# UCSC Genome Browser Workshop

*June 22-23, 2017*

*Holden Auditorium, FLTC*

**Workshop led by ROBERT KUHN, a Co-PI of the Genome Browser project.**

**Hosted by WUSM, Musculoskeletal Research Center**

[http://www.musculoskeletalcore.wustl.edu/](http://www.musculoskeletalcore.wustl.edu/)

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# AGENDA
**Day 1 |** *9:00 AM – 5:00 PM*

*Intro to the UCSC Genome Browser (beginning/novice user material).*

* Browser paradigm
* General overview of the Browser, what it is, history
* Configuring the display
* Track settings
* Exporting Browser images for publication
* Searches: for regions/positions, gene names, motifs, other keywords
* Saving and sharing sessions
* Starting points for browsing our data:
    * genomic position, sequence, gene/motif, variant, publication
* How to find more info about a track or track item

*Coffee Break*

* Most popular data sets
    * Mapping and Sequencing
    * Genes and Gene Predictions
    * Comparative Genomics
    * Variation - SNPs and CNVs
* NGS sequencing data -- paired ends, BAM files, variant calling/display
* Uploading your data into Custom Tracks -- incl. RNA-seq, etc.
* Gene info - getting sequences, position and functional info
* How to get DNA for the region you are viewing
* Intro to the Table Browser
* Getting gene sequences

*Lunch Break*

* Working through problem set

## Day 2 | *9:00 AM – 5:00 PM*

***Getting more out of the Browser***

* Exon-only Display mode
* Alt sequences in hg38
* Table Browser advanced examples:
        * Intersection
        * Filtering
        * Finding the table that goes with your track
* Details about Comparative genomics data
* Track Hubs
        * How to make your own track hub

Browsing variant data and sensitive data
* The Variant Annotation Integrator: annotation for your variants all in one place
* Genome Browser in a Box: Hosting a local copy of the Genome Browser on your laptop

***Lunch Break***

Advanced problem session to work on example problems
1-on-1 conversations about whatever comes up