

Institute for Computational Medicine

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Data, technology and populations for genomewide association studies

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Abstract:

The pervasive effect of genetic variation on medically important phenotypes provides a means for dissecting their underlying mechanisms by identifying variants that are associated with traits of interest. Current trends in human genetics now facilitate, for the first time, pursuing this potential by execution of large scale studies that scan the entire genome for potentially associated variants.

Specifically, the talk will present

- The International HapMap Project, a data resource we participated in developing to enable genomewide association studies, and what our analyses of these data tell us about human variation.
- The current generation of SNP array technology, and how computation and statistics improvements allow it to cover the majority of common human variants.
- The tale of an isolated population in Micronesia, where we show association scans are more promising than elsewhere, though we expose practical complexities of real data and the computational challenges they present.

Some of the research presented was performed as part of the International HapMap Analysis Team, or in collaborations with Affymetrix Inc. and the Friedman lab at Rockefeller University.