



## Advanced Analysis of Imaging Mass Spectrometry Data

Friday, October 11, 2019 | 9:00 am - 4:00 pm

**TO REGISTER for the special pre-conference workshop** cost is \$100 payable through IMSS website at <https://www.imagingmssociety.org/>

**ASILOMAR GUEST ROOM LODGING** within ASMS Asilomar Conference room block is available on Thursday, October 10 for those interested in participating in this special pre-conference workshop. Asilomar reservation info here: <https://www.asms.org/conferences/asilomar-conference/lodging-at-asilomar>

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**Workshop Chair: Chris Anderton**, Ph.D, Pacific Northwest National Laboratories

9-9:10 am: **Introduction/Program Overview**

9:10-10:25 am: **MetaSpace: platform for metabolite annotation of imaging mass spectrometry data**

1. Principles and pitfalls of metabolite and lipid annotation in imaging MS
2. How to use METASPACE for automated annotation (tutorial, examples, QA)
3. Advanced features and scenarios of using METASPACE (offsample filtering, co-localized ions, neutral losses, derivatization, programmatic access)

The url to the software website is <https://metaspace2020.eu/>

10:25-10:45 am: *Break*

10:45 am-Noon: **MSiReader: open source Matlab GUI and function library for visualization and analysis of Mass Spectrometry Imaging data sets**

1. Peak finding, normalization and untargeted analysis
2. Image correlation and principal components analysis
3. Algorithm development with the application programming interface

The url to the software website is <http://msireader.com>

12:00-1:15 pm: *Lunch for Asilomar lodgers. If you are not lodging at Asilomar, front desk may have tickets for sale.*

1:15-2:30 pm: **Cardinal MSI: a mass spectrometry imaging toolbox for statistical analysis**

1. Cardinal/R basics
2. Data import/export
3. Visualization
4. Pre-processing (briefly)
5. Unsupervised analysis (image segmentation)
6. Supervised analysis (classification + cross-validation)
7. Statistical hypothesis testing

The url to the software website is <https://cardinalmsi.org/>

2:30-2:45 pm: *Break*

2:45-4:00 pm: **SCiLS: Interpretation of MALDI imaging mass spectrometry data**

1. Quantitation
2. Tissue typing
3. Metabolite identification