Diptavo Dutta

Dept. of Biostatistics
Johns Hopkins University
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Current Position

Postdoctoral Fellow
Dept. of Biostatistics, Johns Hopkins University
Advisors: Dr. Nilanjan Chatterjee and Dr. Alexis Battle

Education

PhD. in Biostatistics 2014 - 2019
Dept. of Biostatistics, University of Michigan

- Dissertation: Statistical Methods for Gene-based and Gene-Set Analysis
- Advisor: Dr. Seunggeun (Shawn) Lee
- Committee Members: Dr. Michael Boehnke, Dr. Laura J. Scott, Dr. Ananda Sen

M.Stat 2012 - 2014
Indian Statistical Institute

- Graduate with 1^{st} class Distinction
- Specialization: Biostatistics and Data Analysis

B.Sc (Statistics Hons.) 2009 - 2012
St. Xavier's College, University of Calcutta

- Graduate with 1^{st} class Distinction
- Auxiliary subjects: Mathematics, Computer Science

Past Employment

Summer Intern, HEOR Oncology June, 2017 - August, 2017
AbbVie Inc.

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

Research Assistant Sept., 2014 - June, 2019
Dept. of Biostatistics, University of Michigan
Advisors: Dr. Seunggeun (Shawn) Lee & Dr. Laura J. Scott

Summer Intern May, 2013 - July, 2013
Central Statistical Organization, Govt. of India

Publication & Preprints

- **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
- **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.**, 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
- Arvanitis, M., Tampakakis, E., Zhang, Y., Wang, W., Auton, A., 23andMe Research Team, **Dutta, D.**, Glavaris, S., Keramati, A., Chatterjee, N., Chi, N. C., Ren, B., Post, W. S., 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.**, 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
- 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*
- Grams, M. E., Surapaneni, A., Chen, J., Zhou, L., Yu, Z., **Dutta,D.**, $\cdots$, Coresh, J. (2021) Proteins Associated with Risk of Kidney Function Decline in the General Population. *Journal of the American Society of Nephrology (To appear).*
- Qi, G. [†], **Dutta, D.**[†], Leroux, A., Ray, D., Crainiceanu, C., Chatterjee, N. (2021) Genome-wide association studies of 27 accelerometry-derived physical activity measurements identifies novel loci and genetic mechanisms. *(Under Review).* doi: 10.1101/2021.02.15.21251499. Preprint available on medRXiv.
- Zhang, J., **Dutta, D.**, Kottgen, A., $\cdots$, Chatterjee, N. (2021) Large Bi-Ethnic Study of Plasma Proteome Leads to Comprehensive Mapping of cis-pQTL and Models for Proteome-wide Association Studies. (2021). *(Under revision in Nature Genetics)* doi: 10.1101/2021.03.15.435533. Preprint available on bioRXiv.
- **Dutta, D.**, He, Y., Saha, A., Arvanitis, M., Battle, A., Chatterjee, N. (2020) Novel Aggregative trans-eQTL Association Analysis of Known Genetic Variants Detect Trait-specific Target Gene-sets. Preprint available on medRXiv. doi: 10.1101/2020.09.29.20204388 *(Under Review).*
- Rhee, E., Surapaneni, A., Zheng, Z., Zhou, L., **Dutta, D.**, $\cdots$, Grams, M. E. (2021) A Trans-ethnic Genome-wide Association Study of Blood Metabolites in the Chronic Renal Insufficiency Cohort (CRIC) Study. *(Under Review).*
- Kumthekar, P., Dixit, K. S., Kamalakar, R., **Dutta, D.**, Holen, K., Shaikh, N. I., Ganguli, A. (2019) Treatment Patterns and Survival in Patients with Glioblastoma Multiforme: A Retrospective Database Analysis Using US Electronic Health Records (EHR). *(Under Review)*

[†]: Joint first author

Papers in progress

- **Dutta, D.** & Chatterjee, N. Fast and efficient liability model for binary phenotypes in Biobanks.
- **Dutta, D.**, Sen, A., Satagopan, J. Sparse canonical correlation identifies copy number variation-regulated genes for multiple breast cancer outcomes.

- **Dutta, D.**, Zhang, J., $\cdots$, Chatterjee, N. Novel sparse canonical correlation analysis to identify trans-regulated protein networks associated with known complex trait variants.
- Shabani, M., **Dutta, D.**, $\cdots$, Lima, J. Rare genetic variants associated with Myocardial Fibrosis in Multi Ethnic Study of Atherosclerosis (MESA).
- Shabani, M., **Dutta, D.**, $\cdots$, Lima, J. Rare Genetic Variants in Individuals with Low ASCVD Risk and Hard CHD or High Coronary Artery Disease: Multi-Ethnic Study of Atherosclerosis.
- Qi, G., **Dutta, D.**, $\cdots$, Chatterjee, N. A large-scale pleiotropic analysis identifies trait-specific loci and functional mechanisms.
- Chhetri, S., **Dutta, D.**, $\cdots$, Battle, A. A colocalization approach to determine shared heritability of diseases across ethnicities.

Presentations

- Michigan Student Symposium for Interdisciplinary Statistical Sciences, Ann Arbor: Poster (2016), Speed Oral presentation (2017)
- Joint Statistical Meetings: Contributed Talk (2016)
- American Society for Human Genetics Annual Meeting: Poster (2016), Platform talk (2018), Poster (2019), Poster (2020)
- International Genetics Epidemiology Society Annual Meeting: Poster (2017), Platform talk (2019)
- International Conference, Institute for Applied Statistics Sri Lanka, 2017, Colombo: Invited Talk
- Projects at AbbVie presented at SNO, 2017 and ASH, 2017.
- Genome Informatics: Poster (2020)

Awards & Achievements

Williams Award Finalist: IGES Meeting (2019)
Rackham Travel Grant: University of Michigan
INSPIRE Scholarship: Dept. of Science and technology, Govt. of India.

R-Packages

- MultiSKAT: GitHub
- Meta-MultiSKAT: GitHub
- GAUSS: GitHub

Professional Membership

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

Peer Review

- PLoS Genetics
- PLoS Computational Biology
- Annals of Applied Statistics
- NAR Genomics and Bioinformatics
- PLoS One
- BMC Medical Genomics
- NPJ Genomic Medicine
- International Journal of Cancer

- Journal for Trauma Nursing

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

Technical Skills

Programming Languages: R, Python, C++, C
Operations Technologies: Google Cloud, AWS
Operating Systems: Linux, Windows
Statistical Softwares: SAS, Minitab, SPSS
High-performance computing clusters

References

Available upon request.