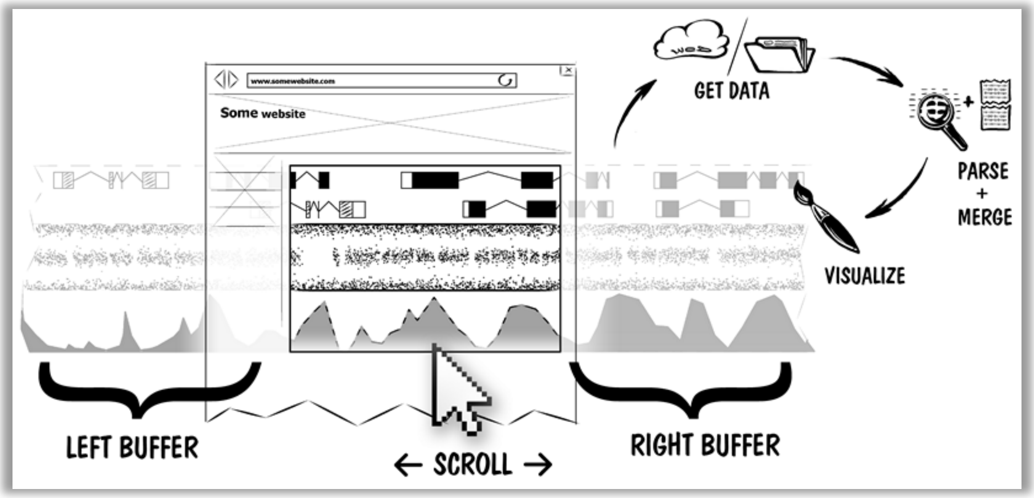
Genoverse

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

Genoverse can be installed on any website and show data from a wide range of online or local sources, working with a variety of formats, such as XML, JSON, GFF, GFF3, BED (try drag-n-drop one), and can be customised to parse and display any data source as required.

How it works



When integrated into a web page, Genoverse deploys itself automatically from the configuration provided. At first, Genoverse tracks make initial AJAX data requests for the current coordinates, as well as left and right buffers, in order to make the data ready for smooth scrolling and zooming operations.

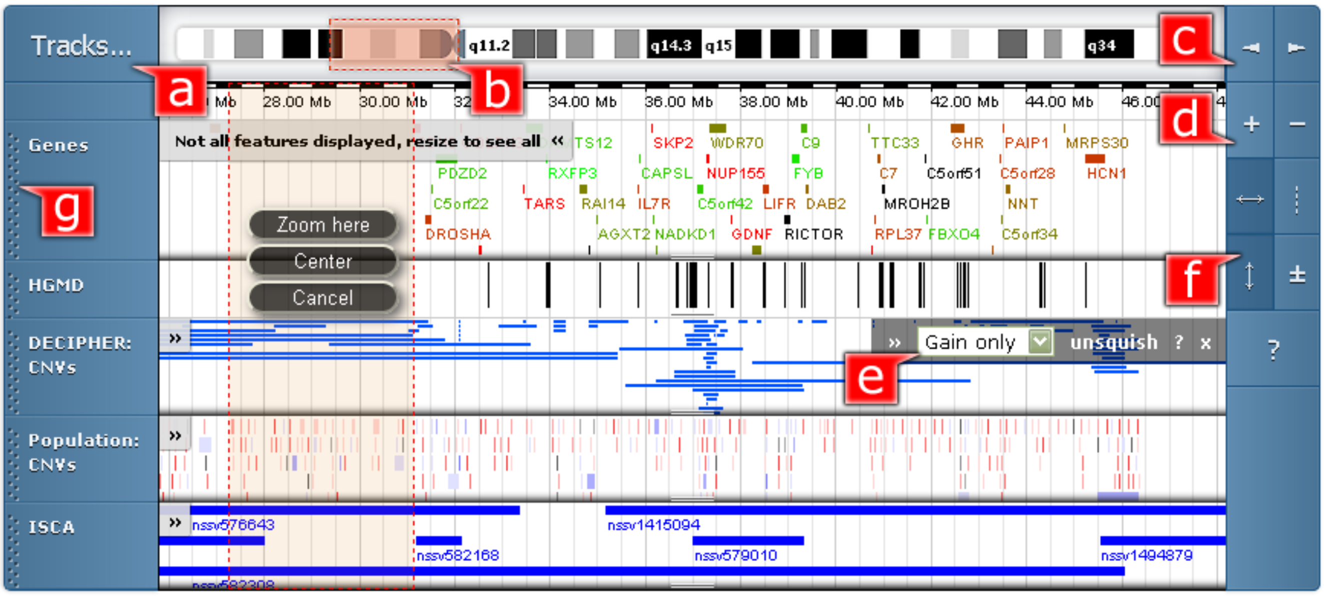
How to embed

Genoverse can be easily integrated into 3d party websites. Typical embedding code looks something like:

```
<script type="text/javascript" src="/js/genoverse.combined.js"></script>
<script type="text/javascript" src="SequenceVariation.js"></script>
<script>
  var genoverseConfig = {
    container : '#genoverse',
    width     : 1366,
    genome    : 'tomato',
    plugins   : [ 'controlPanel', 'karyotype', 'trackControls', 'resizer', 'tooltips', 'fileDrop' ],
```

```
    tracks   : [
     Genoverse.Track.Scalebar,
     Genoverse.Track.extend({
      name       : 'Fasta',
      controller : Genoverse.Track.Controller.Sequence,
      model      : Genoverse.Track.Model.Sequence.Fasta,
      view       : Genoverse.Track.View.Sequence,
      url        :
'http://genoverse.org/examples/tomato/data/Solanum_lycopersicum.SL2.40.18.dna.chromosome.__CHR__.fa',
      resizable  : false,
      30000      : false
     }),
   document.addEventListener('DOMContentLoaded', function () { window.genoverse = new
Genoverse(genoverseConfig); });
  </script>
```

How to Navigate



As is common for genome browsers, Genoverse 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 (c). It is also possible to navigate by dragging the karyotype viewpoint (b) or clicking on a chromosomal band. Tracks can be reordered with a mouse by dragging the track’s handle bar on the left (g). If information on the track does not fit its current vertical space, the user can resize it by clicking or dragging the bottom border. 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 (f) is on (off by default). The user can also zoom in by selecting a region with a mouse while holding the SHIFT key.
Clicking on a specific feature (e.g. a gene) inside a track will open a popup menu with more information if present. Track controls (e) include standard buttons, such as

"*close*" and "*more info*" as well as track-specific controls, where configured. More tracks can be added from the tracks library in the general configuration menu, accessed via the top-left button (a). Genoverse supports a number of static file formats, such as BED, VCF, GFF, GFF3 and others. Local files can simply be dragged and dropped directly onto Genoverse from the file manager, which will trigger the parsing of the data within the browser, and visualise it as a new track without uploading the file online.

Contact

If you have any questions, please contact **info@genoverse.org**