

The Next Genome Browser

Introduction

In the exploratory phase, most datasets can be viewed as features along the genome. These features can be qualitative and/or quantitative and are generally linked with external references to searchable public data (e.g. Ensembl). Our aim is to provide an user interaction layer on top of a simple dynamic genomic data viewer. Without the will to replace what was done before, we first focus on data viewing and rely on other browsers to references public data. Then we work on the analysis of the data, the ability of doing basic, then advanced analysis. This part is covered by the gFeatMiner plugin also developed by the BBCF team.

Features

Visualization

A novel genome visualization tool is proposed where the user interface remains simple. Using technology from Berkley University working entirely inside the web browser, a special focus is put on the interactivensess and intuitively of the GUI.

The browser can display several types of features such as qualitative data that represents features of interest on a genome, like an exon, intron, or UTR, as well as quantitative data where each base pair of a genomic region is associated with a score. One can simply drag to move and double click to zoom. and incorporates a set of common statistical analysis functions. A selection on a particular zone of interest can be made using the lasso tool.

Data center

Genomic files are easily uploaded and processed by the browser. GDV accept a large choice of formats (GTF, BED, WIG, ...) and different sources (Ensembl, UCSC, ...).

With another tool developed by the BBCF team : *GenRep*, GDV know which data correspond to what. ??develop??

Once uploaded, your data can be viewed at any time and can be exported to another format if you need it.

Collaborative

One important feature of GDV is that you can share your data with people. You can be a circle of person working together on the same project analysis of the data. Or you may just want to share the 'view' of your project with other people.

With different levels of sharing, you can tweak which person you want to work/share with.

Descriptive statistics

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Genomics manipulations

A set of tools that can manipulating and compute descriptive statistics on genomic features. Thus GDV incorporate *gFeatMiner* directly on the visualization. The aim is to launch jobs that can be viewed in the GDV interface.

Screenshot

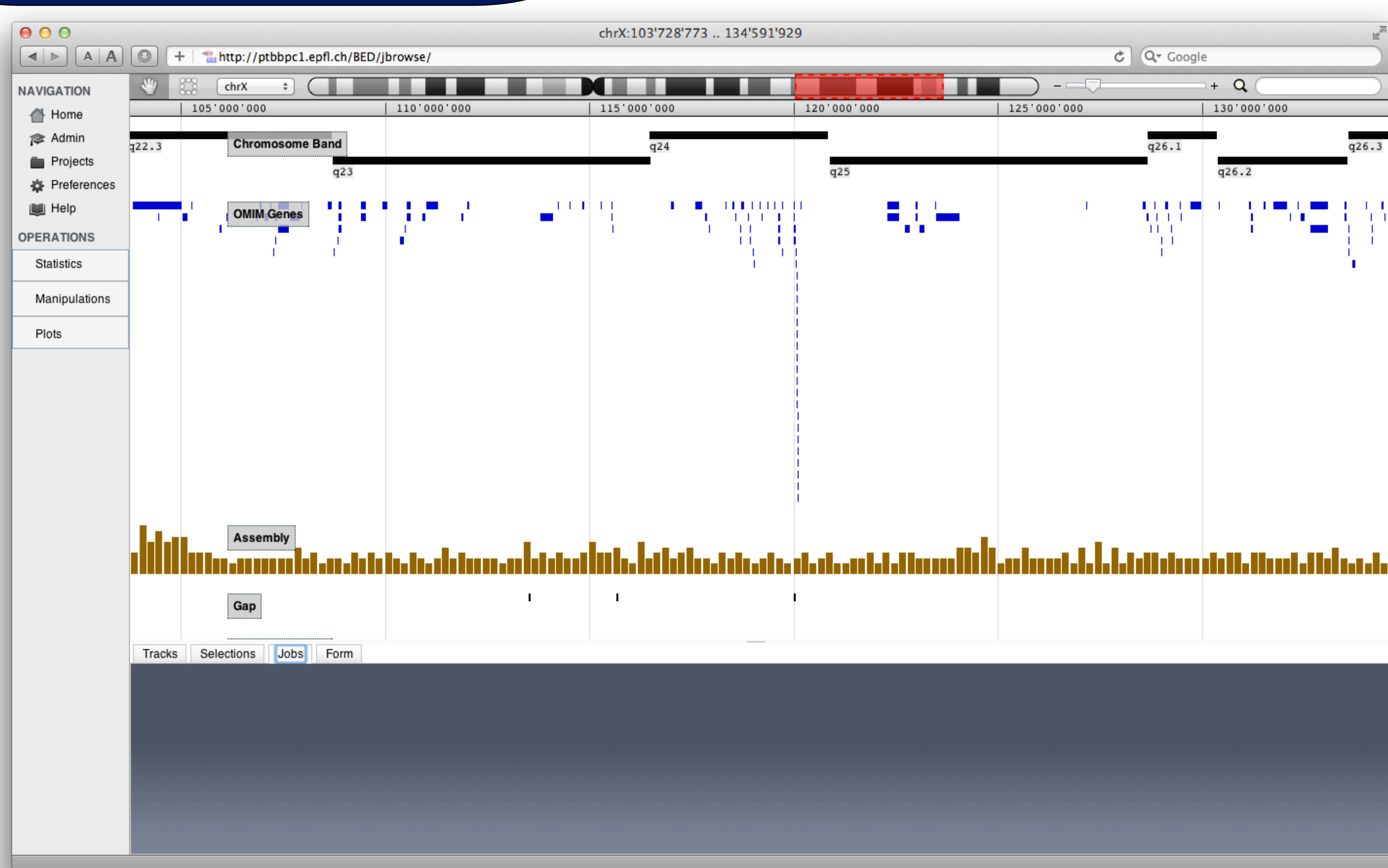


Figure 1: The main view of the online genome browser rendered in Safari.

Data center figure



Figure 2: The permission management view of online genome browser.

Descriptive statistics

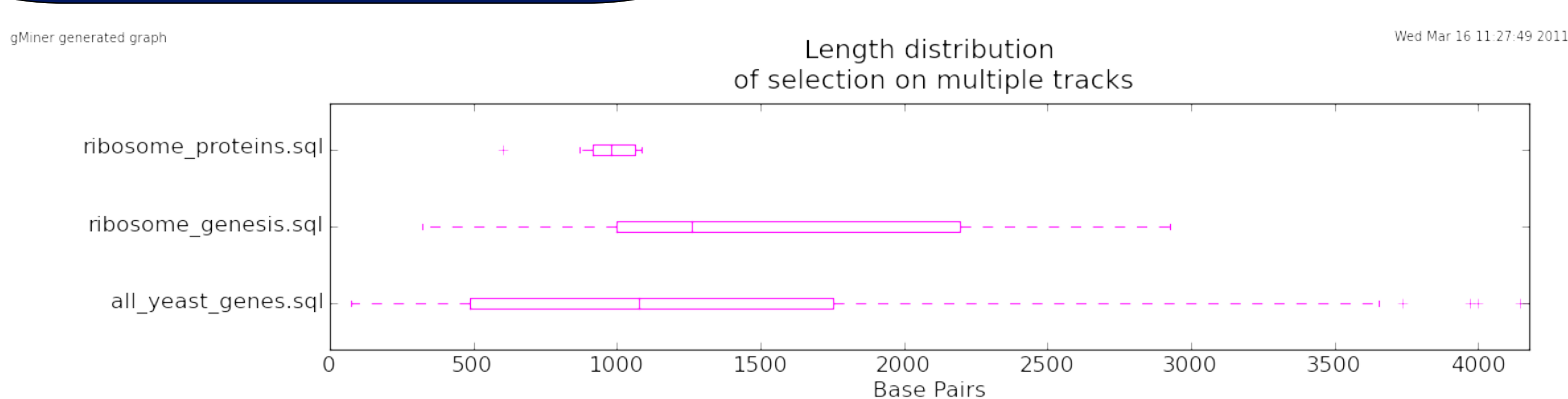


Figure 3: An example statistic computed on three different tracks.

Genomic manipulation



Figure 4: A schematic of a genomic manipulation. A and B are two different input tracks. The result is the boolean AND operation. This could be useful, for instance, if A were a list of gene candidates and B a list of HIV integration site. The manipulation would reveal which genes parts can be infected.

Conclusion

As the age of computational biology approaches, tools like GDV will become increasingly important as petabytes of data overwhelm the field. The ability to aggregate and analyze data from diverse sources will be valuable to generating new hypotheses and discovering new biological processes.