Nilanjan Chatterjee, Ph.D.

Titles & Department
Bloomberg Distinguished Professor with appointments in Biostatistics and Epidemiology; Fellow of American Statistical Association

Specialization Areas
Big data, epidemiologic study design, genetic association studies, risk prediction, and statistical genetics.

Summary of Research & Work
Dr. Chatterjee's work is focused on modeling disease risk associated with genetic, lifestyle, biomarkers and other factors using modern population-based biomedical science. He leads a broad research program in quantitative research that cuts across multiple areas of modern population-based biomedical science including statistical genetics/genomics, precision medicine and big data. The scientific goals of his studies include discovery of new biomarkers, understanding disease mechanisms, characterizing disease risk, and developing risk-stratified approaches to disease prevention. He has extensively collaborated in recent genome-wide association studies that have led to identification new cancer susceptibility SNPs, provided characterization of heritability, genetic architecture, and gene-environment interaction, and led to better understanding of potential for genetic risk stratification for cancer prevention. Prior to joining Hopkins, Dr. Chatterjee worked at the National Cancer Institute for 16 years and led the Biostatistics Branch of the Division of Cancer Epidemiology and Genetics during 2008-2015.

Publications
- Wasm-iCARE: a portable and privacy-preserving web module to build, validate, and apply absolute risk models
- Heterogeneous Transfer Learning for Building High-Dimensional Generalized Linear Models with Disparate Datasets
- MUSSEL: enhanced Bayesian polygenic risk prediction leveraging information across multiple ancestry groups
- A Robust Bayesian Method for Building Polygenic Risk Scores using Projected Summary Statistics and Bridge Prior