

Galaxy **wishlist** from the mass spectrometry imaging (MSI) community

Melanie Föll

melanie.foell@mol-med.uni-freiburg.de

 [@MCFoell](https://twitter.com/MCFoell)

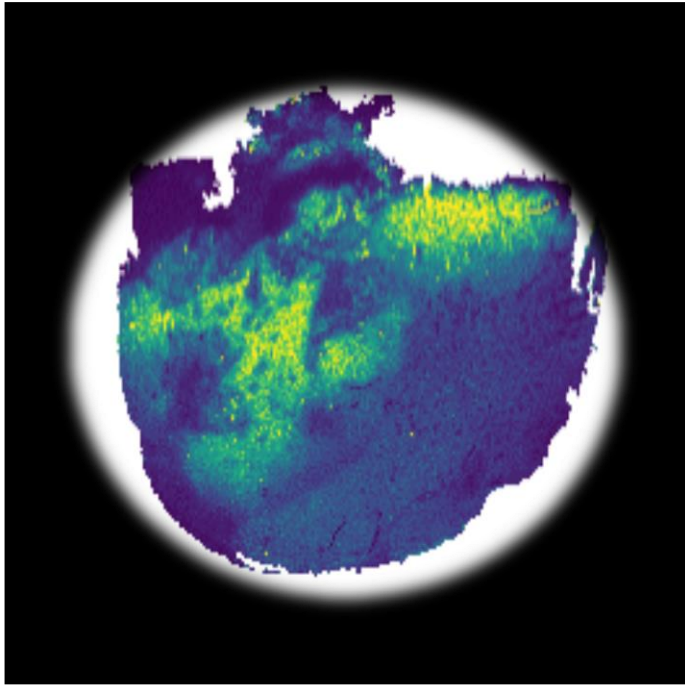
Institute for Surgical Pathology
University Medical Center Freiburg, Germany

&

Khoury College of Computer Sciences
Northeastern University, USA

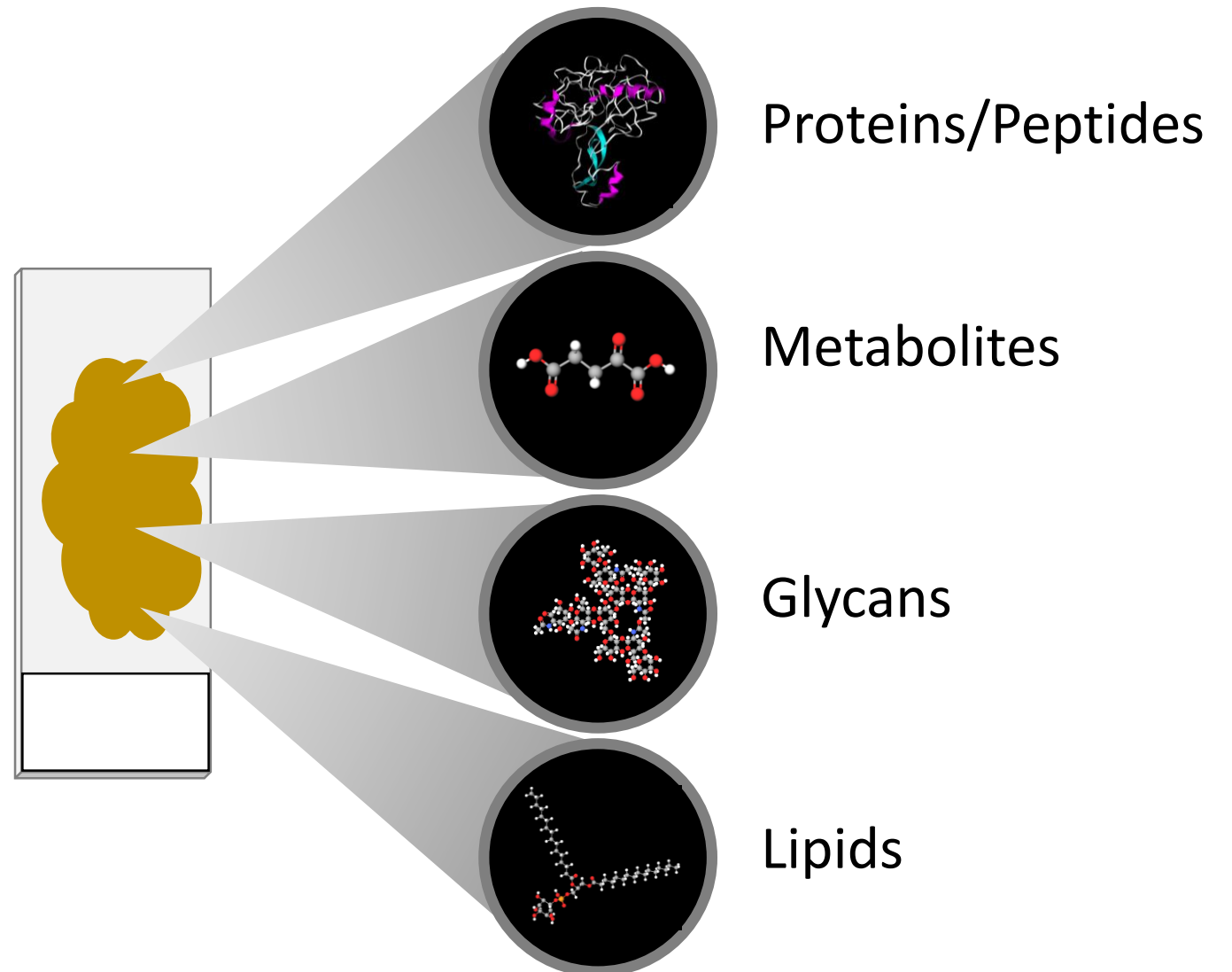
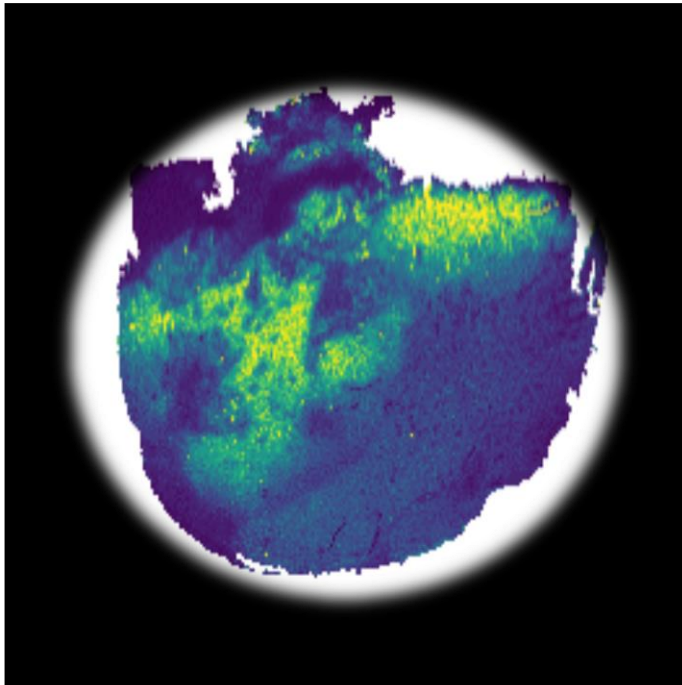


Mass spectrometry imaging enables molecular microscopy



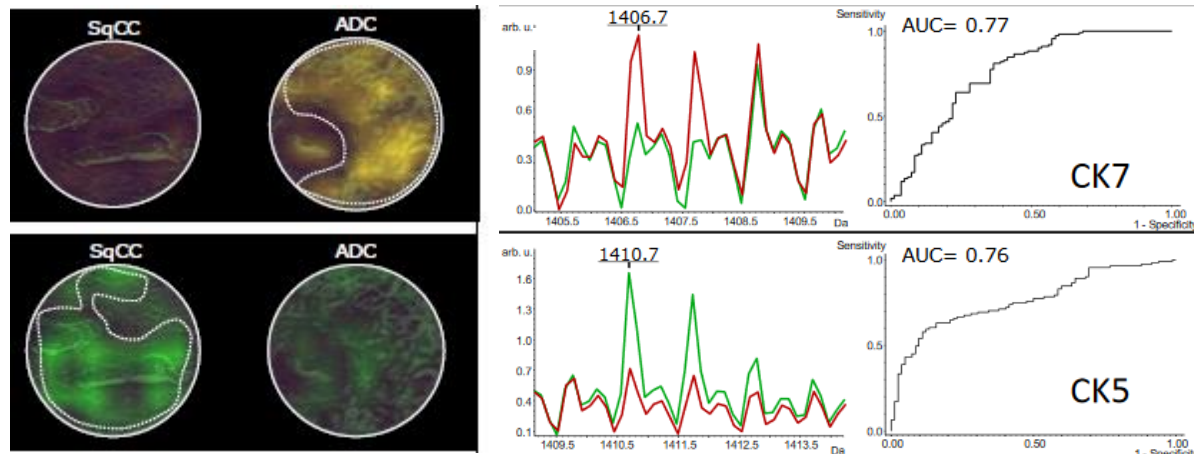
Mass spectrometry imaging enables molecular microscopy

Endogenous and exogenous analytes



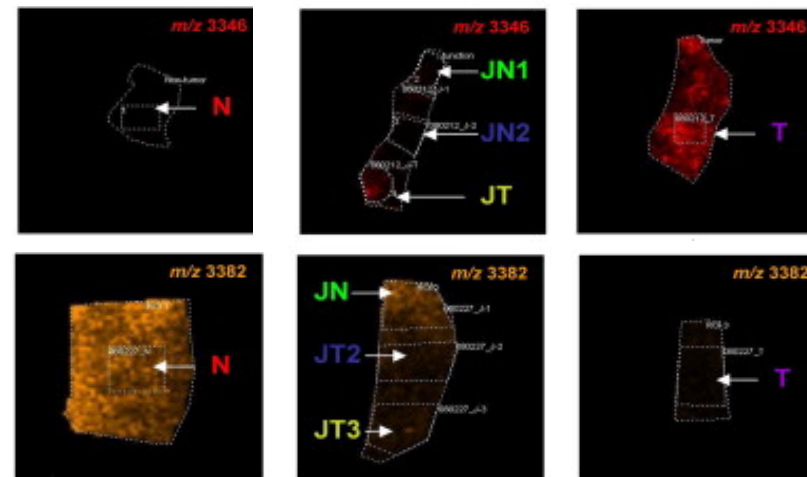
Mass spectrometry imaging in tumor research

Tumor subtyping



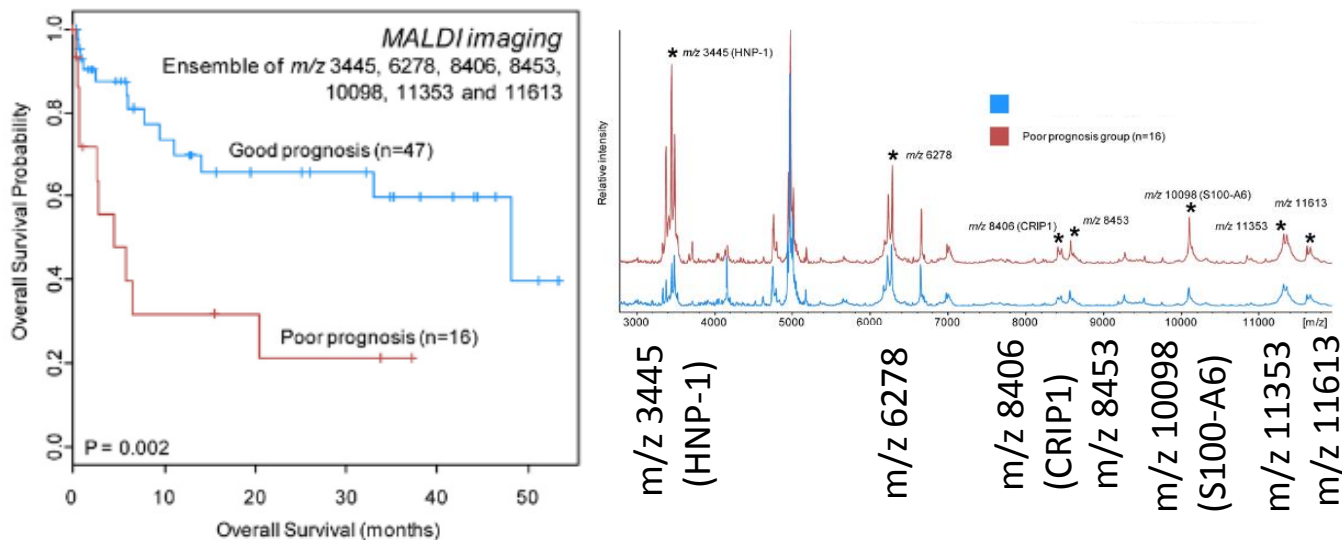
Kriegsmann 2016, Molecular & Cellular Proteomics

Resection margins / heterogeneity



Han et al. 2011, Clinica Chimica Acta

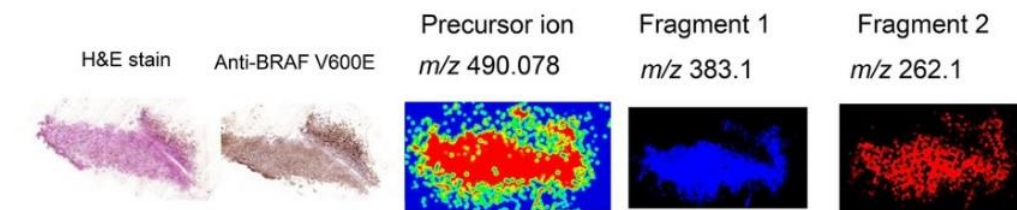
Risk stratification



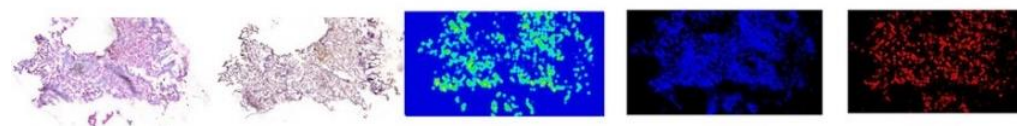
Balluff et al. 2011, The American journal of pathology

Drug imaging

MM tissue with BRAF V600E



MM tissue with BRAF Wild type

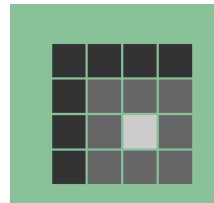


Sugihara et al. 2014, Proteomics

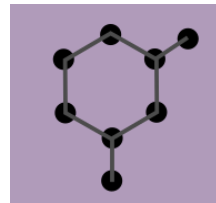
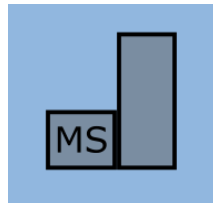
Challenges in MSI data analysis



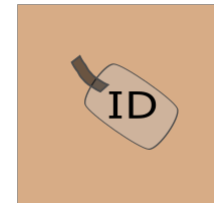
- Large datasets



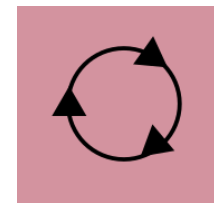
- Spatial dependence between spectra



- Diverse mass spectrometers and analytes

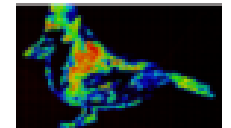


- Analyte identification

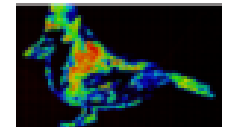


- Reproducibility via shared data and code

Our solutions



Cardinal

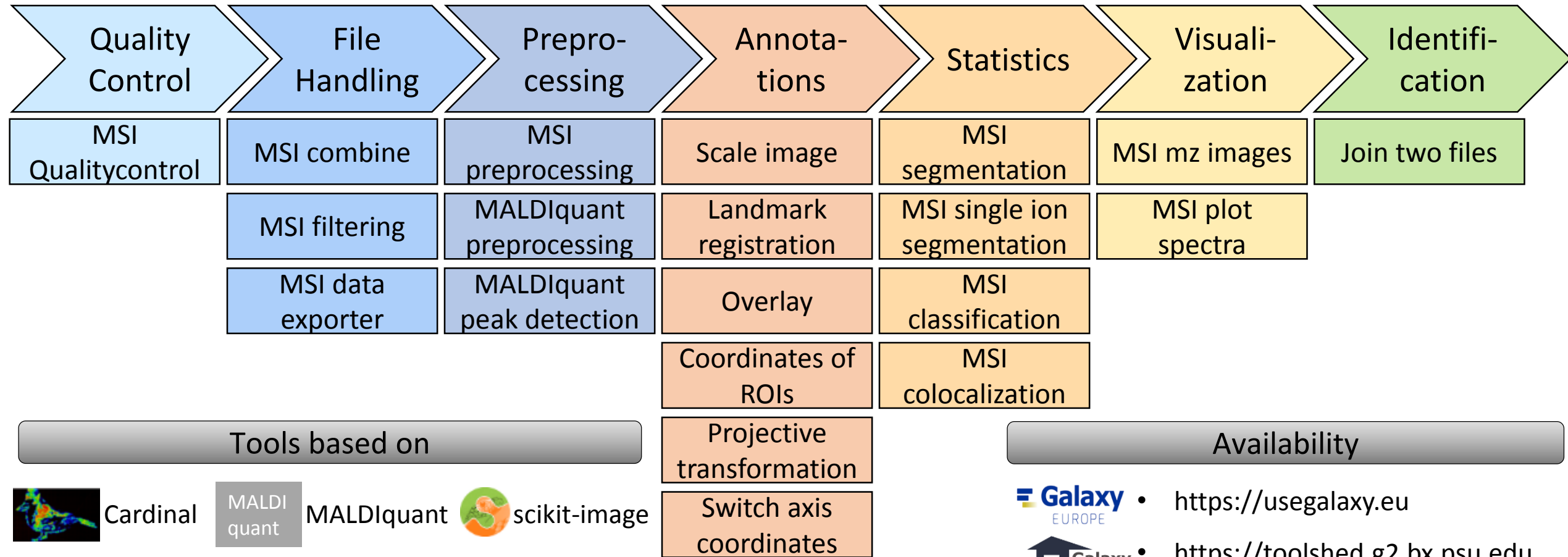


Cardinal

Only partially solved in the field,
common option: LC-MS/MS



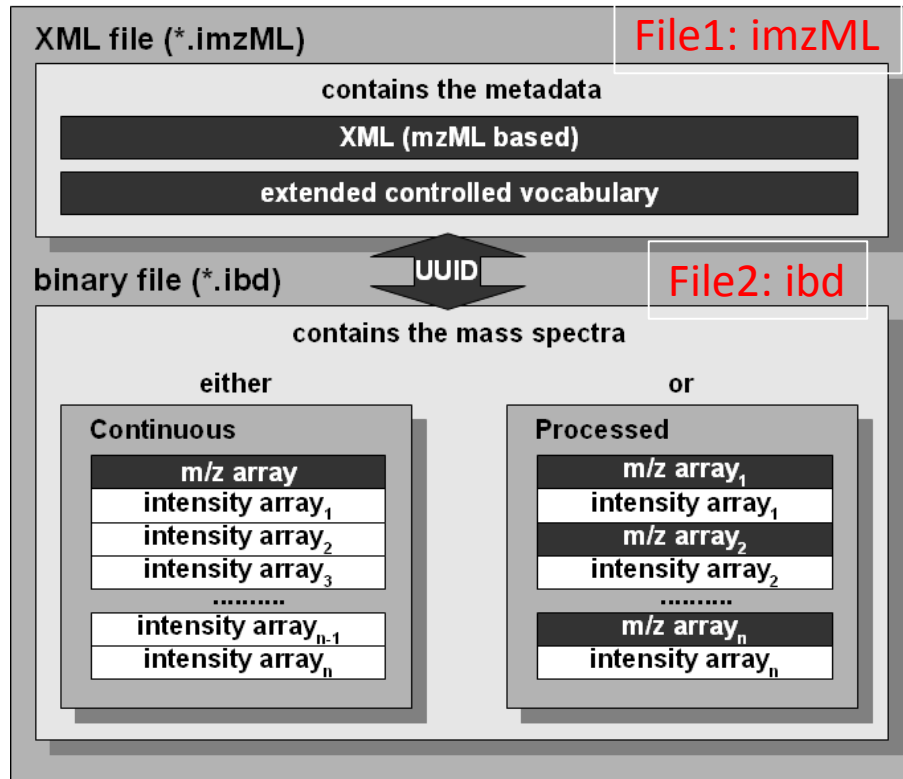
MSI data analysis tools in Galaxy



File formats: composite

imzML open standard file format

Composite upload in Galaxy



Alternative file format:
Analyze 7.5 = hdr + img + t2m

☆wishlist

- Tests for composite upload (imzML and Analyze 7.5) for new Galaxy versions
- Parallel upload of multiple composite files (collection)

File sizes

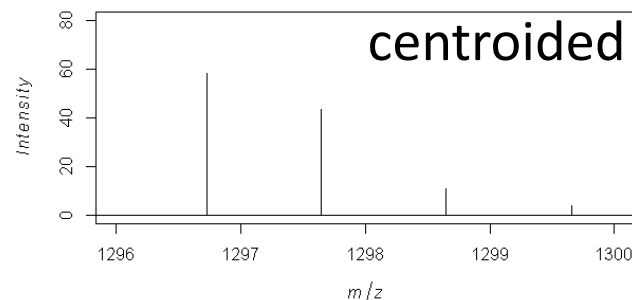
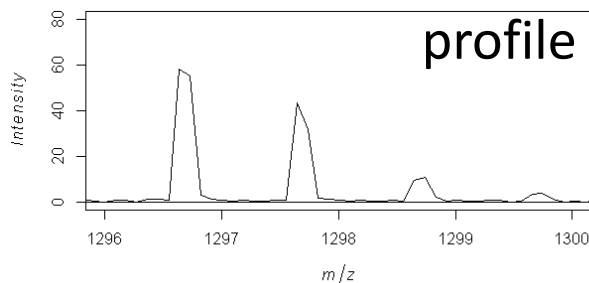
Depend on:

- Size of the tissue / sample
- Type of mass spectrometer
- Options set in the mass spectrometer
 - Spatial resolution
 - Mass resolution
 - Ion mobility
- Profile or centroided data

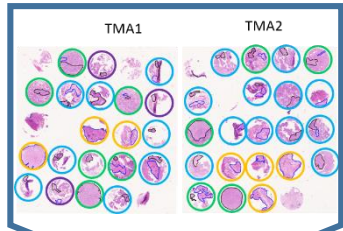
File sizes of our raw files:
0.5 - 800 GB (single file)

☆wishlist

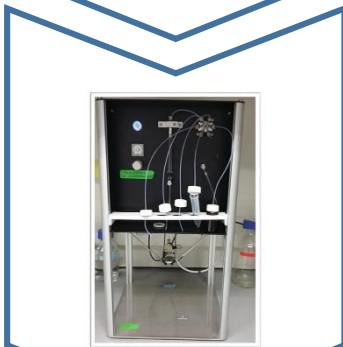
- Ideas / Suggestions for resulting problems:
- Need >>> 250 GB available per user in EU
- Need this for >>> 1 year
- Adjustment of cores and RAM for MSI tools according to input file sizes?



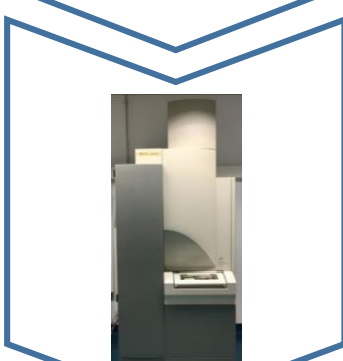
Urothelial carcinoma cohort - Workflow



39 urothelial tissue cores



Sample preparation



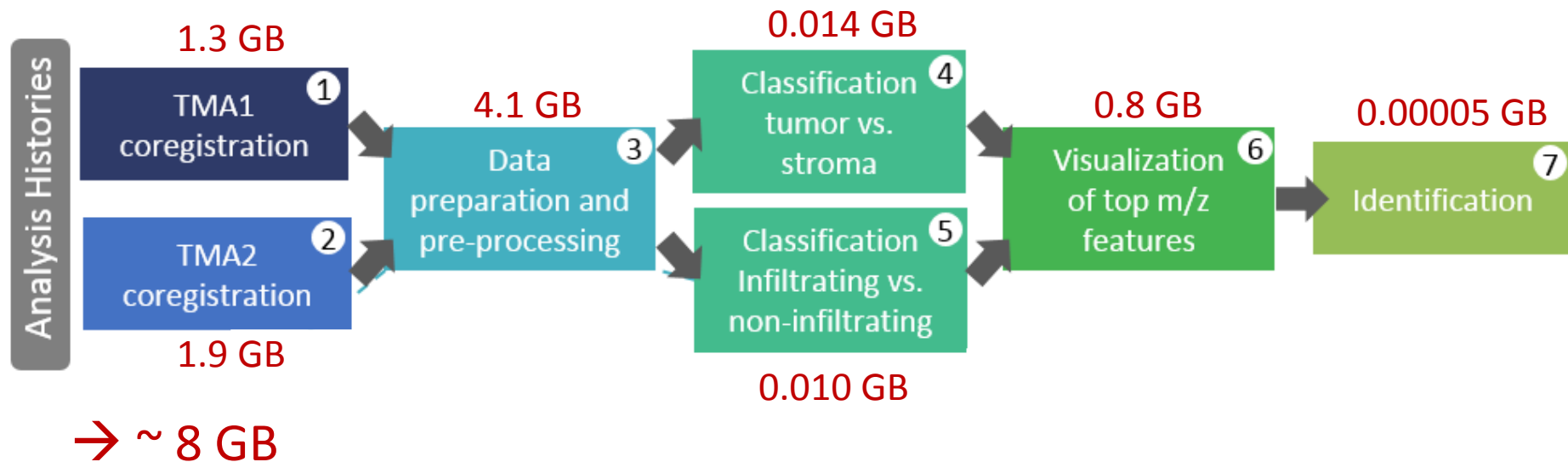
Data acquisition



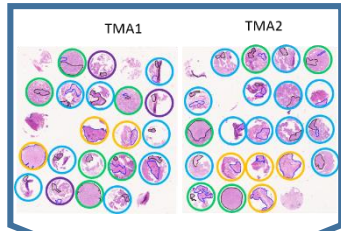
Data analysis



Analysis histories and workflows shared in Galaxy



Urothelial carcinoma cohort - Workflow



39 urothelial tissue cores



Sample preparation



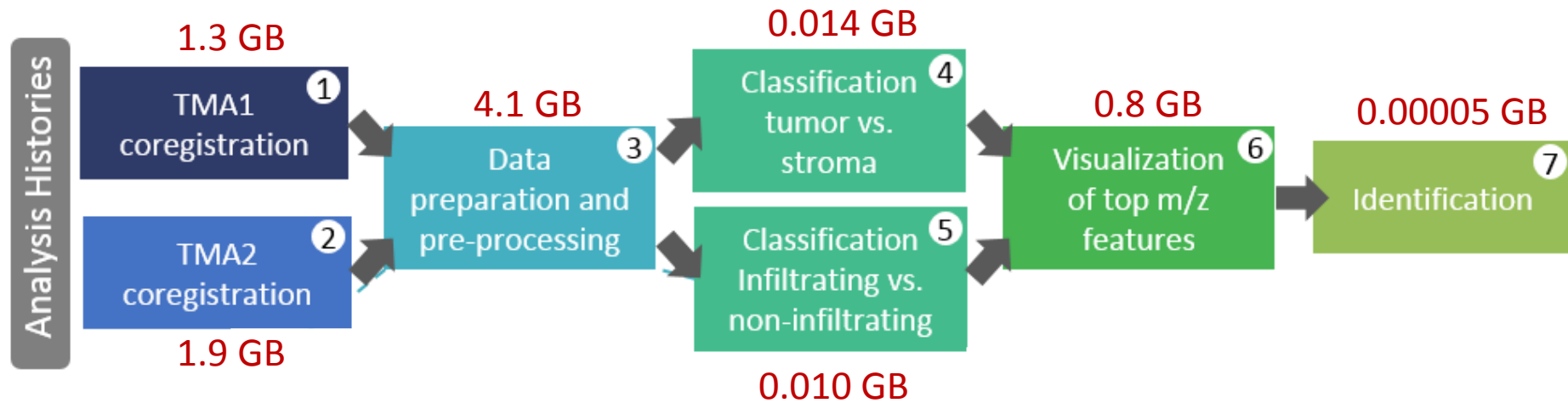
Data acquisition



Data analysis



Analysis histories and workflows shared in Galaxy

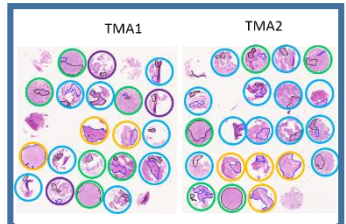


→ ~ 8 GB

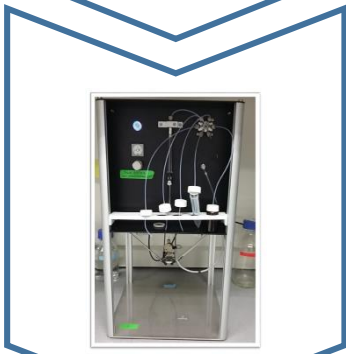
☆wishlist

- Galaxy „publication service“ → Histories shared with publications in peer-reviewed journals are removed from a users quota, stored for X years
- Option to „lock“ published histories

Urothelial carcinoma cohort - Workflow



39 urothelial tissue cores



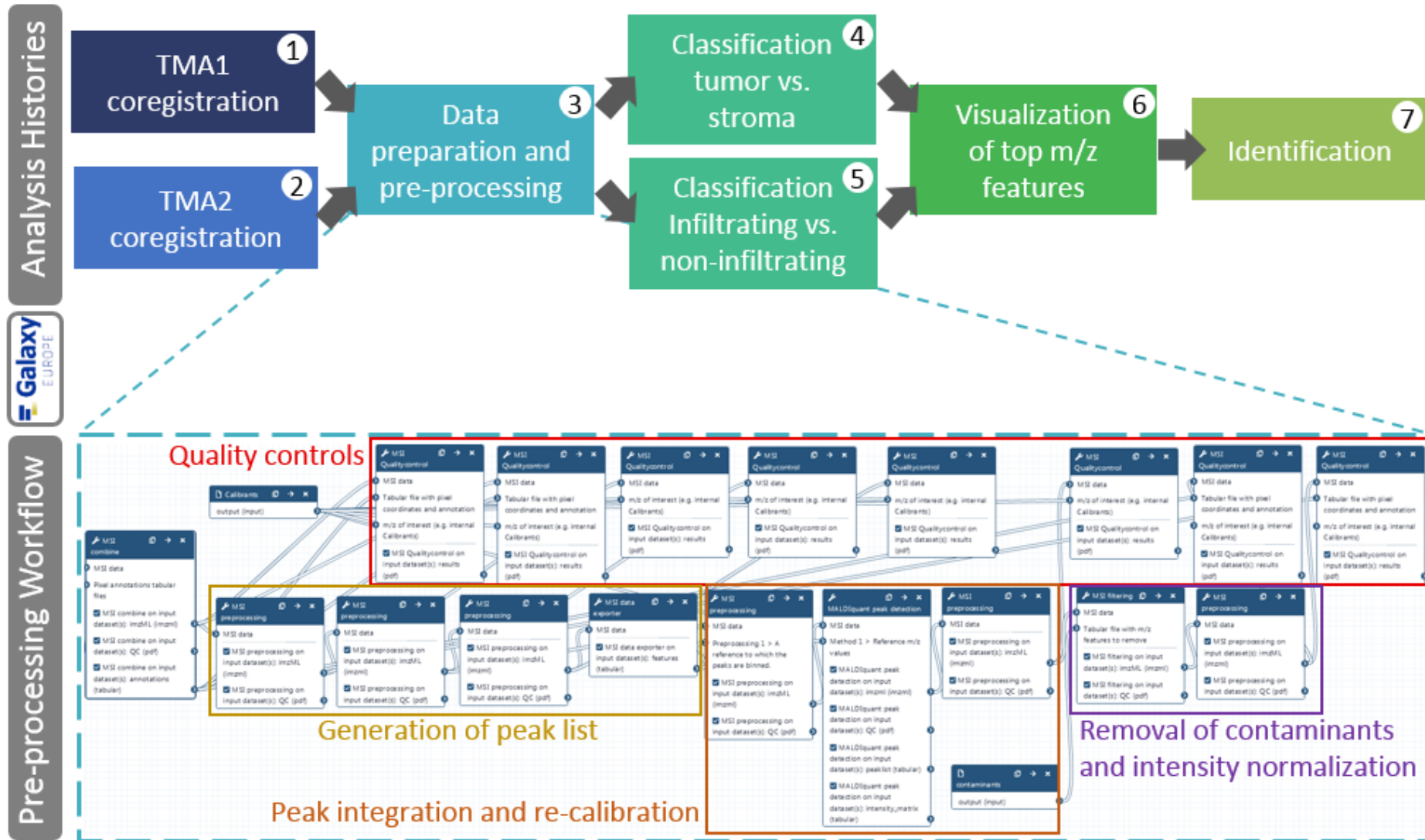
Sample preparation



Data acquisition

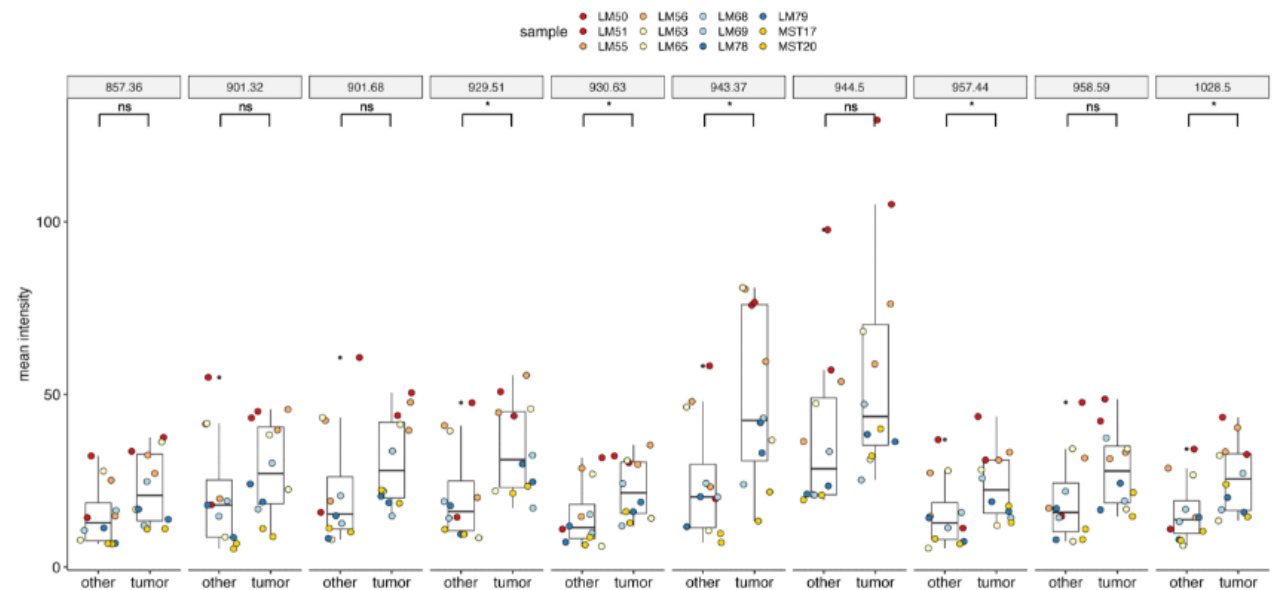
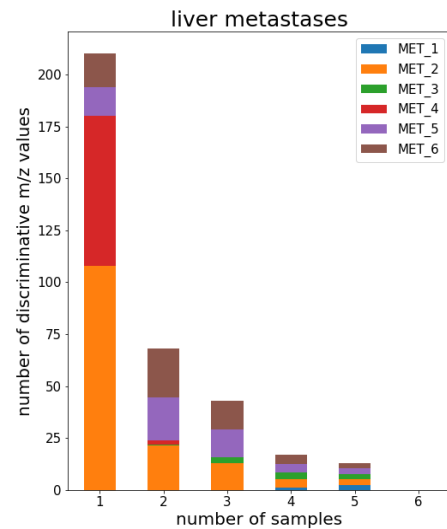
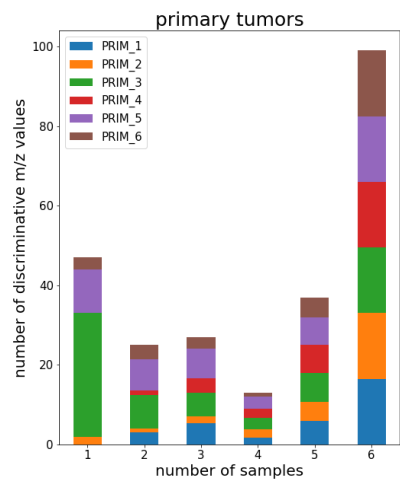


Data analysis



- Colouring of each tool box in workflow editor
- Drawing colourful boxes / annotations

- Basic visualizations in publishable quality for tabular files
 - Barplots
 - Boxplots
 - Scatter plots
 - Line plots
 - Heatmaps



- Option to configure output file from normal tool run
 - Dataset name
 - Tags

Configure Output: 'out_file1' 🔗

Label

Provide a short, unique name to describe this output.

Rename dataset

This action will rename the output dataset. [Click here for more information.](#) Valid input variables are:

- **input**(Input file)

Change datatype

Leave unchanged
▼

This action will change the datatype of the output to the indicated datatype.

Add Tags

This action will set tags for the dataset.

Remove Tags

This action will remove tags for the dataset.

Just like in the workflow editor...

Acknowledgement



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Björn Grüning

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Sai Lakkimsetty

MALDI imaging group

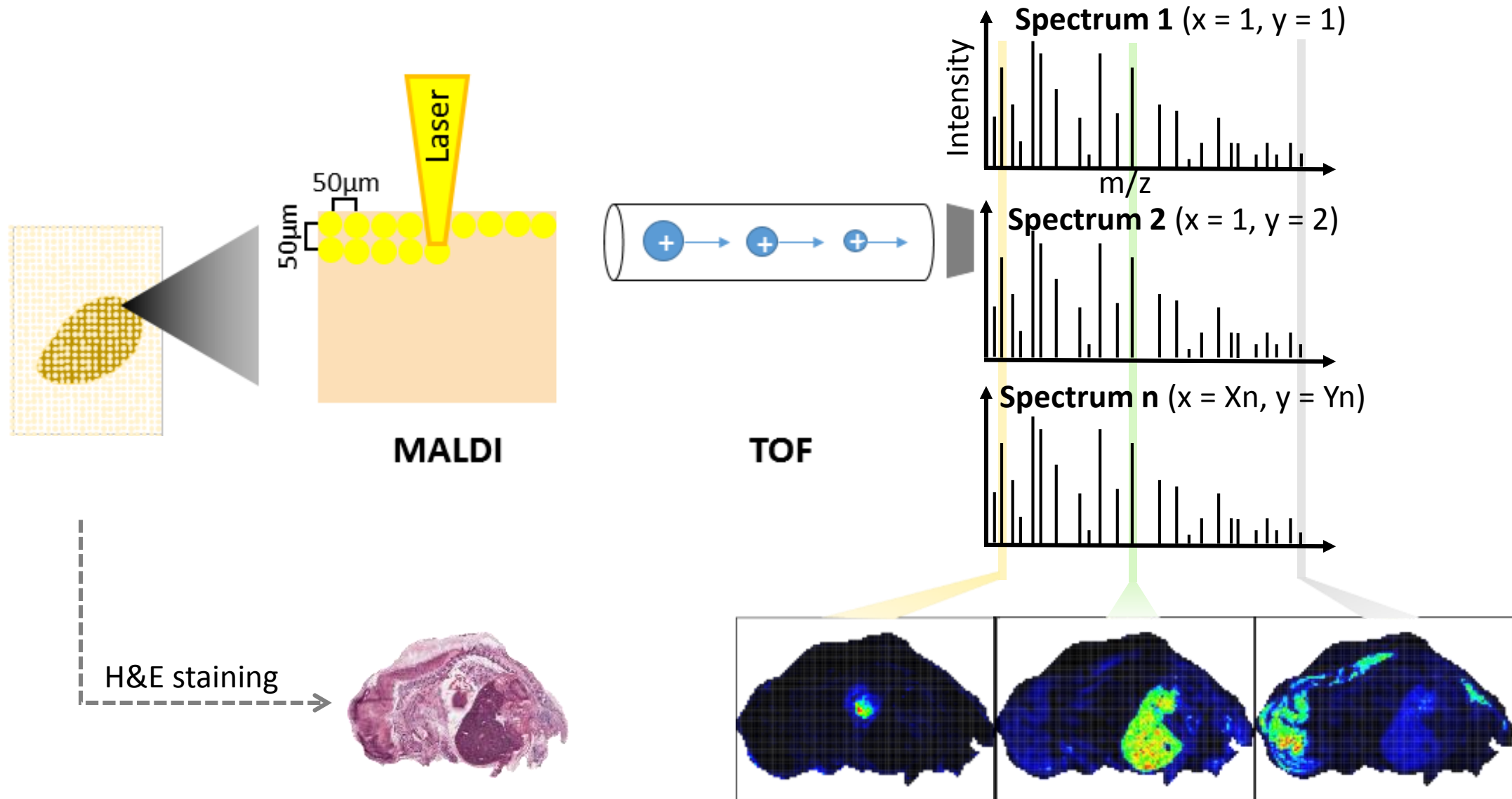
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Niko Pinter
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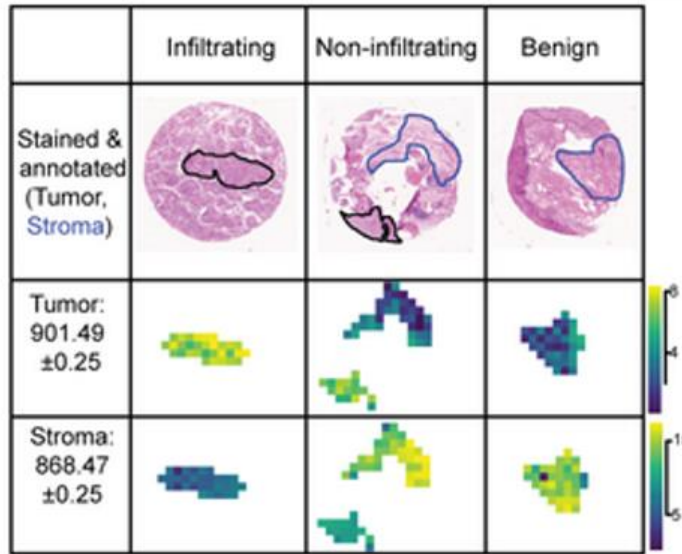
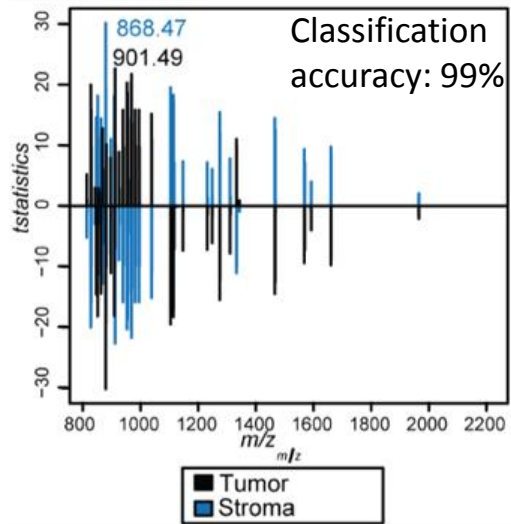


Mass spectrometry imaging

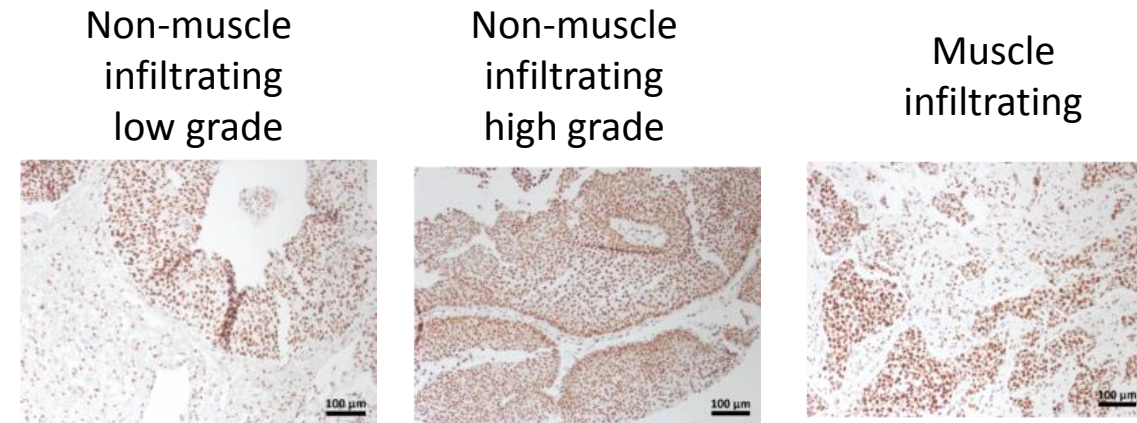


1) Urothelial carcinoma classification & IHC

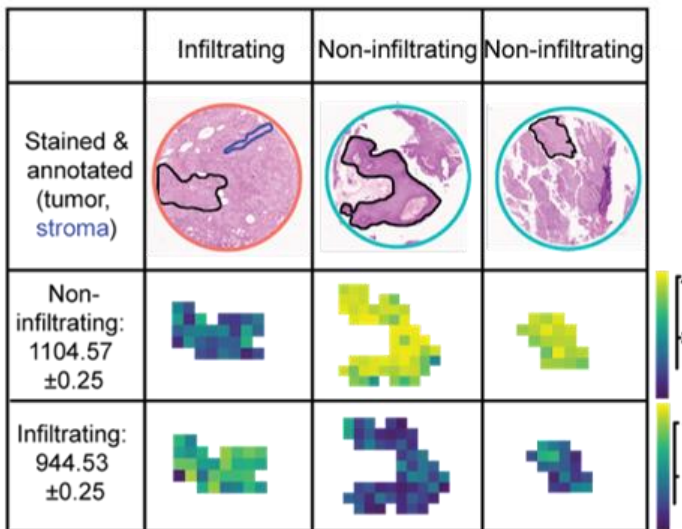
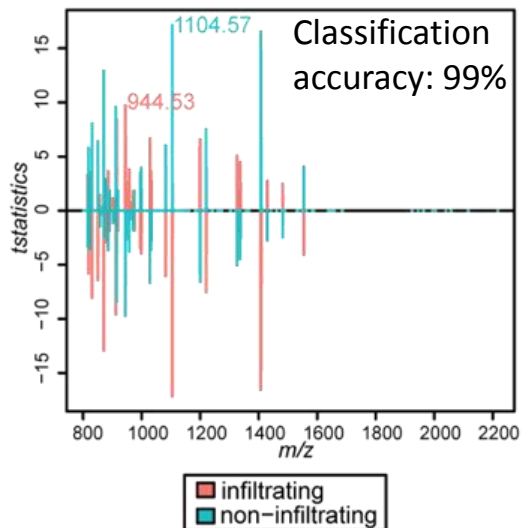
Tumor vs. stroma



Immunohistochemistry of Histone H2A

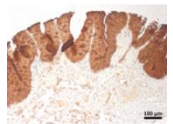
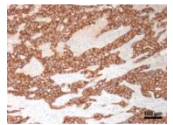
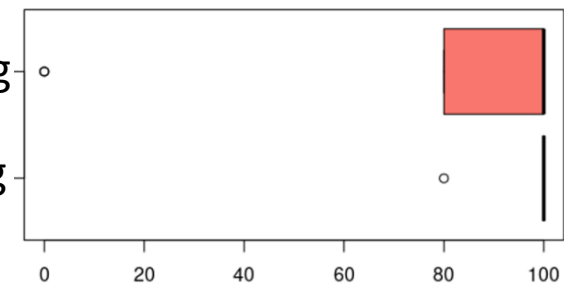


Muscle-infiltration



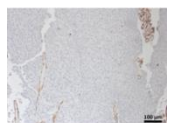
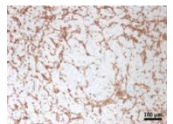
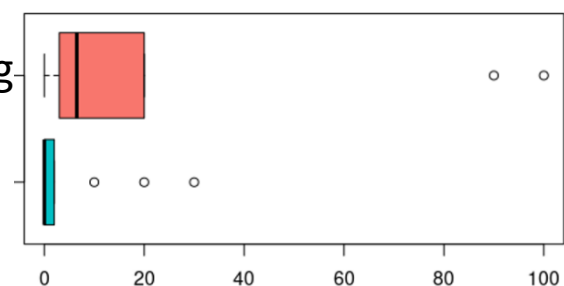
Cytokeratine 7

Infiltrating
Non-infiltrating



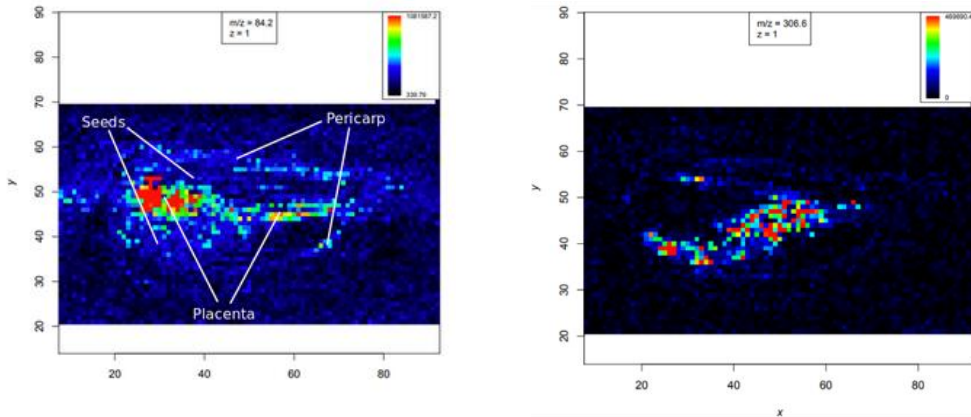
Vimentin

Infiltrating
Non-infiltrating

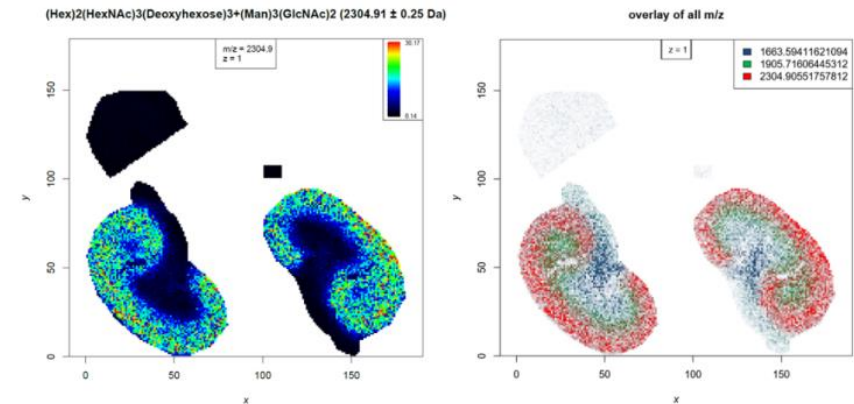


Galaxy MSI tutorials

1) Distribution of volatile metabolites in a chilli section



2) N-linked glycan distribution in mouse kidney tissue



3) Quality control of peptide distribution in mouse kidney tissue

