TEXAS STATE VITA

I. Academic/Professional Background

A. Name: Shuying Sun Title: Professor
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B. Educational Background

Degree	Year	University	Major	Thesis/Dissertation
PhD	2007	University of Toronto, Canada	Statistics	Haplotype inference using a Hidden Markov Model with efficient Markov chain sampling
MS	2002	McMaster University, Canada	Statistics	Post-blackening and other bootstrap methods for time series
MS BS	2000 1997	Hebei Normal University, China	Mathematics	Cohomology complex projective space with actions of G_5 (Master's thesis)

C. University Experience

Position	University	Dates
Professor	Texas State University	2023/09 – present
Associate Professor	Texas State University	2017/09 – 2023/08
Assistant Professor	Texas State University	2013/09 – 2017/08
Assistant Professor	Case Western Reserve University	2009/08 – 2013/08
Postdoctoral Researcher	The Ohio State University	2007/01 – 2009/07

** For my tenure-track period, I have a 2-year credit from my previous experience at Case Western Reserve University.

Brief Summary

Research: My research interests are statistical genetics and bioinformatics. I have been applying statistical methods to address challenging cancer genetics and epigenetics questions with a focus on DNA methylation data analysis. I have published more than 30 peer-reviewed articles in high-impact journals. The average impact factor of these journals is 5 and their average H-index is 167. My H-index is 18 (i.e., I have ≥ 18 publications, each of which has been cited ≥18 times). The total citations of all my papers are > 1,000 times (>30 citations per paper). I have multiple internal and external grants to fund my research projects and I have presented my research many times at national and international conferences.
** My google scholar citation: https://scholar.google.com/citations?hl=en&user=iQ9YkMcAAAAJ

- ***Teaching:*** My goal of teaching is to help students to reach their greatest potential and succeed. With this goal in mind, I have taught 13 statistics courses (10 graduate and 3 undergraduate levels) at Texas State and have had a positive impact on students from different disciplines. My average teaching evaluation score 4.5 (out of 5) with an average of 85% response rate for the last 5 years. I have led students by conducting published research, which laid a solid foundation for many young next generation scientists' and mathematicians' career development. Since 2013, I have published 16 papers based on my research work with 40 students. I mentored 28 of these students on research since I was granted tenure in 2017.

- ***Service:*** I have built a graduate program in statistics as a committee chair (in 2017) and graduate advisor (2018 – present) at Texas State. This program has grown exceedingly well. 21 students graduated in 6 years (2019/05 – 2025/05), 4 are enrolled in Fall 2025. I have been serving as a reviewer for 19 high-impact journals since 2008. I have also led by serving as a career mentor for young researchers and as a poster judge at national and international conferences.

II. TEACHING

A. Teaching Honors and Awards:

1. Teaching Excellence Award, Department of Mathematics, Texas State University (12/03/2021)
2. Presidential Distinction Award for Excellence in Teaching, Texas State University, $2,000 (08/25/2017)
3. Favorite Professor of *Alpha Chi* National College Honor Society (2017)
4. Associate Doctoral Faculty, Materials Science, Engineering & Commercialization (MSEC) Ph.D. program, Texas State University (01/2018 – present)
5. Named/recognized by 3 undergraduate students as a person at Texas State University who made a contribution to their academic careers (in 2019, 2016, 2015)
6. Graduate faculty approved by the Graduate College, Texas State University (2016-present)
7. Teaching Excellence Award, Department of Mathematics, Texas State University (12/09/2016)

B. Courses Taught:

1. Department of Mathematics, Texas State University (10 graduate and 3 undergraduate courses)

MATH7335	Statistics II (Time: Spring 2024, Spring 2021, Fall 2017, Fall 2016)
MATH7325	Statistics I (Time: Fall 2023, Fall 2020, Spring 2017, Spring 2016)
MATH5399A	Thesis (Time: Fall 2018)
MATH5399B	Thesis (Time: Fall 2018)
MATH5390	Statistics (Time: Spring 2017)
MATH5376A	Design & analysis of experiments (Time: Spring 2022, Fall 2020, Fall 2018, Fall 2014)
MATH5376D	Statistical applications in genetics and bioinformatics (Fall 2021, Fall 2024)
MATH5345	Regression analysis (Time: Spring 2024, Spring 2021, Fall 2017)
MATH5336	Studies in applied mathematics (Time: Spring 2018)
MATH5305	Advanced statistics (Time: Fall 2023, Fall 2020, Spring 2017, Spring 2016)
MATH4305	Probability and statistics (Time: 2024 (Spring, Fall), 2023 (Spring, Fall), 2022 (Spring, Fall), Springs of 2018-2019, 2014 -2016)
MATH3305	Intro to probability and statistics (Time: Falls of 2021-2022 & 2013-2018, Springs of 2014 and 2025)
HON3398O	Intro to statistical genetics and bioinformatics (Time: Springs of 2021, 2019, 2018)

2. Department of Epidemiology and Biostatistics, Case Western Reserve University

EPBI476:	Introduction to next generation sequencing data analysis (Time: Fall 2012, Fall 2011) *(EPBI476 is a new graduate course developed by myself based on interdisciplinary cutting-edge research topics)*
EPBI492:	Cohort study design and analysis (Time: Fall 2010)

3. Department of Statistics, University of Toronto, Canada

STAT220:	Introduction to probability and statistics (Time: Fall 2006)

C. Graduate Theses/Dissertations, Honors Theses, or Exit Committees (*if supervisor, please indicate):*

Note: I am the thesis or research supervisor for <u>more than 40 students</u> listed in the following table.

Time	Students	**Mentoring/Advising Activity, Research Work, and Achievement**
08/2022 – Present	2 Under-graduates	**Activity:** Working with 2 REU students (*Neo Eloff and Mayla Ward*). **Research Project**: Comparative analysis of six correlation metrics on identifying DNA co-methylation patterns. Their manuscript was submitted in 08/2024.
06/2022 – Present	4 high schoolers	**Activity:** Advising a 4-student team (*Brandon Peng, Juhi Pandit, Jackson Zane, and Alice Zhong*) for the Honors Summer Math Camp, Mathworks, at Texas State. **Research Project**: Housekeeping Genes' DNA Methylation Patterns in Breast and Endometrial Cancers. **Achievement:** Students presented their research work at the camp (July 27, 2022). Their manuscript was submitted to *Statistics In Biosciences* in 07/2025
07/2022 – 12/2023	1 Under- & 1 graduate	**Activity:** Working with 1 undergraduate (*Christian Tian*) and 1 graduate student (Ashley Pritchard). **Research Project**: Breast Cancer DNA methylation age estimation.

		Achievement: Their manuscript will be submitted in 12/2025
08/2021 – 06/2023	2 Under-graduates 1 High schooler	**Activity:** Working with 2 former REU students and 1 high school student *(Ashley Pritchard, Emma McFall, and Christine Tian).* **Research Project**: Methylation patterns of tumor suppressor genes. **Achievement:** Students' research work was presented at the Eastern North American Region (ENAR) Conference (Mar 30, 2022) and at the Texas State Health Scholar Showcase (Apr 8, 2022).
06/2022 – 08/2022 *Completed*	4 REU Under-graduates	**Activity:** Worked with 4 REU students (*Neo Eloff, Lilah Board, Eric Ren, and Mayla Ward*). **Research Project**: Co-methylation study using different correlation metrics. **Achievement:** Students presented their research work at the CoSE Summer Research Symposium (Aug 5, 2022).
06/2021 – 08/2021 *Completed*	3 REU Under-graduate students	**Activity:** Worked with 3 REU students (*Ashley Pritchard, Emma McFall, and Raymond Jiang*). **Research Project**: Methylation Patterns of Three Types of Genes in Breast Cancer. **Achievement:** Students presented their research work at the 2021 International Chinese Statistician Association (ICSA) meeting (Sept 13, 2021).
06/2020 – 02/2022 *Completed*	3 high school students	**Activity:** Advised a 3-student team (*Jael Dammann, Pierce Lai, Christine Tian*) for the Honors Summer Math Camp, Mathworks, at Texas State. **Research Project:** DNA co-methylation patterns in breast cancer. **Achievement:** This team's project was presented at our department's Statistics Seminar on Mar 26, 2021, the 2021 American Society of Human Genetics meeting on Oct 18, 2021, and Math Graduate Expo on Nov 6, 2021. Their paper was published in *BMC Genomic Data* in 2022.
06/2020 – 05/2022 *Completed*	4 high school students	**Activity:** Advised a 4-student team (*Sarah Wei, Daphne Han, Flora Cheng, Alice Zhong*) for the Honors Summer Math Camp (HSMC), Mathworks, at Texas State. **Research Project:** Comparative analysis of haplotype analysis. **Achievement:** This team presented at the Math Graduate Programs Expo (Nov 2020), the ICSA 2020 Applied Statistics Symposium (Dec 2020), and the Health Scholar Showcase (Apr 8, 2022). Their research paper was submitted in June 2022.
06/2019 – 12/2020	1 Under-graduate	**Activity:** Worked with the undergraduate student Sherwin Massoudian. **Research Project**: Performance of multiple haplotype assembly algorithms. **Achievement:** Sherwin presented a poster at the Math Graduate Expo, Texas State University (Nov 6, 2020). *Poster permalink: https://mediaflo.txstate.edu/Watch/MIHA*
06/2019 – 08/2019 *Completed*	3 REU Under-graduate students	**Activity:** Worked with 3 REU students (*Austin Zane, Carrie Fulton, and Jas Phillipoom*). **Research Project**: Hemimethylation patterns of lung cancer patients. **Achievement:** These students presented their research work at the Summer Undergraduate Research Symposium (Aug 2, 201) and at the American Society of Human Genetics (ASHG) annual meeting (Oct 18, 2019). Their research paper was published in *BMC cancer* in March 2021.
05/2018 – 03/2020 *Completed*	1 Under-graduate	**Activity:** Worked with undergraduate student Allison B Johnson. **Research Project**: Haplotype assembly of DNA sequencing data. **Achievement:** Allison presented this project in the Rapid-Fire Research section during the Math Graduate Programs Expo on Nov 2, 2018 and the Women in Science and Engineering (WISE) conference on Mar 8, 2019. Johnson and I also presented a poster on Oct 18, 2019 at the ASHG annual meeting.
12/2017 – 04/2019 *Completed*	1 Graduate student	**Activity:** Mentored math graduate student, Ryan Zamora, on his Master's thesis. **Research Project**: Multicollinearity in regression. **Achievement:** Zamora presented his thesis work (a poster) at Conference for Texas Statisticians in April 2018 and presented 3 times at Texas State University. Zamora defended his thesis on Mar 26, 2019 and graduated in May 2019.

06/2017 – 09/2017 *Completed*	3 high school students	**Activity:** Advised a 3-student team (*Catherine Li, Juyon Lee, Jessica Ding*) for the Honors Summer Math Camp, Mathworks, at Texas State University. **Research Paper:** Integrative analysis of gene expression and methylation data for breast cancer cell lines. **Achievement:** This team was named as a Regional Semi-Finalist in the 2017 Siemens Competition. Their paper was published in *BioData Mining* in June 2018.
06/2016 – 09/2016 *Completed*	3 high school students	**Activity:** Advised a 3-student team (*Surya Namboodiri, Lillian Sun, and Emily Chen*) for the Honors Summer Math Camp, Mathworks, at Texas State University. **Research Paper:** DNA co-methylation patterns in cancerous and normal tissues. **Achievement:** This team was named as a Regional Semi-Finalist in the 2016 Siemens Competition. Their paper was published to *Cancer Informatics in 2019.*
06/2015 – 09/2015 *Completed*	3 high school students	**Activity:** Advised a 3-student team (*Sunny Tian, Karina Bertelsmann, and Linda Yu*) for the Honors Summer Math Camp, Mathworks, at Texas State University. **Research Paper:** Methylation heterogeneity patterns in breast cancer cell lines. **Achievement:** This paper was published in *Cancer Informatics* in August 2016.
01/2014 – 05/2015 *Completed*	1 Under-graduate *Brittany Enfield*	**Activity**: Advised the math major student, *Brittany Enfield*, for her honors thesis (Summer 2014 to Spring 2015) and honors course project (Spring 2014). **Honors thesis:** Identifying hemimethylation sites in breast cancer cell lines using statistical and bioinformatic methods. **Achievement**: Brittany presented her project (a poster) in the Graduate Open House in October 2014 and at the Conference of Texas Statisticians in April 2015.
06/2014 – 09/2014 *Completed*	3 high school students	**Activity:** Advised a 3-student team (*Lily Xu, Simantini Mitra-Behura, and Brandon Alston*) for the Honors Summer Math Camp, Mathworks, at Texas State. **Research Paper:** Identifying DNA methylation variation patterns for breast cancer biomarker genes (this paper was published in 2015). **Achievement:** This team was named as a Regional Finalist in the 2014 Siemens Competition. Only 5 teams were selected to receive this award in each region.
09/2010 – 06/2014 *Completed*	1 Doctoral student *Xiaoqing Yu*	**Activity:** Advised the Ph.D. candidate, *Xiaoqing Yu,* in the Department of Epidemiology and Biostatistics, Case Western Reserve University. **Xiaoqing Yu's Thesis**: Statistical methods and analyses for next generation sequencing data. Thesis: http://hal.case.edu/~sun/XiaoqingYu.dissertation.pdf **Achievement**: Xiaoqing Yu finished her thesis defense on June 6, 2014.
10/2009 – 09/2013 *Completed*	4 Under-graduate &graduate students	**Activity**: Mentoring four research assistants at Case Western Reserve University: *Zhengyi Chen* (statistics graduate), *Stephen Hatch* (computer science (CS) undergraduate), *Aaron Noviski* (CS undergraduate), and *Peng Li* (CS graduate). **Achievement**: Published several papers with the above students.

D. Course Prepared and Curriculum Development

1. Built the graduate program in statistics (i.e., the Master of Math Statistics Concentration) as the committee chair from Feb 2017 to Dec 2017 (*Proposal submitted in September 2017, approved in December 2017*)
2. Created and taught an interdisciplinary course for the Honors College: HON3398O Introduction to Statistical Genetics and Bioinformatics (*Proposal approved in Summer 2017, taught in Springs 2018, 2019, and 2021*)
3. Developed and taught a new graduate level topic course for Department of Mathematics: MATH5376D Statistical Applications in Genetics and Bioinformatics (*Proposal approved in Fall 2017, taught in Fall 2021 and Fall 2024*)

III. SCHOLARLY/CREATIVE

A. Works in Print (including works accepted, forthcoming, in press)

1. Book and Book Chapter: *(Note: Authors are listed in alphabetical order in the following book and chapters)*

- Edited Book: Elston R. C., Satagopan J, **Sun S** *(Editors,* 2012). Statistical Human Genetics: Methods and Protocols (Methods in Molecular Biology). *Humana Press, USA. Springer Protocols. [Citation: 24 times]*
  - Book Chapter: Elston R. C., Satagopan J, **Sun S** *(Authors,* 2012). Genetic Terminology. Chapter 1 in Statistical Human Genetics: Methods and Protocols. *Humana Press, USA. Springer Protocols.* https://link.springer.com/protocol/10.1007/978-1-61779-555-8_1 *[Citation: 49 times]*
  - Book Chapter: Elston R. C, Satagopan J, **Sun S.** (2017) Statistical genetic terminology. Chapter 1 in *Statistical Human Genetics* (pp. 1-9). Humana Press, New York, NY. *[Citation: 2 times]* https://link.springer.com/protocol/10.1007/978-1-4939-7274-6_1

2. Refereed Articles: Total citation: 993 times. My H-index is 18 (September, 2023)

Impact factor, H-index, and Google Scholar citation are provided.
PA: Primary Author; CA: Corresponding Author; DST: Doctoral Student; GST: Graduate; UST: Undergraduate; HST: High school

Google scholar citations: https://scholar.google.com/citations?user=iQ9YkMcAAAAJ

1) **Sun S** (PA, CA), Pandit J (UST), Peng B (UST), Zane J(UST), Zhong A (UST) (2025) Housekeeping Genes' DNA Methylation Patterns in Breast and Endometrial Cancers, *Submitted to Statistics in Biosciences in 07/2025.*
2) Ward M (UST), Eloff (UST), and **Sun S** (PA, CA) (2025) Comparative Analysis of Six Correlation Metrics on Identifying DNA Co-Methylation Patterns. *Submitted in 08/2025.*
3) **Sun S** PA, CA), Pritchard A (UST), McFall E (UST), and Tian C (UST) (2025) Statistical analysis of DNA methylation patterns of tumor suppressor genes in breast cancer. *Epigenetics Insights, 18(1) [Impact factor: 0.81; H-index: 15]*
4) **Sun S** (PA, CA), Zamora R (GST) (2024). Mcperturb: A new 5-step perturbation-based multicollinearity diagnostic package. *Statistics in Biosciences, Page 1-32. https://doi.org/10.1007/s12561-024-09468-z [Impact factor: 0.9; H-index: 20]*
5) **Sun S** (PA, CA), Cheng F (HST), Han D (UST), Wei S (UST), Zhong A (HST), Massoudian S (UST), Johnson AB (GST) (2023). Pairwise comparative analysis of six haplotype assembly methods based on users' experience. *BMC Genomics Data,* 24(1), 35, Page 1-20. *[Impact factor: 3.295; H-index: 80]*
6) **Sun S** (PA, CA), Dammann, J (HST), Lai P (UST), & Tian C (HST) (2022). Thorough statistical analyses of breast cancer co-methylation patterns. *BMC Genomics Data*, 23(1), Page 1-23. *[Impact factor: 3.295; H-index: 80]*
7) **Sun S** (PA, CA), Zane A (UST), Fulton C (UST) & Philipoom J (UST). Statistical and bioinformatic analysis of hemimethylation patterns in non-small cell lung cancer. *BMC Cancer* 2021, 21:268. *[Impact factor: 4.42; H-index: 139; Citation: 2].*
8) Sun L (UST), Namboodiri S (UST), Chen E (UST) (2019), **Sun S** (PA, CA) (2019). Preliminary analysis of within-sample co-methylation patterns in normal and cancerous breast samples. *Cancer Informatics 2019* (18):1-14. *[Impact factor: 2.4; H-index: 33; Citation: 6].*
9) Sun L (UST), **Sun S** (PA, CA) (2019). Within-sample co-methylation patterns in normal tissues. *BioData Mining* 2019, 12:9 . *[Impact factor: 3.6; H-index: 32; Citation: 6].*
10) **Sun S** (PA, CA), Lee YR (UST), Enfield BE (UST) (2019). Hemimethylation patterns in breast cancer cell lines. *Cancer Informatics 2019* (18):1-12. *[Impact factor: 2.4; H-index: 33; Citation: 5].*
11) Li C (HST), Lee J (HST), Ding J (HST), **Sun S** (PA, CA) (2018). Integrative analysis of gene expression and methylation data for breast cancer cell lines. *BioData Mining* 2018, 11:13. *[Impact factor: 3.6; H-index: 32; Citation: 8].*
12) **Sun S** (PA, CA), Yu X (DST) (2016). HMM-Fisher: Identifying differential methylation using a hidden Markov model and Fisher's exact test. *Statistical Applications in Genetics and Molecular Biology 2016,*15(1):55-67. *[Impact factor: 0.67; H-index: 47; Citation: 27].*
13) Yu X (DST), **Sun S** (PA, CA) (2016). HMM-DM: Identifying differentially methylated regions using a hidden Markov model. *Statistical Applications in Genetics and Molecular Biology 2016,*15(1):69-81. *[Impact factor: 0.67; H-index: 47; Citation: 29].*

14) Yu X (DST), **Sun S** (PA, CA) (2016). Comparing five statistical methods of differential methylation identification using bisulfite sequencing data. *Statistical Applications in Genetics and Molecular Biology 2016*, 15(2) 173-191. *[Impact factor: 0.67; H-index: 47; Citation: 21].*
15) Tian S (HST), Bertelsmann K (HST), Yu L (HST), **Sun S** (PA, CA) (2016). DNA methylation heterogeneity patterns in breast cancer cell lines. *Cancer Informatics 2016,* (Suppl 4):1-9. *[Impact factor: 2.4; H-index: 33; Citation: 4].*
16) Kenyon J, Nickel-Meester G, Qing Y, Santos-Guasch G, Drake E, Fu P, **Sun S**, Bai X, Wald D, Arts E, Gerson SL. (2016). Epigenetic loss of MLH1 expression in normal human hematopoietic stem cell clones is defined by the promoter CpG methylation pattern observed by high-throughput methylation specific sequencing. *International journal of stem cell research and therapy 2016*, *3*(2). [*Impact factor: 1.599; Citation: 8].*
17) **Sun S** (PA, CA), Li P (GST) (2015). HMPL: A pipeline for identifying hemimethylation patterns by comparing two samples. *Cancer Informatics 2015*, 14(Suppl 2):235–245. *[Impact factor: 2.4; H-index: 33; Citation: 7].*
18) Xu L (PA, HST), Mitra-Behura S (PA, HST), Alston B (HST), Zong Z, **Sun S** (PA, CA) (2015). Identifying DNA methylation variation patterns to obtain potential breast cancer biomarker genes. *International Journal of Biomedical Data Mining 2015,* 4:115. *[Citation: 4].*
19) **Sun S** (PA, CA), Noviski A (UST), Yu X (DST) (2013). MethyQA: a pipeline for bisulfite-treated methylation sequencing quality assessment. *BMC Bioinformatics 2013,* 14:259. *[Impact factor: 3.39; H-index: 218; Citation: 22].*
20) Yu X (DST), **Sun S** (PA, CA) (2013). Comparing a few SNP calling algorithms using low-coverage sequencing data. *BMC Bioinformatics 2013,*14:274. *[Impact factor: 3.39; H-index: 218; Citation: 138].*
21) Adams M, Veigl M, Wang Z, Molyneux N, **Sun S**, Guda K, Yu X (DST), Markowitz S, Willis J (2012). Global mutational profiling of formalin fixed human colon cancers from a pathology archive. *Modern Pathology 2012,* 25:1599-1608. *[Impact factor: 7.59; H-index:159; Citation: 23].*
22) Yu X (DST), Guda K, Willis J, Veigl M, Wang Z, Markowitz S, Adams MD, and **Sun S** (PA, CA) (2012). How do alignment programs perform on sequencing data with varying qualities and from repetitive regions? *BioData Mining 2012*, 5:6. *[Impact factor: 3.6; H-index: 32; Citation: 61].*
23) **Sun S** (PA, CA), Chen Z (GST), Yan P, Huang Y, Huang T, Lin S (2011). Identifying hypermethylated CpG islands using a quantile regression model. *BMC Bioinformatics 2011,* 12:54. *[Impact factor: 3.39; H-index: 218; Citation: 8].*
24) **Sun S** (PA, CA), Huang Y, Yan P, Huang T, Lin S (2011). Preprocessing differential methylation hybridization microarray data. *BioData Mining 2011,* 4:13. *[Impact factor: 3.6; H-index: 32; Citation: 20].*
25) Han L, Zheng S, **Sun S**, Huang T, Zhao Z (2010). Genome-wide DNA methylation profiling in 40 breast cancer cell lines. *Advanced Intelligent Computing Theories and Applications. Lecture Notes in Computer Science 2010*, 6215:277-284. *[Citation: 3].*
26) Greenwood C, **Sun S**, Veenstra J (UST), Hamel N, Niell B, Gruber S, Foulkes W (2010). How old is this mutation? – a study of three Ashkenazi Jewish founder mutations. *BMC Genetics 2010,* 11:39. *[Impact factor: 3.295; H-index: 80; Citation:24].*
27) **Sun S** (PA, CA), Yan P, Huang T, Lin S (2009). Identifying differentially methylated genes using mixed effect and generalized least square models. *BMC Bioinformatics 2009,* 10:404. *[Impact factor: 3.39; H-index: 218; Citation: 7].*
28) Clendenning M, Baze ME, **Sun S,** Walsh K, Liyanarachchi S, Fix D, Schumemann V, Comeras I, Deacon M, Wenstrup RJ, Thibodeau ST, Lynch HT, Hampel H, de la Chapelle A (2008). Origins and prevalence of the American founder mutation of MSH2. *Cancer Research 2008,* 68(7):2145-2153. *[Impact factor: 9.24; H-index: 466; Citation: 46].*
29) Clendenning M, Senter L, Hampel H, Robinson K L, **Sun S,** Buchanan D, Walsh MD, Nilbert M, Green JS, Potter J, Lindblom A, de la Chapelle A (2008). A frame-shift mutation of *PMS2* is a widespread cause of

Lynch syndrome. *Journal of Medical Genetics 2008*, 45: 340-345. *[Impact factor: 5.33; H-index: 177; Citation: 59].*

30) Lin HL, Zuo T, Lin C, Kuo CT, Liyanarachchi S, **Sun S,** Shen R, Deatherage DE, Potter D, Asamoto L, Lin S, Yan P, Cheng A, Ostrowski M, Huang TH (2008). Breast cancer-associated fibroblasts confer AKT1-mediated epigenetic silencing of cystatin M in epithelial cells. *Cancer Research 2008,* 68:10257-10266. *[Impact factor: 9.24; H-index: 466; Citation:70].*
31) **Sun S** (PA, CA)**,** Greenwood CM, Neal RM (2007). Haplotype inference using a Bayesian Hidden Markov Model. *Genetic Epidemiology 2007*, 31(8):937-948. *[Impact factor: 2.344; H-index: 99; Citation: 31].*
32) Rahman P, **Sun S,** Peddle L, Snelgrove T, Greenwood CM, Gladman D (2006). Association between the interleukin-1 family gene cluster and psoriatic arthritis. *Arthritis & Rheumatism 2006*, 54 (7): 2321-2325. *[Impact factor: 15.483, H-index 352; Citation: 152].*
33) **Sun S** (PA)**,** Greenwood CM, Thiffault I, Hamel N, Chong G, Foulkes WD (2005). The HNPCC associated MSH2*1906G->C founder mutation probably originated between 1440 CE and 1715 CE in the Ashkenazi Jewish population. *Journal of Medical Genetics 2005*, 42: 766-768. *[Impact factor:5.33; H-index: 177; Citation: 24].*
34) Butt C, **Sun S,** Peddle L, Greenwood CM, Hamilton S, Gladman D, Rahman P (2005). Association of nuclear factor-kB in psoriatic arthritis. *Journal of Rheumatology 2005,* 32:1742-1744. *[Impact factor: 3.21; H-index: 186; Citation: 30].*
35) Butt C, **Sun S,** Greenwood CM, Gladman D, Rahman P. (2005) Lack of association of SLC22A4, SLC22A5, SLC9A3R1 and RUNX1 variants in psoriatic arthritis, *Rheumatology 2005*; 44:820-821. *[Impact factor: 3.65; H-index: 181; Citation:9]*
36) **Sun S** (PA, CA)**,** Liu Z (2000). Cohomology complex projective space with actions of G_5. *Northeastern Mathematical Journal 2000,* 16(3):307-314.

3. Conference Proceedings: N/A
4. Abstracts: N/A
5. Reports: N/A
6. Book Review: N/A
7. Other Works in Print: **Sun S,** Zhao Q, Liu J. (1995) Managing program for operating overhead traveling cranes. *National First Prize winner paper of Mathematical Contest in Modeling in China.*
8. Statistical and Bioinformatic Software Packages:
    1) Mcperturb (2021): Multicollinearity diagnostic package *https://github.com/ss355/mcperturb*
    2) HMM-Fisher (2016) & HMM-DM (2016): Two R software packages for differential methylation identification: *https://github.com/xxy39/HMM-Fisher* & *https://github.com/xxy39/HMM-DM*
    3) HMPL (2015): A pipeline for identifying hemimethylation patterns by comparing two samples. http://hal.case.edu/~sun/HMPL/HMPL.*zip* (HMPL was developed using Perl & R).
    4) MethyQA (2013): A pipeline for methylation sequencing quality assessment. http://hal.case.edu/~sun/MethyQA.v2.*zip* (MethyQA was developed using Perl & R).
    5) HMM.hap (2007): R program for haplotype inference.

B. Works not in Print

1. Papers presented at professional meetings with presenters underlined
    1) **Sun S**, Ren E, Ward M, Board L, Eloff N. Comparative Analysis of Six Correlation Metrics on DNA Co-Methylation. *Poster presented at the CoSE Summer Research Symposium (Aug 5, 2022)*
    2) **Sun S,** Pritchard A, McFall E, and Tian C. Statistical analysis of tumor suppressor genes' methylation patterns in various breast cancer samples. *Poster presented at the Texas State Health Scholar Showcase (Apr 8, 2022)*
    3) **Sun S,** Cheng F, Han D, Wei S, Zhong A. Haplotype Assembly Using DNA Sequencing Data - Users' Experience and Perspective. *Poster presented at the Texas State Health Scholar Showcase (Apr 8, 2022)*
    4) **Sun S,** Dammann J, Lai P, Tian C. Thorough statistical analyses of breast cancer co-methylation patterns. *Poster presentation at the annual meeting of American Society of Human Genetics at Houston (Oct 18, 2021)* and *Math Graduate Expo, Texas State University (Nov 5, 2021)*

5) **Sun S,** Pritchard A, McFall E, and Jiang R. Statistical analyses of housekeeping genes' methylation patterns in breast cancer. *Poster presented at the ICSA 2021 Applied Statistics Symposium (Sept 13, 2021)*
6) **Sun S**, Cheng F, Han D, Wei S, Zhong A. Comparative Analysis of Haplotype Assembly Algorithms. *Poster presented at ICSA 2020 Applied Statistics Symposium (Dec 14, 2020) and at Math Graduate Expo, Texas State University (Nov 6, 2020).* Poster permalink: https://mediaflo.txstate.edu/Watch/HA.compare
7) **Sun S** and Sherwin Massoudian. Performance of multiple individual haplotype assembly algorithms. *Poster presented at Math Graduate Expo, Texas State University (Nov 6, 2020).* Poster permalink: https://mediaflo.txstate.edu/Watch/MIHA
8) Johnson AB, Massoudian S, and **Sun S**. Comparing haplotype assembly approaches. *Poster presentation at the annual meeting of American Society of Human Genetics at Houston (Oct 17, 2019)*
9) **Sun S**, Zane A, Fulton C, and Philipoom J. Hemimethylation patterns of lung cancer patients. *Poster presentation at the annual meeting of American Society of Human Genetics at Houston (Oct 18, 2019)*
10) **Sun S** and Johnson AB. A survey of statistical and computational approaches for haplotype assembly. *Poster presented the Women in Science and Engineering (WISE) conference (Mar 8, 2019)*
11) Zamora R and **Sun S**. A new 5-step perturbation-based multicollinearity diagnostics package. *Talk given at the Statistics Seminar, Texas State University (Nov 30, 2018)*
12) Zamora R and **Sun S**. Exploring multicollinearity diagnostics: A new 5-step perturbation procedure. *Poster presented at the 10th Annual International Research Conference, Graduate College, Texas State University (Nov 13, 2018)*
13) Johnson AB and **Sun S**. A survey of recent statistical and computational approaches for haplotype assembly. *Rapid Fire Research, Math Graduate Expo, Texas State University (Nov 2, 2018)*
14) Zamora R and **Sun S**. Multicollinearity in regression: looking beyond the lines. *Poster presentation at Conference of Texas Statisticians (COTS) (April 13, 2018)*
15) **Sun S** and Lee YR. Hemimethylation patterns in breast cancer cell lines. *Poster presented at the Math Graduate Open House*, *Texas State University (Nov 10, 2017)*
16) Li C, Lee J, Ding J, **Sun S**. Integrative analysis on DNA methylation & gene expression data. *Poster presented at the Math Graduate Open House*, *Texas State University (Nov 10, 2017)*
17) **Sun S** and Lee YR. Hemimethylation analysis using Wilcoxon signed-rank tests and bioinformatics approaches. *Poster presentation at Conference of Texas Statisticians (COTS)* (March 24, 2017). This poster won the 3rd prize in the 2017 COTS poster competition.
18) Sun L, Namboodiri S, Chen E., **Sun S.** DNA Co-methylation Patterns in Normal and Cancerous Tissues. *Poster Presentation at the International Conference on Intelligent Biology and Medicine (ICIBM) (December 8, 2016)*
19) **Sun S**, Yu X. Challenges and opportunities of differential methylation identification using bisulfite sequencing data. *Poster Presentation at the Great Lakes Bioinformatics Conference (May 18, 2016)*
20) **Sun S**, Yu X. A comprehensive comparative analysis of statistical methods for differential methylation identification. *Poster presentation at Conference of Texas Statisticians (COTS) (April 8, 2016)*
21) Tian S, Bertelsmann K, Yu L, **Sun S**. DNA methylation heterogeneity patterns in breast cancer cell lines. *Poster presentation at the Graduate Math Open House, Texas State University (October 16, 2015)*
22) Enfield B, **Sun S**. Identifying hemimethylation sites for breast cancer using statistical and bioinformatic methods. *Poster presentation at COTS (April 10, 2015)*
23) Xu L, Simantini MB, Alston B, Zong Z, **Sun S.** Identifying DNA methylation variation patterns to obtain potential breast cancer biomarker genes. *Poster presentation at COTS (April 10, 2015)*. This poster won the 3rd prize in the 2015 COTS poster competition.
24) Enfield B, **Sun S**. Identifying hemimethylation sites in breast cancer cell lines. *Poster presented at the Math Graduate Open House, Texas State University (October 17, 2014)*
25) **Sun S,** Yu X, and Li P. Identifying hemimethylation and differential methylation patterns using statistical and computational methods. *Poster presentation at COTS (March 22, 2014)*
26) Yu X, **Sun S**. HMM-DM: Identifying differentially methylated regions using a hidden Markov model. *Poster presentation at the Research Showcase, Case Western Reserve* University (April *18, 2014. http://research.case.edu/ShowCASE/Index.cfm)*

27) **Sun S**. Identifying DNA methylation patterns using statistical and computational methods. *Poster presentation at the Graduate Math Open House, Texas State University (November 8, 2013)*
28) Yu X, **Sun S.** Comparing a few SNP calling algorithms using low-coverage sequencing data. *Poster presentation at the annual meeting of American Society of Human Genetics (October, 2013)*
29) Yu X, **Sun S.** Comparing a few SNP calling algorithms using low-coverage sequencing data. *Poster Presentation at the Great Lakes Bioinformatics Conference (GLBIO, May, 2013)*
30) **Sun S**, Li P. HMPL: A pipeline for identifying hemimethylation patterns. *Poster Presentation at the Great Lakes Bioinformatics Conference (GLBIO, May, 2013)*
31) Yu X, **Sun S**. HMM-DM: identifying differential methylation patterns using a Hidden Markov Model. *Poster presentation at the annual meeting of American Society of Human Genetics (November, 2012)*
32) **Sun S**, Yu X. HMM-Fisher: A Hidden Markov Model based model for identifying differential methylation. *Poster presentation at the American Society of Human Genetics meeting (November, 2012)*
33) Yu X, Guda K, Willis J, Veigl M, Wang Z, Markowitz S, Adam M, **Sun S.** Finding a needle in a haystack: identifying SNPs using high throughput sequencing data. *Statistical Methods for Very Large Datasets Conference (June, 2011)*
34) **Sun S,** Yu X., Noviski A. A software package for examining bisulfite conversion rate in methylation sequencing data. *Poster presentation at American Society of Human Genetics meeting (October, 2011)*
35) **Sun S,** Yu X. Comparisons of next generation sequencing alignment programs. *Poster presentation at the 60th annual meeting of American Society of Human Genetics (November, 2010)*
36) Yu X, Guda K, Willis J, Veigl M, Wang Z, Markowitz S, Adam M, **Sun S.** How do sequencing quality issues affect SNP calling? *Poster presentation at the American Society of Human Genetics meeting (November, 2010)*
37) **Sun S.** Integrating methylation and gene expression microarray data obtained from breast cancer cell lines. *Poster presentation at the Breast Cancer Retreat, Case Cancer Center (October, 2009)*
38) **Sun S.** Methylation and gene expression microarray data integration using correlation analysis. *Poster presentation at the annual meeting of American Society of Human Genetics (October, 2009)*
39) **Sun S,** Yan P, Huang T, Lin S. Preprocessing differentially hybridization methylation microarray data. *Poster presentation at Ohio Collaborative Conference on Bioinformatics (June, 2009)*
40) Zuo T, Lin HL, Kuo CT, Potter D, Deatherage DE, Chan MY, Liyanarachchi S, **Sun S,** Asamoto L, Yan P, Shen R, Lin S, Ostrowski MC, Huang TH. Tumor microenvironment: an integral player in triggering epigenetic silencing in breast epithelial cells. *Oral presentation at the annual meeting of American Association of Cancer Research (AACR, April, 2008)*
41) **Sun S,** Potter D, Yan P, Huang T, Lin S. Using a quantile approach to identify methylated genes. *Poster presentation at the International Symposium on Bioinformatics Research and Applications (May, 2008)*
42) **Sun S,** Potter D, Yan P, Huang T, Lin S. Identifying methylated genes using a quantile regression model. *Poster presentation Statistical Society of Canada (SSC, May, 2008)*
43) **Sun S.** Integrating methylation and gene expression microarray data using linear models. *Poster presentation at the Intelligent Systems for Molecular Biology (ISMB, July, 2008)*
44) **Sun S**, Das D, Spellman P, Lapuk A, Liyanarachch S, Yan P, Huang T, Yaswen P, Gray J, Speed T, and Lin S. Integrating methylation and gene expression microarray data for breast cancer cell lines*.* *Poster presentation at Junior Investigator workshop, Integrative Cancer Biology Program (August, 2008)*
45) Senter L, Clendenning M, **Sun S**, Panescu J, Gallinger S, Mackay J, Haidle JL, Greenblatt M, Young J, de la Chapelle A. Founder mutations in the PMS2 gene. *Poster presentation at the 58th annual meeting of American Society of Human Genetics (ASHG, November, 2008)*
46) **Sun S,** Lin S. Identifying methylated genes using the reversible jump Markov Chain Monte Carlo method. *Poster presentation at the 11th International Conference on Research in Computational Molecular Biology (RECOMB, April, 2007)*

47) **Sun S,** Greenwood CM, Neal RM. Haplotype inference. *Poster Presentation at The 3rd International Hapmap Project Annual Meeting (May, 2006)*
48) **Sun S,** Greenwood CM, Neal RM. Haplotype inference using a Hidden Markov Model with efficient Markov Chain sampling. *Poster presentation at the 6th annual meeting of Mathematics of Information Technology and Complex System (MITACS, May, 2005)*
49) **Sun S,** Greenwood CM, Neal RM. Haplotype inference using a Hidden Markov Model with efficient Markov Chain sampling. *Contributed talk given at the joint meeting of Institute of Mathematical Statistics and Chinese Society of Probability and Statistics (IMS & CSPS, July, 2005)*
50) **Sun S,** Thiffault I, Hamel N, Foulkes WD, Greenwood CM. Dating a recent mutation in MSH2 that increases risk for colorectal cancer. *Poster presentation at the 13th annual meeting of International Genetic Epidemiology Society (October, 2004)*
51) **Sun S,** Greenwood CM, Neal RM. Haplotype inference using a Hidden Markov Model with efficient Markov Chain sampling. *Poster presentation at the 54th annual meeting of American Society of Human Genetics (ASHG, October, 2004)*

2. Talks given at different seminars and conferences
   1) Statistics Seminar, Department of Mathematics, Texas State University (April 14, 2023)
   2) Advances in Statistical and Computational Methods for Analysis of Biomedical, Genetic, and Omics Data at The University of Texas at Dallas, Richardson, Texas, United States (Mar 19, 2023). Conference web page: https://sites.google.com/view/abgod2023/home
   3) Joint Statistics and Data Science Conference, Beijing, China, (July 12, 2023)
   4) Discrete Math Seminar, Texas State University (Apr 22, 2022)
   5) Eastern North American Region (ENAR) Conference (Mar 30, 2022)
   6) Statistics Seminar, Department of Mathematics, Texas State University (Nov 19, 2021)
   7) Invited talk given at the Conference of Texas Statisticians (COTS) (Oct 9, 2021)
   8) Statistics Seminar, Department of Mathematics, Texas State University (Mar 26, 2021)
   9) The Mathematical and Computational Methods in Biology Workshop, organized by the Mathematical Biosciences Institute (May 5, 2020). See the abstract & presentation video of the 2nd paper: https://mbi.osu.edu/events/mathematical-and-computational-methods-biology (*Please click "Parallel Talk Titles and Abstracts" and then search "Sun" or "Shuying Sun")*
   10) Statistics Seminar, Department of Mathematics, Texas State University (April 26, 2019, Co-presented with Dr. Vera Ioudina)
   11) Graduate Math Open House, Department of Mathematics, Texas State University (November 10, 2017)
   12) Discrete Math Seminar, Department of Mathematics, Texas State University (September 18, 2016)
   13) Harmony Science Academy (May 13, 2016)
   14) Conference of Texas Statisticians 2016, Trinity University (April 9, 2016)
   15) Department of Statistical Science, Southern Methodist University (November 13, 2015)
   16) Graduate Math Open House, Department of Mathematics, Texas State University (October 16, 2015)
   17) Department of Biology, Texas State University (February 14, 2014)
   18) Department of Chemistry and Biochemistry, Texas State University (March 31, 2014)
   19) Discrete Math Seminar, Department of Mathematics, Texas State University (April 11, 2014)
   20) Women In Science and Engineering annual meeting, Texas State University (November 22, 2013)
   21) Department of Computer Science, Texas State University (November 1, 2013)
   22) University of Texas Health Science Center, San Antonio (October 16, 2013)
   23) Department of Mathematics and Statistics, South Dakota State University (February 22, 2013)
   24) Mathematical Sciences Department, The University of Texas at Dallas (February 12, 2013)
   25) Department of Biostatistics, Virginia Commonwealth University (December 18, 2012)

26) BIT's 5th Annual World Cancer Congress (May 19, 2012)
27) Biostatistics Facility and Department of Biostatistics, University of Pittsburgh (April 23, 2012)
28) Mathematical Sciences Department, University of Missouri-Kansas City (April 4, 2012)
29) Department of Epidemiology, The University of Iowa (March 29, 2012)
30) Department of Statistics, University of North Dakota (February 22, 2012)
31) Center for Proteomics and Bioinformatics, Case Western Reserve University (February, 2010)
32) Cleveland State University (November, 2009)
33) Virginia Commonwealth University (March, 2009)
34) University of Pennsylvania (February, 2009)
35) University of Nebraska, Omaha (February, 2009)
36) University of Minnesota (February, 2009)
37) Case Western Reserve University (January, 2009)
38) University of North Carolina, Chapel Hill (January, 2009)
39) Michigan Technological University (January, 2009)
40) McMaster University, Canada (September, 2008)
41) Department of Statistics, University of California, Berkeley (April, 2008)
42) Division of Biostatistics, University of California, San Francisco (March, 2008)
43) Integrative Cancer Biology Program at the Lawrence Berkeley Lab, Berkeley, California (March, 2008)
44) The 34th annual meeting of Statistical Society of Canada (May, 2006)

3. Consultancies: Texas State University (2013 – Present), Case Western Reserve University (2009 – 2013), University of Toronto (2002 – 2005)
4. Workshops: N/A
5. Other Works not in Print:
   a. Works "submitted" or "under review"
      1) **Sun S** PA, CA), Pritchard A (UST), McFall E (UST), and Tian C (UST). Statistical analysis of DNA methylation patterns of tumor suppressor genes in breast cancer. *Submitted to Epigenetics Insights*, 10/2024.

   b. Works "in progress"
      1) Tian C (HST), **Sun S.** Breast Cancer DNA methylation, age, and methylation age analysis (*90% done, ongoing)*
      2) **Sun S,** Peng B (HST), Pandit J (HST), Zane J (HST), and Zhong A (HST). Analyzing housekeeping genes' methylation patterns in breast and endometrial cancers. (*80% done, ongoing)*
      3) **Sun S,** Eloff N (UST), and Ward M (UST). Comparative Analysis of Six Correlation Metrics on DNA Co-Methylation (*80% done, ongoing)*
      4) **Sun S**, Han D (UST), Wei S (UST), Johnson AB (GST). A survey of haplotype assembly algorithms. (*50% done, ongoing)*
      5) **Sun S**, Massoudian S (UST), Performance of multiple individual haplotype assembly algorithms. (*50% done, ongoing)*

C. Grants and Contracts

1. Funded External Grants and Contracts:

Grant 1: NIH T32 training grant (T32GM154636)- Texas Doctoral Bridge Program.
PI: Steven T. Whitten Time Period: 08/01/2024 –07/31/2029.
Total amount : $2,836,154. **Sun S**: Senior/Key Personnel (Preceptor)

Grant 2: NSF REU Site: Algebra, Combinatorics, and Statistics #2150205
Time period: 03/01/2022 – 02/28/2025
PI: Yong Yang and Tomas Keller. **Sun S**: Senior Personnel. Total Amount: $305,417

Grant 3: NIH-R21 Yoga & Hypertension: Effects of Practice Temperature on Mechanistic Outcomes
Time Period: 12/01/2021–11/30/2023
PI: Dr. Stacy Hunter. **Sun S**: Statistical Consultant. Total amount: $408,493

Grant 4: NSF REU Site: Algebra, Combinatorics, and Statistics #1757233
Time period: 09/01/2018 – 08/31/2021
PI: Yong Yang and Tomas Keller. **Sun S**: Senior Personnel. Total Amount: $269,696

Grant 5: NSF Infrastructure grant -- NSF CC*IIE Networking Infrastructure: Enabling and Improving Data-Driven Research at Texas State University, total amount $499,896.
Time period: 08/19/2014 – 08/18/2016 **Sun S** (Senior Personnel, Person-month per year: acad 0.5)

Grant 5: NIH National Cancer Institute Early Detection Research Network Award (1UO1CA152756-01)
Time period: 08/25/2010 – 08/31/2011 **Sun S** (Co-Investigator with 6% effort/salary)

Grant 6: NIH/NCI Specialized Program of Research Excellence Grant (1P50CA15096401A1)
Time period: 10/01/2009 – 08/31/2011 **Sun S** (Co-Investigator with 25% effort/salary)

2. Submitted, but not Funded, External Grants and Contracts:

a. Grants with my role as the Principal Investigator (PI).

For the following proposals, the major goal is to develop new statistical methods to identify methylation patterns and biomarkers for cancers.

Grant 1: USDA education grant: Hispanic-Serving Institutions Education Grants Program
GRANT14065360. Funds requested: $1,200,000. Proposal *Submitted on Feb 7, 2024.* (*Unfunded*)

Grant 2: NSF Mid-scale Research Infrastructure-1 Mid-scale RI-1 (M1:IP): Mathematical Information Science Collaborative (MISC). Funds requested: $17,529,101.
PI: Lucas Rusnak. My Role: Co-PI. Preliminary Proposal Submitted on Jan 5, 2023.

Grant 3: Tensor Women & Mathematics Grant ($6,000). Submitted on Feb 8, 2022

Grant 4: The 2022-2023 Joan and Joseph Birman Fellowship for Women Scholars ($50,000)
Submitted on Nov 20, 2021 for the funding period of 09/2022-08/2023.

Grant 5: The 2021-2022 Joan and Joseph Birman Fellowship for Women Scholars ($50,000)
Submitted on Nov 24, 2020 for the funding period of 09/2021-08/2022.

Grant 6: NIH-R21: Secondary Analysis and Integration of Existing Data to Elucidate the Genetic Architecture of Cancer Risk and Related Outcomes PA-17-243 ($367,804).
Title: Secondary analysis of lung cancer methylation sequencing data. Submitted on Feb 7, 2020.

Grant 7: The 2020-2021 Joan and Joseph Birman Fellowship for Women Scholars ($50,000.00)
Submitted on Nov 25, 2019 for the funding period of 09/2020-08/2021.

Grant 8: The 2019-2020 Joan and Joseph Birman Fellowship for Women Scholars ($50,000.00),
Submitted on Nov 15, 2018 for the funding period of 09/2019-08/2020.

Grant 9: Association for Women in Mathematics Travel Grant, October 29, 2016
Title: Traveling to build collaborations on statistical genetics and bioinformatics

Grant 10: Simons Foundation Collaboration Grants for Mathematicians, January 27, 2016
Title: A collaboration grant for statistical geneticists and bioinformaticians

Grant 11: NCI-R21 NCI Exploratory/Developmental Research Grant Program, November 5, 2015
Title: DNA methylation heterogeneity patterns in breast cancer cell lines

Grant 12: NIH-R21 NIH Exploratory/Developmental Research Grant program, October 9, 2012
Title: A Bayesian hidden Markov model for methylation sequencing data analysis

Grant 13: NIH-R03 Small Grants Program for Cancer Epidemiology, July 9, 2012
Title: Statistical approaches and pipelines for mining methylation sequencing data

Grant 14: NCI-R03 Cancer Prevention Research Small Grant Program, December 12, 2011
Title: Identifying breast cancer methylation biomarkers using a new statistical method

Grant 15: NCI-K25 Mentored Quantitative Research Career Development Award, October 8, 2010
Title: Studying colon cancer methylation patterns using novel statistical methods

b. Grants with my role as a key/senior personnel or participant (but not a Principal Investigator)

Grant 1: NCI R21 grant, Resubmitted in November 2019
Project: Yoga & Hypertension: Effects of Practice Temperature on Mechanistic Outcomes
PI: Dr. Stacy Hunter. My role: Statistical Consultant.

Grant 2: CPRIT Geospatial and Cancer Communication Technology core research facility grant

(CPRIT: Cancer Prevention & Research Institute of Texas). Submitted on Jan 17, 2017.
PI: Dr. Melinda Villagran. My Role: Key User (or Collaborator), No co-PIs are allowed.
Grant 3: NSF S-STEM Math Scholars Program, Submitted in March 2017
PI: Dr. Max Warshauer and Robert Sigley. My role: Senior Personnel or Research Mentor.

3. Funded Internal Grants and Contracts:
Grant 1: Texas State University Research Enhancement Program (REP) Award ($8,000)
Time Period: 01/01/2023 – 05/31/2024 **Sun S**. (PI)
Project: Investigating the performance of six correlation metrics on DNA co-methylation analysis
Grant 2: Texas State University Research Enhancement Program (REP) Award ($8,000)
Time Period: 01/01/2021 – 05/31/2022 **Sun S**. (PI)
Project: Identifying breast cancer co-methylation patterns using statistical methods
Grant 3: Texas State University Research Enhancement Program (REP) Award ($8,000)
Time Period: 01/01/2018 – 05/31/2019 **Sun S**. (PI)
Project: Developing a statistical and bioinformatic approach for breast cancer data integration
Grant 4: Texas State University Research Enhancement Program (REP) Award ($6,556)
Time Period: 01/01/2016 – 05/31/2017 **Sun S**. (PI)
Goal: Developing a new statistical tool for analyzing cancer methylation heterogeneity patterns
Grant 5: Texas State University Research Enhancement Program (REP) Award ($8,000)
Time Period: 01/14/2014 – 03/31/2015 **Sun S**. (PI)
Goal: Developing a new statistical approach for identifying differential methylation
Grant 6: Texas State University Library Research Grant ($655.90 for 5 books)
Time period: 12/03/2014 – 12/02/2015 **Sun S**. (PI)
Goal: Developing change point analysis for DNA methylation events
Grant 7: Texas State University Library Research Grant ($420 for 6 books)
Time period: 12/01/2013 – 11/30/2014 **Sun S**. (PI)
Goal: Addressing challenging genetic and epigenetic questions using statistical methods
Grant 7: Case Western Reserve University Clinical & Translational Science Collaborative (CTSC) translational methodology grant ($9,000)
Time period: 01/15/2010 – 12/31/2010 **Sun S**. (PI)
Goal: SNP calling analysis using DNA sequencing data

4. Submitted, but not Funded, Internal Grants and Contracts:
Grant 1: Texas State University Research Enhancement Program (REP) Award ($8,000)
Time Period: 01/01/2025 – 05/31/2026 **Sun S**. (PI)
Project: New analysis of DNA methylation age and gene clock identification for breast cancer.
Proposal *Submitted on Oct 7, 2024.*
Grant 2: Texas State University Research Enhancement Program (REP) Award ($8,000)
Time Period: 01/01/2020 – 05/31/2021 **Sun S**. (PI)
Project: Statistical and bioinformatic analysis of lung cancer hemimethylation patterns

5. Pending Grants and Contracts:
Grant 1: REU Site: Algebra, Combinatorics, and Statistics
(Fund requested: $346,568). PI: Yong Yang
My Role: Key Personnel (Research Mentor). *Submitted in September, 2024*
Anticipated Funding Period: 03/2025 – 02//2028

D. Fellowships, Awards, and Honors

2022	Service Excellence Award, Department of Mathematics, Texas State University (12/2022)
2021	Teaching Excellence Award, Department of Mathematics, Texas State University (12/2021)
2020	College Achievement Award for Excellence in Scholarly/Creative Activities, College of Science and Engineering, Texas State University (08/2020)
2019	Research Excellence Award, Department of Mathematics, Texas State University (12/2019)
2019	Faculty Development Leave Supplemental Award (09/2019 –05/2020)

2018 LBJ Institute Faculty Research Fellow for the 2018-2019 cohort (09/2018-05/2019)
2018 The First Prize winner of the 2018 CoSearch team project (Title: *TELeHealth Goes To School*)
2017 The second Prize winner of the 2017 CoSearch team project (Title: *Pain Management: Arts-Based Therapies To Reduce Dependencies On Pain Medication*).
2017 Presidential Distinction Award for Excellence in Teaching, Texas State University
2017 Research Enhancement Program Award, Texas State University
2016 Teaching Excellence Award, Department of Mathematics, Texas State University
2015 Research Enhancement Program Award, Texas State University
2013 Research Enhancement Program Award, Texas State University
2009 Named as the top postdoctoral scholar of the Mathematical Biosciences Institute (MBI) to introduce my research in the newsletter of MBI, The Ohio State University
2008 Integrative Cancer Biology Program (ICBP) Junior Investigator Award
2008 Intelligent Systems for Molecular Biology (ISMB) Travel Award
2007 Mathematical Systems Biology of Cancer II Workshop Travel Award
2006 The 3rd International HapMap Project Annual Meeting Travel Award
1996 Hebei Normal University Award of *Top 10 Outstanding Students* (out of 12,000 students)
1995 National First Prize Award in the Mathematical Contest in Modeling in China

IV. SERVICE

A. Institutional

1. University:
   - [1] Supported the 2022 Health Scholar Showcase by presenting two posters (04/08/2022)
   - [2] Served/helped in the COVID-Testing Verification Event (08/15/2021)
   - [3] Submitted a *Big Idea* proposal on Building a Statistics and Bioinformatics Program at Texas State University (10/27/2020). This proposal was selected for funding raising by the University Advancement.
   - [4] Presented a poster with the title *Statistical Genetics and Bioinformatics @ TxState* for the 2018 Health Scholar Showcase (02/23/2018)
   - [5] Provided statistical consulting service to Dr. Melinda Hester and her graduate student Ms. Danielle Green from St. David's School of Nursing, College of Health Professions, and served as key personnel on their research project (08/2017 – 05/2018)
   - [6] Served as a mentor for Allison Johnson through the Bobcat Bond Program (10/2017 – 05/2018)
   - [7] Attended many workshops for professional development to better serve at Texas State (2013- present)
   - [8] Contributed as a key collaborator in CPRIT Geospatial and Cancer Communication Technology core research facility grant submission (PI: Dr. Melinda Villagran). This is a grant application with the participation of several colleges at Texas State University (11/2016 – 01/2017)
   - [9] Volunteered for the *Bobcat Preview* (08/13/2015 and 08/21/2016)
   - [10] Participated as one of Texas State team members in the application for the Joint Venture Partnership with the National Technical Information Service for Data Innovation Support (08/2016)
   - [11] Reviewed an honors course proposal with Dr. Alex White and the Honors College (10/13/2015)

2. College:
   - [1] Served as a Graduate Marshal on May 12, 2022
   - [2] Served in the collaborative postdoc line committee with colleagues in other departments (02/2018 – 05/2022)
   - [3] Served as a thesis committee member for Anjani Chaudhary, graduate student of the Ingram School of Engineering (Thesis defense done on Nov 2, 2020)
   - [4] Served as a poster judge for the Women In Science and Engineering (WISE) conference (03/02/2018 and 03/08/2019)
   - [5] Served as an associate doctoral faculty for the Materials Science, Engineering & Commercialization (MSEC) Ph.D. program (01/2018 – present) (Served in the MSEC admission committee in Spring 2018)

[6] Led the *Cancer, Genetics, and Bioinformatics* theme poster preparation for the Health Scholar Showcase in collaboration with 8 investigators in College of Science and Engineering (01/2017)
[7] Provided statistical and bioinformatic consultation to a postdoc in the Department of Chemistry and Biochemistry (12/2013 and 12/2016) and one faculty member in the Department of Biology (06/2016)
[8] Contributed to support the NSF grant proposal submitted by Texas State University Computer Science faculty members, Dr. Hongshi Chi, Dr. Xiao Chen, and IT department colleagues. This grant proposal was approved in August 2014 with a total amount of $499,896 (03/2014)
[9] Attended a mental health training workshop to better support students' growth and success (01/2014)
[10] Supported the Women In Science and Engineering conference with an invited talk (11/23/2013)

3. Department/School:

[1] Led the new statistics program by serving as a graduate advisor for the Math MS Statistics Concentration (02/2017 – present, except when I was on faculty development leave from 09/2019 to 05/2020).
[2] Submitted a *Big Initiative* draft proposal on growing our graduate program in statistics to the College of Science and Engineering (02/02/2022).
[3] Attended the monthly ParaDIGMS advisor meeting (Spring 2021)
[4] Supported the Math Department Grad Expo event by presenting posters every year (2013 – present), meeting prospective students as a graduate advisor (2018 -present), as a judge for the "Math in the Picture" posters (11/2017), and as a table host (2014, 2015, 2017)
[5] Served as a mentor for junior faculty members and graduate students:
- Tenure track faculty: Dr. Xiaoxi Shen (09/2021 – present)
- Tenure track faculty: Dr. Yong Yang (03/2018 – 05/2019)
- Tenure track faculty: Dr. Wade Hindes (09/2018 – 05/2019)
- Lecturer: Dr. Vivian Healey (09/2020 – 05/2022)
- Lecturer: Dr. Abby Train (09/2018 – 05/2019)
- Lecturer: Dr. Bahaudin Hashmi (09/2017 – 05/2018)
- Lecturer: Dr. Vera Ioudina (09/2016 – 05/2017)
- Lecturer: Dr. Bikai Nie (09/2015 – 05/2016)
- Graduate student: Holly Tidwell (01/2023 – present)
- Graduate student: Emet Bethany (09/2021 – 12/2021)
- Graduate student: Robert Zhan (09/2020 – 05/2021)
- Graduate student: Ashraf Demian (09/2017 – 05/2018)

[6] Invited and hosted external speakers for department seminars:
- Dr. Longhai Li, University of Saskatchewan, Canada (03/08/2024)
- Dr. Celia Greenwood, McGill University (02/24/2023)
- Dr. Xiaoqing Yu, Moffitt Cancer Center and Research Institute (03/24/2023)
- Dr. Lei Sun, University of Toronto, (09/29/2023)
- Dr. Steve Qin, Emory University, (11/10/2023)
- Dr. Yuting Jia, from Microsoft (02/25/2022)
- Dr. Kui Zhang, from Michigan Technological University (03/04/2022)
- Dr. David Sankoff, from University of Ottawa (04/09/2021)
- Dr. Vivian Li, from Rutgers University (04/30/2021)
- Dr. Mingyao Li, from University of Pennsylvania (10/08/2021)
- Dr. Sherry Wang, from Southern Methodist University (11/13/2021)
- Dr. Sue Geller, from Texas A & M University (02/15/2019)
- Dr. Peter Muller, from University of Texas at Austin (09/28/2018)
- Dr. Tony Ng, from Southern Methodist University (11/06/2015)

[7] Served as a member in different department committees:
- Merit committee (09/2024 – 05/2025)
- Hiring committee for a probability position (04/2023 –05/2024)
- Prepared for and graded Math Education doctoral qualifying exams and comprehensive exams for

Math MS program (05/2022, 01/2022, 05/2021, 01/2021, 05/2018, 01/2018, 05/2017, 01/2017, 01/2014, in 05/2024, 08/2024, and 01/2025.)
- Budget committee (09/2023 – 05/2024)
- Hiring committee for a computational math and statistics position (04/2023 –05/2024)
- The scheduling oversight committee (Fall 2020 – present)
- Math PhD Proposal Committee (09/2020 – 07/2024).
- The math Ph.D. and graduate committee (08/2018 – 05/2019 and 09/2020 – 05/2021).
  [I attended the 1-2 hour committee meeting every week for about 30 weeks in two semesters]
- The hiring committee for the statistics tenure-track faculty position (09/2019 – 05/2021)
  [I committed at least 6 full days for the whole hiring process when I am on leave from Fall 2019 to Spring 2020. In Spring 2021, we reviewed many application files, zoom interviewed 20 candidates (30 minutes/each) in one week]
- The hiring committee for two math tenure-track faculty positions (08/2018 – 05/2019)
- Math PhD proposal committee (09/2018 – 05/2019, and 09/2020 – present).
- The program and curriculum committee (09/2021 – 05/2022)
- Math department's library committee (Fall 2013 – 05/2021)
- The lecturer review committee, as a by-large faculty member (09/2017 – 08/2019)
- Statistics Concentration Committee, as a committee chair (02/2017 – 12/2017)
- Statistics qualifying exam committee, as a chair for Math Education PhD. Program (2016 –2018)
- Committee for the expedite statistics position (09/2016 – 02/2017)

[8] Named/Recognized by Anna Cowsar, Matthew Adams, and Sheryl Rosenthal as a person at Texas State who made a contribution to their academic career (07/03/2019, 07/20/2016, and 07/13/2015)

[9] Served as a committee member for the following graduate students' Master theses: Anjani Chaudhary (02/2018 – 12/2020), Martin Schmidt's (02/2018 – 04/2018), and Jamtsho Jamtsho (10/2015 – 04/2016)

[10] Served on the Graduate and Professional Fair Day (02/12/2018)

[11] Served as a presenter on the Math Award Day, Texas State University (04/2018, 04/2017, 04/2014)

[12] Provided advanced statistics questions and solutions for the Math Lab tutor recruitment (Spring 2017)

[13] Served as a research mentor for undergraduate student, Yu-Ri Lee, on a project (05/2016 – 12/2017)

[14] Mentored the math major student, Brittany Enfield, for her honors thesis (08/2014 – 05/2015) and her honors course project in Math4305, Texas State University (01/2014-05/2014)

[15] Served on Bobcat Days, Department of Mathematics (04/2014 & 02/2016)

[16] Supported students' events (e.g., Halloween Party & Talk Math 2 Me) (Fall 2013)

[17] Participated in developing a new course, MATH2428, in collaboration with other colleagues in the Department of Mathematics, Texas State University (Fall 2013)

B. Professional

1. Promoted to be an Associate Editor (by invitation) of *Cancer Genetics* (specialty section of *Frontiers in Oncology* and *Frontiers in Genetics*), 06/2022-12/2023
2. Served as a Review Editor on the Editorial Board for two sections of *Frontiers in Genetics* (07/15/2020-present for the section of *Cancer Genetics*, and 10/19/2015 – present for the section of *Statistical Genetics and Methodology*)
3. Served as a Handling Editor (i.e., Guest Associate Editor) for the section of *Statistical Genetics and Methodology* of *Frontier Genetics* (06/2021 - 08/2021)
4. Elected as a Reviewer of the Month (June 2021) for the international journal of *Translational Cancer Research* (TCR). https://tcr.amegroups.com/post/view/reviewer-of-the-month-2020-21
5. Served as a career mentor for young researchers at the *American Society of Human Genetics* (ASHG) annual meeting on Oct 12, 2021
6. Served as an invited reviewer for the following high-impact international journals (2008–present): (1) *Statistical Applications in Genetics and Molecular Biology*, (2) *Biometrical Journal*, (3) *Computational Statistics and Data Analysis*, (4) *Physiological Genomics*, (5) *Surveys in Mathematics and Its Applications*, (6) *BMC Medical Genomics*, (7) *Bioinformatics*, (8) *Statistics in Medicine*, (9) *Scientific Reports*, (10) *PLOS One*, (11) *Statistics and Probability Letters*, (12) *Statistics in Biosciences*, (13) *Biometrics*, (14) *Nature Communications*, (15) *BMC Bioinformatics*, (16) *Annals of Applied Statistics*, (17) *Journal of*

American Statistical Association, (18) *Frontiers Genetics*, (19) *Translational Cancer Research,* and (20) Journal of the Royal Statistical Society: Series C. [<u>I review 3 ~5 papers each year for different journals</u>].

7. Conferences/workshops/seminars - served as an organizer (or co-organizer) or session chairs
   [1] Served as a session chair for the conference entitled Advances in Statistical and Computational Methods for Analysis of Biomedical, Genetic, and Omics Data at The University of Texas at Dallas, Richardson, Texas, United States (Mar 17, 2023)
   [2] Served as a session chair for the Joint Statistics and Data Science Conference, Beijing, China, (July 12, 2023)
   [3] Served as a poster judge for the Conference of Texas Statisticians (COTS) (10/09/2021, 04/08/2016)
   [4] Organized Sequencing Data Interest Group (SDIG) meetings (09/2009 – 05/2013)
   [5] Served as an abstract reviewer, Ohio Collaborative Conference on Bioinformatics (2010)
   [6] Co-organized ICBP Junior Investigators Meeting (2008)
   [7] Co-organized Workshop for Young Researchers in Math Biology (2007 & 2008)

Updated on September 1, 2025