UCSC Genome Browser Basics. Part Two: Configuring the Browser

Welcome to Part Two of the Basic Browser video series. In Part One of the series, we focused on the use of accession names – the many ways that identifiers of various kinds can be used to locate genomic locations and gene annotations. We also saw a few configuration options for setting up the Browser. In this installment, we will focus on many more ways that the Browser image can be configured to show the data the way you want it.

At the end of Part One, we found ourselves on chromosome 11, with several datasets turned on. To make it easy to find that location again, we have saved the configuration for easy access.

[0:41] Load Saved Sesson

The Saved Sessions feature is the subject of a separate video in the UCSC Browser video collection, so it will not be presented here.

The session was saved under the username videoDemo1 and the session name hg19_nav1. The session can be accessed directly in any browser using the url:

https://genome.ucsc.edu/s/videoDemo1/hg19_nav1

This returns us to that same location with all the configuration options intact.

[1:20] Export .png image

It is possible to export an image from the browser in a number of ways. If we use the right mouse button to view the image, then it'll draw the Browser image from the middle of the screen. And then you can save the image to a directory as a .png file. A .png image will get pixelated, however, if you try to zoom in and is only at screen resolution.

[1:47] Export .pdf image

Let's go back and look at the browser. There is another way to view the image, which is useful for getting a graphic for a publication, which is required to be at much higher resolution. So, if I click the "PDF/PS" link up here in the "View" menu, then you're able to download the current browser graphic in PDF format. And, if I open it with Adobe Acrobat, I have a PDF version, and then this PDF version can be viewed at very high resolution and because it's vector graphics, it doesn't get pixelated when you zoom in, and so you can save this and then open it up in an application such as Photoshop, where you're able to modify the

resolution, save it at three hundred dots per inch or even higher so that you can grab just a part of the screen.

[2:40] Adjust image by changing the screen width

So if I go back now using the `Back` button, back to the Browser graphic, an interesting feature to know about the Browser is, in case you wanted to save an image that wasn't quite as wide as this one, the browser will redraw the screen for you if you just shrink the size of your Firefox or Chrome browser window and make it a little narrower. There's a button below the browser graphic called "`resize`," which lets you choose the size of the window that you have and then your graphic is redrawn to fit the window with all of the annotations on the screen. So you're not faced with the prospect of making it smaller and then making the type misshapen if you resize it asymmetrically.

[3:23] Change font size

Speaking of type size, there's a `configuration` button below the Browser graphic that gives you the option to change the font size. You can change the text size, for example, from 8 to 12 and make it really large and then submit that and go back to the Browser graphic and it will redraw the Browser with text at that larger size.

So I will reset the browser window to the size the window we had before. Scroll down below the graphic and resize it so that it's back at its original size. If you go to the "`Genome Browser`" pulldown and select "`configure`," which has the same effect as the button below the browser graphic, then you can go back to the default text size of 8. Note that this a global configuration, distinct from the bar at the left side of the data tracks, which is a configuration option for that track only.

[4:21] Drag-and-Zoom

Let's have another look at ways to get around in the Browser and configure some of the options. To do that, let's go this gene, NELL1, we'll put our mouse over the Base Position at the top and move just a bit to the right and catch that exon, put the exon in the window, and we'll do it one more time and zoom into this exon right here. And you'll see that we have the stripes that show the alternating colors. And when we put the mouse over it, you can see that this is exon number six out of 20.

This little double-headed arrow on the end says Previous Exon and on the other side of the screen it says, Next Exon. This gives us the options to jump from exon six to exon five.

[5:19] Next / Previous Item arrows

There's another configuration option that helps you get around in the Browser. If you click again on "configure," you see the only unchecked box on the configuration page, "Next/Prev Item" navigation.

Let's click on that one and submit. And now you get these gray double-headed arrows. Each track has one on the very top of the data, at the same location in the horizontal dimension as the long label for the track. And so let's click on the double-headed arrow for the UCSC Genes track, and it will go to the next gene in the window, SLC6A5. To confirm that it really worked the way we think it did, let's zoom out by a factor of 10 and then another factor 10. And here we pick up the NELL1 gene, which is the gene we are on before.

[6:16] Remove blue gridlines

Let's go back to the configuration page. I'll use the button below the Browser graphic this time. And we'll turn off the Next/Prev Item navigation and we'll also turn off the light blue guidelines that are in the Browser image. Some people prefer to make images for their papers or posters without the light blue lines. And if we submit that, you see we have the same image we had before without the blue lines in the graphic image.

[6:47] Remove chromosome ideogram

You'll notice that we've seen before the chromosome ideogram at the top when we navigated to this page in a previous video. It's optional whether you want to display this or not. So we'll go to the configure page, turn off the ideogram and the image will disappear. We'll also turn on the blue bars while we're here.

[7:16] Remove dialog box for drag-and-zoom

Let's configure one more time. The other options are fairly obvious what they are going to do: Display the labels. Display the description. There is one that can be a bit surprising, however. If you unclick the "Enable highlight with drag-and select" option, then the dialog box that showed up earlier when we drug our mouse to the right over the exon will disappear and you automatically zoom, which fine unless you forget you did it

and then it's problematic. You have to remember to come back in here to the configuration page and turn it back on.

So let's unclick the box and go back to Browser. And you can see that if we put the mouse on either side of the 3'-end exon at the end of the SLC6A5 gene, it automatically zooms directly to the location and we no longer have the option to add the highlight. Note that here, you can see the way the untranslated regions, UTRs, at the ends of gene are represented. They are a half-height box. The stop or start codon is colored green or red. Here you see the stop is colored red.

[8:33] Right-click highlight

We can still add a highlight to the whole gene using the right mouse button on the gene annotation itself in the window. You can highlight the gene, zoom out by a factor 10 and another factor of 10, you can see that the gene itself is fully highlighted right to its very edge. This works for any annotation on the screen, but if you want to put a highlight over any other, randomly selected region, then you have to go back to the configuration menu and check the box.

[9:06] Track controls under main graphic

Another checkbox on this page, "`Show track controls under the main graphic`" is a way to speed up the loading the Browser image. The screen will draw faster if the track controls below the graphic are not there. But you must come back to this configuration page to turn on any other tracks.

Let's uncheck that box and we'll look at this page first. And you can see that on this page we have the same bluebar groups with all the tracks; they are all expanded. And for each one of the tracks you have the Short Label.

This is the label that appears below the Browser graphic near the pulldown menus, but these will not appear on the main page when we go back after unchecking this box. And we also have the Long Label, which is the description of the track you get at the top of the data in the Browser image.

Let's go back to the top of the page and submit. You see that now we have the Browser without the track controls below the Browser graphic.

Let's go back once more to the configuration page, but before we do, let's make note of the Long Label here. "Chromosome Bands Localized by FISH Mapping Clones". That's the long label that you see in the track controls on the configuration page in the Mapping and Sequencing Group.

You can see the “Chromosome Bands Localized by FISH Mapping Clones”. The track is turned on to “`pack`” and is one of the tracks turned on in the Browser image.

Let’s go back now and turn the track controls back on in the image. We’ll turn the ideogram back on as well. And hit “`submit`.” You can see that the Long Label is in the image there, and it’s also what you get when you put the mouse over the label above the track control pulldown menu below the Browser graphic.

That concludes our conversation about the configuration page and a number of configuration options for setting up the Browser the way you like.

This conversation about configuration will be continued in Part Three of the Browser Basic series of videos. In Part Three we will also look at navigation in the Browser using DNA sequence.

Please note that we conduct full-day and two-day on-site trainings at your institutions. Prices are reasonable:

http://genome.ucsc.edu/training/

Thanks for watching and thanks for using the UCSC Genome Browser.