nmrML

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nmrML: a community supported open data standard for the description, storage, and exchange of NMR data

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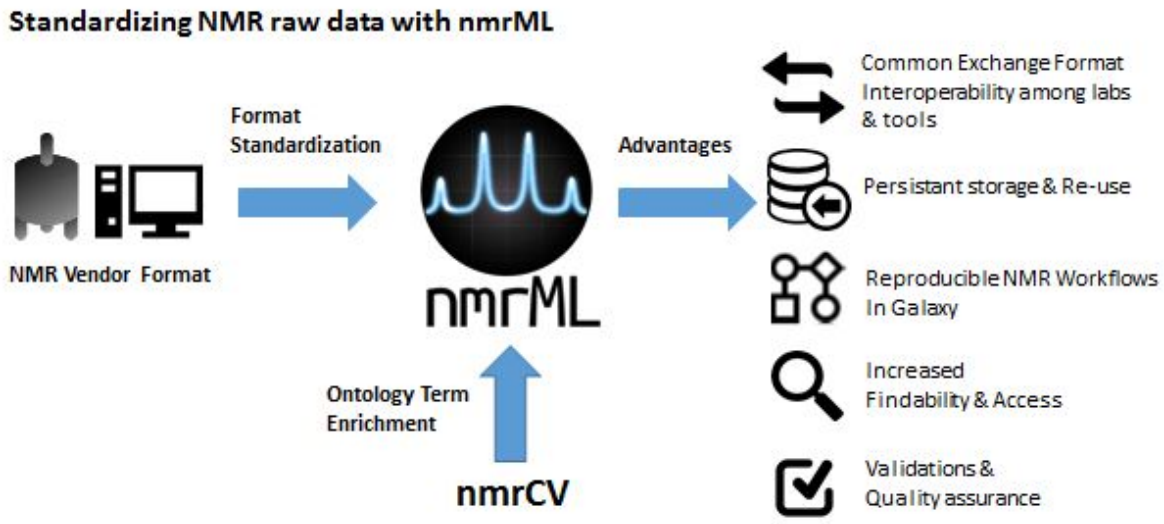
Running title
nmrML, an open NMR data standard and vocabulary

Summary

NMR is a widely used analytical technique with a growing number of repositories available. As a result, demands for a vendor-agnostic, open data format for long-term archiving of NMR data have emerged with the aim to ease and encourage sharing, comparison and reuse of NMR data. Here we present nmrML, an open XML-based exchange and storage format for NMR spectral data. The nmrML format is intended to be fully compatible with existing NMR data for chemical, biochemical and metabolomics experiments. nmrML can capture raw NMR data, spectral data acquisition parameters and, where available, spectral metadata such as chemical structures associated with spectral assignments. The nmrML format is compatible with pure-compound NMR data for reference spectral libraries as well as NMR data from complex bio-mixtures i.e. metabolomics experiments. To facilitate format conversions, we provide nmrML converters for Bruker and Agilent/Varian vendor formats. In addition, easy-to-use web-based spectral viewing, processing and spectral assignment tools that read and write nmrML have been developed. Software libraries and web services for data validation are available for tool developers and end-users. The nmrML format has already been adopted for capturing and disseminating 1D NMR data for small molecules by several open source data processing tools and metabolomics reference spectral libraries, e.g. serving as storage format for the MetaboLights data repository. The nmrML open access data standard has been endorsed by the Metabolomics Standards Initiative (MSI) and we here encourage user feedback to increase usability and make it a successful standard.

Keywords: nuclear magnetic resonance spectroscopy, NMR, XML, open source, data standard, MSI, ontology, controlled vocabulary, validation, metabolomics, workflows



Introduction

Nuclear magnetic resonance (NMR) spectroscopy is an important analytical tool in organic chemistry, biochemistry, natural products research, structural biology and metabolomics. Recently the need for an open NMR data standard covering the free induction decay (FID) to support data reproducibility has been acknowledged [1]. As instrument vendors typically provide the data processing software and produce evolving data formats together with the instrument hardware, developers of third party NMR analysis software often need to devote considerable effort into reading and writing these vendor-specific formats. This applies both to commercial software and to community developed open-source tools such as the BATMAN R package [2], Bayesil [3], NMRProcFlow [4], rNMR [5] and MetaboLab [6]. With the recent termination of the Agilent/Varian NMR spectrometer range, the question of long-term readability of discontinued vendor formats has become paramount for a growing NMR community. Data in proprietary formats

can age quickly and NMR data stored in such formats can become obsolete, making valuable results inaccessible and irreproducible in the long term. Also, spectra processing and quantification tools would benefit from a standardized storage format for processed NMR data, i.e. serving workflow systems. For NMR data repositories such as MetaboLights [7], Metabolomics WorkBench [8], Human Metabolome Database HMDB [9] and BioMagResBank [10], key questions regarding long term data persistence, i.e. on sustainability, usability and accessibility are arising.

Currently, the most widely used open data exchange format for NMR data is JCAMP-DX version 6.0 [11], but due to the broad scope and complexity of this format, many different vendor-dependent variants exist. Coordinated updating for all variants - in order to reflect the state of the art in NMR methodology - is rarely seen in this thirty year old format. This variability can lead to incompatibilities between different software packages, and as a result no content-based (semantic) validation of JCAMP-DX is available. While JCAMP-DX is likely to remain in use for NMR data capture for many years, it is clear that alternative approaches, such as XML or JavaScript Object Notation (JSON) with peer-maintained ontologies, would be beneficial.

The first efforts towards establishing an XML-based open NMR standard and controlled vocabulary were discussed in 2007 by the ontology working group [12] of the Metabolomics Standards Initiative (MSI) [13] and a consortium of UK universities discussing minimal reporting guidelines [14]. In 2011 a series of initiatives by members of the NMR-based metabolomics and biomolecular NMR communities were launched to explore the creation of a new community standard for NMR data exchange and storage. This included meetings attended by NMR stakeholders including metabolomics database representatives and vendors. This initiative and subsequent meetings were then taken over by the COSMOS (COordination of Standards in MetabOlomicS) EU FP7 consortium [15], aiming to coordinate the establishment of a persistent NMR data format and open source data analysis tools for the NMR community. The main goals were:

- *Data sharing in an open vendor-agnostic manner,* so that users, tool developers and public repositories can import or export data to support integrated (meta-)analysis and secondary data usage.

- *Search & retrieval of relevant results,* minimizing alternate ways of encoding the same information, so that data sets with a similar setup can be identified and compared.
- *Spreading best practices and evaluation of the results*, whereby the data quality can be assessed in light of intelligibility and completeness along minimum information standards supported by automatic validation aids.
- *Improved data persistence and traceability over time,* delivering a self-describing easy-to-use, yet robust raw data storage format to support long-term archiving.

From such efforts, it was decided that the new data format would be called nmrML (for NMR Markup Language) and it should:

- Be compatible with existing vendor formats (Varian/Agilent, Bruker) and partially compatible with certain variants of JCAMP-DX.
- Be XML-based, so as to be similar to established XML formats by the Proteomics Standard Initiatives (PSI) *i.e.* mzML for mass spectrometry [16].
- Support the use of controlled vocabularies/ontologies to annotate spectral data and metadata with standardized descriptors, which can be maintained in a decentralized peer production manner.
- Initially focus on the capture of small molecule NMR data (with macromolecular NMR data being addressed in succession).
- Be easy to understand and integrate into existing open analysis and processing software.
- Contain sufficient spectrometer data, acquisition and processing metadata to permit the reconstruction of the NMR spectrum and experiment.
- Capture coarse-grained spectral assignment data for molecule identification and quantification in chemical mixtures. Capture fine-grained assignment and chemical structure data of pure-compound spectra for use in organic synthesis and natural product studies, medicinal chemistry and reference NMR spectral libraries.

Under these development constraints, members of the nmrML COSMOS team created the nmrML data standard, the necessary software support, and fostered support from databases to both accept and display nmrML data. Fig. 1

summarizes available nmrML compliant tools and functionalities in support of a typical NMR data handling workflow for a metabolomics or similar experiment.

[Fig. 1]

Material and Methods

The nmrML format specification is composed of an XML Schema Definition (XSD) and an accompanying controlled vocabulary called nmrCV. Leveraging on existing efforts, the nmrML development started by updating a predecessor XSD developed[1] at The Metabolomics Innovation Centre (TMIC) in Edmonton, Canada, with additional elements and structures from a BML-NMR XSD developed at the University of Birmingham [17]. Both of these efforts were integrated, expanding the TMIC predecessor, as it was already capturing the basic raw data and had the CV reference mechanism in place. The nmrML CV referencing mechanism and basic XML architecture was inspired by mzML, the PSI standard mass spectrometry data format used in proteomics and metabolomics [16]. The mzML community standard captures raw MS spectral data, instrument parameters, experiment metadata, and peak assignment, as well as compound quantitation data. Given the similarity in data capture, storage, and retrieval between modern MS and NMR experiments, many of the successful features found in mzML were transferred and adapted to nmrML. The nmr.owl CV by the MSI [12], and a parallel TMIC effort nmr CV[1], developed to serve the TMIC XSD, were integrated. The merged nmrCV organizes common and essential NMR terms into a simple is-a class hierarchy (taxonomy). The nmrML 1.0.rc1 format presented here is the outcome of these integration efforts and will serve as the MSI recommended common data standard and terminology for open access NMR data. While the nmrML.xsd mostly covers raw data, it also provides for some NMR data elements computed by open access NMR processing and quantification tools. Development was coordinated via mailing lists, video conferences, and during multiple workshops and hackathons. The choice of XML was motivated by technical maturity, flexibility and universality of XML in both capturing and presenting scientific data. There is an abundant XML expertise to leverage on, as XML resides at the base of the semantic web stack. The appearance of all knowledge capture XML

[1] http://www.metabolomicscentre.ca/exchangeformats.htm

elements can be controlled via the XSD (mandatory vs. optional) and hence allows for content completeness checks. We implemented converter webservices to generate valid nmrML from vendor raw data files. Links to nmrML compliant databases as well as NMR processing and spectrum visualisation software are provided in Tab. 1. Format parsers, application program interfaces (APIs), and validation webservices have been set up. All code libraries, an issue tracker as well as a file versioning and release policy are available on the developer's GitHub pages at https://github.com/nmrML/nmrML.

Results

The nmrML core specification, including the XSD and nmrCV, can be found at nmrml.org, together with tutorials. The referenced nmrCV.owl currently contains over 600 terms and is indexed under the NCBO Bioportal ontology library [18]. Our documentation website (http://nmrml.org/examples), provides tutorial material and videos, code examples for single compound reference spectra as well as mixed-compound NMR spectra.

nmrML Architecture

The nmrML XSD element hierarchy contains multiple sections that organize the information that can appear in an nmrML XML data file in a community-agreed and self-explanatory way. This facilitates understanding of the format by both humans and by data processing software alike. The current top level XSD structure provides high-level base elements for the grouping and capture of NMR data, describing the nmrML version, the sources of the controlled vocabularies or ontologies used for metadata annotation, the data depositor contact, source files/formats, software lists, the instrument configuration, sample information (e.g. solvent and reference standards), acquisition settings, and data processing information. This is followed by the spectral FID raw data, as a base64-encoded binary. In addition to such a ‘minimal’ nmrML data file, additional information such as molecule identification/spectral assignment metadata and quantification data can also be included. For example, if the NMR data is for a pure reference compound or a newly isolated/synthesized single chemical, the nmrML file can include data on the chemical structure and corresponding atom-specific peak feature assignments (see example generated by

nmrML-Assign in Fig. 2 or http://nmrml.org/examples/3). If the NMR data is for a complex mixture, consisting of many different compounds from an analytical setting, the nmrML file can include data on peak positions, integrated peak areas and putative peak assignments, together with relative or absolute concentrations of some or all of the compounds, but no annotation of individual peak features to atom environments (see http://nmrml.org/examples/4). Code examples of a minimal nmrML data XML file, as well as for the expanded metadata case are provided on the examples page[2].

The nmrML structure consists of an XSD that allows it to reference a dedicated NMR controlled vocabulary (nmrCV). The XSD defines the allowed XML structure, whereas the controlled vocabulary provides the terminology to describe the NMR data in detail using standardized textual values for XML-defined tags. In areas where the terminology is likely to change faster than the nmrML XSD can be updated, the representation is branched out from XSD to CV-usage. This approach can accommodate rapid technology/terminology changes in a flexible way, as the CV can be maintained externally by a larger NMR user peer group: for example, terms for new NMR probes can be represented in a nmrML file by requesting the addition of corresponding new CV terms in the nmrCV, without the need for a full XSD and any subsequent software revisions. The combined usage of XML and a separate CV also allows multiple validation levels to be established (see below). The CV referencing mechanism is explained in detail on the documentation pages.

Tools compatible with nmrML

We have created web-based easy-to-use tools make nmrML more accessible to the broader organic chemistry and metabolomics communities. To ensure that nmrML will be broadly adopted by life sciences and chemical researchers, these tools cover a large fraction of a typical NMR data acquisition, processing and storage workflow to generate, convert, process, validate and publish nmrML files (Fig. 1). Additionally, we have worked closely with open source and commercial tool developers to encourage nmrML format support and adoption. We have summarized efforts already leveraging on the nmrML format in Tab. 1.

[2] *http://nmrml.org/examples*

[Tab. 1]

nmrML Converters, Parsers and Validators

Format converters translate the exchange syntax from vendor raw data formats into XSD-compliant nmrML by means of mappings from Bruker 'acqus' or Varian 'procpar' raw files to nmrML elements and CV terms. An extensive parameter mapping table is available in the documentation pages. A comprehensive JAVA-based converter automatically generates valid nmrML files from Bruker and Agilent/Varian 1D raw files. It is also available as a webservice (http://nmrml.org/converter) and can be run in batch mode for high-throughput batch conversion of zipped raw data. A python-based converter that uses the nmrGlue API [19] to access the vendor parameters is also available. Also an nmrML2ISA parser [20], written in Python, has the ability to read experimental NMR data and metadata from nmrML data files and passing it over to an autogenerated ISA-Tab [21] assay file, i.e. defining a basic metadata backbone ISA-Tab format for submission to the MetaboLights repository [7]. In addition, nmrML bindings for multiple programming languages (Java, Python, Ruby), as well as for widespread data analysis tools like the R statistics package, MATLAB(R) and open source NMR tools exist. A parser called nmRIO makes nmrML content available to R-based tools such as Batman and rNMR for higher level analysis. A MATLAB parser renders nmrML data available to the MATLAB(R) tool for further statistical processing. An nmrML semantic validator allows the revisal of the correct implementation of manually populated or enriched nmrML files, with regard to XML schema compliance, CV term usage and allowed term cardinalities. At the core, the XML syntax and structural validity of nmrML XML instances, such as XML element and attribute position, order and cardinality, can be checked by any validating XML parser against the nmrML.xsd, which defines these allowed elements and their expected characteristics. On the next higher layer, so-called mapping rules can enforce semantic validity [22] of the ontological descriptions used, by testing which CV terms are allowed in which elements. The elements with their allowed CV descriptor hierarchies are outlined in a mapping rule file. The OpenMS/Topp-based [23] nmrML validator (http://nmrml.org/validator) checks that these higher level semantic criteria are being met in a given XML instance. For example, a validation rule file can enforce minimal reporting guidelines such as the MSI-sanctioned Core

Information for Metabolomics Reporting (CIMR)[3]. These validation scenarios make nmrML more easily accessible to quality assurance than JCAMP-DX or other more verbose and equivocal formats that do not rely on controlled vocabularies.

nmrML Data Processors and Viewers

The following tools facilitate NMR data processing and compound identification. nmrML-Assign (http://nmrml.bayesil.ca) is a JavaScript web application based on Bayesil, that allows users to upload vendor formatted 1D NMR raw data or nmrML and to then interactively add compound identification metadata (see Fig. 2, Example 3). The Bayesil-generated interactive spectrum allows assigning peaks to specific atoms in a proposed molecule after the Bayesil webservice [3] was used to upload a chemical structure and perform a spectral prediction to help with the assignment process. The assigned atoms are displayed on both the spectrum and the molecule image. Once the assignment process is complete, the annotated file can be saved as enriched nmrML file, which can then be re-loaded and interactively viewed and edited or submitted to HMDB. nmrML-Assign works both with ^{1}H and ^{13}C NMR spectra in Bruker or Agilent/Varian format. Bayesil also allows users to upload 1D spectra of biological mixtures (e.g. serum, plasma, cerebrospinal fluid) as shown in Example 4 on our website, and to perform an automated assignment and quantification of all visible peaks.

[Fig. 2]

The Batman R package estimates metabolite relative concentrations from spectral data and automatically assigns them to metabolites from a target list. Batman can access nmrML data and is using the nmRIO parser. rNMR [5] is a region-of-interest rather than peak-list-based software for visualizing, assigning, and quantifying metabolites in complex 1D and 2D NMR data. The upcoming version of rNMR will read nmrML files directly and can convert them into its native data format. NMRProcFlow is a pipeline tool for the reproducible processing and visualization of 1D NMR data in metabolomics. It allows to pipe processed NMR data as tabular data matrix to statistics workflow tools like biostatflow.org. It relies on the NMR spectra viewer

[3] http://mibbi.sourceforge.net/projects/CIMR.shtml

(https://github.com/nmrML/nmrML/tree/master/tools/Visualizers/PMB_NMRviewer), as its design acknowledges iterative parameter adjustments by means of repeated visual inspection by the user.

nmrML compatible Databases

A principal objective behind the establishment of nmrML is to ensure data continuity and persistence in NMR repositories and reference libraries. Several key NMR experiment and reference databases now support the upload, storage, display and download of nmrML data. HMDB, with more than 1500 1D ^{1}H and ^{13}C NMR spectra collected at 500 and 600 MHz[4], describes more than 1000 reference spectra for pure compounds in the Human Metabolome Library (HML)[5]. More than 600 metabolites in HMDB now include NMR reference spectra with complete spectral assignments. These metabolites have 1D NMR annotated spectra available and are downloadable in the nmrML format. Other databases such as DrugBank [24], YMDB [25] and ECMDB [26] plan to support nmrML compatible reference spectra in the future. BMRB entries are available in XML and RDF, as common open representations of NMR-STAR data format [27]. BMRB has archives of time-domain data and fully assigned nmrML files are accessible, which were generated from BMRB/XML files via the BMSxNmrML converter (see Tab.1). In addition to the growing collection of reference spectral libraries, the open access NMR data repository MetaboLights [7], has experimental NMR data archival, that now accepts nmrML data from depositors and allows to extract basic ISA-Tab metadata from it (see above). It now handles nmrML data from biological mixtures as well as from pure reference compounds. The MeRy-B [28] plant metabolomics NMR knowledge base accepts both JCAMP-DX and nmrML format with the plan to fully adopt nmrML in order to leverage on ontological spectra preprocessing terms embedded within nmrML. Work is underway to have the Metabolomics WorkBench [8] accept nmrML data as part of the international MetabolomeXchange[6] initiative.

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[4] "Human Metabolome Database: Database Statistics." http://www.hmdb.ca/statistics, accessed 15 May. 2017.
[5] "HML - Human Metabolome Database." http://www.hmdb.ca/hml, accessed 15 May. 2017.
[6] metabolomexchange.org/

Pipelines and Workflow support

With the recent push to standardize and facilitate the access to data processing workflows [29], devoted workflow environments such as Galaxy [30] have gained more weight, the intent here being transparency, traceability and reproducibility of pipeline-generated data and audit. Galaxy-based metabolomics analysis pipelines are emerging [31] and some are in development for NMR data, such as W4M-NMR[7] [31] and SOMA:tameNMR[8]. The NMR processing tool NMRProcFlow [4] uses nmrML as its native spectral data format and containerization of modules for workflow integration is progressing. To foster nmrML as input format for Galaxy workflow pipelines, the PhenoMeNal projects App library portal[9] already provides nmrML-aware tools (like the nmrML converter) as containers for NMR workflow integration.

Discussion

This manuscript describes the first iteration of nmrML (version 1.0.rc1). We have designed and developed a flexible, open standard data format called the NMR Markup Language (nmrML) for capturing and disseminating 1D NMR data for small molecules. This represents a community-driven effort that involved extensive consultations and many metabolomics, NMR spectroscopy, chemoinformatics and computing science laboratories from across Europe and North America. Further enhancements are planned for nmrML and these will include extensions to 2D and nD NMR data and the inclusion of macromolecular data in the XML and additional terms in nmrCV. Currently, only basic processed data is captured, e.g. for molecule identification and quantification, and the latter is equivalent to what mzTab stores for MS data and what is captured in mzIdentML [32] and mzQuantML [33]. The introduction of nmrML hence brings NMR spectroscopy in alignment with existing data standardization efforts in metabolomics, such as mzML for mass spectrometry and will ultimately contribute to cross-technology and multiple omics data comparison. We hope further tools like XEASY [34] for macromolecular NMR analysis and nmrPIPE [35] for nD NMR will leverage on nmrML in the future. MetaboLab [6] provides high-throughput pre-processing for MATLAB(R) driven

[7] http://workflow4metabolomics.org/the-nmr-workflow
[8] https://github.com/pgb-liv/tameNMR
[9] http://portal.phenomenal-h2020.eu/app-library

NMR statistics and is currently implementing an nmrML parser for standardized data import. In addition, further metadata will be added to nmrML, i.e. as required to store nD spectra. In addition to the persistent data storage/exchange standard and CV, we have also described and developed database support and software tools that make use of nmrML. These tools include nmrML viewers, nmrML data converters, processors and annotators and these will facilitate the widespread adoption of nmrML and permit the facile generation of nmrML data from proprietary vendor formats[10].

The use of nmrML validators will allow users to check nmrML files with regard to consistency and content completeness. Together with ISA-Tab metadata validation, this will greatly contribute to overall quality assurance and traceability of NMR data. The use of nmrML in workflow tools like tameNMR, and the re-use of containerized workflow components in re-combinable app libraries will allow NMR data processing to be more traceable and re-runnable in different (local or cloud) environments. To capture selected basic metadata within the same nmrML file as the data, eases pipeline development as it reduces the complexity of file tracking in Galaxy, as data moves between modules. Overall the nmrML specification and the expandable nmrCV will allow for a detailed standardized description of NMR workflow functionalities.

A recent survey[11] on data standards usage among the metabolomics community indicated that 13.5% of NMR practitioners are already using nmrML, about the same number of people indicating that they use JCAMP. Further testing of the current XSD with diverse experimental configurations is required to increase coverage, fitness of purpose and future flexibility. We hence welcome any community feedback and engagement via our email list[12] to improve and evaluate this first nmrML release. Remarks, suggested changes and extension requests should be sent to info@nmrml.org. By standardizing data descriptions, nmrML and its accompanying nmrCV will help make NMR

[10] Bruker Corp. indicated willingness to incorporate the nmrML converter into their TopSpin(R) software as nmrML file format export option.
[11] http://phenomenal-h2020.eu/home/wp-content/uploads/2016/09/Deliverable8.1.pdf
[12] https://groups.google.com/forum/?hl=en#!forum/nmrml/join

data *Findable, Accessible, Interoperable, and Reusable,* FAIR [36]. This is particularly relevant in light of the recent push by funding bodies to have scientists conduct and publish more reproducible research.

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Abbreviations

API: Application Program Interface
CIMR: Core Information for Metabolomics Reporting
COSMOS: Coordination of Standards in Metabolomics
CV: Controlled Vocabulary
FAIR: Findable, Accessible, Interoperable, and Reusable
FID: Free Induction Decay
JSON: JavaScript Object Notation
LOD: Linked Open Data
MSI: Metabolomics Standards Initiative
mzML: Mass Spectrometry Markup Language
NCBO: National Center for Biomedical Ontology
NMR: Nuclear Magnetic Resonance
nmrCV: Nuclear Magnetic Resonance spectroscopy Controlled Vocabulary
nmrML: Nuclear Magnetic Resonance spectroscopy Markup Language
OWG: Ontology Working Group
PSI: Proteomics Standard Initiative
XSD: XML Schema Definition

Author contributions

DS drafted the manuscript, coordinated the nmrML updates, contacted NMR data repository developers and created tutorial material. DS, DJ, MW and PRS implemented the nmrCV. DS and SN set up the semantic validator and created the mapping files. MW created and updated the nmrML.xsd, set up the Git and nmrML.org home pages and wrote the Python parser. DJ updated the nmrML.xsd, created and maintains the JAVA converter. DJ created example nmrML files and coordinated NMRProcFlow interactions. JAC created the predecessor nmrML XSD and an nmrCV predecessor. AMa and JRG deployed the nmrML Assign web server, added assigned spectra for HMDB compounds and coordinated Bayesil interactions. AMo and CD supervised the Java converter development, MeryB example generation, and provided feedback as wet-lab NMR and metabolomics database users. LFdF, KH, and RS helped integrating nmrML format with the MetaboLights repository. LFdF contributed to the initial version of the JAVA converter and created example nmrML files. PRS worked on and advised on CV and ontology reuse and coordinated the nmrML to ISA converter development with ML and RS. TE and JH contributed the MATLAB parser and BATMAN advice. ChL, JE and ULG were instrumental in aligning the initial XSD to BML-NMR repository needs. CLt and AR were initial driving forces overseeing the overall NMR data standards coordination. MSK and IAL worked towards rNMR integration. JLM coordinated BMRB and NMRFAM interactions and provided overall advice. ARJ and AG were contributing the NMR workflow tool tameNMR. ML implemented the nmrML2ISA converter. MY developed an nmrML converter for BMRB with guidance from JLM and NK. AP tested the vendor to nmr parameter mappings. JLG, MRV and DS contributed to the first round of nmrCV and CIMR MSI development. DW initiated the project and hosted the first round of XSD development and HMDB oversight. CS and RS initiated and coordinated the COSMOS EU project. RS advised on NMR and database issues and created example data sets. RS contributed to the nmrCV and nmrML development and MSI approval. SN contributed the nmrRIO parser, alignments to the semantic validator and helped with the Git. All authors contributed to, reviewed and approved the manuscript.

Figure and Table Legends

Fig. 1:

A prototypical metabolomics workflow for NMR data processing and storage is shown and nmrML-aware tools supporting each workflow step are illustrated. Vendor to nmrML converters, NMR data processing and visualization tools, as well as public repositories that accept nmrML as standard data format are highlighted. Parsers for MATLAB(R) and R, which make nmrML data accessible to statistics tools, and content validators that assist in data quality control and workflow reproducibility are shown. Many of our tools already run in Galaxy-based workflow management environments.

Fig. 2:

Assignment of an identified molecule in a single compound spectrum, generated in nmrML-Assign and displayed using the JSpectraViewer (JSV). An uploaded raw FID for the *2-oxobutanoic acid* reference compound was automatically processed with Bayesil. The resulting interactive JSV spectrum then allows the assignment of peaks to specific atoms, using the nmrML-Assign tool. The assignment metadata is then saved in the nmrML format (see https://github.com/nmrML/nmrML/tree/master/examples/reference_spectra_examples/hmdb). An excerpt view of the corresponding nmrML code (blue code inset) is shown for the quadruplet assignment (Multiplet #1) of the second peak (bold code). The corresponding HMDB entry is available from http://www.hmdb.ca/metabolites/HMDB00005, with the ^{1}H spectrum found at http://www.hmdb.ca/spectra/nmr_one_d/1024.

Tab. 1:

Non-exhaustive list of nmrML compatible open source software, clustered by tool category.

Figures

Fig.1:

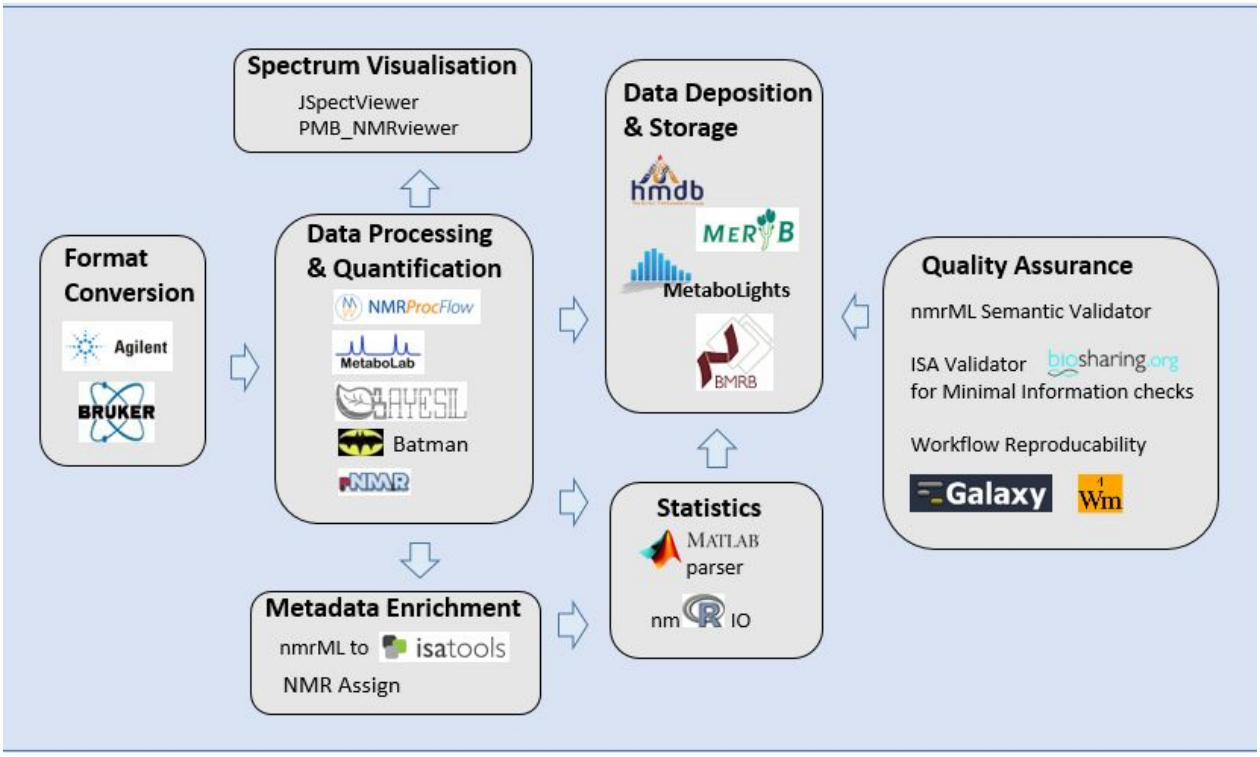

Fig.2:

Tables

Tab. 1:

Tool Category	Tool name	Key Functions	URL	Developer

Format Converters	nmrML converter (Java)	Converts vendor to nmrML format (*recommended*)	https://github.com/nmrML/nmrML/tree/master/tools/Parser_and_Converters/Java	Institut National de la Recherche Agronomique (INRA), France
	nmrML converter (Python)	Converts vendor to nmrML format	https://github.com/nmrML/nmrML/tree/master/tools/Parser_and_Converters/python/pynmrml	The Metabolomics Innovation Center (TMIC), Canada
	nmrML to ISA converter	Generates pre-populated ISA files from nmrML files	https://github.com/ISA-tools/nmrml2isa	EMBL-EBI, UK
	BMSxNmrML	Converts BMRB metabolomics entries to nmrML format	http://bmrbdep.pdbj.org/en/bmsxnmrml.html	Institute for Protein Research (IPR), Japan
Parsers	MATLAB parser	MATLAB(R) functions parsing and decoding nmrML files, and also writing MATLAB data into nmrML format.	https://github.com/nmrML/nmrML/tree/master/tools/Parser_and_Converters/Matlab	Imperial College London (ICL), United Kingdom
	nmRIO	R package for parsing and decoding nmrML files	https://github.com/nmrML/nmrML/tree/master/tools/Parser_and_Converters/R/nmRIO	Leibniz Institute of Plant Biochemistry (IPB), Germany
	nmrGlue	modules for working with NMR data in Python; for processing, analyzing, and inspecting NMR data	https://github.com/jjhelmus/nmrglue	Argonne National Laboratoriy (ANL), Il, USA
Data Validators	nmrML semantic validator	XML Schema compliance and rule-based validation of CV term usage	http://nmrml.org/validator	Leibniz Institute of Plant Biochemistry (IPB), Germany
Spectrum Viewers	JSpectraViewer (JSV)	Interactive 1D NMR Spectral viewer used in tools such as Bayesil and nmrML-Assign	http://nmrml.bayesil.ca	The Metabolomics Innovation Center (TMIC), Canada
NMR Processing, and Identification/ Quantification tools	NMRProcFlow	Interactive 1D NMR spectral viewer, spectral processing and quantification tool dedicated to metabolomics	http://nmrprocflow.org	Institut National de la Recherche Agronomique (INRA), France

	Bayesil	Automated compound identification, quantification and annotation from 1D NMR spectra	http://bayesil.ca, http://tmic.bayesil.ca	The Metabolomics Innovation Center (TMIC), Canada
	nmrML-Assign	nmrML conversion, annotation and peak assignment to compounds for reference 1D NMR spectra	http://nmrml.bayesil.ca	The Metabolomics Innovation Center (TMIC), Canada
	Batman	Bayesian deconvolution and automated quantification of metabolites from 1D NMR spectra	http://batman.r-forge.r-project.org	Imperial College London (ICL), United Kingdom
	rNMR	Region-of-interest based NMR spectra quantification from 1D and 2D NMR spectra	http://rnmr.nmrfam.wisc.edu	University of Calgary (U of C), Canada
Workflow Tools	PhenoMeNal app library	Lists containerized nmrML aware tools to build Galaxy NMR workflows	http://portal.phenomenal-h2020.eu/app-library	EMBL-EBI, UK
	SOMA:tameNMR	NMR data processing and analysis via Galaxy Workflows	https://github.com/pgb-liv/tameNMR	University of Liverpool (UoL), United Kingdom

Supporting Information

[Add authors, affiliations, title, Abstract …]

Supporting Information:

1. A pdf serialisation of the nmrML.xsd as Schema description
2. Documentary material with FAQ and tutorial