

# The International HapMap Project and its Applications to Association Studies

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**Abstract:** The HapMap project will generate enormous amount of data on human genomic variation. Due to high linkage disequilibrium in many regions, a small fraction of SNPs (tag SNPs) are sufficient to capture most of the haplotype structure of the human genome. We developed a suite of dynamic algorithms for haplotype block partition and tag SNP selection to minimize the total number of tag SNPs across the region of interest or the whole genome. Our algorithm can be applied to both haplotype and genotype data as well as any pedigree structures. We also studied the power issues in association studies related to tag SNP selection using both simulated data and real data.