

Utilising a Large Computing Resource for Your Proteomics Research the Australian Proteomics Computational Facility - Using the APCF for Biomarker Discovery

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Diseases such as colorectal cancer (CRC) is a leading cause of cancer death in the Western World. Early detection is the single most important factor influencing outcome of CRC patients. If identified while the disease is still localized, CRC is treatable. To improve outcomes for CRC patients there is a pressing need to identify biomarkers for the early detection (diagnostic markers), prognosis (prognostic indicators), tumor responses (predictive markers) and disease recurrence (monitoring markers). Despite recent advances in the use of genomic analysis for risk assessment, in the area of biomarker identification genomic methods have yet to produce reliable candidate markers for CRC. For this reason, attention is now being directed towards protein chemistry or proteomics as an analytical tool for biomarker identification. Here, we present a large high-performance computing cluster to aid researchers in the use of large-scale proteomics technologies. Our approach for addressing the metrics of large scale mass spectrometry data analysis, the Achilles' heel of current proteomic analyses, will be discussed with the presentation of our national strategy for Proteomics mass spectrometry data analysis through the establishment of the Australian Proteomics Computational Facility (APCF).

In 2007, the APCF established and installed an advanced high-performance multi-processor computing cluster based on multi-socket quad-core processors and infrastructure for scientists at proteomics center's from all over Australia to access. In addition, through the collective management by proteomics researchers from every state in Australia as well as internationally, the Management committee as well as the Scientific Advisory committee have

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guided the hardware usage as well as the software development to enable multi-algorithm usage of the APCF. To date, over 40,000 individual data searches have been performed by many groups independent of distance from the central server. Further software developments will be described that will enable secure remote access to additional algorithms as requested by the user community as well as the addition of both varied public and proprietary sequence databases.

This unique world's first integrated approach to proteomics computing and the sharing of databases will place Australia at the forefront of efforts to identify the proteins associated with the early detection of major human diseases as well as many other programs such as plant, animal, microbe and many other agriculture proteomic analysis. In addition, the APCF gathers together expertise to provide leadership for proteomic data interpretation on locally generated data. This data can also be used in the contribution to other world-wide large-scale proteomic efforts. The APCF can be accessed to analyse mass spectrometry data through a simple web interface by a secure user account which can be obtained from the APCF at www.apcf.edu.au. The APCF is open to all Australian and New Zealand researchers with the possibility of expanding the system for use by other countries such as many of the neighbouring countries in Asia through the Asian Oceania Human Proteome Organization.

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