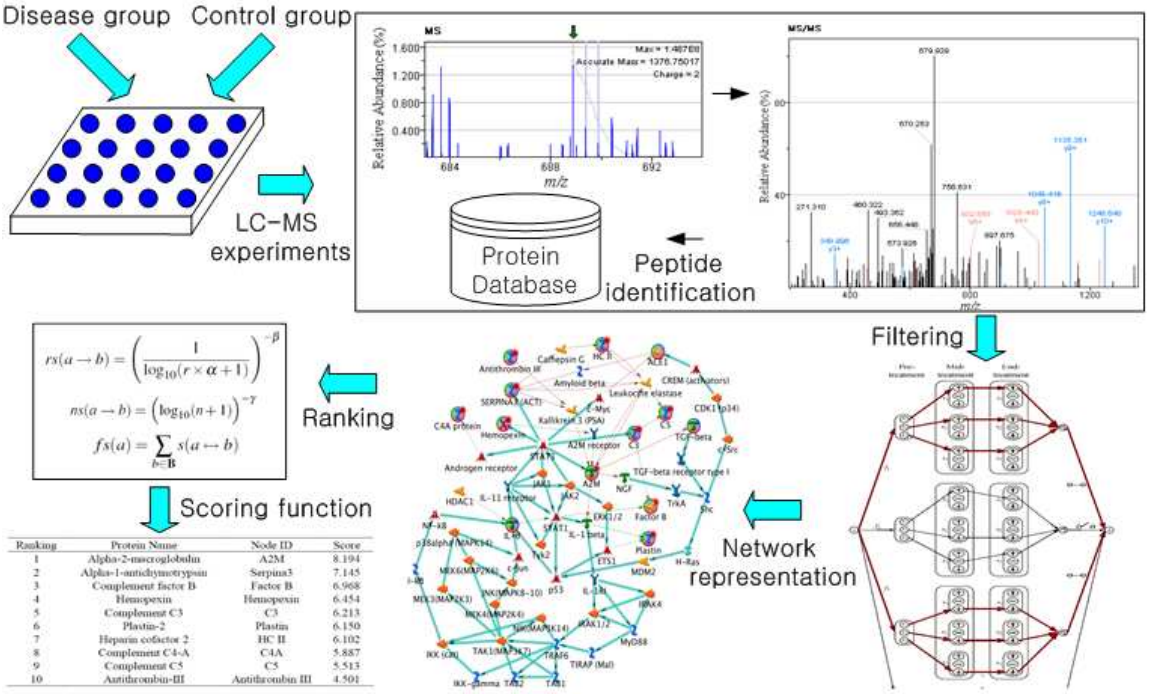
A Bioinformatics Approach for Biomarker Identification in Radiation-Induced Lung Inflammation from Limited Proteomics Data

Jung Hun Oh, Jeffrey M. Craft, Reid Townsend, Joseph O. Deasy, Jeffrey D. Bradley, and Issam El Naqa



Ranking	Protein Name	Node ID	Score
1	Alpha-2-macroglobulin	A2M	8.194
2	Alpha-1-antichymotrypsin	Serpina3	7.145
3	Complement factor B	Factor B	6.968
4	Hemopexin	Hemopexin	6.454
5	Complement C3	C3	6.213
6	Plastin-2	Plastin	6.150
7	Heparin cofactor 2	HC II	6.102
8	Complement C4-A	C4A	5.887
9	Complement C5	C5	5.513
10	Antithrombin-III	Antithrombin III	4.501

Widespread utilization of proteomics analysis for biomarkers discovery in oncology is impeded by prohibitive sample size requirements. In this work, we propose a novel graph-based scoring function to rank and identify the most robust biomarkers from limited proteomics data. The methodology is demonstrated for identifying biomarkers for radiation pneumonitis in lung cancer patients. Our preliminary results suggest that the proposed approach is promising for biomarker identification in sample-limited clinical applications.