Application number/Title: 32285 - Detecting pleiotropic effects through integration of omics data

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Keywords provided by the Applicant PI to describe the research project:

omics, pleiotropy

Application Lay Summary:

Using omics data, we will attempt to identify shared genetic variants that play a role in a number of common traits and diseases that have a high public health significance that include: asthma, obesity, type 2 diabetes, blood pressure and blood lipid profiles. We will accomplish these goals by using the UK Biobank data and a second dataset with gene expression and genome sequence data on a small set of subjects. We will use statistical methods to detect shared genetic effects and perform biological validation in order to bring about a better understanding of the role shared genetics plays in complex disease. The co-occurrence of common traits and diseases pose a critical public health challenge; this co-occurrence may be explained, in part, by genetic loci shared between these traits and diseases.

Identifying shared genetic loci for pairs of traits/diseases will advance our understanding of the mechanistic links between them. These loci have the potential to serve as targets for a single intervention that simultaneously treats both diseases. We will implement previously developed statistical methods and extend existing methods to analyze imputed and rare genetic variants to identify variants associated with two of the diseases/traits listed in 1a. All methods will be implemented in software developed by one of the investigators on this proposal, Dr. Suzanne Leal, which uses parallel processing to make it feasible to analyze hundreds of thousands of samples efficiently and quickly. We plan to analyze the full cohort of approximately 500,000 subjects with genotype and phenotype data.