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statistical approaches or strategies to address G x E and G x G interactions with high-throughput sequenced data, including two-stage procedures to identify G x E and G x G interactions, marker-set approaches to assessing interactions at the gene level, and the use of a partial-least square (PLS) approach.

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The single study GSCA approach is most similar to GSEA (or SAFE) in that a single statistic is calculated for each gene set and calibrated via permutations across samples. The results of single study GSCA are therefore compared with GSEA in Section 4.1.

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In this chapter we will discuss the current statistical methods for probe annotation, background estimation, normalization and summarization, and approaches that can be used to test the effectiveness of these methods on the resulting data. I. General Overview A. Gene Expression Microarrays Over the past decade, gene expression microarray has revolutionized the way we measure the level of gene transcripts in biological organisms.

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The contributors first present different statistical approaches or strategies to address G x E and G x G interactions with high-throughput sequenced data, including two-stage procedures to identify G x E and G x G interactions, marker-set approaches to assessing interactions at the gene level, and the use of a partial-least square (PLS) approach.

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Genetic interactions (gene-gene and gene-environment) substantially contribute to complex traits and diseases and could be one of the main sources of the missing heritability. This paper provides an overview of the available statistical methods and related computer software for identifying genetic interactions in animal and plant experimental crosses and human genetic association studies.

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