The Computational Challenges of Personal Genomes

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The genomic revolution will soon provide each of us the ability to obtain our own complete genetic information. What does this information tell us and how will we use it? Over the past few years, novel genomic technologies have led to the discovery of hundreds of genetic risk factors for common disease such as hypertension, diabetes, Alzheimer's disease, and cancer. These discoveries will have a tremendous impact on medicine in many ways. These technologies have also shed light on both human history and provides insight into our ancestry. However, despite the success of these initial studies, many challenges and open questions remain on how to interpret personal genomes. Many of these challenges involve computational and statistical questions and provide great opportunities for contributions by engineers.