

# Shaopeng Liu

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State College, PA

## Education

<b>Ph.D. in Bioinformatics and Genomics (ongoing), GPA 3.9 / 4.0</b> The Pennsylvania State University, The Huck Institutes of Life Science	<b>State College, PA</b> Aug 2019 – now
<b>Master of Science in Biostatistics, GPA 3.7 / 4.0</b> Washington University in St. Louis (WUSTL), Division of Biostatistics	<b>St. Louis, MO</b> June 2016 – Dec 2017
<b>Bachelor of Science: Biology, GPA 3.5 / 4.0</b> Wuhan University, College of Life Science	<b>Wuhan, China</b> Sep 2010 – June 2014

## Research Experience

<b>Research assistant advised by Dr. David Koslicki (PSU)</b>	May 2020 – now
<b>Bioinformatician supervised by Dr. Bo Zhang and Dr. Ting Wang (WUSTL)</b>	Jan 2018 – April 2019
<b>Research assistant supervised by Dr. Bo Zhang (WUSTL)</b>	Aug 2016 – Dec 2017

## Projects:

- Computational methods for metagenomic analysis** (2020-now, advised by Dr. David Koslicki):
  - Proved, implemented and benchmarked a truncation-based containment MinHash algorithm, which can efficiently estimate multi-resolution Jaccard and containment indices, in metagenomic analysis;
  - Production code and manuscript are in progress.
- The National Center for Advancing Translational Sciences (NCATS)** (2021-now, supervised by Dr. David Koslicki):
  - Worked in the ARAX team that aims at providing a graph-based reasoning tool to explore biomedical questions;
  - Worked in the Translator API team that aims at normalizing query communications between the user and the knowledge database.
- Methodology improvement for ATAC-seq analysis** (2018-2019, with Dr. Bo Zhang and Dr. Ting Wang):
  - based on the biological nature of Tn5 insertion, improved the ENCODE ATAC-seq analysis pipeline by adjusting signal reading process;
  - incorporated statistical ideas from DEG and genomic footprint into the pipeline to discover differentially opened DNA regions and insertion free DNA regions as downstream analysis;
  - explored rodent-specific TE rewired gene regulatory network from ENCODE ATAC-seq data;
- TaRGET II epigenome data analysis** (2018-2019, with Dr. Bo Zhang and Dr. Ting Wang):
  - worked in Data Coordination Center (DCC) of TaRGET II Consortium, streamlined and setup the routine pipelines for RNA-seq, ChIP-seq, WGBS, and ATAC-seq data; and processed part of data with preliminary quality analysis;
  - implemented pipelines into Docker and Singularity;
  - explored the empirical distribution of key quality factors and provided schemes for data quality estimate.
- Various bioinformatic collaborations** (2016-2019, with Dr. Bo Zhang):
  - performed single-cell RNA analysis by Seurat and scdiff / SC3 for trajectory prediction;
  - profiled epigenetic signature changes under different conditions based on ATAC-seq and RNA-seq data;
  - analyzed ChIP-seq data of NKX2, Twist1 transcription factors in human and mouse samples;
- Synthetic biology: biobricks for tandem promoter** (2013-2014, IGEM project):
  - created biobricks with tandem promoters combined with specific guide-RNA targets
  - utilized GFP to validate the multi-stage promoter function triggered by dCas9+Transcription factor protein complex

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## Publications

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- **Shaopeng Liu**, David Koslicki. "CMash: fast, multi-resolution estimation of k-mer-based Jaccard and containment indices." (In preparation)
- **Shaopeng Liu**, Daofeng Li, Cheny Lyu, Paul Gontarz, Ting Wang, Bo Zhang. "AIAP: A Quality Control and Integrative Analysis Package to Improve ATAC-seq Data Analysis." (In Press) *Genomics, Proteomics & Bioinformatics*, 2021
- Matthew J McCoy, Kitra Cates, Yangjian Liu, Daniel G Abernathy, Bo Zhang, **Shaopeng Liu**, Paul Gontarz, Woo Kyung Kim, Shawei Chen, Wenjun Kong, Harrison W Gabel, Samantha A Morris, Andrew Yoo. "Deconstructing Stepwise Fate Conversion of Human Fibroblasts to Neurons by MicroRNAs." *CELL STEM CELL*, 2021
- Paul Gontarz, Shuhua Fu, Xiaoyun Xing, **Shaopeng Liu**, Benpeng Miao, Viktoriia Bazylianska, Akhil Sharma, Pamela Madden, Kitra Cates, Andrew Yoo, Anna Moszczynska, Ting Wang, Bo Zhang. "Comparison of differential accessibility analysis strategies for ATAC-seq data." *Scientific reports* 10.1 (2020): 1-13.
- Jennifer L David, Linda Cox, Christine Shao, Cheng Lyu, **Shaopeng Liu**, Rajeev Aurora, Deborah J Veis. "Conditional Activation of NF- $\kappa$ B Inducing Kinase (NIK) in the Osteolineage Enhances Both Basal and Loading-Induced Bone Formation." *Journal of Bone and Mineral Research*, 2019
- Yanchun Pan, Ying Zhu, Wei Yang, Eric Tycksen, **Shaopeng Liu**, Linjian Zhu, Mukesh K Sharma, Albert H Kim, Bo Zhang, Hiroko Yano. "The role of Twist1 in mutant huntingtin-induced transcriptional alterations and neurotoxicity." *Journal of Biological Chemistry*, 2018
- Kesavan Meganathan , Emily MA Lewis , Paul Gontarz , **Shaopeng Liu** , Ed Stanley , Andrew G Elefanty , James E. Huettner , Bo Zhang , Kristen L Kroll. "Regulatory networks specifying cortical interneurons from human embryonic stem cells reveal roles for CHD2 in interneuron development." *Proceedings of the National Academy of Sciences*, 2017
- Hangxing Jia, Tong Liang, Zhaoning Wang, Zhaoren He, Yang Liu, Lei Yang, Yan Zeng, **Shaopeng Liu**, Linyi Tang, Jianbo Wang, Yu Chen, and Zhixiong Xie. "Multistage Regulator Based on Tandem Promoters and CRISPR/Cas." *ACS Synthetic Biology*, 2014

## Skills

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- Programming: Shell, Python, R, Rust, Git, and SQL
- Domain of knowledge: Bioinformatics, Statistics, Algorithm, and Data mining

## Teaching and Mentoring

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- TA in class "Statistical Computing with SAS", 2017

## Awards

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| • The J. Lloyd Huck Graduate Fellowship; Pennsylvania State University | 2019-2020 |
| • The Graham Endowed Fellowship; Pennsylvania State University         | 2019-2021 |
| • The Braddock Scholarship; Pennsylvania State University              | 2019-2020 |
| • WU Scholarship and Grants; Washington University in St. Louis        | 2016-2017 |
| • Golden medal; International Genetically Engineered Machine (IGEM)    | 2013-2014 |
| • College Scholarship; Wuhan University                                | 2010-2012 |