Siyao Liu

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SUMMARY OF PROFESSIONAL GOALS

My career goal is to help solving important societal needs in global food security and human health through the development and application of statistical methods and computational tools for the analysis of genetic and genomic data.

EDUCATION

PhD, Bioinformatics & Computational Biology — Expected May 2022
Department of Genetics, University of North Carolina at Chapel Hill

- *Dissertation:* Clustering Single Cell RNA-seq Data in Cancer
- *Committee:* Drs. Charles Perou (major advisor), Steve Marron, Joel Parker (chair), Katie Hoadley, Benjamin Vincent
- *Written exam completed in May, 2018*
- *Oral exam expect to complete in May, 2020*

MS, Plant Breeding & Genetics, **GPA**: 3.96/4.0 — May 2015 (degree conferred)
Department of Crop Sciences, University of Illinois at Urbana-Champaign

- *Master's Thesis:* High Density Genetic Mapping of *Miscanthus sinensis* reveals inheritance of zebra stripe
- *Committee:* Drs. Erik Sacks (major advisor), John Juvik, Brian Diers, Patrick Brown

BS, *cum laude*, Turfgrass Management — May 2012
Department of Crop and Soil Sciences, Michigan State University, **GPA**: 3.94/4.0
College of Forestry, Beijing Forestry University, **GPA**: 91.13/100

SUMMARY OF RESEARCH SKILLS

Project Management, Research Methodology & Design, Data Collection & Management, Statistical Analysis (R, Matlab, SAS, JMP, JMP Genomics, UNIX), Grant and Proposal Writing, Oral Presentations, Public Speaking

RESEARCH INTERESTS

Bioinformatics, Statistical Genetics, Data Science, Data Visualization, Predictive Modeling, Predictive Breeding, Genomic Selection, Cancer Genomics, Precision Medicine

AWARDS AND HONORS

- UIUC The Lawrence E. Schrader and Elfriede Massier Plant Physiology Fellowship, August 2012
- UIUC Graduate College Conference Travel Award, November 2012
- UIUC Energy Biosciences Institute Travel Award, November 2012

RESEARCH EXPERIENCE

Dissertation Research — August 2017 – Present
UNC School of Medicine, Department of Genetics, Chapel Hill, NC
Major Advisor: Dr. Charles Perou
The goal of my research project is twofold: 1) develop statistical methods and computation tools for analyzing genetic and genomic data (primarily single cell RNA-seq data); 2) apply both existing and newly developed methods to gene expression data in order to understand tumor heterogeneity as well as how the immune system responds to and shapes intratumor heterogeneity. The goal is to develop more effective personalized cancer therapies for patients.

Rotation Research
UNC School of Medicine, Department of Genetics, Chapel Hill, NC
Stein Lab (Rotation PI: Dr. Jason Stein)
Project: Unearthing the Evolutionary History of Genetic Variants Influencing Human Cortical Surface Area

- Performed Singleton Density Score (SDS) analysis on human cortical surface area (ENIGMA3)
- Presented a poster at the program poster session

Valdar & Heise Labs (Rotation PIs: Drs. William Valder & Mark Heise)
Project: Identifying Quantitative Genetic Loci (QTL) for Host Genetic Responses to Influenza A Virus Infection in a Collaborative Cross Recombinant Intercross (CC-RIX) Population

- Analyzed time-course antibody response data in the CC-RIX population
- Performed Principal Component Analysis for IgM antibody data
- Wrote a report for this project

Perou Lab (Rotation PI: Dr. Charles Perou, collaborated with Dr. Steve Marron)
Project: Single-cell RNA sequencing to Identify Cell Types in Adult Mouse Normal Mammary Gland

- Performed clustering analysis on single cell RNA-seq data taken from two adult mouse normal mammary glands
- Gave a professional talk at the BCB

Thesis Research August 2012 – January 2015
UIUC Department of Crop Sciences, Urbana-Champaign, IL
Major Advisor: Dr. Erik Sacks
- Constructed high density genetic map for *Miscanthus sinensis* (a bioenergy grass) using next-generation genotyping-by-sequencing technique
- Identified quantitative trait loci for biomass yield and adaptation traits in *Miscanthus*
- Trained undergraduate student workers in molecular and field work related to my research project

Undergraduate Student Intern August 2011 – February 2012
MSU Hancock Turfgrass Research Center, East Lansing, MI
Supervisor: Dr. Kevin Frank
- Conducted three independent research studies on fall nitrogen fertility in cool-season turfgrass, 15N fall fertility, cooling degree days and dandelion roots after fall herbicide application
- Assisted instructor with teaching CSS292 Management of Turfgrass Weeds Class
- Participated in experiment design, field trials set up, data collection, and reports delivery

TEACHING EXPERIENCE

Graduate Teaching Assistant Spring 2019
Statistical Genetics and Genomics (BCB 723)
- Graded homework assignments
- Held regular office hours

Graduate Teaching Assistant Fall 2018
Introduction to Statistical Modeling (BCB 720)
- Graded homework assignments
- Held regular office hours
- Participated in preparing and teaching the first class lecture

Teacher How to Learn to Code Summer Program Summer 2018
Teaching How to Learn to Code
- Prepared lectures for Beginners R class
- Taught and assisted teaching classes for 6 weeks

Graduate Teaching Assistant Spring 2014
Applied Statistics II (CPSC542: experimental designs for science majors)
- Assisted professor with teaching lab sessions twice a week
- Wrote answer keys and graded homework and exams
- Held regular office hours and review sessions

PROFESSIONAL EXPERIENCE

Assistant Genetic Project Lead, Cereals January 2015 – December 2017
Syngenta, Slater, Iowa, USA
- Performed statistical data analyses of genetic linkage mapping, QTL mapping, genome-wide single-SNP and haplotype association mapping, genomic selection
- Interpreted data and communicated and presented results to various groups
- Participated in evaluating and improving data analysis tools and methods for both conventional and predictive breeding
- Established synergies with wheat breeders and scientists working in other crops
- Actively participated in formulating ideas for existing and potential projects in genomic selection applied to wheat breeding

PUBLICATIONS AND POSTERS

Publications
- Hollern D.P., Xu N., Thennavan A., Glodowski C., Garcia Recio S., Mott K.R., He X., Garay J.P., Carey-Ewend K., Marron D., Ford J., **Liu S.**, Vick S.C., Martin M., Parker J.S., Vincent B.G., Serody J.S., Perou C.M., B cells and T follicular helper cells mediate response to checkpoint inhibitors in high mutation burden mouse models of breast cancer, Cell, 2019
- Tilot A.K., Khramtsova E.A., Grasby K., Jahansha N., Painter J., Colodro-Conde L., Bralten J., Hibar D.P., Lind P.A., **Liu S.,** Brotman S., Thompson P.M., Medland S.E., Macciardi F., Stranger B.E., Davis L.K., Fisher S.E., Stein J.L., The Evolutionary History of Common Genetic Variants Influencing Human Cortical Surface Area (submitted)

- Mitros et al., Genome biology of the paleotetraploid perennial C4 grass *Miscanthus*
- **Liu S.**, Clark L.V., Swaminathan K., Gifford J.M., Juvik J. A., Sacks E.J. (2015) High-density genetic map of *Miscanthus sinensis* reveals inheritance of zebra stripe. Global Change Biology Bioenergy, 8, 616–630.
- Dong, H., **Liu, S.**, Clark, L. V., Sharma, S., Gifford, J. M., Juvik, J. A., … Sacks, E. J. (2018). Winter hardiness of *Miscanthus* (II): Genetic mapping for overwintering ability and adaptation traits in three interconnected Miscanthus populations. https://doi.org/10.1111/gcbb.12587
- Dong H., **Liu S.**, Clark L. V., Sharma S., Gifford J. M., Juvik J. A., … Sacks E. J. (2018). Genetic mapping of biomass yield in three interconnected *Miscanthus* populations. Global Change Biology Bioenergy, 10, 165–185.

Posters
- 2018 The Department of Genetics Retreat in Wilmington, NC (Poster title: "Characterizing T cell Diversity across Various Human Cancer Cohorts by Single Cell RNA-seq")
- 2017 BBSP Poster Session, Chapel Hill, NC (Poster title: "Unearthing the Evolutionary History of Genetic Variants Influencing Human Cortical Surface Area")
- 2014 ASA-CSSA-SSSA meeting in Long Beach, CA (Poster title: "A High-Density Genetic Map for *Miscanthus sinensis* that Integrates RAD-seq and GoldenGate SNPs: Mapping Zebra Stripe Trait")

Oral Presentations
- 2018 BCB New Student Symposium (Talk title: "Single-cell RNA sequencing to Identify Cell Types in Adult Mouse Normal Mammary Gland")

CONFERENCES AND WORKSHOPS
- 2019 Komen Young Researchers Round Table, Durham, NC
- 2019 Computational Medicine Program Inaugural Symposium, Chapel Hill, NC
- 43rd Annual UNC Lineberger Scientific Symposium, Chapel Hill, NC

RELEVANT COURSEWORK
PhD

The First Year Group (Faulty Group Leader: Dr. Samir Kelad, Co Mentors: Drs. Jason Stein, Folami Iderabdullah, Uma Nagarajan, Mike Madden, and Joe Harrison), Introduction to Statistical Modeling (High Pass), Object Oriented Data Analysis (High Pass), Statistical Theory I (Pass), Applied Statistics II - Linear Models (Pass), Mathematical Modeling (High Pass), Topics in Population Genetics (Pass), Sequence Analysis (High Pass), Structural Bioinformatics (Pass), Topics in Statistical Genetics (High Pass), Cancer Pathobiology (High Pass), Cancer Genomics and Class Discovery (High Pass)

MS

Applied Multivariate Statistics, Applied Statistical Methods I, Applied Statistical Methods II - Experiment Design, Evolution Genetics and Genomics, Genomics for Plant Improvement, Horticultural Plant Breeding, Molecular Marker Data Analyses, Plant Breeding Literature, Population Genetics, Principles of Plant Breeding

CERTIFICATES
- The 21st Summer Institute in Statistical Genetics at University of Washington, Seattle, WA (2016)
- edX Verified Certificate for Data Science and Machine Learning Essentials (issued October 2015)
- Michigan Test for Teacher Certification (MTTC)

ACTIVITIES AND SERVICE
Curriculum Bioinformatics and Computational Biology Steering Committee Member September 2019 – Present
- Evaluate new faculty applicants
- Help craft program policies
- Provide student perspective on policies and decisions

Trainee Johnson Controls Business Immersion Program August 2010 – August 2011

This program selected 30 excellent college students from awarded teams in 2010 SIFE China National Business Competition
- Participated in two sessions of on-site intense training and one-year student business project to improve Johnson Controls' brand awareness
- Gained advanced business knowledge and practical skills about project management, enterprise financing, leadership development, public speaking, and communication skills
- Specific training topics included LEM Business Model, How to initiate a benchmark, DISC Model, Team Work, Interview Skills, Distant Collaboration

President of SIFE (Students in Free Enterprise) BFU September 2008 - June 2010
- Implemented 7 projects to help people in the community acquire financial independence and improve their life quality (impacting over 5000 people)

- Led the team winning the TOP 16, TOP 20 team & the Johnson Controls Environmental Award in SIFE China National Business Competition
- Interviewed by 21-Century Newspaper

APPENDIX: SUMMARY OF ACHIEVEMENTS

Academic Experience

University of North Carolina at Chapel Hill, NC, USA (2017 - Present)

I. *Analysis of Single Cell RNA-seq data from data QC, batch correction to downstream analyses such as clustering, differential gene expression, cell trajectory.*
II. *Developing novel methods for clustering single cell RNA-seq data and assessing the optimal number of groups*

University of Illinois at Urbana-Champaign, IL, USA (2012 - 2014)

III. Four mapping populations for *Miscanthus* phenotyped and genotyped
IV. A pipeline developed for SNP filtering for mapping purposes in Miscanthus using high-throughput sequencing data
V. High-density genetic maps constructed for *Miscanthus sinensis* using next generation high-throughput genotyping-by-sequencing technique
VI. QTL for zebra stripe and biomass yield traits identified in one of the mapping populations
VII. A graduate-level Statistics course in experimental design prepared and taught

Industry Experience

Syngenta Seeds, Slater, IA, USA (2015 - 2017)

I. Bi-parental QTL mapping conducted for agronomic, disease resistance, producibility, abiotic/biotic stress traits in wheat
II. Genome-wide association mapping analysis in wheat implemented (two on global diversity panels and one on regional panel)
III. Genomic selection analyses performed for yield and quality traits in two wheat breeding programs
IV. Conventional and hybrid wheat breeding programs in North America engaged in discussions on how genomic tools could help increase breeding efficiencies