

CPH Seminar in Precision Medicine

"CHALLENGES IN HTS DATA ANALYSIS AND CLINICAL APPLICATIONS"

Yuriy Fofanov, Ph.D.

Department of Pharmacology & Toxicology,
Director of Genomics and Bioinformatics Lab at
The Sealy Center for Structural Biology & Molecular Biophysics (SCSMB)
University of Texas Medical Branch (Galveston)

The price of High Throughput Sequencing (HTS) has dropped dramatically, while the speed of the instruments has also improved. As such, three major challenges remain to be resolved before this technology will be able to move from being nearly exclusively a research tool to routine diagnostic use:

1. The absence of standard data analysis algorithms and reference databases;
2. The large and complicated output of available HTS data analysis pipelines which usually require PhD level scientists to interpret the analysis results;
3. Large amount of data and computational complexity of the available HTS analysis tools which require data to be stored away of the place of its origin, separating sequencing from the analysis and decision making process as well as raising security and privacy concerns.

This talk will focus on the strengths and weaknesses of available approaches to resolve these challenges.

Friday, January 27, 2017. 12p – 1p. UCT.1414

rosalinda.molina@uth.tmc.edu

713.500.3912

 **#SBMIseminar**

