Tutorial: Viewing sequencing data in the UCSC Genome Browser
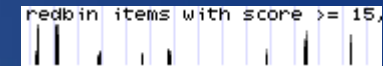
Angie Hinrichs, Bob Kuhn
UCSC Genome Bioinformatics Group
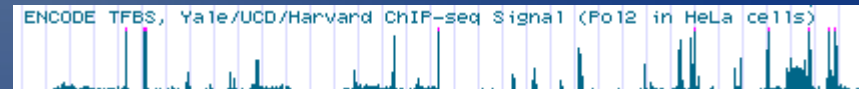genome@ucsc.edu

Overview

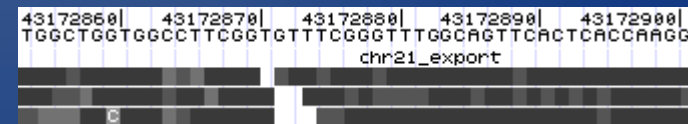- Genome Graphs with .sgr data
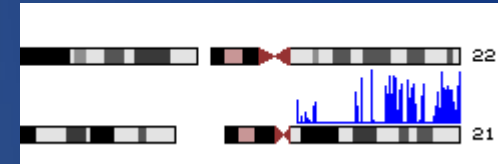
- Transforming .sgr into bedGraph for Genome Browser

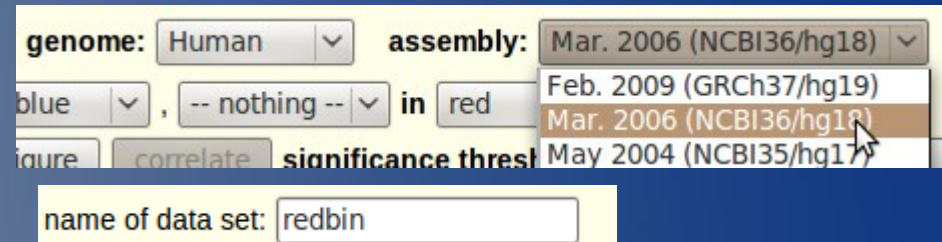- Comparing with UCSC-hosted data

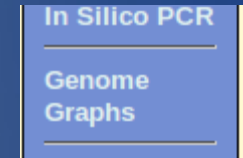- Transforming ELAND export read alignments to BAM for Genome Browser

Genome Graphs with .sgr data

- http://genome.ucsc.edu/

- Choose assembly

- Click upload button

- Paste URLs or data:

  http://genome-test.cse.ucsc.edu/ABRF2010/chr21_extended.txt_redbin.sgr

- Click on a peak to go to Genome Browser

Genome Graphs data in Genome Browser

- Clicking on Genome Graphs → 1Mbase region
- Genome Graphs uploaded data appears:
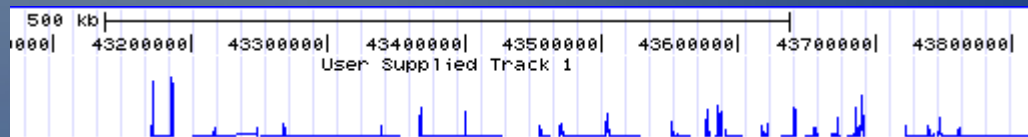
Transforming .sgr into bedGraph for Genome Browser viewing
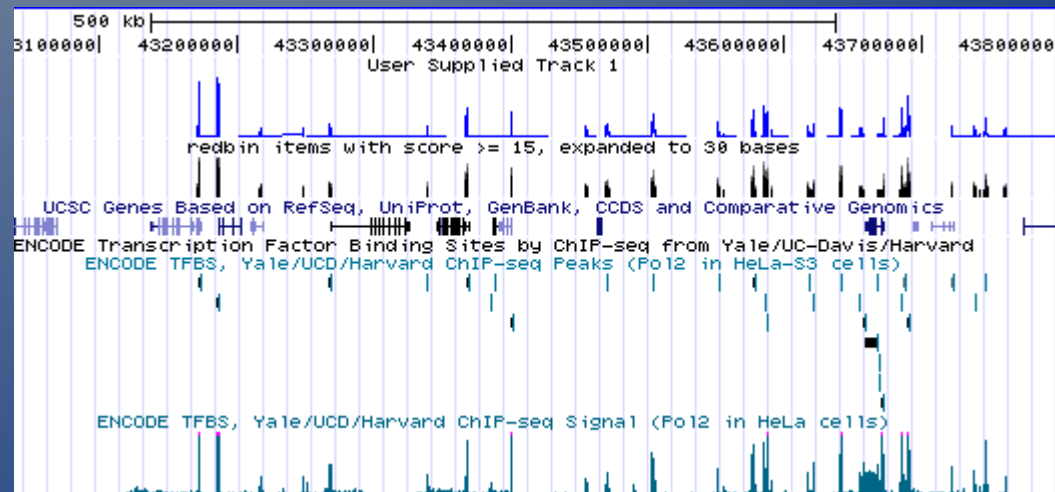
- Perl to the rescue!

```
perl -wpe '@w=split("\t"); $_ = "$w[0]\t" . ($w[1]-1) .
"\t" . ($w[1]+29) . "\t$w[2]"; \

           if ($w[2] < 15) {$_ = "";}' \

chr21_extended.txt_redbin.sgr > redbinGt15.bed
```
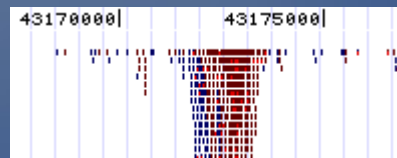
Comparing with UCSC-hosted data
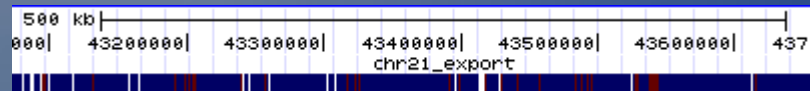
- ENCODE data: "Yale TFBS" track in Regulation section

BAM for read alignments

- Add custom track:

  track name=chr21_export type=bam bigDataUrl=http://genome-test.cse.ucsc.edu/ABRF2010/chr21.bam visibility=pack

ELAND export to indexed BAM

- Samtools script export2sam.pl:

```
export2sam.pl --read1=chr21_export.txt \
    | perl -wpe 's/(chr.*)\.fa/$1/' \
        > chr21.sam
```

- Add header lines at beginning of chr21.sam:

```
@HD    VN:1.0   GO:none  SO:coordinate
@SQ    SN:chr21 LN:46944323
```

- Samtools:

```
samtools view -bSo chr21.unsorted.bam chr21.sam
samtools sort chr21.unsorted.bam chr21
samtools index chr21.bam
```