

Ryan Sun

CONTACT INFORMATION

Department of Biostatistics
University of Texas M.D. Anderson Cancer Center
1400 Pressler Street, Unit 1410
Houston, Texas 77030

Office: (713) 745-0373
E-mail: rsun3@mdanderson.org
Website: <https://ryanrsun.github.io/>
Citizenship: United States, Canada

EDUCATION

Harvard University, Boston, Massachusetts

Ph.D., Biostatistics, May 2017

- Dissertation Title: “Methods for High-Dimensional Inference in Genetic Association Studies”
- Advisor: Professor Xihong Lin

M.A., Biostatistics, May 2014

Columbia University, New York City, New York

B.S., Applied Mathematics, May 2012

HONORS AND AWARDS

Travel Award for IMS New Researchers Conference, 2018

Harvard Program in Quantitative Genomics Postdoctoral Travel Award, 2017

ENAR Distinguished Student Paper Award, 2017

Harvard University Distinction in Teaching Award, 2014-2015

Cyprus National Government Environmental Health Travel Scholarship, 2013

Columbia University Lauren P. Breakiron Scholarship, 2008-2012

ACADEMIC EXPERIENCE

University of Texas MD Anderson Cancer Center, Houston, Texas

Associate Professor, Department of Biostatistics

September 2025 - Present

Assistant Professor, Department of Biostatistics

July 2019 - August 2025

Rice University, Houston, Texas

Adjunct Assistant Professor, Department of Statistics

July 2020 - Present

Harvard School of Public Health, Boston, Massachusetts

Postdoctoral Research Fellow

May 2017 - June 2019

Developed statistical methods for the analysis of high-dimensional biomedical data. Collaborations include the EPA Superfund project and the International Lung Cancer Consortium (ILCCO).

Harvard School of Public Health, Boston, Massachusetts

Instructor

July 2016 - August 2016

Redesigned and delivered real analysis course for incoming Biostatistics Ph.D. students. Planned lectures, created class materials, and taught all sessions.

Teaching Assistant

September 2012 - June 2016

Assigned to three doctoral-level biostatistics courses and one introductory statistics course.

PROFESSIONAL EXPERIENCE

Empiric Asset Management, New York, New York

Analyst

May 2011 - May 2012

Quantitative analyst for hedge fund with equity market neutral strategy.

PUBLICATIONS:
FIRST AUTHOR,
LAST AUTHOR, &
STATISTICAL
COLLABORATIONS

*Indicates equal contribution as first authors.

#Indicates author was a trainee in the Sun Lab at time of work.

1. **Sun R**, Bouchard MB, Hillman EM. SPLASH: Open source software for camera-based high-speed, multispectral in-vivo optical image acquisition. *Biomed Opt Express*. 2010 Aug 01; 1(2):385-397. PMID: 21258475.
2. **Sun R**, Carroll RJ, Christiani DC, Lin X. Testing for gene-environment interaction under exposure misspecification. *Biometrics*. 2018 Jun 01; 74(2):653-662. PMID: 29120492.
3. **Sun R**, Hui S, Bader GD, Lin X, Kraft P. Powerful gene set analysis in GWAS with the Generalized Berk-Jones statistic. *PLoS Genet*. 2019 Mar 01; 15(3):e1007530. PMID: 30875371.
4. Gaynor SM*, **Sun R***, Lin X, Quackenbush J. Identification of differentially expressed gene sets using the Generalized Berk-Jones statistic. *Bioinformatics*. 2019 Nov 01; 35(22):4568-4576. PMID: 31062858.
5. Zhu, L, Tong, X, Cai, D, Li, Y, **Sun, R**, Srivastava, DK, Hudson, MM. Maximum likelihood estimation for the proportional odds model with mixed interval-censored failure time data. *J Appl Stat*. 2020 Jan 01; :1-17. PMID: 34349336.
6. **Sun R**, Lin X. Genetic Variant Set-Based Tests Using the Generalized Berk-Jones Statistic with Application to a Genome-Wide Association Study of Breast Cancer. *J Am Stat Assoc*. 2020 Jan 01; 115(531):1079-1091. PMID: 33041403.
7. Li X, Li Z, Zhou H, Gaynor SM, Liu Y, Chen H, **Sun R**, Dey R, Arnett DK, Aslibekyan S, Ballantyne CM, Bielak LF, Blangero J, Boerwinkle E, Bowden DW, Broome JG, Conomos MP, Correa A, Cupples LA, Curran JE, Freedman BI, Guo X, Hindy G, Irvin MR, Kardia SLR, Kathiresan S, Khan AT, Kooperberg CL, Laurie CC, Liu XS, Mahaney MC, Manichaikul AW, Martin LW, Mathias RA, McGarvey ST, Mitchell BD, Montasser ME, Moore JE, Morrison AC, O'Connell JR, Palmer ND, Pampana A, Peralta JM, Peyser PA, Psaty BM, Redline S, Rice KM, Rich SS, Smith JA, Tiwari HK, Tsai MY, Vasan RS, Wang FF, Weeks DE, Weng Z, Wilson JG, Yanek LR, (TOPMed) Consortium NTFPM, Working Group TL, Neale BM, Sunyaev SR, Abecasis GR, Rotter JI, Willer CJ, Peloso GM, Natarajan P, Lin X. Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. *Nat Genet*. 2020 Sep 01; 52(9):969-983. PMID: 32839606.
8. **Sun R**, Wang Z, Claus Henn B, Su L, Lu Q, Lin X, Wright RO, Bellinger DC, Kile M, Mazumdar M, Tellez-Rojo MM, Schnaas L, Christiani DC. Identification of novel loci associated with infant cognitive ability. *Mol Psychiatry*. 2020 Nov 01; 25(11):3010-3019. PMID: 30120420.
9. Kim DH, Li X, Bian S, Wei LJ, **Sun R**. Utility of Restricted Mean Survival Time for Analyzing Time to Nursing Home Placement Among Patients With Dementia. *JAMA Netw Open*. 2021 Jan 28; 4(1):e2034745. PMID: 33507253.
10. **Sun R**, Xu M, Li X, Gaynor S, Zhou H, Li Z, Bossé Y, Lam S, Tsao MS, Tardon A, Chen C, Doherty J, Goodman G, Bojesen SE, Landi MT, Johansson M, Field JK, Bickeböller H, Wichmann HE, Risch A, Rennert G, Arnold S, Wu X, Melander O, Brunnström H, Le Marchand L, Liu G, Andrew A, Duell E, Kiemeny LA, Shen H, Haugen A, Johansson M, Grankvist K, Caporaso N, Woll P, Dawn Teare M, Scelo G, Hong YC, Yuan JM, Lazarus P, Schabath MB, Aldrich MC, Albanes D, Mak R, Barbie D, Brennan P, Hung RJ, Amos CI, Christiani DC, Lin X. Integration of multiomic annotation data to prioritize and characterize inflammation and immune-related risk variants in squamous cell lung cancer. *Genet Epidemiol*. 2021 Feb 01; 45(1):99-114. PMID: 32924180.
11. **Sun R***, McCaw Z*, Tian L, Uno H, Hong F, Kim DH, Wei LJ. Moving beyond conventional stratified analysis to assess the treatment effect in a comparative oncology study. *J Immunother Cancer*. 2021 Nov 01; 9(11) PMID: 34799398.
12. Li X, Yung G, Zhou H, **Sun R**, Li Z, Hou K, Zhang MJ, Liu Y, Arapoglou T, Wang C, Ionita-Laza I, Lin X. A multi-dimensional integrative scoring framework for predicting functional variants in the human genome. *Am J Hum Genet*. 2022 Mar 01; 109(3):446-456. PMID: 35216679.

13. Yam C*, Abuhadra N*, **Sun R***, Adrada BE, Ding QQ, White JB, Ravenberg EE, Clayborn AR, Valero V, Tripathy D, Damodaran S, Arun BK, Litton JK, Ueno NT, Murthy RK, Lim B, Baez L, Li X, Buzdar AU, Hortobagyi GN, Thompson AM, Mittendorf EA, Rauch GM, Candelaria RP, Huo L, Moulder SL, Chang JT. Molecular Characterization and Prospective Evaluation of Pathologic Response and Outcomes with Neoadjuvant Therapy in Metaplastic Triple-Negative Breast Cancer. *Clin Cancer Res.* 2022 Jul 01; 28(13):2878-2889. PMID: 35507014.
14. Huang B*, **Sun R***, Claggett B, Tian L, Ludmir EB, Wei LJ. Handling Informative Premature Treatment or Study Discontinuation for Assessing Between-Group Differences in a Comparative Oncology Trial. *JAMA Oncol.* 2022 Oct 01; 8(10):1502-1503. PMID: 35980612.
15. Li, Z, Li, X, Zhou, H, Gaynor, SM, Selvaraj, MS, Arapoglou, T, Quick, C, Liu, Y, Chen, H, **Sun, R**, Dey, R, Arnett, DK, Auer, PL, Bielak, LF, Bis, JC, Blackwell, T, Blangero, J, Boerwinkle, E, Bowden, DW, Brody, JA, Cade, BE, Conomos, MP, Correa, A, Cupples, LA, Curran, JE, de Vries, PS, Duggirala, R, Franceschini, N, Freedman, BI, Göring, HH, Guo, X, Kalyani, RR, Kooperberg, C, Kral, BG, Lange, LA, Lin, BM, Manichaikul, AW, Manning, AK, Martin, LW, Mathias, R, Meigs, JB, Mitchell, BD, Montasser, ME, Morrison, AC, Naseri, T, O'connell, Jr, Palmer, ND, Peyser, PA, Psaty, BM, Raffield, LM. A framework for detecting noncoding rare-variant associations of large-scale whole-genome sequencing studies. *Nat Methods.* 2022 Dec 01; PMID: 36303018.
16. Li, X, Quick, C, Zhou, H, Gaynor, SM, Liu, Y, Chen, H, Selvaraj, MS, **Sun, R**, Dey, R, Arnett, DK, Bielak, LF, Bis, JC, Blangero, J, Boerwinkle, E, Bowden, DW, Brody, JA, Cade, BE, Correa, A, Cupples, LA, Curran, JE, de Vries, PS, Duggirala, R, Freedman, BI, Göring, HH, Guo, X, Haessler, J, Kalyani, RR, Kooperberg, C, Kral, BG, Lange, LA, Manichaikul, AW, Martin, LW, McGarvey, ST, Mitchell, BD, Montasser, ME, Morrison, AC, Naseri, T, O'Connell, JR, Palmer, ND, Peyser, PA, Psaty, BM, Raffield, LM, Redline, S, Reiner, AP, Reupena, MS, Rice, K, Rich, SS, Sitlani, CM, Smith, JA, Menon, VK. Powerful, scalable and resource-efficient meta-analysis of rare variant associations in large whole genome sequencing studies. *Nat Genet.* 2023 Jan; 55(1):154-164. PMID: 36564505.
17. Parseghian CM*, **Sun R***, Woods M*, Napolitano S*, Lee HM, Alshenaifi J, Willis J, Nunez S, Raghav KP, Morris VK, Shen JP, Eluri M, Sorokin A, Kanikarla P, Vilar E, Rehn M, Ang A, Troiani T, Kopetz S. Resistance Mechanisms to Anti-EGFR Therapy in RAS/RAF Wildtype Colorectal Cancer Vary by Regimen and Line of Therapy. *J Clin Oncol.* 2023 Jan 20; 41(3):101200JCO2201423. PMID: 36351210.
18. McCaw ZR, Gaynor SM, **Sun R**, Lin X. Leveraging a surrogate outcome to improve inference on a partially missing target outcome. *Biometrics.* 2023 Jun 01; 79(2):1472-1484. PMID: 35218565.
19. **Sun R**, Zhu L, Li Y, Yasui Y, Robison L. Inference for Set-Based Effects in Genetic Association Studies with Interval Censored Outcomes. *Biometrics.* 2023 Jun 01; 79(2):1573-1585. PMID: 35165890.
20. Napolitano S, Parikh AR, Henry J, Parseghian CM, Willis J, Raghav KP, Morris VK, Johnson B, Kee BK, Dasari AN, Overman MJ, Luthra R, Drusbosky LM, Corcoran RB, Kopetz S, **Sun R**. Novel Clinical Tool to Estimate Risk of False-Negative KRAS Mutations in Circulating Tumor DNA Testing. *JCO Precis Oncol.* 2023 Sep; 7:e2300228. PMID: 37824798.
21. **Sun R**, Sun D, Zhu L, Sun J. Regression analysis of general mixed recurrent event data. *Lifetime Data Anal.* 2023 Oct 01; 29(4):807-822. PMID: 37438585.
22. **Sun R**, Shi A, Lin X. Differences in set-based tests for sparse alternatives when testing sets of outcomes compared to sets of explanatory factors in genetic association studies. *Biostatistics.* 2024 Jan 01; 25(1):171-187. PMID: 36000269.
23. Zhu H#, Choi J#, Kui N#, Yang T, Wei P, Li D, **Sun R**. Identification of pancreatic cancer germline risk variants with effects that are modified by smoking. *JCO Precis Oncol.* 2024 Mar; 8:e2300355. PMID: 38564682.
24. Choi J#, Xu Z#, **Sun R**. Variance-components tests for genetic association with multiple interval-censored outcomes. *Stat Med.* 2024 Jun 15; 43(13):2560-2574. PMID: 38636557.

25. Xu Z[#], Choi J[#], **Sun R**. Set-based tests for genetic association studies with interval-censored competing risks outcomes. *Statistics in Biosciences*. 2024 Jul 13.
26. **Sun, R**, McCaw Z, Lin, X. Testing a large number of composite null hypotheses using conditionally symmetric multidimensional gaussian mixtures in genome-wide studies. *Journal of the American Statistical Association*. 2025 Jan 01; 120(550):605-617.
27. Li, X, Chen, H, Selvaraj, MS, Van Buren, E, Zhou, H, Wang, Y, **Sun, R**, McCaw, ZR, Yu, Z, Jiang, MZ, Dicorpo, D, Gaynor, SM, Dey, R, Arnett, D, Benjamin, EJ, Bis, JC, Blangero, J, Boerwinkle, E, Bowden, DW, Brody, JA, Cade, BE, Carson, A, Carlson, JC, Chami, N, Chen, YI, Curran, JE, De Vries, PS, Fornage, M, Franceschini, N, Freedman, BI, Gu, C, Heard-Costa, NL, He, J, Hou, L, Hung, YJ, Irvin, MR, Kaplan, RC, Kardia, SL, Kelly, TN, Konigsberg, I, Kooperberg, C, Kral, BG, Li, C, Li, Y, Lin, H, Liu, CT, Loos, RJ, Mahaney, MC, Martin, LW, Menon, VK. A statistical framework for multi-trait rare variant analysis in large-scale whole-genome sequencing studies. *Nature Computational Science*. 2025 Feb 01; 5(2):125-143. PMID: 39920506.
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34. Yam C, Rauch GM, Rahman T, Karuturi M, Ravenberg E, White J, Clayborn A, McCarthy P, Abouharb S, Lim B, Litton JK, Ramirez DL, Saleem S, Stec J, Symmans WF, Huo L, Damodaran S, **Sun R**, Moulder SL. A phase II study of Mirvetuximab Soravtansine in triple-negative breast cancer. *Invest New Drugs*. 2021 Apr 01; 39(2):509-515. PMID: 32984932.
35. Bhamidipati, D, Colina, A, Hwang, H, Wang, H, Katz, MH, Fournier, KF, Serpas Higbie, V, Thomas, J, **Sun, R**, Wolff, RA, Raghav, KS, Overman, MJ. Metastatic small bowel adenocarcinoma: role of metastasectomy and systemic chemotherapy. *ESMO Open*. 2021 Jun 01; 6(3) PMID: 33940348.
36. Strati P, Ahmed S, Furqan F, Fayad LE, Lee HJ, Iyer SP, Nair R, Nastoupil LJ, Parmar S, Rodriguez MA, Samaniego F, Steiner RE, Wang M, Pinnix CC, Horowitz SB, Feng L, **Sun R**, Claussen CM, Hawkins MC, Johnson NA, Singh P, Mistry H, Johncy S, Adkins S, Kebriaei P,

- Shpall EJ, Green MR, Flowers CR, Westin J, Neelapu SS. Prognostic Impact of Corticosteroids on Efficacy of Chimeric Antigen Receptor T-cell Therapy in Large B-cell Lymphoma. *Blood*. 2021 Jun 10; 137(23):3272-3276. PMID: 33534891.
37. Han G, Yang G, Hao D, Lu Y, Thein K, Simpson BS, Chen J, **Sun R**, Alhalabi O, Wang R, Dang M, Dai E, Zhang S, Nie F, Zhao S, Guo C, Hamza A, Czerniak B, Cheng C, Siefker-Radtke A, Bhat K, Futreal A, Peng G, Wargo J, Peng W, Kadara H, Ajani J, Swanton C, Litchfield K, Ahnert JR, Gao J, Wang L. 9p21 loss confers a cold tumor immune microenvironment and primary resistance to immune checkpoint therapy. *Nat Commun*. 2021 Sep 23; 12(1):5606. PMID: 34556668.
 38. Yam C, Yen EY, Chang JT, Bassett RL, Alatrash G, Garber H, Huo L, Yang F, Philips AV, Ding QQ, Lim B, Ueno NT, Kannan K, Sun X, Sun B, Parra Cuentas ER, Symmans WF, White JB, Ravenberg E, Seth S, Guerriero JL, Rauch GM, Damodaran S, Litton JK, Wargo JA, Hortobagyi GN, Futreal A, Wistuba II, **Sun R**, Moulder SL, Mittendorf EA. Immune Phenotype and Response to Neoadjuvant Therapy in Triple-Negative Breast Cancer. *Clin Cancer Res*. 2021 Oct 01; 27(19):5365-5375. PMID: 34253579.
 39. Alhalabi, O, Soomro, Z, **Sun, R**, Hasanov, E, Albittar, A, Tripathy, D, Valero, V, Ibrahim, NK. Outcomes of changing systemic therapy in patients with relapsed breast cancer and 1 to 3 brain metastases. *npj Breast Cancer*. 2021 Dec 01; 7(1) PMID: 33742001.
 40. Abuhadra N, **Sun R**, Litton JK, Rauch GM, Yam C, Chang JT, Seth S, Bassett R, Lim B, Thompson AM, Mittendorf E, Adrada BE, Damodaran S, White J, Ravenberg E, Candelaria R, Arun B, Ueno NT, Santiago L, Saleem S, Abouharb S, Murthy RK, Ibrahim N, Sahin AA, Valero V, Symmans WF, Tripathy D, Moulder S, Huo L. Prognostic Impact of High Baseline Stromal Tumor-Infiltrating Lymphocytes in the Absence of Pathologic Complete Response in Early-Stage Triple-Negative Breast Cancer. *Cancers (Basel)*. 2022 Mar 01; 14(5) PMID: 35267631.
 41. Grover P, Veilleux O, Tian L, **Sun R**, Previtera M, Curran E, Muffly L. Chimeric antigen receptor T-cell therapy in adults with B-cell acute lymphoblastic leukemia. *Blood Adv*. 2022 Mar 01; 6(5):1608-1618. PMID: 34610109.
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 43. Cherng HJ, **Sun R**, Sugg B, Irwin R, Yang H, Le CC, Deng Q, Fayad L, Fowler NH, Parmar S, Steiner R, Hagemester F, Nair R, Lee HJ, Rodriguez M, Samaniego F, Iyer SP, Flowers CR, Wang L, Nastoupil LJ, Neelapu SS, Ahmed S, Strati P, Green MR, Westin J. Risk assessment with low-pass whole-genome sequencing of cell-free DNA before CD19 CAR T-cell therapy for large B-cell lymphoma. *Blood*. 2022 Aug 01; 140(5):504-515. PMID: 35512184.
 44. Byun J, Han Y, Li Y, Xia J, Long E, Choi J, Xiao X, Zhu M, Zhou W, **Sun R**, Bossé Y, Song Z, Schwartz A, Lusk C, Rafnar T, Stefansson K, Zhang T, Zhao W, Pettit RW, Liu Y, Li X, Zhou H, Walsh KM, Gorlov I, Gorlova O, Zhu D, Rosenberg SM, Pinney S, Bailey-Wilson JE, Mandal D, de Andrade M, Gaba C, Willey JC, You M, Anderson M, Wiencke JK, Albanes D, Lam S, Tardon A, Chen C, Goodman G, Bojesen S, Brenner H, Landi MT, Chanock SJ, Johansson M, Muley T, Risch A, Wichmann HE, Bickeböllér H, Christiani DC, Rennert G, Arnold S, Field JK, Shete S, Le Marchand L, Melander O, Brunnstrom H, Liu G, Andrew AS, Kiemeny LA, Shen H, Zienoldiny S, Grankvist K, Johansson M, Caporaso N, Cox A, Hong YC, Yuan JM, Lazarus P, Schabath MB, Aldrich MC, Patel A, Lan Q, Rothman N, Taylor F, Kachuri L, Witte JS, Sakoda LC, Spitz M, Brennan P, Lin X, McKay J, Hung RJ, Amos CI. Cross-ancestry genome-wide meta-analysis of 61,047 cases and 947,237 controls identifies new susceptibility loci contributing to lung cancer. *Nat Genet*. 2022 Aug 01; 54(8):1167-1177. PMID: 35915169
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PUBLISHED
CORRESPONDENCE

1. **Sun R**, Horiguchi M, Wei LJ. Interpreting the Benefit of Trifluridine/Tipiracil in Metastatic Colorectal Cancer With Respect to Progression-Free Survival and Overall Survival. *J Clin Oncol*. 2018 May 01; 36(13):1378-1379. PMID: 29558278.

2. **Sun R**, Rich MW, Wei LJ. Pembrolizumab plus Chemotherapy in Lung Cancer. *N Engl J Med*. 2018 Sep 13; 379(11):e18. PMID: 30211499.

3. **Sun R**, Nie L, Huang B, Kim DH, Wei LJ. Quantifying Immunoscore performance. *Lancet*. 2018 Nov 03; 392(10158):1624. PMID: 30496077.

4. **Sun R**, Wei LJ. Regional Hyperthermia With Neoadjuvant Chemotherapy for Treatment of Soft Tissue Sarcoma. *JAMA Oncol*. 2019 Jan 01; 5(1):112-113. PMID: 30489612.

5. **Sun R**, Lee H, Wei LJ. Interpreting the Long-term Prognostic Value of Total Mesorectal Excision Plane Quality in Rectal Adenocarcinoma. *JAMA Surg*. 2019 Jan 01; 154(1):96. PMID: 30427976.

6. **Sun R**, Zhu H, Wei LJ. Assessing the Prognostic Value of the Automated Bone Scan Index for Prostate Cancer. *JAMA Oncol*. 2019 Feb 01; 5(2):270. PMID: 30543368.

7. Wei LJ, **Sun R**, Orkaby AR, Kim DH, Zhu H. Biodegradable-polymer stents versus durable-polymer stents. *Lancet*. 2019 May 11; 393(10184):1932-1933. PMID: 31084958.

8. **Sun R**, Kim DH, Wei LJ. Analysis of Overall Survival Benefit of Abemaciclib Plus Fulvestrant in Hormone Receptor-Positive, ERBB2-Negative Breast Cancer. *JAMA Oncol*. 2020 Jul 01; 6(7):1121-1122. PMID: 32463424.

9. **Sun R**, Messick C, Wei LJ. Two-Stage Turnbull-Cutait Pull-Through Coloanal Anastomosis for Low Rectal Cancers. *JAMA Surg*. 2021 Feb 01; 156(2):202-203. PMID: 33175112.

10. **Sun R**, Tian L, Wei LJ. Evaluating Long-term Efficacy of Neoadjuvant Chemoradiotherapy Plus Surgery for the Treatment of Locally Advanced Esophageal Squamous Cell Carcinoma. *JAMA Surg.* 2022 May 01; 157(5):458-459. PMID: 35080625.
11. **Sun R**, Wei, LJ. Pembrolizumab in Triple-Negative Breast Cancer. *N Engl J Med.* 2022 Oct 13; 387(15):1435-1436. PMID: 36239657.
12. **Sun R**, Wei LJ. Quantifying Clinical Utility of Adjuvant Abemaciclib in Patients With High-risk Early Breast Cancer Who Received Neoadjuvant Chemotherapy. *JAMA Oncol.* 2022 Nov 01; 8(11):1701. PMID: 36173642.
13. **Sun R**, Wei LJ. Quantifying Clinical Utility of Enzalutamide for Overall Survival in Metastatic Hormone-Sensitive Prostate Cancer. *J Clin Oncol.* 2022 Dec 20; 40(36):JCO2201084. PMID: 35985008.
14. **Sun R**, Huang B, Wei LJ. Comparing Short- and Long-Term Treatment Duration of Bevacizumab for Advanced Ovarian Cancer. *J Clin Oncol.* 2023 Apr 01; 41(10):1952-1953. PMID: 36763910.
15. **Sun R**, Wei LJ. Efficacy, Safety, and Analysis Issues in a Study of Intraoperative Hyperthermic Intraperitoneal Chemotherapy for Locally Advanced Colon Cancer. *JAMA Surg.* 2023 Dec 13; 158(12):1357-1358. PMID: 37585200.
16. **Sun R**, Seibert, TM, Wei, LJ. Predictability of Olfactory Neuroblastoma Staging Systems. *JAMA Otolaryngol Head Neck Surg.* 2024 Jan 11; 150(1):84-85. PMID: 37971764.
17. **Sun R**, Liu, J, Wei, LJ. Assessing Predictability of Pathologic Lymph Node Regression for Recurrence and Survival in Esophageal Adenocarcinoma. *J Clin Oncol.* 2024 Jan 20; 42(3):366-367. PMID: 37988644.
18. **Sun R** Wei, LJ. Is Pertuzumab Plus Trastuzumab Without Chemotherapy a Reasonable Treatment for ERBB2-Positive Metastatic Breast Cancer? *JAMA Oncol.* 2024 Apr 18; 10(4):537. PMID: 38329744.
19. **Sun R**, Moraleda JM, Wei LJ. Quantification of Treatment Effect of Tislelizumab vs Sorafenib for Hepatocellular Carcinoma. *JAMA Oncol.* 2024 May 01; 10(5):674. PMID: 38483380.
20. **Sun R**, Wei LJ. Benralizumab versus Mepolizumab for Eosinophilic Granulomatosis with Polyangiitis. *New England Journal of Medicine.* 2024 May 30; 390(20):1939. PMID: 38810203.
21. **Sun R**, Wei, LJ. Aspirin vs Placebo as Adjuvant Therapy for Breast Cancer. *JAMA.* 2024 Oct 01; 332(13):1112. PMID: 39235794.
22. **Sun R**, Seibert, TM, Wei, LJ. Pembrolizumab in Early-Stage Triple-Negative Breast Cancer. *New England Journal of Medicine.* 2025 Mar 13; 392(11):1141. PMID: 40073317.

PENDING AND
CURRENT FUNDING

1. **Principal Investigator**, Development of large-scale composite null hypothesis testing approaches to perform translational genetics analyses, NIH/NIGMS (PI: Ryan Sun), 1R35GM154843, 9/2024-8/2029, (\$1,250,000 direct costs)
2. **Core Co-Director**, Lymphoma Outcomes SPORE, NIH/NCI (PI: Christopher Flowers), U54CA302435, 8/2025-7/2030
3. **Core Co-Director**, Epigenetic basis and therapeutic targeting of the unique lymphoma immunological niche, NIH/NCI (PI: Christopher Flowers), 1P01CA272295, 10/2024-9/2029
4. **Core Co-Director**, Translating molecular profiles into treatment approaches to target disparities in lymphoma, Leukemia & Lymphoma Society (PI: Jean Koff), 7038-25, 10/2024-9/2029
5. **Co-Investigator**, A phase II and biomarker study of dual VEGF/PD-L1 blockade in neoadjuvant setting in resectable HCC patients, NIH/NCI (PI: Ahmed Kaseb), R01CA260872, 4/2021-3/2026
6. **Co-Investigator**, Functional characterization and rational therapeutic targeting of 18q DNA copy number gains in diffuse large B-cell lymphoma, NIH/NCI (PI: Michael Green), R01CA240839, 12/2020-11/2025

7. **Co-Investigator**, Roles of coactivator-associated arginine methyltransferase 1 in B cell activation and lymphomagenesis, NIH/NCI (PI: Margarida Santos), R01CA247883, 4/2021-3/2026
8. **Co-Investigator**, Targeting SMARCA4 mutations in pediatric Burkitt lymphoma, Cancer Prevention & Research Institute of Texas (PI: Michael Green), RP220208, 3/2022-2/2026
9. **Co-Investigator**, Therapeutic approaches for TGF-beta-enriched minimal residual disease in patients with colorectal cancer, Cancer Prevention & Research Institute of Texas (PI: Van Morris), RP220416, 3/2022-2/2025
10. **Co-Investigator**, Rescuing CD19 CAR T-cell therapy in DLBCL, Sanofi Pharmaceuticals (PI: Michael Green), 57754, 11/2021-1/2024
11. **Biostatistician**, Therapeutic targeting of multiple glioblastoma phagocytosis checkpoints using a novel bispecific antibody, NIH/NINDS (PI: Wen Jiang), R01NS117828, 6/2021-4/2026
12. **Co-Investigator**, Recruitment of established investigators, Cancer Prevention & Research Institute of Texas (PI: Christopher Flowers), RR190079, 8/2019-8/2024
13. **Co-Investigator**, Identifying/targeting mechanisms of lymphomagenesis driven by CREBBP inactivation, NIH/NCI (PI: Michael Green), R01CA201380, 4/2022-3/2027
14. **Co-Investigator**, Developing appendix cancer specific chemotherapy, Conquer Cancer Foundation (PI: J.P. Shen), 14192, 7/2022-6/2025
15. **Co-Investigator**, BAF complex deregulation in lymphoma, NIH/NCI (PI: Michael Green), R01CA266279, 8/2022-7/2027
16. **Co-Investigator**, Overcoming adaptive resistance to KRAS inhibition in colorectal cancer, NIH/NCI (PI: Scott Kopetz), R01CA262805, 4/2022-3/2027
17. **Co-Investigator**, Tumor cell lineage diversity and composition in gastric cancer progression and therapy resistance, NIH/NCI (PI: Linghua Wang), R01CA266280, 7/2022-6/2027
18. **Co-Investigator**, Targeting adaptive and acquired resistance to direct KRAS inhibition, Massachusetts General Hospital (PI: Scott Kopetz), FP00014745, 2/2022-1/2025
19. **Co-Investigator**, Role of DKK3 in triple negative breast cancer tumor progression and resistance to therapy, Department of Defense (PI: Rosa Hwang), W81XWH2210097, 3/2022-2/2028
20. **Co-Investigator**, Evaluation of a novel CD79b-targeting chimeric antigen receptor T-cell therapy in patients with relapsed/refractory B-cell lymphomas, Conquer Cancer Foundation (PI: Kunwha Kim), 7/2024-6/2025
21. **Biostatistician**, Listeriolysin O drives innate and adaptive immune responses to CD47 immunotherapy, Conquer Cancer Foundation (PI: Benjamin Schrank), 7/2024-6/2025
22. **Principal Investigator**, Innovative statistical analysis for genome-wide data with general interval-censored outcomes of oral health in childhood cancer survivors, NIH, R03DE029238
23. **Core Co-Director**, MD Anderson Cancer Center SPORE in gastrointestinal cancer, NIH/NCI (PI: Scott Kopetz),
24. **Co-Investigator**, Colorectal cancer molecular subtype assay development and validation, NIH/NCI (PI: Dipen Maru),
25. **Statistician**, Adaptive mutability in colorectal cancers treated with epidermal growth factor receptor inhibition, Conquer Cancer Foundation (PI: Madhulika Eluri)
26. **Co-Investigator**, Activating p53 for colorectal cancer prevention, NIH/NCI (PI: Xiangwei Wu)
27. **Co-Investigator**, Circulating tumor DNA-defined minimal residual disease in colorectal cancer, Cancer Prevention & Research Institute of Texas (PI: Arvind Dasari)
28. **Co-Investigator**, Microsimulation modeling to evaluate the clinical effectiveness of novel cancer therapies, Burroughs Wellcome Fund (PI: Christopher Flowers)

SELECTED
COMPLETED OR
RELINQUISHED
FUNDING SINCE
2020

29. **Co-Investigator**, Overcoming PARP inhibitor resistance in patients with breast cancer who have germline BRCA mutations, Cancer Prevention & Research Institute of Texas (PI: Banu Arun)
30. **Co-Investigator**, Longitudinal therapeutic monitoring of colorectal cancer patients using exosome-based liquid biopsies, NIH/NCI (PI: Anirban Maitra)
31. **Co-Investigator**, Vimentin phospho-malleability is critical for maintaining stemness and metastatic properties, NIH/NCI (PI: Mani Sendurai)
32. **Co-Investigator**, Targeting myeloid cells to mitigate immune effector cell-associated neurotoxicity syndrome in large B-cell lymphoma, NIH/NCI (PI: Paolo Strati)
33. **Co-Investigator**, The microbiota-immune axis and response to neoadjuvant chemotherapy in triple-negative breast cancer, Conquer Cancer Foundation (PI: Clinton Yam)
34. **Co-Investigator**, CD38 as a targetable antigen in large B cell lymphoma to improve the efficacy of CD19 directed chimeric antigen receptor T cell therapy and mitigate CD19 negative relapse, Conquer Cancer Foundation (PI: Patrick Reville)
35. **Co-Investigator**, Strategic alliance agreement, Allogene Therapeutics (PI: Michael Green)
36. **Biostatistician**, Minimal residual disease assessment in colorectal cancer, Guardant Health (PI: Christine Parseghian)
37. **Biostatistician**, MD Anderson oropharynx program biostatistics and data integration grant, Stiefel Research Fund (PI: Jack Lee)
38. **Biostatistician**, Strategic alliance agreement, Kite Pharma Inc (PI: Michael Green)
39. **Co-Investigator**, WRN inhibition in microsatellite instability high colorectal cancer, Conquer Cancer Foundation (PI: Deepak Bhamidipati)
40. **Co-Investigator**, Tracking alloreactive T-cells to improve efficacy of allogeneic CAR T-cell therapy, Conquer Cancer Foundation (PI: Andrew Jallouk)
41. **Co-Investigator**, Prediction of treatment failure following CD19 CAR T-cell therapy in large B-cell lymphoma by measurement of circulating tumor DNA, Conquer Cancer Foundation (PI: Hua-Jay Cherng)
42. **Biostatistician**, Breast Cancer Moon Shot, MD Anderson Moonshot Program (PI: Stacy Moulder)
43. **Co-Investigator**, Clinical correlations of ctDNA in locally advanced rectal cancer, Conquer Cancer Foundation (PI: Andrew Pellatt)
44. **Co-Investigator**, Targeting aggressive NK-cell leukemia and other CD94-expressing NK/T-cell lymphoproliferative disorders with CAR T-cell therapy, Conquer Cancer Foundation (PI: Owhofasa Agbedia)
45. **Co-Investigator**, ASH Minority Hematology Fellow Award, American Society of Hematology (PI: Owhofasa Agbedia)
46. **Co-Investigator**, Validation of biomarkers of autophagic flux in patients with RAS mutant tumors, Conquer Cancer Foundation (PI: Jason Henry)
47. **Co-Investigator**, Implementation of a geriatric care survivorship intervention in older adults who have completed curative intent therapy for early-stage breast cancer, MD Anderson IRG (PI: Meghan Karuturi)

INVITED TALKS

Testing for gene-environment interaction under misspecification of the environment. Harvard School of Public Health Program in Genetic Epidemiology and Statistical Genetics. Boston, Massachusetts. April 2016.

Pathway analysis and gene-based inference in genomic data with the Generalized Berk-Jones statistic. Harvard T.H. Chan School of Public Health P01 Environmental Statistics Retreat. Wellesley, Massachusetts. October 2016.

Set-based tests using the Generalized Berk-Jones statistic in genetic association studies. Broad Institute Statistical Genetics Meeting. Boston, Massachusetts. January 2017.

Set-based tests using the Generalized Berk-Jones statistic in genetic association studies. Channing Division of Network Medicine Statistical Genetics and Networks Science Meeting. Boston, Massachusetts. January 2017.

Methods for high-dimensional inference in genetic association studies. University of New Hampshire Statistics Graduate Seminar. Durham, New Hampshire. May 2017.

The role of inflammation pathways in lung cancer and coronary artery disease. Broad Institute Statistical Genetics Meeting. Boston, Massachusetts. October 2017.

A unified framework for composite null inference in mediation, pleiotropy, and replicability analyses related to genetic association studies. Harvard T.H. Chan School of Public Health P01 Environmental Statistics Retreat. Boston, Massachusetts. October 2017.

A unified framework for composite null inference in mediation, pleiotropy, and replicability analyses related to genetic association studies. Harvard School of Public Health Program in Genetic Epidemiology and Statistical Genetics. Boston, Massachusetts. February 2018.

Set-based tests using the Generalized Berk-Jones statistic in genetic association studies. Jilin University School of Mathematics Statistics Colloquium. Changchun, Jilin, China. May 2018.

Identification of inflammation and immune-related risk variants associated with squamous cell lung cancer. International Lung Cancer Consortium Annual Meeting. Toronto, Ontario, Canada. September 2018.

Set-based inference for analysis of genetic compendiums (cancelled due to COVID19). Georgia State University 8th Workshop on Biostatistics and Bioinformatics. Atlanta, Georgia. May 2020.

Set-based inference for analysis of genetic compendiums (cancelled due to COVID19). International Chinese Statistical Association China Conference. Wuhan, China. July 2020.

Set-based inference for analysis of genetic compendiums (given online due to COVID19). Statistics Department Seminar, University of Haifa. Haifa, Israel. July 2020.

Set-based inference for analysis of genetic compendiums (given online due to COVID19). Human Genetics Center Seminar, UTHealth School of Public Health. Houston, Texas. October 2020.

Inference for set-based effects in genetic association studies with interval-censored outcomes. Conference of Texas Statisticians. Zoom. October 2021.

Strategies for performing set-based inference in modern genetics studies. Biostatistics Department Seminar, UTHealth School of Public Health. Zoom. October 2021.

Projecting omic data into clinical studies: vignettes from statistical analysis of ctDNA, germline, tumor sequencing, and similar data. University of Texas MD Anderson Data Science & Modeling Forum. Zoom. October 2021.

Strategies for performing set-based inference in modern genetics studies. Biostatistics Department Seminar, University of Nebraska Medical Center. Zoom. February 2022.

Strategies for performing set-based inference in modern genetics studies. Statistics Department Seminar, University of Toronto. Zoom. March 2022.

Conditionally symmetric multidimensional gaussian mixtures for testing composite null hypotheses in genetic association studies. Statistics Department Seminar, Southwestern University of Finance and Engineering China. Zoom. May 2022.

Conditionally symmetric multidimensional gaussian mixtures for testing composite null hypotheses in genetic association studies. Statistics Department Seminar, Texas A&M University. April 2023.

Differences in set-based tests for sparse alternatives when testing sets of outcomes compared to sets of explanatory factors in genetic association studies. Joint Statistical Meetings. Toronto, Ontario, Canada. August 2023.

Bayesian variable selection for interval-censored outcomes in genetic association studies. CMStatistics 2023. Berlin, Germany. Zoom. December 2023.

Interpretable large-scale testing of composite null hypotheses for translational genetics studies in modern biobanks. OHSU Biostatistics Seminar. Portland, Oregon. January 2024.

Interpretable large-scale testing of composite null hypotheses for translational genetics studies in modern biobanks. Georgetown University Medical Center Bio3 Seminar. Washington DC. February 2024.

Interpretable large-scale testing of composite null hypotheses for translational genetics studies in modern biobanks. University of Maryland Biostatistics & Epidemiology Seminar. College Park, Maryland. March 2024.

Interpretable large-scale testing of composite null hypotheses for translational genetics studies in modern biobanks. The 9th Workshop on Biostatistics & Bioinformatics. Atlanta, Georgia. May 2024.

Interpretable large-scale testing of composite null hypotheses for translational genetics studies in modern biobanks. Mediation Days. Montreal, Quebec, Canada. September 2024.

Interpretable large-scale testing of composite null hypotheses for translational genetics studies in modern biobanks. Department of Mathematics and Statistical Sciences Seminar. Milwaukee, Wisconsin. April 2025.

Interpretable large-scale testing of composite null hypotheses for translational genetics studies in modern biobanks. Joint Statistical Meetings. Nashville, Tennessee. August 2025.

CONTRIBUTED
TALKS AND
POSTERS

Testing for gene-environment interaction under misspecification of the environment. Joint Statistical Meetings. Seattle, Washington. August 2015.

Testing for gene-environment interaction under misspecification of the environment. International Chinese Statistical Association - Canada Chapter Statistics and Data Science Symposium. Calgary,

Alberta. August 2015.

Testing for gene-environment interaction under misspecification of the environment. Superfund Research Program Annual Meeting. San Juan, Puerto Rico. November 2015.

The Generalized Berk-Jones statistic for SNP-set tests in genetic association studies. Eastern North Atlantic Region Spring Meeting. Austin, Texas. March 2016.

The Generalized Berk-Jones statistic for SNP-set tests in genetic association studies. Joint Statistical Meetings. Chicago, Illinois. August 2016.

Pathway analysis and gene-based inference in genomic data with the Generalized Berk-Jones statistic. Harvard T.H. Chan School of Public Health Program in Quantitative Genomics Conference. Boston, Massachusetts. November 2016.

Set-based tests using the Generalized Berk-Jones statistic in genetic association studies. Eastern North Atlantic Region Spring Meeting. Washington, District of Columbia. March 2017.

Set-based tests using the Generalized Berk-Jones statistic in genetic association studies. Joint Statistical Meetings. Baltimore, Maryland. August 2017.

A unified framework for inference in mediation, pleiotropy, and replicability analyses related to genetic association studies. Joint Statistical Meetings. Vancouver, British Columbia, Canada. August 2018.

Inference for set-based effects in genetic association studies with interval-censored outcomes. Joint Statistical Meetings. Zoom. August 2021.

PROFESSIONAL
SERVICE

Associate Editor, *Scientific Reports*, 2023-
Associate Editor, *Statistics in Biosciences*, 2023-
Member of Program Committee, 12th International Chinese Statistical Association International Conference, Hong Kong, 2023
Member of Program Committee, 2022 International Chinese Statistical Association China Conference, Xian, China, 2020
Member of Local Organizing Committee, 2020 International Chinese Statistical Association Applied Statistics Symposium, Houston, 2020
Invited Session Organizer, Eastern North Atlantic Region Biometrics Conference, Nashville, 2020
Section Chair, Methods for Single Cell Genomic Analysis, Joint Statistical Meetings, Baltimore, 2017

REVIEWER

Annals of Applied Statistics, Bioinformatics, Biometrics, bmjOpen, Clinical Cancer Research, Frontiers in Genetics, Journal of the American Statistical Association, Journal of the Royal Statistical Society Series C, Molecular Genetics and Genomics, Molecular Psychiatry, Nature Communications, Nature Medicine, npj Schizophrenia, npj Systems Biology, Nucleic Acids Research Genomics and Bioinformatics, PeerJ, PLOS Genetics, Scientific Reports, Statistics in Biosciences, Statistics in Medicine, Statistical Methods in Medical Research

INSTITUTIONAL
SERVICE

MD Anderson Graduate School of Biomedical Sciences Admissions Committee, 2022-2023
MD Anderson Department of Biostatistics Visiting Guest Lecturer Committee, 2021-
MD Anderson ARTEMIS Breast Cancer Resource Committee, 2021-
MD Anderson Breast Cancer Moonshot Steering Committee, 2021-2023
MD Anderson Lymphoma/Myeloma IEC Steering Committee, 2020-
MD Anderson Scientific Review Committee, 2020-

MD Anderson Graduate School of Biomedical Sciences Curriculum Committee, 2020-2021
MD Anderson Graduate School of Biomedical Sciences Quantitative Sciences Committee, 2019-
MD Anderson Young Faculty Committee, 2019-
Co-organizer, Program in Quantitative Genomics Seminar, 2018-2019
Owner and Administrator, Harvard Biostatistics Department Slack Messaging Space, 2017-2019
Mentor, Harvard StatStart and Harvard Summer Program in Biostatistics and Computational Biology, 2015-2018

TEACHING

Course Director:

- MDACC Survival Analysis, Spring 2021
- MDACC Survival Analysis, Spring 2023

Instructor:

- Harvard Biostatistics Summer Course in Real Analysis, Summer 2017

SOFTWARE PACKAGES

ICSKAT: An R package for performing the interval-censored sequence kernel association test, interval-censored burden test, and interval-censored sequence kernel association test-optimal in genetic association studies.

GBJ: An R package for calculating the Generalized Berk-Jones statistic and its p-value. Also provides test statistic and corrected p-value for Higher Criticism, Generalized Higher Criticism, and Berk-Jones statistics when factors in a set are correlated.

GEint: An R package to calculate the exact bias of interaction coefficients in misspecified gene-environment interaction models. Also implements the Bootstrap Inference with Corrected Sandwich (BICS) procedure for testing of gene-environment interaction terms in generalized linear models.

reconstructKM: An R package to reconstruct individual-level patient data from Kaplan-Meier curves published in academic journals.

GOFexactPvalue: A C++ binary to calculate the exact p-value of Goodness-of-Fit statistics (Higher Criticism, Generalized Berk-Jones, etc.) when there are only a small number (less than 10) of correlated factors in a set.

PHD THESIS PRIMARY MENTORSHIP

Jaihee Choi, Rice University Statistics PhD Primary Advisor (2020-2024)
Current Position: Tenure-Track Assistant Professor, Department of Mathematical & Statistical Sciences, Marquette University)
Naishu Kui, UTHealth Biostatistics PhD Primary Advisor (2022-)
Emily Oppold, Rice University Statistics PhD Primary Advisor (2024-)
Co-Mentored with Dr. Christine Peterson

OTHER MENTORSHIP

Jessica Valdebenito, UTHealth GSBS PhD Candidacy Exam Committee (2022-2022)
JingJing Cao, UTHealth GSBS PhD Thesis Committee (2022-)
Zhichao Xu, UTHealth GSBS PhD Thesis Committee (2022-)
Hayden Scott, UTHealth GSBS MS/PhD Thesis Committee (2021-)
Xiaoyun Cheng, UTHealth GSBS MS Thesis Committee (2021-2023)
Shu-Hsien Cho, UTHealth GSBS PhD Thesis Committee (2020-)
Carlos Vera Rocio, UTHealth GSBS MS Thesis Committee (2020-2022)
Vahid Bahrambeigi, UTHealth GSBS PhD Thesis Committee (2020-2024)
Ziqiao Wang, UTHealth GSBS PhD Thesis Committee (2019-2022)
Chao Yang, UTHealth GSBS PhD Thesis Committee (2019-2024)