MYTRACK: AN APPLICATION THAT INTEGRATES WITH THE UCSC GENOME BROWSER TO PROMOTE ORGANIZATION, CUSTOMIZATION AND SHARING OF GENOMIC DATA

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Rapidly-evolving high-throughput sequencing technology is making huge volumes of sequencing data available for analysis. Faced with this mass of data, researchers are challenged to organize it, customize it and collaborate efficiently with it. To address these challenges, we developed a web application called ‘MyTrack’. In addition to managing data, MyTrack integrates and interacts with the University of California Santa Cruz (UCSC) Genome Browser, providing high-quality data visualization. The UCSC Genome Browser is the most current visual analysis tool capable of processing high-throughput technologies like next generation sequencing, array-related technology, and SNP genotyping. As a web-based application, MyTrack is implemented using PHP with a CakePHP framework. Information is stored in a MySQL database. MyTrack organizes experimental data on three levels: project management (each project is a collection of data defined by the project manager), track management (each track represents the data of one sample from within a project) and session management (each session is a collection of user-selected tracks). Once logged in to MyTrack, users can access the projects for which they are authorized, and create sessions by selecting tracks from those projects. Users can then employ advanced features of UCSC Genome Browser, visualizing sequencing data on different levels, from single nucleotide resolution to entire chromosomes. Another feature of MyTrack is the ability of principal investigators and authorized researchers to share notes and data with selected collaborators. In addition to managing high-throughput data from next generation sequencing, MyTrack can host microarray data, exon array data, SNP genotyping data, and many others.