UCSC Genome Browser Short Course

This 2-day short course is designed so that attendees will leave with a strong foundational understanding of the UCSC Genome Browser, including hands-on experience with its core functions and an introduction to its more advanced features. While not intended to create expert-level users, attendees should expect that this course will equip them with the skills and confidence needed to navigate and more effectively use the Genome Browser in their work. Attendees should make sure to bring their laptops to fully participate.

The UCSC Genome Browser is an essential tool widely used in research and clinical laboratories. The Browser is a web-based visualization interface into a large database. A genomic-coordinate-based display allows access to data at any scale from a single nucleotide to an entire chromosome. The underlying data vary from one genome assembly to another, but essentially, anything that can be localized to a genomic coordinate can be displayed on the Browser. These data include mRNA mappings (gene models), transcription-factor binding sites, histone- and DNA-modification locations, expression data, conservation and importantly, variants (SNVs and CNVs) both pathogenic and benign. This arrangement allows the user to pursue biological inquiries by accessing the data directly and quickly.

During its 25 years of growth, the expanding capabilities of the Browser have been both exciting and daunting. Much like Photoshop or Excel, the Browser is used by many, but few are adept at more than a subset of the features.

Day 1

UCSC Genome Browser – Session I
Monday October 13, 2025. 2 - 5 pm

The first Browser short course session will present the Browser visual display paradigm and feature navigation and configuration options. Through demonstration and hands-on exercises, participants will

- Understand the display modes: dense, squish, pack and full in several contexts. The modes vary across different data types, discussion of which serves as an introduction to several of the main data types in use in the Browser display.
- Configure Browser-wide options to optimize their viewpoint – allowing the data to show what is important to the user.
- Rearrange data ordering, zooming in and out and highlighting.
- Investigate default tracks.
- Investigate the differences among human genome assemblies, hg19, hg38, hs1 (T2T).
- Search/Navigate the genome, using gene names, HGVS nomenclature and accession names and numbers (RefSeq, OMIM, GENCODE and more).
- Appreciate right-click menu features.
- Click into details pages for individual items in various datasets and from there to the original data sources.
- Access Track Descriptions, which describe the data, the process of collecting and configuring it and, importantly, color conventions used in the track.
- Explore track-specific configuration options.
- Export .pdf images of Browser views.

Questions will be encouraged throughout.

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Day 2

UCSC Genome Browser – Session II
Tuesday October 14, 2025. 9 am – 12pm (noon)

The second Browser short course session will present more advanced features of the Browser. Through demonstration and hands-on exercises, participants will

- Explore a variety of datasets through the Recommended Track Sets – shortcuts to enable tracks relevant to interpretation of SNVs or CNVs, including pathogenic and benign variants and splice predictions.
- Investigate multiple subtracks within composite tracks that sometimes obscure the full extent of available data.
- Load their own data into the Browser as Custom Tracks in a variety of formats.
- Use the Table Brower to export subsets of data from large data tables, including exporting coordinates for genes discontinuous in the genome.
- Save sessions for future use, publication and/or sharing with colleagues (stable links).

Questions will be encouraged throughout.

UCSC Genome Browser – Session III
Tuesday October 14, 2025. 1 - 3 pm

The third Browser short course session will present still more advanced features of the Browser. Through demonstration and hands-on exercises, participants will

- Appreciate Comparative Genomics datasets: Chain, Net, multiz and liftOver.
- Enable Multi-Region mode, which allows user-supplied discontinuous regions to be displayed together – including Exon-only mode.
- Import, export and search sequences: BLAT, isPCR, Short Match and Get DNA.
- Perform Table Browser queries with filters.
- Download data using the Table Browser and the API.

Questions will be encouraged throughout.