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ChromoViz-Web: mapping and multimodal visualizing gene expression data with integrated major bio resources onto chromosomes using scalable vector graphics



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Short Abstract: ChromoViz-Web is a web-based service for the visualization of microarray gene expression data, cross-species and cross-platform comparisons, as well as non-expression genomic data obtained from public databases onto chromosomes using Scalable Vector Graphics. In addition, it provides a function for mapping gene expression data with integrated major bio databases.

Long Abstract:

Mapping gene expression data in chromosomal order with associated annotations is a powerful tool for understanding the higher-level chromatin structures coordinating transcriptional regulation. Recently, developed tools (Sturn et al., 2002; Gentleman 2003), however, have some limitations. It is not easy to add tracks for informative non-expression data for chromosomal analysis such as CpG islands, gene density, variations, repeats and genomic DNA copy number alterations from array CGH. Applying comparative genomic information may uncover patterns of gene expression conserved between human and mouse. ChromoViz-Web (<http://www.snubi.org/software/ChromoViz>) is a web-based service for the visualization of microarray gene expression data, cross-species and cross-platform comparisons, as well as non-expression genomic data obtained from public databases onto chromosomes. In addition, it provides a function for mapping gene expression data with integrated major bio databases such as NCBI's GenBank, UniGene, LocusLink, RefSeq, Homologene, UCSC Golden Path's refGene, knownGene, all_mRNA, all_est, NetAffyx and NCBI's report for chromosome and cytogenetic band.

To clearly separate the data layer from its procedure layer, ChromoViz-Web uses a data format called Chromosomal Visualization Format (C.V.F) to store the position, value and other data associated with tracks (i.e. tab-delimited with the nine attributes, track/taxonomy/chromosome/strand/begin/end/id/value/title). A Web site, <http://www.snubi.org/software/ChromoViz/>, has been provided to generate CVF files with human-mouse homology tracks from accession numbers and expression levels. Moreover, ChromoViz-Web provides a service that generates CVF files automatically by being entered another input, preCVF (i.e. tab-delimited attributes, track name/species/accession-number/expression-level).

Microarray datasets for human and mouse stem cell differentiation are mapped onto human chromosomes with cytoband, mouse-human homology and cross-platform-comparison information for the purpose of illustration.

From its input, a CVF file, ChromoViz-Web produces JavaScript-enabled Scalable Vector

Graphics for web-enabled interactive visualization of gene expression data onto chromosomes.

Integrated visualization and the function for providing associated annotations onto chromosomes will benefit biological knowledge discovery.