

# Yu Deng

CONTACT INFORMATION	Feinberg School of Medicine, 303 E Superior street, Chicago, IL	Email:yudeng2015@u.northwestern.edu
RESEARCH INTEREST	I am a PhD student majoring in biomedical informatics. My focus is on applying supervised and unsupervised learning methods for clinical research. I have applied various unsupervised learning techniques to find disease subtypes and novel risk factors. I have used joint modeling techniques to improve prediction performance using longitudinal data as well as using Natural Language Processing (NLP) for computational phenotyping.	
EDUCATION	<b>Northwestern University, Chicago, IL, USA</b> <ul style="list-style-type: none"><li>• PhD Candidate, biomedical informatics, Feinberg School of Medicine, expected graduation June 2020</li><li>• Major GPA: 3.79/4.00</li><li>• Coursework: Programming for Big Data, Advanced Biostatistics, Deep Learning From Scratch</li></ul>	
SKILLS	<b>Programming Skills</b> <ul style="list-style-type: none"><li>• Python (sklearn, numpy, pandas), R, SQL</li></ul> <b>Machine Learning Algorithms</b> <ul style="list-style-type: none"><li>• Classical &amp; Penalized Regression Methods (LASSO, Ridge), SVM, Random Forest, K-nearest Neighbors, Adaboosting, Deep Learning (MLP, RNN), Cox regression</li><li>• K-means, hierarchical clustering, Partition Around Medoid (PAM), Latent Class Analysis (LCA), non-Negative Tensor Factorization (NTF), non-negative Matrix Factorization (NMF)</li><li>• Feature Engineering (e.g. PCA, tensor factorization, forward/backward selection), Regularization</li><li>• Experimental Design, Hypothesis Testing, A/B Testing</li></ul> <b>Tools</b> <ul style="list-style-type: none"><li>• SQLServer, Spark, Tensorflow</li></ul>	
WORK EXPERIENCE	<b>Center for Health Information Partnerships, Northwestern University, Chicago</b> <ul style="list-style-type: none"><li>• Graduate Research Assistant, July 2016-Present</li><li>• Used SQL to extract clinical data. Developed various algorithms to model disease progression and subtypes</li></ul> <b>Bioinformatics Laboratory, Tsinghua University, Beijing, China</b> <ul style="list-style-type: none"><li>• Research Assistant, Dec 2014-August 2015</li><li>• Developed pipeline for genetic data analysis (i.e.RNA-seq, DNA-seq) on computing cluster</li></ul>	
HONOURS AND DISTINCTIONS	<ul style="list-style-type: none"><li>• <b>Honorable Mention in Student Poster Competition</b>, International Chinese Statistical Association (ICSA), 2018</li><li>• <b>First Prize in Student Poster Competition</b>, Northwestern Biomedical Informatics Day, 2017</li><li>• Driskill Graduate Program Full Scholarship, Northwestern University 2015 – 2017</li><li>• Outstanding Study Abroad Undergraduate Scholarship, Chinese Scholarship Council, 2013</li></ul>	
SELECTED PUBLICATIONS/CONFERENCES	<b>Use of Clinical Phenotypes and Non-negative Tensor Factorization for Heart Failure Prediction</b> Deng Y., Furmanchuk A., Chen R., Ahmad F., Sun J., Kho A.(2017). <i>AMIA Annual Symposium. Podium Presentation</i> <b>Use of Repeated Measurements for Cardiovascular Disease Prediction: the Application of Joint Model</b> Deng Y., Zhong Y., Kho A., Zhao L.(2019). ENAR 2019. Poster presentation <b>Identification of Systemic Lupus Erythematosus Subtypes using Latent Class Analysis</b> Deng Y., Ghosh A., Luo Y., Kho A., Goldman R., Walunas T.(2019). Medinfo. Podium Presentation (submitted) <b>Natural Language Processing for EHR-Based Computational Phenotyping</b> Zeng, Z., Deng, Y., Li, X., Naumann, T., & Luo, Y. (2018). Natural Language Processing for EHR-Based Computational Phenotyping. arXiv preprint arXiv:1806.04820. <b>Characterizing Design Patterns of EHR-Driven Phenotype Extraction Algorithms</b> Zhong, Y., Rasmussen L., Deng Y., Pacheco J., Smith M., Starren J., Wei W., Walton N., Hripesak G., Chute C., Luo Y. Characterizing Design Patterns of EHR-Driven Phenotype Extraction Algorithms. IEEE on Bioinformatics and Biomedicine (paper accepted) <b>Measuring Nascent Transcripts by Nascent-seq. Methods in Molecular Biology</b> Chen, F. X., Marshall, S. A., Deng, Y., & Tianjiao, S. (2018). Measuring Nascent Transcripts by Nascent-seq. In Next Generation Sequencing (pp. 19-26). Humana Press, New York, NY.	
SELECTED RESEARCH PROJECTS	<b>Use of Clinical Phenotypes and Non-negative Tensor Factorization for Heart Failure (HF) Prediction, 2017</b> <ul style="list-style-type: none"><li>• Performed NTF on large scale, sparse medical record data; Generated latent clusters</li><li>• Performed dimension reduction including NTF, MTF, PCA on medical record data to get important features</li><li>• Compared model performance between dimension reduction techniques and random forest using the top features</li></ul> <b>Developed/customized joint multivariate Bayesian Model for Cardiovascular Disease (CVD) Prediction, 2017</b> <ul style="list-style-type: none"><li>• Built joint multivariate Bayesian model using longitudinal data to predict CVD time-to-event</li><li>• Imputed missing data using multivariate imputation by chained equation</li><li>• Evaluated model performance using AUC and NRI. Improved AUC from 0.85 to 0.87 with statistical significance.</li></ul> <b>Using Deep Learning for Post-Operative Atrial Fibrillation (AF) prediction, 2018 -</b> <ul style="list-style-type: none"><li>• Extracted data from Northwestern Memorial Hospital data warehouse using SQL</li><li>• Trained supervised learning models including LASSO, Random Forest, deep learning (on tensorflow)</li><li>• Trained and fine-tuned deep learning model by changing number of epochs, number of hidden layers, learning rate</li></ul>	