Improving Estimates of Compensatory *cis–trans* Regulatory Divergence

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In this article, I regretfully neglected to cite a paper [1] in which the authors proposed separating RNA-seq technical replicates (the same library sequenced on different lanes) to estimate *cis* and *trans* components of gene expression divergence. While similar in spirit to the approach that I proposed, it should be noted that separating technical but not biological replicates will still lead to an artifactual negative *cis–trans* correlation if there is any error in allele-specific expression estimates driven either by biological variation among samples or by variation in library construction (e.g., due to PCR 'jackpots').

Reference

1. Emerson JJ et al. (2010) Natural selection on *cis* and *trans* regulation in yeasts. Genome Res. 20, 826–836 [PubMed: 20445163]

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