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Sommario/riassunto	Genome-wide association studies (GWAS) for complex disorders with large case-control populations have been performed on hundreds of traits in more than 1200 published studies (http://www.genome.gov/gwastudies/) but the variants detected by GWAS account for little of the heritability of these traits, leading to an increasing interest in using family based designs. While GWAS studies are designed to find common variants with low to moderate attributable risks, family based studies are expected to find rare variants with high attributable risk. Because family-based designs can better control both genetic and environmental background, this study design is robust to heterogeneity and population stratification. Moreover, in family-based analysis, the background genetic variation can be modeled to control the residual variance which could increase the power to identify disease associated rare variants. Analysis of families can also help us gain knowledge about disease transmission and inheritance patterns. Although a family-based design has the advantage of being robust to false positives, novel and powerful methods to analyze families in genetic epidemiology continue to be needed, especially for the interaction between genetic and environmental factors associated with disease. Moreover, with the rapid development of sequencing technology, advances in approaches to the design and analysis of sequencing data in families are also greatly needed. The 11 articles in this book all introduce new methodology and, using family data, substantial new

findings are presented in the areas of infectious diseases, diabetes, eye traits, autism spectrum disorder and prostate cancer.