CHUN SU

Bioinformatics Scientist | Computational Biologist

I have 10+ years of hands-on experience in bioinformatics. Skilled in both molecular cloning and computational analysis of next generation sequencing (NGS) data. Proficient in a variety of programming languages, HPC cluster systems, cutting-edge bioinformatic software, and multivariate statistical analysis. Knowledgeable about molecular cell biology and immunology. 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

Ph.D, Biology
2017 | 2011
University of Virginia — 📍 Charlottesville, VA

- Thesis: Uncovering the molecular mechanism underlying the virulence of Striga gesnerioides

B.S Biology
2011 | 2007
Huazhong Agricultural University — 📍 Wuhan, China

💼 PROFESSIONAL EXPERIENCE

Scientist, Computational Biology
Current | 2022
Amgen, Inc — 📍 Remote

Bioinformatics Scientist
2022 | 2018
Children's Hospital of Philadelphia — 📍 Philadelphia, PA

- Established in-house bioinformatics analysis pipelines and standard operating procedures (SOP) for the various types of NGS data.
- Predicted candidate gene targets for drug repurposing 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 14 scientific publications of which 4 are first-authored and 10 are peer-reviewed
- Presented research at national and international scientific conferences
- Recruited and trained bioinformatics fellows and graduate students.
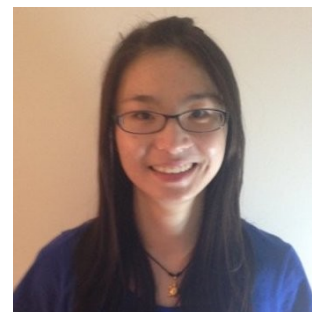
CONTACT INFO

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- ⌗ @sckinta
- 🌐 learniningwithsckinta
- in chun-su-a031087b
- G chun-su

SKILL HIGHLIGHTS

- ⊙ NGS analysis
- ⊙ single cell
- ⊙ Programming with R, Perl, Python, Shell and Matlab
- ⊙ Database management with SQL and FileMaker
- ⊙ Web application development with R shiny
- ⊙ High-performance computing with PBS, SLURM and SGE
- ⊙ Version control with Git and GitHub

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 gesneriodies.
- 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)

LEADERSHIP EXPERIENCE

Current
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2019

Co-organizer
R ladies Philly   📍 Philadelphia, PA

- Organized monthly meetup https://www.meetup.com/rladies_philly/
- Authored blogs to summarize events.
- Designed an outreach brochure and developed the mentorship/speaker application shiny dashboard https://rladiesphilly.shinyapps.io/mentorship/
- Organized and led data hackathon projects to help local non-profit organizations

2017
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2012

Teaching Assistant
University of Virginia, Department of Biology   📍 Charlottesville, VA

- Taught Introduction to Biology Lab (Head TA), Genetics Lecture, Plant Pathology Lab
- Explained challenging biological concepts and demonstrated laboratory techniques to undergraduate students.
- Led and coordinated graduate teaching assistants to maximize learning opportunities for students.

AWARDS AND HONORS

2020

Poster Winner
Penn joint epigenetics and immunology symposium   📍 Philadelphia, PA

2019

Reviewers' Choice Abstract
American Society of Human Genetics (ASHG)   📍 Houston, Texa

2015

Best Poster Award
The 13th World Congress on Parasitic Plants   📍 Kunming, China

2015   **Graduate Student and Postdoc Association Travel Award**
University of Virginia, Department of Biology   📍 Charlottesville, VA

2011   **First Year Fellowship**
University of Virginia, Department of Biology   📍 Charlottesville, VA

2011   **Outstanding Undergraduate Thesis Award**
Huazhong Agricultural University   📍 Wuhan, China

2011
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2010   **Monsanto Fellowship**
Monsanto Inc & Huazhong Agricultural University   📍 Wuhan, China

2011
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2010   **National Fund for Fostering Talents of Basic Science**
National Natural Science Foundation of China   📍 Wuhan, China

👥 POSTER AND PRESENTATION

2020   **3D promoter architecture reorganization during iPSC-derived neuronal cell differentiation implicates target genes for neurodevelopment disorders (Poster)**
American Society of Human Genetics (ASHG)   📍 Virtual

2020   **Immune cell promoter connectomes suggest mechanistic bases of genetic susceptibility to autoimmune diseases (Poster and Presentation)**
Penn joint epigenetics and immunology symposium   📍 Philadelphia, PA

2019   **Network analysis workshop (Presentation)**
R ladies Philly   📍 Philadelphia, PA

2019   **3D promoter-open chromatin connectomes in human immune cells yield insight into cell-specific gene regulatory architectures and the genetic basis of multiple autoimmune diseases (Poster)**
American Society of Human Genetics (ASHG)   📍 Houston, Texa

2019   **Whole Genome Sequencing (WGS) of saliva and osteochondroma-derived DNA from Hereditary Multiple Exostoses (HME) families reveals new insights into pathogenesis (Poster)**
American Society for Bone and Mineral Research (ASBMR)   📍 Orlando, Florida

2015   **Identification of Parasite Effectors Mediating Striga gesnerioides-Host Plant Interactions (Poster)**
The 13th World Congress on Parasitic Plants   📍 Kunming, China

2015   **Comparison of transcriptome profiling in different races of Striga gesnerioides during its interaction with Vigna unguiculata L. Walp (Presentation)**
Annual Conference for Parasite Plant Genomics Project   📍 State College, PA

📖 SELECTED PUBLICATIONS

2022   **Implicating effector genes at COVID-19 GWAS loci using promoter-focused Capture-C in disease-relevant immune cell types**
Genome Biology

- Matthew C Pahl, Carole Le Coz, Chun Su, Prabhat Sharma, Rajan M Thomas, James A Pippin, Emylette Cruz Cabrera, Matthew E Johnson, Michelle E Leonard, Sumei Lu, Alessandra Chesi, Kathleen E Sullivan, Neil Romberg, Struan FA Grant, Andrew D Wells
- https://genomebiology.biomedcentral.com/articles/10.1186/s13059 022 02691 1

2021 — **The three-dimensional chromatin structure of the major human pancreatic cell types reveals lineage-specific regulatory architecture of T2D risk**
bioRxiv
- Su Chun, Long Gao, Catherine L. May, James A. Pippin, Keith Boehm, Michelle Lee, Chengyang Liu, Matthew C. Pahl, Maria L. Golson, Ali Naji, the HPAP Consortium, Struan F.A. Grant, Andrew D. Wells, Klaus H. Kaestner.
- https://doi.org/10.1101/2021.11.30.470653

2021 — **Cis-regulatory architecture of human ESC-derived hypothalamic neuron differentiation aids in variant-to-gene mapping of relevant complex traits**
Nature Communication
- Matthew C. Pahl, Claudia A. Doege, Kenyaita M. Hodge, Sheridan H. Littleton, Michelle E. Leonard, Sumei Lu, Rick Rausch, James A. Pippin, Maria Caterina De Rosa, Alisha Basak, Jonathan P. Bradfield, Reza K. Hammond, Keith Boehm, Robert I. Berkowitz, Chiara Lasconi, Chun Su, Alessandra Chesi, Matthew E. Johnson, Andrew D. Wells, Benjamin F. Voight, Rudolph L. Leibel, Diana L. Cousminer & Struan F. A.
- https://doi.org/10.1038/s41467-021-27001-4

2021 — **Restriction enzyme selection dictates detection range sensitivity in chromatin conformation capture-based variant-to-gene mapping approaches**
Human Genetics
- Su, C., Pahl, M.C., Grant, S.F.A. Wells, A.D
- https://doi.org/10.1007/s00439-021-02326-8

2021 — **Projecting genetic associations through gene expression patterns highlights disease etiology and drug mechanisms**
bioRxiv
- Milton Pividori, Sumei Lu, Binglan Li, Chun Su, Matthew E. Johnson, Wei-Qi Wei, Qiping Feng, Bahram Namjou, Krzysztof Kiryluk, Iftikhar Kullo, Yuan Luo, Blair D. Sullivan, Benjamin F. Voight, Carsten Skarke, Marylyn D. Ritchie, Struan F.A. Grant, Casey S. Greene
- https://doi.org/10.1101/2021.07.05.450786

2021 — **Constrained chromatin accessibility in PU.1-mutated agammaglobulinemia patients**
Journal of Experimental Medicine
- Le Coz C, Nguyen DN, Su C, Nolan BE, Albrecht AV, Xhani S, Sun D, Demaree B, Pillarisetti P, Khanna C, Wright F, Chen PA, Yoon S, Stiegler AL, Maurer K, Garifallou JP, Rymaszewski A, Kroft SH, Olson TS, Seif AE, Wertheim G, Grant SFA, Vo LT, Puck JM, Sullivan KE, Routes JM, Zakharova V, Shcherbina A, Mukhina A, Rudy NL, Hurst ACE, Atkinson TP, Boggon TJ, Hakonarson H, Abate AR, Hajjar J, Nicholas SK, Lupski JR, Verbsky J, Chinn IK, Gonzalez MV, Wells AD, Marson A, Poon GMK, Romberg N.
- https://doi.org/10.1084/jem.20201750

2021 — **3D promoter architecture reorganization during iPSC-derived neuronal cell differentiation implicates target genes for neurodevelopmental disorders**
Progress in Neurobiology
- Su, C., Argenziano, M., Lu, S., Pippin, J. A., Pahl, M. C., Leonard, M. E., Cousminer, D. L., Johnson, M. E., Lasconi, C., Wells, A. D., Chesi, A., & Grant, S. F.
- https://doi.org/10.1016/j.pneurobio.2021.102000

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, Kenyaita M. Hodge, Alessandra Chesi, James Pippin, Neil Romberg, Struan F. A. Grant and Andrew D. Wells
- https://doi.org/10.1038/s41467-020-17089-5

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
- https://doi.org/10.1111/nph.16351

2019

Genome-scale Capture C promoter interactions implicate effector genes at GWAS loci for bone mineral density
Nature Communications
- Alessandra Chesi, Yadav Wagley, Matthew E. Johnson, Elisabetta Manduchi, Chun Su, Sumei Lu, Michelle E. Leonard, Kenyaita M. Hodge, James A. Pippin, Kurt D. Hankenson, Andrew D. Wells & Struan F. A. Grant.
- https://doi.org/10.1038/s41467-019-09302-x

2016

Horizontal gene transfer is more frequent with increased heterotrophy and contributes to parasite adaptation
PNAS
- Zhenzhen Yang, Yeting Zhang, Eric K. Wafula, Loren A. Honaas, Paula E. Ralph, Sam Jones, Christopher R. Clarke, Siming Liu, Chun Su, Huiting Zhang, Naomi S. Altman, Stephan C. Schuster, Michael P. Timko, John I. Yoder, James H. Westwood, and Claude W. dePamphilis
- https://doi.org/10.1073/pnas.1608765113

2014

Identification and characterization of a subset of microRNAs in wheat
Genomics
- Chun Su, Xiaozeng Yang, Shiqing Gao, Yimiao Tang, Changping Zhao, Lei Li.
- https://doi.org/10.1016/j.ygeno.2014.03.002