Bioinformatics Seminar

Sponsored by Genome Sequencing Facility (CTRC NGS Shared Resources), Greehey Children's Cancer Research Institute, UTHSCSA

QIAGEN Advanced Genomics

IPA

If you have gene (including RNAseq), protein and metabolic expression data, you should be using IPA to guide you with the biological interpretation of your data. Using IPA you will learn how to rapidly understand:

- Pathway involvement and change
- Effected biological processes
- Causal regulators and their directional effect on genes, functions and diseases across multiple time points or doses.

You will also learn to explore IPA's knowledge and discovery tools that allow you to relate the most Recent literature findings to your research.

CLC bio

INGENUITY PATHWAY ANALYSIS

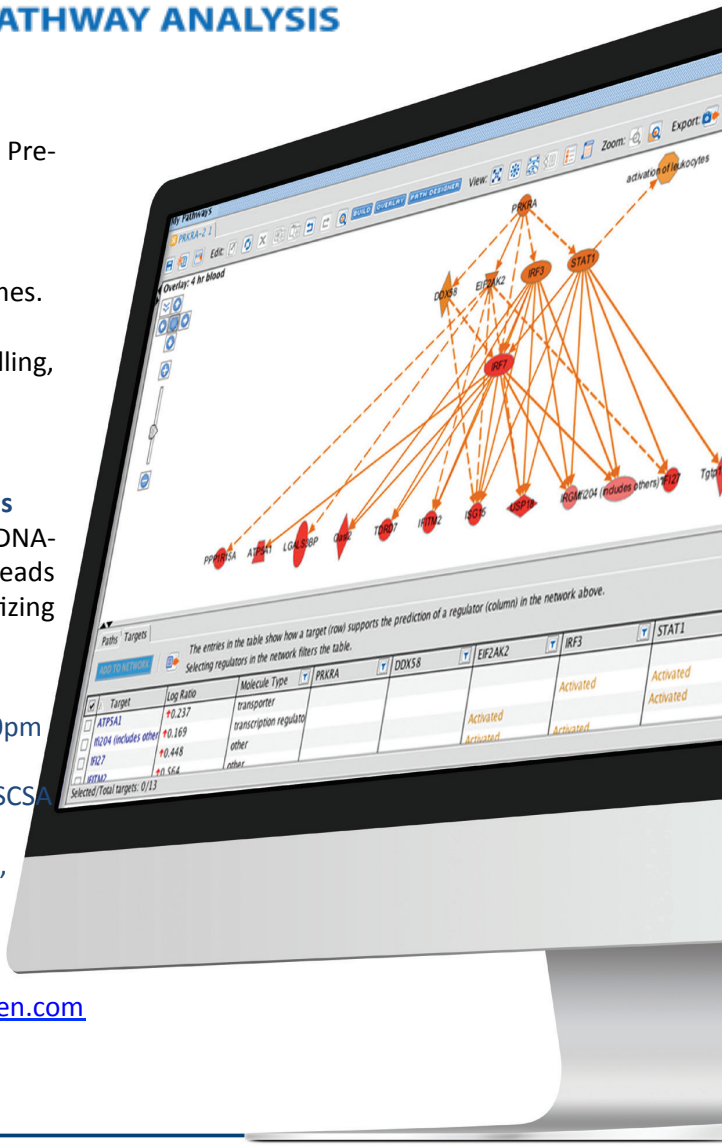
CLC Genomics Workbench

Overview of Application, Importing NGS read data, QC & Pre-processing

- Overview of Microbial Modules (Finishing & Microbial Genomics)
- De novo assembly – Genomes & Transcriptomes. Characterizing Contigs, Joining & Finishing
- Mapping/Alignment to Reference, Variant Calling, Annotation & Filtering
- RNA Seq Analysis Workflow & Tools

CLC Biomedical Workbench & Ingenuity Variant Analysis

- Prebuilt intuitive pipeline for your human DNA-seq data that allows you to quickly go from reads or called variants to identifying and prioritizing the casual variants.



WHEN: Tuesday, November 15, 2016 from 11:00 – 12:30pm

WHERE: GCCRI Classroom 2.150. Greehey Campus, UTHSCSA

PRESENTER: Neja Jalan, PhD - Field Application Scientist,

Lunch Provided by Panera

Register/Questions: Jason Garner at jason.garner@qiagen.com