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MetaboNews

This month in metabolomics

January, 2024
Vol 14, Issue 1

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

METABOLOMICS
SOCIETY

TMIC
The Metabolomics Innovation Centre

In This Issue

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- **María Eugenia Monge**

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Metabolomics Society News

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

Conference Corner

Happy New Year to the metabolomics community! We are busy planning the in-person conference in Osaka, at the ATC Hall located right on the bay. Join us in Japan, June 16-20, 2024, for plenary sessions, a busy exhibit hall with industry partners, a huge poster gallery, workshops, and over 25 scientific sessions!

Website: **www.metabolomics2024.org**
Hosted by: The Metabolomics Society
When: June 16 – 20, 2024

Abstract Submission- Now Open!

Abstract submission is now open. Submissions for oral abstracts will be accepted through March 7. Poster abstracts will continue to be accepted through May 16. Take a moment to review the webpage for abstract guidelines, themes, sub-topics and scoring rubric.

There are several Travel Awards available to support all types of participants. Review the details online before submitting your abstract, you might be eligible!

Conference registration will be available in the next couple of weeks.
Abstract Info: https://www.metabolomics2024.org/abstract-submissions

Sponsorship

The **Sponsorship Brochure** is available for Metabolomics 2024.

Sponsorship packages are still available. Visit the website to view the brochure and available packages. We expect the limited number of Platinum spots to be sold out soon, so don’t delay!

Members' Corner

Board of Directors

Dear Society Members,

I wish you all a very Happy New Year. I hope that 2024 will treat you well, bring happiness, peace and prosperity to you, your family and friends; especially so as we have another day to enjoy this leap year!

At our recent Board of Directors meeting, we discussed our Society Awards and this is our time to celebrate our successes and bestow honours to our most worth metabolomers. Regarding these awards, the nominations for our Metabolomics Society 2024 awards will be opened very soon (during February) on our website (https://metabolomicssociety.org). So, now is the time to think about nominating colleagues for consideration of these awards and brief details of each of these are provided below:

- An Honorary Fellowship is a significant lifetime award granted by the Society to exceptional members of our community. We normally award two of these per year. Nominees have either made outstanding contributions to the Metabolomics Society or have been recognised as making a pioneering and sustained contribution to the science of metabolomics.
- The Metabolomics Society Medal is for mid-career members of the society. This medal is open to those members who have been awarded a PhD 10-15 years prior to the closing date for nominations in each round. We usually award one of these medals per annum.
- The President’s Award again recognizes outstanding achievements in metabolomics. This time for those earlier in their careers and is for Society members who have been awarded a PhD no more than 5-10 years prior to the closing date prior to the closing date for nominations in each round. We usually award one President’s Award per annum.

Please get thinking about nominations!!!

When you visit our society website you will notice a nice new look. Many thanks to Rick Dunn as chair of the Website & Communications Committee and to Leslie and her SnapIT team for the coordination and delivery of this revamp – I hope you like it.

Those of you who were in Niagara Falls will remember that last year’s Honorary Fellows gave plenary lectures at our annual meeting. I am certainly looking forward to hearing the latest developments in metabolomics from Jules Griffin and Pieter Dorrestein in Osaka. In addition, we hope that this year's recipients of the Society Medal and The President's Award awardees will be able to present their work as keynote speakers during this conference.

I hope you are making your travel plans to Japan and remembering to check any visa requirements that you may need. Note: Japan visa is only valid for 3 months, so you should not apply before middle March. If you apply sooner, your visa will be expired before the conference in June.

Details of the meeting and travel are available here: https://www.metabolomics2024.org and more local details on visa here: https://www.mofa.go.jp/j_info/visit/visa/short/novisa.html
I hope to see you in June.

That's all the news for January. All the Board of Directors hope you have a great leap year!

All the very best.

Roy Goodacre, University of Liverpool, UK

President, Metabolomics Society

CanMetCon
Canadian Metabolomics Conference
Save the Date!!!
5th Annual Canadian Metabolomics Conference 2024
"Integrating metabolomics with other omics"
Date : Thursday, 25 April 2024 - Friday, 26 April 2024
Venue : Jack Poole Hall
University of British Columbia, Vancouver, BC
TMIC
The Metabolomics Innovation Centre
UBC THE UNIVERSITY OF BRITISH COLUMBIA

We are delighted to extend an invitation for you to participate at the 5th Annual Canadian Metabolomics Conference (CanMetCon 2024), scheduled for Thursday, 25 April to Friday, 26 April 2024, at the Jack Poole Hall, The University of British Columbia, Vancouver, BC, co-hosted by The Metabolomics Innovation Centre (TMIC) and the UBC Department of

Chemistry.

This year's conference is themed "Integrating Metabolomics with Other Omics", featuring four broad topics in the applications of Biological and Cellular Systems, Omics in Clinical Studies and Biomarker Discovery, Agricultural and Nutritional Applications, and Public Health and the Epigenome.
More information about the program is available here

Registration is open now! Important dates:

- Early Bird Registration deadline: **February 29, 2024**
- **Abstract Submission** Deadline: **March 15, 2024** to be considered for Oral Presentation, **March 22, 2024** for Posters
- Registration Deadline: **March 22, 2024**

Early bird registration fees are **CAD 150** for students and **CAD 250 plus applicable taxes and fees**. Your registration fee includes a welcome reception on April 25, breakfast and lunch on April 25–26, and light refreshments during morning and afternoon coffee breaks. See you in Vancouver!

International Affiliates' Corner

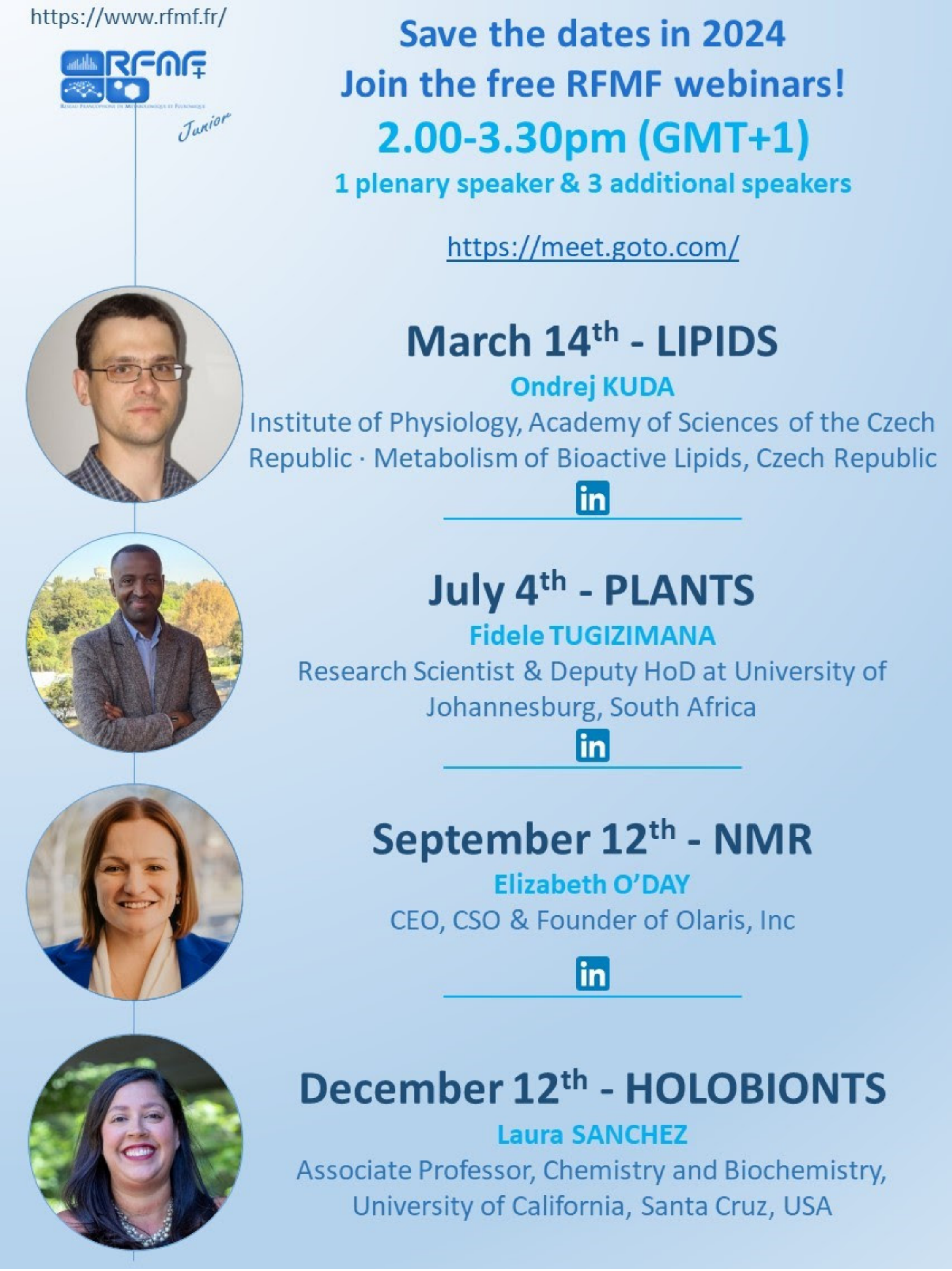
Réseau Français de Métabolomique et Fluxomique (RFMF)

Visit: http://www.rfmf.fr/

A network dedicated to providing financial support for conferences and training courses
One of the missions of the French-speaking Network of Metabolomics and Fluxomics is to promote access to conferences and training courses for international students and young researchers. In 2023, 17 travel grants were awarded, including 2 for attendance at the MetSoc meeting in Canada (Thomas Dussarrat, Nathan Carriot). In addition, 3 training grants have been offered to acquire new skills and expertise in analytical methods in metabolomics and fluxomics.

Keynote speakers for the 2024 RFMF webinars

On a different note, the keynote speakers for the RFMF webinars in 2024 have all confirmed their contributions. Four exciting sessions (2-3:30 pm, GMT+1) will focus on specific topics: 14 March on lipids (Ondrej KUDA), 4 July on plants (Fidele TUGIZIMANA), 12 September on NMR (Elizabeth O’DAY) and 12 December on holobionts (Laura SANCHEZ).



https://www.rfmf.fr/

Save the dates in 2024
Join the free RFMF webinars!
2.00-3.30pm (GMT+1)
1 plenary speaker & 3 additional speakers

https://meet.goto.com/

March 14th - LIPIDS
Ondrej KUDA
Institute of Physiology, Academy of Sciences of the Czech Republic · Metabolism of Bioactive Lipids, Czech Republic

July 4th - PLANTS
Fidele TUGIZIMANA
Research Scientist & Deputy HoD at University of Johannesburg, South Africa

September 12th - NMR
Elizabeth O’DAY
CEO, CSO & Founder of Olaris, Inc

December 12th - HOLOBIONTS
Laura SANCHEZ
Associate Professor, Chemistry and Biochemistry, University of California, Santa Cruz, USA

Metabolomics Association of North America (MANA)

Visit: https://metabolomicsna.org

In this New Year, MANA will enhance its efforts in DEIA and in prioritizing early career members, corporate members, and providing opportunities, through our conference and virtual events, that bring together the entire metabolomics community. MANA currently has 7 Interest Groups (Early Career Members, WomiX, Software and Data Exchange, Metabolomics in Precision Medicine, Microbiome, Metabolomics Core, and NMR) and updates to their activities are highlighted on our main website and newsletter. We encourage participation in these activities and please reach out to mana@metabolomicsna.org should you have any feedback, questions, or new ideas!

Also, a note to save the date for our next MANA conference, hosted by Tim Garrett (University of Florida) & John Koomen (Moffitt Cancer Center), to be held in Tampa, Florida, USA, on October 22-24th 2024. Stay tuned for abstract submission and registration details!

Netherlands Metabolomics Centre (NMC)

Visit: www.metabolomicscentre.nl/

February 29, Metabolomics & Fermented Foods 2024, Danone Nutricia, Utrecht

In September 2022 NMC organized the first edition of **Metabolomics & the Microbiome**, which was a great success! This second meeting on the 29th of February, is a follow-up and aims at broadening our knowledge and network in the field of **Metabolomics and**

Fermented Foods. We like to initiate an open discussion on how metabolomics is contributing to answering complex questions in the field of Fermented Foods concerning monitoring health and food safety issues. The main focus is mammalian health and food production.

Among the **eight excellent international keynote speakers from around Europe** are Paul Cotter (Teagasc Food Research Centre, IR), Barbara Korousic Seljak (JSI, SI), Kiran Raosaheb Patil (University of Cambrigde, UK), Corinna Dawid (TUM, DE), Julien Tap (INRAE, FR), Klaartje Houben (DSM-Frimenich), Christian Chervaux, (Danone Nutricia, FR) and Guus Roeselers (Danone Nutricia, NL) who is our host for the last day in February. We also will feature a **panel discussion** and a **poster session!**

Check the programme and the conference website. You can subscribe here. The poster deadline is the 12th of February! Questions concerning this event please contact: meike.bunger@health-ri.nl

Polish Society of Metabolomics

Visit: https://ptmet.pl/

The Polish Proteomics Society and the Polish Society of Metabolomics invite you to a lecture titled **"Decoding the chemical language of plants."** The lecture will be given by Tomáš Pluskal from the Institute of Organic Chemistry and Biochemistry of the Czech Academy of Sciences.

The online event will be held on **Thursday, February 8, 2024, at 4 pm CET** via the ZOOM platform.

Meeting details:

https://zoom.us/j/98182779464?pwd=S2x1RTR6cEtsK0N3cjB0SUE5WkRNdz09
Meeting ID: 981 8277 9464
Passcode: 345644

Please feel free to share the information with any colleagues who may be interested.

We are looking forward to your participation.

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MetaboInterview

María Eugenia Monge

Independent Researcher
Centro de Investigaciones en Bionanociencias/ Center for Bionanoscience Research (CIBION) – CONICET
https://cibion.conicet.gov.ar/

Biography

María Eugenia Monge is an Independent Researcher of the National Scientific and Technical Research Council of Argentina (CONICET) and works at the *Centro de Investigaciones en Bionanociencias* (CIBION). In 2006, she earned her Ph.D. in analytical and physical chemistry from the University of Buenos Aires. Between 2007 and 2014, she held postdoctoral positions in Italy, France, and the USA. In 2014, she was recruited by CONICET to set up a new laboratory in CIBION, which was a new research center in Argentina, where she leads the Bioanalytical Mass Spectrometry Group and the Mass Spectrometry facility. Her research group develops MS-based metabolomics and lipidomics analytical methods with applications in health and the environment. As well, her group contributes with pipelines for preprocessing LC-MS data for quality control procedures in untargeted workflows. She is co-author of >50 peer-reviewed publications.

Since 2014, she has coordinated hands-on metabolomics courses at CIBION for South American students, and has participated in strengthening the Latin American community through teaching in Brazil, Colombia, Mexico, and Argentina. In 2021, she became a Founding Member of LAMPS and has been instrumental in integrating this young network with the Metabolomics Society as an International Affiliate. Since 2019, she has been a member of the metabolomics quality assurance and quality control consortium (mQACC), and she has been a member of the Metabolomics Society. In 2022, she was awarded the Metabolomics Society Medal and was elected to the Society Board of Directors. She currently serves as co-chair of the Membership Committee and of the newly established LipidMet Task Group of the Metabolomics Society. Additionally, since 2022, she has been the vice-president of the Argentinean Mass Spectrometry Society. She has also contributed as a guest editor for the journal *Metabolites* and serves on the editorial board of *GigaByte*.

How did you get involved in metabolomics?

I got involved in this field in 2012, when I accepted the challenging offer to return to Argentina in 2014 to set up a new mass spectrometry (MS) laboratory at the Center for Bionanoscience Research (CIBION, created in 2012), with the goal in starting new research projects in a field that was underdeveloped in the country at that time. My recruitment was framed in a national scientific program that aimed to promote the return of Argentine researchers living abroad to develop new research lines in the country.

During my doctoral thesis, I studied gas-phase fingerprints provided by food flavors and essential oils released from polysaccharide gels using electronic noses in combination with chemometric tools, and I evaluated correlations between the release of volatile organic compounds and the rheological properties of the gels. Additionally, I characterized the chemical composition of the encapsulated flavors and the polysaccharides using GC-MS and MALDI-TOF-MS, respectively. During my doctoral studies, I conducted a stance at the Biophysical Institute of Palermo-CNR, Italy, and a stance at the University of Antwerp, Belgium. In 2006, I obtained my Ph.D. in Inorganic, Analytical, and Physical Chemistry from the University of Buenos Aires, Argentina. After my doctoral studies, I conducted a brief postdoctoral stance in the research group of Pier Luigi San Biagio at the Biophysical Institute of Palermo-CNR, Italy, to work with e-noses, chemometric tools, and GC-MS. Between 2008 and 2011, I held a postdoctoral position in the research group of Christian George at IRCELYON-CNRS, France, to study photoinduced transformations of atmospheric aerosol particles using mass spectrometry. In 2010, I was offered the possibility of returning to Argentina and joining the research staff of CIBION to start a research group in a scientific field that was new to my country. Therefore, in 2012, I moved from France to the USA to work for 2 years as a research scientist in the group of Facundo Fernández at the Georgia Institute of Technology. There, I applied UPLC-HRMS, UPLC-QqQ-MS, UPLC-TWIMS-HRMS, and ambient-MS instrumentation to address different biological questions in the field of mass spectrometry-based metabolomics for biomarker discovery as well as to develop quantitative methods for biological and pharmaceutical sample analyses. At Georgia Tech, I also served as co-advisor of a Ph.D. student. In 2013, I applied for a research staff position at CONICET (the National Scientific and Technical Research Council of Argentina) and returned to Argentina in January 2014. That same month, I started setting-up my new lab at CIBION, and in May 2014, my daughter Maite was born on my birthday.

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

Some of the most exciting aspects of my work in metabolomics include being the mentor of an interdisciplinary group, and training students and postdocs with no previous knowledge in mass spectrometry or metabolomics, but with a solid background in analytical chemistry, biochemistry, biology, or computing science. This gives me the possibility of sharing my passion for science, and my belief that MS-based technologies can be transformative for disease diagnosis and contribute to global health equity.

One of the goals of my research group is to develop alternative analytical strategies to improve the performance of existing diagnosis and prognosis methods that are currently implemented in the clinics and to understand altered pathways in disease progression. To achieve our goals, we collaborate with a biobanking system and three hospitals in Buenos Aires. Our initial untargeted metabolomics efforts focused on clear cell renal cell carcinoma (ccRCC) biomarker discovery and the understanding of disease pathophysiology. Findings from my group provided a proof of concept that conditioned media can be used as a serum proxy to obtain disease-related metabolic signatures; and we validated results from metabolic profiling experiments targeting the endometabolome of *in vitro* models with biological and bioinformatics assays. In addition, we obtained lipid panels for ccRCC detection and early diagnosis through an untargeted serum lipidomics-machine learning strategy. As well, metabolic and lipid fingerprints differentiated phenotypes associated with metabolic restoration after surgery, representing a serum signature of metabolic phenoreversion toward a healthy metabolic state. Based on these results, we are currently exploring new high-throughput analytical methods for ccRCC detection. Another ongoing project is focused on improving prostate cancer detection by evaluating findings from previous biomarker discovery studies on an Argentine cohort. My team has also developed quantitative targeted assays to contribute to the diagnosis of pediatric endocrine disorders, to address the limited specificity of immunoassays, which is the gold standard technique currently used in Argentina. The developed methods have been translated to the clinical setting in public hospitals in the country, and we have been involved in staff training to achieve the translation.

Furthermore, my research group is continuously updating and expanding the capabilities of TidyMS, a Python-based package for preprocessing LC-MS data for quality control procedures in untargeted metabolomics workflows. In this sense, we are working on additional open tools within TidyMS to facilitate ambient MS data processing.

With the workflows and procedures developed in my group, we have expanded into other untargeted and semi-targeted metabolomics collaborations with several colleagues, and we are moving beyond biomarker discovery toward the understanding of biochemical mechanisms to answer different biological questions. In this sense, we are applying pharmacometabolomics strategies for assessing new antivirals for dengue and chikungunya; and we aim to enhance our understanding of dengue biology in the South American population, where the disease is endemic. In a different interdisciplinary project in collaboration with IBioBA-CONICET-Max Planck Society Partner, we are in search of the neuronal metabolome by investigating the effect of different stimuli on neurons from animal models to extend results to different models of the nervous system. In addition, my group collaborates to investigate the metabolic reprogramming of macrophages induced by macrophage-trophoblast interactions during the early stages of gestation using semi-targeted and untargeted metabolomics strategies.

As well, my research group has also participated in the ring trial for ceramide quantitation in human plasma reference materials, which was led by the Singapore Lipidomics Incubator and the National University of Singapore.

Dr. María Eugenia Monge´s research group members. The top, left-corner picture also includes Dr. Bronzel, an invited researcher from NuBBE-IQ-UNESP, Brazil.

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

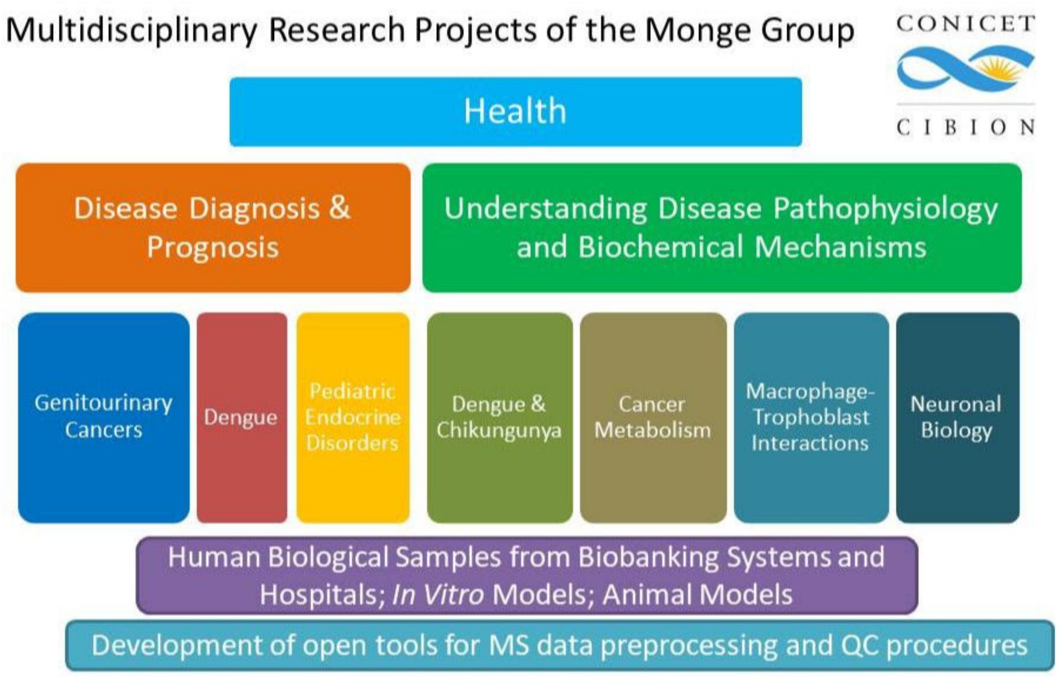
One of the goals of CIBION is to develop alternative analytical strategies to improve the performance of existing diagnosis and prognosis methods that are currently implemented in the clinics. In this sense, we have different ongoing projects in the oncometabolomics field, mainly focused on the study of genitourinary tumors, which are feasible based on strong collaborations with national health centers and biobanking systems.

In addition, my research group collaborates with the Medicinal Chemistry Group of CIBION, led by Dr. Mariela Bollini, to investigate dengue and chikungunya diseases and treatment, with a combined pharmacometabolomics and biomarker discovery approach, using untargeted and semi-targeted approaches in combination with the design of new open tools for data processing.

As well, within CIBION we aim to train new staff on MS techniques and MS-based methods to be translated into the clinical setting. My group is involved in several collaborative projects with other national academic institutions to apply metabolomics workflows to address health-related scientific questions in the fields of cancer metabolism, immunometabolism, and molecular neurobiology, using in vitro and in vivo models.

In addition, my team collaborates with the group of Dr. Pablo Hoijemberg, who leads the Bioanalytical NMR lab at CIBION, to address biological questions with metabolomics strategies using two complementary technologies.

At the regional level, my group collaborates with the research groups of Dr. Ian Castro-Gamboa, UNESP-Brazil, and Dr. Mónica Cala, MetCore-UniAndes, Colombia, to train students and postdocs on this research field as well as to harmonize quality control procedures.



Research Projects at Monge Group, CIBION-CONICET

What is happening in Argentina in terms of metabolomics?

As I mentioned above, I was recruited by the CONICET to address health-related scientific questions through MS-based metabolomics, which was a new research field for the country in 2014. Since then, I have been able to set up a new mass spectrometry laboratory for bioanalytical applications in a recently created center and train students and postdocs in an emerging field in Argentina. Since then, I have been able to set up a new mass spectrometry laboratory for bioanalytical applications and train students and postdocs in an emerging field in Argentina.

From my perspective, technological developments utilized in metabolomics have not been distributed or shared equally worldwide. Since my return to Argentina in 2014, I have actively engaged in coordinating and instructing metabolomics courses for South American students. Additionally, I have contributed to promoting the understanding and benefits of metabolomics across various Latin American countries, aiming to broaden and reinforce the South American community. In line with this mission, I am privileged to be a Founding Member of the Latin American Metabolic Profiling Society (LAMPS), established in 2020. LAMPS is a young network that pursues strengthening collaborations across the continent as well as promoting emerging technologies and practices that help to make science more reproducible and open. Since 2019, I have also been a member of the Metabolomics Society Membership Committee, to contribute to designing and implementing strategies for increasing the representation of the South American community in the Society.

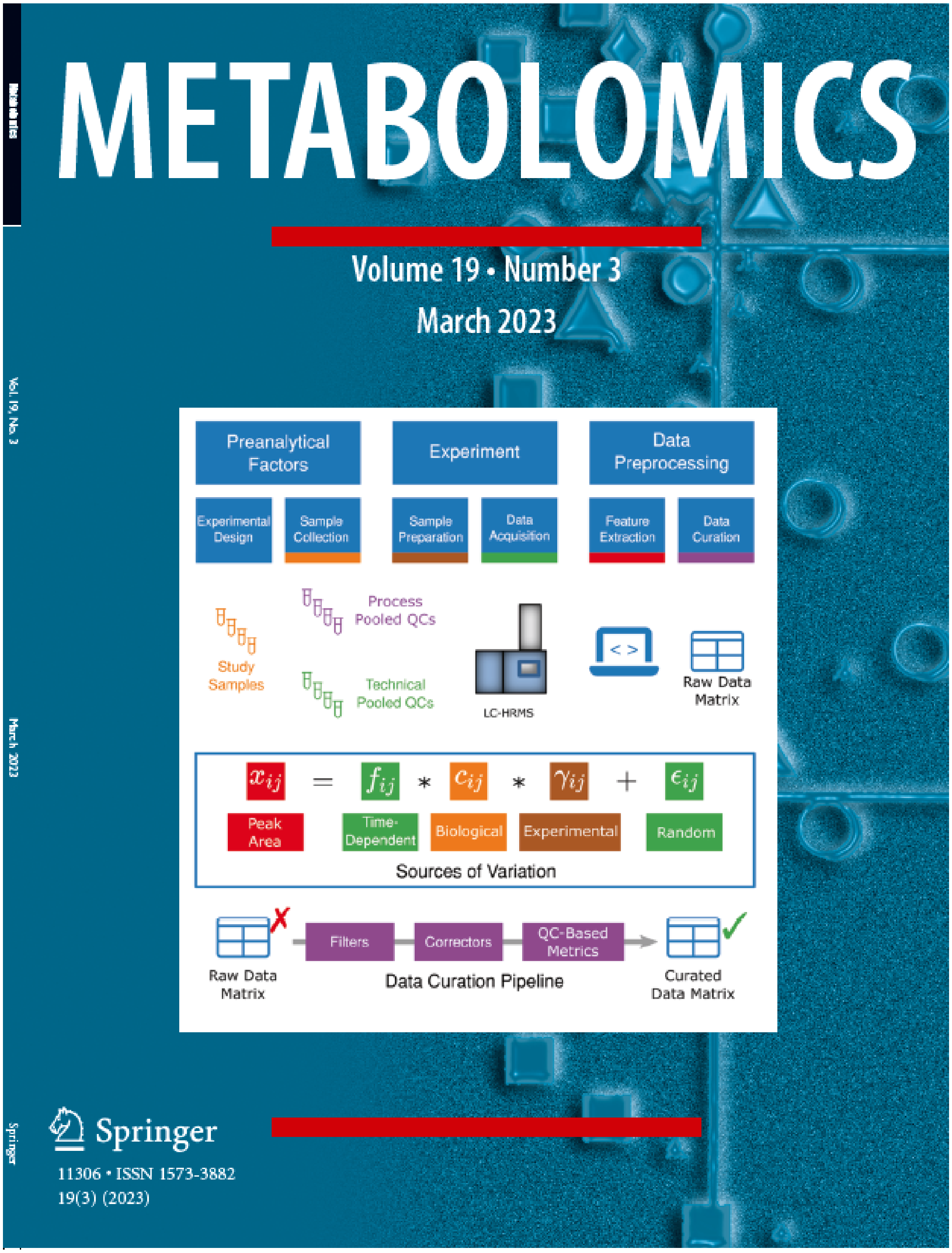
This month marks the 10th anniversary of my lab at CIBION. I am very proud of having served as a mentor for Ph.D. students, postdocs, and technicians, as well as visiting researchers and students from Europe and South America, and for the national and international awards that my group has received, which has become a reference in Latin America in the field. As well, I am also proud of having provided more than 90 services to our local industry and academia in the frame of the MS Facility that I lead at CIBION. As Vice president of the Argentine Mass Spectrometry Society, I will organize this year the V Argentine Mass Spectrometry Conference, which will have a dedicated session to highlight results from metabolomics projects conducted in the country and the region.

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

I see my work in metabolomics as a powerful tool to improve our current understanding of alterations in metabolic pathways in living organisms and models; to connect the phenotypes with health and disease statuses; to contribute to drug discovery; to improve clinical readouts. My work has also provided tools to bridge marine and atmospheric chemistry, which directly impact air quality, climate change, and human health.

I envision that metabolite panels are promising for translating metabolomics research into clinical applications, particularly as diagnostic and prognostic tools, with the potential to change the current diagnostic paradigm. In addition, ambient and direct-to-mass spectrometry (MS) methods combined with machine learning techniques have the potential to offer molecular diagnosis methods in the clinical setting globally. I also foresee technologies becoming faster and more cost-effective for *in situ* use, thereby contributing to global health equity. Moreover, I anticipate an increased number of international collaboration initiatives aimed at validating results across different laboratories through standardized quality control practices, which will further advance this field. I am particularly optimistic about the prospects in South America, where I expect growth in the metabolomics field, increased access to technological advancements, and substantial contributions from this region. In this context, collaborative initiatives are likely to create mutually beneficial opportunities.

About my research group, we are expanding our analytical platforms, which would allow us to tackle new scientific questions and challenges with more sophisticated and complementary technologies. In addition, we are expanding the capabilities of open and free data processing tools within TidyMS, and hope to continue contributing to the national, regional, and international metabolomics community.



Cover of the *Metabolomics* issue 11306/19/3 that illustrates a recent contribution from the Monge team (Riquelme, G., et al.)

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

Among the greatest strengths of metabolomics, I would include the collection of biochemically-based fingerprints of diagnostic, prognostic, or classification value; the identification of potential biomarkers that reflect actual biological processes; the fact that it is not necessary to have the genome sequence of all of the organisms involved in the study; the possibility of using biofluids collected noninvasively or minimally invasively for diagnosing or studying human disease; the possibility of analyzing time-dependent metabolic patterns of change in response to disease, drug effects, or other stimuli to be measured; the possibility to contribute to precision medicine. In addition, I consider very valuable the efforts of the metabolomics community toward producing transparent and reproducible science.

What do you see as the greatest barriers for metabolomics?

In my opinion, the greatest barriers are associated with limited replication and validation studies, mainly in the sub-field of biomarker discovery. Potential biomarker candidates suggested by different research groups should be validated in independent sample sets and compared through interlaboratory studies in larger and different cohorts using QA/QC practices established by the community before possible translation to the clinic. As well, biobanks are required worldwide to collect samples from individuals with different ethnicity, gender, and geographical regions, using standard operating procedures. Data pre-processing and processing steps should be clearly reported, and confidence levels of identified features in untargeted studies should be indicated to allow further validation of results and interpretation of disease biology. Finally, data should be shared on public repositories such as MetaboLights or Metabolomics Workbench, to comply with the minimum standards of reporting scientific research and follow the principles of FAIR (Findable, Accessible, Interoperable, and Reusable) to enrich the metabolomics community and allow for future data analysis. In low and middle-income countries, I consider that financial support, training in the use of sophisticated analytical platforms, and collaborative initiatives overseas are needed to move the field forward.

What improvements, technological or otherwise, need to take place for metabolomics to really take off?

I think that metabolomics is rapidly advancing in developed countries. However, it faces challenges, particularly in the use of standards for harmonization and validation of results. The metabolomics community is expanding quickly, and this growth needs to be supported by a solid consensus on best practices and reporting standards. In particular, mass spectrometry (MS) technologies and commercial software packages are becoming increasingly accessible to professionals from various fields. However, in my opinion, despite these advancements, it is crucial to maintain synergistic communication among analytical chemists, mass spectrometrists, bioinformaticians, biochemists, medical doctors, epidemiologists, and professionals with different expertise for producing data that is both usable and interpretable.

The Metabolomics Standards Initiative and more recently the metabolomics QA and QC consortium (mQACC) and the Lipidomics Standards Initiative are addressing the need for improved standards. In particular, I believe that mQACC is making a great contribution to the community with its outputs.

In addition, I think that the lipidomics and the metabolomics community should increase their communication in terms of analytical strategies, optimization, and harmonization of workflows for comprehensive coverage of metabolites and lipids, as well as bioinformatics tools. In this sense, I'm serving as co-chair of the recently created LipidMet Task Group of the Metabolomics Society, which is chaired by Dr. Maria Fedorova, who is a leader in the lipidomics field, to achieve these goals.

The scenario in South America is different since technological developments have not been equally distributed worldwide. However, I am optimistic about future contributions from this region. I believe that collaborative and international initiatives focused on training and research can lead to mutually beneficial opportunities. In this context, the LAMPS community has shown significant growth since its inaugural meeting in Lima, Peru, in 2014. Currently, we have 141 LAMPS members, and since 2023, we have broadened our initiatives to include virtual seminars and a virtual podium, in addition to our biannual in-person conferences. This year, the V LAMPS Meeting, which is a key metabolomics event in our region, will take place in Montevideo, Uruguay, from October 30 to November 1st. The event aims to foster and strengthen continental collaborations, highlight emerging technologies, and discuss practices that improve reproducibility and advance open science. As a member of the Scientific Organizing Committee of the V LAMPS Meeting, I envision a successful event with the attendance of students and young researchers from various countries in our region, and the participation of invited speakers from around the world who will help to build new networks in the region.

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

In low and middle-income countries, funding constraints for metabolomics research affect the speed of development in this field. Specifically, in Argentina, access to cutting-edge instrumentation is limited, and there is a shortage of trained personnel. Additionally, the cost of maintaining such instrumentation is considerably higher compared to developed countries. We have outlined some of these local and regional challenges in our LAMPS charter.

What role can metabolomics standards play?

Standards play a crucial role in overcoming some of the present barriers that I have previously described. They would allow replication and validation of results and translation of discoveries to the clinical setting. Validation of results in independent sample sets and through interlaboratory comparisons using QA and QC practices is required. These actions combined with data sharing would also support the reproducibility of results and transparency.

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

I believe that metabolomics technologies have the potential to revolutionize disease diagnosis and prognosis, significantly contributing to global health equity and precision medicine. The use of metabolite panels or fingerprints is promising in translating metabolomics findings into the clinical setting. This approach may change the current diagnostic paradigm.

Looking ahead, I anticipate a deeper understanding of how metabolites of microbial origin impact disease diagnosis. Furthermore, I think that mass spectrometry (MS) techniques could offer more accurate assessments of tumor margins compared to traditional histological methods. This advancement may introduce molecular-based diagnostic alternatives that could be globally implemented in clinical settings, especially when integrated with machine learning methods. Additionally, the development of portable technologies will allow studying additional biological systems, enhancing our capabilities in different research areas.

I am convinced that this is an exciting field that allows broadening our knowledge by addressing biological problems through a synergistic approach constructed with interdisciplinary teams. Personally, I hope that the Latin American region will continue growing in the field, and I really appreciate having had this opportunity to share my thoughts.

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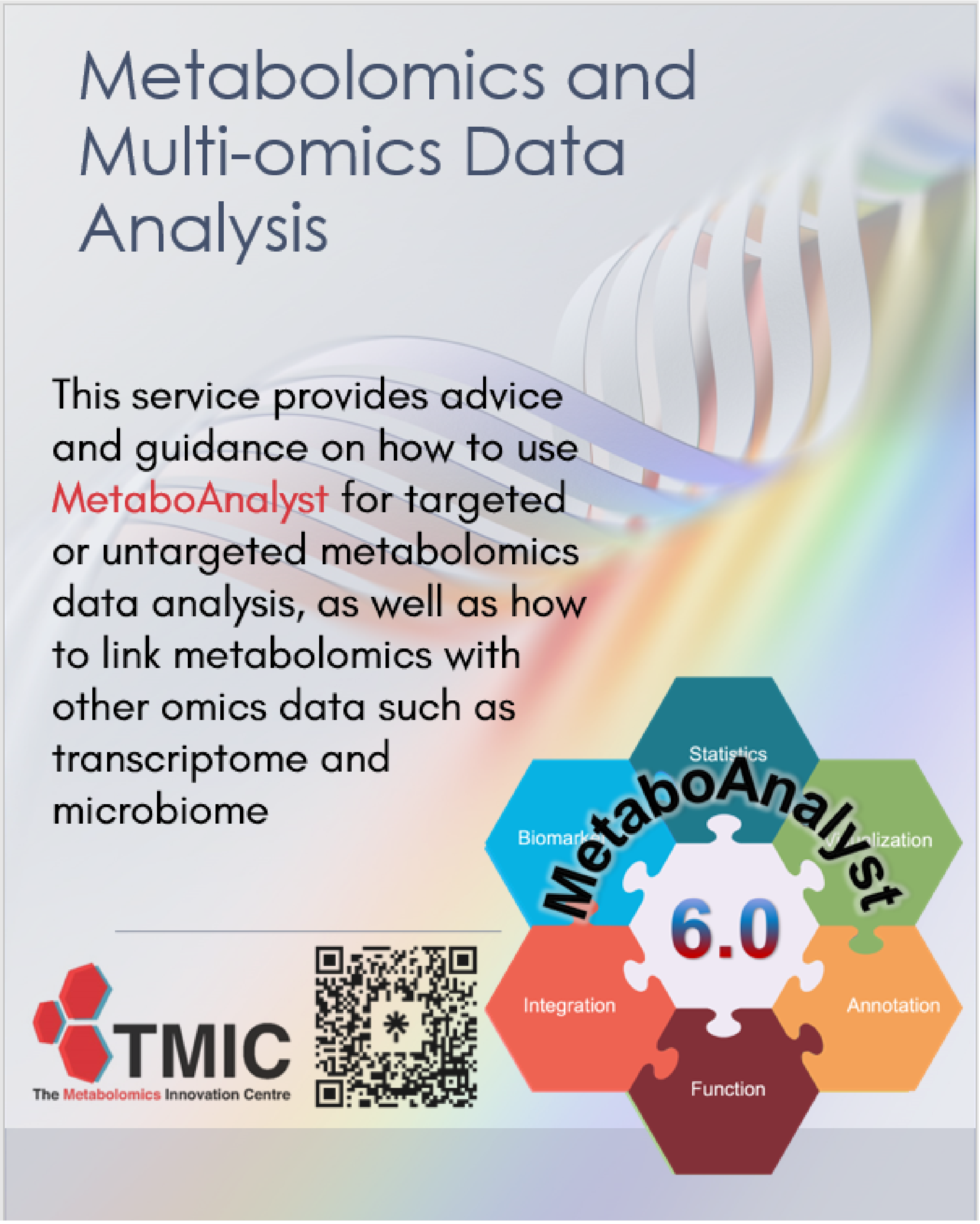

Metabolomics and Multi-omics Data Analysis

This service provides advice and guidance on how to use MetaboAnalyst for targeted or untargeted metabolomics data analysis, as well as how to link metabolomics with other omics data such as transcriptome and microbiome

TMIC

The Metabolomics Innovation Centre

Recent Publications

Reviews:

- Atlas of fetal metabolism during mid-to-late gestation and diabetic pregnancy (Open access)

- Current Practices in LC-MS Untargeted Metabolomics: A Scoping Review on the Use of Pooled Quality Control Samples (Open access)
- Mass spectrometry-based single-cell lipidomics: Advancements, challenges, and the path forward

Articles:

- Adaptive response of triploid Fujian oyster (Crassostrea angulata) to nanoplastic stress: Insights from physiological, metabolomic, and microbial community analyses
- Analysis of gut microbiome, host genetics, and plasma metabolites reveals gut microbiome-host interactions in the Japanese population (Open access)
- Chemical Composition of Commercial Cannabis (Open access)
- Combining stable isotope, multielement and untargeted metabolomics with chemometrics to discriminate the geographical origins of ginger (Zingiber officinale Roscoe)
- Controlling pre-analytical process in human serum/plasma metabolomics
- Current status and advances in untargeted LC-MS tissue lipidomics studies in cardiovascular health
- EISA-EXPOSOME: One Highly Sensitive and Autonomous Exposomic Platform with Enhanced in-Source Fragmentation/Annotation
- Fast mass spectrometry search and clustering of untargeted metabolomics data
- Identification of blood metabolites associated with risk of Alzheimer's disease by integrating genomics and metabolomics data
- Integrated spatial transcriptomics and lipidomics of precursor lesions of pancreatic cancer identifies enrichment of long chain sulfatide biosynthesis as an early metabolic alteration
- Machine learning model for predicting age in healthy individuals using age-related gut microbes and urine metabolites (Open access)
- Metabolic biomarkers using nuclear magnetic resonance metabolomics assay for the prediction of aging-related disease risk and mortality: a prospective, longitudinal, observational, cohort study based on the UK Biobank
- Metabolomic Biomarker Signatures for Bipolar and Unipolar Depression (Open access)
- Plasmid-encoded toxin defence mediates mutualistic microbial interactions (Open access)
- Unbiased Single-Cell Sequencing of Hematopoietic and Immune Cells from Aplastic Anemia Reveals the Contributors of Hematopoiesis Failure and Dysfunctional Immune Regulation (Open access)

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Metabolomics Events

Bits & Bites # 01: Mastering Lipidomics: From Biology to Advanced Techniques

January 25, 2024

Venue: Online

Bits & Bites 2024 is a flexible learning experience tailored for busy researchers seeking condensed yet impactful sessions. Now in its fourth year, this series continues to bridge the gap for those unable to commit to 1- or 2-week intensive courses.

10-part short course series will feature in-depth topics in untargeted metabolomics such as mass spectrometry applications, mass spectrometry imaging, statistics with both MetaboAnalyst and R, GNPS, MS-DIAL, 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 approximately 4 hours. The
courses will be conducted in a highly interactive manner, with the use of freely available software and databases. The tuition is $175 USD per Bite, except for #10. The tuition for #10 is $350 USD as it will take approximately 8 hours.

This 1st course (for 2024) is taught by Dr. Tong Shen from UC Davis and no prior knowledge or software is required. In this short course, the focus will be on lipidomics, where systems-level lipid analysis will be covered through practical case studies. The course will explore mass spectrometry-based lipid analysis, encompassing advanced separation techniques and emerging technologies. Throughout, best practices for the entire experimental pipeline will be provided—from crafting experimental designs and sample extraction to emphasizing the crucial role of quality control. This ensures the reliability and accuracy of lipidomics research, offering a practical and comprehensive learning experience.

Check for more details

Bits & Bites # 02: Mass Spectrometry for Metabolomics

February 8, 2024

Venue: Online

This 2nd course (for 2024) is taught by Dr. Uri Keshet from UC Davis, and no prior knowledge or software is required. Mass spectrometry (MS) holds a crucial role in metabolomics, being one of the most widely used analytical techniques in the field. In this comprehensive yet short course, participants will cover various MS systems and models like TOF, QQQ, and Orbitrap, understanding their application in metabolomics. Participants will also learn how to make informed decisions when selecting the right MS instrument, method, and parameters tailored to their research needs. Lastly, participants will gain practical insights on how to optimize their workflow with tips and tricks for developing high-throughput MS methods, such as a short 5-minute method, designed for practical use in metabolomics research

Check for more details

MANA SODAMeet

February 13, 2024

Venue: Online

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), two speakers will present on software or data they would like to share with the community, emphasizing how these software/data are used. Speakers will be requested to fill out a form on our SODA website so that we collect relevant information on these software/data presented.

Join the web seminar

World Critical Care and Anesthesiology Conference 2024 (WCAC24)

March 09 – 10, 2024

Venue: Bangkok, Thailand

World Critical Care and Anesthesiology Conference 2024 (WCAC24) is the 6th Edition educational event which is designed to advance knowledge and expertise in critical care and anesthesiology that rotates between continents and is organized in collaboration with national and international Anesthesiology and Critical Care societies and associations. The conference is targeted to the international Critical Care Medicine community as well as other healthcare professionals involved in multidisciplinary critical care surgical challenges; For every community, there continues to be a need for surgical and medical teams to evaluate and treat severely injured patients. Check out more information at the conference website.

- Speaker and Presenter's Registration Deadline extended: **January 30, 2024**

Learn More Here

Computational Mass Spectrometry Workshop

April 15 – 17, 2024

Venue: in-person, IOCB Prague, Czech Republic

Focused on non-target LC-MS metabolomics data processing, this workshop is suited for beginners, expert users, and software developers. The workshop aims for a high percentage of hands-on lectures, and registration is **free of charge.**

Register by January 31, 2024

5th Annual Canadian Metabolomics Conference (CanMetCon) 2024

April 25 – 26, 2024

Venue: Vancouver, Canada

The 5th Annual Canadian Metabolomics Conference (CanMetCon) 2024 will be held in April 25-26, 2024 at the University of British Columbia, Vancouver, BC, Canada. This year, the conference presents an exciting two-day agenda: Day 1 is dedicated to "Metabolomics Technology and Integration", offering deep dives into the latest advancements and methodologies, while Day 2 focuses on "Multiomics and Applications". Registration for the conference is open, inviting researchers, students, and professionals to join this vibrant gathering of the metabolomics community!

Important dates:

- Early Bird Registration deadline: **February 29, 2024**
- Abstract Submission Deadline: **March 15, 2024** to be considered for Oral Presentation **March 22, 2024** for Posters
- Registration Deadline: **March 22, 2024**

Early bird registration fees are CAD 150 for students and CAD 250 plus applicable taxes and fees. Your registration fee includes a welcome reception on April 25, breakfast and lunch on April 25–26, and light refreshments during morning and afternoon coffee breaks.

Check out our updated conference program here.

Register now

EMBL-EBI Introduction to Metabolomics Analysis

May 14 – 17, 2024

Venue: European Bioinformatics Institute, United Kingdom

This course will provide an introduction to metabolomics through lectures and hands-on sessions, using publicly available data, software, and tools. Participants will become familiar with standardised workflows as well as with the current state of experimental design, data acquisition (LC-MS, MS imaging), processing, and modelling. In addition, they will learn about community standards and sharing in metabolomics, particularly through the use of EMBL-EBI's MetaboLights repository and Galaxy infrastructure. Participants will learn through hands-on tutorials to use tools available for data analysis and data submission. Additionally, case studies will be discussed to show how to employ the week's learning.

Applications close on **January 28, 2024.**

Learn more and apply now

20th Annual Conference of the Metabolomics Society

Metabolomics 2024

June 16 – 20, 2024

Venue: Osaka, Japan

20th Annual International Metabolomics Conference of the Metabolomics Society will be held on June 16-20, 2024 in Osaka, Japan. Save the upcoming dates:

- Abstract submission is open
- Oral Abstract deadline: March 7, 2024
- Poster Abstract deadline: May 16, 2024

Scientists in academia, government, industry, and others working in the field of metabolomics are invited to submit abstracts in the following scientific themes:

- Metabolomics in Human Health and Disease
- Plants, Food, Environment and Microbes
- Technology Advancements
- Computational Metabolomics, Statistics & Bioinformatics
- Industry Spotlight: Metabolomics in Pharma and Biotech

Learn more here

16th Mass Spectrometry School in Biotechnology and Medicine

July 7 – 13, 2024

Venue: Dubrovnik, Croatia

The MSBM program is taught through a combination of lectures, workshops and tutorials. It is suitable for attendees from a wide variety of backgrounds, and the standard core syllabus covered every year is as follows:

- Mass spectrometry basics
- Introductions to main classes of mass analysers – ToF, ion traps, quadrupoles, FTMS etc.
- Ionization sources – ESI, MALDI etc.
- Ion mobility
- Separations methods – LC, CE, HILIC, fractionation etc.
- Tandem MS – CID, ECD, UVPD, SRM, MSM, DDA, DIA etc.
- Mass spectrometry systems – e.g. LC-ESI-QToF, IMS-MSMS etc.
- Proteomics – bottom-up, top-down, quantitative etc.
- Other omics – lipidomics, metabolomics, glyomics etc.
- MS data processing and Informatics

Registration is open now and will close on **June 12, 2024.**
For more information, please visit msbm.org or send an email to msbm.dubrovnik@gmail.com

Learn more here

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NIST SRM 1950 Beyond the Certificate of Analysis: mQACC Call to Provide Qualitative and Quantitative Data

Certified reference materials (CRM) values provide a known and standardized reference point against which the results of a metabolomic study can be compared. However, the certification of hundreds of individual metabolites is a cumbersome and time-consuming process. The Standard Reference Material (SRM) 1950, Metabolites in Frozen Human Plasma, is by far the most used reference material by the metabolomics community. NIST SRM 1950 provides certified and/or reference values for select metabolites and lipids such as fatty acids, electrolytes, vitamins, hormones, and amino acids. The metabolomics community would greatly benefit from consensus values and identification of metabolites and lipids in SRM 1950 that are not tied to a single analytical platform or method. This increases the accuracy, reliability, harmonization, and meaningful comparisons of metabolomic studies utilizing the material. Additionally, having more values and information available for SRM 1950 metabolites and lipids would allow researchers to investigate a broader range of analytes in their studies, which in turn could lead to a better understanding of the underlying biology of the metabolic processes. To that end, the Reference and Test Materials Working Group of mQACC is actively collecting information on qualitative identifications and quantitative values of metabolites and lipids in NIST SRM 1950 beyond those listed on the NIST Certificate of Analysis. Any data from instrumental platforms with compound identification (LC-MS, GC-MS, NMR) are welcome to participate. The data was combined in order to produce a publicly available database of community-generated 1) consensus concentration values for quantified metabolites and lipids of critical interest within the community and 2) compounds identified but not quantified in SRM 1950.

More information and an example reporting form can be found at https://www.mqacc.org/srm1950

Metabolomics Jobs

Metabolomics Jobs

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

We may remove a listing after 6 months if we do not receive a confirmation that it is still necessary. However, if you would like us to repost it, please contact us.

Job Title	Employer	Location	Source
Experimental Officer in Metabolomics	School of Biosciences, University of Birmingham	Edgbaston, Birmingham, UK	Metabolomics Society
Canada Research Chair (CRC) Tier 2 in Metabolomics	Schulich School of Medicine and Dentistry, Western University	London, ON, Canada	Western University
Chemical Biologist/Ecologist	The Monell Chemical Senses Center	Philadelphia, PA, USA	The Monell Chemical Senses Center
ORISE Postdoctoral Fellowship in Pharmacology/Toxicology	National Center for Toxicological Research U.S. Food and Drug Administration	Jefferson, AR, USA	Metabolomics Society
ORISE Postdoctoral Fellowship in Neuroscience/ Neurotoxicology	National Center for Toxicological Research U.S. Food and Drug Administration	Jefferson, AR, USA	Metabolomics Society
Post-Doctoral Fellow	Department of Medical Microbiology & Immunology, University of Alberta	Edmonton, AB, Canada	University of Alberta Careers
Operations Assistant	NovaMT and TMIC Li Node at the University of Alberta	Edmonton, Alberta, Canada	Dr. Liang Li (please contact liang.li@ualberta.ca)
Postdoctoral Research Fellow (LC-MS and Data Science for Metabolomics)	The Li Lab and the Li Node of TMIC, University of Alberta	Edmonton, Alberta, Canada	University of Alberta

MetaboNews Feedback Form

Thank you for being a part of MetaboNews! Your input means a lot to us, and we're eager to hear your thoughts on how we can improve our newsletter. We've put together a brief, anonymous survey with just two mandatory questions that won't take more than a minute of your time. Your feedback is invaluable, so please take a moment to share your opinions with us.

[Fill Out Your Survey Here]

If you have any questions, don't hesitate to contact us at metabolomics.innovation@gmail.com

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Our mailing address is:
metabolomics.innovation@gmail.com