

# GENOME BROWSER WORKSHOP

- Speaker:** Robert Kuhn, PhD  
Associate Director UCSC Genome Browser  
UC Santa Cruz Genomics Institute, Santa Cruz, CA, USA
- Venue:** National Supercomputing Centre (NSCC)  
1 Fusionopolis Way, #17-01 Connexis South, Singapore 138632
- Dates:** 21 (Thurs) – 22 (Fri) March 2019
- Registration:** First come-first-serve basis. Limited space as this is a hands-on workshop.  
Nominal Fee applies (**special reduced rate for APSHG members**)  
Enquire to [paegtix@nus.edu.sg](mailto:paegtix@nus.edu.sg)



Organized by: BRETSS Department of Paediatrics, National University of Singapore

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## About the workshop

The typical molecular biologist is now generating data at an increasing pace, as research turns to sequencing in all its forms, including RNA-seq, whole-genome, whole-exome, ChIP-seq, 3-C and 5-C and others to solve problems. The initial human sequence generated by the human genome project together with the genomes of thousands of eukaryotic and prokaryotic genomes have produced complex and voluminous data which have to be interpreted and visualized in a simple manner.

Genome browsers provide a unique graphical interface for users to browse, search, retrieve and analyze genomic sequence and annotated data efficiently and conveniently through a web-based visualization interface. Browsers typically integrate genome sequences and other annotations from heterogeneous data to allow information to be extracted and summarized from raw data.

The UCSC Genome Browser is an on-line, and downloadable, genome browser hosted by the University of California, Santa Cruz (UCSC). The Browser is a graphical viewer optimized to support fast interactive performance and is an open-source, web-based tool suite built on top of a MySQL database for rapid visualization, examination, and querying of the data at many levels. The UCSC Genome Browser presents a diverse collection of annotation datasets (known as "tracks" and presented graphically), including mRNA alignments, mappings of DNA repeat elements, gene predictions, gene-expression data, disease-association data (representing the relationships of genes to diseases), and mappings of commercially available gene chips (e.g., Illumina and Agilent). Tracks for Mapping and Sequencing, Genes and Gene Predictions, Phenotype and Literature, mRNA and EST, Expression, Regulation, Comparative Genomics, Variation, and Repeats can be visualized on the browser.

## About the Speaker

Dr Robert Kuhn has a PhD in Biochemistry and Molecular Biology. He has been part of the team that developed the browser since the early days, and has been on the project since 2003. In recent years, he has been conducting training and workshops on how to use the Browser and its associated bioinformatics tools. He has also been interacting with the medical genetics community to acquire useful datasets for the Browser and to learn about how to make it more useful to the scientific community.