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MetaboNews is a monthly newsletter published in a partnership between The Metabolomics Innovation Centre (TMIC) and the Metabolomics Society.

Metabolomics Society News

Conference Corner



There is still time to attend the remainder of [Metabolomics 2022](#).

For those already in attendance, enjoy your time at the conference and your stay in Valencia!

Members' Corner

Early-career Members Network (EMN)

Travel Award

After a difficult and careful blind evaluation by all the EMN members, four applicants were selected from among more than thirty applications to receive the EMN Travel Award for Metabolomics 2022. We congratulate the following candidates: Abhishek Jain, Giorgia La Barbera, Diana Pinto, and Chanel J. Petrorius.

EMN Webinar Series

The EMN would like to thank Prof. Jean-Francois Focant and Dr. Pierre-Hugues Stefanuto, who gave an inspiring presentation about their work on GCxGC-TOFMS in medical volatolomics and in understanding lung inflammation mechanisms. Find all the details about the webinar and watch it [here](#).

EMN Expert Opinion

This month, the EMN is glad to present Professor Eiichiro Fukusaki, who kindly shares his expertise and experience in the field of food metabolomics. Read his interview [here](#).

Roy Goodacre, PhD FRSC FLSW



Chair in Biological Chemistry at the University of Liverpool; Head of a multidisciplinary Metabolomics and Raman spectroscopy research group in the Institute of Systems, Molecular and Integrative Biology (ISMIB), and co-leader of ISMIB's Centre for Metabolomics Research

Biography

Roy is the founder and current Editor-in-Chief of *Metabolomics* (since 2005) and an editorial advisory board member for *Analyst* (since 2014), *Journal of Analytical and Applied Pyrolysis* (since 1997), and *Spectrochimica Acta A: Molecular and Biomolecular Spectroscopy* (since 2016). He also helped establish the Metabolomics Society (Director: 2005-2015, 2020-present) and since 2008 is a Director of the Metabolic Profiling Forum.

Roy has two international patents, published more than 450 peer-reviewed research articles, and edited two books on metabolomics.

For more information on Roy's background and research:

- Twitter: <https://twitter.com/RoyGoodacre>
- Goggle Scholar: <https://scholar.google.com/citations?hl=en&user=Dszi0U8AAAAJ>
- Wikipedia: https://en.wikipedia.org/wiki/Roy_Goodacre

Interview Q&A

How did you get involved in metabolomics?

I guess I was there before it started. I did my PhD at Bristol University in the UK in the late 1980s and at that time was using mass spectrometry to characterize biological systems. In particular I was investigating the changes in phenotypes of bacteria when you altered their genotype. Hopefully from that

you can see the analogy between this and modern metabolomics, which is very much employed for generating a phenotypic read-out of what genes are doing. My first paper highlighted that you could tell the difference between the same bacteria carrying different plasmids. Later I showed that transposons inserted into genes encoding enzymes altered the mass spectrum and, in particular, when you disrupt tryptophanase, *E. coli*

could no longer produce indole. I went on then to look at the effects of feeding tryptophan and linking this to the level of indole production. This mechanistic work is why a lot of us use metabolomics, as we want to know how and why a measured phenotype in one system is different from another. This could be for functional genomics (as in the example above), for understanding health and disease processes, for improved plant breeding, or for understanding antimicrobial resistance (AMR). All of these require mechanistic understanding of the system.

What are some of the most exciting aspects of your work in metabolomics?

I think it's fair to say that the most exciting aspect is

that metabolomics is a group effort and I've worked with many great researchers. When I was in Manchester with Doug Kell, Rick Dunn and David Broadhurst, as well as Ian Wilson, and many others, we established a quality control (QC) pipeline that allowed fusion of metabolomics data collected over years rather than days. This meant that you could start to analyse 1000s of samples rather than 10s-100s. I'm particularly proud to have been involved in that.

All our metabolomics studies have embedded within them QAs and QCs, as we can use these to assess analytical performance and apply corrections where necessary. We have used untargeted metabolomics to look at what I might call epidemiological scale studies

where we profiled 2000 people and were able to differentiate biochemically between a human resilient phenotype and individuals who were considered frail. That was some work led by Nik Rattray when he was in our group. It's very nice work and indicates that part of the mechanism behind frailty is down to dysregulation of carnitine shuttle and vitamin E pathways which play a role in the risk of frailty. Moreover, it shows that this metabolic 'frailty' measurement has the potential to contribute greatly to the standardization of frailty assessment, which currently is observational and open to human interpretation. (See Figure 1.)

What key metabolomics initiatives are you pursuing at your research centre or institute?

The initial initiative when I moved to Liverpool in November 2018 was to help establish the [Centre for Metabolomics Research \(CMR\)](#). I'm delighted that we have done so well!

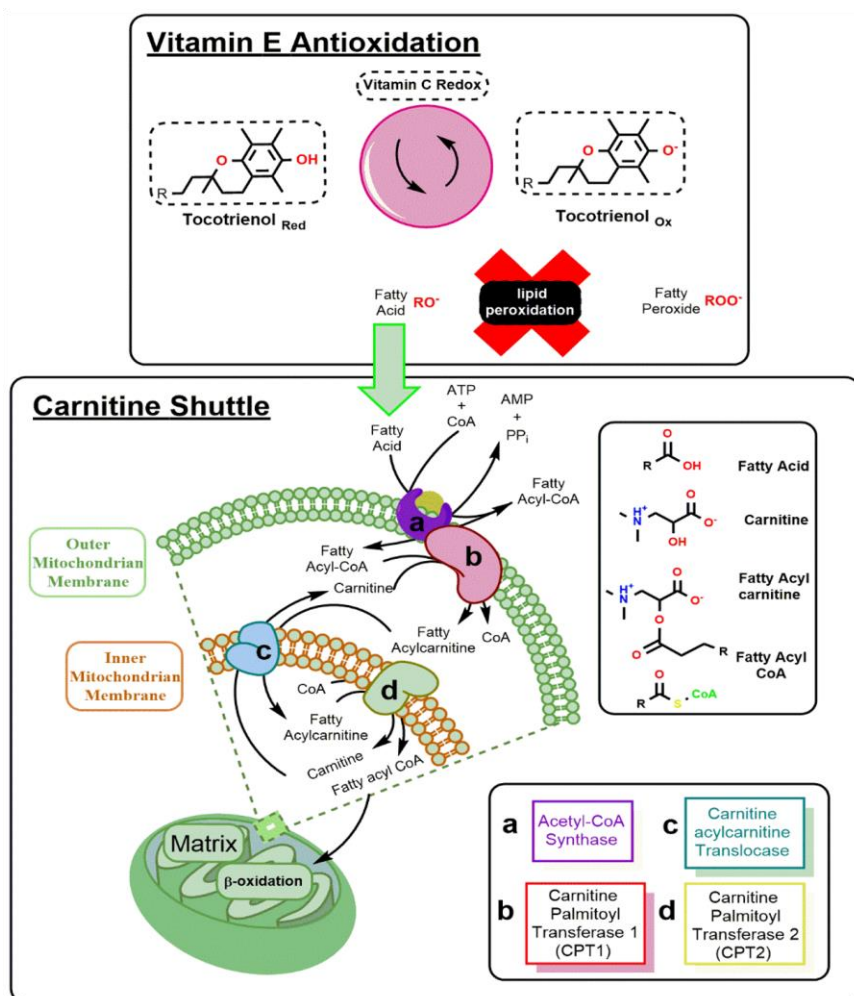


Figure 1: An image highlighting the key biochemical pathways that are altered in the human frail phenotype as discussed in [Nature Communications](#), **10**, art. 5027 (2019).

The CMR comprises a variety of mass spec platforms with upfront GC or LC as well as high mass resolution detectors and triple quads for untargeted and targeted work. Instruments are important but more important are my colleagues in the CMR who include Doug Kell who joined Liverpool at the same time as I did. Howbeer Muhamadali joined the team a year later as a tenure track fellow and last year we were delighted that Rick Dunn joined us as Professor of Analytical and Clinical Metabolomics, and Ian Wilson as an honorary professor. This team covers many areas of metabolomics from human health and disease, animal and plant sciences through to microbiology. Cate Winder also joined us last year: she leads our Liverpool Training Centre for Metabolomics, and this means we can help train and mentor the next generation of metabolomics scientists. In addition, Marie Phelan leads the NMR spectroscopy centre for metabolomics in Liverpool, so we also have access to NMR via three instruments (600, 700, 800 MHz)

equipped with cryoprobes and autosamplers.

Although many people may not think of vibrational spectroscopy as mainstream metabolomics, Howbeer and I do! We have been developing these techniques for imaging tissues and single cells, which of course many researchers do. However, our forte is to use Raman spectroscopy (including CARS and SRS) to look at metabolism in action and to use stable isotopes to probe cellular metabolism at the single-cell level. We have also developed optical photothermal infrared spectroscopy (O-PTIR) (see Figure 2) to probe single bacterial cells and use this to probe dynamics in metabolism. We're very excited by this.

What is happening in your country in terms of metabolomics?

I think the most significant is a funded initiative called the UK Consortium for MetAbolic Phenotyping

MANA 2022

September 16-18, 2022 - Edmonton, Alberta, Canada

Plenary Speakers

- Dr. Philip Britz-McKibbin
- Dr. Nadja Cech
- Dr. Russell Jones
- Dr. Yamilé López Hernández
- Dr. Laura-Isobel McCall
- Kathryn McCauley, MPH

[Workshops](#)

[Networking](#)

[Awards](#)

[Events](#)

Revised Deadlines

Oral Abstracts – July 8
Poster Abstracts – July 22

Check [MANA2022.net](https://mana2022.net)
for themes

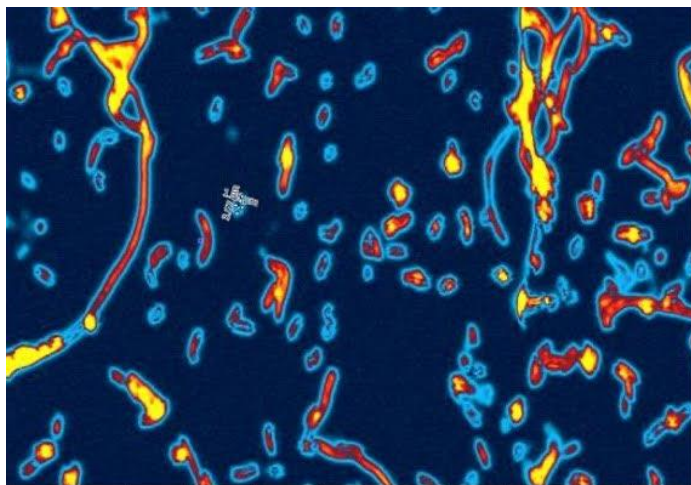


Figure 2: O-PTIR image at 1655 cm^{-1} (showing protein content from C=O vibration from amide I). The image was generated at 200-nm step sizes on a mIRage infrared microscope (Photothermal Spectroscopy Corp., Santa Barbara, USA) and was kindly provided by Mustafa Kansiz.

([MAP/UK](#)) project which is supported by the UK Medical Research Council and so is clinically focussed. I think we can agree that metabolic phenotyping can be used to help understand human physiology and pathology throughout the life course. The problem is that many of us do this in different ways and therefore harmonization of techniques and best practices, as well as how these are reported, are important for the metabolomics community. Therefore, within MAP/UK we are establishing some forms of unification within the platforms that we use to make sure that metabolic phenotyping is a robust routine and therefore can be reproducibly applied across the UK. This is a multicentre effort which we are involved in, with many colleagues from Imperial, Birmingham, Cardiff, Aberdeen, Leicester, Aberystwyth as well as EMBL-EBI.

Whilst this does of course have a clinical focus, the same approaches can be easily applied across the whole of the life sciences. Indeed, many of the consortium members have interests outside of human biology.

How do you see your work in metabolomics being applied today or in the future?

I think it's clear that the future is not to continue bringing the sample to the instrument but *vice versa* and effectively move metabolomics out of the laboratory and into the field using so-called point-and-shoot technologies.

While I know there are several activities in portable mass spectrometry, these are probably well off being used routinely. Yet, by contrast, if you look at spectroscopy, in particular Raman spectroscopy, these are already being deployed as handheld instruments and therefore can be used in remote settings. Indeed, these remote settings can be low-resource settings without a main power supply. I did this myself the summer before covid lockdown where I spent a few weeks in Kimberley in Western Australia analysing rocks and [Aboriginal rock art](#). This was only possible with a portable Raman instrument.



Therefore, I think that where our work will go in the future is having bedside, point-of-care/use devices that measure specific metabolites, or specific combinations of metabolites, that can be linked with disease. Raman is also inherently quantitative, so it has that advantage as well. These will be used to screen people very rapidly. If what we call analytical 'truth' is needed – which at least in the forensics area is based on mass and abundance – then one could of course do offline mass spec.

I don't think this is a step too far in health and disease screening as portable instruments are already being used in everyday life, for instance, if we consider a roadside breath test, which is a handheld instrument based on fuel cell technology used to measure alcohol levels in breath. This screening measurement can then be used to trigger further testing of blood or urine, which is measured using GC-MS and provides a much stronger basis for conviction.

As you see it, what are metabolomics' greatest strengths?

Many know that the genome tells you what's possible and the metabolome (along with the proteome and transcriptome) what is actually happening. When a physiological process is embedded in metabolism then metabolomics' greatest strength is getting closer to the biochemical mechanism that is occurring. Metabolites are more than just biomarkers and moving beyond this towards mechanism is an important move for the community. Some of this is summarized beautifully in a review by Caroline Johnson, Julijana Ivanisevic, and Gary Siuzdak: "[Metabolomics: beyond biomarkers and towards mechanisms](#)" (*Nature Reviews Molecular Cell Biology*, **17**, 451 (2016)).

What do you see as the greatest barriers for metabolomics? And what improvements, technological or otherwise, need to take place for metabolomics to really take off?

I think the biggest barriers in the field is actually a threat: far too many metabolomics studies that are published are underpowered. What I mean by this is that they do not contain the correct samples needed to address the problem, contain the wrong controls, or have too few samples. Therefore, one doesn't know whether the study reported is separating based on the disease process or indeed some other non-random variable that happens to be correlated with the disease process being scrutinized. This threat can be addressed by judicious design of experiments, and doing this before collecting any samples.

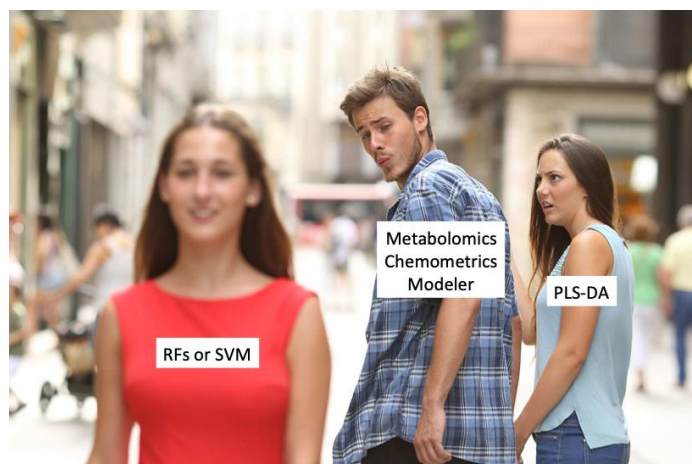
Hand-in-hand with this is that a lot of studies are too preliminary with no validation, and often when there is validation, it is performed on a very small subset using resampling. One software company's default cross-validation setting is to do k -fold validation where $k = 7$. This is done where some people have only 6 samples in each class of a case-control study. Clearly this is bonkers! It also irks me when they refer to these as cohorts. This is because the standard

definition of a cohort – at least in the dictionary – is where a cohort is an ancient Roman military unit, comprising 6 centuries, equal to one tenth of a legion. 600, not 6... I was reminded of this recently when I was discussing metabolomics with Ian Wilson.

Even when validation is done, those who use partial least squares-discriminant analysis (PLS-DA) for classification purposes show scores plots. This is a pet hate of mine. Of course these scores plots will show separation, as PLS-DA is entirely designed to do so and these scores plots are for the training data only. What large proportions of the metabolomics community seem to have forgotten is that PLS-DA predicts a Y -variable that is binary and coded: i.e., a '0' represents the absence and a '1' the presence of a particular trait. This is what people should be reporting. In other words, how close are you to predicting zero (e.g., absence of, say, a disease), or how close are you to a 1 (e.g., that the sample comes from someone with disease). These are the correct metrics to report and many in the community miss this.

So, when I see a paper that has a PLS-DA scores plot with 6 to 10 individuals in each group that shows perfect separation, and in the orthogonal version (OPLS-DA) perfect separation in the first component, I won't read the paper any further as I do not think the science is valid. Now of course some papers contain PCA scores plots with separation, and these therefore may have some power – in this case the PCA loadings vectors which are ample to do metabolite feature selection.

I appreciate that it is expensive to replicate studies, but some level of biological validation is also important. Very few published studies include any biological validation either in terms of having two discovery data sets or a validation set where specific metabolites 'discovered' in the discovery phase are analyzed in larger samples (may be the size of a real cohort!).



A reminder to metabolomics researchers that there is more to life than PLS-DA and that other chemometric algorithms exist including random forests and support vector machines, as well as other discriminant algorithms, as discussed in our tutorial review in [Analytica Chimica Acta, 879, 10 \(2015\)](#).

How does the future look in terms of funding for metabolomics?

Turbulent! And I mean this for all funding of science in the UK. I'd rather not be drawn into politics on this issue. I've said enough (probably too much!) on Twitter.

What role can metabolomics standards play?

A HUGE one! And I'm here thinking of standardization of practices and not metabolite standards which are obviously needed to effect metabolite identification and for metabolite quantification.

I was involved in the Metabolomics Standards Initiative that published a set of reporting standards in 2007. The idea with these standards was to try and standardize the reports of how experiments were done, and not to dictate **how** the experiments themselves were done. This way the reader can understand how the experiment was designed, how the metabolomics data were collected, and how these data were processed. This would then help the reader appreciate the work that was done and come to their own opinion. These do need updating and there are

ongoing international initiatives, some led by the Metabolomics Society, to address this.

In other areas the use of quality control and quality assurance samples is being encouraged within the community. There is a consortium called the Metabolomics Quality Assurance & Quality Control Consortium ([mQACC](#)) that is promoting, disseminating, and trying to harmonize best QA and QC practices in untargeted metabolomics. Another very worthy effort.

There will be many of these conducted globally and hopefully they will lead to harmonization of best practices for our community.

Do you have any other comments that you wish to share about metabolomics?

If I reflect on my answer to the first question – I've clearly been around for some considerable time! I've seen the birth of metabolomics, watched it emerge as an important omics research tool in many biological fields, and I think we can consider metabolomics a robust science.

My closing comments go to anyone new to the field: it is important to walk before you run. Metabolomics is a highly multidisciplinary field. In addition to the biological question being asked, there are considerable skills needed in analytical sciences as well as a requirement for expertise in informatics. Very few have skills in all of these areas, so it's important to work with research teams where the support and mentoring is available across these different disciplines.

It's also important to engage with other metabolomics research groups which is why I am looking forward to flying to Valencia this weekend for the Metabolomics Society annual meeting: 19-23 June 2022 [interview answers provided before meeting]. This will be our 18th international conference and I'm looking forward to seeing many old faces and making new metabolomics friends.

Recent Publications

Recently published papers in metabolomics

- [A Multidimensional Bioinformatic Platform for the Study of Human Response to Surgery](#)
- [Alterations of the gut microbiota and metabolomics in children with e-waste lead exposure](#)
- [Aquifer system and depth specific chemical patterns in fractured-rock groundwater from the Critical Zone revealed by untargeted LC-MS-based metabolomics](#) (Open Access)
- [Association of nanoparticle exposure with serum metabolic disorders of healthy adults in printing centers](#)
- [Determination of adulteration, geographical origins, and species of food by mass spectrometry](#) (Review)
- [Gene-environment interaction analysis of redox-related metals and genetic variants with plasma metabolic patterns in a general population from Spain: The Hortega Study](#) (Open Access)
- [Gut microbiota-derived ursodeoxycholic acid from neonatal dairy calves improves intestinal homeostasis and colitis to attenuate extended-spectrum \$\beta\$ -lactamase-producing enteroaggregative *Escherichia coli* infection](#) (Open Access)
- [Impact of PM_{2.5} exposure on plasma metabolome in healthy adults during air pollution waves: A randomized, crossover trial](#)
- [Integrated physiological, transcriptomic and metabolomic analysis of the response of *Trifolium pratense* L. to Pb toxicity](#)
- [Integrative metabolomic characterisation identifies altered portal vein serum metabolome contributing to human hepatocellular carcinoma](#) (Open Access)
- [Multi-omics analysis reveals the influence of tetracycline on the growth of ryegrass root](#)
- [Occurrence of antibiotics in Lettuce \(*Lactuca sativa* L.\) and Radish \(*Raphanus sativus* L.\) following organic soil fertilisation under plot-scale conditions: Crop and human health implications](#)
- [OmicsNet 2.0: a web-based platform for multi-omics integration and network visual analytics](#) (Open Access)
- [Recent advances in LC-MS-based metabolomics for clinical biomarker discovery](#) (Review)
- [Serum metabolome associated with severity of acute traumatic brain injury](#) (Open Access)
- [Spatial metabolomics for evaluating response to neoadjuvant therapy in non-small cell lung cancer patients](#) (Open Access)



Metabolomics Events

The Association of Biomolecular Resources Facilities (ABRF) Metabolomics Research Group invites participants to its 2022 “Compound Identification” study

[Learn More Here](#)

Overview

Consistent and accurate compound identification is a major challenge for LC-MS-based metabolomics. A combination of accurate mass MS1, MS2 fragmentation, and retention time (RT) of external standards is frequently used to provide a high-confidence, though unconfirmed, compound identification. However, given this information it is unclear how much compound identification success will vary from lab to lab. The aim of this study is to quantify inter-personal and inter-lab variability of compound identification. The target population of this study are PIs, trainees, and professional staff of metabolomics laboratories. The response deadline has been extended to December 31.

May 29-June 2, 2022

19th International GCxGC Symposium

Venue: Online

[Learn More Here](#)

Overview

While we had planned to host the meeting in beautiful Canmore, Alberta, Canada, we are now moving to a fully virtual event. The technical program includes the 2022 John B. Phillips and Scientific Achievement Award Lectures, 3.5 full days of live talks, posters and discussion sessions, and opportunities to contribute virtual talks and posters.

Update: We held the conference already but you can still access the conference platform until September 2.

June 18-23, 2022

HPLC 2022

Venue: San Diego, California, USA

[Learn More Here](#)

Overview

The HPLC symposia are the longest-running, largest, and most recognized international chromatographic conference series in the world. The symposium covers all aspects of separations and analyses carried out in liquid phase.

The goal of HPLC 2022 is to bring together scientists at all professional levels involved with all aspects of liquid-phase separations from fundamental research to practice, to provide a dynamic program with cutting-edge presentations and engaging scientific sessions, and to offer wide opportunities for training, networking, and informal discussion. Scientists and researchers will present the latest trends and issues in areas such as column technologies, 3D-printing, 2D-LC, capillary LC, micro- and nanofluidics, sample preparation, theory of the chromatographic separation processes, mass spectrometry detection, and a myriad of other topics related to liquid-phase separations and analyses.

July 11-15, 2022

Hands-on Data Analysis for Metabolic Profiling

Venue: London, UK

[Learn More Here](#)

Overview

This 5-day course provides a comprehensive overview of data analysis for metabolic profiling studies focusing on data from NMR spectroscopy and liquid chromatography-mass spectrometry. It combines lectures and tutorial sessions using open-source software to ensure a thorough understanding of the theory and practical applications.

July 15, 2022

Symposium: Stable Isotope-Resolved Metabolomics: From Bench to Bedside

Venue: Kentucky, USA

[Learn More Here](#)

Overview

Hear and meet speakers who use advanced techniques to investigate metabolism in different biological systems including the immune system, the brain, and cancer. There will also be poster sessions and exhibitor tables. Abstracts for posters are due June 30.



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

General Enquiries

info@metabolomicssociety.org

Membership Enquiries

membership@metabolomicssociety.org

August 5, 2022

MANA Early-Career Members (ECM) Virtual Job Fair

Venue: Online

[Learn More Here](#)

Overview

Hiring new members? Looking for a new position? Gathering information for the next step in your career? Join the ECM Virtual Job Fair!

As an employer or recruiter, you'll get the opportunity to meet potential candidates. As someone who is in the market, this is a great opportunity for you to meet potential employers from different tracks (i.e., Academia, Industry, or Government/Nonprofit). We will help employers and potential candidates meet effortlessly in a virtual capacity via Zoom! Using Breakout Rooms, we'll set up and manage interviews and/or informal meetings.

August 7-12, 2022

Gordon Research Conference on Lipidomics

Venue: Newry, Maine, USA

[Learn More Here](#)

Overview

In this Gordon Conference series, we will highlight recent developments in standardization, omics integration, and state-of-the-art technologies and their impact on applications to study human health and disease. The time is critical to set the future cornerstones in how to powerfully, adequately, and transparently define the lipidomics rules of new and existing platforms in basic research, and most importantly, in a regulatory environment. Overall, the future of lipidomics in the clinical and biological realms will be discussed at this conference, aligning with other ongoing consortia, with an anticipated active involvement of researchers across all important arenas (academic, industry, government) and different stages of their career (established and young scientists).

Applications for this meeting must be submitted by **July 10, 2022**. Apply early to avoid disappointment! The conference chair is currently developing their detailed program, which will include the complete meeting schedule, as well as the titles of talks for all speakers.

August 9, 2022

MANA SODAMeet

Venue: Online

[Learn More Here](#)

Overview

The goal of SODA is to provide a community-driven resource of actively-maintained software, test datasets used for software benchmarking, and results produced by software. SODAMeets is a platform where data generators and computational scientists can share their use of software/data. During SODAMeets (every 2 months), we will have two speakers present on software or data they would like to share with the community, emphasizing how these software/data are used.

August 22-September 2, 2022

International Summer Sessions in Metabolomics

Venue: Online or Davis, California, USA (Hybrid)

[Learn More Here](#)

Overview

This course at UC Davis has been completely redesigned for a hybrid format and will also be recorded for the participants to view at a later time. All software training has transitioned to a virtual machine environment so training can be done from any location. Virtual machines are hosted by Amazon Web Services and can be accessed using either a PC or a Mac computer. Every unit is taught using interactive tools such as polling, using the annotation tool, utilizing non-verbal feedback, live questions, and group work.

September 6-9, 2022

The 2nd Nordic Metabolomics Conference (2022)

Venue: Copenhagen, Denmark

[Learn More Here](#)

Overview

The conference aims to highlight and discuss the latest metabolomics research in the Nordic countries and abroad, and we are proud to present an outstanding scientific program. The meeting will start with a session dedicated to early-career scientists, followed by an opening keynote lecture and a welcome reception at Copenhagen Town Hall. We have invited outstanding speakers from Europe including the Nordic countries. The meeting will also host a panel debate and a session dedicated to our sponsors. The majority of talks will be based on submitted abstracts. Early-bird registration, abstract submission, and travel grant application submission deadline is June 30.

September 8-9, 2022

Bits & Bites #7: Identification of unknown compounds in untargeted metabolomics using freely available software

Venue: Online

[Learn More Here](#)

Overview

This 10-part short course series will feature in-depth topics in untargeted metabolomics such as Bayesian statistics, a deeper look into MS-DIAL, fundamental courses in mass spectrometry, lipidomics, and so many others. Each short course can be taken individually or you can select multiple Bites. Participants will gain a deeper insight into current software, methods, and pitfalls. Each session starts promptly at 9 a.m. (Pacific Time) and will take approx. 4 hours. The courses will be conducted in a highly interactive manner, with the use of freely available software and databases. The tuition is \$150 USD per Bite.

The 7th course is “Identification of unknown compounds in untargeted metabolomics using freely available software”, taught by Dr. Arpana Vaniya. Compound identification is known as the bottleneck in metabolomics. However, there are many approaches one may consider while tackling this challenge (e.g., mass spectral library search, *in silico* fragmentation tools, database searching). This short course will provide an overview of the current status of compound identification in metabolomics. Participants will learn how to use freely available *in silico* fragmentation tools MS-FINDER and SIRIUS+CSI:FingerID, and apply those skills to some unknown challenges.

In session 2, participants will continue learning additional tools and compound identification approaches. In this short course, participants will learn how to use web-based tools such as MetFrag and CFM-ID and learn how to use MassBank of North America in NIST MS Search. Participants will get a chance to practise on unknown challenges.

Take the Lead in Metabolomics with Agilent

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metabolomics research

[Learn more](#)



September 9-10, 2022

2022 World Endocrine & Obesity Conference

Venue: Online (no longer hybrid)

[Learn More Here](#)

Overview

The 2022 World Endocrine & Obesity Conference (2022WEOC) in collaboration with Thyroid Federation International is scheduled for September 9-10, 2022. Their focus is to bring together leading experts, researchers, and clinicians to exchange and share their experiences of various treatment procedures on endocrine care and obesity. Abstract submission is due June 30 and speaker registration is due July 15.

September 11-15, 2022

Metabolism in Action – From Genome to Function

Venue: Hillerød, Denmark

[Learn More Here](#)

Overview

The goal of this meeting is to bring together leading experts with the brightest post-doctoral and doctoral students, to create an inspiring, international, and open environment to explore the influence of molecular and tissue-specific regulation of metabolism.

September 16-18, 2022

4th Annual MANA Conference

Venue: Edmonton, Alberta, Canada

[Learn More Here](#)

Overview

The 4th Annual Conference of the Metabolomics Association of North America (MANA) will be hosted by the University of Alberta and The Metabolomics Innovation Centre (TMIC), and the organizers have developed an engaging preliminary program. Check out the website for program information, speakers, events, registration, awards, and more. Deadlines have been extended to July 8 for early-bird registration and oral abstract submission and July 22 for poster abstract submission.

October 14, 2022

4th MANA Fall Symposium

Venue: Online

[Learn More Here](#)

Overview

The 4th Fall Symposium of the Metabolomics Association of North America is entitled “We are what we eat: Metabolomics leading the way for nutritional research”.

October 24-28, 2022

EMBO Practical Course on Metabolomics Bioinformatics for Life Scientists

Venue: Wageningen, Netherlands

[Learn More Here](#)

Overview

This course will provide an overview of key issues that affect metabolomics studies, handling datasets and procedures for the analysis of metabolomics data using bioinformatics tools. It will be delivered using a mixture of lectures, computer-based practical sessions and interactive discussions. The course will provide a platform for discussion of the key questions and challenges in the field of metabolomics, from study design to metabolite identification. The application deadline is September 1.

October 25-27, 2022

2nd International Diabetes and Metabolic Surgery Summit

Venue: Tel Aviv, Israel

[Learn More Here](#)

Overview

The focus of IDMSS 2022 will be the relationship between obesity and type 2 diabetes and their associated complications and the beneficial results obtainable from metabolic/bariatric surgery. The Summit will bring together many of the world’s experts in the fields of metabolic surgery and medicine. The range and scope of the program are a must for all clinicians caring for patients suffering from metabolic diseases.

Metabolomics Jobs

If you have a job to post, please email the MetaboNews team at metabolomics.innovation@gmail.com.

Jobs Offered

Job Title	Employer	Location	Posted	Closes	Source
Postdoctoral Research Fellow in Metabolomics (Diabetes)	Lund University	Lund, Sweden	15-June-2022	Until filled	MetaboNews Jobs
Developer of Scientific / Bioinformatics applications for the Reprocessing of High Resolution Spectrometric Data	Oniris	Nantes, France	9-June-2022	7-July-2022	Laberca
Senior Research Associate in Mass Spectrometry	Chan Zuckerberg Biohub	Stanford, California, USA	27-May-2022	Until filled	CZ Biohub
Postdoctoral Research Fellow (Exometabolomics)	North Carolina State University	Raleigh, North Carolina, USA	13-May-2022	Until filled	North Carolina State University
Senior Associate Researcher in Mass Spectrometry	Icahn School of Medicine at Mount Sinai	New York City, New York, USA	6-May-2022	Until filled	Icahn School of Medicine at Mount Sinai
Postdoctoral Research Fellow	University of Alberta	Edmonton, Alberta, Canada	4-May-2022	Until filled	University of Alberta
Assistant Professor in Metabolomics of Adaptive Responses	University of California, Riverside	Riverside, California, USA	15-April-2022	Until filled	University of California, Riverside
Operations Manager (TMIC-The Metabolomics Innovation Centre)	University of Alberta	Edmonton, Alberta, Canada	14-April-2022	Until filled	University of Alberta
Research Technician (Mass Spectrometry)	University of Alberta	Edmonton, Alberta, Canada	5-April-2022	Until filled	University of Alberta
Postdoc in Mass Spectrometry	University of Alberta	Edmonton, Alberta, Canada	1-Mar-2022	Until filled	University of Alberta
Postdoc in Metabolomics/ Exposomics	University of Vienna	Vienna, Austria	4-Feb-2022	Until filled	University of Vienna

Jobs Offered

Job Title	Employer	Location	Posted	Closes	Source
Postdoctoral Research Associate (Sumner Lab)	University of North Carolina at Chapel Hill	Kannapolis, North Carolina, USA	12-Jan-2022	Until filled	University of North Carolina Careers
Various Positions	Various	Various (within North America)	Various	Various	Metabolomics Association of North America

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 the MetaboNews team at metabolomics.innovation@gmail.com. Upon review, a limited number of job submissions will be selected for publication in the Jobs Wanted section.

NEW

MEGA Assays for Rapid Metabolomics Analysis

Comprehensive *Quantitative* *LC-MS-based*

Highlights

- Fully quantitative
- High throughput (96-well plate compatible)
- Up to 21 chemical families, including:
 - Amino acids
 - Organic acids
 - Vitamins
 - Lipids

Clinical Biomarker Assay

- Quantifies up to 900 metabolites and ratios
- Validated for blood, serum and plasma

Microbiome Metabolism Assay

- Quantifies up to 900 metabolites and ratios in fecal material, and up to 350 metabolites and ratios in urine
- Validated for urine, fecal extract and more

The diagram illustrates a four-step workflow for metabolomics analysis. Step 1: 'SAMPLE REGISTRATION & PREPARATION' (20 MIN) involves a pipette and a 96-well plate. Step 2: 'SAMPLE MEASUREMENT' (5 HOURS) features an LC-MS instrument. Step 3: 'DATA PROCESSING & QUANTIFICATION' (36 HOURS) shows a chromatogram. Step 4: 'DATA PROCESSING & QUANTIFICATION' (2 HOURS) and 'DATA PROCESSING & QUANTIFICATION' (30 MIN) are represented by a clipboard icon.

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