# Chong Wu

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## RESEARCH INTERESTS

Statistical genomics (TWAS, GWAS, multi-omics, integrative analysis, polygenic risk score)
Machine learning (unsupervised learning, supervised learning)
Causal inference (Mendelian randomization, instrumental variables regression)

## EMPLOYMENT

**Assistant Professor** Sept. 2022–Present
Department of Biostatistics, The University of Texas MD Anderson Cancer Center

**Assistant Professor** Aug. 2018–Aug. 2022
Department of Statistics, Florida State University

## EDUCATION

**University of Minnesota** Minneapolis, MN
**Ph.D., Biostatistics** Jun. 2018
Advisors: Drs. Weihua Guan & Wei Pan
Thesis: Statistical methods for high-dimensional genetic and genomic data

**Huazhong University of Science & Technology** Wuhan, China
**B.S., Applied Mathematics** Jun. 2013
Advisor: Dr. Xiaoyang Zhou

## PEER-REVIEWED ARTICLES

* Corresponding author; † Co-first author; ‡ Students advised by C Wu

### —Theory & Methods

1. Meng, Z.‡, **Wu, C.***, & Lin, L*. (2022). The effect direction should be taken into account when assessing small-study effects. *Journal of Evidence-Based Dental Practice*, 101830.
2. Guo, X., Wei, W., Liu, M., Cai, T., **Wu, C.**, & Wang, J. (2022+). Assessing heterogeneous risk of type 2 diabetes associated with statins usage: Evidence from electronic health record data. *Journal of the American Statistical Association*, Accepted.
3. Ma, X., Wang, J., & **Wu, C.** (2022+). Breaking the winner's curse in Mendelian randomization: Rerandomized inverse variance weighted estimator. *Annals of Statistics*, Accepted. (Alphabetical order)
4. Song, M., Greenbaum, J., IV J., Zhou, W. **Wu, C.**, ..., Deng, HW., Zhang, C. (2022). An autoencoder-based deep learning method for genotype imputation. *Frontiers in Artificial Intelligence*, 5:1028978. (Highlights from the MCBIOS 2022 Conference.)
5. Wei, W., Laan, M., **Wu, C.***, & Wang, J.* (2022+). Efficient targeted learning of treatment

effects for multiple subgroups in observational studies. *Biometrics*, accepted.
(An earlier version won the Best Presentation and Best Student Paper Awards, Nonparametric Statistics Section, American Statistics Association.)

6. Zhang, Z.‡, Bae, Y.‡, Bradley, J., Wu, L, & **Wu, C.*** (2022). SUMMIT: An integrative approach for better transcriptomic data imputation improves causal gene identification. *Nature Communications*, 13, 6336.
(An earlier version won a poster talk (top 10% of all posters) and Reviewers' Choice at ASHG 2021).
7. He, Y., Xu, G., **Wu, C.**, & Pan, W. (2021). Asymptotically independent U-statistics in high-dimensional testing. *Annals of Statistics*, 49(1), 154–181.
8. **Wu, C.***, Bradley, J., Li, Y., Wu, L., & Deng, H. (2021). A gene-level methylome-wide association analysis identifies novel Alzheimer's disease genes. *Bioinformatics*, 37(14), 1933–1940.
9. Bae Y.‡, Wu, L., & **Wu, C.*** (2021). InTACT: An adaptive and powerful framework for joint-tissue transcriptome-wide association studies. *Genetic Epidemiology*, 45(8), 848–859.
(Editor's pick paper for Issue 8)
10. **Wu, C.***, Xu, G., Shen, X., & Pan, W.* (2020). A regularization-based adaptive test for high-dimensional generalized linear models. *Journal of Machine Learning Research*, 21, 1–67.
(An earlier version won the 2019 ENAR Distinguished Student Paper Award.)
11. Xue, H., **Wu, C.**, & Pan, W. (2020). Leveraging existing GWAS summary data to improve power for a new GWAS. *Genetic Epidemiology*, 44(7), 717–732.
12. **Wu, C.** (2020). Multi-trait genome-wide analyses of the brain imaging phenotypes in UK Biobank. *Genetics*, 215(4), 947–958.
(This paper won a platform presentation at the American Society of Human Genetics (ASHG) 2019 Annual Meeting; highlighted in *Genetics* August issue)
13. Yang, T., **Wu, C.**, Wei, P., & Pan, W. (2020). Integrating DNA sequencing and transcriptomic data for association analyses of low-frequency variants and lipid traits. *Human Molecular Genetics*, 29(3), 515–526.
14. Yang, T., Kim, J., **Wu, C.**, Ma, Y., Wei, P., & Pan, W. (2020). An adaptive test for meta-analysis of rare variant association studies. *Genetic Epidemiology*, 44(1), 104–116.
15. **Wu, C.***, & Pan, W.* (2020). A powerful fine-mapping method for transcriptome-wide association studies. *Human Genetics*, 139, 199–213.
16. **Wu, C.***, & Pan, W.* (2019) Integration of methylation QTL and enhancer-target gene maps with schizophrenia GWAS summary results identifies novel genes. *Bioinformatics*, 35(19), 3576–3583.
17. **Wu, C.***, Xu, G., & Pan, W.* (2019). An adaptive test on high dimensional parameters in generalized linear models. *Statistica Sinica*, 29, 2163–2186.
18. **Wu, C.**, & Pan, W. (2018). Integration of enhancer-promoter interactions with GWAS summary results identifies novel schizophrenia-associated genes and pathways. *Genetics*, 209(3), 699–709.
19. **Wu, C.**, & Pan, W. (2018). Integrating eQTL data with GWAS summary statistics in pathway-based analysis. *Genetic Epidemiology*, 42(3), 303–316.
(Highlighted by International Genetic Epidemiology Society (IGES). This paper won a poster talk at the ASHG 2017 Annual Meeting.)
20. Park, J.Y., **Wu, C.**, Basu, S., McGue, M., & Pan, W. (2018). Adaptive SNP set association test-

ing in generalized linear mixed models with application to family studies. *Behavior Genetics*, 48(1), 55–66.

21. Xu, Z., **Wu, C.**, Wei, P., & Pan, W. (2017). A powerful framework for integrating eQTL and GWAS summary data. *Genetics*, 207(3), 893–902.
22. Liu, B., **Wu, C.**, Shen, X., & Pan, W. (2017). A novel and efficient algorithm for de novo discovery of mutated driver pathways. *Annals of Applied Statistics*, 11(3), 1481–1512.
23. Xu, Z., **Wu, C.**, Pan, W., & Alzheimer's Disease Neuroimaging Initiative (ADNI). (2017). Imaging-wide association study: Integrating imaging endophenotypes in GWAS. *NeuroImage*, 159, 159–169.
    (This paper won a platform presentation at the ASHG 2017 Annual Meeting.)
24. **Wu, C.**[†], Kwon, S.[†], Shen, X., & Pan, W. (2016). A new algorithm and theory for penalized regression-based clustering. *Journal of Machine Learning Research*, 17(188), 1–25.
25. **Wu, C.**, Chen, J., Kim, J., & Pan, W. (2016). An adaptive association test for microbiome data. *Genome Medicine*, 8(1), 1–12.
    (This paper won the 2016 Joint Statistical Meetings (JSM) Distinguished Student Paper Award on Statistics in Genomics and Genetics Section.)
26. **Wu, C.**, Demerath, E. W., Pankow, J. S., Bressler, J., Fornage, M., Grove, M. L., Chen, W., & Guan, W. (2016). Imputation of missing covariate values in epigenome-wide analysis of DNA methylation data. *Epigenetics*, 11(2), 132–139.

### —Applications & Collaborations

27. King, A.[‡], Wu, L., Deng, HW., & **Wu, C.*** (2022). Polygenic risk score improves the accuracy of a clinical risk score for coronary artery disease. *BMC Medicine*, 20, 385.
28. Xie, T., Xu, C., Shi, X., **Wu, C.**, Meng, R., Meng, X., Yu, G., Wang, K., Xiao, H., & Deng, H. (2021). Accurate recognition of colorectal cancer with semi-supervised deep learning on pathological images. *Nature Communications*, 12, 6311.
29. **Wu, C.***, Zhu, J., King, A.[‡], Tong, X., Lu, Q., Park, J. Y., ... & Wu, L.* (2021). Novel strategy for disease risk prediction incorporating predicted gene expression and DNA methylation data: a multi-phased study of prostate cancer. *Cancer Communications*, 1–11.
30. Wu, L.*, Zhu, J., Liu, D., Sun, Y., & **Wu, C.*** (2021). An integrative multiomics analysis identifies putative causal genes for COVID-19 severity. *Genetics in Medicine*, 1–11.
31. **Wu, C.***, Wu, L., Wang, J., Lin, L., Li, Y., Lu, Q., & Deng, H. (2021). Systematic identification of modifiable risk factors and drug repurposing options for Alzheimer's disease: Mendelian randomization analyses. *Alzheimer's Dement*, 7:e12148.
32. Sun, Y., Zhou, D., Rahman, R., **Wu, C.**, Zhu, J., Cox NJ., Beach TG., Wu, C., Gamazon, ER., & Wu, L. (2021). A transcriptome-wide association study identifies novel blood-based gene biomarker candidates for Alzheimer's disease risk. *Human Molecular Genetics*, ddab229.
33. Sun, Y., Zhu, J., Zhou, D., Canchi, S., **Wu, C.**, Cox NJ., Rissman, RA. Gamazon, ER., & Wu, L. (2021). A transcriptome-wide association study of Alzheimer's disease using prediction models of related tissues identifies novel candidate susceptibility genes. *Genome Medicine*, 13(1), 1–11.
34. Wang, K. S., Yu, G., Xu, C., ..., **Wu, C.**, ... & Deng, H. W. (2021). Accurate diagnosis of colorectal cancer based on histopathology images using artificial intelligence. *BMC Medicine*, 19(1), 1–12.

35. Liu, D., Zhu, J., Zhou, D., ..., **Wu, C.**, ..., & Wu, L. (2021). A transcriptome-wide association study identifies novel candidate susceptibility genes for prostate cancer risk. *International Journal of Cancer*, 1–11.
36. Zhu, J., **Wu, C.**, & Wu, L. (2021). Associations between genetically predicted protein levels and COVID-19 severity. *The Journal of Infectious Diseases*, 223(1), 19–22.
37. Liu, D., Zhou, D., Sun, Y., Zhu, J., Ghoneim, D., **Wu, C.**, Yao, Q., Gamazon, E.R., Cox, N.J., & Wu, L. (2020). A transcriptome-wide association study identifies candidate susceptibility genes for pancreatic cancer risk. *Cancer Research*, 80(20), 4346–4354.
38. Wu L., Yang Y., Guo X., ..., **Wu C.**, ..., & Long, J., The Practical Consortium (2020). An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. *Nature Communications*, 11(1), 1–11.
39. Song, M., Greenbaum, J., Luttrell IV, J., Zhou, W., **Wu, C.**, Shen, H., Gong P., Zhang C., & Deng, H. W. (2020). A review of integrative imputation for multi-omics datasets. *Frontiers in Genetics*, 11.
40. Zhu, J., Shu, X., Guo, X., ..., **Wu, C.**, ..., & Wu L. (2020). Associations between genetically predicted blood protein biomarkers and pancreatic cancer risk. *Cancer Epidemiology, Biomarkers & Prevention*, 29(7), 1501–1508.
41. Zhu, L., Li, Y., Chen, Y., Carrera, C., **Wu, C.**, & Fork, A. (2018). Comparison between two post-dentin bond strength measurement methods. *Scientific Reports*, 8(1), 2350.
42. Bose, M., **Wu, C.**, Pankow, J. S., Demerath, E. W., Bressler, J., Fornage, M., Grove, M. L., Mosley, T. H., Hicks, C., North, K., Kao, W. H., Zhang, Y., Boerwinkle, E., & Guan, W. (2014). Evaluation of microarray-based DNA methylation measurement using technical replicates: the Atherosclerosis Risk In Communities (ARIC) Study. *BMC Bioinformatics*, 15(1), 1–10.

### —Peer-reviewed Proceedings

43. Park, J. Y., **Wu, C.**, & Pan, W. (2018). An adaptive gene-level association test for pedigree data. *BMC Genetics*, 19(1), 68.
44. **Wu, C.**, Park, J.Y., Guan, W., & Pan, W. (2018). A powerful gene-based test for methylation data. *BMC Proceedings*, 12(9), 60.

### —Book Chapter

45. **Wu, C.** (2022). Using R for Cell-Type Composition Imputation in Epigenome-Wide Association Studies. In *Epigenome-Wide Association Studies* (pp. 49-56). Humana, New York, NY.

## SUBMITTED MANUSCRIPTS

* Corresponding author; † Co-first author; ‡ Students advised by C Wu

46. Meng, Z.‡, Wang, J., Lin, L.*, & **Wu, C.***. An iterative method for detecting outlying studies in meta-analysis. Submitted.
47. Meng, Z.‡, **Wu, C.***, & Lin, L.*. The effect direction should be accounted for when assessing small-study effects. Under revision.
48. Sun, Y., Zhu, J., Yang, Y., Nowakowski, R., Long, J., **Wu, C.**, & Wu, L. (2021+). Identification of candidate DNA methylation biomarkers related to Alzheimer's disease risk by integrative multi-omics analysis. Submitted.
49. Xu, X., Masca, A., Zhu, J., Yang, T., Ghoneim, D., Surendran, P., Liu, T., Platz, E., Yao, Q., Liu, T., Fahle, S., Butterworth, A., **Wu, C.***, & Wu, L*. Associations between genetically predicted

blood protein levels and pancreatic ductal adenocarcinoma risk: a study using protein genetic prediction models. Submitted.

50. Zhong, X., Xu, X., Zhu, J., Ghoneim, D., Surendran, P., Fahle, S., Butterworth, A., **Wu, C.***, & Wu, L*. Identification of genetically predicted blood protein biomarkers associated with prostate cancer risk using genetic prediction models: analysis of over 140,000 subjects. Submitted.
51. Sun, Y.[†], Bae, YE.[†‡], Zhu, J., **Wu, C.***, & Wu, L.* (2021+) A splicing transcriptome-wide association study identifies novel altered splicing in Alzheimer's disease susceptibility. To be submitted.
52. Zhu, J., Xu, X., Walker, K., Ghoneim, D., Zhang, Z.[‡], Surendran, P., Fahle, S., Butterworth, A., **Wu, C.***, & Wu, L.* (2021+) Associations between genetically predicted protein concentrations in plasma and Alzheimer's disease risk. Submitted.
53. Li, Y., Kang, J., **Wu, C.**, Dinov, I., Chalise, P., & Mahnken, J. (2021+). A machine-learning approach for detection of local brain networks and marginally weak signals identifies novel AD/MCI differentiating connectomic neuroimaging biomarkers. To be Submitted. An earlier version is on bioRxiv.
54. Hidalgo, B., Lent, S., ..., **Wu, C.**, ..., Hivert, M.F., & Pankow J.S. for the CHARGE consortium (2021+). DNA methylation associated with glycemic traits and type 2 diabetes in multi-ethnic meta-analyses: CHARGE Consortium. *Nature Communications*. Under revision.

## GRANTS

### —Undergoing

- Novel statistical methods for multi-omics data integration in Alzheimer's disease (Wu, C and Bradley, J) R03
  National Institutes of Health (NIH) 01/01/21–12/31/22
  Role: **Contact PI** 20% efforts
- Uncovering causal protein markers to improve prostate cancer etiology understanding and risk prediction in Africans and Europeans (Wu, L and Wu, C) **R01**
  NIH, NCI 07/01/2022–06/31/2027
  Role: **PI** 15% efforts in Years 1–2, 20% efforts in Years 3–5

### —Completed

- Trans-omics integration of multi-omics studies for osteoporosis: Administrative supplement for COVID-19 studies (Deng, HW) U19
  NIH 09/10/2021–07/31/2022
  Role: Subcontract PI 5% efforts
- Novel statistical methods for transcriptome-wide association studies
  First Year Assistant Professor Grant, Florida State University 05/08/19–08/06/19
  Role: Contact PI Total cost: $20,000
- Novel machine learning methods for Alzheimer's disease
  The Committee on Faculty Research Support, Florida State University 05/07/20–06/30/20
  Role: Contact PI Total cost: $14,000

## SOFTWARE

- Owner and maintainer for the following R packages:
  - prclust: Penalized Regression-Based Clustering Methods; 21K downloads
  - MiSPU: Microbiome Based Sum of Powered Score (MiSPU) Tests; 21K downloads
  - aSPU2: A New Version of Adaptive Sum of Powered Score (aSPU) Test;
  - GLMaSPU: Adaptive Tests on High Dimensional Parameters in GLMs; 19K downloads
  - glmtlp: Truncated Lasso Regularized Generalized Linear Models; 14K downloads
- Online software tutorial: `http://wuchong.org/software.html`
- Lab GitHub Repo: `https://github.com/ChongWuLab`

## TEACHING EXPERIENCE

- STA 4321/5323 Introduction to Mathematical Statistics
  - Instructor, Department of Statistics, Florida State University Jan. 2021–April. 2021
  - Instructor, Department of Statistics, Florida State University Jan. 2020–May 2020
  - Instructor, Department of Statistics, Florida State University Aug. 2019–Dec. 2019
  - Instructor, Department of Statistics, Florida State University Jan. 2019–May 2019
  - Instructor, Department of Statistics, Florida State University Aug. 2018–Dec. 2018
- STA 5934 Statistical Genetics (Topic course, redesigned by Wu, C)
  - Instructor, Department of Statistics, Florida State University Aug. 2020–Dec. 2020
  - Instructor, Department of Statistics, Florida State University Aug. 2021–Dec. 2021
- PUBH 6451 Biostatistics (Instructor: Dr. William Thomas)
  - Lab Instructor, Division of Biostatistics, University of Minnesota Jan. 2014–May 2014
- PUBH 6414 Biostatistical Methods (Instructor: Dr. Ann M. Brearley)
  - Teaching Assistant, Division of Biostatistics, University of Minnesota Sept. 2013–Dec. 2013

## STUDENTS

- Ph.D. students who passed the qualifying exam: Shengjie Jiang, Ye Eun Bae, Zhuo Meng, Austin King, Hunter Melton
- Other Ph.D. students: Zichen Zhang, Madison Layfield

## PRESENTATIONS

Most of my presentation slides can be found at `https://wuchong.org/talks.html`.

- "An adaptive association test for microbiome data"
  - Presentation at Eastern North American Region (ENAR) 2016 Spring Meeting
    Austin, TX Mar. 2016
  - Presentation at 2016 Joint Statistical Meetings (JSM)
    Chicago, IL Aug. 2016
- "Iterative PCA in epigenome-wide association studies"
  - Poster presented at American Society of Human Genetics (ASHG) 2016 Annual Meeting
    Vancouver, BC, Canada Oct. 2016
- "A gene-level adaptive association test for methylation data"

  - Presentation at Genetic Analysis Workshop (GAW) 20
    San Diego, CA Mar. 2017
- “An adaptive test on high dimensional parameters in GLMs”
  - Presentation at ENAR 2017 Spring Meeting
    Washington, DC Mar. 2017
  - Poster presented at MSI Research Exhibition
    Minneapolis, MN Apr. 2017
  - Presentation at 2017 JSM
    Baltimore, MD Aug. 2017
- “Imaging-wide association study: Integrating imaging endophenotypes in GWAS”
  - Invited presentation at 2017 JSM (On behalf of Dr. Wei Pan)
    Baltimore, MD Aug. 2017
  - Invited presentation at Third Annual Kliakhandler Conference (On behalf of Dr. Wei Pan)
    Houghton, MI Aug. 2017
- “Integrating eQTL data with GWAS summary statistics in pathway-based analysis”
  - Poster talk at ASHG 2017 Annual Meeting
    Orlando, FL Oct. 2017
- “Integration of methylation QTL and enhancer-target gene maps with schizophrenia GWAS summary results identifies novel genes”
  - Oral presentation at IGES 27th Annual Meeting
    San Diego, CA Oct. 2018
- “An adaptive test for high-dimensional generalized linear models with application to detect gene-environment interactions”
  - Presentation at ENAR 2019 Spring Meeting
    Philadelphia, PA Mar. 2019
- “Complex disease risk prediction via a deep learning method”
  - Presentation at JSM 2019
    Denver, CO Jul. 2019
- “Multi-trait genome-wide analyses of the brain imaging phenotypes in UK Biobank”
  - Platform presentation at ASHG 2019
    Huston, TX Oct. 2019
- “A powerful fine-mapping method for transcriptome-wide association studies”
  - Invited Presentation at JSM 2020
    Virtual Aug. 2020
- “Novel strategy for disease risk prediction incorporating predicted gene expression and DNA methylation: a multi-phased study of prostate cancer”
  - Department seminar at Florida State University School of Medicine
    Virtual Sep. 2020
  - Invited presentation at International Indian Statistical Association (IISA) 2021
    Virtual May 2021
- “A gene-level methylome-wide association analysis identifies novel Alzheimer’s disease genes”
  - Poster presented at ASHG 2020
    Virtual Oct. 2020
- “A regularization-based adaptive test for high-dimensional generalized linear models”

  - Department seminar at Shanghai University of Finance and Economics, Statistics
    Virtual Dec. 2020
  - Department seminar at Washington University School of Medicine, Biostatistics
    Virtual Dec. 2020
- "SUMMIT: An integrative approach for better transcriptomic data imputation improves causal gene identification"
  - Invited presentation at New Investigator in AD and AFAR Grantee Conference
    Virtual Oct. 2021
- "Accounting for winner's curse and pleiotropy in two-sample Mendelian randomization"
  - Department seminar at Tulane Unveristy, Biomedical Informatics & Genomics Center
    Virtual Dec. 2021
  - Department seminar at the Chinese University of Hong Kong, Statistics
    Virtual Dec. 2021
  - Invited presentation at The ICSA 2022 Applied Statistics Symposium
    Gainesville, FL Jun. 2022

## HONORS & AWARDS

- Dean's Faculty Travel Award Apr. 2020
  - Florida State University
- ENAR Distinguished Student Paper Award Mar. 2019
  - Eastern North American Region International Biometric Society
- James R. Boen Student Achievement Award May 2018
  - Division of Biostatistics, University of Minnesota
- Pre-Doctoral Trainee Award Oct. 2017
  - Association of Chinese Geneticists in America (ACGA)
- Poster Award May 2017
  - University of Minnesota Chapter of Sigma Xi
- Elected to Delta Omega (Public Health Honorary Society) May 2017
  - University of Minnesota
- Elected to Sigma Xi (The Scientific Research Society) May 2017
  - University of Minnesota
- Distinguished Student Paper Award, Genomics and Genetics Section Aug. 2016
  - 2016 Joint Statistical Meetings
- Doctoral Dissertation Fellowship 2016–2017
  - University of Minnesota
- Travel Award, Computational Neuroscience Summer School Jul. 2015
  - Statistical and Applied Mathematical Sciences Institute
- Dean's Ph.D. Scholarship Sept. 2013
  - University of Minnesota
- Honorable Mention in Mathematical Contest in Modeling Apr. 2012
  - Consortium for Mathematics and Its Application
- National Scholarship Sept. 2011
  - Ministry of Education, China

## PROFESSIONAL ACTIVITIES

**Manuscript Reviewer**

- Statistics/Biostatistics: Annals of Statistics, Biometrics, Journal of the American Statistical Association, Journal of Machine Learning Research, Statistics in Medicine, Electronic Journal of Statistics, Statistical Applications in Genetics and Molecular Biology, Statistics in Biosciences, Journal of Theoretical Biology, Biometrical Journal, Computational Statistics and Data Analysis
- Genetics/Genomics/Medicine/Bioinformatics: Genetic Epidemiology, Bioinformatics, Genome Biology, Frontiers in Genetics, Alzheimer's & Dementia, Briefings in Bioinformatics, PLOS Computational Biology
- Epidemiology: American Journal of Epidemiology
- Multidisciplinary: Nature Communications, PLOS One, Scientific Reports

**Guest Editor**, *Frontiers in Genetics*

**Education Officer**, mental health statistics section, American Statistical Association (ASA)

**Program Committee Member**, IEEE BIBM 2022

**Invited Session Chair & Organizer**

- Recent Advances of Causal Inferences in Human Genetics, JSM 2021 (with Dr. Jingshen Wang)
- Recent Advances in Mendelian randomization, 2022 ICSA Applied Statistics Symposium

**Grant Reviewer (ad hoc)**

- NIA Special Emphasis panel, ZAG ZIJ-P J2, Functional genomics, 2020
- NCI Informatics Technology for Cancer Research (ITCR) study section, 2020
- NCI ITCR study section, ZCA1 TCRB-Q (M1), 2022
- Lifestyle and Health Behaviors (LHB) study section, 2022