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Visualizing Hi-C chromatin interactions in the UCSC Genome Browser

L. Nassar[1], J. Casper[1], D. Schmelter[1], K. R. Rosenbloom[1], B. J. Raney[1], M. Diekhans[1], N. C. Durand[2],
E. L. Aiden[2], J. T. Robinson[3], M. Haeussler[1], W. J. Kent[1];

[1]Genomics Institute, University of California Santa Cruz, Santa Cruz, CA, USA, [2]Molecular & Human Genetics, Baylor College Medicine, Houston, TX, USA, [3]Department of Medicine, University of California San Diego, La Jolla, CA, USA.

Abstract

The UCSC Genome Browser (https://genome.ucsc.edu/) has a new track format for displaying chromatin conformation capture data (3C, 4C, 5C, Hi-C, etc.). This heatmap visualization shows interaction scores for 3-dimensional contact sequencing methods, which may indicate enhancer-promoter interactions. The heatmaps currently support three draw modes, where color in each mode correlates with the strength of the proximity signal. Additional features include variable resolutions, score normalization options, and different color palettes. This format is used in native Browser tracks and is available to users for their own use through track hubs and custom tracks. We have added two native tracks to demonstrate this display using data from in situ Hi-C and Micro-C XL experiments.

Workflow

FASTQ files

```
@EAS54_6_R1_2_1_413_324
CCCTTCTTGTCTTCAGCGTTTCTCC
+
;;3;;;;;;;;;;;;7;;;;;;;88
@EAS54_6_R1_2_1_540_792
TTGGCAGGCCAAGGCCGATGGATCA
+
;;;;;;;;;;;7;;;;;-;;;3;83
```

Juicer
https://github.com/aidenlab/juicer

Host **.hic** heatmap file:
- AWS
- CyVerse
- Google cloud
- etc.

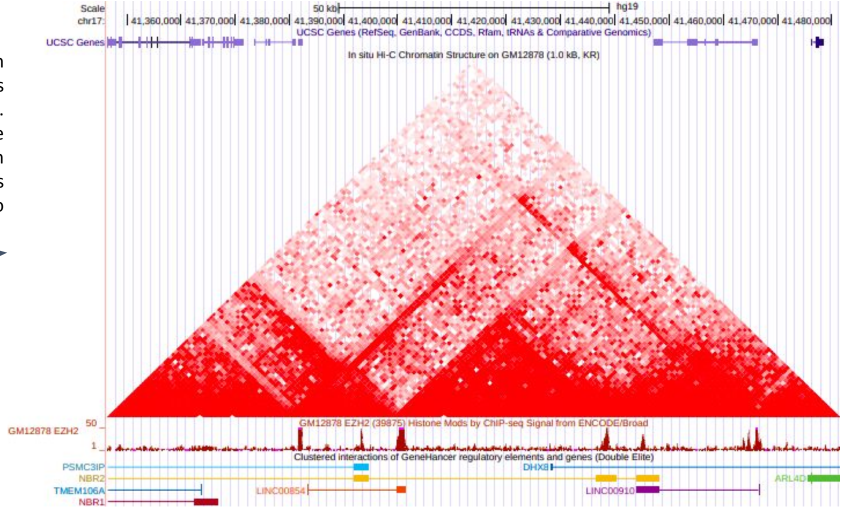

Figure 1: *In situ* Hi-C data (Rao et al.,2014) displayed alongside Genome Browser tracks. Default Hi-C display settings. Explore live: https://genome.ucsc.edu/s/Lou/ASHG1

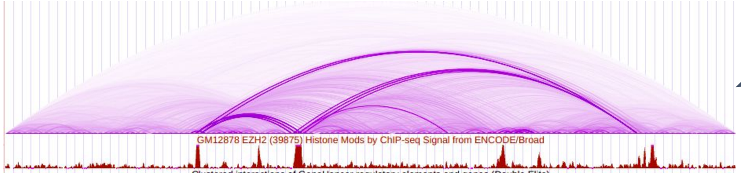

Figure 2: *In situ* Hi-C data (Rao et al.,2014) alongside a ChIP-seq signal track. Custom color, score normalization, and arcs used. Explore live: https://genome.ucsc.edu/s/Lou/ASHG2

Future Directions

Work is ongoing to improve the Hi-C display. These features include support for multi-region mode, annotation of loops and topological associated domains (TADs), and image inversion.

More info: https://genome.ucsc.edu/goldenPath/help/hic.html

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