

Ryan Sun

CONTACT INFORMATION

Department of Biostatistics
University of Texas M.D. Anderson Cancer Center
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Houston, Texas 77030

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Website: <https://ryansun.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

PROFESSIONAL EXPERIENCE

Empiric Asset Management, New York, New York

Analyst

May 2011 - May 2012

Quantitative analyst for hedge fund with equity market neutral strategy.

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

Rice University, Houston, Texas

Adjunct Assistant Professor, Department of Statistics

July 2020 - Present

University of Texas MD Anderson Cancer Center, Houston, Texas

Assistant Professor, Department of Biostatistics

July 2019 - Present

Harvard School of Public Health, Boston, Massachusetts

Postdoctoral Research Fellow

May 2017 - June 2019

Develop 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.

Sun, R.*, Bouchard, M.B.*, and Hillman, E.M.C. SPLASSH: Open source software for camera-based high-speed, multispectral in-vivo optical image acquisition. *Biomedical Optics Express* 2010; 1(2): 385-397.

Wang, Z., Claus-Henn, B., Wang, C., Wei, Y., Su, L., **Sun, R.**, Chen, H., Wagner, P.J., Lu, Q., Lin, X., Wright, R., Bellinger, D., Kile, M., Mazumdar, M., Tellez-Rojo, M.M., Schnaas, L., and Christiani, D.C. Genome-wide gene by Pb exposure interaction analysis identifies UNC5D as a candidate gene for neurodevelopment. *Environmental Health* 2017; 16(1): 81.

Sun, R., Carroll, R.J., Christiani, D.C., and Lin, X. Testing for gene-environment interaction under exposure misspecification. *Biometrics* 2018; 74(2): 653-662.

Orkaby, A., Rich, M.W., **Sun, R.**, Lux, E., Wei, L.J., and Kim, D.H. Pravastatin for primary prevention in older adults: restricted mean survival time analysis. *Journal of the American Geriatrics Society* 2018; 66(10): 1987-1991.

Sun, R., Wang, Z., Claus Henn, B., Su, L., Lu, Q., Lin, X., Wright, R., Bellinger, D., Kile, M., Mazumdar, M., Tellez-Rojo, M.M., Schnaas, L., and Christiani, D.C. Identification of novel loci associated with infant cognitive ability. *Molecular Psychiatry* 2018; 1-10.

Sun, R., Hui, S., Bader, G., Lin, X., and Kraft, P. Powerful gene set analysis in GWAS with the Generalized Berk-Jones statistic. *PLOS Genetics* 2019; 15(3): e1007530.

Gaynor S.*, **Sun, R.***, Lin, X., and Quackenbush, J. Identification of differentially expressed gene sets using the Generalized Berk-Jones statistic. *Bioinformatics* 2019; 35(22): 4568-4576.

Sun, R. and Lin, X. Set-based tests for genetic association using the Generalized Berk-Jones statistic. *Journal of the American Statistical Association* 2020; 115(53): 1079-1091.

Park, H-R., Panganibana, R.A., **Sun, R.**, Shumyatcher, M., Himes, B.E., Christiani, D.C., and Lu, Q. MicroRNA-124 protects neural cells against arsenic-induced endoplasmic reticulum stress and cytotoxicity in vitro and is associated with neurodevelopmental outcomes in children. *Scientific Reports* 2020; 10(1):1-11.

Li, X., Li, Z., Zhou, H., Gaynor, S., Liu, Y., Chen, H., **Sun, R.**, ..., Lin, X. Dynamic incorporation of multiple in-silico functional annotations empowers rare variant association analysis of large whole genome sequencing studies at scale. *Nature Genetics* 2020; 52(9):969-983.

Colina, A., Hwang, H., Wang, H., Katz, M., **Sun, R.**, Lee, J., Tzeng, C., Wolff, R., Raghav, K., Overman, M. Green, M.R. Natural history and prognostic factors for localized small bowel adenocarcinoma. *ESMO Open* 2020; 5(6):e000960.

Deng, Q., Han, G., Puebla-Osorio, N., Ma, M.C.J., Strati, P., Chasen, B., Dai, E., Dang, M., Jain, N., Yang, H., Wang, Y., Zhang, S., Wang, R., Chen, R., Showell, H., Ghosh, S., Patchva, S., Zhang, Q., **Sun, R.**, ..., Green, M.R. Characteristics of anti-CD19 CAR T-cell infusion products associated with efficacy and toxicity in patients with large B-cell lymphomas. *Nature Medicine* 2020; 26(12): 1878-1887.

Zhu, L., Cai, D., Li, Y., Tong, X., **Sun, R.**, Srivastava, D., Hudson, M. Maximum likelihood estimation for the proportional odds model with mixed interval-censored failure time data. *Journal of Applied Statistics* 2021; 48(8):1496-1512.

Sun, R., Xu, M., Li, X., Gaynor, S., Zhou, H., Bossé, Y., Lam, S., Tsao, M., Tardon, A., Chen, C., Doherty, J., Goodman, G., Egil Bojesen, S., Teresa, M.T., Johansson, M., Field, J.K., Bickeböllner,

H, Wichmann, H., Risch, A., Rennert, G., Arnold, S., Wu, X., Melander, O., Brunnström, H., Marchand, L.L., Zong, X., Liu, G., Andrew, A., Duell, E., Kiemeny, L.A., Shen, H., Haugen, A., Johansson, M., Grankvist, K., Caporaso, N., Woll, P., Teare, M.D., Scelo, G., Hong, Y., Yuan, J., Lazarus, P., Schabath, M.B., Aldrich, M.C., Albanes, D., Brennan, P., Barbie, D., Mak, R., Hung, R.J., Amos, C.I., Christiani, D.C., Lin, X. Identification of inflammation and immune-related risk variants associated with squamous cell lung cancer. *Genetic Epidemiology* 2021; 45(1):99-114.

Kim, D., Li, X., Bian, S., Wei, L.J. , **Sun, R.** Utility of restricted mean survival time for analyzing time to nursing home placement among patients with dementia. *JAMA Network Open* 2021; 4(1):e2034745.

Strati, S., Ahmed, S., Furqan, F., ..., **Sun, R.**, Claussen, C., Hawkins, M., Johnson, N., Singh, P., Mistry, H., Johny, S., Adkins, S., Kebriaei, P., Shpall, E., Green, M., Flowers, C., Westin, J., Neelapu, S. Prognostic impact of corticosteroids on efficacy of chimeric antigen receptor t-cell therapy in large b-cell lymphoma. *Blood, The Journal of the American Society of Hematology* 2021; 137(23):3272-3276.

Alhalabi, O., Soomro, Z., **Sun, R.**, Hasanov, E., Albittar, A., Tripathy, D., Valero, V., Ibrahim, N. Outcomes of changing systemic therapy in patients with relapsed breast cancer and 1 to 3 brain metastases. *NPJ Breast Cancer* 2021; 7(1):1-5.

Yam, C., Rauch, G., Rahman, T., Karuturi, M., Ravenberg, E., White, J., Clayborn, A., McCarthy, P., Abouharb, S., Lim, B., Litton, J., Ramirez, D., Saleem, S., Stec, J., Symmans, W., Huo, L., Damodaran, S., **Sun, R.**, Moulder, S. A phase II study of mirvetuximab soravtansine in triple-negative breast cancer. *Investigational New Drugs* 2021; 39(2):509-515.

Han, G., Yang, G., Hao, D., Lu, Y., Thein, K., Chen, J., **Sun, R.**, ..., Wang, L. 9p21 loss confers a cold tumor immune microenvironment and primary resistance to immune checkpoint therapy. *Nature Communications* 2021; 12(1):1-19.

Xu, M., Tapia, C., Hajjar, J., ..., **Sun, R.**, Karp, D., Koay, E., Yang, Y., Wistuba, I., Hwu, P., Meric-Bernstam, F., Naing, A. Implementation of a novel web-based lesion selection tool to improve acquisition of biopsies. *Journal of Immunotherapy and Precision Oncology* 2021; 4(2):45-52.

Yam, Y., Yen, E., Chang, T., ..., **Sun, R.**, Moulder, S., Mittendorf E. Immune phenotype and response to neoadjuvant therapy in triple-negative breast cancer. *Clinical Cancer Research* 2021; 27(19):5356-5375.

Sun, R.*, McCaw, Z.*, Tian, L., Uno, H., Hong, F., Kim, D., Wei, L.J. Moving beyond conventional stratified analysis to assess the treatment effect in a comparative oncology study. *Journal for Immunotherapy of Cancer* 2021; 9(11):e003323.

Kaseb, A., Hasanov, E., Cao, H., ..., **Sun, R.**, Vittorio, C., Beretta, L., Yao, J., Wolff, R., Allison, J., Sharma, P. Perioperative nivolumab monotherapy plus ipilimumab in resectable hepatocellular carcinoma. *The Lancet Gastroenterology & Hepatology* 2022+ (in press).

Li, Y., Xiao, X., Li, J., ..., **Sun, R.**, ..., Willey, J., Gaba, C., Amos, C. Genome-wide interaction analysis identified low-frequency variants with sex disparity in lung cancer risk. *Human Molecular Genetics* 2022+ (in press).

Grover, P., Veilleux O., Tian, L., **Sun, R.**, Previtiera, M., Curran, E., Muffly, L. Chimeric antigen receptor-T cell therapy in adults with B-cell acute lymphoblastic leukemia: a systematic review. *Blood Advances* 2022+ (in press).

McCaw, Z., Gaynor, S., **Sun, R.**, Lin X. Cross-tissue eQTL mapping in the presence of missing data via surrogate outcome analysis. *Biometrics* 2022+ (in press).

Li, X., Yung G., Zhou H., **Sun, R.**, Li, Z., Liu X., Ionita-Laza, I., Lin X. A multi-dimensional integrative scoring framework for predicting functional variants in the human genome. *American Journal of Human Genetics* 2022+ (in press).

Sun, R., Liang, Z., Li, Y., Yutaka, Y., Robison, L. Inference for set-based effects in genetic association studies with interval-censored outcomes. *Biometrics* 2022+ (in press).

Yam, C.,* Abuhadra, N.,* **Sun, R.**,* Ding, Q., ..., Huo, L., Moulder, S., Chang, J. Molecular characterization and prospective evaluation of pathological response and outcomes with neoadjuvant therapy in metaplastic triple-negative breast cancer. *Clinical Cancer Research* 2022+ (in press).

Cherng, H.J., **Sun, R.**, Sugg, B., Yang, H., Irwin, R., Deng, Q., Fayad, L., Fowler, N., Parmar, S., Steiner, R., Hagemester, F., Nair, R., Lee, H.J., Rodriguez, M., Samaniego, F., Iyer, S., Flowers, C., Wang, L., Nasoupi, L.J., Neelapu, S.S., Ahmed, S., Strati, P., Green, M.R., Westin, J. A simple, minimally invasive approach for pre-treatment risk stratification of large B-cell lymphoma patients receiving CD19 CAR T-cell therapy. *Blood* 2022+ (in press).

Huang, B.,* **Sun, R.**,* Claggett, B., Tian, L., Ludmir, E.B., Wei, L.J. *JAMA Oncology* 2022+ (in press).

Sun, R., Shi, A., Lin, X. Differences in genetic set-based inference for sparse signals when testing sets of outcomes compared to sets of explanatory factors. *Biostatistics* 2022+ (in press).

Li, X., Quick C., Zhou, H., Gaynor, S.M., Lu, Y., Chen, H., **Sun, R.**, ..., Lin, X. Powerful, scalable and resource-efficient meta-analysis of rare variant associations in large whole-genome sequencing studies. *Nature Genetics* 2022+ (in press).

Li, Z., Li, X., Zhou, H., Gaynor, S.M., Selvaraj, M.S., Arapoglou, T., Quick, C., Liu, Y., Chen, H., **Sun, R.**, ..., Lin, X. A framework for detecting noncoding rare variant associations of large-scale whole-genome sequencing studies. *Nature Genetics* 2022+ (in press).

Byun, J., Han, Y., Li, Y., Xia, J., Xiao, X., **Sun, R.**, ..., Amos, C. Trans-ethnic genome-wide meta-analysis of 35732 cases and 34424 controls identifies novel genomic cross-ancestry loci contributing to lung cancer susceptibility. *Nature Genetics* 2022+ (in press).

Westin, J., Davis, R., Feng, L., ..., **Sun, R.**, Scott, D., Flowers, C., Neelapu, S., Green, M.R. SmartStart: rituximab, lenalidomide, and ibrutinib in large B-cell lymphoma. *Journal of Clinical Oncology* 2022+ (in press).

PUBLISHED
CORRESPONDENCE

Sun, R., Horiguchi, M., and Wei, L.J. Interpreting the benefit of trifluridine/tipiracil in metastatic colorectal cancer with respect to progression-free survival and overall survival. *Journal of Clinical Oncology* 2018; 36(13): 1378.

Sun, R., Rich, M.W., and Wei, L.J. Pembrolizumab plus chemotherapy in lung cancer. *New England Journal of Medicine* 2018; 379(11): e18.

Sun, R., Nie, L., Huang, B., Kim, D.H., and Wei, L.J. Quantifying immunoscore performance. *The Lancet* 2018; 392(10158): 1624.

Sun, R. and Wei, L.J. Regional Hyperthermia With Neoadjuvant Chemotherapy for Treatment of Soft Tissue Sarcoma. *JAMA Oncology* 2019; 5(1): 112-113.

Sun, R., Zhu, H., and Wei, L.J. Assessing the prognostic value of automated bone scan index in prostate cancer. *JAMA Oncology* 2019; 5(2): 270.

Sun, R., Orkaby, A.O., Kim, D.H., Zhu, H., and Wei, L.J. Interpreting non-inferiority of biodegradable-polymer stents to durable-polymer stents. *The Lancet* 2019; 393(10184): 1932-1933.

Sun, R., Lee, H., and Wei, L.J. Interpreting the long-term prognostic value of total mesorectal excision plane quality in rectal adenocarcinoma. *JAMA Surgery* 2019; 154(1):96.

Sun, R., Kim, D.H., and Wei, L.J. Analysis of overall survival benefit of abemaciclib plus fulvestrant in hormone receptor-positive, ERBB-2 negative breast cancer. *JAMA Oncology* 2020; 6(7):1121-1122.

Sun, R., Messick, C., and Wei, L.J. Two-stage turnbull-cutait pull-through coloanal anastomosis for low rectal cancers. *JAMA Surgery* 2021;156(2):202-203.

Sun, R., Tian, L., and Wei, L.J. Evaluating long-term efficacy of neoadjuvant chemoradiotherapy plus surgery for the treatment of locally advanced esophageal squamous cell carcinoma. *JAMA Surgery* 2022+.

Sun, R. and Wei, L.J. Quantifying clinical utility of enzalutamide for overall survival in metastatic hormone-sensitive prostate cancer. *Journal of Clinical Oncology* 2022+.

Sun, R. and Wei, L.J. Quantifying clinical utility of adjuvant abemaciclib in patients with high-risk early breast cancer who received neoadjuvant chemotherapy. *JAMA Oncology* 2022+.

SUBMITTED PAPERS **Sun, R.**, Sun, D., Liang, Z., Sun, J. Regression analysis of general mixed recurrent event data.

Parseghian, C.,* **Sun, R.**,* Woods, M.,* Napolitano, S.,* Nunez, S., Sorokin, A., Kanikarla, P., Eluri, M., Morris, V.K., Willis, J., Evilar, E., Rehn, M., Ang, A., Troiani, T., Kopetz, S. Acquired alterations are rare after first line therapy with anti-EGFR therapy.

*Indicates equal contribution as first authors.

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. International Chinese Statistical Association China Conference. Zoom. July 2022.

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

Program Committee, International Chinese Statistical Association China Conference Hong Kong, 2022
Program Committee, International Chinese Statistical Association China Conference Wuhan, 2020
Local Committee, 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 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, npj Schizophrenia, npjSystems Biology, Nucleic Acids Research Genomics and Bioinformatics, PeerJ, PLOS Genetics, Scientific Reports, Statistics in Biosciences, Statistics in Medicine

INSTITUTIONAL
SERVICE

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-
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 Graduate School of Biomedical Sciences Biostatistics Admissions Subcommittee, 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

Instructor:

- Harvard Biostatistics Summer Course in Real Analysis, Summer 2017

Teaching Assistant:

- HSPH BIST245 Analysis of Multivariate and Longitudinal Data
- HSPH BIST232 Statistical Methods II (Distinction in Teaching award)
- HSPH BIST230 Probability Theory and Applications I (Distinction in Teaching award)
- HSPH BIO210 Rates and Proportions

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.

GOExactPvalue: 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.

MENTORSHIP

Zhichao Xu, UTHealth GSBS Rotation Student (2022-)
Hayden Scott, UTHealth GSBS MS Thesis Committee (2021-)
Xiaoyun Cheng, UTHealth GSBS MS Thesis Committee (2021-)
Jaihee Choi, Rice University Statistics PhD Research (2020-)
Shu-Hsien Cho, UTHealth GSBS PhD Thesis Committee (2020-)
Carlos Vera Rocio, UTHealth GSBS PhD Thesis Committee (2020-)
Vahid Bahrambeigi, UTHealth GSBS PhD Thesis Committee (2020-)
Ziqiao Wang, UTHealth GSBS PhD Thesis Committee (2019-)
Chao Yang, UTHealth GSBS PhD Thesis Committee (2019-)
Mengting Li, Harvard Biostatistics MS Thesis Committee (2018)

PATENTS

SPLASSH: Open source software for camera-based high-speed, multispectral in-vivo optical image acquisition.