**mz5**: Space- and Time-efficient Storage of Mass Spectrometry Data Sets*

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Across a host of MS-driven-omics fields, researchers witness the acquisition of ever increasing amounts of high throughput MS data and face the need for their compact yet efficiently accessible storage. Addressing the need for an open data exchange format, the Proteomics Standards Initiative and the Seattle Proteome Center at the Institute for Systems Biology independently developed the mzData and mzXML formats, respectively. In a subsequent joint effort, they defined an ontology and associated controlled vocabulary that specifies the contents of MS data files, implemented as the newer mzML format. All three formats are based on XML and are thus not particularly efficient in either storage space requirements or read/write speed. This contribution introduces mz5, a complete reimplementation of the mzML ontology that is based on the efficient, industrial strength storage backend HDF5. Compared with the current mzML standard, this strategy yields an average file size reduction to ~54% and increases linear read and write speeds ~3–4-fold. The format is implemented as part of the ProteoWizard project and is available under a permissive Apache license. Additional information and download links are available from http://software.steenlab.org/mz5. Molecular & Cellular Proteomics 11: 10.1074/mcp.O111.011379, 1–5, 2012.

MS data are acquired on a wide variety of mass analyzer technologies and brands that deliver data sets in various proprietary data formats and make use of a multitude of architecture-dependent libraries. In the past, this situation has severely complicated the development and application of alternative, vendor-independent data analysis pipelines (1–3), highlighting the need for and fueling the development of a common and open storage format for MS data sets (4, 5).

The Proteomics Standards Initiative and the Seattle Proteome Center at the Institute for Systems Biology independently developed the mzData and mzXML formats, respectively (4, 6). They subsequently merged their efforts, leading to the development of mzML (7), which features a generic ontology for the representation of MS data. The mzML format is universally applicable, and combined with the readily available open source reference implementation ProteoWizard (1), it significantly simplifies data import and export as well as general data handling. Most notably, mzML introduces a controlled vocabulary that enables the addition of novel as well as user-defined data types without requiring changes to the underlying XML schema. As a consequence, laboratories are able to store, analyze, and share MS data using an open exchange format, even for highly specialized workflows (8–11).

Continuous improvements in mass resolution and acquisition speed pose a serious challenge for existing data formats: current MS setups commonly acquire several hundreds of megabytes of data for each run, and space requirements for complete proteomics experiments easily exceed tens of gigabytes. As a consequence, the space and time efficiency of data format implementations have become increasingly critical.

Although based on excellent ontologies, relying on the extended markup language (XML)1 for the straightforward implementation of mzData, mzXML, and mzML makes for a major efficiency bottleneck. XML was designed to be a human readable, textual data format with considerable inherent verbosity and redundancy. XML was not designed for efficient bulk data storage, and the general modus operandi requires reading complete files to construct the XML parse tree. The mzXML and mzML formats partly circumvent these limitations by using base-64 encoding and (optional) compression of the raw MS scan data in combination with an application-specific indexing system. Despite the improvements gained from these efforts, vendor formats in general outperform mzXML and mzML in terms of space requirements, as well as in read and write efficiency.

This contribution introduces mz5, a novel data representation that combines the merits of the mzML ontology with the efficiency of the Hierarchical Data Format (HDF5) (12). HDF5 is an established industrial standard for efficient storage and

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1 The abbreviations used are: XML, extended markup language; HDF5, Hierarchical Data Format, version 5; I/O, Input/Output.
retrieval of large amounts of complex data and is based on a portable binary representation. HDF5 was specifically designed for large data sets; the key features used in our mz5 implementation are its native support for compression and cached partial read and write access. HDF5 library implementations are available for a range of languages and computational platforms, and the format is distributed under a permissive licensing scheme. Introduced more than 20 years ago, the continued use of HDF5 as the standard format for the NASA earth observing system, as well as its adaption as a prime format for data intensive applications in fields as diverse as astronomy, geology, remote sensing, and avionics (13–16), ensures broad, ongoing use and technical support for many years to come.

Our analyses show that mz5 dramatically outperforms the XML-based representations of the mzXML and mzML formats in terms of both space requirements and Input/Output (I/O) speed and is competitive with proprietary vendor formats in terms of space requirements (Fig. 1). Because mz5 is implemented inside the ProteoWizard (1) framework, it is already available for use by the mass spectrometry community, and mz5 files can immediately be created from all open or proprietary formats supported by ProteoWizard (Fig. 2).

**EXPERIMENTAL PROCEDURES AND RESULTS**

Twenty LC-MS/MS runs of fractionated HeLa S3 cell lysate were acquired in data-dependent acquisition mode on an LTQ/Orbitrap classic (Thermo Scientific) system hyphenated to a nanoflow HPLC system (Eksigent). The survey scan range was limited to m/z 400–2000 at a nominal resolution of 60,000, and MS/MS scans were limited to the eight most abundant precursor ions. The resulting raw data files were converted to mzML using the ProteoWizard (1) tool set, mzXML files were converted to mz5, and the identity of the mzML and mz5 file contents was confirmed. For all formats, the data were stored in compressed double precision. For the mzXML and mzML formats, indexing was turned on. All of the experiments were conducted using the same hardware, with all resources dedicated to the test runs (no parallel jobs). Overall, we consider the selected data set to be a reasonably common example of LC-MS/MS data acquisition and hence expect that the results generalize to a large majority of practical use cases.

To assess mz5 performance, we conducted three types of comparative experiments, testing (i) write performance; (ii) read performance; and (iii) space requirements. For each of the 20 input files, we generated a set of 10 subsets of increasing sizes (sets of 900, 1600, up to 8000 spectra, and the complete set of all spectra present in the respective input file). This strategy yielded 220 test cases. All of the time measurements were averaged over 10 repeats for every test case, after discarding the minimum and maximum timings. For performance comparisons between different formats, we fitted linear models with intercepts and determined relative slopes over time and space (see supplemental materials). mz5 files were used to generate each test case for mzXML, mzML, and mz5, to guarantee that all three file formats contain the same data.

To test linear read performance, we measure the time it takes to read each of the test cases from the file it is stored in. Fig. 1a shows the linear read times of all test cases versus the number of (m/z, abundance) pairs. The mz5 format outperforms the mzXML and mzML formats by factors of −2.3 and −3.7, respectively. We note in passing that the mz5 gains over mzML are not strictly linear; this indicates optimization opportunities for the parsing of smaller mzML files. Interestingly, the mz5 linear read times also exhibit smaller variation compared with mzXML and, in particular, mzML read times.

For strictly random reading, mz5 is significantly faster than mzML but performs slightly slower than mzXML. This is due to the underlying HDF5 caching/compression tradeoff. We focused on the vast majority of conceivable use cases and geared the tradeoff toward efficient linear reading. The random read and initialization performance tests, as well as benchmarks for different mass analyzer types, can be found in the supplemental materials.

To test write performance, we extracted every test case from the respective mz5 input file and measured the time it takes to write the data to disk, using mzXML, mzML, and mz5. Consequently, potential read time delays only cause a constant offset that is identical between the different formats and does not affect the slopes. Supplemental Fig. 1a illustrates the results for all 220 test cases. Time measurements for mzXML, mzML, and mz5 are shown as circles, triangles, and circles, respectively. It is apparent that mz5 is consistently faster than mzXML and mzML. The read time-corrected relative slopes show improvements of a factor of ~4.7 for mz5 over mzXML and ~3.9 over mzML (Table I).

Fig. 1b illustrates storage consumption versus the number of (m/z, abundance) pairs. It is evident that the mz5 format requires little more than half the disk space (54%) of the mzXML and mzML formats. The mzXML and mzML storage requirements are practically identical. Fig. 1c illustrates that mz5 even supersedes XML-based formats that are compressed at the file and spectrum levels for off-line long term storage. Hence, mz5 provides better compression levels while still offering immediate data access and avoiding the need for time-consuming file level compression and decompression.

**Implementation**—The mz5 format maps the mzML compound data types, which correspond to classical abstract data types. Collections of compounds are stored in instances of a multidimensional array type (H5::dataset). Instances are compressed and stored to disk. It should be noted that the straightforward representation of mzML tags in terms of HDF5 groups is not a viable solution, because such an approach would prohibit data compression for technical reasons.

The HDF5 library is already highly optimized for file I/O (17). The mz5 implementation guarantees optimized buffer sizes to minimize the number of necessary I/O operations, collecting raw data before bulk writes are performed. HDF5 natively supports compression filters, and to optimize compression rates, our implementation makes heavy use of HDF5 data types that are amenable to compression, in particular avoiding variable length data types where possible. In addition, mz5 removes zero intensity scans and encodes m/z measurements in a delta mass representation, storing distances between consecutive m/z observations. The latter two measures yield a stor-
age requirement reduction of 55%. Tests showed that there were no numerical errors introduced by delta storage.

The implementation at hand features considerable versatility: it is possible to adapt the data type of raw data (float/double), configure compression level and filtering strategies, and configure HDF5 buffer sizes. The default configuration provides a reasonable parameter setting for most common use cases.

`mz5` is currently limited to collections of \((m/z, \text{abundance})\) and \((\text{time, abundance})\) for spectral and chromatographic measurements, respectively. The extension to other forms of measurements is possible and straightforward.

**Application**—For practical applications, the main impact of the `mz5` format is likely going to be the significant decrease in storage space requirements. Many proteomics core facilities have substantial data storage and archiving costs, and the efficient use of available space can help to reduce these costs. Although standard database searches as they are currently performed are unlikely to benefit from increased read and write speeds, we expect that `mz5` will be of particular interest for spectral library searches, which are likely to become more relevant in the future (18, 19). Furthermore, `mz5` will be of interest for data processing pipeline setups because the read and write performance is significantly improved.

**TABLE 1**

Average read/write times and space requirements for \(10^6\) \((m/z, \text{abundance})\) pairs for the `mz5`, `mzML`, and `mzXML` file formats

|            | `mz5` | `mzML` | `mzXML` | `mzML/mz5` | `mzXML/mz5` |
|------------|-------|--------|---------|------------|-------------|
| `t_{lr}`   | 0.13  | 0.49   | 0.3     | 3.65       | 2.28        |
| `t_{w}`    | 0.63  | 2.08   | 2.46    | 3.28       | 3.9         |
| `t_{w}/t_{lr}` | 0.5  | 1.95   | 2.33    | 3.89       | 4.66        |
| `t_{w} - t_{w}^{mz5}` | 0.5  | 1.95   | 2.33    | 3.89       | 4.66        |
| `Space`   | 7.57  | 13.72  | 14.13   | 1.81       | 1.87        |

**Fig. 1.** Linear read/write times and storage space requirements for different file formats on 22 file fragments over 10 repeats. Linear read and write speeds are measured in \(10^6\) \((m/z, \text{abundance})\) pairs/s; storage space is measured in MB/10^6 \((m/z, \text{abundance})\) pairs. All `mz5`, `mzXML`, and `mzML` measurements are shown as circles, diamonds, and triangles, respectively. a, the `mz5` format exhibits a 2.28-fold increase in reading speed compared with `mzXML` and a 3.65-fold increase compared with `mzML`. b, `mz5` roughly halves the storage space requirements when compared with `mzXML` (53%) and `mzML` (55%). c, space requirements for `mzXML`, `mzML`, `mzML` with file level compression (gzip), and `mz5` relative to Thermo raw, Bruker yep, and ABSciex wiff format (dashed line). The `mz5` format minimizes storage requirements while providing fast raw data I/O.
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**Fig. 2. The mz5 format and its relation to common input and output formats.** Format conversions that are supported by the ProteoWizard (1) framework are represented by solid arrows; format conversions that currently require additional software are shown with dashed arrows. Because the mz5 format has been implemented within the ProteoWizard framework, it can readily be generated from a wide range of proprietary vendor raw formats.

write speeds and storage space requirements offered by mz5 will increase the efficiency of data exchange between different components of a tool chain and reduce the impact caused by data conversion from proprietary vendor formats to an open standard. To enable the transparent, straightforward use of the mz5 format in existing and future software applications, we have implemented mz5 within the ProteoWizard library; hence, any application that already makes use of ProteoWizard-based transparent data file access will automatically support mz5. This eliminates the need for any mz5-specific conversion tools or software adoptions because the ProteoWizard interface already enables the use of many proprietary and open formats and requires only a single implementation effort on the user side. We have successfully used the mz5/ProteoWizard combination under Windows, Linux, and Mac OSX.

Summary—This contribution introduces an efficient open data format for bulk mass spectrometry storage termed mz5. It combines the merits of HDF5, an established industry standard, and the mzXML ontology developed by the HUPO Proteomics Standards Initiative. The mz5 format offers dramatically faster I/O than the mzXML and mzXML formats and requires only approximately half (54%) of the storage space. The current mz5 implementation is fully integrated into the ProteinWizard library and supports conversion operations for all proprietary data formats supported by ProteoWizard itself. All software is available from: http://software.steenlab.org/mz5.

The mz5 format is a first step toward providing extended capabilities for MS data storage. Depending on future mzML ontology development and forthcoming HDF functionality, this may include physical and logical merging of large experimental data sets, distributed read and write access for high throughput workflows, and novel strategies for large data repositories (20, 21).

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