

UCSC Genome Browser Training Schedule

Day 1

9:00 - 10:30 Intro to the UCSC Genome Browser - features and navigation.

A guided tour of the basic parts of the UCSC Genome Browser:

- General overview of the Browser, what it is, history
- Display configuration
- Track settings
- Exporting Browser images for publication
- Searches: for regions/positions, gene names, motifs, other keywords
- Searches: BLAT, short match track for sequences
- Searches: PCR for primers
- Demo of example searches: Gene of interest, regions of interest, dataset/publication of interest
- Navigation: drag-and-zoom, drag-reorder tracks, switching genome assemblies and organisms via homology
- Keeping track of your thinking by saving and sharing sessions

10:30 - 10:45 Coffee break

10:45 - 12:00 More Genome Browser - data

A short tour of our data

- Starting points for browsing our data:
- Genomic position
- Sequence
- Gene
- Variants -- CNVs and SNPs, benign and pathogenic
- Comparative genomics -- synteny and evolution
- Publication
- How to find more info about a track or track item
- Table Browser and extracting data
- Custom tracks - uploading and displaying your own data in the Browser

- Custom track examples - BED files. Sequences data: coverage (BAM files), variant calls (VCF), RNA-seq (wiggle)
- Public Assembly Hubs
- How to download our data
- How to get DNA for the region you are viewing
- Gentle intro to the Table Browser
- Getting gene sequences using the Table Browser
- Getting track information using the Table Browser

Day 2

9:00 -10:30 Getting more out of the Browser

- Multi-Region mode
- Exon-only display
- Viewing regions of your own choice, including discontinuous (e.g., pathways)
- Alternate haplotypes in human genome assemblies
- Public sessions - sharing your data with everyone
- Table Browser advanced examples:
- Intersection
- Filtering
- Finding the table that goes with your track
- Track Hubs
- How to make your own track hub
- Assembly Hubs
- Make a track hub for your genome of interest

10:30 - 10:45 Coffee break

10:45 - 12:00 Browsing variant data and sensitive data

- Understanding various SNP tracks
- The Variant Annotation Integrator: predicting biochemical consequences of short variants
- Genome Browser in a Box: Hosting a local copy of the Genome Browser on your laptop
- GBiB as Browser inside your firewall
- Using GBiB and Assembly hubs to explore sensitive data

12:00 - 1:00 Lunch on your own