

Diptavo Dutta

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Website

Current Position	Earl Stadtman Tenure Track Investigator Integrative Tumor Epidemiology Branch Division of Cancer Epidemiology and Genetics National Cancer Institute National Institutes of Health	Aug, 2022 - Present
Education and Training	<i>Postdoctoral Fellow</i> Dept. of Biostatistics, Johns Hopkins University Advisors: Dr. Nilanjan Chatterjee and Dr. Alexis Battle	2019 - 2022
	<i>PhD. in Biostatistics</i> Dept. of Biostatistics, University of Michigan Dissertation: Statistical Methods for Gene-based and Gene-Set Analysis Advisor: Dr. Seunggeun (Shawn) Lee	2014 - 2019
	<i>M.Stat</i> Indian Statistical Institute Graduate with 1 st class Distinction Specialization: Biostatistics and Data Analysis	2012 - 2014
	<i>B.Sc (Statistics Hons.)</i> St. Xavier's College, University of Calcutta Graduate with 1 st class Distinction	2009 - 2012
Professional Experience	<i>Summer Intern, HEOR Oncology</i> AbbVie Inc. <ol style="list-style-type: none">1. Treatment Patterns and Survival in Patients with Glioblastoma: A Retrospective Database Analysis Using US Electronic Health Records (EHR)2. Treatment Patterns in Patients with Chronic Lymphocytic Leukemia (CLL) Treated with B-Cell Receptor Inhibitors (BCRIs) in Canada : A Medical Chart Review Study	June, 2017 - August, 2017
	<i>Research Assistant</i> Dept. of Biostatistics, University of Michigan Advisors: Dr. Seunggeun (Shawn) Lee & Dr. Laura J. Scott	Sept., 2014 - June, 2019
	<i>Summer Intern</i> Central Statistical Organization, Govt. of India	May, 2013 - July, 2013

Peer reviewed
Publications

- Guo, X., Chatterjee, N., **Dutta, D.** Subset-based method for cross tissue transcriptome wide association studies improves power and interpretability. Preprint available on medRxiv. (In press *HGG Advances*).
- Purdue, M. †, **Dutta, D.** †, ···, Chanock, S. J. Multi-ancestry genome-wide association study of kidney cancer identifies 63 susceptibility regions. (In Press *Nature Genetics*).
- Koutros, S., ···, **Dutta, D.**, ···, Rothman, N. (2023) Genome-wide association study of bladder cancer reveals new biological and translational insights. *European Urology*; 84(1) 127-137.
- Maity, S., **Dutta, D.**, Terhorst, J., Sun, Y., Banerjee, M. (2023) A linear adjustment based approach to posterior drift in transfer learning. *Biometrika*; Link.
- **Dutta, D.**, Sen, A., Satagopan, J. (2022) Sparse canonical correlation to identify copy number aberration-regulated genes for multiple breast cancer outcomes. *Plos One*; 17 (12); e0276886
- Surapaneni, A., ···, **Dutta, D.**, Coresh, J., Rhee, E., Grams, M. E. (2022) Identification of 969 protein quantitative trait loci in an African American population with kidney disease attributed to hypertension. *Kidney International*; 102(5) 1167-1177
- **Dutta, D.**, He, Y., Saha, A., Arvanitis, M., Battle, A., Chatterjee, N. (2022) Aggregative trans-eQTL analysis detects trait-specific target gene sets in whole blood. *Nature Communications*. 13, 4323.
- Shabani, M., **Dutta, D.**, ···, Lima, J. (2022) Rare genetic variants associated with Myocardial Fibrosis in Multi Ethnic Study of Atherosclerosis (MESA). *Frontiers in Cardiovascular Medicine*; 9: 804788.
- Rhee, E., Surapaneni, A., Zheng, Z., Zhou, L., **Dutta, D.**, ···, Grams, M. E. (2022) A Trans-ethnic Genome-wide Association Study of Blood Metabolites in the Chronic Renal Insufficiency Cohort (CRIC) Study. *Kidney International*; 101(4) 814-823.
- Qi, G. †, **Dutta, D.** †, Leroux, A., Ray, D., Crainiceanu, C., Chatterjee, N. (2022) Genome-wide association studies of 27 accelerometry-derived physical activity measurements identifies novel loci and genetic mechanisms. *Genetic Epidemiology*; 46(2) 122-138.
- Zhang, J., **Dutta, D.**, Kottgen, A., ···, Chatterjee, N. (2022) Plasma proteome analyses in individuals of European and African ancestry identify cis-pQTLs and models for proteome-wide association studies. *Nature Genetics*; 54(5) 593-602.
- Grams, M. E., Surapaneni, A., Chen, J., Zhou, L., Yu, Z., **Dutta, D.**, ···, Coresh, J. (2021) Proteins Associated with Risk of Kidney Function Decline in the General Population. *Journal of the American Society of Nephrology*; 32(9) 2291-2302 .
- Cox, C. K., Zawitowski, M. , Pandit, A., **Dutta, D.**, Narla, G., Swenson, C. W. (2021) Genome Wide Association Study of Pelvic Organ Prolapse using the Michigan Genomics Initiative. *Female Pelvic Medicine & Reconstructive Surgery*; 27(8) 502-506.
- **Dutta, D.**, VandeHaar, P., Fritsche, L. G., Zollner, S., Boehnke, M., Scott, L. J., Lee, S. (2021) A powerful subset-based gene-set analysis method identifies novel associations and improves interpretation in UK Biobank. *The American Journal of Human Genetics*; 108(4) 669-681

- Arvanitis, M., Tampakakis, E., Zhang, Y., Wang, W., Auton, A., 23andMe Research Team, **Dutta, D.**, ..., Battle, A. (2020) Genome-wide association and multi-omic analyses reveal ACTN2 as a gene linked to heart failure. *Nature Communications*; 11(1), 1-12
- **Dutta, D.**, Brummett, C., Fritsche, L., Moser, S., Tsodikov, A., Lee, S., Clauw, D., Scott, L. (2020) Heritability of the fibromyalgia phenotype varies by age. *Arthritis & Rheumatology*; 72(5), 815-823
- **Dutta, D.**, Gagliano, S. A., Weinstock, J., Zawistowski, Sidore, C., Fritsche, L., M., Cucca, F., Schlessinger, D., Abecasis, G., Brummett, C., Lee, S. (2019) Meta-MultiSKAT: Region-based rare variant meta-analysis of multiple phenotypes using summary statistics. *Genetic Epidemiology*; 43(7), 800-814
- **Dutta, D.**, Scott, L., Boehnke, M., Lee, S. (2019) Multi-SKAT: General framework to test multiple phenotype associations of rare variants. *Genetic Epidemiology*; 43(1), 1-20

†: Joint first author

Publications under revision or submitted

- **Dutta, D.**, Sen, A., Satagopan J. Joint sparse canonical correlation to identify genes associated with stage at diagnosis of renal clear cell carcinoma. (Under revision in *Genetic Epidemiology*)
- **Dutta, D.**, Guo, X., Winter, T. D., Jahagirdar, O. B., ..., Purdue, M. P. Transcriptome and proteome-wide association studies identify genes associated with renal cell carcinoma. (Under Review)
- Qi, G., Chhetri, S., Ray, D., **Dutta, D.**, ..., Chatterjee, N. Genome-Wide Large-Scale Multi-Trait Analysis Characterizes Global Patterns of Pleiotropy and Unique Trait-Specific Variants Preprint available on biorXiv. (Under Revision *Nature Communications*)

Invited Presentations

- Departmental Seminar, Dept. of Biostatistics and Epidemiology, University of South Carolina
- 23rd annual conference of the International Indian Statistical Association. June, 2023.
- Advances in Statistical and Computational Methods for Analysis of Biomedical, Genetic, and Omics Data. University of Texas at Dallas. Mar, 2023.
- 22nd annual conference of the International Indian Statistical Association. Dec, 2022.
- Integrated multi-omics analyses symposium organized by the IBS working group population genetics and genome analysis. Oct, 2022.
- International Conference, Institute for Applied Statistics Sri Lanka. Dec, 2017.

Contributed Presentations

- Genome Informatics: Poster (2020)
- American Society for Human Genetics Annual Meeting, Virtual: Poster (2020)
- International Genetics Epidemiology Society Annual Meeting, Houston: Platform talk (2019)
- American Society for Human Genetics Annual Meeting, Houston: Poster (2019)
- American Society for Human Genetics Annual Meeting, San Diego: Platform talk (2018)

- International Genetics Epidemiology Society Annual Meeting, Cambridge: Poster (2017)
- MSSISS, Ann Arbor: Speed Oral presentation (2017)
- American Society for Human Genetics Annual Meeting, Vancouver: Poster (2016)
- Joint Statistical Meetings, Chicago: Contributed Talk (2016)
- MSSISS (Michigan Student Symposium for Interdisciplinary Statistical Sciences), Ann Arbor: Poster (2016).
- Projects at AbbVie presented at SNO, 2017 and ASH, 2017.

Awards & Achievements

Pamela Anne Cafritz Renal Cell Carcinoma Awards: National Cancer Institute, 2022 (Role: PI)
Williams Award Finalist: IGES Meeting (2019)
Rackham Travel Grant: University of Michigan
INSPIRE Scholarship: Dept. of Science and technology, Govt. of India.

R-Packages & Software

- MultiSKAT: Rare variant association tests for multiple phenotypes
- Meta-MultiSKAT: Meta analysis of rare variant association tests for multiple phenotypes.
- GAUSS: Gene-set association analysis using GWAS summary statistics
- PathWeb: Visualization for results for application of GAUSS on UK Biobank data.
- PWAS: Visualization of proteome-wide association analysis on ARIC data for European and African Americans.
- ARCHIE: trans-regulated gene modules for known trait-related genetic variants using sparse canonical correlation

Professional Membership

American Society for Human Genetics, International Genetic Epidemiology Society, American Statistical Association.

Peer Review

Nature Communications, Nature Neuroscience, The American Journal of Human Genetics, PLoS Genetics, PLoS Computational Biology, Biostatistics, Genetic Epidemiology, Frontiers in Psychiatry, Frontiers in Genetics, Biostatistics, Annals of Applied Statistics, Annals of Human Genetics, Scientific Reports, NAR Genomics and Bioinformatics, PLoS One, BMC Medical Genomics, NPJ Genomic Medicine, International Journal of Cancer, Health Services and Outcomes Research Methodology, Journal for Trauma Nursing, International Journal of Biostatistics

Sub-reviewer: *Machine Learning in Computational Biology, International Conference on Machine Learning (Computational Biology workshop)*

Organization

- Statistical Genetics Working Group Seminar, Dept. of Biostatistics, Johns Hopkins University, Fall 2021 and Spring 2022
- Statistical Genetics Journal Club, Dept. of Biostatistics, University of Michigan, Fall 2015