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by

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A Phenotype based genomic interval storage and viewing system

ABSTRACT

Disease-oriented research often includes mapping of genome intervals that are associated or linked with a disease. This data is typically only accessible through thousands of journal articles in the scientific literature. Interval is a resource to store, manage, and retrieve genetic interval related information. The goal of this project is to develop a system to store interval information for diseases along with corresponding phenotype information. The system is Java-based and allows the scientific community to upload and view data stored in the database. Each interval is associated with one or more publications. Basic operations (i.e. union, intersection) on intervals will allow researchers to refine intervals and genomic data interactively. Using the UCSC genome database, candidate gene lists for intervals (or sub-intervals) can be integrated. Extended analyses can be performed over multiple intervals with similar phenotypes, based upon the presence of similar genes (e.g., Paralogs, present in the same pathways, similar expression, etc).