

CHUN SU

Bioinformatics Scientist | Computational Biologist

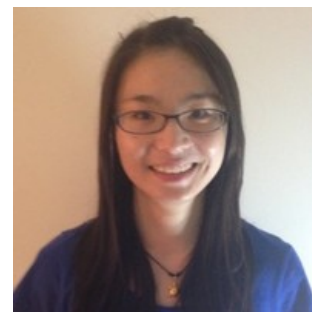
Scientist with 10+ years of hands-on experience in both bioinformatics and molecular biology. Proven experience in troubleshooting and meeting challenging deadlines in a fast-paced work environment. Excellent professional communication and leadership skills developed through community service and extensive teaching experiences.

EDUCATION

- 2017 | 2011
● **Ph.D, Biology**
University of Virginia
Charlottesville, VA
• Thesis: Uncovering the molecular mechanism underlying the virulence of *Striga gesnerioides*
- 2011 | 2007
● **B.S Biology**
Huazhong Agricultural University
Wuhan, China

PROFESSIONAL EXPERIENCE

- Current | 2022
● **Scientist, Computational Biology**
Amgen, Inc
Remote
- 2022 | 2018
● **Bioinformatics Scientist**
Children's Hospital of Philadelphia
Philadelphia, PA
• Established in-house bioinformatics analysis pipelines and SOP for the various types of NGS analysis including RNA-seq, ChIP-seq, ATAC-seq, Capture-C and Hi-C.
• Predicted candidate targets by integrating human genetics (eg. GWAS, rare variants) with functional genomics data in immune, neurological, and metabolic contexts
• Innovated computational workflows to analyze data from high-throughput screening, including CRISPR screen, MPRA (Massive Parallel Reporter Assay) and HiDRA (High-resolution Dissection of Regulatory Activity).
• Designed and maintained Laboratory Information Management System (LIMS) using relationship database application FileMaker
• Developed and maintained web applications using R Shiny.
• Authored 11 peer-reviewed publications of which 4 are first-authored
• Presented research at national and international scientific conferences
• Recruited and trained bioinformatics fellows and graduate students.



CONTACT INFO

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- 📧 @sckinta
- 🌐 learningwithsckinta
- in LinkedIn
- 🔍 Google Scholar

SKILL

HIGHLIGHTS

- 🔍 NGS analysis
- 🔍 Single cell multiomics
- 🔍 Human Genetics
- 🔍 Phylogenetics
- 🔍 R | Bash | Perl | Python
- 🔍 R shiny
- 🔍 SQL & FileMaker
- 🔍 HPC & AWS cloud computing
- 🔍 Git & GitHub

Last updated on 2023-01-31.

Prepared by {Pagedown}

- 2017
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2013

Graduate Researcher

University of Virginia (Timko Lab)

Charlottesville, VA

 - Initiated and led a research project characterizing the genetic basis for virulence variance of a major African crop pest *Striga gesnerioides*.
 - Implemented large-scale data mining and developed custom bioinformatic scripts to identify expression pattern differences under different biological conditions.
 - Collaborated with external research groups on comparative functional genomics of parasitic plants
 - Designed and performed experiments testing putative parasitism genes
 - Authored scientific publications and assisted in writing government-funded grants
 - Mentored and trained undergraduate students
- 2013
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2011

Graduate Researcher

University of Virginia (Li Lab)

Charlottesville, VA

 - Standardized computational pipeline to predict microRNA on multiple crop species using small RNA sequencing analysis on HPC clusters
 - Modified and optimized microRNA prediction Perl package for mining Expression Short Tags (ESTs) data
 - Identified novel microRNAs using Northern Blotting and qPCR
- 2010
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2010

Summer Intern

Beijing Genomics Institute (BGI)

Shenzhen, China

 - Designed custom code to parse small RNA sequencing and degradome data to predict small RNA and their targets in *Arabidopsis*
 - Assisted with alignment algorithm development for Short Oligonucleotide Analysis Package (SOAP)



SELECTED PUBLICATIONS

- 2022

3D chromatin maps of the human pancreas reveal lineage-specific regulatory architecture of T2D risk

Cell Metabolism

 - Su C**, Gao L, May CL, Pippin JA, Boehm K, Lee M, Liu C, Pahl MC, Golson ML, Naji A; HPAP Consortium, Grant SFA, Wells AD, Kaestner KH.
- 2020

Mapping effector genes at lupus GWAS loci using promoter Capture-C in follicular helper T cells

Nature Communication

 - Chun Su**, Matthew E. Johnson, Annabel Torres, Rajan M. Thomas, Elisabetta Manduchi, Prabhat Sharma, Carole Le Coz, Michelle E. Leonard, Sumei Lu, Kenyatta M. Hodge, Alessandra Chesi, James Pippin, Neil Romberg, Struan F. A. Grant and Andrew D. Wells
- 2020

SHR4z, a novel decoy effector from the haustorium of the parasitic weed *Striga gesnerioides*, suppresses host plant immunity

New Phytologist

 - Chun Su**, Hai Liu, Eric K. Wafula, Loren Honaas, Claude W. dePamphilis, Michael P. Timko
- 2014

Identification and characterization of a subset of microRNAs in wheat

Genomics

 - Chun Su**, Xiaozeng Yang, Shiqing Gao, Yimiao Tang, Changping Zhao, Lei Li.