

Zichen Wang, PhD

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ABOUT

Assistant Professor in biomedical informatics, with intensive experiences in bioinformatics, systems pharmacology, transcriptomics and next-gen sequencing data analysis. I have been actively applying Machine Learning/Deep Learning methods in my research. I am also interested and experienced in interactive data visualization and web development.

EXPERIENCE

Icahn School of Medicine at Mount Sinai, New York, NY — Assistant Professor

JUN 2017 - PRESENT

Conduct research in Bioinformatics and Computational Systems Biology using high-dimensional molecular and clinical big data.

Icahn School of Medicine at Mount Sinai, New York, NY — Postdoctoral Fellow

JAN 2017 - JUN 2017

Developed a Deep Learning model leveraging clinical variables from the EMR to study physiological aging.

EDUCATION

Icahn School of Medicine at Mount Sinai, New York, NY — PhD in Biomedical Science (bioinformatics and genomics)

AUG 2012 - DEC 2016

Developed computational and mathematical methods to study the complexity of regulatory networks in mammalian systems.

China Agricultural University, Beijing, China — BS in Biochemistry and Molecular Biology

SEP 2008 - JUN 2012

SELECTED PUBLICATIONS

Wang Z, Lachmann A, Keenan AB, Ma'ayan A: L1000FWD: Fireworks visualization of drug-induced transcriptomic signatures. *Bioinformatics* 2018, 34(12): 2150–2152

Developed a large-scale interactive visualization engine (l1000fwd.net) for over 17,000 drug-induced transcriptomic signatures to facilitate drug discovery.

SKILLS

Data science: Exploratory Analysis, Classification, Clustering, Regression, Interactive Data Visualization, Natural Language Processing, Deep Learning, Reinforcement Learning

Software development: Flask, Shiny, MongoDB, Docker, Apache Mesos, Bootstrap, Backbone.js, d3.js, THREE.js

Bioinformatics: Electronic Medical Records, Next-gen sequencing data analysis, Transcriptomics, Network analysis, Cheminformatics

LANGUAGES

Programming: Python, R, Javascript, SQL, Bash, php, MATLAB, HTML, CSS

Natural: English, Mandarin

SOCIAL MEDIA

GitHub: [wangz10](https://github.com/wangz10)

LinkedIn: [zichenwang](https://www.linkedin.com/in/zichenwang)

Kaggle: [zichen](https://www.kaggle.com/zichen)

StackOverflow: [2340065/zichen-wang](https://stackoverflow.com/users/2340065/zichen-wang)

Google scholar: [bwLMCp4AAAAJ](https://scholar.google.com/citations?user=bwLMCp4AAAAJ)

Personal website: wangz10.github.io

Wang Z, Li L, Glucksberg BS, Israel A, Dudley JT, Ma'ayan A: Predicting Age by Mining Electronic Medical Records with Deep Learning Characterizes Differences between Chronological and Physiological Age. *Journal of Biomedical Informatics* 2017, 76: 59–68

Employed deep neural network to predict physiological age for over 300,000 patients using the Electronic Medical Record (EMR) data and performed large-scale statistical association studies to reveal clinical and genetic factors contribute to disparities in aging.

Wang Z, Monteiro CD, Jagodnik KM, Fernandez NF, Gundersen GW et al: Extraction and analysis of signatures from the gene expression omnibus by the crowd. *Nature Communications* 2016 7, 12846.

Built a crowdsourcing microtask platform to enable over 70 citizen scientists to collaboratively work on curation of gene expression signatures from public repository and achieved one of the largest high-quality collection of signatures themed by genetic perturbation, drug treatment and diseases: <http://amp.pharm.mssm.edu/CREEDS/>.

Wang Z, Ma'ayan A: An open RNA-Seq data analysis pipeline tutorial with an example of reprocessing data from a recent Zika virus study. *F1000Research* 2016, 5(1574).

Developed one of the first transparent and reproducible computational pipeline implemented in Dockerized Jupyter notebook with equipped diverse interactive visualization widgets to analyze RNA-seq data from scratch: <https://github.com/MaayanLab/Zika-RNAseq-Pipeline>.

Wang Z, Clark NR, Ma'ayan A: Drug-induced adverse events prediction with the LINCS L1000 data. *Bioinformatics* 2016, 32(15):2338–2345.

Developed a novel multi-label classification framework to predict adverse drug reactions using features from drug-induced gene expression data and chemical structures: <http://maayanlab.net/SEP-L1000/>.

Wang Z, Clark NR, Ma'ayan A: Dynamics of the discovery process of protein-protein interactions from low content studies. *BMC Systems Biology*, 2015, 9(1):26.

Introduced a mathematical network discovery model to investigate the existence and consequences of research focus biases in biological networks from the literature.

SELECTED SOFTWARES

<http://amp.pharm.mssm.edu/L1000FWD/>

<http://amp.pharm.mssm.edu/CREEDS/>

<http://amp.pharm.mssm.edu/LJP/>

<http://hair-gel.net/>