

MEETING ABSTRACT

Open Access

Bioinformatic challenges for proteomic biomarkers of cancer

David L Tabb^{1*}, Daniel C Liebler²

From 10th Annual UT-ORNL-KBRIN Bioinformatics Summit 2011
Memphis, TN, USA. 1-3 April 2011

Background

Proteomic biomarkers are sets of proteins that may be detected in biofluids for disease detection, prognosis, and treatment selection. Vanderbilt University is taking part in two National Cancer Institute initiatives to establish a basis for clinical biomarkers. The first, Clinical Proteomic Technology Assessment for Cancer (CPTAC), characterizes proteomic technologies for discovery and validation of biomarkers. The second, the Early Detection Research Network (EDRN), attempts to develop new sets of biomarkers and evaluate their effectiveness in clinically relevant samples. The quest for biomarkers is fraught with challenges for both “bench” experiments and bioinformatics. Here, we examine sources of discrepancy at several levels. The search engines that identify peptides from LC-MS/MS experiments differ significantly in the set of spectra that they identify from experiments. Parsimonious protein assembly may prune out proteins in one experiment and retain them in another. Protein differentiation tools may yield divergent results, even when starting from the same data sets. Verifying biomarkers through targeted proteomics has only recently been supported by tools that can work across instruments from different vendors. Translating cancer biology knowledge into clinically relevant tests for this disease will require care at all these levels.

Author details

¹Biomedical Informatics, Vanderbilt University, Nashville, TN, 37232-8575, USA.

²Biochemistry, Vanderbilt University, Nashville, TN, 37232-6350, USA.

Published: 5 August 2011

* Correspondence: david.l.tabb@vanderbilt.edu

¹Biomedical Informatics, Vanderbilt University, Nashville, TN, 37232-8575, USA
Full list of author information is available at the end of the article

doi:10.1186/1471-2105-12-S7-A17

Cite this article as: Tabb and Liebler: Bioinformatic challenges for proteomic biomarkers of cancer. *BMC Bioinformatics* 2011 **12**(Suppl 7):A17.

Submit your next manuscript to BioMed Central and take full advantage of:

- Convenient online submission
- Thorough peer review
- No space constraints or color figure charges
- Immediate publication on acceptance
- Inclusion in PubMed, CAS, Scopus and Google Scholar
- Research which is freely available for redistribution

Submit your manuscript at
www.biomedcentral.com/submit

