Biodalliance: a fast, extensible, genome browser

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Project website: http://www.biodalliance.org/
Source download: http://github.com/dasmoth/dalliance
License: BSD

Genome browsers are a vital part of the genomics workflow. Inspection of annotations and experimental data have proved indispensable for spotting unexpected correlations, formulating new hypotheses, or simply sanity-checking new data sets. The sequencing revolution has made this even more important. Today, even small labs are routinely applying techniques like ChIP-seq, RNA-seq, or genome sequencing, often with limited bioinformatic support. To keep pace with these trends we need tools that make integrating and visualisation large datasets as effortless as possible.

Dalliance [1] is a genome browser which makes aggressive use of modern web technologies to offer a high level of interactivity and powerful navigation and exploration tools while running within a normal web browser. The display can be freely scrolled and zoomed with mouse gestures and keyboard controls. Shortcuts for navigation between features allows sparse datasets to be rapidly explored. We have adopted a fully distributed approach, with no backend server between the datasets and the web-application client. Data can be accessed directly from a number of standard indexed binary file formats, such as BigWig, BigBed, BAM, and VCF. Direct file access makes integrating new genomic datasets, particularly the results of high-throughput sequencing experiments, very quick, and accessible to occasional bioinformaticians who often have limited sysadmin experience – and limited enthusiasm for installing extra server software. It also allows instant access to datasets in this format from remote web servers without time-consuming downloading (e.g. ENCODE datasets from EBI). Unusually for a web-based application, Dalliance also allows viewing of data directly from local disk on your own machine, without any helper processes or servers.

Recent developments include support for more file formats (VCF, non-binary BED and WIG), support for UCSC-style "track hub" metadata, and hooks to allow user code to interact with the displays and control the integration of data from multiple sources.

[1] Down TA, Piipari M, Hubbard TJ. *Dalliance: interactive genome viewing on the web* Bioinformatics (2011) 27:889-890