TCAG New Technologies Seminar

Interpreting Variants from Human Genome, Exome and Targeted Panel Sequencing: A Rapid, Point-and-Click Approach

Date: Tuesday Nov. 5
Time: 11:00 – 12:00 pm
Location: 2nd Floor, Room 02.9230 (publicly accessible)
Peter Gilgan Centre for Research and Learning
686 Bay St., Toronto
Speaker: David Dailey, PhD
NGS Specialist
Ingenuity Systems

Classification and prioritization of variants is challenging, not just because of the number and uniqueness of variants of potential interest, but also due to the wide range of information sources useful to the prioritization process. Ingenuity's software aims to bring together information on variant and gene function, pathways, processes and disease models within an intuitive system that enables investigators and clinical researchers to ask many questions of their data and see the results in seconds, with direct access to the supporting findings to guide decisions on which variants to carry forward. Examples pertinent to rare disease, germ line and somatic cancer, will be presented.

Hosted by The Centre for Applied Genomics and the Ontario Genomics Institute

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