

This is an Open Access document downloaded from ORCA, Cardiff University's institutional repository: <https://orca.cardiff.ac.uk/id/eprint/157134/>

This is the author's version of a work that was submitted to / accepted for publication.

Citation for final published version:

Ni, Zhixu, Wölk, Michele, Jukes, Geoff, Mendivelso Espinosa, Karla, Ahrends, Robert, Aimo, Lucila, Alvarez-Jarreta, Jorge, Andrews, Simon, Andrews, Robert, Bridge, Alan, Clair, Jeremy C., Conroy, Matthew J., Fahy, Eoin, Gaud, Caroline, Goracci, Laura, Hartler, Jürgen, Hoffmann, Nils, Kopczyński, Dominik, Korf, Ansgar, Lopez-Clavijo, Andrea F., Malik, Adnan, Ackerman, Jacobo Miranda, Molenaar, Martijn R., O'Donovan, Claire, Pluskal, Tomáš, Shevchenko, Andrej, Slenter, Denise, Siuzdak, Gary, Kutmon, Martina, Tsugawa, Hiroshi, Willighagen, Egon L., Xia, Jianguo, O'Donnell, Valerie B. and Fedorova, Maria 2022. Guiding the choice of informatics software and tools for lipidomics research applications. *Nature Methods* 20 (2) , pp. 193-204. 10.1038/s41592-022-01710-0

Publishers page: <http://dx.doi.org/10.1038/s41592-022-01710-0>

Please note:

Changes made as a result of publishing processes such as copy-editing, formatting and page numbers may not be reflected in this version. For the definitive version of this publication, please refer to the published source. You are advised to consult the publisher's version if you wish to cite this paper.

This version is being made available in accordance with publisher policies. See <http://orca.cf.ac.uk/policies.html> for usage policies. Copyright and moral rights for publications made available in ORCA are retained by the copyright holders.



Guiding the choice of informatics software and tools for lipidomics biomedical research applications.

Zhixu Ni¹, Michele Wölk¹, Geoff Jukes², Karla Mendivelso Espinosa², Robert Ahrends³, Lucila Aimó⁴, Jorge Alvarez-Jarreta^{2,5}, Simon Andrews⁸, Robert Andrews², Alan Bridge⁴, Jeremy C Clair⁶, Matthew J Conroy², Eoin Fahy⁷, Caroline Gaud⁸, Laura Goracci⁹, Jürgen Hartler^{10,11}, Nils Hoffmann¹², Dominik Kopczyński³, Ansgar Korf¹³, Andrea F. Lopez-Clavijo⁸, Adnan Malik⁵, Jacobo Miranda Ackerman¹⁴, Martijn R Molenaar¹⁵, Claire O'Donovan⁵, Tomáš Pluskal¹⁶, Andrej Shevchenko¹⁴, Denise Slenter¹⁷, Gary Siuzdak¹⁸, Martina Kutmon^{17,19}, Hiroshi Tsugawa^{21,22,23,24}, Egon L Willighagen¹⁷, Jianguo Xia²⁴, Valerie B O'Donnell^{2,*} and Maria Fedorova^{1,*}

¹Center of Membrane Biochemistry and Lipid Research, Faculty of Medicine Carl Gustav Carus of TU Dresden, Germany; ²Systems Immunity Research Institute, School of Medicine, Cardiff University, UK; ³Department of Analytical Chemistry, University of Vienna, Vienna, Austria; ⁴Swiss-Prot group, SIB Swiss Institute of Bioinformatics, Centre Medical Universitaire, Geneva, Switzerland; ⁵European Molecular Biology Laboratory, European Bioinformatics Institute, Wellcome Genome Campus, Hinxton, Cambridge, UK; ⁶Biological Science Division, Pacific Northwest National Laboratory, Richland, Washington, USA; ⁷Department of Bioengineering, University of California, San Diego, La Jolla, USA; ⁸Babraham Institute, Babraham Research Campus, Cambridge, UK; ⁹Department of Chemistry, Biology and Biotechnology, University of Perugia, Italy; ¹⁰Institute of Pharmaceutical Sciences, University of Graz, Austria; ¹¹Field of Excellence BioHealth – University of Graz, Austria; ¹²Center for Biotechnology (CeBiTec), University of Bielefeld, Germany; ¹³Bruker Daltonics GmbH & Co. KG, Bremen, Germany; ¹⁴Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany; ¹⁵Structural and Computational Biology Unit, European Molecular Biology Laboratory, Heidelberg, Germany; ¹⁶Institute of Organic Chemistry and Biochemistry of the Czech Academy of Sciences, Prague, Czech Republic; ¹⁷Department of Bioinformatics – BiGCaT, NUTRIM, Maastricht University, The Netherlands; ¹⁸Scripps Center for Metabolomics and Mass Spectrometry, The Scripps Research Institute, La Jolla, USA; ¹⁹Maastricht Centre for Systems Biology (MaCSBio), Maastricht University, The Netherlands; ²⁰Department of Biotechnology and Life Science, Tokyo University of Agriculture and Technology, Japan; ²¹RIKEN Center for Sustainable Resource Science, Yokohama, Japan; ²²RIKEN Center for Integrative Medical Sciences, Yokohama, Japan; ²³Graduate School of Medical Life Science, Yokohama City University, Japan; ²⁴Institute of Parasitology, McGill University, Montreal, Canada.

Corresponding authors:

* Maria Fedorova, Lipid Metabolism: Analysis and Integration, Center of Membrane Biochemistry and Lipid Research, Faculty of Medicine Carl Gustav Carus of TU Dresden, Germany; E-mail: maria.fedorova@tu-dresden.de

* Valerie B O'Donnell, Systems Immunity Research Institute, School of Medicine, Cardiff University, CF14 4XN, UK; O-DonnellVB@cardiff.ac.uk

Abstract

Recent progress in mass spectrometry (MS) lipidomics has led to a rapid proliferation of studies across biology and biomedicine facilitating important discoveries. These generate extremely large raw datasets requiring sophisticated tailored solutions to support automated data processing. To address this, numerous software tools have been developed, tailored for specific tasks in the data analysis pipeline. However, for researchers, deciding which approach best suits their application relies on *ad hoc* testing, which is inefficient and time-consuming. Here, we first review the data processing pipeline, summarizing the number and scope of available tools. Next, to support researchers, LIPID MAPS provides an interactive online portal listing open-access tools with a graphical user interface. This guides users towards appropriate solutions within major areas in data processing, including (1) lipid-oriented databases, (2) MS data repositories, (3) analysis of targeted lipidomics datasets, (4) lipid identification, and (5) quantification from untargeted lipidomics datasets, (6) statistical analysis and visualization, and (7) data integration solutions. Detailed descriptions of functions and requirements are provided to guide customized data analysis workflows.

Main text

Lipidomics is a rapidly growing sub-area of metabolomics, reporting on the generation and metabolism of small molecule hydrophobic species during health and disease¹⁻⁵. There is increasing interest in the use of lipidomics to identify biomarkers and new targets for intervention in disease progression, as well as to delineate underpinning mechanisms⁶⁻⁸. Over the last 10 years, there has been an explosion in the establishment and application of lipidomics mass spectrometry (MS) approaches for biomedical research. Newer generation MS instruments, particularly high-resolution time-of-flight and orbitrap configurations, enable the generation of large “omics” type datasets that can report on literally thousands of lipids in a single analytical run. With the current drive in the field being to analyse large numbers of samples (e.g., blood plasmas, tissue extracts), the amount of data generated experimentally is increasing exponentially. This is leading to significant challenges in both data processing and downstream storage for later (open access) re-use that requires computational solutions.

Researchers have responded strongly to the emerging challenges of data analytics in lipidomics through developing new algorithms and tools that enable effective computational processing of data. These tools have already begun to enable the application of new lipidomics methods to the characterisation of diverse biological processes, in many cases leading to significant discoveries, and some examples are listed here. Several tools have been applied to the profiling of plasma lipidomes, for example LipidXplorer, LipidFinder, and Lipid Data Analyser (LDA).^{9,10} LDA has also contributed to a diverse range of biochemical studies, including adipocyte-derived extracellular vesicle characterisation¹¹, determining the role of phosphatidylserine in autophagy¹² analysis of the role of lipids in flavivirus replication¹³ and how the lipid bilayer stabilises the 5HT receptor¹⁴. Meanwhile, LipidFinder performed an extended clean-up of

high-resolution MS data for the first report of the SARS-CoV2 envelope composition¹⁵. As further examples, the Lipid Ontology enrichment web tool, LION/web¹⁶ enabled the investigation of the role of lipids in bone-marrow neutrophils during aging¹⁷ and the effect of sex and genetics on the metabolic response to calorie restriction¹⁸. Several of the tools described in this review, including LionWeb and XCMS have enabled the investigation of metabolic states in non-alcoholic fatty liver disease (NAFLD)^{19,20}. Furthermore, XCMS enabled a role for sphingolipids in neuropathic pain to be identified²¹. Although this is only a small illustrative list of studies using existing tools, the number and diversity of biological applications for lipidomics tools is increasing significantly as more and more researchers enter the field. Evidencing the significant user base for lipidomics, LIPID MAPS has around 72K users globally, with the LIPID MAPS Structure Database downloaded >4.6K times and viewed ~380K times in 2021, along with ~2.5K citations in publications during 2020/2021 (Google Scholar, Google Analytics data).

When it comes to the choice of which approach to use, researchers need to consider the underlying data structure and also the research questions being asked. They also need to understand the underlying approaches used by algorithms in order to determine whether they will perform as expected for their particular data. However, making decisions on the most appropriate software is currently based on *ad hoc* processes, such as manual searching of the literature and testing packages individually. This is time-consuming and inefficient since implementing tools requires extensive training and familiarisation. Furthermore, the inappropriate use of software can lead to significant errors, for example, incorrect annotation of lipid identifications or erroneous interpretation of noise as peaks to suggest the presence of lipids in samples.

To address these issues, and to support researchers with identification and testing of appropriate computational solutions for lipidomics, LIPID MAPS has generated a Lipidomics Tools Guide, accessible through our home page. This comprises an interactive display that guides researchers towards appropriate solutions and provides detailed descriptions of key features and performance of individual tools, enabling informed decision-making on processing pipelines (Figure 1). To accompany the tool, in this review, we provide full details on the Lipidomics Tools Guide and listed software, together with practical advice from the individual developers relating to the primary and secondary applications of each tool. Additionally, two tutorials provided in the Supplementary Note illustrate the interoperability of different tools, exemplified for targeted and untargeted lipidomics experiments.

On the LIPID MAPS website, the tools are represented in the form of an interactive flow chart ([https://www.lipidmaps.org/resources/tools?page=flow chart](https://www.lipidmaps.org/resources/tools?page=flow_chart)) which covers available, open access solutions supported by a graphical user interface (GUI) for different types of lipidomics derived datasets. This is integrated into LIPID MAPS with links, descriptions, video tutorials, and contact details for software developers. The new tool comprehensively covers the seven major areas in lipidomics data processing, as follows: (1) lipid-oriented databases, (2) MS data repositories, (3) analysis of targeted

lipidomics datasets, (4) lipid identification, and (5) quantification from untargeted lipidomics datasets, (6) statistical analysis and visualization, and (7) data integration solutions (Figure 2). To support informed decision making by lipidomics analysts, for each software, a short description is provided, highlighting the main functionalities and the areas of applications, followed by the specific features listed under “**Technical information**” and “**Task specific information**” tabs (Figures 3 and 4). Additionally, users can review simplified, tabular representation of the available functions for each tool in a given section by using the “Tools Overview” tab.

In the “**Technical information**” section, users can view the type of the license under which the tool is distributed, the availability of desktop and/or web platform-based interfaces, data input/output formats, and compatibility with different operating systems (e.g., Windows, Linux, macOS). There is also information accessible via clickable links, which allow the downloading of the tool together with related documentation, user guides, and training datasets. Additional fields list how to use the tool through the command line, or via API interfaces for advanced users wishing to construct their own customized pipelines. “**Task specific information**” tabs navigate users to pages describing functionalities of the software for particular tasks covering the seven areas outlined above (Figures 1 and 2). Some comprehensive tools have multiple functions integrated into one combined package and can be configured for a wide range of workflows. These tools are assigned to each task with associated descriptions accordingly, and the list of tools is shown in Table 1. In the next section, we provide more details about each area and its associated software and tools.

The categories of lipidomics tools

1. Lipid oriented databases:

Databases that curate individual lipid structures, both from historical and new publications, into organised repositories are essential for researchers who aim to identify the specific molecules present in their biological samples. Databases also serve as a foundation for many data analysis pipelines as well as key knowledge bases for lipid research. Over the last 5-10 years, the size of lipidomics research datasets generated using MS and MS/MS has increased massively, and their routine analysis requires automated programmatic approaches to enable database searching. To support the selection of the databases suitable for a particular application, the “**Task specific information**” tabs within **Lipid Oriented Databases** section provide an overview of the database functionalities, including the number of included lipid structures, structural ontology, covered lipid (sub)classes, levels of curation and annotation. Automated approaches to support data searchability and utility are described, including used identifiers, structural representation, availability of spectral libraries, and calculated physicochemical properties when available.

The most widely used lipid-specific databases are provided by LIPID MAPS and SwissLipids. **LIPID MAPS** hosts several databases in which lipid structures are

catalogued according to the LIPID MAPS nomenclature and classification^{22,46,47}. Specific databases provide utility for different use-cases as follows. **LIPID MAPS Structure Database (LMSD)**²² contains over 47K lipids (August 2022) obtained from sources that include experimental work performed by the LIPID MAPS consortium, from other lipid databases, from the scientific literature, and also some that are computationally generated based on commonly occurring fatty acid chains in mammalian lipids. LMSD can return either bulk (lipid species) annotations for MS data, based on the shorthand nomenclature described by Liebisch *et al.*⁴⁷, or fully annotated names (structure-defined lipids), where users already have additional structural information, e.g., from tandem mass spectrometry experiments. LMSD has recently implemented a display of reaction data to link together lipid species by biochemical transformations. This was initially obtained from Rhea⁴⁸, WikiPathways⁴⁵, Reactome⁴⁹, and other sources and is now in place for many generic lipids. This is in the process of being cascaded down to individual lipid species. In the case of (high resolution) MS experiments, the user may only have information on the *m/z* value of detected lipid ions. In this case, searching databases will provide information on elemental compositions and, using this, generate putative matches. It is recommended to use the BULK search tool on LIPID MAPS in order to perform this operation since this returns shorthand nomenclature as a first step. Putative matches based on MS indicate the number of carbons in fatty acyl chains, and double bonds/rings present, but not how these are distributed between/within acyl chains in the molecule. For some users, the LIPID MAPS **Computationally-generated Bulk Lipids (COMP_DB)**²² may be a more suitable resource to query. This database contains over 59,000 lipid species in shorthand format (in the major classes such as fatty acyls, glycerol and glycerophospholipids, sterols, and sphingolipids), computationally generated from a list of commonly occurring acyl and alkyl chains. Most entries in this database represent hierarchical structures that could map to many different specific annotations. The LIPID MAPS **In Silico Structure Database (LMISSD)**²² contains over 1.1M entries derived from the computational expansion of headgroups and chains for common lipid classes. These are provided as specific structural annotations but can also be provided as a hierarchy of sum composition and chain composition. Last, **The Lipidomic Ion Mobility Database**²² was developed using data from the McLean and Griffin labs^{50–52} to provide collisional cross section measurements for drift tube MS experiments.

The **SwissLipids knowledgebase**²³ was developed to aid lipidomics researchers in interpreting experimental datasets and integrating them with prior biological knowledge, allowing also for data exploration and hypothesis generation. In SwissLipids, experimentally characterized lipids are curated from peer-reviewed literature using the ChEBI⁵³ ontology (www.ebi.ac.uk/chebi/). Lipid metabolism is described using the Rhea knowledgebase⁴⁸ for biochemical and transport reactions (www.rhea-db.org), itself based on ChEBI, while enzymes, transporters, and interacting proteins are described using the UniProt Knowledgebase UniProtKB⁵⁴ (www.uniprot.org), for which Rhea is the reference vocabulary for such annotation.⁵⁵ As the number of experimentally characterized lipid structures represents only a small fraction of the possible structures that may exist in nature, expert-curated knowledge of lipid structures and metabolism in ChEBI, Rhea, and

UniProt is used to design and create a library of all theoretically feasible lipid structures *in silico*, which is fully mapped to these three resources. The current version of the SwissLipids library contains almost 600,000 lipid structures from over 550 lipid classes, organized into two distinct hierarchical lipid classifications – one that parallels the structural classification of LIPID MAPS⁵⁶, and one based on the shorthand notation for MS-data⁵⁷ that links lipid identifications from MS-based experiments to structures and biological knowledge.

2. MS data repositories:

Raw and/or processed data deposition using free repositories services, although a standard task prior to publication of the results in the field of proteomics for many years, is only now finding its way into the lipidomics community⁵⁸. MS data repositories increase data transparency and reproducibility, allow reanalysis for new discoveries and data-driven hypothesis generation, as well as benchmarking of new software tools⁵⁹. Although numerous platforms for upload of raw MS datasets exist (e.g., MassIVE: <https://massive.ucsd.edu/>, ProteomeXchange: <http://www.proteomexchange.org/>), specific functionalities to support metadata, sample preparation protocols, and data matrices are necessary to improve the reusability of the deposited datasets following FAIR principles⁶⁰. To select the optimal solution for data upload/download, users would need to be informed about the types of stored raw, processed, and metadata, curation strategy, total number of available datasets, and species coverage.

Repositories tuned for metabolomics and lipidomics data, such as **Metabolomics Workbench**²⁴ and **MetaboLights**²⁵ have the functionality to associate deposited data with compound query results to enhance the reusability of the datasets, allowing further interrogation. Each dataset is assigned a unique project accession ID, sufficient space to host the raw and/or processed data, supported by detailed information, including study design, associated metadata, details on sample preparation, and analysis protocols. Datasets can be browsed and searched by specific keywords, organisms of origin, and reported compounds and are usually associated with a source publication. **MetaboLights** has unique fields for data transformation and metabolite identification and provides an online viewer to review lipid identifiers, quantities, and corresponding structures, while **Metabolomics Workbench** is bundled with the **RefMet**⁴² data resource (containing over 160,000 annotated metabolite species, including a large collection of lipids) and a suite of online data analysis tools. Metabolights and Metabolomics Workbench are accepted by mainstream journals as data repositories for publications of lipidomics datasets.

3. Analysis of targeted lipidomics datasets:

Lipidomics data acquisition strategies can be generally subdivided into targeted and untargeted workflows. In targeted lipidomics, a predefined set of lipids with a known mass-to-charge ratio (m/z) of the precursor and fragment/product ion(s) need to be provided by the user before data acquisition. Moreover, optimisation of ionization and MS parameters for each pair of precursor–product ions (so-called “transition”) must be

performed to optimise the sensitivity of the method. Targeted analysis using single or multiple reaction monitoring (SRM, MRM) on triple quadrupole instruments and, more recently, parallel reaction monitoring (PRM) on orbitrap and QTOF based instruments are successfully applied to the quantification of selected sets of lipids as well as hundreds of lipids in large sample cohorts (e.g., over 600 lipid species in one LC-MS/MS analysis⁶¹). However, to quantify a large number of lipids in a correspondingly large sample cohort targeted lipidomics workflows should be quick to establish, and obtained results should be easy to inspect and validate. This process can be extremely time-consuming and most often is not accessible to non-experts. Thus, specialized tools can be used to facilitate both method design and data processing steps. For software-assisted method design, the user should define the type of the targeted acquisition method planned (SRM/MRM, or PRM) and lipid (sub)classes/species aimed to be covered. The selection of transitions can be done among experimentally validated or computationally optimized or can be even predicted on-fly based on common knowledge of lipid subclass-specific gas phase fragmentation chemistry. The set of fragment ions and their yield will strongly depend on class, the number of double bonds and fatty acyl length and even the type of instrument on which data were acquired. For instance, with **LipidCreator**²⁶ the targeted assay can be generated in three steps. In brief, during step 1 the user would select the lipid category and class to work with and define fatty acyl, double bonds, hydroxyl group, and adduct constrains (precursor selection) as well as the polarity mode to analyse lipids of interest. In step 2 the monitored fragments at MS/MS level can be defined. In step 3 the designed molecules can be added to the target list, reviewed, and transferred to the MS instrument for data acquisition. **METLIN-MRM**²⁷ is another data rich resource where users can choose from experimentally and/or computationally optimized transitions or even public repository transitions with links to corresponding DOIs.

Although method design requires careful optimization and is time-consuming, post-acquisition data processing of targeted lipidomics datasets is relatively straightforward and follows general rules of LC-MS/MS-based targeted quantification accepted in both the proteomics and metabolomics communities. Indeed, several open access tools originally developed for targeted analysis of peptides (Skyline) or metabolites (XCMS-MRM) have been adapted for lipidomics applications. Thus, **LipidCreator** is fully integrated with **Skyline**⁶² for small molecules, making it a vendor-independent software. METLIN-MRM-assisted method development can be directly extended to post-acquisition data processing using the **XCMS-MRM**²⁷ platform. Both Skyline and XCMS-MRM tools provide automated solutions for peak integration, relative and absolute quantification, and data quality control.

4. Lipid identification from untargeted lipidomics datasets:

A second analytical strategy commonly used in lipidomics relates to untargeted workflows based on data dependent (DDA) or data independent acquisition (DIA). Here users perform MS analysis of a lipidome in so-called “discovery” mode without prior knowledge of the exact set of lipids to be analysed in the sample. Generally, the main aim of

untargeted lipidomics is to analyse and ideally identify as many lipid species as possible (ultimately all ionizable constituents extracted from the sample). Both DDA and DIA experiments rely on the iteration of instrument cycles which include MS1 survey scans (usually acquired at high resolution to define the elemental composition of the lipid ions) and a number of MS/MS spectra in which lipid ions, selected based on their abundance (DDA) or within a given m/z range (DIA), undergo collision-induced-dissociation (CID). MS/MS information is then used to assign lipids to particular molecular species based on their known gas phase fragmentation patterns. Thus, untargeted lipidomics experiments can support lipid identification at different levels of structural assignment with high-resolution MS spectra providing elemental composition and thus the putative bulk composition of the lipid (e.g., PC 36:4) only, but with additional MS/MS information supporting the identification of lipids at molecular species levels (e.g., PC 16:0_20:4). Although this is possible by manually checking MS and corresponding MS/MS spectra, lipid identification requires automated solutions to support analysis throughput, as within commonly used LC-MS/MS DDA setups, thousands of individual MS/MS spectra are generated within a single analysis.

Due to the high demand and popularity of untargeted lipidomics workflows, numerous tools have been developed to support this area. Thus, the section of the interactive chart for untargeted lipidomics is represented by 9 software tools with open access for academic users. By clicking on the corresponding “Task specific information” tabs, users can get familiar with the tools which support specific acquisition strategies only versus other tools which cover larger application areas. To support the selection of the optimal identification tool, the user can select between high-resolution MS applications (**Lipid Data Analyzer (LDA)**⁶³, **LipidFinder**²⁹, **MS-DIAL**³⁰, **XCMS on-line**³¹, DDA (**LDA**^{28,64}, **MS-DIAL**, **LipidHunter2**³², **LipidXplorer**³³, **Lipostar2**³⁴, and **MZmine**^{35,65,66}), DIA (**MS-DIAL** and **Lipostar2**), and even datasets acquired using ion mobility methods which provide orthogonal to LC-MS/MS separation (**MS-DIAL**, **MZmine**, **Lipostar2**). Furthermore, analysis of epilipidomics datasets focusing on the identification of oxidized lipids can be supported by **LDA**⁶⁷, **Lipostar2**, **LPptiger**³⁶, and **MS-DIAL** tools. For each particular application listed above, the “Task specific information” tab provides information about the main principles of operation and scoring, and accuracy measures.

5. Lipid quantification from untargeted lipidomics datasets

The quantification of lipids provides their abundance (relative or absolute) in a biological sample, enabling comparison with other samples. Quantified values aid harmonization across lipidomics datasets. Quantitative analysis can be performed using data acquired from targeted and untargeted approaches regardless of whether they were acquired using Full-MS, DDA, or DIA modes. Untargeted lipidomics quantification can be subdivided into relative (e.g. fold change between condition 1 vs. condition 2) and semi-absolute (e.g., expressed in pmol/ μ g of proteins). Due to the extremely large diversity of lipid structures in natural lipidomes and relatively limited numbers of commercially available lipid standards, it is not feasible to perform absolute quantification at true lipidome level^{68,69}.

On the other hand, due to the close similarity in ionization and MS behavior of lipids from the same subclass, the use of one or a small number of internal standards (ISTD) per subclass is currently considered as a compromise. Isotopic correction algorithms can be used during data processing to minimize the effect of structural differences between internal standards and individual lipid molecular species⁷⁰. Lipids present a particular challenge for accurate identification since there will be several hundreds of lipids distributed over a relatively narrow m/z range (e.g., from 400 to 900 m/z), as well as a high number of isobaric and even isomeric species. Additionally, lipids are detected over a large dynamic range of concentrations in natural lipidomes. These issues result in significant challenges for accurate peak assignment and integration and downstream accurate quantification⁶⁹. Tools for processing quantitative lipidomics datasets have benefited from previously developed software solutions designed for quantitative proteomics and metabolomics. However, due to the special properties of lipids as outlined above, additional optimizations are necessary to ensure the accuracy of lipidomics data processing. For instance, data normalization using a preconfigured set of ISTD (e.g., **Lipostar 2** and **MS-DIAL**) is introduced to simplify the normalization process and reduce the post-processing of the data matrix. Additionally, robust peak picking and peak boundary selection algorithms are critical for obtaining accurate peak areas for quantitative analysis. Though several robust peak picking algorithms are available, manual adjustment and re-integration is often required due to the high number of isobaric and isomeric species. Additional features integrated within data processing tools such as peak alignment and deconvolution are important to handle lipid species with multiple adducts types and to process DIA datasets. Current available quantification tools such as **LDA**, **Lipostar 2**, **MS-DIAL**, **MZmine**, and **XCMS on-line** generally provide integrated pipelines from lipid identification up to quantification including essential normalization functions. For each tool, the “**Task specific information**” section within the LIPID MAPS Lipidomics Tools Guide displays multiple features to guide the choice of the tool based on user requirements, including details on quantification methods and accuracy measures.

6. Statistical analysis and visualization of lipidomics datasets:

Lipidomics research generates large datasets, and the complexity of experimental design is also increasing. Therefore, a critical bottleneck in lipidomics data processing is often the statistical analysis, which requires extensive use of tailored approaches that take into account the specific characteristics of lipid data. Different methods are available for the analysis of lipidomics data, each one with its own advantages and pitfalls. The choice of statistical methods to be applied should be first guided by the aim of the lipidomic study. When testing for statistical significance between pre-defined groups is desired (e.g., health vs. disease), differences between groups of samples are usually evaluated by applying parametric (e.g., t-test, ANOVA) or non-parametric (e.g. Wilcoxon signed-rank test, Kruskal-Wallis) statistical hypothesis tests⁷¹. With thousands of lipids being considered in some lipidomics experiments, the high number of variables increases the chance to find spurious correlated variables (false positives). Therefore, correction for

multiple comparison testing is required. In addition, in lipidomics, variables (lipids) are usually not all truly independent (for example, one lipid can be represented by several ions/adducts), meaning that corrections commonly applied for genomics/transcriptomics, such as Bonferroni or Benjamini Hochberg can significantly overcorrect. Here, softer corrections, such as Sequential Goodness of Fit, represent an alternative that may be more appropriate⁷².

Another consideration is that detected features might not always follow a normal distribution⁷³. Thus, multivariate statistical approaches, in which all the variables are considered simultaneously, often by assuming they are correlated and not fully independent, are extensively applied in lipidomics. For explorative purposes, principal component analysis (PCA)⁷⁴ represents the most widely used approach in omics, including lipidomics⁷⁵. Using PCA, the original dataset is represented in a lower-dimensional subspace that maintains most of the relevant information (variance). Being an unsupervised method, PCA does not require a priori knowledge of the dataset and can be used not only to explore clusters of samples eventually formed but also for interpretation without imposing any information on classification or cluster association. Hierarchical or non-hierarchical clustering methods aim at grouping samples by similarity, which is measured utilizing statistical distances or similarities between samples⁷⁶. Supervised regression algorithms for dimensionality reduction, such as linear discriminant analysis^{77,78} or partial least squares discriminant analysis (PLS-DA)^{79,80}, are also available to evaluate and classify sample identity. In addition to PLS-based methods, other machine learning approaches have been also used in lipidomics applications. Among them, supervised methods like support vector machine⁸¹ and random forest⁸² were used for classification purposes and can also be used for feature selection. Despite the wide availability of statistical tools applied to lipidomics, several potential issues need to be considered. For example, in large studies, the so-called “batch-effect” can hamper statistical analysis, and correction with internal standards and/or quality controls has to be made before the application of statistical tools. Also, missing data, which are the result of molecule concentrations below detection limits and very common in lipidomics, can be detrimental in model generation and interpretation, with some tools more sensitive than others⁷⁵. Nevertheless, several strategies for missing data imputation have been proposed⁸³.

Generally, the multi-functional tools described above for quantitative lipidomics all provide integrated platforms for statistical analysis and data visualization (**LDA**, **Lipostar 2**, **MS-DIAL**, **MZmine**, and **XCMS on-line**). Additionally, several tools were specifically developed to support chemometrics analysis and result visualization of metabolomics and lipidomics data (**LIPID MAPS Statistical Analysis Tools**³⁷ and **MetaboAnalyst 5.0**³⁸). Integrated statistical analysis and visualization functions provide easy access to most common functions, including univariate (parametric and non-parametric testing) as well as multivariate (non-supervised and supervised) solutions with a close interactive connection to the corresponding lipid quantification data matrix and often bundled with data pre-treatments including normalization, scaling, and visualization of filtered data

subset. Dedicated tools (**LIPID MAPS Statistical Analysis Tools** and **MetaboAnalyst 5.0**) might require researchers to transform the quantification data according to specific templates for dataset import but can provide a more extensive set of statistical and visualization functions with detailed customizable configurations. MetaboAnalyst 5.0, for instance, has a dedicated utility for batch-effect correction, which contains nine methods well established in the field of metabolomics as well as eight methods for missing value imputation⁸⁴.

7. Data integration solutions:

The ultimate aim of many lipidomics studies is to investigate biological relevance and mechanisms behind lipidome remodelling driven by the specific biological conditions. Considering the nature of “big data” produced by lipidomics experiments, manual evaluation of the biological significance of obtained results would be extremely time-consuming and require extensive knowledge in diverse areas of biochemistry and cell biology. Such advanced data integration goes well beyond single lipidomics data matrices and extends into related multiomics approaches using curated pathways or network analysis strategies. The combination and utilization of multiomics data from different sources require sophisticated data pre-treatments, including manual curation and advanced bioinformatics solutions. This type of workflow can be generally divided into three steps: conversion of lipid annotations to their corresponding IDs within knowledge and ontology databases, lipid ontology enrichment, and advanced pathway/network analysis.

Tools that are capable of bridging lipid annotations supported by purely lipidomics software with the structural or functional IDs in data integration tools provide the first critical step towards systems biology integration of lipidomics datasets. To reduce the complexity of ID cross-validation and database queries, several tools are available to assist this conversion (**Goslin**⁴⁰, **LipidLynxX**⁴¹, and **RefMet**⁴²) and to link lipid identifiers to various databases (**BridgeDb**³⁹, **Goslin**, **LipidLynxX**, and **RefMet**). For example, BridgeDb has mappings to other databases for almost 19K LIPID MAPS identifiers⁸⁵.

Biological interpretation of lipidomics data is often driven by the focus on individual lipids. Although this approach is useful in biomarker discovery, it obscures the possible effects of shared properties of molecules related to the biological phenomenon. A way to circumvent this is to manually curate lipid groups that share specific properties (e.g., lipid class, level of unsaturation) and report aggregate statistics. However, the manual construction of these groups is often laborious due to the ambiguity in lipid nomenclature and introduces a risk of cherry-picking. Ontologies, formalizations of concepts, and their relations have been successful in other omics fields to provide frameworks for constructing groups of molecules with shared biological properties. For lipidomics data, several ontologies, such as **Lipid Ontology (LION/Web)**¹⁶ and **Lipid Mini-On**⁴³, are useful in aiding in the biological interpretation. Currently, LION links over 50,000 lipids to chemical (e.g., LIPID MAPS classification, fatty acid associations), physiochemical (e.g., membrane fluidity, intrinsic curvature), and cell biological (e.g., predominant subcellular

localization) properties and Lipid Mini-On uses a text mining strategy to attribute Lipid Ontology (LO) structural terms to lipids.

Typically, ontology-derived groups of molecules ('terms') are analysed using enrichment analysis approaches. In these analyses, a given term is enriched if the molecules belonging to the term are overrepresented in a target-list or are higher ranked in a list of molecules ordered by a statistic (e.g., fold-change, P-value) than expected by chance. Both **LION/web** and **Lipid Mini-On** are freely available online tools that perform ontology-term enrichment analysis of user-provided lipidomics data. **LION/web** allows specific LION-term categories to be included for analysis. After submission, LION/web reports descriptive matching statistics and enrichment analysis, as well as publication-ready figures. Traditionally, enrichment analyses compare two groups of samples. To analyse datasets with more sample groups, LION/web was recently expanded with the PCA-LION heatmap module. This module generates a heatmap showing the most dynamic LION-terms for all samples based on the enrichment analysis of a given number of principle components. Lipid IDs of significantly enriched terms can be further mapped to available pathways and networks to investigate the changes at the systems level. **Lipid Mini-On** enables to generate a variety of visualization of lipid enrichment by structural characteristics. Lipids and their associated LO terms can be visualized as a network to hierarchize interpretations of the enrichment performed.

Several tools are available to support pathway, and network analysis of lipidomics datasets, including integrated pathway graph analysis modules in **Lipostar 2**, stand-alone web application **BioPAN**⁴⁴, which allows the visualisation of quantitative lipidomics data in the context of known biosynthetic pathways as well as the central hub of community-driven pathways represented by the **Lipid Portal on WikiPathways**⁴⁵, in collaboration with LIPID MAPS. Though more advanced analysis can be performed with highly customized programs and scripts by experienced bioinformaticians, these tools provide simple interfaces for researchers to begin to map lipidomics data to obtain essential lipid centric analysis results from predefined pathways and networks in, e.g., PathVisio⁸⁶ and Cytoscape⁸⁷. Furthermore, the pathways from WikiPathways can be easily converted to a network through the WikiPathways App⁸⁸, after which these networks can be extended with additional knowledge such as miRNAs, transcription factors, or drugs through the CyTargetLinker⁸⁹ app.

Lipidomics is a fast-growing field which increasingly is supporting the analysis of ever larger datasets of high complexity. To assist with high-throughput data processing, many new software tools have been developed by academic researchers and are now openly available on developers' websites. To guide the user and provide a point of contact for finding these tools, in this review, we provide detailed specifications on the most widely used software packages for lipidomics along with a complimentary interactive Lipidomics Tools Guide available on LIPID MAPS. Two tutorials are provided as Supplementary Notes to exemplify the interoperability of the Guide and how to combine different tools for targeted and untargeted lipidomics experiments. This portal can help researchers to

construct a complete lipidomics data analysis workflow starting with lipid identification and quantification till advanced visualization and data integration using open access software solutions with the clickable graphical user interface. The lipidomics Tools Guide will be regularly reviewed and updated to reflect new developments in the field as well as continuous support the listed tools. Moreover, the Guide can be updated upon request by authors of the software within the scope of this resource. The LIPID MAPS interactive Lipidomics Tools Guide (https://www.lipidmaps.org/resources/tools?page=flow_chart) summarizes essential information about each tools to assist beginners in lipidomics as well as advanced data scientists in selecting the most suitable tool for each of the steps in the processing of MS-derived lipidomics data.

Acknowledgements:

This publication is based upon work from COST Action EpiLipidNET, Pan-European Network in Lipidomics and Epilipidomics (CA19105; <https://www.epilipid.net>), supported by COST (European Cooperation in Science and Technology). Funding from the Wellcome Trust is gratefully acknowledged for LIPID MAPS (203014/Z/16/Z). LIPID MAPS receives sponsorship from Cayman Chemical, Merck and Avanti Polar Lipids. T.P. is supported by the Czech Science Foundation Grant 21-11563M. Funding from the FWF P33298-B and Human Frontiers Science Program RGP0002/2022 is gratefully acknowledged. “Sonderzuweisung zur Unterstützung profilbestimmender Struktureinheiten 2021” by the SMWK is gratefully acknowledged. JSPS KAKENHI (21K18216 to Hiroshi T.), the National Cancer Center Research and Development Fund (2020-A-9, H.T.), AMED Japan Program for Infectious Diseases Research and Infrastructure (21wm0325036h0001, H.T. and M.A.), JST National Bioscience Database Center (NBDC, H.T.), JST ERATO “Arita Lipidome Atlas Project” (JPMJER2101 to H.T.).

Author Contributions:

The manuscript was written through contributions of all authors who have given approval to the final version of the manuscript. M.F. and V.B.O. conceived the original idea and supervise the project. Z.N., M.F. and V.B.O. contributed to review of the tools and data collection. M.F., Z.N, and M.W. contributed to figures. M.W. designed and tested the workflows and tutorials. G.J., K.M.E., R. An. developed the website with the help from Z.N. and M.F.. Software developers Z.N., R.Ah., L.A., J.A.J., S.A., A.B., G.C.C., M.J.C., E.F., C.G., L.G., J.H., N.H., D.K., A.K., A.F.L., A.M., J.M.A, M.R.M., C.O., T.P., A.S., D.S, G.S., M.K., H.T., E.L.W., and J.X. contribute to sections of corresponding software tools in both manuscript and website.

Competing Interests:

A.K. is employed at Bruker Daltonics GmbH & Co. KG, Bremen, Germany

References

1. Wenk, M. R. The emerging field of lipidomics. *Nature Reviews Drug Discovery* **4**, 594–610 (2005).
2. Yang, K. & Han, X. Lipidomics: Techniques, Applications, and Outcomes Related to Biomedical Sciences. *Trends in Biochemical Sciences* **41**, 954–969 (2016).
3. Wood, P. L. Lipidomics of Alzheimer's disease: Current status. *Alzheimer's Research and Therapy* **4**, 1–10 (2012).
4. Meikle, P. J., Wong, G., Barlow, C. K. & Kingwell, B. A. Lipidomics: Potential role in risk prediction and therapeutic monitoring for diabetes and cardiovascular disease. *Pharmacology & Therapeutics* **143**, 12–23 (2014).
5. Yang, L. *et al.* Recent advances in lipidomics for disease research. *Journal of Separation Science* **39**, 38–50 (2016).
6. Watson, A. D. Thematic review series: Systems Biology Approaches to Metabolic and Cardiovascular Disorders. Lipidomics: a global approach to lipid analysis in biological systems. *Journal of Lipid Research* **47**, 2101–2111 (2006).
7. Hu, C. *et al.* Analytical strategies in lipidomics and applications in disease biomarker discovery. *Journal of Chromatography B* **877**, 2836–2846 (2009).
8. Shevchenko, A. & Simons, K. Lipidomics: coming to grips with lipid diversity. *Nature Reviews Molecular Cell Biology* **11**, 593–598 (2010).
9. Vvedenskaya, O. *et al.* Nonalcoholic fatty liver disease stratification by liver lipidomics. *Journal of Lipid Research* **62**, 100104–100105 (2021).
10. Vvedenskaya, O., Wang, Y., Ackerman, J. M., Knittelfelder, O. & Shevchenko, A. Analytical challenges in human plasma lipidomics: A winding path towards the truth. *Trends in Analytical Chemistry* **120**, 115277 (2019).
11. Durcin, M. *et al.* Characterisation of adipocyte-derived extracellular vesicle subtypes identifies distinct protein and lipid signatures for large and small extracellular vesicles. *Journal of Extracellular Vesicles* **6**, (2017).
12. Durgan, J. *et al.* Non-canonical autophagy drives alternative ATG8 conjugation to phosphatidylserine. *Molecular Cell* **81**, 2031-2040.e8 (2021).
13. Zhuang, X. *et al.* The circadian clock components BMAL1 and REV-ERB α regulate flavivirus replication. *Nature Communications* **10**, 1–13 (2019).
14. Zhang, Y. *et al.* Asymmetric opening of the homopentameric 5-HT_{3A} serotonin receptor in lipid bilayers. *Nature Communications* **12**, 1–15 (2021).
15. Saud, Z. *et al.* The SARS-CoV2 envelope differs from host cells, exposes procoagulant lipids, and is disrupted in vivo by oral rinses. *Journal of Lipid Research* **63**, 100208 (2022).
16. Molenaar, M. R. *et al.* LION/web: A web-based ontology enrichment tool for lipidomic data analysis. *Gigascience* **8**, 1–10 (2019).
17. Lu, R. J. *et al.* Multi-omic profiling of primary mouse neutrophils predicts a pattern of sex- and age-related functional regulation. *Nature Aging* **1**, 715–733 (2021).
18. Green, C. L. *et al.* Sex and genetic background define the metabolic, physiologic, and molecular response to protein restriction. *Cell Metabolism* **34**, 209-226.e5 (2022).
19. Beyer, B. A. *et al.* Metabolomics-based discovery of a metabolite that enhances oligodendrocyte maturation. *Nature Chemical Biology* **14**, 22–28 (2017).
20. Rappez, L. *et al.* SpaceM reveals metabolic states of single cells. *Nature Methods* **18**, 799–805 (2021).
21. Patti, G. J. *et al.* Metabolomics implicates altered sphingolipids in chronic pain of neuropathic origin. *Nature Chemical Biology* **8**, 232–234 (2012).

22. Sud, M. *et al.* LMSD: LIPID MAPS structure database. *Nucleic Acids Research* **35**, D527–D532 (2007).
23. Aimo, L. *et al.* The SwissLipids knowledgebase for lipid biology. *Bioinformatics* **31**, 2860–2866 (2015).
24. Sud, M. *et al.* Metabolomics Workbench: An international repository for metabolomics data and metadata, metabolite standards, protocols, tutorials and training, and analysis tools. *Nucleic Acids Research* **44**, D463–D470 (2016).
25. Haug, K. *et al.* MetaboLights: a resource evolving in response to the needs of its scientific community. *Nucleic Acids Research* **48**, D440–D444 (2020).
26. Peng, B. *et al.* LipidCreator workbench to probe the lipidomic landscape. *Nature Communications* **11**, 1–14 (2020).
27. Domingo-Almenara, X. *et al.* XCMS-MRM and METLIN-MRM: a cloud library and public resource for targeted analysis of small molecules. *Nature Methods* **15**, 681–684 (2018).
28. Hartler, J. *et al.* Deciphering lipid structures based on platform-independent decision rules. *Nature Methods* **14**, 1171–1174 (2017).
29. Fahy, E. *et al.* LipidFinder on LIPID MAPS: peak filtering, MS searching and statistical analysis for lipidomics. *Bioinformatics* **35**, 685–687 (2018).
30. Tsugawa, H. *et al.* A lipidome atlas in MS-DIAL 4. *Nature Biotechnology* **38**, 1159–1163 (2020).
31. Tautenhahn, R., Patti, G. J., Rinehart, D. & Siuzdak, G. XCMS online: A web-based platform to process untargeted metabolomic data. *Analytical Chemistry* **84**, 5035–5039 (2012).
32. Ni, Z., Angelidou, G., Lange, M., Hoffmann, R. & Fedorova, M. LipidHunter Identifies Phospholipids by High-Throughput Processing of LC-MS and Shotgun Lipidomics Datasets. *Analytical Chemistry* **89**, 8800–8807 (2017).
33. Herzog, R. *et al.* LipidXplorer: A Software for Consensual Cross-Platform Lipidomics. *PLOS ONE* **7**, e29851 (2012).
34. Goracci, L. *et al.* Lipostar, a Comprehensive Platform-Neutral Cheminformatics Tool for Lipidomics. *Analytical Chemistry* **89**, 6257–6264 (2017).
35. Pluskal, T., Castillo, S., Villar-Briones, A. & Orešič, M. MZmine 2: Modular framework for processing, visualizing, and analyzing mass spectrometry-based molecular profile data. *BMC Bioinformatics* **11**, 1–11 (2010).
36. Ni, Z., Angelidou, G., Hoffmann, R. & Fedorova, M. LPPTiger software for lipidome-specific prediction and identification of oxidized phospholipids from LC-MS datasets. *Scientific Reports* **7**, 15138 (2017).
37. Fahy, E., Sud, M., Cotter, D. & Subramaniam, S. LIPID MAPS online tools for lipid research. *Nucleic Acids Research* **35**, W606–W612 (2007).
38. Pang, Z. *et al.* MetaboAnalyst 5.0: narrowing the gap between raw spectra and functional insights. *Nucleic Acids Research* **49**, W388–W396 (2021).
39. Ding, D. *et al.* The BridgeDb framework: standardized access to gene, protein and metabolite identifier mapping services. *BMC Bioinformatics* **11**, (2010).
40. Kopczynski, D., Hoffmann, N., Peng, B. & Ahrends, R. Goslin: A grammar of succinct lipid nomenclature. *Analytical Chemistry* **92**, 10957–10960 (2020).
41. Ni, Z. & Fedorova, M. LipidLynxX: a data transfer hub to support integration of large scale lipidomics datasets. *bioRxiv* (2020) doi:10.1101/2020.04.09.033894.
42. Fahy, E. & Subramaniam, S. RefMet: a reference nomenclature for metabolomics. *Nat Methods* **17**, 1173–1174 (2020).
43. Clair, G. *et al.* Lipid Mini-On: Mining and ontology tool for enrichment analysis of lipidomic data. *Bioinformatics* **35**, 4507–4508 (2019).

44. Gaud, C. *et al.* BioPAN: a web-based tool to explore mammalian lipidome metabolic pathways on LIPID MAPS. *F1000Res* **10**, 4 (2021).
45. Martens, M. *et al.* WikiPathways: connecting communities. *Nucleic Acids Research* **49**, D613–D621 (2021).
46. Fahy, E. *et al.* Update of the LIPID MAPS comprehensive classification system for lipids. *Journal of Lipid Research* vol. 50 S9–S14 (2009).
47. Liebisch, G. *et al.* Update on LIPID MAPS Classification, Nomenclature and Shorthand Notation for MS-derived Lipid Structures. *Journal of lipid research* **61**, 1539–1555 (2020).
48. Bansal, P. *et al.* Rhea, the reaction knowledgebase in 2022. *Nucleic Acids Res* **50**, D693–D700 (2022).
49. Gillespie, M. *et al.* The reactome pathway knowledgebase 2022. *Nucleic Acids Research* **50**, D687–D692 (2022).
50. Stow, S. M. *et al.* An Interlaboratory Evaluation of Drift Tube Ion Mobility-Mass Spectrometry Collision Cross Section Measurements. *Analytical Chemistry* **89**, 9048–9055 (2017).
51. Hinz, C. *et al.* A Comprehensive UHPLC Ion Mobility Quadrupole Time-of-Flight Method for Profiling and Quantification of Eicosanoids, Other Oxylipins, and Fatty Acids. *Analytical Chemistry* **91**, 8025–8035 (2019).
52. Leaptrot, K. L., May, J. C., Dodds, J. N. & McLean, J. A. Ion mobility conformational lipid atlas for high confidence lipidomics. *Nature Communications* **10**, 985 (2019).
53. Hastings, J. *et al.* ChEBI in 2016: Improved services and an expanding collection of metabolites. *Nucleic Acids Res* **44**, D1214–D1219 (2016).
54. Bateman, A. *et al.* UniProt: the universal protein knowledgebase in 2021. *Nucleic Acids Research* **49**, D480–D489 (2021).
55. Morgat, A. *et al.* Enzyme annotation in UniProtKB using Rhea. *Bioinformatics* **36**, 1896–1901 (2020).
56. Fahy, E. *et al.* A comprehensive classification system for lipids. *Journal of Lipid Research* **46**, 839–861 (2005).
57. Liebisch, G. *et al.* Shorthand notation for lipid structures derived from mass spectrometry. *Journal of Lipid Research* **54**, 1523–30 (2013).
58. O'Donnell, V. B. *et al.* Steps Toward Minimal Reporting Standards for Lipidomics Mass Spectrometry in Biomedical Research Publications. *Circulation: Genomic and Precision Medicine* **13**, e003019 (2020).
59. Tsugawa, H. *et al.* Mass Spectrometry Data Repository Enhances Novel Metabolite Discoveries with Advances in Computational Metabolomics. *Metabolites* **9**, 119 (2019).
60. Wilkinson, M. D. *et al.* The FAIR Guiding Principles for scientific data management and stewardship. *Sci Data* **3**, 160018 (2016).
61. Huynh, K. *et al.* High-Throughput Plasma Lipidomics: Detailed Mapping of the Associations with Cardiometabolic Risk Factors. *Cell Chemical Biology* **26**, 71–84.e4 (2019).
62. Adams, K. J. *et al.* Skyline for Small Molecules: A Unifying Software Package for Quantitative Metabolomics. *Journal of Proteome Research* **19**, 1447–1458 (2020).
63. Hartler, J. *et al.* Lipid Data Analyzer: unattended identification and quantitation of lipids in LC-MS data. *Bioinformatics* **27**, 572–577 (2010).
64. Hartler, J. *et al.* Automated Annotation of Sphingolipids including Accurate Identification of Hydroxylation Sites Using MS nData. *Analytical Chemistry* **92**, 14054–14062 (2020).

65. Korf, A. *et al.* Three-dimensional Kendrick mass plots as a tool for graphical lipid identification. *Rapid Communications in Mass Spectrometry* **32**, 981–991 (2018).
66. Korf, A., Jeck, V., Schmid, R., Helmer, P. O. & Hayen, H. Lipid Species Annotation at Double Bond Position Level with Custom Databases by Extension of the MZmine 2 Open-Source Software Package. *Analytical Chemistry* **91**, 5098–5105 (2019).
67. Krettler, C. A., Hartler, J. & Thallinger, G. G. Identification and Quantification of Oxidized Lipids in LC-MS Lipidomics Data. *Studies in Health Technology and Informatics* **271**, 39–48 (2020).
68. Wang, M., Wang, C. & Han, X. Selection of internal standards for accurate quantification of complex lipid species in biological extracts by electrospray ionization mass spectrometry—What, how and why? *Mass Spectrometry Reviews* **36**, 693–714 (2017).
69. Khoury, S. *et al.* Quantification of Lipids: Model, Reality, and Compromise. *Biomolecules* **8**, (2018).
70. Lange, M. & Fedorova, M. Evaluation of lipid quantification accuracy using HILIC and RPLC MS on the example of NIST® SRM® 1950 metabolites in human plasma. *Analytical and Bioanalytical Chemistry* **412**, 3573–3584 (2020).
71. Miller, J. N. and Miller, J. C. Statistics and Chemometrics for Analytical Chemistry Ch. 7 (Pearson Education, 4th Edition, 2000).
72. Carvajal-Rodríguez, A., de Uña-Alvarez, J. & Rolán-Alvarez, E. A new multitest correction (SGoF) that increases its statistical power when increasing the number of tests. *BMC Bioinformatics* **10**, 209 (2009).
73. Griffin, J. L., Liggi, S. & Hall, Z. CHAPTER 2:Multivariate Statistics in Lipidomics. in *Lipidomics* 25–48 (2020).
74. Wold, S., Esbensen, K. & Geladi, P. Principal component analysis. *Chemometrics and Intelligent Laboratory Systems* **2**, 37–52 (1987).
75. Checa, A., Bedia, C. & Jaumot, J. Lipidomic data analysis: Tutorial, practical guidelines and applications. *Analytica Chimica Acta* **885**, 1–16 (2015).
76. Kaya Gülağız, F. & Şahin, S. Comparison of Hierarchical and Non-Hierarchical Clustering Algorithms. *International Journal of Computer Engineering and Information Technology* **9**, 6–14 (2017).
77. Mika, S., Ratsch, G., Weston, J., Scholkopf, B. & Muller, K. R. Fisher discriminant analysis with kernels. *Neural Networks for Signal Processing - Proceedings of the IEEE Workshop* 41–48 (1999).
78. Tharwat, A., Gaber, T., Ibrahim, A. & Hassanien, A. E. Linear discriminant analysis: A detailed tutorial. *AI Communications* **30**, 169–190 (2017).
79. Wold, S., Sjöström, M. & Eriksson, L. PLS-regression: a basic tool of chemometrics. *Chemometrics and Intelligent Laboratory Systems* **58**, 109–130 (2001).
80. Lee, L. C., Liong, C. Y. & Jemain, A. A. Partial least squares-discriminant analysis (PLS-DA) for classification of high-dimensional (HD) data: a review of contemporary practice strategies and knowledge gaps. *Analyst* **143**, 3526–3539 (2018).
81. Cortes, C., Vapnik, V. & Saitta, L. Support-vector networks. *Machine Learning 1995 20:3* **20**, 273–297 (1995).
82. Breiman, L. Random Forests. *Machine Learning 2001 45:1* **45**, 5–32 (2001).
83. Gromski, P. S. *et al.* Influence of Missing Values Substitutes on Multivariate Analysis of Metabolomics Data. *Metabolites* **2014**, **4**, 433–452 (2014).
84. Stacklies, W., Redestig, H., Scholz, M., Walther, D. & Selbig, J. pcaMethods--a bioconductor package providing PCA methods for incomplete data. *Bioinformatics* **23**, 1164–1167 (2007).

85. Slenter, D. Metabolite BridgeDb ID Mapping Database (20210109). (2021) doi:10.6084/m9.figshare.13550384.v1.
86. Kutmon, M. *et al.* PathVisio 3: an extendable pathway analysis toolbox. *PLoS Computational Biology* **11**, (2015).
87. Shannon, P. *et al.* Cytoscape: A Software Environment for Integrated Models of Biomolecular Interaction Networks. *Genome Research* **13**, 2498–2504 (2003).
88. Kutmon, M., Lotia, S., Evelo, C. T. & Pico, A. R. WikiPathways App for Cytoscape: Making biological pathways amenable to network analysis and visualization. *F1000Research* **3**, 152 (2014).
89. Kutmon, M., Ehrhart, F., Willighagen, E. L., Evelo, C. T. & Coort, S. L. CyTargetLinker app update: A flexible solution for network extension in Cytoscape. *F1000Research* **7**, 743 (2019).

Figure legends:

Figure 1. A screenshot of Lipidomics Tools Guide guiding the choice of the tools organized by the major tasks for lipidomics data processing. Each task is marked by a clickable button to redirect the user to the list of corresponding tools and their descriptions.

Figure 2. List of tools represented within LIPID MAPS Lipidomics Tools Guide assigned for each of the seven data processing categories These include (1) lipid-oriented databases, (2) MS data repositories, (3) analysis of targeted lipidomics datasets, (4) lipid identification, and (5) quantification from untargeted lipidomics datasets, (6) statistical analysis and visualization, and (7) data integration solutions.

Figure 3. A screenshot example of individual tool details pages from LIPID MAPS Structure Database. Each tool has three sections: a “**Description**” section for the brief introduction of the tool, a “**Technical Information**” section listing all essential technical information from links to compatible file formats, and a “**Task specific information**” section containing detailed features tailored to the corresponding task. Hovering on the underlined text field displays further features for the section.

Figure 4. A screenshot example of individual tool details pages LipidLynxX. Each tool has three sections: a “**Description**” section for the brief introduction of the tool, a “**Technical Information**” section listing all essential technical information from links to compatible file formats, and a “**Task specific information**” section containing detailed features tailored to the corresponding task. Hovering on the underlined text field displays further features for the section.

Tables:

Table 1. The list of tools covered by the interactive LIPID MAP Lipidomics Tools Guide assigned with the corresponding task. URL, links to video tutorials (when available) and reference are provided for each tool.

Task	Tool	URL	Video tutorial	ref
1	LIPID MAPS® Structure Database (LMSD)	https://lipidmaps.org/resources/databases/index.php?tab=lmsd	https://youtu.be/WNxsatndc2E	22
1	LIPID MAPS® Computationally-generated Bulk Lipids (COMP_DB)	https://lipidmaps.org/resources/databases/index.php?tab=comp_db	https://youtu.be/WNxsatndc2E	22
1	LIPID MAPS® Lipidomic Ion Mobility Database	https://lipidmaps.org/resources/databases/index.php?tab=ion_mobility	https://youtu.be/WNxsatndc2E	22
1	LIPID MAPS® In-Silico Structure Database (LMISSD)	https://lipidmaps.org/resources/databases/index.php?tab=lmissd&intro=full	https://youtu.be/WNxsatndc2E	22
1	SwissLipids Knowledgebase	http://www.swisslipids.org/		23
2	Metabolomics Workbench	https://metabolomicsworkbench.org		24
2	MetaboLights	https://www.ebi.ac.uk/metabolights/		25
3	LipidCreator	https://lifs-tools.org/lipidcreator.html	https://youtu.be/1QjcFTah1YI	26
3	METLIN-MRM/XCMS-MRM	http://metlin.scripps.edu/ ; http://xcmsonline-mrm.scripps.edu		27
4.1, 4.2, 4.5, 5 and 6	Lipid Data Analyzer (LDA)	http://genome.tugraz.at/lda2/lda_description.shtml	https://youtu.be/GiKM-urfNIg	28
4.1	LipidFinder	https://lipidmaps.org/resources/tools/lipidfinder/	https://youtu.be/ULHt5FKo1E	29
4.1, 4.2, 4.3, 4.5, 5 and 6	MS-DIAL	http://prime.psc.riken.jp/compms/index.html http	https://youtu.be/ozowb75vHXc	30
4.1, 5 and 6	XCMS_online	https://xcmsonline.scripps.edu/	https://youtu.be/D9vBMw78_qI	31
4.2	LipidHunter 2	https://github.com/SysMedOs/lipidhunter/releases		32
4.2	LipidXplorer	https://lifs-tools.org/lipidexplorer	https://cloud.mpi-cbg.de/index.php/s/cAOv62Gwy2YXvHw	33
4.2, 4.3, 4.4, 4.5, 5, 6 and 7.3	Lipostar 2.0	https://www.moldiscovery.com/software/lipostar/		34
4.2, 5 and 6	MZmine	www.mzmine.org	https://youtu.be/vRSh4GmnrH8	35
4.5	LPptiger	https://github.com/SysMedOs/lpptiger/releases/	https://youtu.be/0eRkO9RzT3c	36
6	LIPID MAPS Statistical Analysis Tools	https://lipidmaps.org/data/stats/		37
6	MetaboAnalyst 5.0	https://www.metaboanalyst.ca		38
7.1	BridgeDb	https://bridgedb.github.io/		39
7.1	Goslin	https://lifs-tools.org/goslin.html		40
7.1	LipidLynxX	http://www.lipidmaps.org/lipidlynxx/	https://youtu.be/6WBzZgiAyLc	41
7.1	RefMet	https://www.metabolomicsworkbench.org/databases/refmet/		42
7.2	LION/web	http://www.lipidontology.com/	https://youtu.be/KkO5mUJu-8g	16
7.2	Lipid Mini-On	https://omicstools.pnnl.gov/shiny/lipid-mini-on/		43
7.3	BioPAN	https://lipidmaps.org/biopan	https://youtu.be/3OrJRzbCB04	44

7.3	WikiPathways (lipid portal)	https://www.wikipathways.org/index.php/Portal:Lipids	https://www.youtube.com/playlist?list=PL-Z5Z7-ljMwb2wBi3yL5wvB3nG7-ewYK-	45
-----	-----------------------------	---	---	----