

## **Epidemiology in the “omics” era.**

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New technologies offer the potential to improve our ability to discover the distribution and determinants of disease. However, these technologies bring with them new questions of scale, expense, data analysis, and, in some circumstances, research ethics. The most immediate technology is the application of whole genome single nucleotide polymorphism (SNP) scans, which leverage the sequence data from the Human Genome Project and the HapMap, along with new technologies to measure up to a million SNPs in a single sample. These technologies permit the Descriptive Epidemiology of the Genome, and are being applied in case-control studies to identify common gene variants that underlie the well-established contribution of family history to most diseases. Challenges to epidemiologists include: the increased need for multi-disciplinary collaboration, the need for networks to obtain large-scale replication of findings, the development of new methods to analyze high-dimensional data, and the integration of a strain of genetic determinism into our view of disease causation. Only well-designed epidemiologic studies will be able to use these new data to develop accurate measures of penetrance and population attributable risk that will be necessary to appropriately use knowledge about inherited gene variants and disease in population-based activities such as screening. Other new technologies have been less used to date by epidemiologists. Gene expression arrays offer the possibility of defining disease subtypes that may have different etiologies. Proteomic approaches have been promoted as the key to early disease detection, however, experience to date has reinforced the need for rigorous study design rather than providing robust and reproducible results. An epidemiologic approach to utilizing these new technologies in etiologic research is needed, yet epidemiologists are under-represented in the design and conduct of such studies.