Genome Browser

Genome browser is a genomic viewer that allows to visuazile in different zones of visualization(trakcs) different features (genes, snp, variations...).

Architecture

The genome browser is composed of 2 panels showing the careotype and chromosomes of the selected species (blue) and in the lower part different tracks or zones of visualization of genomic features (green).
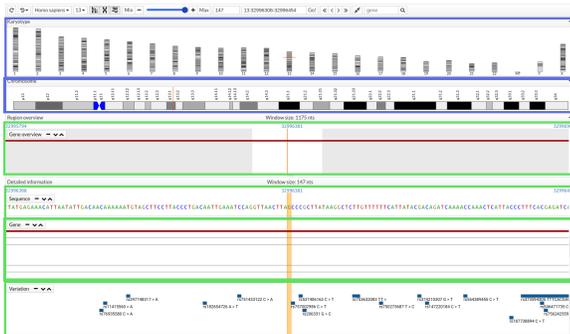
The panels are defined when you instantiate the Genome Browser, the tracks are added later.

One of the main characteristics is their joint movement. When you move to a zone of the genome all the tracks move together to visualize the same zone of genome.

The navigation bar is shown at the top. Ih this bar you can select setiings that will affect the entire genome browser, such as the species selector. From left to right it shows:

- Recharge button: This button reloads the genome browser locating it in the initial position.
- Region history button: In this button you can reposition your genome browser in a position previosly searched.
- Species selector: In this selector the user can change species. The available species are those available in the cellbase database. (Cellbase species)
- Chromosome selector: This selector is a quick way to change the chromosome.
- Toggle Karyotype panel: Show or hide the karyotype panel.
- Toggle chromosome panel: Show or hide the chromosome panel.
- Toggle overview panel: Show or hide the overview panel.
- Min button: Minimun windows size.
- "-" button: In this button the user can decrease the zoom by making the area to be displayed larger.
- Zoom scrollbar: Scrollbar to adjusted to the desired zoom by the user.
- "+" button: In this button the user can increase the zoom by making the area appear smaller.
- Max button: Maximun windows size.
- Windows size button: Show the window size in nucleotides.
- Position: This display shows the region where the tracks are located. The structure of region is "chromosome:start-end". This input is editable, the user can write the desired position and then click on the go button to change the region.
- Go!: This button positions the genome browser in the position shown in the display position.
- <<, <, >, >>: These buttons are to scroll through the genome browser. If the user wishes instead of clicking and dragging on the track to move, you can press these buttons to move laaterally within the genome. The "<<" and ">>" buttons will make a big jump in their directions while the movement when pressing "<" or ">" will be smaller.
- Compact button: if this button is pressed the tracks will be shown in extended mode occupying all the space necessary to show the information contined in its entirety. If the botion is not pressed, the tracks will have the predefined height in their creation and a lateral scroll bar will be shown when the information they contain is greater than the size they have.
- Gene display and search: For more comfort the user genome browser can be located in the region that occupies a certain gene. For this, the user can enter a gene in the display and give the magnifying glass to search.

Tracks and Panels

- **Karyotype:** All human chromosomes are shown. The current display area is indicated by an orange line.

- **Chromosome**: The selected chromosome is displayed. The current display area is indicated by an orange line.
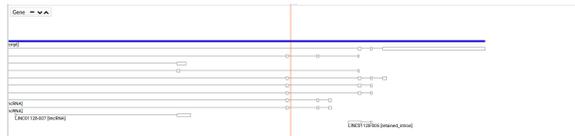

- **Gene overview:** Region genes shown. This area is less than the area zoom genes. It is to have a global vision to the user that there are genes around.

- **Sequence:** Bases of chromosomal sequence. If the viewing area is very large sequence it will not be shown.

- **Gene:** Gene and transcripts found in that region.

In a closer view we can see exons painted red when they are protein coding. When you place the mouse on top of the exon, the track show the amino acid and a tooltip which exon description.

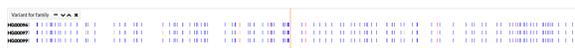- **SNP:** SNP found in that region.

If the size of the region is no longer, the snp be displayed , if not a histogram of these .

- **Variant browser - compact mode:** In this mode the variants are displayed in mode browser.

- **Variant genotype - extended mode:** In this mode there are samples. The genotypes of the samples are drawn, showing in blue 0/0, in yellow 0/1 and red 1/1.

- **Bam:** The coverage is shown at the top. In the lower part the readings are shown.