Tulane Cancer Center Bioinformatics Core

The capacity to perform Second Generation sequence analysis has become essential in biomedical research. At Tulane, this need is met by the Tulane Cancer Center Bioinformatics Core.

The Core trains individual lab members in the analysis of their specific data, giving them hands-on training and access to an array of analysis programs. The core is overseen by Dr. **Erik Flemington**, who also maintains his own research program with a focus on understanding the Epstein-Barr Virus (EBV) transcriptome and the effects of the virus on human health and disease.

Global Viral Transcriptome Architecture

Viral genomes are tightly constrained and contain many overlapping genes. As a result, mapping gene expression data and definitely determining even the number of individual viral genes that can be expressed from second generation sequencing data is challenging.

Dr. Flemington has developed a computational method to combine sequencing data from three different sequencing platforms to resolve the viral transcriptome architecture. Synthesizing data from EBV obtained using Illumina, PacBio, and CAGE sequencing, the lab discovered that EBV expresses approximately 300 genes, in a significantly improved contrast to the previously identified 70 total genes.

This data analysis pipeline has applications beyond viral transcriptomics, and could be utilized to analyze the global transcriptome architecture of genetically complex human cells, most obviously cancer or tumor cells.

Cancer Biology
Bioinformatic Analysis

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Single Cell RNA Analysis: Complex Mixtures Unraveled

Single-Cell RNAseq analysis promises to revolutionize the way we understand complex mixtures of cells. Instead of looking at RNA data from many cells with no way to tell them apart, this method allows for the identification of rare cell types in a mixed population by analyzing the individual gene expression profiles (or fingerprints) of single cells.

This method of analysis can also identify new cell populations, resolving them into distinct, clustered populations based on their common fingerprints. Dr. Flemington and the Core are applying this technology to EBV-infected cells to try and understand what causes cells to switch from one infection program to another, and what genes expressed by the EBV itself can contribute to this process.

Ultimately, the core endeavors to understand the complex mixture of cells that comprise a solid tumor –and its associated microenvironment – through their transcriptional profiles. This will allow for more accurate prognostic and treatment options to be delivered based on a fuller knowledge of the genes expressed in the complex cellular mixture.

Contact & Further Info:
James R Zanewicz
Chief Business Officer
zanewicz@tulane.edu

Find Us:
engage.tulane.edu

t: @zanewicz
t: @engagetulane

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