MetaboNews

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Metabolomics Society News

Notes from the Chair

Dear Colleagues,

This month we have been busy organising Metabolomics 2020 (http://metabolomics2020.org/), our first on-line virtual meeting which will take place on the 27th-29th October. This has been a steep learning curve trying to turn a concept into an actual conference, but we think we have an exciting and enjoyable conference in the making. Hopefully by the time this goes out we will have the online portal live and you will be able to submit your abstracts for either a talk or a poster. We should also have announced officially our plenaries – and this time we have representatives from every continent apart from Antarctica - now there is a challenge for a future speaker! If you are one of the society's sponsors you should have been contacted by ASK about sponsorship opportunities. We will also have several workshops provided by our affiliate networks and task groups. Notice that I haven't said that you can register for the conference this year. We decided to make the virtual conference free for all members in part to reflect what has been a very tough year for everyone.

Another reason for renewing your membership if you haven't done so already is the approaching elections. All members can take part in the elections and we have a number of director positions available this year. In addition, Nichole, Krista and I will stand down as officers so members will also be voting in the elections of a new President, Treasurer and Secretary to the Society. Unlike some Presidents, I will definitely be stepping down on time so I can focus on the virtual meeting. I hope you and your families are well in these difficult times and I look forward to 'seeing virtually' as many of you as possible online in October.

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METABOLOMICS SOCIETY

METABOLOMICS SOCIETY
EARLY- CAREER MEMBERS NETWORK

The Metabolomics Society is an independent non-profit organisation dedicated to promoting the growth, use and understanding of metabolomics in the life sciences.

General Enquiries
info@metabolomicssociety.org
Membership Enquiries

Board of Directors Election – Voting Now Open!

All members of the Metabolomics Society are welcomed and encouraged to participate in the 2020 Board of Directors election. Voting is open now through **August 30, 2020** at 11:59pm USA CST.

You can find a list of the nominees as well as their biographies and statements of interest on the website. Visit www.metabolomicssociety.org home page for details and the link to vote.

NOTE: The Society has launched a NEW membership system. ALL members are required to create a new record in this new platform.

If you have not signed up for membership in 2020, sign up here: 2020 Membership

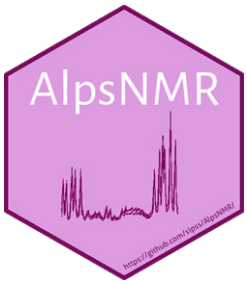
Select the option: Create a new user account, even if you have previously been a member of the Society.

NEW MEMBERSHIP BENEFITS: Your membership will be valid for one full year, and you'll receive complimentary access to the **Metabolomics 2020 Online** event in October!

There are 11 open positions on the Board this year, making this election incredibly important! Please contribute to shaping the future of our Society by voting and playing an active role.

Best,
Krista Zanetti (Chair of Nominations Committee and Secretary)
Jules Griffin (President)

SpOtlight



Spotlight article contributed by Francisco Madrid-Gambin, Luis Fernandez, Sofia Moco and Santiago Marco

The Institute for Bioengineering of Catalonia (IBEC), Barcelona, Spain

Nestlé Research, EPFL Innovation Park, Lausanne, Switzerland

NMR-based metabolomics is widely used to explore metabolic fingerprints from biological samples. Targeted metabolomics workflows aim to detect and quantify a set of pre-defined, known metabolites. Untargeted approaches, in contrast, comprehensively extract metabolite features derived from the entire spectra, including both known and unknown compounds. While there are various computational tools developed for targeted metabolomics that require previous knowledge about the list of metabolites to monitor, there is a lack of open source tools in fully untargeted metabolomics. We developed AlpsNMR (Automated spectraL Processing System for NMR), an R package that allows for an automated untargeted NMR-based metabolomics analysis (Madrid-Gambin et al., 2020). The AlpsNMR R package and tutorial is freely available to download from http://github.com/sipss/AlpsNMR.

The AlpsNMR workflow includes a sequential procedure from data import to identification (Figure 1). In the load spectra step, the 'nmr_read_samples' function imports the directory containing multiple instrumental spectra. The external or clinical metadata can be automatically merged to the dataset from a Microsoft Excel file. The list of raw spectral vectors is combined into a single matrix, performing the cubic spline process in the interpolation step to get a unique ppm axis (Kohl et al., 2012). Visualization of the dataset may be interactively displayed with plotly in an HTML file that can be zoomed and saved as a picture (PNG plot). Then, spectra are ready for the exclusion of the solvent region (e.g., water). The robust Principal Component Analysis is used for the outlier detection step. Figure 2 shows an example of outlier diagnostics based on quantiles for Q residual and T2 score values (Hubert and Engelen, 2004). The peak detection step includes visualization of detected signals, so it allows for adjustment of the sensitivity of the algorithm based on an automated calculation of the noise level, signal-to-noise ratio and the size of the window to detect a peak. The obtained peak list is aligned based on hierarchical cluster-based peak alignment (Vu et al., 2011) from the speaq package (Beirnaert et al., 2018). In the normalization step, the dataset can be normalized by probabilistic quotient normalization (PQN) (Dieterle et al., 2006), total sum of the spectral area, an internal calibrant, among others. The peak integration step is performed either automatically or manually, and allows users to select a specific region and width. Then, the final peak table is ready for the machine learning step. For modelling of the data, the package includes the possibility to perform machine learning using repeated double cross-validation optimized for unbiased variable selection (Figure 3) from the MUVR package (Shi et al., 2018). Subsequently, auto-selected variables are ranked according to the cumulated VIP values. Finally, the identification step uses the source of the biological samples (e.g., plasma/serum, urine and cells) generating ranked metabolite candidates obtained according to the Human Metabolome Database (http://www.hmdb.ca).

AlpsNMR was employed on an openly available dataset from the MetaboLights repository (Haug et al., 2013). The MTBLS242 dataset of human serum was acquired from a human clinical study of bariatric surgery (Gralka et al., 2015). The AlpsNMR workflow took less than 30 min to evaluate this dataset in a twelve-core workstation. The obtained output allowed us to identify the discriminant compounds, in agreement with the previously reported ones by Gralka and colleagues. Hence, this R-package may prove to be of interest to the NMR metabolomics community due to its automated pipeline, working in a fully untargeted manner.

Figure 1. Step-by-step workflow for untargeted NMR-based metabolomics analysis using AlpsNMR.

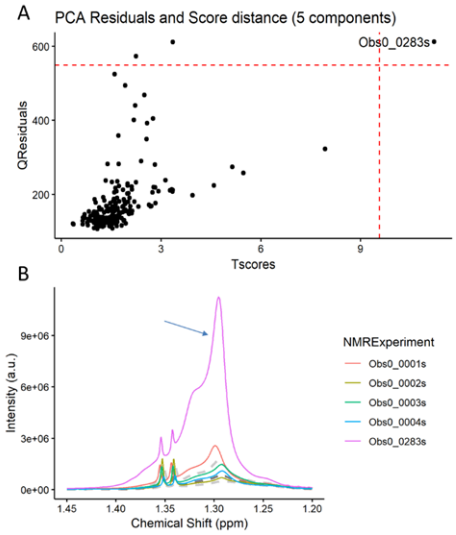


Figure 2. Output from the outlier detection step in an example dataset. The plot of rPCA residuals (A) indicates that the sample "Obs0_0283s" differs greatly on Q-residuals and T-scores from other samples, while spectral visualization (bottom plot) confirmed this behaviour at the spectral level (B).

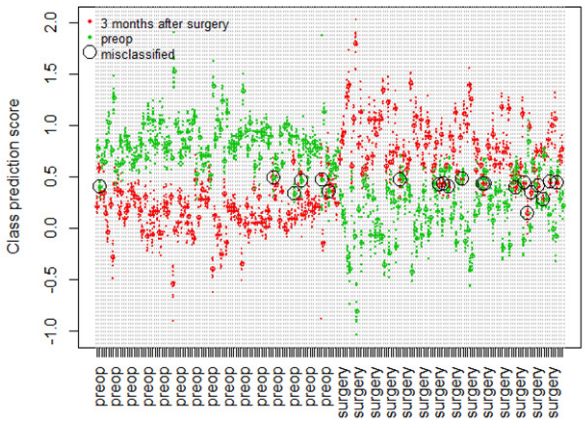


Figure 3. Misclassification plot from a repeated double cross-validated Partial Least Squares Discriminant Analysis model in the MTBLS242 dataset. The misclassification plot shows each sample predicted as "preop" (pre-operation samples) and "surgery" (after bariatric surgery). The first half of the horizontal axis represents actual preop samples, while the second half represents actual "surgery" samples. Bold points are the average predicted samples, while grey points display predictions from each iteration. Misclassifications are differences between predicted samples compared to the actual ones, as shown by black circles.

References

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Dieterle, F. et al. (2006) Probabilistic quotient normalization as robust method to account for dilution of complex biological mixtures. Application in 1H NMR metabonomics. Anal. Chem., 78, 4281–4290.

Gralka, E. et al. (2015) Metabolomic fingerprint of severe obesity is dynamically affected by bariatric surgery in a procedure-dependent manner. Am. J. Clin. Nutr., 102, 1313–1322.

Haug, K. et al. (2013) MetaboLights—an open-access general-purpose repository for metabolomics studies and associated meta-data. Nucleic Acids Res., 41, D781–D786.

Hubert, M. and Engelen, S. (2004) Robust PCA and classification in biosciences. Bioinformatics, 20, 1728–1736.
Kohl,S.M. et al. (2012) State-of-the art data normalization methods improve NMR-based metabolomic analysis. Metabolomics, 8, 146–160.

Madrid-Gambin, F. et al. (2020) AlpsNMR: an R package for signal processing of fully untargeted NMR-based metabolomics. Bioinformatics.

Shi, L. et al. (2018) Variable selection and validation in multivariate modelling. Bioinformatics.

Vu, T.N. et al. (2011) An integrated workflow for robust alignment and simplified quantitative analysis of NMR spectrometry data. BMC Bioinformatics, 12, 405.

Recent Publications

Recently published papers in metabolomics

- Choline-related metabolites influenced by feeding patterns in preterm and term infants
- Prenatal Exposure to Perfluoroalkyl Substances Associated with Increased Susceptibility to Liver Injury in Children
- A blood-based metabolomics test to distinguish relapsing-remitting and secondary progressive multiple sclerosis: addressing practical considerations for clinical application
- Integrated Datasets of Proteomic and Metabolomic Biomarkers to Predict Its Impacts on Comorbidities of Type 2 Diabetes Mellitus
- Effects of Elevated p CO 2 on the Survival and Growth of Portunus trituberculatus
- Systematic Multi-Omics Integration (MOI) Approach in Plant Systems Biology
- Introduction to high throughput platforms in kidney cancer: Genomics, transcriptomics, and metabolomics urologic oncology: Seminars and original investigations
- GlycA Levels during the Earliest Stages of Rheumatoid Arthritis: Potential Use as a Biomarker of Subclinical Cardiovascular Disease
- Plasma Metabolites Related to Peripheral and Hepatic Insulin Sensitivity Are Not Directly Linked to Gut Microbiota Composition
- Metabolomic Biomarkers for Detection, Prognosis and Identifying Recurrence in Endometrial Cancer
- An Integrated Metabolomics Study of Glucosinolate Metabolism in Different Brassicaceae Genera
- Proteomics and Metabolomics for Cystic Fibrosis Research

Metabolomics Events

14-16 Sep 2020

Metabolomics Association of North America (MANA)
2nd Annual MANA Conference

Venue:
Online

Confirmed speakers
- Joshua Rabinowitz, Princeton University
- Nima Sharifi, Cleveland Clinic
- Charles Serhan, Harvard University
- Wassim Labaki, University of Michigan

Overview
The conference will feature oral presentations, poster sessions and interactive forums with live discussion of key challenges in different metabolomics subfields.

Abstract submission deadline: July 17, 2020

Course link
Information and registration: https://www.mana2020.org

23-25 Sep 2020

Multiple Biofluid and Tissue Types, From Sample Preparation to Analysis Strategies for Metabolomics

Venue:
Birmingham Metabolomics Training Centre, University of Birmingham, United Kingdom

Overview
This 3-day course provides a theoretical overview and hands-on training to apply multiple sample preparation and UPLC-MS methods to characterise the metabolomes of complex biological samples using the mass spectrometer (Xevo QToF G2-XS - a maximum of 4 people working on the instrument in a session). The course is led by experts in the field who have experience of the analysis of microbial, plant and mammalian samples, and illustrates the different approaches that are available to analyse a range of biological samples and applying complementary liquid chromatography approaches to maximise the coverage of the metabolome.

Topics covered
- Introduction to dealing with the complexity of biological samples using UPLC-MS
- Overview of different sample collection, sample quenching and sample extraction methods
- The challenges of working with cellular and tissue samples
- Overview of different UPLC methods including HILIC and reversed phase methods
- Hands-on sample preparation of plasma, urine, cell and tissue samples
- Monophasic and biphasic solvent extraction methods to target polar and non-polar metabolites
- SPE and liquid-liquid sample clean-up methods
- Hands-on HILIC and reversed-phase liquid chromatography
- Hands-on UPLC-MS analysis for untargeted studies (maximum of 4 people)
- Overview of data analysis and metabolite identification
- Problem solving and tips and tricks session with the experts

Course link
More information available here.

7-9 Oct 2020

Introduction to Metabolomics for the Microbiologist

Venue
Birmingham Metabolomics Training Centre, University of Birmingham, United Kingdom

Overview
This three-day course introduces how untargeted metabolomics can be applied to study microbial systems in academic and industrial research. The course provides an overview of the metabolomics pipeline, experimental design, sample preparation and data acquisition. The course is led by experts in the field of metabolomics and will include lectures, hands-on laboratory sessions in sample preparation and data acquisition and computer workshops focused on data processing and data analysis.

Topics Covered

- Introduction to metabolomics, both targeted and untargeted approaches
- Experimental design and the importance of quality control samples in untargeted metabolomics
- Analytical strategies applied in metabolomics with a focus on mass spectrometry
- Hands-on laboratory sessions focused on sample preparation and to include metabolic quenching and extraction procedures, intracellular and exometabolome samples and polar and non-polar extraction methods
- Hands-on laboratory sessions focused on sample analysis for untargeted metabolomics studies using an Acquity UPLC coupled to a Xevo QToF mass spectrometer
- Hands-on workshop focused on data processing and data analysis
- Hands-on workshop focused on an introduction to metabolite identification
- Question and answer session with the experts

Course link

More information available here.

2-4 Nov 2020

Metabolomics with the Q Exactive

Venue

Birmingham Metabolomics Training Centre, University of Birmingham, United Kingdom

Overview

This 3-day course introduces you to using the Q Exactive mass spectrometer in your metabolomics investigations. The course is led by experts in the field of metabolomics and includes lectures, laboratory sessions and computer workshops to provide a detailed overview of the metabolomics pipeline applying the Q Exactive mass spectrometer.

Topics covered

- Introduction to Metabolomics on the Q Exactive, the metabolomics workflow, and case studies using the Q Exactive
- Using the Q Exactive family of instruments in your metabolomics investigations
- Experimental design and the importance of quality control samples
- Sample preparation including polar and non-polar preparation methods on biofluids (urine and plasma) and tissue samples
- Preparation of samples for profiling and targeted analyses on the Q Exactive
- Hands-on data acquisition for profiling and targeted studies, setting up the Vanquish UHPLC coupled to the Q Exactive MS
- Data processing workshop
- Data analysis workshop (univariate and multivariate analysis)
- Introduction to metabolite identification applying Data Dependent Analysis and Data
- Independent Analysis
- Question and answer session with a panel of experts
- Tips and tricks
- Problem solving

Course link

More information available here.

5-6 Nov 2020

Metabolite identification with the Q Exactive and LTQ Orbitrap Elite

Venue
Birmingham Metabolomics Training Centre, University of Birmingham, United Kingdom

Overview
This 2-day course will provide a hands-on approach to teach the attendees about the latest techniques and tools available to perform metabolite identification in non-targeted metabolomics studies. The course will be led by experts working within the fields of metabolomics and chemical analysis and will include a significant proportion of hands-on experience of using mass spectrometers, software tools and databases. A maximum of four people will be working on each mass spectrometer in a session. We will apply these tools on the Q Exactive and LTQ-Orbitrap family of mass spectrometers.

Topics Covered
- Importance of mass spectral interpretation
- Types of data which can be collected on the QE and LTQ-Orbitrap (*m/z*, retention time, MS/MS, MSn)
- Conversion of raw data to molecular formula and putative metabolite annotations
  MS/MS experiments in metabolic phenotyping for on-line data acquisition using the QE (DDA, DIA, all-ion)

Topics Covered
- MS/MS and MSn experiments for sample fractions using the LTQ-Orbitrap
- Mass spectral libraries (using mzCloud)
- Searching mass spectral libraries
- Tools for mass spectral interpretation
- Reporting standards for metabolite identification
- Question and answer session with the experts

Course link
More information available here.

Postponed Until 2021

The Third Annual Canadian Metabolomics Conference

Venue
Edmonton, Alberta, Canada

Overview
The Third Annual Canadian Metabolomics Conference has been postponed until 2021. The conference will highlight work by leading researchers, including new technologies and approaches for metabolomics research, and applications in various fields. The conference will feature networking opportunities and a poster session designed for trainees to present their work. Our goal is to highlight the exceptional metabolomics science that is being done in Canada and abroad, and foster Canada's leadership role in the global research community.

We look forward to seeing you in 2021!

Conference link
https://www.canmetcon.ca/

6-7 April 2021

Targeting CNS Tumor Metabolism Symposium

Venue
NIH Campus, Bethesda, Maryland

Overview
This is the first conference that focuses on the tumor metabolism and it is expected to be a didactic and collegial learning environment. Metabolic investigations for these tumors have been conducted in isolation and the goal of this meeting is to bring together the clinicians with the experts in metabolism to increase the utilization of metabolic investigations in the clinical settings. This will, in turn, enhance partnerships and advance the treatment for patients.

In addition to oral and poster presentations selected from the submitted abstracts, the conference will feature invited lectures from an internationally recognized faculty, including keynote talks from Craig Thompson, MD (President and CEO of Memorial Sloan Kettering Cancer Center) and Paul Mischel, MD (Distinguished Professor, University of California San Diego).

Abstract submission deadline is December 1, 2020.

Course link
https://www.soc-neuro-onc.org/SNO/2020METAB/Home.aspx

15-16 Apr 2021

Data Analysis for Metabolomics

Venue
Wageningen Campus, The Netherlands

Overview
Event postponed from June 4-5, 2020 to now April 15-16, 2021

Metabolomics experiments based on mass spectrometry (MS) or nuclear magnetic resonance (NMR) produce large and complex data sets. This course will introduce approaches to process and analyze data and design high-quality experiments. Through hands-on workshops and lectures highlighting the different concepts you will get a thorough basis for tackling the challenges in metabolomics data analysis.

Course link
https://www.wur.nl/en/Education-Programmes/Wageningen-Academy/Plant/Course-Data-analysis-for-Metabolomics.htm

Metabolomics Jobs & Collaborations

If you have a job you would like posted, please email Shelby Soke (soke@ualberta.ca).

Jobs Offered

Job Title	Employer	Location	Posted	Closes	Source
Various Positions			29-July-20		Metabolomics Association of North America Jobs
Scientific Software Engineer	Universität Jena	Jena, Germany	1-July-2020	Until filled	MetaboNews
Postdoctoral scholar	University of California San Francisco (UCSF)	San Francisco, CA, USA	24-June-20	31-Dec-20 or until filled	Metabolomics Society Jobs
Are you a skilled metabolomics expert/ analytical chemist?	MS-Omics	Vedbaek/ Copenhagen, Denmark	26-May-20	1-Sep-20	Metabolomics Society Jobs
Postdoctoral Researcher in Metabolomics/ Computational Metabolomics	Institute for Biomedicine, Eurac Research	Bolzano, Italy	13-May-20	Until filled	Metabolomics Society Jobs
Postdoctoral Associate	Yale School of Public Health	New Haven, Connecticut	5-Feb-20	Until filled	Metabolomics Society Jobs

Jobs Wanted

This section is intended for very highly qualified individuals (e.g., lab managers, professors, directors, executives with extensive experience) who are seeking employment in metabolomics.

We encourage these individuals to submit their position requests to Shelby Soke (soke@ualberta.ca). Upon review, a limited number of job submissions will be selected for publication in the Jobs Wanted section.