Big Data Training for Cancer Research

Special Lecture Series

Using Polygenic Risk Scores to Inform Cancer Screening

Dr. Peter Kraft

June 9, 2020, 1:00 – 2:30 PM (EST)

Speaker Bio:

Peter Kraft is Professor of Epidemiology and Biostatistics and Director of the Program in Genetic Epidemiology and Statistical Genetics at the Harvard T.H. Chan School of Public Health. His research concentrates on the design and analysis of genetic association studies, with particular emphasis on the genetic epidemiology of cancer. He has participated in many international consortia studying genetics and environmental exposures in relation to cancer risk over the last fifteen years, including the Breast and Prostate Cancer Cohort Consortium (BPC3); the NCI's PanScan and Cancer Genetic Markers of Susceptibility (CGEMS) projects; the NCI's "post-GWAS" GAME-ON consortium; the Breast Cancer Association Consortium (BCAC); and the Cancer Risk Estimates Related to Susceptibility Genes (CARRIERS) consortium, which is sequencing cancer predisposition genes in a large population-based breast cancer case-control sample.

His methodological work has focused on efficient and interpretable "gene x environment interaction" analyses; building and evaluating risk prediction models incorporating high dimensional genetic data; and integrative analyses combining genetic and environmental risk factors with intermediate biomarkers (gene expression, metabolomics). He has taught introductory and advanced courses in genetic epidemiology and statistical learning at the Harvard Chan School since 2004 and co-chaired the American Association for Cancer Research's Integrative Molecular Epidemiology workshop since it started in 2013. Dr. Kraft is currently President-Elect of the International Genetic Epidemiology Society.

Abstract:

Polygenic scores aggregate information on many common germline markers across the genome to inform prediction models for complex diseases and traits. These scores may help disease prevention, early diagnosis and treatment by refining available risk stratification tools. In this talk I review methods for developing polygenic scores and evaluating their accuracy and generalizability, using breast cancer as an example. I also discuss a framework for establishing the clinical or public health utility of polygenic scores, which emphasizes clinical context (available interventions, risks associated with polygenic testing and interventions, potential benefits of a risk stratified approach to intervention, etc.).

Series Schedule:

June 12: Dr. Sean Davis – The National Cancer Institute
June 15: Dr. Daniel Raftery – University of Washington
June 16: Dr. Constantine Gatsonis – Brown University
June 18: Dr. Mark Kelley – Indiana University
June 19: Dr. Warren Kibbe – Duke University

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