

## Scientists at THSTI developed a HyperQuant – A computational pipeline to relieve analytical nightmares of proteomic researchers

A group of researchers from at Department of Biotechnology's institute, the Translational Health Science and Technology Institute (THSTI) have taken a leap forward to develop modern tools of computational biology, following their latest innovation called HyperQuant.



Aimed at relieving the analytical nightmares of proteomic researchers, HyperQuant is an open source tool made available for achieving better data processing for high order multiplexing experiments. Multiplexing is a gigantic task of quantifying several samples in a single experiment, wherein mass spectroscopy, following either label-free or label-based quantification is often utilized. When topped with additional layer of higher order multiplexing involving the combination of data from double MS quantification events, it becomes one big data trove. It is where HyperQuant comes to the rescue which collates the quantifiable data from MS1 and MS2, deconvolutes the labels, summarizes and calculates normalized protein intensities. Moreover, the tool is flexible to be used with results from different search engines for identifying and quantifying the MS results.

HyperQuant also overcomes the challenges of data loss and fidelity of quantitation by combining protein spectrum matches (PSMs), rescuing protein identification, increasing the peptide data points, and removing outliers of poor quantitation values. The efficacy and flexibility of the technique was demonstrated by analyzing 18-plex hyperplexing data and quantifying newly synthesized secretome for *Mycobacterium* infection of human macrophages.

The nature and tools of investigations into working of biological systems evolved with evolving queries of the scientific minds. Currently, amongst the array of investigative branches of research, omics-driven research continues to expand. One of the many branches in omics, the proteomics, occupies significant stance, as it entails the large-scale study of proteins, which sustain and perform a multitude of functions in living organisms. As the entire complement of proteins are analysed to gain insight into structure and physiological functions, a large amount of study data are generated. To support the processing of large-scale raw data for deriving meaningful conclusions, the modern tools of computational biology support the scientists. With every challenge faced in processing of data computational biologists device improved methods.

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