

Haoran Chen

CONTACT INFORMATION	280 E Broad St. Apt 906 Rochester, NY USA (979) 446-7880	<i>E-mail:</i> hrchen@tamu.edu <i>Website:</i> https://hrch3n.github.io/ <i>Github:</i> https://github.com/hrch3n/
RESEARCH INTERESTS	Unravel the mechanisms underlying complex genetic diseases and explore novel and customized clinical treatments <ul style="list-style-type: none">• Computational Modeling• Artificial and Biological Intelligence• Cancer Systems Biology• Machine Learning	
EDUCATION	Master of Science in Electrical Engineering Texas A&M University, College Station, Texas USA <ul style="list-style-type: none">• Thesis: Improving Molecular-level Protein Docking and Interpreting System-level Cancer Mechanisms through Machine Learning• Advisor: Prof. Yang Shen, Nicholas Duffield, Aniruddha Datta, Sing-Hoi Sze	08/2018
	Bachelor of Engineering in Electrical Engineering and Automation South China University of Technology, Guangzhou, Guangdong China	06/2015
RESEARCH EXPERIENCE	Graduate Research Assistant TAMU, Department of Electrical and Computer Engineering Project: Quantify, predict, and understand mutational effects (leader) <ul style="list-style-type: none">• Designed a machine learning framework to predict cancer driver genes based on functional circuits in Protein-Protein Interaction (PPI) network• Extracted and integrated cancer mechanisms of the propagation of mutational effects in PPI network• Techniques: Random Forest, Sparse Group LASSO, Association Rule Learning Project: Prediction of protein complex conformation change (leader) <ul style="list-style-type: none">• Proposed an entropy-inspired machine learning algorithm to predict the extent of protein complex conformational change between unbound / homology and bound structures• Developed a proof-by-contradiction pipeline based on protein energy calculation and protein interface displacement for fast assessing rigidity assumption of protein complex docking• Built a web server providing protein structures change prediction, rigidity assumption assessment and protein normal mode visualization• Techniques: Normal Mode Analysis, Kernel Ridge Regression, CHARMM Project: Pan-Cancer Atlas - Genomic and molecular landscape of DNA Damage Repair (DDR) deficiency <ul style="list-style-type: none">• Utilized the STRING and UniProt databases to locate the binding partners and their structures of three tumor suppressor genes, BRCA1, BRCA2 and RAD50• Calculated the change of protein folding energy to identify mutations which potentially have a functional impact• Techniques: CHARMM	06/2016 - 08/2017, 01/2018 - 05/2018

Project: CAGI 5 - Variants of BRCA1 and BRCA2: predict which variants are associated with increased risk of breast cancer by ENIGMA

- Designed objective function and features of ordinal regression for predicting categorical clinical outcomes of BRCA1, BRCA2 and CHEK2 mutations
- Techniques: Ordinal Regression, feature engineering

Project: DREAM Challenge - AstraZeneca-Sanger Drug Combination Prediction

- Developed DNA methylation and drug-cell line kernel features for predicting the effects of drug synergy
- Techniques: Kernel Support Vector Machine, feature engineering

Undergraduate Research Assistant

09/2013 - 01/2015

SCUT, Department of Electrical Engineering

Project: Monitoring and predicting the safe working condition of 10kV three-core cable

- Designed and executed a field experiment with state-of-the-art accuracy for a thermal rising test of 10kV three-core cables
- Designed an ANSYS finite element analysis to model the thermal resistivity of 10kV three-core cable in terms of various impacts from materials, temperature and conditions
- Techniques: ANSYS, MATLAB

PUBLICATIONS

Chen, H., Sun, Y., & Shen, Y. (2017). Predicting protein conformational changes for unbound and homology docking: learning from intrinsic and induced flexibility. *Proteins: Structure, Function, and Bioinformatics*, 85(3), 544-556.

Knijnenburg, T. A., Wang, L., Zimmermann, M. T., Chambwe, N., Gao, G. F., Cherniack, A. D., Fan, H., Shen, H., Way, G. P., Greene, C. S., Liu, Y., Akbani, R., Feng, B., Donehower, L. A., Miller, C., Shen, Y., Karimi, M., **Chen, H.**, Kim, P., Jia, P., Shinbrot, E., Zhang, S., Liu, J., Hui, H., Bailey, M. H., Yau, C., Wolf, D., Zhao, Z., Weinstein, J., Li, L., Ding, L., Mills, G. B., Laird, P. W., Wheeler, D. A., Shmulevich, I., The Cancer Genome Atlas Research Network, Monnat, R. J., Jr., Xiao & Y., Wang, C. (2018). Genomic and molecular landscape of DNA damage repair deficiency across The Cancer Genome Atlas. *Cell Reports*, 23(1), 239.

Menden, M. P., Wang, D., Guan, Y., Mason, M., Szalai, B., Bulusu, K. C., Yu, T., Kang, J., Jeon, M., Wolfinger, R., Nguyen, T., Zaslavskiy, M., **AstraZeneca-Sanger Drug Combination DREAM Consorti**, Jang, I. S., Ghazoui, Z., Ahsen, M. E., Vogel, R., Neto, E. C., Norman, T., Tang, E. KY., Garnett, M. J., Di Veroli, G., Fawell, S., Stolovitzky, G., Guinney, J., Dry & J. R., Saez-Rodriguez, J. (2018). A cancer pharmacogenomic screen powering crowd-sourced advancement of drug combination prediction. *bioRxiv*, 200451.

Chen, H., Hu, Q. (2014) Impact of thermal resistivity value of materials on calculation for conductor temperature of 10 kV three-core cable. *Guangdong Electric Power*, 27(4) 86-90.

PAPERS IN PREPARATION

Karimi, M., Sun, Y., Cao, Y., **Chen, H.**, Moronfoye, O., & Shen, Y. (2018). Predicting missense mutational effects on protein functions and cancer pathogenicity. *Submitted*

Sun, Y., **Chen, H.**, & Shen Y. (2018) PredPro: Predicting Protein conformational change and assessing rigidity assumption. *Manuscript in preparation*.

Chen, H., Shen Y. (2018). Interpreting system-level cancer mechanisms through machine learning. *Manuscript in preparation*.

TEACHING EXPERIENCE	Teaching Assistant, Electrical Circuit Theory	09/2017 - 12/2017
	TAMU, Department of Electrical and Computer Engineering <ul style="list-style-type: none"> Selected as a teaching assistant for Electrical Circuit Theory, one of the core courses for electrical engineering Led 10-hour weekly lab sections and discussion sections for a group of 80 students Designed course materials including study problems and lab exams 	
	Grader, Algorithms in Structural Bioinformatics	01/2016 - 05/2016
	TAMU, Department of Electrical and Computer Engineering <ul style="list-style-type: none"> Graded weekly assignments and exams 	
HONORS AND AWARDS	• Academic Performance Scholarship	10/2014
	• Academic Improvement Scholarship	10/2013
	• Social Activities Award	02/2013 & 09/2013
	• Outstanding Cadres of Student Association Award	05/2013
DATABASES	<ul style="list-style-type: none"> Cancer: TCGA, Xena, COSMIC, ClinVar Pathway: PathwayCommons, KEGG Protein structure and interaction: PDB, UniProt, STRING 	
ALGORITHMS	<ul style="list-style-type: none"> Machine Learning: Ridge, LASSO, SVM, Random Forest, Gradient Boosting, AdaBoost Deep Learning: CNN, RNN, LSTM, GAN, VAE Probabilistic Graphical Models: Bayesian Network, Dynamic Bayesian Network, Hidden Markov Model, Conditional Random Field Data Mining: Association Rule Learning, DBSCAN, Kernel Density Estimation, PCA, LDA, K-mean, Hierarchical Clustering Protein Modeling: Normal Mode Analysis 	
COMPUTER SKILLS	<ul style="list-style-type: none"> Languages: Python, R, Shell, L^AT_EX, MATLAB, Pascal, VB Software: Pymol, CHARMM, ANSYS 	