

DEVELOPMENT OF TOOLS FOR SOYKB: SNPviz,
DIFFERENTIAL EXPRESSION AND PROTEIN BIOVIEWER

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ABSTRACT

Soybean Knowledge Base (SoyKB) is a comprehensive website, which contains lots of web sources for soybean. By integrating multi omics data and solving data storage problem, SoyKB is able to build connection between multiple datasets. Lots of hands-on tools has been designed and developed into SoyKB. And three of them, SNPviz, Differential Expression and Protein BioViewer, will be introduced in detailed methodology and function demonstration.

SNPviz is a simple-to-use SNP haplotype viewer. Its variety of options to view haplotypes from designated gene areas to larger chromosomal areas makes users able to scrutinize on different levels with ease. Its dataset selection function increases its convenience to use as it allows users to put in SNP-array files along with annotation files. SNPviz collects all the samples and composes a phylogeny tree according to the identity of haplotypes.

Differential Expression is for visualizing all kinds of data including Transcriptomics RNA-Seq, Microarray, Metabolites and Proteomics data, which all come from public sources and collaborators. It features six functions: Gene Lists, Venn Diagram, Volcano Plot, Function Information, Path Information and Enrichment Analysis. They will be used based on thresholds settings (p-value/q-value, fold change) by users' input.

Protein BioViewer is designed to show the primary protein sequence, predicted secondary structures, phosphorylation positions, amino acid characteristics, functional domain positions and transmembrane helix positions