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**Kai Kang\*** (kangkai0714@gmail.com), MA. *A reference-based Bayesian method for sample-specific complete deconvolution.*

Tremendous efforts have been made to determine quantitative trait loci (QTLs) across human tissues. Nevertheless, most such findings were made using bulk measurements, therefore obscuring the cell-type-specificity of genetic regulatory effects and subsequently confining their biological interpretation. Our goal is to characterize the cellular specificity of genetic effects across human tissues and to investigate the impact of these effects to phenotypic traits. Existing studies aiming to alleviate this issue employ partial deconvolution methods to estimate cell-type proportions and use them as covariates to estimate cell type-interaction QTLs. However, due to the limitation of current deconvolution tools, the cell-type-specific QTLs mapping is still out of reach.

To this end, we propose a reference-based complete deconvolution framework which is able to estimate cell-type-specific gene expression and their proportions simultaneously for a single bulk RNAseq sample. We employ a Bayesian modeling strategy and provide a Monte Carlo algorithm for parameter estimations. Benchmarking studies show our method outperforms existing sample-specific deconvolution tools. This method would grant us to better explore bulk data and help decipher sample heterogeneity. (Received January 24, 2022)