CLSA Approved Project

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Project Title
Interactive visualization of genetic variant-trait associations in the CLSA dataset

Project Summary
The CLSA study collected data on thousands of traits and hundreds of millions of genetic variants in almost thirty thousand Canadians. Manually sifting through all the resulting gene-disease association results, trait by trait and variant by variant, is neither an efficient nor comprehensive way to foster discoveries. Efficiently translating such massive amounts of results into new understandings of health and disease for Canadians requires making the association results from large-scale genetic studies accessible to researchers in an intuitive and easy-to-use manner. In this project, we will build an instance of PheWeb - our web-based interactive tool for visualizing and browsing through hundreds or thousands of genetic association results efficiently and intuitively - to make all CLSA association results available to researchers at their fingertips, which will facilitate data sharing and collaboration among the community members.

Keywords
genome-wide association, phenome-wide association, interactive browser, data sharing