Tutorial: Viewing sequencing data in the UCSC Genome Browser

Workshop: Tools to Facilitate Management, Analysis and Visualization of 2nd Generation Sequencing Data, ABRF 2010.

Angie Hinrichs, Bob Kuhn UCSC Genome Bioinformatics Group genome@ucsc.edu

Overview

Genome Graphs with .sgr data



r III. . Er flendag

- 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



In Silico PC

Genome

Graphs

Genome Graphs data in Genome Browser

- Clicking on Genome Graphs \rightarrow 1Mbase region
- Genome Graphs uploaded data appears:

500 1000	kb 43200000	43300000 43400000 43500000 User Supplied Track 1			43600000	43800000	
					11_	الاندارة	<u></u>

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

Scale chr21:	43000000	500 kb⊨ 43100000 4320	0000 4330000	0 43400000	43500000	3600000 43700000
redbin 1				User Supplied	Track 1	. 0 1. 14
redbinGt15			redbin items w	ith score >= 15	, expanded to	30 bases
					166	i ii u i i ii

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://genometest.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