Metabo News

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http://www.metabonews.ca/archive.html

Metabolomics Society News

Members' Corner

Board of Directors: Message from Roy Goodacre, President

Dear Society Members,

I hope this finds you all well.

This is my first time writing this and as the new President, I am looking forward to serving the Metabolomics Society. I also look forward to your support over the next couple of years and to hearing your thoughts about our Society. Hopefully, some of you would like to become involved in running the Society.

For our latest Board of Directors meeting, we welcomed Warwick Dunn, María Monge, Tomáš Pluskal, Candice Ulmer, and Lynn Vanhaecke as new Directors. We also welcomed back Natasa Giallourou, Fabien Jourdan, Matej Orešič, Stacey Reinke, Fidele Tugizimana, and Michael Witting who join Evelina Charidemou, Kati Hanhineva, and myself as the new Board of Directors. As you know, we elect a new Board every year and members are asked to serve for two years, with the potential for a second 2-year term. It is with great relief that with 12 positions open this year that we have so many returning board members who bring with them valuable experiences of supporting our Society. On a personal note, I am very much looking forward to working with the new Board, as well as with Candice (Treasurer) and Fabien (Secretary), who were also elected to serve as Officers of the Metabolomics Society.

You'll be pleased to know that we have Jessica Lasky-Su on speed dial, and her leadership as President of the Metabolomics Society over the last two years has put the Society in such excellent shape. Thanks ever so much, Jessica. We shall certainly be relying on her support and guidance.

For those of you who don't know me, I look forward hopefully to meeting you at future events. On this note, I am very pleased to report that plans for Metabolomics 2023 are developing very nicely and we are all very thankful to Natasa and her team. There will be news on this conference to be held in Niagara Falls, Canada, soon. For now, please make a note of the dates in your diaries: June 18-22.

Finally, as a Society, we are seeing immense growth within our field, with new colleagues from very diverse fields and scientific backgrounds using
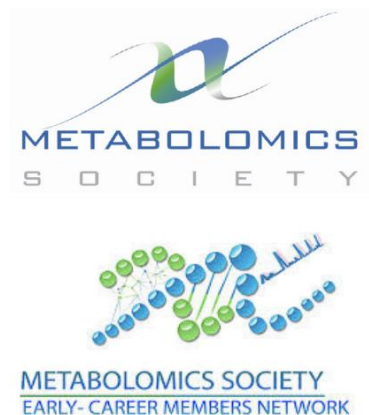
The Metabolomics Society is an independent, non-profit organization dedicated to promoting the growth, use, and understanding of metabolomics in the life sciences.

General Enquiries
info@metabolomicssociety.org

Membership Enquiries
membership@metabolomicssociety.org

metabolomics to answer biochemical questions in just about every area of clinical and biological sciences. It's an exciting time and we continue to look forward to welcoming newcomers to our exciting field.

All the very best,

Roy Goodacre, University of Liverpool, UK
President, Metabolomics Society

Early-career Members Network (EMN)

New Committee
The EMN Committee is delighted to welcome the following new members for 2022-2023:
• Anza-Tshilidzi Ramabulana
• Silvia Radenkovic
• Domenica Berardi
• Millena Cristina Barros Santos
• Marvin Nathanael Iman
• Daniel Mutithu

We would also like to congratulate Evelina Charidemou as the EMN Committee Chair for the second year. The new team is motivated to maintain the initiatives of the EMN but also to bring new ideas to the Committee. We would like to thank all our former members for their contributions to the EMN.

International Affiliates' Corner

Metabolomics Association of North America (MANA)

Visit https://metabolomicsna.org

Call for Nominations – 2023 WomiX Mentorship Award

The WomiX organizing committee is seeking nominations for the 2023 WomiX Mentorship Award! This award will honour a woman/womxn in metabolomics that has demonstrated strong mentorship and leadership skills and has made a large impact on other researchers in their field.

Eligibility criteria for nomination:
1) Any woman/womxn MANA member or WomiX member may be nominated! Collective nominations for a mentor are also encouraged!
2) Any MANA member or WomiX member may nominate someone for the mentorship award. Self-nominations are also encouraged!
3) The nominee should be an outstanding woman/womxn who has demonstrated mentorship and leadership skills in the metabolomics community.
4) The nominee must work in the field of metabolomics.
5) The nominee does not need to be part of a formal mentorship program.

Award information:

The recipient of this year's award will receive a $500 cash award and a commemorative plaque to recognize the awardee's achievements as an inspiring mentor to the metabolomics community.

Deadline: December 9, 2022

Don't miss this opportunity to nominate your mentor. Submit nominations here!

Recent ECM Activities

The first MANA ECM Postdoc Webinar, "Showcase of Emerging and Innovative Research", was held on Nov 8, 2022.

Four MANA ECM postdocs were selected to present a 10-minute flash talk. This was an opportunity to highlight & celebrate MANA ECM postdocs and their research.

• Dr. Stephanie Bishop: "Identifying the metabolic underpinnings of pulmonary infection: insights from a new device for studying the metabolism of polymicrobial cultures"

• Dr. Emily Hill: "Unique-to-salmon compounds increase in plasma and are associated with cardiovascular health following a Mediterranean diet intervention"

• Dr. Xingxing Li: "Identification of bioactive specialized metabolites from bioenergy crop switchgrass (*Panicum virgatum*)"

• Dr. Insha Zahoor: "Profiling blood-based markers in multiple sclerosis using a combination of highly sensitive single molecule array technology (SIMOA) and untargeted metabolomics"

MANA ECM will be bringing more quarterly opportunities in 2023 for early-career members to showcase their research. We'll have a webinar for postdocs, graduate students, and undergraduate students, so keep an eye out for more information coming soon!

2023 WomiX Mentorship Award
Call for Nomination

WomiX would like to recognize a scholar in the metabolomics and WomiX community who has excelled at mentoring others in achieving their career objectives.

The recipient of this year's award will receive a $500 cash award and a commemorative plaque recognize the awardee's achievements as an inspiring mentor to the metabolomics community!

WomiX

Eligibility criteria for nomination:
1) Any woman/womxn MANA member or WomiX member may be nominated! Collective nominations for a mentor are also encouraged!
2) Any MANA member or WomiX member may nominate someone for the mentorship award. Self-nominations are also encouraged!
3) The nominee should be an outstanding womxn who has demonstrated mentorship and leadership skills in the metabolomics community.
4) The nominee must work in the field of metabolomics.
5) The nominee does not need to be part of a formal mentorship program.

Stay connected & follow us on social media!
@womi_x

@manaecm https://metabolomicsna.org/ Date : **Nov 8, 2022** Time : **12:00PM–1:30PM (EST)**

MANA ECM PRESENTS:
Showcase of Emerging and Innovative Metabolomics Research

A webinar highlighting the exciting research by MANA early-career postdoctoral researchers

Stephanie Bishop

Identifying the metabolic underpinnings of pulmonary infection: insights from a new device for studying the metabolism of polymicrobial cultures

Emily Hill

Unique-to-salmon Compounds Increase in Plasma and are Associated with Cardiovascular Health Following a Mediterranean Diet Intervention

Xingxing Li

Identification of bioactive specialized metabolites from bioenergy crop switchgrass (Panicum virgatum)

Insha Zahoor

Profiling blood-based markers in multiple sclerosis using a combination of highly sensitive single molecule array technology (SIMOA) and untargeted metabolomics

Scottish Metabolomics Network
Visit https://www.scottishmetabolomics.net/

The Scottish Metabolomics Network held their annual conference on November 3-4 at the P&J Live exhibition centre in Aberdeen. This year's conference was organized by Prof. Wendy Russell and Prof. Jules Griffin who are based at the Rowett Institute at the University of Aberdeen. The Rowett Institute's research is based upon food nutrition and human health, two areas that were strongly represented by our two guest plenary lecturers. The conference was opened with the plenary lecture of Prof. Rick Dunn of the University of Liverpool who presented on his research on the application of metabolomics within precision medicine. Following on with the theme of human health and nutrition, our closing plenary lecture was given by Prof. Kati Hanhineva from the University of Turku, Finland. Kati presented her work applying metabolomics at the interface between food nutrition and human health with a special focus upon the 'Nordic' diet. We would like to express our sincere thanks to both plenary lecturers for their fantastic and thought-provoking talks. Between the plenary presentations, we had our usual array of poster and oral presentations from early-career researchers and group leaders from across the Scottish institutes. The breadth of Scottish metabolomics research impacts all fields of application, from plants and microbes in food, nutritional and natural product research, through to an array of clinical areas, as well as biotechnological endeavours and those pushing the development of computational metabolomics, mass spectrometry imaging, and real-time analysis. This year's meeting attracted near to 150 participants from across academia and industry. It's fantastic to see our annual attendance figures increasing with each year; it truly reflects that the SMN and Scottish metabolomics research is in a fantastic state of health and growth.

-Will Allwood (Chair of the SMN)

Photo of P&J Live conference venue used with permission courtesy of P&J Live, Aberdeen, UK.

Profs. Rick Dunn and Jules Griffin

Prof. Kati Hanhineva

~The 2nd and 3rd photos above are used with permission of Sphamandla Ntshangase of the University of Edinburgh.

Other News

National Institutes of Health – RFI

Dear Metabolomics Society Members,

We would like to draw your attention to a recently-published Request for Information (RFI) from the US National Institutes of Health that is relevant to the metabolomics community. Through this RFI, the National Cancer Institute (NCI) is currently seeking input from a broad cross-section of biomedical research scientists on best practices for metabolomics data storage, management, and use/reuse. The Institute is interested in hearing from everyone across the fundamental to clinical spectrum – core facility managers and data generators, as well as those who use and reuse metabolomics data – on the following subjects:

• your experience generating, using, and reusing metabolomics data sets;

• the data and metadata most necessary for you to reproduce results reported by metabolomics studies;

• your experience selecting and using software and informatics tools for metabolomics;

• your experience incorporating metabolomics data into multi-omics studies;

• how the interoperability of different file formats has promoted or impeded your ability to reuse metabolomics data;

• any other comments that you would like to share about cancer metabolomics data storage, management, and use/reuse.

Responses are voluntary, and the information collected is for planning purposes only. Understanding the current experiences and challenges of scientists working in the many fields that generate, rely on, and/or contribute to metabolomics data and tools to advance cancer research, including those supported by other institutes at NIH, will help us better serve your community. Learn more by reading NOT-CA-23-007, and to share your thoughts, please visit the submission website. All responses must be submitted by **11:59 pm ET on December 23, 2022.**

Kristine Willis, Ph.D.
Program Director, Division of Cancer Biology
National Cancer Institute, NIH

MANA 2022 Conference Presenters

We are pleased to present interviews from presenters at the 2022 conference of the Metabolomics Association of North America that took place in Edmonton, Canada. Check out the work of these outstanding, early-career researchers!

Dr. Tao Huan

Tao is an Assistant Professor in the Department of Chemistry at the University of British Columbia (Vancouver, Canada). He received his PhD training in Analytical Chemistry from the University of Alberta under the supervision of Dr. Liang Li. After graduation, Tao did postdoctoral work with Dr. Gary Siuzdak at the Scripps Research Institute (La Jolla, California, USA). In July 2018, he was hired as an Assistant Professor in the Department of Chemistry at the University of British Columbia (UBC). At UBC, his research focusses on the synergistic development of analytical chemistry and bioinformatics for mass spectrometry-based metabolomics. He has published 70 peer-reviewed publications in high-impact journals, including *Nature Methods*, *Nature Protocols*, and *Analytical Chemistry* with over 2950 citations and an h-index of 25. He is currently a steering committee and faculty member of the UBC Social Exposome Research Cluster. In addition, Tao is one of the affiliated faculty members in the Graduate Program in Bioinformatics, Genome Science and Technology (GSAT) program, and Djavad Mowafaghian Centre for Brain Health.

Tao was recently awarded the Early Career Rising Star Award during the 4th Annual Metabolomics Association of North America (MANA) Conference, given for his work in the development of analytical and bioinformatics tools for improving data acquisition and analysis of LC-MS-based metabolomics. His awardee lecture was entitled "Addressing Big Data Challenges in Untargeted Metabolomics". This MANA Early Career Award is a competitive award for the most accomplished Early Career Members (ECM) who have exhibited exceptional novelty or have pushed the boundaries of metabolomics, or whose early career efforts, after obtaining a PhD, MD, or MD-PhD, have resulted in sustained, substantial, and noteworthy contributions to the field.

What is the key point or highlight that you want the audience to take away from your presentation?

In this presentation, I described three overlooked issues in processing untargeted metabolomics data, including fold change compression, sample size estimation, and feature-specific data transformation. I hope to convince the audience that extracting high-quality metabolic features for downstream data interpretation is still challenging and that there is a lot of room to improve the bioinformatic pipeline.

Can you summarize your presentation in a 30-second elevator pitch?

Advancements in computer science and software engineering have greatly facilitated mass spectrometry (MS)-based untargeted metabolomics. However, in the "omics" era, we are faced with new challenges, the big data challenges, of how to accurately and efficiently process raw data, extract biological information, and visualize results from the gigantic amount of collected data. In this presentation, I first described the issues of fold change compression. Fold changes calculated using MS signal intensities can be biased, even in the linear signal response ranges. Next, I used a study of Monte Carlo simulations to highlight the importance of using enough samples to improve the true positive rate of identifying statistically significant features. Finally, I questioned the commonly used log transformation in improving data normality. Our study shows that conventional log or power transformations do not work well for given feature-specific data distributions in untargeted metabolomics. My lab proposed an adaptive box-cox transformation, which considers the original data distributions and improves data normality to extract more statistically significant features.

Where do you think the future of this technology lies?

Despite the development of sensitive mass spectrometry analyses, metabolomics data processing is still time-consuming and contains many challenges. By working together with others in the metabolomics community, my lab aims to further advance analytical and bioinformatic methods to make metabolomics data processing as convenient as "one-click".

Metabolomics and Human Health
Gordon Research Conference

Examining the Intersection Between Systemic and Cellular Metabolism and Lifestyle Factors to Understand Health and Disease

March 12-17, 2023

Venue: Barga, Lucca, Italy

Chairs: Steven S. Gross
                 Lorraine Brennan

Vice Chairs: Susan Jenkins Sumner
                 Warwick Dunn

The Metabolomics and Human Health Gordon Research Conference (March 2023) will highlight state-of-the-art metabolomics technologies and how such technologies can be used to study human health. Places are limited and filling up, so we encourage early submission to avoid disappointment.

To apply, click here.

Dr. Sadjad Fakouri Baygi

Sadjad is a National Institutes of Health T32 postdoctoral fellow at the Icahn School of Medicine at Mount Sinai, New York, within the Department of Environmental Medicine and Public Health. [T32 is an institutional research training grant program within the NIH.]. He has been working in the field of computational mass spectrometry from his PhD through his postdoctoral fellowship. A number of computational pipelines developed by him are utilized to process mass spectrometry data from various fields, such as metabolomics, lipidomics, exposomics, and environmental studies. His research philosophy in computational mass spectrometry is to develop computational tools that are able to offer maximum automation levels, the highest precision, versatility to use in various analytical platforms, and simplicity for users to minimize laboratory efforts. He is currently working on developing a computational tool to discover natural products from mass spectrometry data. He is interested in incorporating quantum computing in mass spectrometry data processing pipelines to maximize the precision of untargeted workflows for high-throughput multi-omics projects.

Sadjad received the Mark P. Styczynski Early Career Award from the MANA 2022 conference for his accomplishments in the design, development, and support of new algorithms for processing untargeted high-resolution mass spectrometry data in the metabolomics and exposomics fields. This research was conducted under the mentorship of Dr. Dinesh Barupal. His ECM awardee lecture presented during the last day of the conference was "New computational workflows to generate comprehensive, diverse and inclusive metabolomic datasets".

What is the key point or highlight that you want the audience to take away from your presentation?

I want scientists to know that there is a lot of complexity in metabolomics and more in the data interpretation methods that are required to unravel more biological questions. Metabolomics heavily depends on mass spectrometry data processing techniques; therefore, I attempted to present the efficacy of incorporating the chemistry of mass spectrometry instruments in the metabolomics data interpretation workflows for data interpretation. The main takeaway of my presentation was to show that more needs to be done to develop more accurate computational metabolomics workflows.
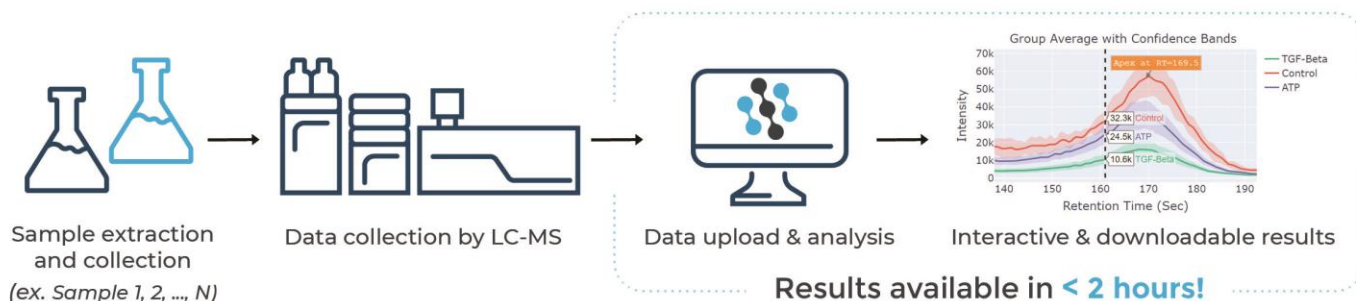
Can you summarize your presentation in a 30-second elevator pitch?

To gain biological insights, complex mass spectrometry data are required to be processed using accurate computational mass spectrometry tools. I have developed a number of computational pipelines to
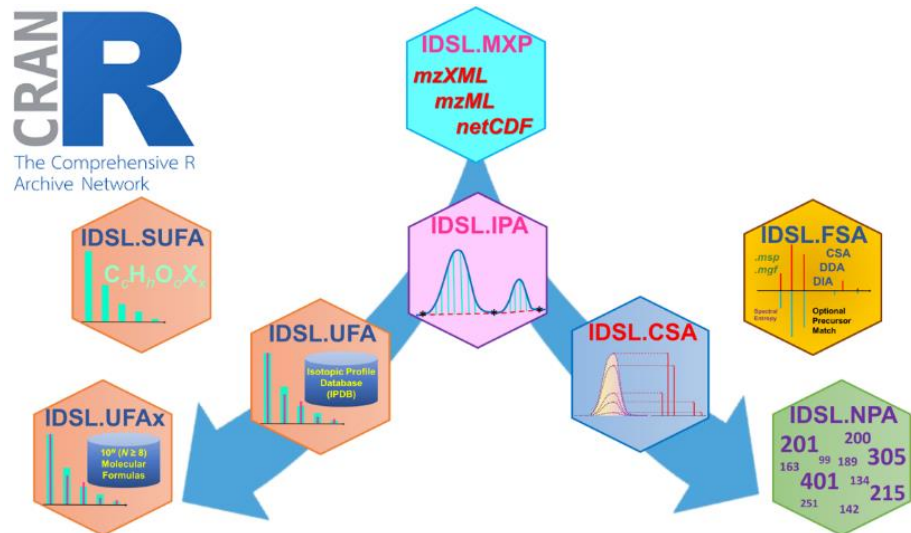
reduce the complexity of mass spectrometry data into multiple layers using fundamental chemistry principles. In the first layer of data processing, random electronic noises are minimized and mass spectrometry features of solely organic compounds are isolated using natural carbon signatures. Next, the mass spectrometry features are annotated by predicting the chemical space of the sample. These data processing workflows were successful in suggesting the presence of an emerging class of toxic substances known as chlorinated perfluorotriether alcohols (Cl-PFTrEAs) in human populations. IDSL.MXP, IDSL.IPA, IDSL.UFA, IDSL.UFAx, and IDSL.SUFA computational pipelines were developed in the R programming language and are available on online repositories for public use. Currently, I am working on IDSL.FSA, IDSL.CSA, and IDSL.NPA computational pipelines to provide integrated mass spectrometry data processing pipelines. I also published the scientific concepts embedded in these tools in the

Journal of Proteome Research and *Analytical Chemistry*. [IDSL refers to the Integrated Data Science Laboratory of Metabolomics and Exposomics.]

Where do you think the future of this technology lies?

High-resolution mass spectrometry instruments are utilized to understand responses to drugs and therapies in many biomedical fields. The computational pipelines that I have developed can be utilized to deconvolute mass spectrometry data with higher precision when combining metabolomics with other biomedical fields such as proteomics, genomics, lipidomics, and exposomics. Therefore, I expect to see these computational pipelines used in multi-omics analyses. I should also mention that I am committed to maintaining these computational pipelines to steadily improve their performance.

Sara Londoño-Osorio
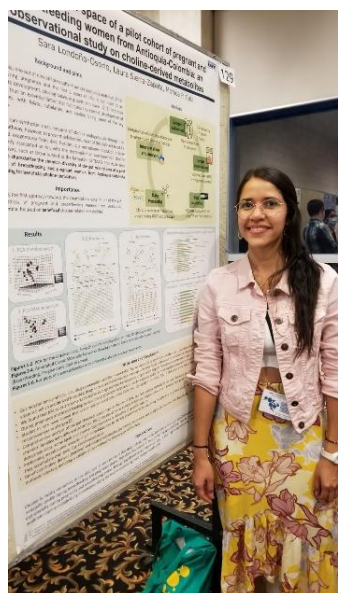
Sara is currently a Master of Science candidate in Biosciences at Universidad EAFIT (Colombia) with a fellowship award from Minciencias (Ministry of Science, Technology and Innovation, Colombia), and earned her degree in Biological Engineering from Universidad Nacional de Colombia. She is part of the CIBIOP (Biological Sciences and Bioprocesses) research group where she is working on her thesis on "Chemical and microbial diversity of the gut microbiome in pregnant and lactating women", using omics techniques. Sara has experience in bioinformatics, Molecular biology, data science, and biomarker obtainment and detection technologies. Sara also has experience with Python, R Studio, Qiime2, GNPS, and MetaboAnalyst. She received the Mitacs Globalink Research Award for an internship at McMaster University (Hamilton, Canada) (2022). She is also a co-founder of the Startup Astrolab Bio in microbiome diagnosis and therapies.

Sara presented her poster during the MANA 2022 conference with the title, "Total chemical space of pregnant and breastfeeding women from Antioquia, Colombia: an observational study on choline-derived metabolites". Before heading to the MANA conference in Edmonton, Sara just finished her 3-month internship as a visiting student at Dr. Philip Britz-McKibbin's laboratory at McMaster University. Research in the Britz-McKibbin group is focussed on both fundamental and applied studies in bio-analytical chemistry when using multi-segment injection-capillary electrophoresis-mass spectrometry (MSI-CE-MS) for rapidly expanding metabolomic initiatives.

What is the key point or highlight that you want the audience to take away from your presentation?

Comprehensive analysis of the gut chemical space requires the use of different metabolomic methods. In this case, the use of two columns allows us to identify different chemical families with different polarities. The hydrophilic interaction chromatography (HILIC) column allows us to identify betaine, phytonutrients, and, generally, polar substances. The C_{18} column, on the other hand, helps to detect bile acids, some lipids, and diverse food derivative metabolites of a lipophilic nature. Also, gut metabolomics reflects diet, drug consumption, and pharmacokinetics. For example, we were able to identify metabolites such as coumarin, omega-3 and omega-6 fatty acids, and vitamin E, which are derived from the diet; and drugs such as antihistamines and anticoagulants were found in the volunteers that declared their consumption.

Can you summarize your presentation in a 30-second elevator pitch?

It is very interesting to explore the microbial and chemical diversity of the gut microbiota in breastfeeding and pregnant women, where choline is an essential nutrient that helps to improve IQ levels and the development of babies. This work was focussed on studying the gut metabolome from stool samples, performing LC-MS (using a C_{18} and HILIC column), and using molecular networking to analyze the data. I expect to integrate these results with microbial data and also compare them with the metabolites found performing MSI-CE-MS at Dr. Britz-McKibbin's lab.

Where do you think the future of this technology lies?

- Being able to integrate meta-barcoding and metabolomic data using the DIABLO framework;
- Complementing the metabolome profile with the data obtained from MSI-CE-MS;
- Conducting this study in a larger cohort supplementing with choline-rich dietary sources, such as eggs, and a potential biotherapeutic we have in development to see if it increases the bioavailability of choline derivatives, especially in women who are in these stages.

Parker Bremer

Parker is a PhD student in Chemistry from the Fiehn Lab and West Coast Metabolomics Center, University of California, Davis (USA). He first experienced STEM data science while clustering molecular-dynamics simulations of proteins from Folding@home. Since then, he has had the privilege of improving his mass spectrometry, software engineering, and statistical knowledge in Oliver Fiehn's lab as well as at the Chan Zuckerberg Biohub. He is interested in any research where he can deploy modern technology to have a tangible impact, so he is looking forward to any data challenges that come his way.

The Fiehn laboratory at UC Davis develops metabolomics technologies in cheminformatics and analytical chemistry and applies these methods in biomedical projects and basic science. Parker worked with Gert Wohlgemuth and Dr. Oliver Fiehn and did an oral presentation entitled "A database query interface across 160,000 metabolomic samples in GC-TOF mass spectrometry". [GC-TOF mass spectrometry: gas chromatography-time of flight mass spectrometry].

What is the key point or highlight that you want the audience to take away from your presentation?

The community can use our "ontologically-grouped differential analysis" to extract compound trends that persist throughout disparate studies. Because of this, we can perform an instantaneous meta-analysis and transform large databases into actionable summaries.

Can you summarize your presentation in a 30-second elevator pitch?

We designed a web tool or application programming interface (API) that implements our "ontologically-grouped differential analysis" on a 160,000-sample dataset from the UC Davis/West Coast Metabolomics Center. The user only needs to express a comparison query involving groups (e.g., "Human Gut" vs. "Bacterial Cells") and they will receive tabular and visual results that describe the trends coming from all of the studies involving those sample metadata. This is made possible by using ontologies to transform generic terms like "Bacterial" into sets of species for which we have data.

Where do you think the future of this technology lies?

This line of thinking is valid for any metadata attribute and any -omics (the procedure can be feature-agnostic if desired). We would love to see it implemented in

community-wide repositories such as the Metabolomics Workbench. We also believe that transitioning to Graph/NoSQL [SQL: Structured Query Language] databases might further attempt to "capture the essence" of a study, which would aid metadata-focussed analyses such as this.

Oluwatosin Kuteyi

Oluwatosin Racheal Kuteyi is a current PhD candidate at Concordia University, (Montreal, Canada), under the supervision of Dr. Dajana Vuckovic. In 2007, she graduated at the top of the department with her bachelor's degree with honours as an industrial chemist from Osun State University, Nigeria. To further advance her hunger and love for knowledge in the analytical field, she obtained her distinction in her master's degree in Analytical Chemistry at Loughborough University, United Kingdom, in 2015. Her goal as a research scientist is to be able to identify and provide scientific innovation that can improve the metabolomics field, especially in biochemical and clinical studies. Oluwatosin made a poster presentation entitled "Stability of oxylipins stored on biocompatible solid-phase micro-extraction (SPME) devices".

What is the key point or highlight that you want the audience to take away from your presentation?

Biocompatible microextraction devices can improve the stability of oxylipins, during sampling, transportation, and storage to enable accurate quantitation and remote/at-home sample collection.

Can you summarize your presentation in a 30-second elevator pitch?

We extracted the oxylipins on an SPME device and performed a 3-cycle freeze-and-thaw study and an 18-day room temperature stability study. SPME significantly improved the stability of oxylipins, with the exciting result that only one oxylipin was found to be unstable during the 18-day storage at room temperature. For unstable oxylipins, we further performed forced degradation studies in order to map out their degradation pathways and examine if the resulting degradation products could interfere with the analysis of stable oxylipins.

In vivo SPME device

Where do you think the future of this technology lies?

This study further establishes biocompatible SPME as an excellent sampling and sample preparation approach for oxylipins. The next steps involve the design and validation of personalized sampling devices in both *in vivo* and *ex vivo* formats. In addition, we hope to see the incorporation of micro-extraction technology into other at-home blood, saliva, and urine collection devices. We are currently mapping the possible degradation pathways of the unstable compounds and investigating whether antioxidant addition before or after extraction on SPME can further stabilize the few unstable oxylipins reported in our work. We are also currently evaluating the results for a broad range of lipids beyond oxylipins, including phospholipids, sphingolipids, and glycerolipids.

Recent Publications

Recently published papers in metabolomics

- [A multi-omics framework reveals strawberry flavor genes and their regulatory elements](#) (Open access)

- [Discovering a trans-omics biomarker signature that predisposes high risk diabetic patients to diabetic kidney disease](#) (Open access)

- [Furan fatty acid metabolite in newborns predicts risk of asthma](#)

- [Influence of the microbiome, diet and genetics on inter-individual variation in the human plasma metabolome](#) (Open access)

- [LargeMetabo: an out-of-the-box tool for processing and analyzing large-scale metabolomic data](#)

- [Metabolic Rewiring of Kynurenine Pathway during Hepatic Ischemia–Reperfusion Injury Exacerbates Liver Damage by Impairing NAD Homeostasis](#) (Open access)

- [Metabolomic and lipidomic signatures in autosomal dominant and late-onset Alzheimer's disease brains](#) (Open access)

- [Metabolomics analysis insight into medicinal plant science](#) (Review)

- [Metabolomics of soybean (*Glycine max* L.) response to co-exposure of pyrene and three metal oxide engineered nanomaterials](#)

- [Multi-omics research strategies in ischemic stroke: A multidimensional perspective](#) (Review)

- [Nanoplastics induce molecular toxicity in earthworm: Integrated multi-omics, morphological, and intestinal microorganism analyses](#)

- [Not just a gut feeling: a deep exploration of functional bacterial metabolites that can modulate host health](#) (Review, Open access)

- [Nuclear Magnetic Resonance Metabolomic Profiling and Urine Chemistries in Incident Kidney Stone Formers Compared with Controls](#)

- [Reassessment of adipocyte technology for cellular agriculture of alternative fat](#) (Review)

- [Revisiting the bioavailability of flavan-3-ols in humans: A systematic review and comprehensive data analysis](#) (Review, Open access)

Metabolomics Events

March 12-17, 2023

Metabolomics and Human Health *Gordon Research Conference*
Examining the Intersection Between Systemic and Cellular Metabolism and
Lifestyle Factors to Understand Health and Disease
Venue: Barga, Lucca, Italy
Learn More Here

Overview

Chairs: Steven S. Gross and Lorraine Brennan
Vice Chairs: Susan Jenkins Sumner and Warwick Dunn
The Metabolomics and Human Health Gordon Research Conference (March 2023) will highlight state-of-the-art metabolomics technologies and how such technologies can be used to study human health. Places are limited and filling up, so we encourage early submission to avoid disappointment.

To apply click here

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December 1, 2022

Bits & Bites #10: How to navigate demands in Metabolomics core services
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.

This last, 10th course (for 2022) is taught by Dr. Oliver Fiehn from UC Davis, and no prior knowledge or software is required. Biologists and biomedical investigators need metabolomic data but must rely on services from metabolomic service providers in Universities or private companies. Interests in metabolomics services are very diverse, ranging from PK/PD to untargeted metabolomics, and from flux analysis to absolute quantifications of pathway intermediates. How can metabolomic service cores manage such demands and expectations with limited resources? At UC Davis, we have run metabolomics services for the past 16 years. In this short course, we will provide a strategic overview on how to deploy tools, spot and fill bottlenecks, assess your core's capacity, scale up from small studies to 1000s of samples and provide high-throughput / high-quality services in a time and cost-efficient manner. We discuss how to consult with clients, how to provide educational resources, and how to manage staff and budgets. Recognizing that there is no one-size-fits-all strategy, we will survey measures on how to best engage your research community to utilize metabolomics services.

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December 4-7, 2022

The Human Microbiome: Ecology and Evolution
Venue: Banff, Alberta, Canada; Online (Hybrid)
Learn More Here

Overview
This Keystone Symposia conference will explore the evolutionary and ecological forces shaping the interplay between the human host and microbiome., and is held jointly with the conference "Novel Approaches Against Emerging Antimicrobial Resistance". The microbiome is implicated in a widening set of disease conditions, yet many questions remain as to how its diversity and composition are assembled and maintained.

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December 13, 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), 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.

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January 27-28, 2023

IX Metabolomics Circle Meeting
Venue: Wrocław, Lower Silesian, Poland
Learn More Here

Overview
The Polish Metabolomics Society (Polskie Towarzystwo Metabolomiczne) is inviting participants to the 9th Metabolomics Circle Meeting, which will be organized by Professor Piotr Młynarz from the Wrocław University of Science and Technology. Information about abstract submission and registration will soon be posted on the webpage.

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March 28-31, 2023

EMBL-EBI course | Introduction to Metabolomics Analysis
Venue: Hinxton, Cambridgeshire, United Kingdom
Learn More Here

Overview
The European Bioinformatics Institute (EMBL-EBI) is organizing an on-site course at the EMBL-EBI Wellcome Genome Campus in Hinxton. This course will provide an introduction to metabolomics through lectures and hands-on sessions, using publicly available data, software, and tools. It is an open application with a selection for 26 seats. Please submit all required documents for the application process by **January 4, 2023.**

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June 18-22, 2023

19th Annual Conference of the Metabolomics Society
Venue: Niagara Falls, Ontario, Canada
Learn More Here

Overview
Save the date! Visit the website for updates over the coming weeks.
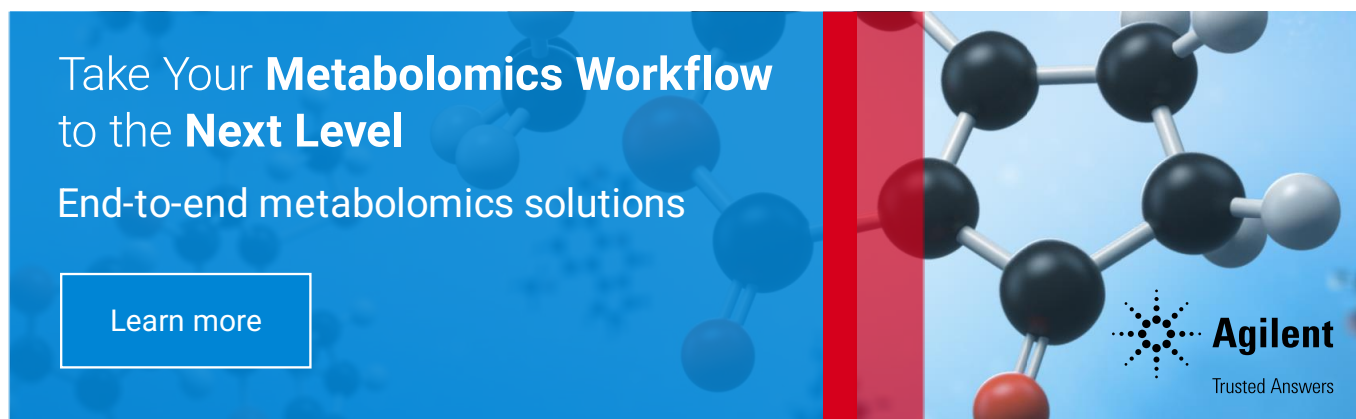
Metabolomics Jobs

Jobs Offered

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	Deadline	Source
Postdoctoral Fellows (Metabolomics, Proteomics, and Informatics - Microbial Infections)	University of Calgary	Calgary, Alberta, Canada	Until filled	Lewis Research Group
Research Director – In vitro Diagnostics	Metabolomic Technologies Inc.	Edmonton, Alberta, Canada	Until filled	MetaboNews Jobs
Postdoctoral Position in Metabolomics and Proteomics	Brigham and Women's Hospital	Boston, Massachusetts, USA	Until filled	Brigham and Women's Hospital
Postdoctoral Research Fellow in Metabolomics (Diabetes)	Lund University	Lund, Sweden	Until filled	MetaboNews Jobs
Postdoctoral Research Fellow (Exometabolomics)	North Carolina State University	Raleigh, North Carolina, USA	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	Until filled	Icahn School of Medicine at Mount Sinai
Postdoctoral Research Fellow (LC-MS and Data Science for Metabolomics)	University of Alberta	Edmonton, Alberta, Canada	Until filled	University of Alberta
Assistant Professor in Metabolomics of Adaptive Responses	University of California, Riverside	Riverside, California, USA	Until filled	University of California, Riverside
Various Positions	Various	Various (within North America)	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.