Jianyu **Yang**

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Education

Preclinical Medicine (Batchelor's Degree) — *Guangzhou, China*
SOUTHERN MEDICAL UNIVERSITY — *Sep. 2012 - Jun. 2017*

Developmental Biology (Master's Degree) — *Guangzhou, China*
SOUTHERN MEDICAL UNIVERSITY — *Sep. 2017 - Jun. 2020*

Bioinformatics and Genomics Program (Ph.D. candidate) — *State College, US*
PENNSYLVANIA STATE UNIVERSITY — *Aug. 2020 -*

Skills

Programming	Python, JAVA, R, Tensorflow, Pytorch, Pytorch-lightning
Machine learning	Bayesian method, Deep learning

Research Experience

RUNX1 upregulates CENPE to promote leukemia cell proliferation

MASTER — *Sep. 2020 - April. 2021*

- Find Runx1 downstream target genes by analysis on RNA-seq and ChIP-seq data
- Investigating the function of Runx1 in THP-1 cells

Size-based expectation maximization for characterizing nucleosome positions and subtypes

PH.D. — *Sep. 2017 - April. 2024*

- Design and implement a nucleosome calling package using Gaussian Mixture model
- Features the unique ability of distinguishing various nucleosome types

Joint sequence & chromatin neural networks characterize the differential abilities of Forkhead transcription factors to engage inaccessible chromatin

PH.D. — *Jan. 2022 - Sep. 2023*

- Apply deep neuron network to predict various Fox factors bindings in mouse embryonic stem cell
- Employ feature attribution techniques to understand preexisting chromatin determinants of Fox factors bindings

Systematic Dissection of Sequence Features Affecting the Binding Specificity of a Pioneer Factor Reveals Binding Synergy Between FOXA1 and AP-1

PH.D. — *Jan. 2022 - Oct. 2023*

- Apply a bimodal neuron network to dissect the influence of sequence and chromatin to understand FoxA1 binding mechanism

Honors & Awards

2018	**1st Prize**, National Scholarship for Graduate students	*Guangzhou, China*
2018	**1st Prize**, Excellent Graduate Student of Southern Medical University	*Guangzhou, China*
2024	**Travel Fellowship**, 16th Great Lakes Bioinformatics conference	*Pittsburgh, US*

Presentations

2024	**Talk**, Jointly characterizing the sequence and chromatin binding preferences of transcription factors using neural networks	*16th Great Lakes Bioinformatics conference*
2024	**Proceeding talk (selected for Genome Research)**, SEM: size-based expectation maximization for characterizing nucleosome positions and subtypes	*RECOMB 2024*

Publications

Link to Google Scholar

Comprehensive understanding of Tn5 insertion preference improves transcription regulatory element identification *10.1093/nargab/lqab094*

NAR Genomics and Bioinformatics *2021*

Houyu Zhang, Ting Lu, Shan Liu, Jianyu Yang, Guohuan Sun, Tao Cheng, Jin Xu, Fangyao Chen, Kuangyu Yen

RUNX1 upregulates CENPE to promote leukemic cell proliferation *10.3389/fmolb.2021.692880*

Frontiers in Molecular Biosciences *2021*

Shan Liu, Jianyu Yang, Guohuan Sun, Yawen Zhang, Cong Cheng, Jin Xu, Kuangyu Yen, Ting Lu

Systematic Dissection of Sequence Features Affecting the Binding Specificity of a Pioneer Factor Reveals Binding Synergy Between FOXA1 and AP1 *10.1101/2023.11.08.566246*

Biorxiv *2023*

Cheng Xu, Holly Kleinschmidt, Jianyu Yang, Erik Leith, Jenna Johnson, Song Tan, Shaun Mahony, Lu Bai

SEM: size-based expectation maximization for characterizing nucleosome positions and subtypes *10.1101/2023.10.17.562727*

Biorxiv *2023*

Jianyu Yang, Kuangyu Yen, Shaun Mahony

Joint sequence & chromatin neural networks characterize the differential abilities of Forkhead transcription factors to engage inaccessible chromatin *10.1101/2023.10.06.561228*

Biorxiv *2023*

Sonny Arora, Jianyu Yang, Tomohiko Akiyama, Daniela Q James, Alexis Morrissey, Thomas R Blanda, Nitika Badjatia, William KM Lai, Minoru SH Ko, B Franklin Pugh, Shaun Mahony