Building a Predictive Quantitative Genomics Framework for Identifying Endophenotypes in Opioid-Dependent Patients

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Our research group is developing a machine-learning interface to peruse relevant gene expression data sets that are related to acquired clinical data from publicly-available databases. We have built an algorithm for automated meta-analysis of gene expression sets and comparison to clinical data sets using the programming language, R. This provides a computational framework for prediction tasks using quantitative genomics data. In this project, we present the basis of a platform for the Unsupervised Learning Environment using genomic database data, which can be used as a method to use test results to help healthcare providers make earlier diagnostic and treatment decisions. This research focuses on the clinical relevance of endophenotypes, which are quantitative measurements that are correlated with disease via shared genetic causes. Quantitative measurements in medicine can include blood tests, functional tests, tissue staining, serum measures, and imaging analysis—among other clinical values. Through shared genetic causes, these endophenotypes can often precede the physical manifestation of disease, making them a potentially valuable tool for preventive care. Identification of candidate endophenotypes and their clinical utility is often stalled by the lack of genomic databases in individual research groups. Using a newly-distributed public gene expression database, we designed a machine learning interface to find genes of interest in opioid-dependent patients. Here, we present the interface and its ability to identify and validate genes of interest. Going forward, we will use this to associate genomic data with pharmacogenetic and toxicology tests in matching opioid-dependent patient populations. From the sum of these analyses, we can generate candidate endophenotypes.