The Genome Workbench Program

A powerful standalone program designed for genome analysis


Scope and Access
The Genome Workbench program (GBench) from NCBI is a powerful display and analysis tool for studying biological sequence data. GBench is freely available for download, and runs on most major computing platforms (A). GBench enables access to sequence data publicly available at NCBI as well as the ability to upload private data. Many viewing options in GBench allow data interrogation at all levels, from a graphical overview to single nucleotide resolution. Over 15 different analysis tools, such as BLAST, Splign and Phylogenetic Tree Builder, are built into GBench, making it a powerful software tool for performing sophisticated analysis. Download instructions, help documentation, tutorials and links to video How-To's (B) can be found on the GBench homepage (right). The video tutorials, as part of the NCBI video collection, are directly available on the NCBI YouTube channel (www.youtube.com/ncbinlm/).

Opening a Public Genome Record
A common use of GBench is to graphically display a genomic record and its annotation, which can be done using the “File >> Open” dialog box (C). Highlighting an assembly and clicking the “Next” button (D) opens the project dialog box. Clicking the “OK” button (E) adds the project to the project tree. Double-clicking the project opens the Open View window (F). Clicking “Graphical View”, selecting “chr1” and clicking “Finish” button (G) opens the display.
Searching and Browsing Annotated Features

The “Search View” tab (A) allows for searching with names of genes and other features annotated on the genome. A Feature Search with “IL6R” (B) on the selected chromosome (chr 1) retrieves a single gene. Double-clicking the result adds the feature to the project tree view and updates the graphical display (C) to show details of the retrieved gene. Clicking the arrow (D) in the tools strip activates a menu for customizing tracks shown in that graphical panel. Clicking and dragging across a region in the ruler (E) highlights that region. Right-clicking the highlighted region (F) outside the ruler section allows zooming (G) into that region using the “Zoom” menu option. The “Run Tool …” option (H) in the right-click menu provides access to tools for analysis of the displayed sequence. Hovering on an object displays its details in a popup (I).
Searching selected sub-sequences with BLAST

Right-clicking a highlighted feature (A) and selecting “Run Tool” (B) in the menu activates the Run Tool widget. Selecting the “Blast” option (C) allows a BLAST search using the sequence as a query against the selected database (D). An Entrez query, such as “human [orgn] AND biomol_mrna[prop]” (E), helps restrict the search to a specific subset of sequences in the database. Additional databases are available by clicking the folder icon (F). Follow the dialog boxes to add the search to the project (G).

The Project View displays a successfully completed BLAST search as a new node (H). Double-clicking the node followed by “Multiple Alignment View” menu selection (I) displays the search result in a new panel (J).

Clicking the “+” and “−” signs (K) toggles on and off the annotated features to the right. Options in the right-click menu allow the examination of the alignment at the sequence level in selected color scheme (L).
Displaying a region in non-graphical format

GBench can display a feature in Project View, such as the IL6R node (A), in different formats through options in the “Open View” dialog box (B, activated by double-clicking A). The example shows the “SNP Table View” (C) for this region. This table’s display order is resortable through column header click. Context menu (D) activated via right-click allows filtering of displayed SNPs according to their attributes as well as exporting the list to a csv file.

In the “Open View” menu, selecting the “Sequence Text View” option (E) allows GBench to display the selected region, gene, or other feature as a marked up sequence. This display color-codes annotated and projected subregions and mapped SNPs onto the sequence. Untranslated regions (UTR) are shown in blue (F), coding regions are in red (G) with codons separated by black dots (upon hovering, not shown), and introns are in lowercase green (H). Mapped SNPs are shown as black letters (I) under the sequence.

Tutorials & Announcements

The GBench online tutorials provide detailed descriptions on how to use specific functions of GBench. Example links to the “Working with BAM files” section and to the playlist of YouTube video tutorials for GBench are given below:

www.youtube.com/playlist?list=PL60C2D06BE1E0BFDB&feature=plcp

For updates, subscribe to the GBench announcement mailing list: