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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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methods and related computer software for identifying genetic interactions in animal and plant experimental crosses and human genetic association studies.

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