Webinar: Using the New NCBI Variation Viewer to Explore Human Genetic Variation

Hosted by: Cushing/Whitney Medical Library, Yale University

Presenter: National Center for Biotechnology Information

Date/time: Wednesday, August 13, 2014 – 1:00 – 2:00 PM

Location: SHM L Room 101A Yale Medical Library, 333 Cedar St. New Haven CT 06520

Free and open to all Yale affiliates – **Registration required** due to limited seating.

Register here: http://schedule.yale.edu/event.php?id=714947

This presentation will show you how to find human sequence variants by chromosome position, gene, disease names, and database identifiers(RefSNP, Variant region ids) using NCBI's new Variation Viewer (http://www.ncbi.nlm.nih.gov/variation/view). You will learn how to browse the genome, navigate by gene or exon, filter results by one or more categories including allele frequencies from 1000 Genomes or GO-ESP, and link to related information in NCBI's molecular databases and medical genetics resources such as ClinVar, MedGen and GTR. You will also be shown how to upload your own data to add to the display, and download results. Anyone who works with clinical or research variation data will find that the Variation Viewer provides a convenient and powerful way to access human variation data in a genomic context that is fully integrated with all other NCBI tools and databases.

Organizer: Rolando Garcia-Milian - Rolando.milian@yale.edu