

Li, Wei Vivian

683 Hoes Lane West Rm 210
Rutgers, The State University of New Jersey
Piscataway, NJ 08854

Telephone: 732-235-8574
Email: vivian.li@rutgers.edu
Homepage: <http://liw-vivian.appspot.com/>

RESEARCH INTERESTS

I am interested in statistical modeling and algorithm development, as well as their applications to high-throughput sequencing data in bioinformatics and clinical research. Major research topics of my lab include:

- Statistical modeling and experimental design of
 - Single-cell genomic data
 - Bulk-tissue high-throughput sequencing data
 - Biomedical data
- Gene regulatory networks
- Alternative RNA splicing
- Comparative bioinformatics

EDUCATION

University of California, Los Angeles (UCLA) 09/2014 - 06/2019
Department of Statistics
Ph.D. in Statistics
Dissertation: Statistical methods for bulk and single-cell RNA sequencing data
Advisor: Dr. Jingyi Jessica Li

Huazhong University of Science & Technology (HUST) 09/2010 - 06/2014
School of Mathematics and Statistics
B.S. in Statistics

EMPLOYMENT

Assistant Professor 08/2019 -
Department of Biostatistics and Epidemiology
School of Public Health
Rutgers, The State University of New Jersey

Teaching Assistant Consultant 10/2018 - 06/2019
Department of Statistics
University of California, Los Angeles

Graduate Student Researcher 09/2016 - 06/2019
Department of Statistics
University of California, Los Angeles

HONORS AND AWARDS

Busch Biomedical Grant Award , Rutgers	2020
The Caliburn Allocation Award of Research Computing , Rutgers	2020
The Most Outstanding Statistician Award , UCLA	2019
Physical Sciences Entrepreneurship & Innovation Award (co-inventor with Dr. Jessica Li), UCLA	2018
Dissertation Year Fellowship , UCLA	2018
Pearl Cohen Poster Award , UCLA Biomedical & Life Science Innovation Day	2018
Diversity Scholarship , UseR 2016 Conference	2016
Doctoral Student Travel Grant , UCLA	2016
The Most Promising Computational Statistician Award , UCLA	2015
Distinguished Graduate of Class 2014 , HUST	2014
National Fellowship , Ministry of Education, China	2013
Student Award of Excellence (awarded to 20 students per year), HUST	2013
National Fellowship , Ministry of Education, China	2012
National Fellowship , Ministry of Education, China	2011
Outstanding Student Award (awarded to 3 students in each department), HUST	2011

RESEARCH FUNDING

Rutgers Busch Biomedical Grant	10/01/2020 - 09/30/2022
A Novel Approach for Joint Modeling of Multi-patient Single-cell Gene Expression Data	
NJ ACTS Mini-Methods Grant	06/04/2020 - 06/03/2021
Statistical Methods for Single-cell Differential Gene Network Analysis	
Rutgers School of Public Health Pilot Grant	11/01/2019 - 06/01/2021
Understanding Gene Co-expression Patterns in Single Cells	

PUBLICATIONS

* co-first authors [†] corresponding authors — trainees

Preprint:

1. Li, W. V.[†] & Li, Y. (2020). scLink: Inferring Sparse Gene Co-expression Networks from Single-cell Expression Data. *bioRxiv*.
2. Jiang, R., Li, W. V., & Li, J. J.[†] (2020). mbImpute: an accurate and robust imputation method for microbiome data. *bioRxiv*.

3. Roque, W., Cuevas-Mora, K., Sales, D., Li, W. V., Rosas, I. O., & Romero, F.[†] (2020). Transcriptomics, metabolomics and lipidomics of chronically injured alveolar epithelial cells reveals similar features of IPF lung epithelium. *bioRxiv*.

Refereed Article:

4. Wang, J., Deng, F., Zeng, F., Shanahan, A. J., Li, W. V., & Zhang, L.[†] (2020). Predicting long-term multicategory cause of death in patients with prostate cancer: random forest versus multinomial model. *American Journal of Cancer Research*, 10(5), 1344.
5. Xu, J., Cheng, Y., Yuan, X., Li, W. V., & Zhang, L.[†] (2020). Trends and prediction in daily incidence of novel coronavirus infection in China, Hubei Province and Wuhan City: an application of Farr's law. *American Journal of Translational Research*, 12(4), 1355.
6. Li, W. V.^{*}, Li, S.^{*}, Tong, X., Deng, L., Shi, H.[†], & Li, J. J.[†] (2019) AIDE: annotation-assisted isoform discovery with high precision. *Genome Research*, 29, 2056-2072.
7. Li, W. V. & Li, J. J.[†] (2019). A statistical simulator scDesign for rational scRNA-seq experimental design. *Bioinformatics (ISMB/ECCB 2019)*, 35(14), i41-i50.
8. Ge, X., Zhang, H.[†], Xie, L., Li, W. V., Kwon, S. B., & Li, J. J.[†] (2019). EpiAlign: an alignment-based bioinformatic tool for comparing chromatin state sequences. *Nucleic Acids Research*, gkz287.
9. Li, W. V. & Li, J. J.[†] (2018). An accurate and robust imputation method scImpute for single-cell RNA-seq data. *Nature Communications*, 9, 997.
10. Li, W. V. & Li, J. J.[†] (2018). Modeling and analysis of RNA-seq data: a review from a statistical perspective. *Quantitative Biology*, 6(3), 195-209.
11. Li, W. V., Zhao, A., Zhang, S.[†], & Li, J. J.[†] (2018). MSIQ: joint modeling of multiple RNA-seq samples for accurate isoform quantification. *Annals of Applied Statistics*, 12(1), 510-539.
12. Li, W. V., Chen, Y., & Li, J. J.[†] (2017). TROM: A testing-based method for finding transcriptomic similarity of biological samples. *Statistics in Biosciences*, 9(1), 105-136.
13. Li, W. V., Razaee, Z. S., & Li, J. J.[†] (2016). Epigenome overlap measure (EPOM) for comparing tissue/cell types based on chromatin states. *BMC Genomics*, 17(1), S10.

Dissertation:

14. Li, W. V. (2019). Statistical methods for bulk and single-cell RNA sequencing data. PhD dissertation, UCLA.

Google Scholar: <https://scholar.google.com/citations?user=HzjANkQAAAAJ>

INVITED TALKS AND CONFERENCE PRESENTATIONS

Conference and Symposium Presentations:

1. Talk, 2020 Joint Statistical Meetings, Virtual. 08/2020
AIDE: Annotation-Assisted RNA Transcript Discovery with High Precision

2. Invited Talk, RCAF Forum: Challenges and Opportunities in Computational Biology. 08/2020
Current Computational and Analytical Challenges in Transcriptomics
3. Poster, 28th Conference on Intelligent Systems for Molecular Biology (ISMB 2020). 07/2020
Inferring Gene Co-expression Networks from Single Cell Gene Expression Data
4. Invited Talk, RCAF Webinar Series. 05/2020
Statistical Challenges and Opportunities in Single-cell Studies
5. Invited Talk, ENAR 2020 Spring Meeting, Virtual. 03/2020
A Unified View of Asymmetric Binary Classification
6. Invited Talk, Inaugural Lange Symposium Software Workshop 02/2020
Improving Single-cell RNA-seq Data Analysis with scImpute and scDesign
7. Invited Talk, 2019 Joint Statistical Meetings, Denver, CO. 07/2019
A Unified View of Asymmetric Binary Classification
8. Invited Talk, ENAR 2019 Spring Meeting, Philadelphia, PA. 03/2019
A Unified View of Asymmetric Binary Classification
9. Talk, 8th Annual Southern California Systems Biology Conference, Irvine, CA. 02/2019
AIDE: Annotation-assisted Isoform Discovery with High Precision
10. Invited Talk, 2018 IEEE 8th International Conference on Computational Advances in Bio and Medical Sciences, Las Vegas, NV. 10/2018
scImpute: Accurate and Robust Imputation for Single Cell RNA-seq Data
11. Talk and Poster, Inaugural Symposium on Multiscale Cell Fate, Irvine, CA. 10/2018
scImpute for Imputation of ScRNA-seq Data
12. Talk, UCLA 4th Annual QCBio Retreat, Los Angeles, CA. 09/2018
AIDE for Annotation-assisted mRNA Isoform Reconstruction and Quantification
13. Talk, 2018 Joint Statistical Meetings, Vancouver, Canada. 08/2018
Joint Modeling of Multiple RNA-seq Samples for Accurate Isoform Quantification
14. Talk, 26th Conference on Intelligent Systems for Molecular Biology (ISMB 2018), Chicago, IL. 06/2018
scImpute: Accurate and Robust Imputation for Single Cell RNA-seq Data
15. Poster, UCLA Biomedical & Life Science Innovation Day, Los Angeles, CA. 06/2018
scImpute: Accurate Imputation for Single Cell RNA-seq Data
16. Invited Talk, DahShu Webinar. 04/2018
An Accurate and Robust Imputation Method for Single-cell RNA-seq Data
17. Invited Talk, 3rd Annual NGS Data Analysis & Informatics Conference, San Diego, CA 02/2018
scImpute: Accurate and Robust Imputation for Single Cell RNA-seq Data
18. Poster, UCLA 3rd Annual QCBio Retreat, Los Angeles, CA. 09/2017
scImpute: Accurate and Robust Imputation for Single Cell RNA-seq Data

19. Talk, Asia Pacific Bioinformatics Conference 2016, San Francisco, CA. 01/2016
Epigenome Overlap Measure (EPOM) for Comparing Tissue/cell Types based on Chromatin States
 20. Talk, USC/UCLA Bioinformatics Joint Meeting, Los Angeles, CA. 11/2015
A Testing-based Measure EPOM for Comparing Tissue/cell Types based on Chromatin States
 21. Poster, UCLA 1st Annual QCBio Retreat, Los Angeles, CA. 09/2015
A New Measure for Comparing Epigenetic Profiles in Tissue/cell Types
- Seminar Presentations:**
22. Epigenetics User Group Meeting, Rutgers Department of Genetics 02/2020
Improving Statistical Analysis of Bulk and Single-cell RNA-seq Data
 23. Systems Biology/Bioinformatics Meeting, Rutgers Cancer Institute of New Jersey 10/2019
Improving Statistical Analysis of Bulk and Single-cell RNA-seq Data
 24. Department of Biostatistics and Epidemiology, Rutgers University. 02/2019
Statistical Methods to Uncover Hidden Information from Large-scale Genomic Data
 25. Department of Statistics, University of Wisconsin-Madison. 02/2019
Statistical Methods to Uncover Hidden Information from Large-scale Genomic Data
 26. Department of Public Health, University of California, Merced. 01/2019
Statistical Methods to Uncover Hidden Information from Large-scale Genomic Data
 27. Department of Statistics, Pennsylvania State University. 01/2019
Statistical Methods to Uncover Hidden Information from Large-scale Genomic Data
 28. Department of Statistics, University of Illinois at Urbana-Champaign. 12/2018
Statistical Methods to Uncover Hidden Information from Large-scale Genomic Data
 29. Jonsson Comprehensive Cancer Center Gene Regulation Intramural Meeting, UCLA. 03/2018
scImpute: Accurate and Robust Imputation for Single Cell RNA-seq data

TEACHING EXPERIENCE

Instructor (Rutgers Graduate Courses):

BIST 0725: Generalized Linear Models Spring 2020

Student Instructor (UCLA Graduate Courses):

STATS 495A: Teaching College Statistics Fall 2018

Teaching Assistant (UCLA Graduate Courses):

STATS 207: Statistical Learning with Sparsity Spring 2018

STATS 203: Large Sample Theory, Including Resampling Winter 2017

STATS 205: Hierarchical Linear Models Winter 2017

STATS M254: Statistical Methods in Computational Biology Spring 2016

STATS 200C: Large Sample Theory Spring 2016

Teaching Assistant (UCLA Undergraduate Courses):

STATS 101A: Introduction to Data Analysis and Regression Summer 2016

STATS 13: Introduction to Statistical Methods for the Health and Life Sciences Winter 2016

STATS 10: Introduction to Statistical Reasoning Fall 2015

STATS 100B: Introduction to Mathematical Statistics Summer 2015

Guest Lecturer:

DSO 530: Applied Modern Statistical Learning Methods 04/2020
Marshall School of Business, University of South California
Introduction to Cloud Computing

DSO 530: Applied Modern Statistical Learning Methods 03/2019
Marshall School of Business, University of South California
Cloud Computing with the Amazon Web Services

BIOINFO 201: Bioinformatics Interdisciplinary Research Seminar 10/2018
Bioinformatics Interdepartmental Ph.D. Program, UCLA
Statistical Methods for Isoform Quantification of Multiple Samples

STATS M254: Statistical Methods in Computational Biology 06/2018
Department of Statistics, UCLA
Statistical Methods for Isoform Quantification of Multiple Samples

STATS M254: Statistical Methods in Computational Biology 05/2018
Department of Statistics, UCLA
Imputation Methods for Single-cell RNA-seq Data

DSO 530: Applied Modern Statistical Learning Methods 02/2018
Marshall School of Business, University of South California
Cloud Computing with the Amazon Web Services

DSO 530: Applied Modern Statistical Learning Methods 03/2017
Marshall School of Business, University of South California
Introduction to the Amazon Web Services (AWS)

STUDENT MENTORING & ADVISING

Research Mentor of Graduate Students:

- Dayuan Wang (2020/08 -) MS student in Biostatistics at Rutgers
- Shiwei Fu (2020/06 -) MS student in Statistics at UIUC
- Alireza Naghizadeh (2020/06 - 2020/08) PhD student in Computer Science at Rutgers
- Yanzeng Li (2019/12 - 2020/09) MS student in Biostatistics at Rutgers

Research Mentor of Undergraduate Students:

- Andrew Cheng (09/2020 -) Undergraduate student in Computer Science at Rutgers

Academic Advisor of Graduate Students:

- Phoebe Chu (08/2020 -) MS student in Biostatistics at Rutgers
- Changhan Lin (08/2020 -) MS student in Biostatistics at Rutgers
- Adriel Staana (08/2020 -) MS student in Biostatistics at Rutgers
- Daniel Yen (08/2020 -) MS student in Biostatistics at Rutgers
- Zifan Guo (01/2020 -) MS student in Biostatistics at Rutgers

Thesis Committee Member:

- Wenxuan Xiong (2020 -) PhD student in Biostatistics at Rutgers
- Aysegul Guvenek (2019 - 2020) PhD student in Biomedical Science at Rutgers

PROFESSIONAL SERVICE

Committee Member:

Rutgers School of Public Health Bylaws and Elections Committee	2020 -
Rutgers Bioinformatics and Microbiome Research Committee	2020 -

Reviewer:

Applied Sciences (×1)
Bioinformatics (×8)
BioMed Research International (×1)
Biometrics (×1)
BMC Bioinformatics (×1)
BMC Genomics (×1)
Cells (×1)
Chapman & Hall/CRC Press (×1)
Frontiers in Genetics (×1)
Gene Report (×1)
Genes (×2)
Genome Biology (×1)
Genomics, Proteomics & Bioinformatics (×1)
IEEE Access (×2)
Journal of Molecular Cell Biology (×1)
Laboratory Investigation (×2)
NAR Cancer (×1)
NAR Genomics and Bioinformatics (×1)
Nature Communications (×1)
Nature Methods (×1)
Nucleic Acids Research (×3)
PeerJ (×1)
Plos Computational Biology (×2)
Plos One (×1)
Proteomics (×1)
Quantitative Biology (×1)

PROFESSIONAL AFFILIATIONS

Member:

Rutgers Cancer Institute of New Jersey	2019 -
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Eastern North American Region International Biometric Society	2019 -
American Statistical Association	2019 -
International Chinese Statistical Association	2019 -

Student Member:

International Society for Computational Biology	2017 - 2019
International Chinese Statistical Association	2015 - 2019
American Statistical Association	2014 - 2019

SOFTWARE

R packages:

- **scDesign** for rational scRNA-seq experimental design
<https://github.com/Vivianstats/scDesign>
- **scLink** for constructing single-cell gene co-expression networks
<https://github.com/Vivianstats/scLink>
- **scImpute** for accurate imputation of scRNA-seq data
<https://github.com/Vivianstats/scImpute>
- **AIDE** for annotation-assisted transcript reconstruction and quantification
<https://github.com/Vivianstats/AIDE>
- **MSIQ** for quantifying expression of RNA transcripts from multiple RNA-seq samples
<https://github.com/Vivianstats/MSIQ>
- **TROM** for comparing transcriptomes of biological samples from the same or different species
<https://cran.r-project.org/web/packages/TROM/index.html>