High-Throughput Proteomics Pipeline

Overview:

McGill researchers have developed a bioinformatics pipeline for the high-throughput analysis of data from bottom-up proteomics experiments. The system is built on a comprehensive relational database and incorporates components for laboratory information management, peptide and protein identification from mass spectra, inter-sample comparisons and analysis, annotation, and sophisticated report generation. The system is fully operational and in daily production in the Genome Quebec Proteomics Platform. It is distinguished from other systems in two main ways: 1) it is designed to be used in service platforms and to manage multiple projects in parallel; and 2) the analysis and reporting mechanisms are built to handle complex samples; that is experiments involving comparisons of data sets involving multiple conditions, biological samples, or time points.

Characteristics:

- **Efficient Design**: Relies on data structures and algorithms for the annotations of proteins to assist in inferring biological significance from protein identification. The algorithms allow sorting results into a unified proteomics database for data mining purposes across multiple experiments.

- **Modular Structure**: Compatible with commercial, open source or in-house software to perform various functions.

- **Data Sharing**: Facilitates the overall flow of data between researchers working on different projects in the same or different facilities.

- **Integrated Aspect**: Supports all phases of mass spectrometer proteomics from sample preparation to protein grouping. The software can be tailored to the user needs whether it is a low volume on-demand environment or high-throughput proteomics.

- **Rapid market entry**: Minimal customization and software development efforts required for the market launch of the currently available version of the Pipeline.
**Inventors:** Kearney R.E. et al.

**Profile:**

**Dr. Robert E. Kearney**
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Associate Member, School of Physical & Occupational Therapy  
Associate Member, Mechanical Engineering

Fellow of the Engineering Institute of Canada; American Institute of Medical and Biological Engineering; and Institute of Electrical and Electronics Engineering.

**Research focus:**

**Bioinformatics:** Development of algorithms that improve accuracy and sensitivity of proteomics measurements with focus on: (i) Deployment and operation of a robust, secure information technology infrastructure to support acquisition, analysis and interpretation of proteomics data; (ii) Development of CellMapBase, a custom database and Web-based application for the distributed acquisition and analysis of proteomics data; and (iii) Elucidation and evaluation of new algorithms and tools to assess, validate and improve the efficiency and accuracy of protein identification and abundance measurement.

**Biomedical System Identification and Signal Analysis:** Development of tools and techniques for analysis of biomedical signals and system. The emphasis is on practical methods for the identification of linear-time-varying and nonlinear systems within a continuous-time, nonparametric context. Related to this are methods for relating the structure and parameters of model estimates to the underlying biomedical mechanisms.

**Human Motor Control:** The role of the peripheral neuromuscular system in the control of posture and movement. System identification methods address key questions: (i) The mechanical properties of human joints and how do they vary under normal physiological conditions; (ii) Mechanisms responsible for generating the mechanical behavior; the role of muscle properties and reflex mechanisms; (iii) Understanding the mechanical properties in the control of posture and movement.

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