

Opportunities and challenges for integrated analysis of genomics data resources

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Unraveling the mechanistic underpinnings of genetic associations with complex traits requires characterizing and testing associations with cell and tissue-specific expression profiles. New opportunities exist to bolster this investigation with the growing number of large publicly available -omics level data resources now available. In this talk I describe some of the opportunities and challenges inherent in integrating these big data resources that involve concepts ranging from causal inference to missing data methods. I also present some of my current research on two-stage regression imputation and fully likelihood-based strategies to leverage external resources for robust inference. These methods are applied to an investigation of the genetics of evoked inflammatory response, and a simulation study is described.