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many diseases and traits  
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pattern than previously  
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approach with nine  
existing competitive  
methods was carried on  
six different real crop  
gene expression  
datasets.

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Gene ...

The single study GSCA  
approach is most similar  
to GSEA (or SAFE) in



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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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Statistical methods for  
gene set co-expression  
analysis ...

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set approaches to  
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Genetic interactions  
(gene–gene and  
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substantially contribute

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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

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