msis Society
The Home of Mass Spectrometry Imaging

December 2022

In this issue

Happy Holidays from the MSIS

Dear MSIS members,

Take a deep breath, close your eyes for a few seconds, and congratulate yourself on getting through this last year. Although we may not be out of the woods yet, progress is happening and for that we are very grateful and excited and 2023 has a lot in store for the MS imaging community.

The societies are moving constantly together, and we plan to have IMSIS launched very soon. IMSIS will bring together MSIS and IMSS in a unified society with a mission of advancing the scientific field through collaborative exchange of ideas.

We will jumpstart 2023 with a hybrid conference held at Doshisha University. The organizers included presentations from MSIS and IMSS to highlight how tight-knit our community is. A Spring Workshop in Uppsala will provide ample opportunity to meet colleagues face-to-face and get hands-on experience in data analysis and imaging experiments. And BMSS is hosting a regional event before some of us meet at ASMS in Houston.

But save your excitement for the follow-up event to our beloved OurCon. The "1st IMSIS Conference - Annual Conference on Mass Spectrometry Imaging and Integrated Topic" takes place from Oct 23 to 25, at the Centre Mont-Royal in Montreal, Canada.

Last but not least, It's been fantastic talking and working with you in 2022 and we hope we can continue doing in the forthcoming year. In the meantime, have a wonderful time and a happy holiday season.

On behalf of the MSIS board,

The president,
Martina Marchetti-Deschmann

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Join the **Regional Mass Spectrometry Imaging Spring Workshop**

Mar 27th – 29th, 2023
Uppsala, Sweden

We are pleased to invite you to the in-person Regional Mass Spectrometry Imaging Spring Workshop, a conference style meeting hosted by the Swedish Pharmaceutical Society and the newly formed International Mass Spectrometry Imaging Society (IMSIS) which is comprised of Mass Spectrometry Imaging Society (Europe) and Imaging Mass Spectrometry Society (US).

The scientific program will aim to reflect cutting edge innovations and current developments in mass spectrometry imaging (MSI), alongside new applications in various areas. Our goal for this workshop is to promote and educate academic, industry and government scientists on the latest applications and innovations in MSI applied to biomedical, biological and data science research areas.

We are excited to have a unique three-day scientific agenda packed with oral presentations, workshop discussions, and poster presentations covering the latest developments and applications of MSI by leading and upcoming scientists from academic, government, and industry labs.

We look forward to welcoming you to Uppsala!

Dr. Per Andrén, Uppsala University, Local Organizer

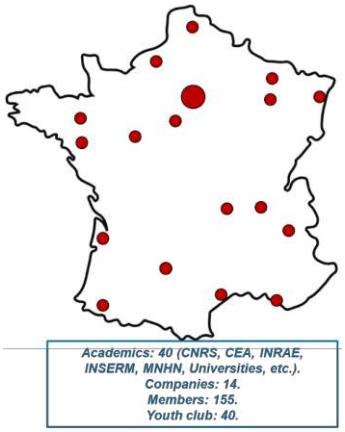
Co-organized with the International Mass Spectrometry Imaging Society and the Swedish Pharmaceutical Society

ANNOUNCEMENTS

Launch of the CNRS Research Network on Mass Spectrometry Imaging (GdR-MSI, GDR2125)

Dear Colleagues,

cnrs GDR Groupement de recherche
MSI Imagerie par Spectrométrie de Masse



It is a great pleasure to inform you on the recent launching (in January 2022) of the CNRS Research Network on Mass Spectrometry Imaging (GdR-MSI, GDR2125) funded for 5 years. The *GdR* is a key tool of the French National Center for Scientific Research (CNRS) to promote exchanges between the main laboratories in a specific field together with academic partners but also industrial partners. It is first focused to partners localized in France but it might be opened to key international stakeholders. The CNRS GdR-MSI aims to establish strong relationships within the community of around two hundred scientists in France focusing their experimental work around two main instrumental subcommunities, namely that around MALDI, DESI and LA ICP-MS, as well as that on surface analysis using SIMS (ToF-SIMS and nano-SIMS).

The Scientific Board of the GdR-MSI, with Nicolas Desbenoit (CBMN UMR 5248, Bordeaux) as Director, and Alain Brunelle (LAMS UMR 8220, Paris) & David Touboul (ICSN UPR 2301, Gif-sur-Yvette) as Deputy Director, includes 19 scientists reflecting the variety of the entire community of mass spectrometry imaging users at the French level. Its main missions are the following ones:

- Bring together the entire French community active in mass spectrometry imaging,
- Make our community visible and attractive at national and European levels,
- Discuss on common and transverse interest topics,
- Share approaches and methods considering the modalities as well as applications,
- Foster collaborations between network teams and facilitate the emergence of national and international projects,
- Reinforce interaction between network teams and industrial partners,
- Help young scientists by promoting their mobility through intra-network exchanges, or by providing grants to attend conferences related to the MSI field.

1st IMSIS Conference Annual Conference on Mass Spectrometry Imaging and Integrated Topics

Oct 23rd -25th, 2023
Centre Mont-Royal, 2200 rue Mansfield
Montreal, QC Canada

This is the first meeting of the of the newly formed International Mass Spectrometry Imaging Society which is comprised of Mass Spectrometry Imaging Society (MSIS) (Europe) and Imaging Mass Spectrometry Society (IMSS) (US). As with the past OurCon conferences that were organized jointly between IMSS and MSIS, this conference is a global forum on mass spectrometry imaging (MSI) research.

For more information on abstract deadlines, registration fees, and scientific programme please visit: **http://www.imsis2023.org/**

BMSS - MSIS Imaging & MALDI SIG

May 10th, 2023
Sheffield, UK

BMSS - MSIS is jointly hosting a one-day **Mass Spectrometry Imaging Special Interest Group Meeting** with the British Mass Spectrometry Society and Sheffield Hallam University at Sheffield Hallam University on **Wednesday 10th May 2023**. Further details on abstract submission and registration in the New Year. For sponsorship information please contact Jillian Newton: **jillian.newton@shu.ac.uk**

To achieve these goals, the GdR-MSI has already started its activities: creation of the Board, setting up a web site (https://gdr-msi.cnrs.fr/gdr-msi/), LinkedIn social network (https://www.linkedin.com/groups/12723584/), publication of a Newsletter, first exchanges on the organization of the first GdR-MSI workshop, as well as organization of webinars with international colleagues. For instance, the first one has been presented by Sebastiaan Van Nuffel from M4i at Maastricht University. The second one will be held in December with Ian Gilmore from NPL. Finally, the third one will be presented next January by Pierre Chaurand from Université de Montréal.

Yours sincerely,
On behalf of the GdR-MSI Scientific Board,
Nicolas Desbenoit

Special Issues

Metabolites | Special Issue : New Frontier in Mass Spectrometry Imaging for Metabolomics and Lipidomics (mdpi.com)

Guest Editors Prof. Dr. Shuichi Shimma and Prof. Dr. Eiichiro Fukusaki (Department of Biotechnology, Graduate School of Engineering, Osaka University)

Deadline for manuscript submissions: 31 January 2023

Pharmaceuticals | Special Issue : Mass Spectrometry Imaging in Pharmaceutical Research (mdpi.com)

Guest Editors Prof. Dr. Carsten Hopf and Dr. Stefania-Alexandra Iakab (Center for Mass Spectrometry and Optical Spectroscopy (CeMOS), Mannheim University of Applied Sciences) and Dr. Michael Becker (Boehringer Ingelheim Pharma GmbH & Co., Germany)

Deadline: 15 March 2023

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MSI Calendar

6th International symposium of the Kyoto biomolecular mass spectrometry society / international symposium on mass spectrometry imaging 2023
Jan 30th – 31st, 2023
Kyoto, Japan and online
Details:
https://en.kbmss.org/sympo6/

18th European Molecular Imaging Meeting | EMIM 2023
Mar 14th – 17th, 2023
Salzburg, Austria
Details:
https://e-smi.eu/meetings/emim/emim-2023/

Regional Mass Spectrometry Imaging Spring Workshop
Mar 27th – 29th, 2023
Uppsala, Sweden
Details:
www.apotekarsocieteten.se/produkt/regional-mass-spectrometry-imaging-spring-workshop/

ANAKON 2023
Apr 11th – 14th, 2023
Vienna, Austria
Details:
www.anakon2023.at/welcome

BMSS - MSIS Imaging & MALDI SIG
May 10th, 2023
Sheffield, UK
Details:
www.bmss.org.uk/special-interest-groups/imaging-and-maldi/

EUROANALYIS MSI Workshop
Aug 27th – 31st, 2023
Geneva, Switzerland
Details:
www.euroanalysis2023.ch/

INTERVIEW:
Meet distinguished members of the MSI community:

Prof. Ingela Lanekoff

Professor in Analytical Chemistry at Uppsala University, Sweden

Ingela Lanekoff is a full Professor of Analytical Chemistry at the Department of Chemistry-BMC, Uppsala University, Sweden. After a PhD in 2011 from the University of Gothenburg, Sweden, she did a post doc at Pacific Northwest National Laboratory, USA. Following, she started her independent career in 2014 at Uppsala University. Her research is focused on developing and applying new mass spectrometry tools for the analysis metabolites and lipids, including low abundant and isomeric species, in tissue and cells. The overall aim to use novel analytical tools to realize the chemistry behind biological function.

How you came to be involved in MSI?

I started my PhD with running LC-MS, but when I heard about MSI I decided to take a course to learn more. Finally, I ended up doing SIMS imaging of single cells for half my PhD. It was a great time! After my PhD I got the opportunity to do my post doc with Dr. Julia Laskin and to develop nano-DESI into a technique for MSI. This really got me hocked on the technique and when I moved back to Sweden to start my independent research group, I brought the technique along with me. It has been, and still is, such a wonderful journey to continuously explore and push nano-DESI MSI for chemical imaging.

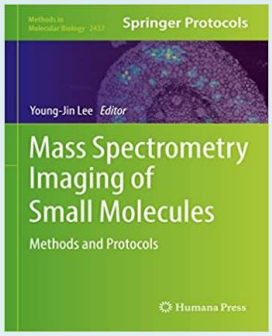
What do you think MSIS brings to the MSI field? What else would you like to see from the society?

I think it is important to have societies such as the MSIS where we can share knowledge, experiences, and laughter. I have found many friends within the MSIS society! For the future, I foresee an even more open society that is inclusive to all MSI techniques and all types of researchers, industrial and academic, young and old. I would embrace more small workshops and visits among the members of MSIS to collaborate, and to learn tools and tricks. Perhaps the society could set aside a small pot of funding for PhD students to experience other labs.

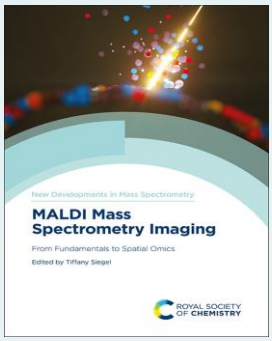
Have you participated in OurCon and if yes what are your best memories?

I attended the first Ourcon in Ourence back in 2012, and have tried to attend all of them since then, but have not always succeeded. I remember the hot weather at Ourence, and where we were playing beach volleyball at Ourcon in Antalya in 2014 and covered the floor with sand! The first time I brought group

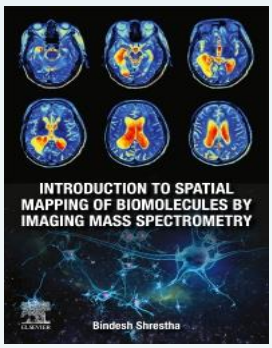
Books published in 2021-2022:



Mass Spectrometry Imaging of Small Molecules | SpringerLink
1st edition 2022
Editor: Young-Jin Lee



MALDI Mass Spectrometry Imaging
1st edition 2021
Editor: Tiffany Porta Siegel



Introduction to Spatial Mapping of Biomolecules by Imaging Mass Spectrometry
1st edition 2021
Author: Bindesh Shrestha

members was to the conference in Pisa in 2015, that was a lot of fun. Although, I remember dinner being extremely late one night because some presenters just kept talking! Doorn in 2017 was a very nice conference as well, with lots of dancing J Also, Saint-Malo in 2019 was wonderful with a nice, but somewhat rainy view – and too many people to fit into the bar at the same time! The Sheffield conference in 2021 was of course less interactive, but the digital social event was still memorable.

What drives your enthusiasm for the field of MS imaging?

I am fascinated to see the intricate chemical differences between different cellular regions in tissue and that we can reveal this with MSI. There are so many things that are still unknown in biology and with our techniques we really have the potential to open, or at least peak into, the chemical complexity. I am also driven by broaden the type molecules that we can detect and image, and by pushing the technology to enable quantitation so that different regions can be compared by concentration fold change, which provides more accurate information than intensity fold change. My enthusiasm of working with nano-DESI stems from the plenthora of possibilities to alter the solvent for quantitation, chemical reactions, and enhanced ionization.

How do you think the field will be in 5-10 years from now?

In 5-10 years I anticipate that the field has expanded more into industrial applications, such as drug development. I think MSI holds a great promise in this field since the location of both the drug and its metabolites can be revealed at the same time as endogenous metabolites can be monitored to ensure that the drug is effective. I also believe that more researchers will realize the added dimension of also learning about the distribution of their analytes in the tissue and turn to MSI to complement their studies in both basic and applied research.

What are the main challenges and the biggest success you have encountered in your career and what do you think can be improved in the field of MSI?

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MSIS membership

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Currently we offer ***active memberships***, and ***early career memberships*** (for active members up to 3 years after their PhD graduation date)

To buy the MSIS membership and for more information, please visit our website:

https://ms-imaging.org/wp/

The main challenge has without a doubt been to establish myself and my research in the academic environment and the communities. In Sweden, there are very few positions in analytical chemistry and I had to get grants to pay my own salary for four years of my independent career. Today, I have a better situation where I can use the grants for group members and research. J The biggest success is on the same theme, I have a wonderful group of 7 PhD students and 1 post doc that I am working with and that I have the fortune to follow as they are growing into more mature scientists.

I think the field of MSI has a lot of potential. I believe that the most important thing to strive for is to generate data that can solve biological questions. But this is difficult since MSI has inherent issues with matrix effects and isomers that we at best can compensate for and at worst will skew our results so that they no longer make sense biologically. We should never stop thinking critically about our data or trying to improve our techniques!

What advice would you give to a student entering an MSc/PhD project?

Read, reflect, and reassess – becoming a researcher has a lot to do with developing your mind set. Also, if possible, choose a position for your studies that has a nice working environment and where there is support from advisors and colleagues. Everything is a lot easier when you are happy so try to enjoy this time of your life! Finally, you will encounter lots of problems. Discuss with others and pick your battles carefully, since some problems will be possible to solve and give great reward while some you may have to let go.

MSIS Executive Committee


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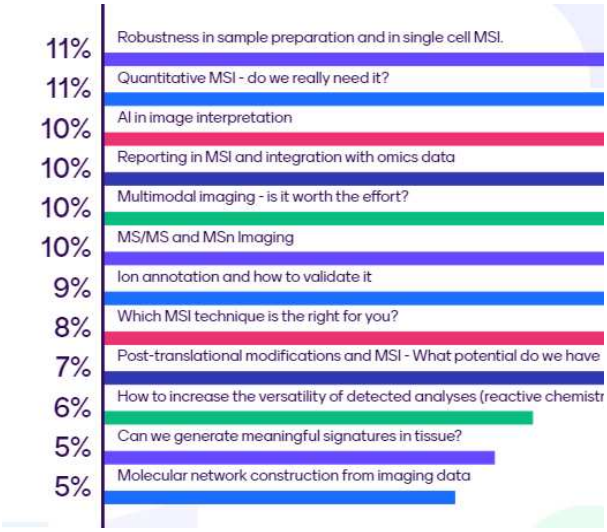
SPECIAL ISSUE – Focus Group on Imaging at IMSC 2022

The 111 attendees of the Focus Group were presented with several topics they could choose from for the follow up discussion. The attendees were then split in 6 groups and could choose to participate to the discussion of their choice, moderated by the organizers of the Focus Group.
The summary of the different discussions are presented in this special issue.



Topic: Robustness in sample preparation and focus towards single cell MSI

The real first point of discussion was actually on the semantics of "single cell." For many attendees, it was not about discerning single cells in a tissue but having the equivalence of 1 pixel = 1 cell. Many felt that a proper distinction would be nice to rule out the confusion quickly. The proposed idea stressed the subtle difference between "single cell analysis" and "single cell resolution." Regarding MSI meant to achieve single cell resolution on tissue sections, an important point was raised: how often do we really need to go to such high spatial resolution? It is important to assess if and when this type of analysis is necessary since achieving cellular resolution also means that a big part of the sample is not analyzed. Moreover, researchers are often prompted with the question: how low can you go? Therefore, the consensus among the participants is clear: It is mandatory to communicate more clearly what can be achieved. Although briefly explored, the application field between attendees was from the lipidomics community. Many were thrilled to learn how much MSI in lipidomics is gaining momentum.
The discussion was then steered to the robustness of sample preparation. Undoubtedly, many pointed out the gravity of this aspect: from obtaining the sample (e.g., cryosection, thickness), to storing conditions tailored to preserve the analytes of interest, and to the many single steps from preparation to MSI analysis. For example, MALDI MSI requires a proper matrix selection, followed by the relative means of application, and storage conditions if not imaged immediately. On this topic, the common idea is to rely on the operator's experience and to use and expand the standardization of sample preparation (e.g., automatic sprayers or sublimation devices). Nonetheless, the responsibility of a good sample prep should not lie entirely with the machine itself. Still, a continuous line for discussion, support, and improvement should be kept open between researchers and vendors. Moreover, robustness is not strictly limited to sample preparation, but it should be expanded to MSI itself. As well known, sources of error like ion suppression, matrix effects, and sample heterogeneity must be addressed. The solution to these problems can sometimes be achieved by specific or fine-tuning settings of the instrument but is often sought by employing specific software, or scripts, that help minimize these errors.
Lastly, many wish for a "general cheat sheet" linking: the instrumentation employed (e.g., SIMS, MALDI, LDI), the

type of sample (e.g., organ-specific, brain, liver, etc.), and the analytes of interest, to show, generally speaking, a guideline for the optimal sample preparation conditions.

Topic: Quantitative MSI: Do we really need it?

During the discussions, we started to ask ourselves which users are performing (absolute) quantification with mass spectrometry imaging (MSI) and for which purpose.
Among the audience, it appeared that mostly MALDI users used quantification approaches, but some (nano-)DESI users were also present.
From the discussion, it emerged that "absolute" quantification is mostly relevant for comparison between labs, and also in toxicology.
For the groups employing MALDI-MSI, it appeared that the experiments were often conducted in parallel to LC-MS/MS from tissue homogenate extracts and/or preceded by laser microdissection from selected and subsequently extracted regions of interest. Several challenges were denoted and discussed, including:
* The extraction of selected molecules and its characterization (e.g. determination of the extraction recovery);
* The fact that the response factors differ from one tissue type from another, rendering challenging larger-scale study comparison;
* Protein binding and the consequence on the detection of selected molecules is under-discussed;
* The thickness of the tissue might introduce a bias in the results generated by quantitative MSI, as there are no evidence whether the extracted molecules are moving not only horizontally, but hypothetically vertically in the sample.

It was noted that these challenges are even more pronounced and difficult to tackle for quantification of endogenous compounds.
We discussed the different strategies that are employed but concluded that there are currently no consensus amongst the community, which is lacking best practice amongst the different labs.
This discussion was a good opportunity to remind the existence of the following white paper published in 2015 by McDonnell *et al.*
Discussion point: reporting guidelines for mass spectrometry imaging - PubMed (nih.gov)
which about guidelines for reporting mass spectrometry imaging data. However, we concluded that these guidelines are not used very often, and that discussions in that direction should be. This would allow to better harmonize the results obtained in between different lab and maximize the chances to reproduce experiments from one lab to another.

Topic: Data Analysis / Artificial Intelligence / Machine Learning

Every round started with the rhetorical question who applies Artificial Intelligence (AI) for data interpretation in MSI and in general there were only very few participants who actually used AI. Rephrasing the question towards machine learning (ML) approaches a few more hands went up. But the discussion showed that even amongst the attendees a different understanding of AI and ML was given. One participant came from the field of chemometrics and correctly stated that many researchers who do MSI use rather chemometric approaches than AI or ML, meaning that chemical information is gathered from MSI data sets. It was agreed between the more experienced participants that for AI and ML a certain amount of data is needed to train for instance a neuronal network. Data which is very often missing. In neither group a clear definition for AI in MSI could be given – it was agreed that AI and ML are general terms describing a broad range of advanced bioinformatics tools but not a data analysis which includes for instance a simple classification task, a hierarchical cluster analysis, principal components analysis or the automatization of a more labor intense data interpretation. The discussion group that included more experienced people (doing actual bioinformatics or starting to use ML

approaches) agreed that large data set for building strong models have to have “good” data sets, meaning bullet proof data sets. But this is so far not defined for MSI. Are we talking raw data? Image data? Histological images with gradings from the professionals? But is a histologist / pathologist actually able to help the MS person to judge data – a close collaboration and good communication is mandatory for this.

The more experienced participants pointed out that for training a model one has to run the analysis and refine the model in many iterations, which is only possible if the ground truth is available. AI and ML makes a “cloud” of seemingly independent data understandable. So AI/ML does not give the answer but helps to judge data sets. However, human common sense is indispensable in the process.

But where to start such a process? There was a clear agreement that one has to always consider the end-users’ research questions from which hypotheses have to be built and then either proven or rejected. If an unsupervised or supervised process is helpful for this has to be decided on the actual research problem.

One participant emphasized in particular, that today a change from clinical applications towards hypothesis generation is necessary and will drive the field of AI/ML application in MSI forward.

At some point all groups came to the finding that valid, huge data sets for model building have to come from databases. But open access databases are missing and if there is a database it is not well curated and important information for hypothesis driven approaches is missing.

The most positive outcome from this discussion group was the fact that everyone acknowledges the effort to involve students in their MSI projects who can bridge the gap from data generation to data handling, i.e. students who are bioinformaticians by training who furthermore developed their skills in an environment that is gernating the data per se. This is a natural way to bring data to a meaningful result. However, from the bioinformaticians point of view there is no clear advice on the programming language - is R, Python or MathLab the best way to go forward? Yet, the end-user requests a simple, ideally WYSIWYG, solution where programming skills are not needed.

A first improvement for the current state of the art would be to offer more courses where wet-bench researchers are working/learning together with bioinformaticians. Only by this we will generate a common acceptance for both sides and meaningful outcome.

Topic: MSI and omics data – how to integrate and report them?

Many workflows exist that combine the largescale omic analysis of different analytes from a single tissue section. Once these image datasets are created, they become quite complex and difficult to integrate. The MSI and ‘omics group had a stimulating discussion on methods, software and current pitfalls related to this topic. Group members reported a broad range of techniques that were being integrated. These included omic level combinations of analytes such as tryptic peptides, proteins, metabolites and lipids. Techniques of nano-DESI and MALDI were the primary imaging modalities. Primary alternative omics techniques combined with the MSI data were transcriptomics and LC-MS/MS proteomics. Nearly all individuals currently report imaging omic data in parallel, instead of in a combined image where analytes could be more closely referenced to each other. A main challenge integrating MSI omics data lies in the available software. Larger labs had in-house personnel resources to help with complex data analysis presented by integrated omics data sets. Smaller labs relied on commercial software or used R coding for small datasets. A comment was made that combining omics datasets causes files to balloon in size using significant data resources and this poses a problem in sharing data. Members described wanting to combine imaging data with differential spatial resolution. An outstanding question remained on same spatial resolution software regarding

normalization processes for the image data. Most agreed that normalization should be to a particular analyte's total ion current and not combine both ion currents prior to normalization. Researchers indicated a desire to combine multi omics datasets as time courses. Overall, there is significant work being done to combine MSI data with other spatial biological analyses and the major gap lies in the available and accessible software to create and evaluate the datasets. New strategies are sought for data sharing/deposit so that combined data can be further studied and utilized by different research groups.

Topic: Multimodal imaging – is it worth the effort?

Multimodal imaging sparked a lively discussion, with a range of different opinions on the topic. We discussed a big variety of imaging modalities, with a special focus of course on mass spectrometric imaging techniques, and mainly MALDI MSI. Other imaging modalities, such as spatial transcriptomics, Raman imaging, and microscopy were brought up during the discussion. One of the main questions risen during the discussion was what are the benefits, and most importantly what are the main applications of multimodal imaging. One of the main uses of multimodal imaging discussed was for the acquisition of orthogonal data, if possible, on the same sample/tissue section, for the construction of molecular networks, and generally to acquire a better, more holistic understanding of the underlying biology. Another application that was discussed, was the use of non-mass spectrometric imaging techniques, for the "correction" / normalisation of the mass spectrometry imaging data, e.g., for the correction of ion suppression, based on Raman imaging.
Challenges and issues associated with multimodal imaging were also considered, with the main one being the destructive nature of mass spectrometry, which does not always allow the imaging of the same tissue section with different modalities. The use of consecutive sections was offered as a solution to this issue, however, many participants argued that the localisation could be significantly altered between consecutive sections, which could create problems during the correlation of the results from the various imaging modalities. Another alternative solution proposed to overcome this issue was the careful consideration of the sequence of the imaging modalities used, starting from non-destructive imaging techniques, such as microscopy, and moving towards the more destructive mass spectrometry imaging technologies.

Topic: MS/MS and MSn imaging

Basically, the need for including MS/MS and/or MSn in the imaging experiment is associated with the analytical questions. Simply, it is not always needed and sometimes offline acquisition of fragmentation spectra is easier achievable.
Pros:
- There is no need for mass spectrometers with high resolving power
- Gain in sensitivity
- Identification of analytes
- Increase in confidence of annotations
- Elucidation of isobars and/or isomers
- Protein identification through proton transfer charge reduction (PTCR)

Cons:
- Reduced duty cycle
- Restriction to specific number of precursor ions (SWATH acquisition could help with this)
- Comparison of fragments solely on intensity does not account for fragmentation efficiency differences

How can we improve the versatility of our detected analytes?
Reactive chemistry approaches provide improved sensitivity and higher degree of selectivity/specificity. Further, the addition of proper dopants can remove molecules that cause ionization suppression and at the same time enhance the detection of difficult to ionize molecules.
Separation methods are powerful and provide complimentary information to the

acquired ion images. However, they are not scaled to the time scale of the imaging experiments and therefore are conducted offline. Proper sample handling is required for maximizing the information acquired through the combined approaches.

Topic: Ion annotation and how to validate it

Annotation of the ions detected with mass spectrometry imaging was discussed together with the different confidence levels of the annotations/tentative identifications, and finally approaches to increase the confidence of the identifications. LC-MS/MS, using standard compounds was proposed by the majority of the participants as the technique of choice for the confirmation of the ions' IDs, coming however with certain limitations, such as the cost of standard compounds. Mass spectrometry imaging in MS/MS or MSn mode and ion mobility were also suggested as alternatives to LC-MS/MS for the identification of selected ions. The conclusion of the discussion was the need for guidelines for the ion annotation in MSI experiments and the reporting of the ions' IDs.

Topic: Isobars and isomers – how can we separate them in MSI?

This topic was discussed shortly. The consensus is to employ instrumentation fitted with ion mobility capabilities. If such technology is unavailable, reactive matrices or derivatization methods are worth exploring.

This Focus Group was organized by:

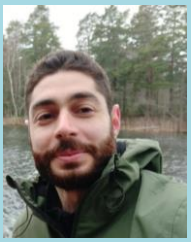
Martina Marchetti-Deschmann
TU Vienna. Austria

Peggi Angel
MUSC, South Carolina

Tiffany Siegel
Boehringer Ingelheim, Germany

Ingela Lanekoff
Uppsala University, Sweden

Samuele Zoratto
TU Vienna, Austria



Leonidas Mavroudakis,
Uppsala University, Sweden

Stefania Maneta-Stavrakaki
Imperial College London, UK