Exon-only mode in the UCSC Genome Browser

This video will demonstrate the new multi-region display mode on the UCSC Genome Browser. In particular, we will show the feature that allows display of exons only, which should be quite useful to those doing whole-exome sequencing, RNA-seq and other experiments.

To begin, go to the main index page, genome.ucsc.edu.

Click the Genome Browser link to go the Gateway page, which allows access to all the organisms hosted on the Browser. Reset the Browser to start at the default position.

[0:31] Now we will change the genome assembly to hg19 because it is still better annotated than the most recent, hg38. "Hide All" to turn off the data tracks, then turn on the UCSC Genes track to "pack". Let's resize the screen to make the most of the width of the web browser. You see a single isoform of the SOD1 gene at the default location, occupying some 10 kb of genomic DNA.

[0:64] To enable the exon-only display mode, go to the View… menu in the blue bar at the top of the page and choose Multi-Region.

Select the second option, "show exons using UCSC Genes." Note the configurable option of 6 bases of padding on each side of the exons. This makes it easier to see the breaks between exons in the Browser display. You see that the display has discarded the introns and now shows only 1.1 kb, with 12 bases between exons.

[1:34] Now let's navigate to a more interesting location, the PCDH15 gene. Note that the alternate isoforms near the right side of the screen show some gaps where certain exons are excluded from some isoforms. Any genomic DNA that is covered by any exon will be shown in this display mode.

Let's zoom out by a factor of 3. Note the red tick marks in the chromosome ideogram above the Browser graphic, showing the interrupted nature of the genomic coverage when exon-only mode is turned on, if the exons are sufficiently far apart.

[2:11] Now we will go to the gene, MCF2, to see another feature of exon-only mode. Zoom out 3x and 1.5x. This will set the window to 22 kb of displayed DNA. Notice several untranslated transcripts on the screen, including an antisense transcript for FGF13 on the left side of the display.

We will turn off the untranslated genes using the configuration options found behind the little bar at the left side of the UCSC Genes track. Unclick the checkbox next to "non-coding genes" and Submit. See that the antisense and other non-translated genes are gone and the Browser is now displaying only 18.6 kb. Turn the multi-region display off and see that this region actually represents 1.5 Mb of genomic DNA.

[3:10] Now we will look the signal in a gene expression data set and show how looking at exons-only enhances the ability to interpret the Browser display.

Below the Browser graphic, find the Expression bluebar group and click into the link above the pulldown menu, "ENCODE RNA-seq…." On the resulting page, click on the "Cold Spring Harbor Long RNA Seq" link to configure the composite track of data from this project.

Set the maximum display mode to "full." Set "Contigs" to "hide," leaving the Plus Signal and Minus Signal tracks on, so we can see RNA that maps to both DNA strands. Now select the minus sign next to the word "All" to turn off all tracks, then turn on all tracks in the Whole Cell column in the track matrix.

Below the list of cell lines, choose "Poly-A+" from the RNA Extract menu and leave Replicate rank to "All," so we can see both replicates in the project. Below the list of selected tracks (74 in all), hit the Submit button.

[4:13] Each cell line has four tracks turned on, all shown in a single color. Notice that the replicates match pretty well and that the genes typically have signal on either one strand or the other. The ATPase gene on the right is expressed in all cell lines, while the FGF13 gene has spikes of signal in some cell lines and not in others.

Now let's go back to exon-only mode, where we can see that the differential gene expression is much more obvious when the display has discarded exons and intergenic regions, especially for genes with narrow exons, such FGF13.

It will take a while for the Browser to slice up 74 wiggle tracks, but when we return to the Browser graphic, notice that the signal for the FGF13 gene is much easier to interpret and it even becomes obvious that different isoforms are expressed in the H1hSC and K562 cell lines, for example. There is no expression at all in the GM12878 line.

Thanks for watching and for being a UCSC Genome Browser user.