Pacific Northwest
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PNNL-31223

Algorithms and file structures to enhance software workflows for ion mobility mass spectrometry (IM-MS)

CRADA 410

April 2021

Aivett Bilbao Pena

U.S. DEPARTMENT OF ENERGY

Prepared for the U.S. Department of Energy
under Contract DE-AC05-76RL01830

PACIFIC NORTHWEST NATIONAL LABORATORY
operated by
BATTELLE
for the
UNITED STATES DEPARTMENT OF ENERGY
under Contract DE-AC05-76RL01830

Printed in the United States of America

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Cooperative Research and Development Agreement (CRADA) Final Report

Report Date: April 27, 2021

In accordance with Requirements set forth in the terms of the CRADA, this document is the CRADA Final Report, including a list of Subject Inventions, to be provided to PNNL Information Release who will forward to the DOE Office of Scientific and Technical Information as part of the commitment to the public to demonstrate results of federally funded research.

Parties to the Agreement:

PNNL/Battelle Memorial Institute
Agilent Technologies, Inc.

CRADA number: 410 (Project No. 72496)

CRADA Title: Algorithms and file structures to enhance software workflows for ion mobility mass spectrometry (IM-MS)

Responsible Technical Contact at DOE Lab:

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DOE Program Office: Not applicable – 100% funds-in CRADA; however, both Todd Anderson and Michael Riches (Office of Science) are informed of this effort.

Joint Work Statement Funding Table showing DOE funding commitment:

Participant: Agilent Technologies, Inc

Duration: 27 months

In-Kind:	$50,000
Funds-In total:	$100,000
Total:	$150,000

Federal Admin Charge on funds-in (if applicable): $2912.62 under base award

Executive Summary of CRADA Work:

The purpose of this project was supporting customizations of algorithms and raw data file structures to enhance software workflows for liquid chromatography (LC), mass spectrometry (MS) and ion mobility mass spectrometry (IM-MS)-based metabolite characterization. PNNL worked with Agilent to evaluate and improve the integration of ion mobility into existing MS data analysis methods of Agilent software tools. The project augmented PNNL's capabilities to analyze complex omics samples. These capabilities are directly beneficial to DOE and PNNL efforts to characterize and analyze compounds in microbial and plant communities. The project assisted Agilent in further developing improved instrument-software solutions combining ion mobility with mass spectrometry for widespread applications in life sciences and other fields.

Summary of Research Results:

During this project, we have implemented and evaluated several improvements in the PNNL PreProcessor software (https://omics.pnl.gov/software/pnnl-preprocessor). These improvements support and enhance LC-IM-MS and LC-MS software workflows for molecular characterization in complex samples and produced a new prototype software workflow for two-dimensional (2D) LC-MS analyses. Specifically:

- We have adapted and evaluated the smoothing algorithm in the PNNL Pre-Processor, initially developed for IM-MS data structures, to TOF and QTOF data structures (i.e., LC-MS data files without IM).
- We have implemented and evaluated a first prototype of a converter for parsing multi-file 2DLC-MS data files to a single LC-IM-MS data file. Conceptually, the first LC dimension corresponds to the LC dimension in the new data file and the second LC dimension corresponds to the ion mobility dimension. This enabled the utilization of the Agilent IM-MS Browser software to visualize and process 2D-LC-MS data by leveraging the algorithms implemented for LC-IM-MS data.
- We have performed a benchmarking of the demultiplexing tools from PNNL and Agilent using metabolite and protein standards. The PNNL demultiplexing algorithm was found to provide better quality results. We next worked on the integration of the PNNL demultiplexing algorithm into the PNNL Pre-Processor, allowing easy access and usage of the software through the PNNL Pre-Processor user-friendly GUI. In addition, we integrated post-demultiplexing smoothing and performed the adaptation and evaluation of the demultiplexing for All Ions data files, which contain both precursor and fragment ion information.
- We have implemented software updates for enabling the processing of data from developmental PNNL ion mobility devices. Specifically, we adapted the PNNL-

PreProcessor algorithms for UIMF files, implemented updates in the UIMF-to-MassHunter converter for proper metadata parsing and performed the adaptation and evaluation of the demultiplexing algorithm for long ion mobility separations using more than 4 bits multiplexing sequence.

- Regarding the initially planned task of prototyping a multaidimensional scoring for metabolite identification, we have implemented a prototype R script for scoring based on accurate mass and collision-cross section. However, by mutual agreement and evaluation of priorities, work on this task did not continue, and instead, the efforts were redirected towards the work for demultiplexing tools.

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