

Mixed Modeling of Copy Number and Exon Data

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Abstract:

We reanalyze two Affymetrix examples. The first, from George et al. (2007), PLoS ONE 2(2) e255, involves allele intensity data from pairs of SNP chip arrays run on blood and tumor samples from children with neuroblastoma. The second, from Kwan et al. (2007), Genome Research, 17: 1210-1218, addresses the heritability of alternative splicing using exon arrays on lymphoblastoid cell lines from a CEPH family. Mixed models provide a useful statistical framework for appropriately handling covariance structure and accurately testing critical scientific hypotheses on a genome-wide scale.