using K means,
\circ Revealed the relation between comorbidity clusters and severity conditions then i clustering method	dentified the most significant

Daily Rounding Report for Inpatient Practice

 $Team \ member$

- $\circ~$ Built Customized application for display of EHR in hospital-based practice
- $\circ~$ Used FHIR to extract patient information and used JavaScript D3 to visualize

Novartis - Tumor Mutation Burden Distribution in Melanoma

 $Team \ member$

- Integrated 13 skin cancer studies, normalized their TMB, and built a R shiny app to visualize TMB distribution according to clinical and genomics factors
- Won second prize during 2 weeks academic hackathon; front end R shiny: https://github.com/tinghe14/TMB

Breast Cancer Data Search

 $Undergraduate\ Executor$

- $\circ~$ Built Breast Cancer Related Mutation Query web application based on Java, HTML, and MySQL
- $\circ~$ Used Decision Tree model to predict unknown classes of patients through WEKA machine learning tool

Health Doctor - Android App

Undergraduate Team Leader

- Led a 6-student team to develop app providing general health improvement recommendations based on medical data
- $\circ~$ Gave a presentation and won 1st prize for provincial competition

PUBLICATION & PRESENTATION

Publication: Taylor, C. O., Lemke, K. W., Richards, T. M., Roe, K. D., **He, T.**, Arruda-Olson, A., ... Kullo, I. (2019). Comorbidity Characterization Among eMERGE Institutions: A Pilot Evaluation with the Johns Hopkins Adjusted Clinical Groups® System. AMIA Summits on Translational Science Proceedings, 2019, 145.

Poster: He T, Taylor CO. (Sept, 2018) Identify symptom cluster in pregnant women experiencing preterm birth. 9th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics

Poster: He T, Kreimeyer K, Botsis T. (March, 2020) Using SemRep to Detect Adverse Drug Events in Biomedical Abstracts. AMIA 2020 Summit

LEADERSHIP EXPERIENCE

NIH - ALL of Us Research Program

Volunteer (Data Provider)

Johns Hopkins Division of Health Sciences Informatics

Graduate Teaching Assistant

 $\circ~$ Introduction to Biomedical and Public Health Informatics - Instructor: Harold Lehmann

• Informatics & Clinical Research Lifescycle: Tools, Techniques and Processes - Instructor: Casey Overby Taylor

RESEARCH AND TECHNICAL SKILLS

Programming: R, Python, SAS, SQL, Shell, R shiny, JavaScriptHealth: FHIR, Coding Standard, Decision SupportModeling: Statistical Modeling, Machine Learning, Natural Language ProcessingTool: SemRep, NLTK, OHDSI

Sep. 2019 - Oct. 2019

arning tool

Jul. 2016 - Aug. 2016

Jul. 2015 - Sep. 2015

Dec. 2019 - Present

Sep. 2018 - Dec. 2018

Oct. 2019 - Nov. 2019