

Paper 116-30

The Human Genome Project and the International HapMap

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ABSTRACT

The Human Genome Project and the International HapMap Project have provided rich and challenging datasets of genetic information. On the one hand, it is now possible to characterize an individual at several million features (single nucleotide polymorphisms or SNPs), although only on relatively few individuals. On the other hand, we know that all human genetic characteristics are controlled by only 20,000 genes. Added to the genetic marker and quantitative trait data, we can now measure expression levels for all genes. Building a coherent picture of the causes and cures for human diseases from these disparate datasets requires substantial resources in statistical computation.

NOTE

No paper was made available for publication. Please contact the author directly.

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