



HAL
open science

Conversion from metabolomics raw data to open format: ensuring MS and MS/MS data quality and software compatibility

Quentin Ruin, Delphine Centeno, Charlotte Joly, Marie Lagree, Stéphanie Durand, Emilien Jamin, Carla Orlandi, François Fenaille, Mélanie Pétéra, Estelle Pujos-Guillot

► **To cite this version:**

Quentin Ruin, Delphine Centeno, Charlotte Joly, Marie Lagree, Stéphanie Durand, et al.. Conversion from metabolomics raw data to open format: ensuring MS and MS/MS data quality and software compatibility. 16èmes Journées Scientifiques du Réseau Francophone de Métabolomique et de Fluxomique, Jun 2024, St Malo, France. hal-04611713

HAL Id: hal-04611713

<https://hal.inrae.fr/hal-04611713>

Submitted on 13 Jun 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Conversion from metabolomics raw data to open format: ensuring MS and MS/MS data quality and software compatibility

Quentin Ruin^a, Delphine Centeno^a, Charlotte Joly^a, Marie Lagree^a, Stéphanie Durand^a, Emilien Jamin^b, Carla Orlandi^b, François Fenaille^c, Mélanie Pétéra^a, Estelle Pujos-Guillot^a

^a Université Clermont Auvergne, INRAE, UNH, Plateforme d'Exploration du Métabolisme, MetaboHUB Clermont, Clermont-Ferrand, France
^b Toxalim (Research Centre in Food Toxicology), Université de Toulouse, INRAE, ENVT, INP-Purpan, UPS, MetaboHUB, 31300 Toulouse, France
^c Université Paris-Saclay, CEA, INRAE, Département Médicaments et Technologies pour la Santé (DMTS), MetaboHUB, 91191 Gif-sur-Yvette, France

[1] The Galaxy Community, "The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2022 update", *Nucleic Acids Research*, Volume 50, Issue W4, 5 July 2022, Pages W345–W351.
 [2] Bruker Daltonics, *Wissenschaft*, France
 [3] DOI: 10.18129/B3.bioc.xcms [4] DOI: 10.1016/j.biocel.2017.07.002 [5] DOI: 10.1038/nbt.2377 [6] Avtonomov D.M. et al. *J. Proteome Res.* June 16, 2016. DOI: 10.1021/acs.jproteome.6b00021.
 [7] DOI: 10.1093/bioinformatics/btq054 [8] https://doi.org/10.1038/41587-020-0531-2

CONTEXT

In the context of information extraction of high-throughput MS/MS metabolomics experiments, open science has led to the necessity of converting raw MS data into open formats capable of handling MS/MS. However, several formats and conversion software exist, involving heterogeneous FAIR adherence in terms of reproducibility, retro-compatibility and interoperability.

MATERIAL AND METHODS

STUDIED FORMATS

Two major formats have become the standard for converting raw data: **mzML** and **mzXML**. Although netCDF is still notably in use, it can only store one specific MS-level as it is not originally designed for spectrometry and tends not to be supported by the latest software solutions.

Moreover, **netCDF** is a mostly encoded format with few to no metadata whereas **mzXML** offers headers containing acquisition and processing information (Figure 1). **mzML** file metadata are even more detailed and structured, in addition to information on each scan; only mass and intensity lists are encoded to reduce file size.

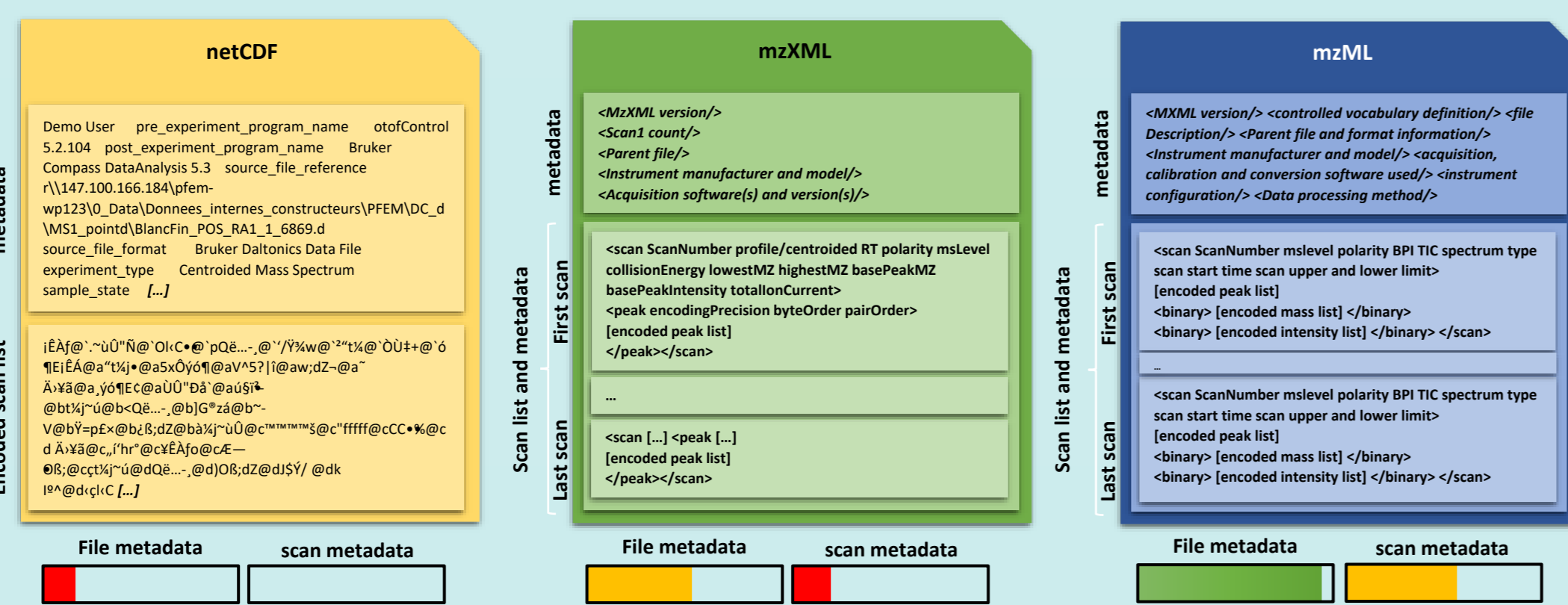


Figure 1: Iconography of files when opened with a text editor. Normal text represents real raw content copied from a file as an example, bold text summarizes bigger content blocks or XML-like tags to enhance readability. The amount of human-readable metadata provided is shown underneath the file diagrams.

RESULTS

INTRA-FORMAT VARIATIONS



Figure 4: Iconography of files when opened with a text editor.

- Different ways to store acquisition software
- Different tag codes, content and organization
- Different ways to store instrument reference
- Instrument name is even false in both cases!
- Different ways to store instrument components:
- Different number of components
- Different tag codes and organization
- Different "name" designation
- Different scan metadata organization
- Different encoding methods (even with the same encoding scheme, e.g. 64-bit)

Same format, different software: several metadata organization and potentially distinct encoding.

FORMAT AND SOFTWARE COMPATIBILITY

Knowing these variations within the same format depending on the conversion software used, especially with regard to encoding, can all conversion methods produce files readable by Galaxy and other common software for MS and MS/MS extraction/visualization? Tested with Galaxy, Batmass^[6], Skyline^[7] and MS-Dial^[8] as target software (Figure 5).

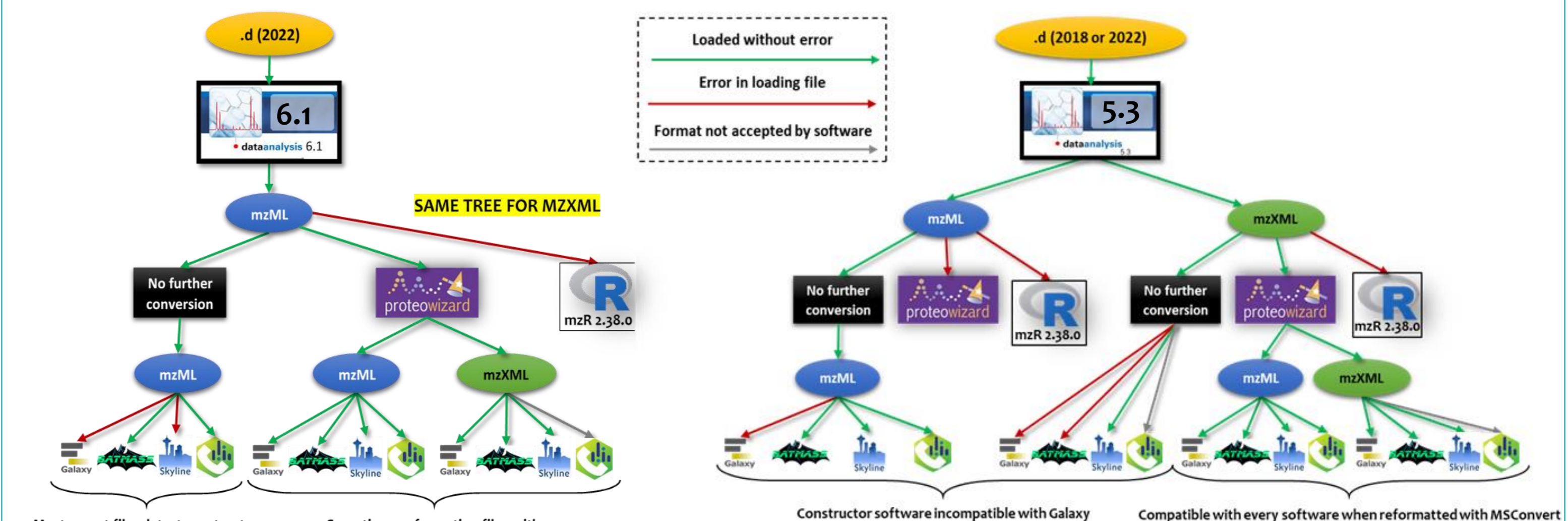


Figure 5: Tree diagram showing the pipelines of conversion tested and their compatibility with the files.

The compatibility of converted files with the used software must be monitored for all conversion software and each time a new version is released!

INTER-FORMAT AND SOFTWARE DEVIATIONS

As DataAnalysis 5.3 did not ensure Galaxy compatibility neither with mzML nor with mzXML (see Figure 5 right tree), we reformatted the mzXML files with MSConvert as the outputs are readable by Galaxy. However, for both mzML and mzXML outputs, important detection divergences as well as mass and RT deviations can be observed in comparison to the original netCDF file. In fact, the number of detected ions differs (20024 vs 15969) and no mutually detected ions (15621) show identical mass and RT (Figure 6). Moreover, 22.88% of them are deviated of at least $10^{-2} Da$ and 1 minute, which are our maximal database matching tolerance. Worse, 11.6% show detection divergence, being detected in one workflow and not in the other.



Figure 6: Heatmap of m/z and RT deviations for ions detected by both Galaxy workflows (2019 common ions, left) and comparison of detection of common ions (right). Transition from zero to non-zero and vice versa shows detection divergence.

None	RT deviation (minutes)										None
	1E-08	1E-07	1E-06	1E-05	1E-04	1E-03	1E-02	1E-01	1		
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0.02	0.08	0.09	0.09	0.09	0.09	1E-08
0	0	0	0.01	0.01	0.12	0.64	0.77	0.79	0.8	0.8	1E-07
0	0	0	0.02	0.12	1.14	5.71	7.1	7.23	7.27	7.27	1E-06
0	0	0	0.05	0.85	9.25	42.62	54.15	55.36	55.80	55.80	1E-05
0	0.01	0.01	0.08	1.04	10.71	50.36	64.57	67.03	70.12	70.12	1E-04
0	0.01	0.01	0.08	1.05	10.79	50.97	66.39	69.63	76.33	76.33	1E-03
0	0.01	0.01	0.08	1.05	10.81	51.02	66.55	69.84	77.12	77.12	1E-02
0	0.01	0.01	0.08	1.05	10.83	51.27	67.26	72.27	84.12	84.12	1E-01
0	0.01	0.01	0.08	1.05	10.92	51.75	69.03	77.33	100	100	1

Same results for Raw file (.d) → DataAnalysis 5.3 → mzXML → proteowizard → mzML vs Raw file (.d) → DataAnalysis 4.3 → .cdf

Figure 6: Heatmap of m/z and RT deviations for ions detected by both Galaxy workflows (2019 common ions, left) and comparison of detection of common ions (right). Transition from zero to non-zero and vice versa shows detection divergence.

Changing your conversion pipeline to ensure software compatibility is risky: beware of mass and RT deviations!

In this poster, we focused on mzXML and mzML, as they are the most widely accepted by recent software solutions.

USED DATA AND SOFTWARE SOLUTIONS

Diverse data sources are essential to address format, manufacturer, instrument, and acquisition time issues. To evaluate temporal reproducibility, software-dependent variations within the same format, and the compatibility of converted files with Galaxy^[1] and recent software solutions, we used data from a Bruker^[2] Impact HDII UHR-QTOF. Analysis workflows in which the aforementioned datasets and software solutions are used, as well as their objectives, are outlined in the figure below.

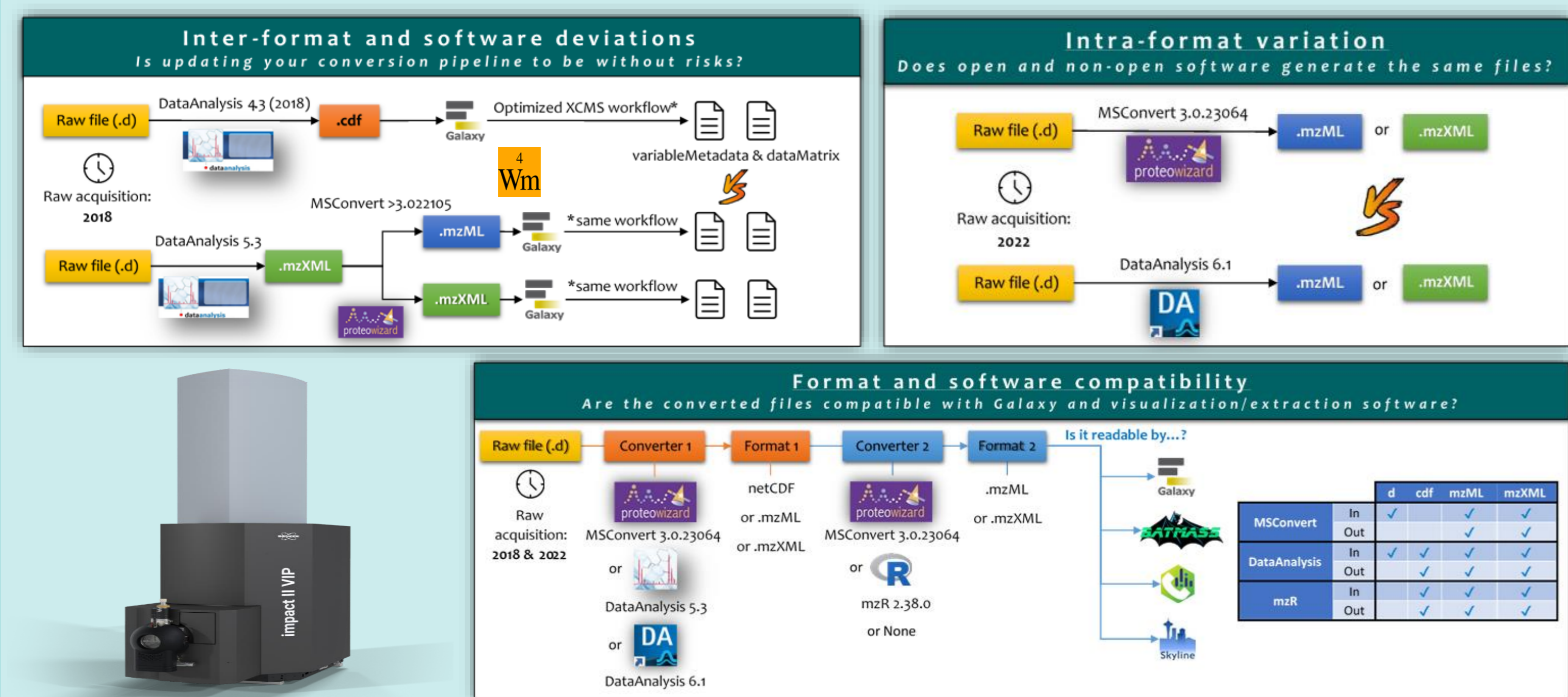


Figure 2: Schematization of the workflow used to perform the tests

DEDICATED TOOLS

To streamline and automate the necessary studies, we developed two specialized Python tools: **mz(x)ml_compare** along with **XCMS_compare** (Figure 3).

The **mz(x)ml_compare** tool is designed to extract metadata from the headers of mzML and mzXML files, compiling this information into a .tsv file without the need to open these large files in text editors. The **XCMS_compare** tool analyzes the variableMetadata and dataMatrix outputs from two XCMS^[3] Galaxy workflows^[4], matching ions by closest mass and retention time (RT) values (within a given window) to identify those detected in both workflows and providing quality indicators that highlight potential deviations in mass, RT, or intensity values.

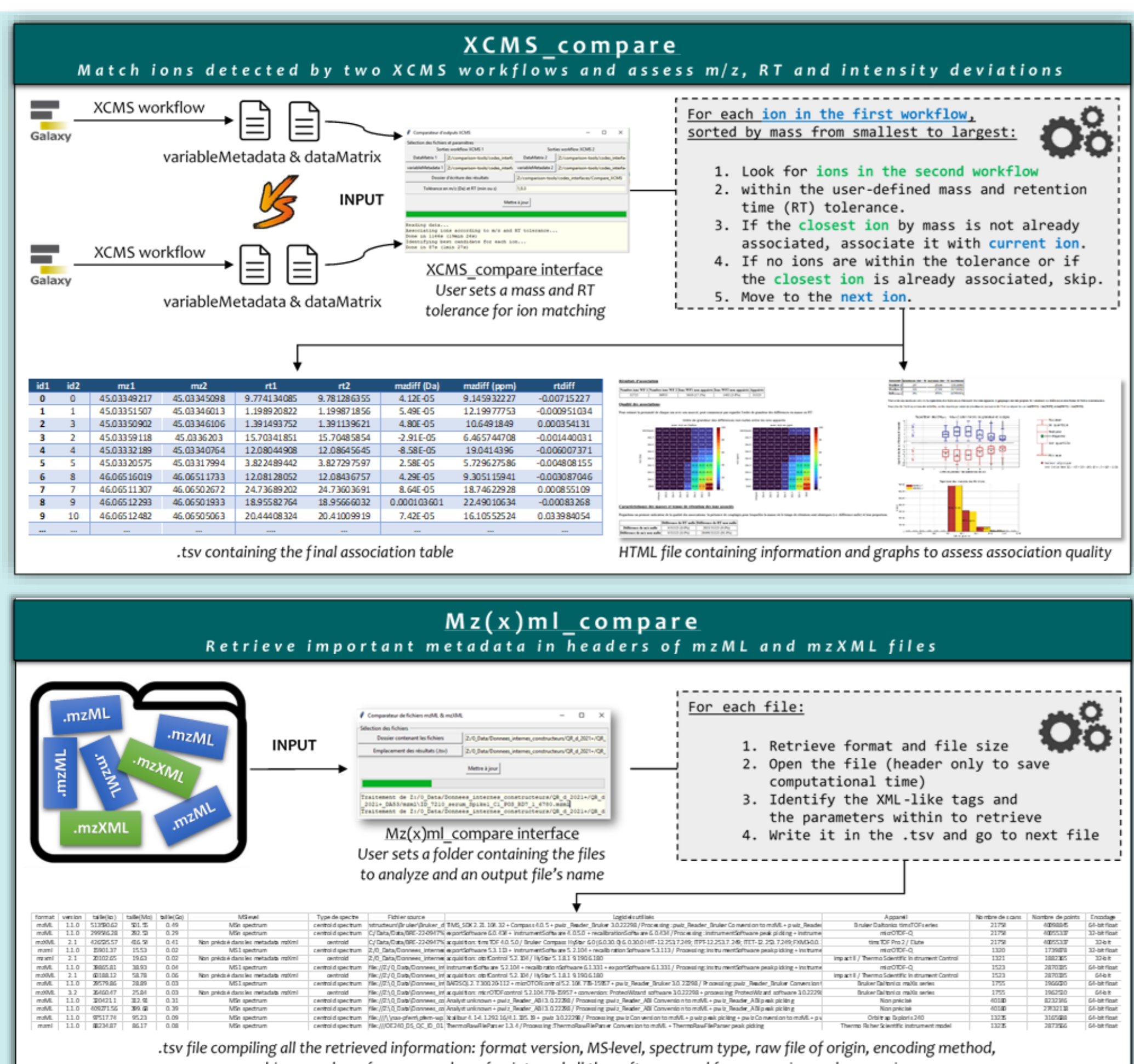


Figure 3: Schematization of the workflow used to perform the tests

CONCLUSION AND PERSPECTIVES

Two popular open formats have become the norm to convert raw spectrometry data: mzML and mzXML. However, there are several software solutions or software pipelines to obtain them but metadata and, even more seriously, masses, retention times and intensities can be subjected to non negligible deviations. Moreover, there is no certainty that converted files could be read by Galaxy and other software until tests have been conducted. This is mainly due to the fact that all software solutions do not write or read the same data encoding pattern. This study revealed a valuable imperative to ensure reproducibility: formats, dates, software and versions used must be monitored and reported!

Now that we know how to obtain qualitative open format data, the perspective of this study will focus on testing and selecting pipelines able to properly extract information from MS/MS high throughput data.

Acknowledgments: This work is supported by the French Ministry of Research and National Research Agency as part of the French metabolomics and fluxomics infrastructure (MetaboHUB: ANR-11-INBS-0010).

quentin.ruin@inrae.fr