Genoverse 2.0

This is only a draft, the content, style and format may differ with the definitive version

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Genoverse 2.0 Documentation

Introduction

Genoverse 2.0 is a customizable, back-end independent JavaScript and HTML5 based genome browser which allows the user to explore data interactively.

Genoverse 2.0 is based in Genoverse, a genome browser created in the early 2010s and developed by Eugene Bragin, a former student of the MSc in Applied Bioinformatics in Cranfield University, with the Wellcome Sanger Institute, original creators of Ensembl.

Description

The first contact of the user with the program is through the welcome page, which displays a list of available Genoverse 2.0 instances, and gives the user the option to sign in using a previously created account. Once logged in, the user gains access to additional features like create a new instance of Genoverse 2.0 or modify the already available ones, both of them redirect to the instance page. A user that does not sign in only have access to the genome browser page.

In the instance page, there are several properties that allow the user to totally customize the new instance that will be created such as the species genome to visualize, the plugins to implement and the tracks to display. In addition, it allows uploading files of different formats to be displayed in the browser.

The genome browser page is where the instances display all the info of the selected genome in different tracks.

How it works

How Genoverse genome browser works
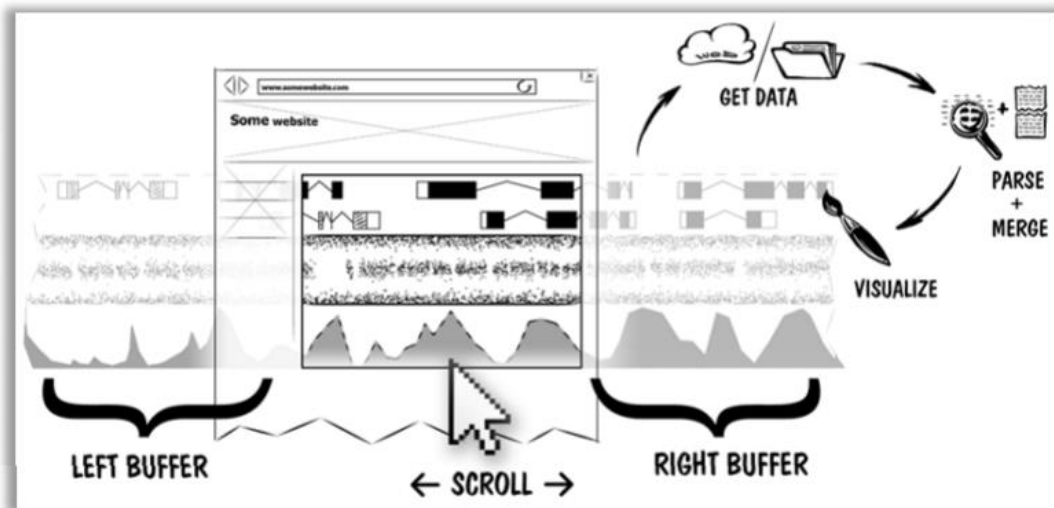
Genoverse 2.0 browser deploys itself automatically from the instance properties and configuration provided. At first, Genoverse tracks make initial AJAX data requests for the current coordinates in the genome, as well as left and right buffers, in order to make the data ready for smooth scrolling and zooming operations.

How to navigate
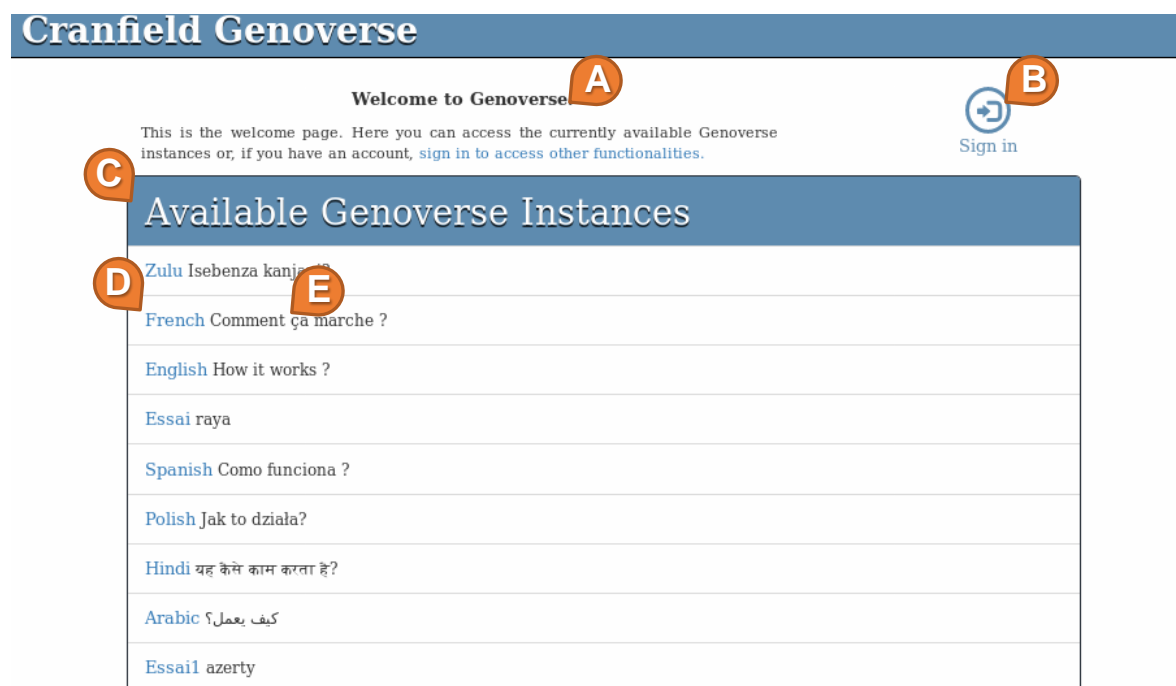
The welcome page is the first encounter of the user with Genoverse 2.0. At the top of the page, there is a brief welcome message and description of what the user can do (A) and a button that allows signing in Genoverse 2.0 (B). Currently, there is no option to create an account, in order to do that, it has to be created manually in the database by the programmer team.

The page displays a list of all the Genoverse 2.0 instances available (C), understanding instance as a custom Genoverse 2.0 genome browser with its own genome, tracks and plugins. In each instance, it is shown the name of the instance (D), which is also a link that redirects to that instance, and a brief description (E).

a) How to Sign in

If you have an account in Genoverse 2.0 and you want to sign in, simply click on the *Sign In* button (B). You will be redirected to the Login Page. Here you will see two forms, put the email that you used to be registered in the first one and your password in the second. Finally, click on *Sign in*. If you do not have an account or just want to go back, you have that option behind the *Sign in* button.

b) Additional features

Once you are logged in, you will have more buttons available on the welcome page.

- *Create a new instance*: If you click here, you will be redirected to the Instance page, which will be explained in the next section.
- *Sign out*: This button will log out your account. Use it when you finish working with Genoverse 2.0 to be sure that no one else enters into your account.
- *Modify*: This button will appear on the list of instances. If you click here, you will be also redirected to the Instance page, where you can modify the properties of the selected instance.

Instance Page

The Instance page is where the user can create or modify a new instance of Genoverse 2.0. On the top of the page, the user can specify the name for the new instance (A), the description of the instance that will appear on the Welcome page (B), the species genome (C), the chromosome in which the instance will be initialized (D), and the start and end

position to be displayed of the chromosome (E, F). If the user prefers to upload a file, clicking in *Ensembl* (G) will change the list of species (C) to a file chooser to upload the desired file. There is also a *Home* button (H) that will redirect the user to the Welcome page.

On the left side, there is a list of all the plugins available for the instance (I), having each one a checkbox to activate/deactivate them (J). In a similar way, on the right side, there is a list of tracks (K) and each one has a checkbox to activate/deactivate them (L). The gene and dbSNPs tracks have a pencil-shape button next to them (M) that allows changing their configuration (Name, info and URL). The rest of the tracks possess a plus-shape button next to them (N) that when is clicked, it displays a pop-up window with the configuration of the track and the option to upload a file. This configuration will be saved and displayed when the user clicks on the track name (O). Finally, the user can submit the configuration on the *Submit* button (P).

Genome browser
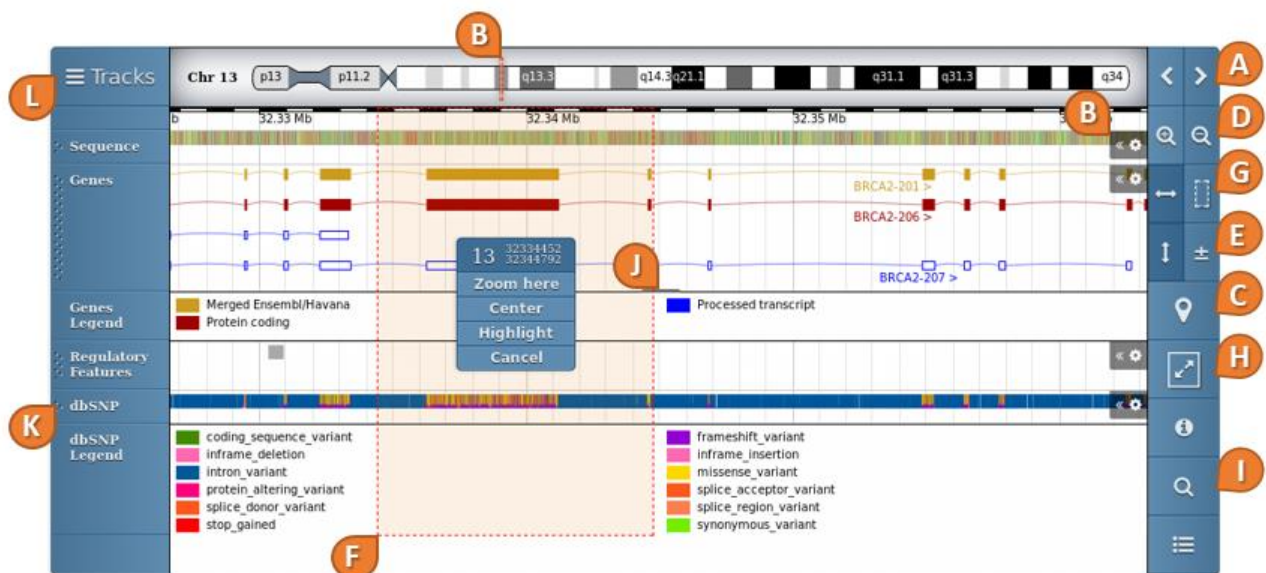
As is common for genome browsers, Genoverse 2.0 consists of a set of "tracks", each representing different data as configured by the webmaster. Navigation along the chromosome can be performed either by dragging tracks sideways with a mouse or by clicking the left/right arrow buttons in the top control panel (**A**). It is also possible to navigate by dragging the karyotype viewpoint (**B**) or clicking on a chromosomal band. To re-centre, the focus back to its original view, click the focus-region button within the control panel (**C**).

Zoom operations can be done with the +/- buttons (**D**) or by double-clicking on a specific location. It is also possible to zoom with a mouse wheel if the switch (**E**) is on (off by default). The user can also zoom in by selecting a region with a mouse while holding the SHIFT key (**F**), this can also be toggled in the control panel menu (**G**). To resize genoverse to fit the full screen, toggle the full-screen button (**H**).

a) How to search by gene or position

When you click the search plugin (**I**) a search menu will open:

From here you can search by gene, search by position or search for a gene within a defined position.

To search by gene across the whole chromosome, leave the position fields blank, to move to a new position and not search a gene, leave the gene field blank.

The result of a gene search will be a table of all the genes that contain those characters:

From here you can move to the position of each gene by clicking on the gene name

b) How to resize, move, add and remove tracks

The resizer (**J**) shows where you can resize tracks. If this is clicked, the track will resize to fit all the information from the track currently visible. If this is dragged, the user can resize as chosen. The handles (**K**) show where you can drag tracks to reorder them.

To add and remove tracks available with the current data loaded, click the track menu (**L**).

From here you can add available tracks and remove currently enabled tracks. You can also search the list of available tracks if you have implemented a large number of datasets

To add more tracks than those available, you can write custom tracks on the welcome page or add more datasets that will make more track options available. This can be done on the welcome page or by dragging and dropping files.

c) How to view details

ENSR00000060898

Focus here   Highlight this feature

Location	13:32340801-32341000
source	Regulatory_Build
feature_type	regulatory
description	Predicted promoter flanking region
seq_region_name	13
strand	0
bound_start	32340801
bound_end	32341000

If you click on a feature within the browser, a menu appears with more details listed and the option to highlight this feature or refocus the view to that region.