

Controlling for False Positive Findings of Trans-Hubs in e-QTL Mapping

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In the fast developing field of expression quantitative traits loci (eQTL) studies, great interests have been concentrated on detecting genomic regions containing transcriptional regulators that influence multiple expression phenotypes (trans-hubs). In this paper, we develop statistical methods for e-QTL mapping and propose a new procedure for investigating candidate trans-hubs. We use data from the Genetic Analysis Workshop 15 to illustrate our methods. After correlations among expressions were accounted for, the previously detected trans-hubs are no longer significant. Our results suggest that conclusions on regulation hot spots should be treated with great caution.

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