

## Yang Li, Ph.D.

Postdoctoral Researcher  
Bioinformatics and Mathematical Biosciences Lab

### CONTACT

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### EDUCATION

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- Ph.D. Operations Research and Control Theory,  
Shandong University, 2013-2019 (Advisor: Prof. Guojun Li)  
Thesis: "Combinatory Motif Discovery and Analysis of Complex Binding  
Patterns for ChIP-seq Data"
- Visiting Bioinformatics,  
Scholar The University of North Carolina at Charlotte, 2014-2015 (Advisor: Prof.  
Zhengchang Su)
- M.D. Operations Research and Control Theory,  
Shandong University, 2011-2013 (Advisor: Prof. Guojun Li)
- B.S. Information and Scientific Computing,  
Shandong University, 2007-2011

### TEACHING

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Teaching Assistant, Mathematical Analysis (Mathematics Base Class), Autumn 2011,  
School of Mathematics, Shandong University.

### PUBLICATIONS

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#### Available

1. Li, Y., Ma, A., Mathé, E.A., Li, L., Liu, B., & Ma, Q. (2020). Elucidation of biological networks across complex diseases using single-cell omics. *Trends in Genetics* (in press).
2. Li, Y., Ni, P., Zhang, S., Li, G., & Su, Z. (2019). An ultra-fast and accurate motif finder in large ChIP-seq datasets for combinatory motif discovery. *Bioinformatics*.
3. Li, Y., Liu, B., Li, J., & Li, G. (2019). Mimod: a new algorithm for mining biological network modules. *IEEE Access*.
4. Qi, E., Wang, D., Li, Y., Li, G., & Su, Z. (2019). Revealing favorable and unfavorable residues in cooperative positions in protease cleavage sites. *Biochemical and Biophysical Research Communications*.
5. Yang, J., Ma, A., Hoppe, A.D., Wang, C., Li, Y., Zhang C., Wang, Y., Liu, B., & Ma, Q.

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- (2019). Prediction of regulatory motifs from human Chip-sequencing data using a deep learning framework. *Nucleic Acids Research*.
6. Lu, S. J., Xie, J., **Li, Y.**, Yu, B., Ma, Q., & Liu, B. Q. (2019). Identification of lncRNAs-gene interactions in transcription regulation based on co-expression analysis of RNA-Seq data. *Math. Biosci. Eng.*
  7. Gao, B. , Zhao, Y., **Li, Y.**, Liu, J., Wang, L., Li, G., & Su, Z. (2018). Prediction of driver modules via balancing exclusive coverages of mutations in cancer samples. *Advanced science*.
  8. Gao, B., Li, G., Liu, J., **Li, Y.**, & Huang, X. (2017). Identification of driver modules in pan-cancer via coordinating coverage and exclusivity. *Oncotarget*.
  9. Liu, B., Yang, J., **Li, Y.**, Mcdermaid, A., & Ma, Q. (2017). An algorithmic perspective of *de novo* cis-regulatory motif finding based on ChIP-seq data. *Briefings in Bioinformatics*.
  10. Qi, E., Wang, D., Gao, B., **Li, Y.**, & Li, G. (2017). Block-based characterization of protease specificity from substrate sequence profile. *BMC Bioinformatics*.

### Pending

1. **Li, Y.**, Ni, P., Zhang, S., Li, G., & Su, Z. (2019). Identification of confounding factors of motif-finding in ChIP-seq datasets reveals complex transcription factor binding patterns. (Completed)
2. Zhang, Q., Li, S., **Li, Y.**, Zhang, Y., Ma, Q., Zhang, Y., & Yu, B. (2020). MpsLDA-ProSVM: predicting multi-label protein subcellular localization by wMLDAe dimensionality reduction and ProSVM classifier. *Artificial Intelligence in Medicine* (Under Review)

### **CONFERENCES**

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1. Interdisciplinary Conference of Mathematics and Bioinformatics. November, 2019. Qingdao, China.
2. Intelligent Computing and Biomedical Big Data Conference. November, 2018. Shanghai, China.
3. Workshop of Graph Theory and its Applications. September, 2016. Jinan, China.
4. Forum of Young Scholars on Interdisciplinary Research in Mathematics, Computer and Life Science. May, 2014. Beijing, China.
5. International Bioinformatics Workshop. July, 2013. Shanghai, China.

### **SOFTWARES**

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1. **ProSampler**: an ultra-fast and accurate motif finder in large ChIP-seq datasets for combinatorial motif discovery. Link: <https://github.com/zhengchangsulab/ProSampler>
2. **MiMod**: a new algorithm for mining biological network modules. Link: <https://github.com/LiYangSDU/SYSTEMS>
3. **PBlock**: block-based characterization of protease specificity from substrate sequence profile. Link: <https://sourceforge.net/projects/PBlock/files/?source=navbar>

**TEACHING**

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1. **Guest lecturer**, Applications of Machine Learning and Artificial Intelligence in Biomedical Informatics (BMI 8050), autumn 2020, Department of Biomedical Informatics, The Ohio State University.
2. **Guest lecturer**, Single-Cell RNA-Sequencing Data Modeling and Analyses, summer class 2020, Iowa State University.

**INVITED PRESENTATIONS**

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1. **Co-lecturer**, Cell-Type-Specific Gene Regulatory Networks Inference Based on Single-Cell Multi-Omics Data. Pelotonia Institute for Immuno-Oncology, The Ohio State University. Oct 9th, 2020.

**REVIEWS**

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*Nature, Genome Biology, Nucleic Acids Research, Bioinformatics, PLoS Computational Biology, BMC Genomics, BMC Bioinformatics, Computational Biology and Chemistry, Molecular Therapy Nucleic Acids, Frontiers, Current Bioinformatics.*