

Tissue Based Proteomics and Biomarker Discovery

Multivariate Data Mining Strategies for Mass Spectral Imaging

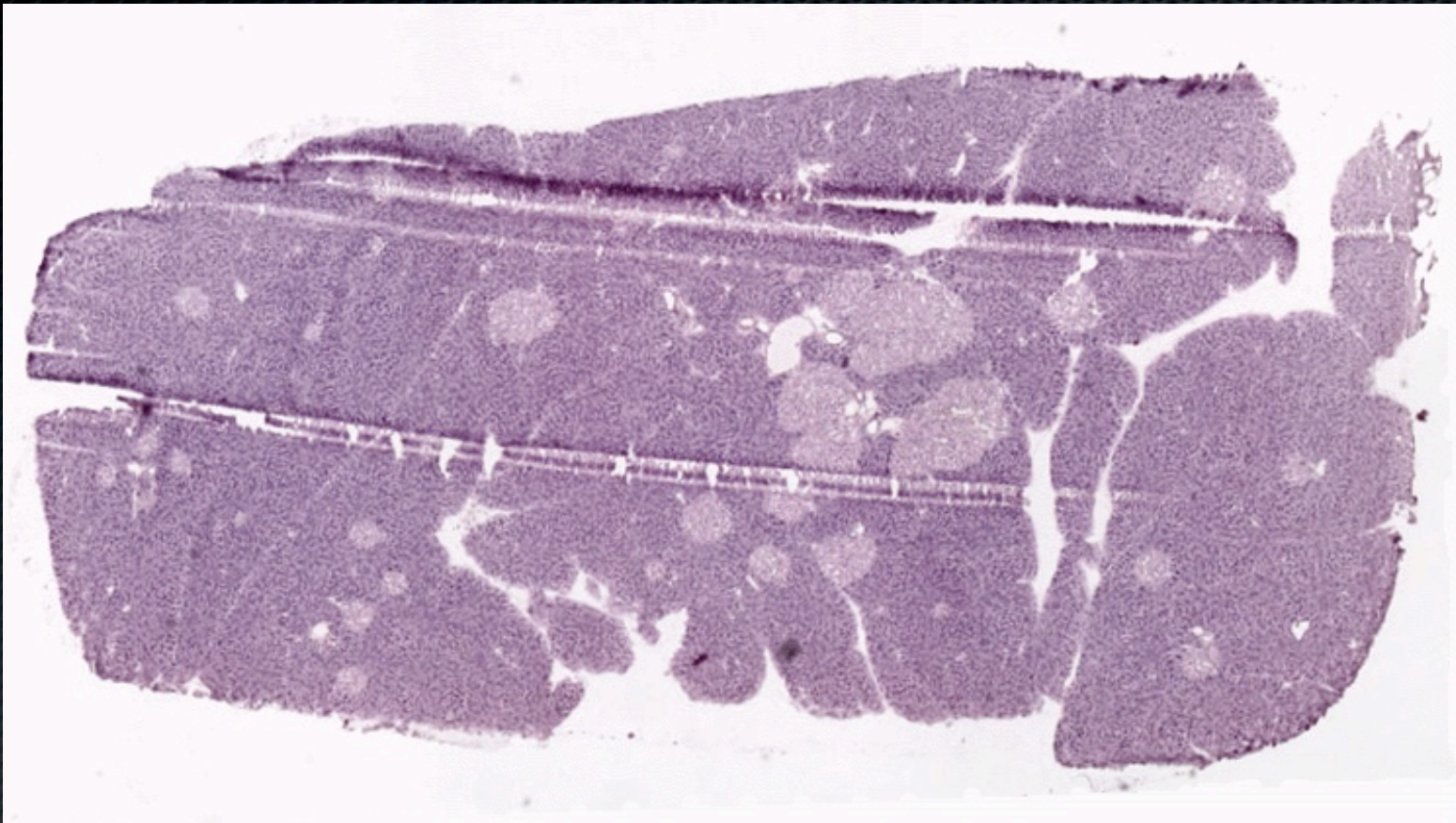
Raf Van de Plas

Promotor
Prof. dr. ir. Bart De Moor

Co-Promotor
Prof. dr. Etienne Waelkens

Katholieke Universiteit Leuven





premise - *The direct analysis of tissue is important for understanding disease.*

problem - *Mass spectral imaging is a promising technology for direct tissue analysis, but is currently hampered by lack of computational techniques.*

goal of this work - *To answer that challenge and develop multivariate data mining techniques to unlock MSI's full potential.*

- Mass Spectral Imaging
- Computational Analysis of MSI Data

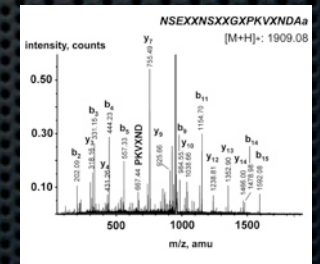
Mass Spectral Imaging

Mass Spectral Imaging

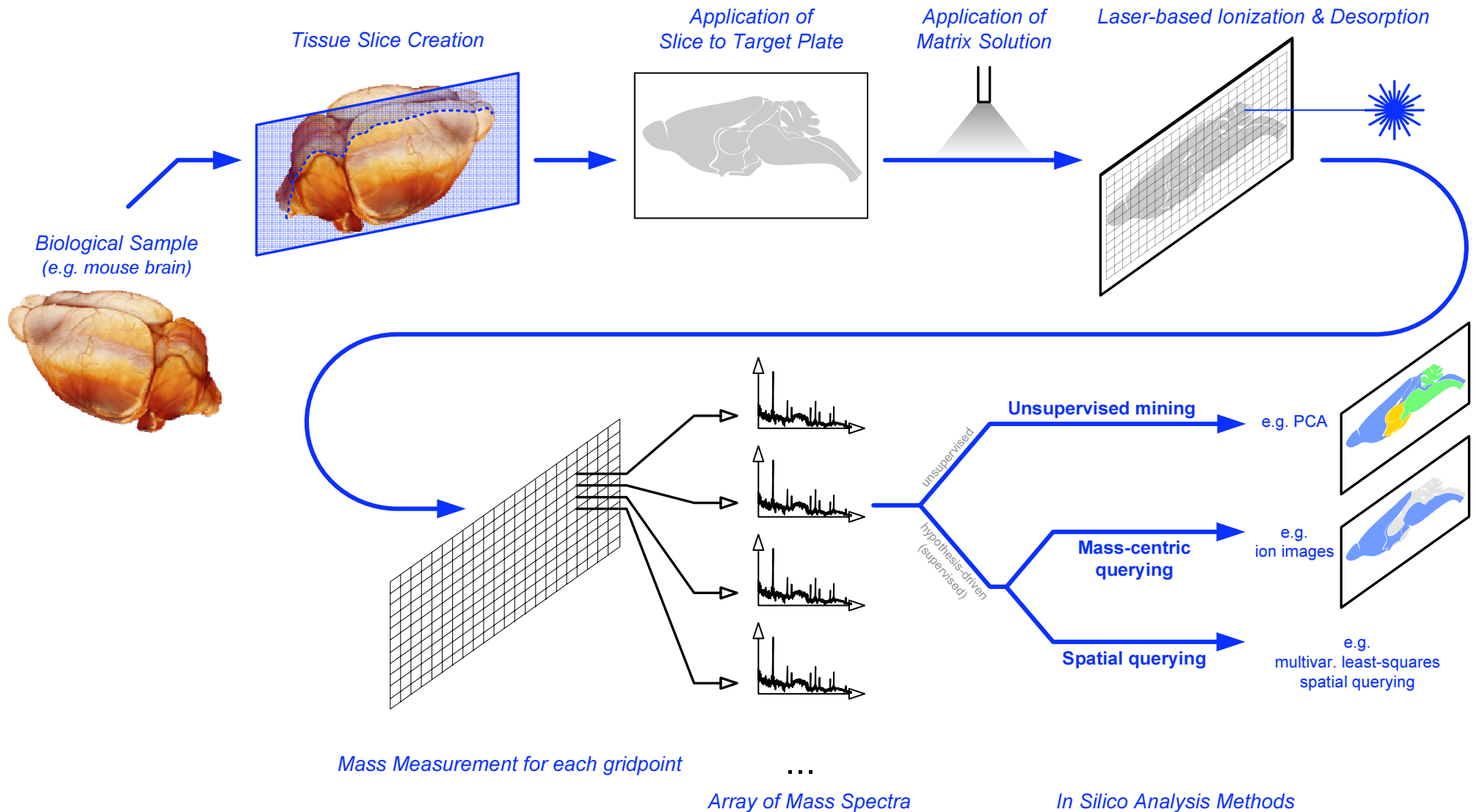
Objective

To link together two aspects:

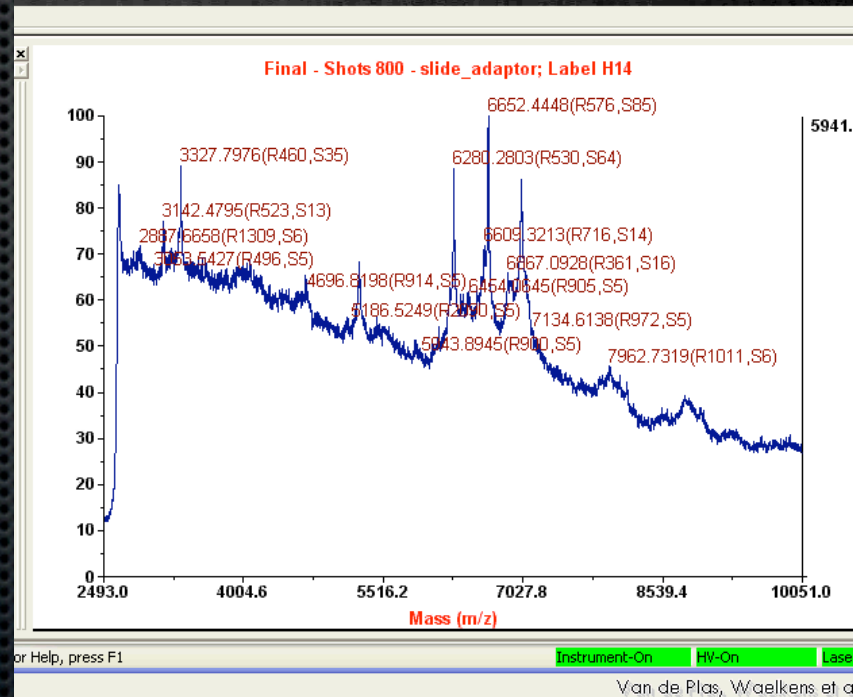
Biochemical characterization



Mass Spectral Imaging



Mass Spectral Imaging



Mass Spectral Imaging

Pros and cons

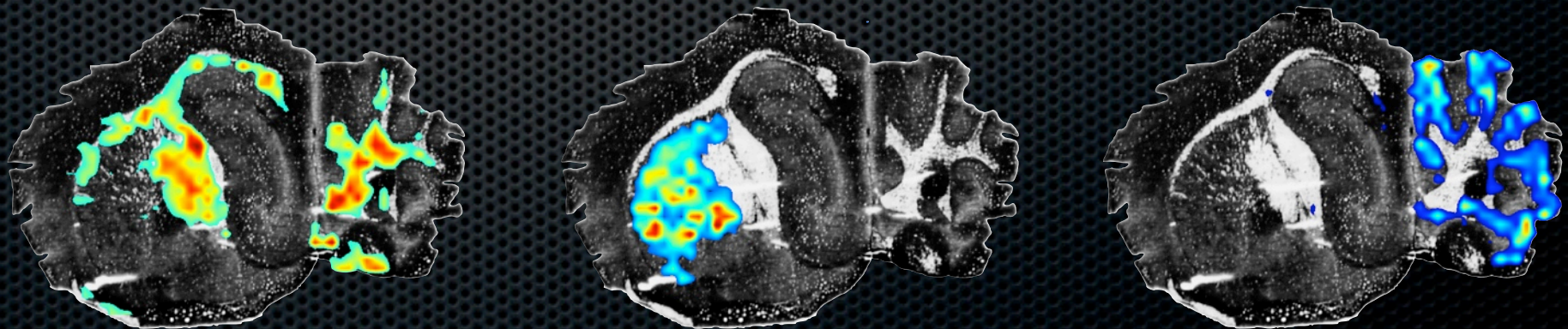
Pros:

- **Requires no chemical labeling of sample**
- **Requires no prior hypothesis** - Excellent exploratory merit
- **Very high specificity** - Better than most immunobodies
- **Massively multiplexed** - Hundreds of ions spatially followed in one experiment
- **Insight into intermolecule relationships** - Inherent multivariate nature

Cons:

- **Relatively low spatial resolution**
- **Sensitivity is tissue-dependent**

Complementary to traditional molecular imaging modalities:



Mass Spectral Imaging

Starting up...

- **Proper sample preparation and extraction**

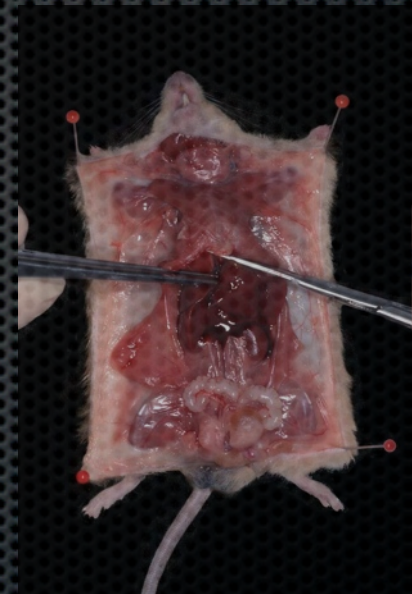
tissue extraction, freezing, washing, cutting, collaboration with pathologists,...

- **Experimentation with matrix deposition**

experimentation with matrix solutions, heterogenous deposition operation (self-made, Labcyte, Shimadzu)

- **Fusing heterogenous equipment**

custom target plate (ABI), ITO conductive glass slides (Bruker), conductive tape (Shimadzu), different MS platforms,...



Conclusion:

Proper MS-related computational analysis requires a lot of physics, biochemistry, and MS-specific context and experience. 'Standardized' computational approaches rarely fit MS or MSI data directly.

Mass Spectral Imaging

Starting up...

Heterogeneous instruments & formats



Applied Biosystems Inc.
4800 MALDI-TOF/TOF Analyzer



Bruker Daltonics
UltraFlex II w/ SmartBeam Laser



Shimadzu AXIMA TOF²

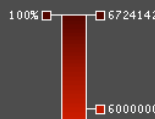
Others...



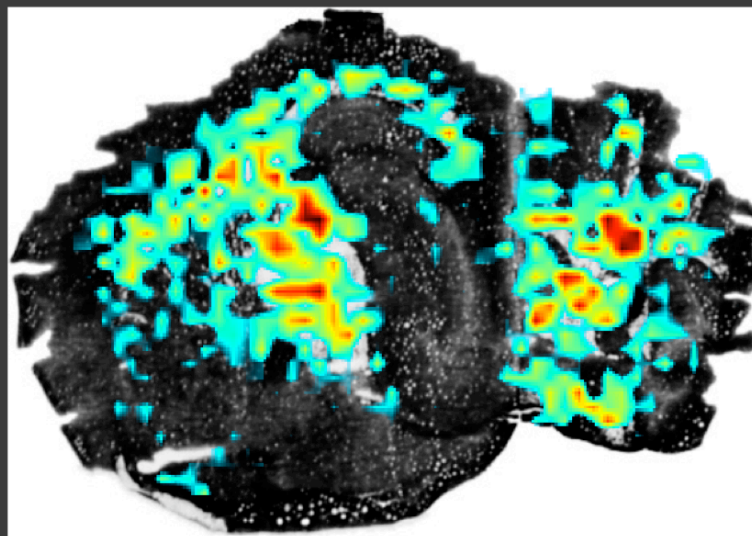
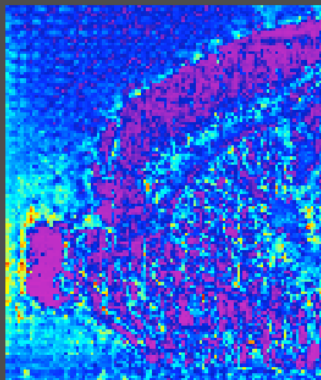
Unravel software
Java-based
20.000 lines of code

Uniform analysis & exploration

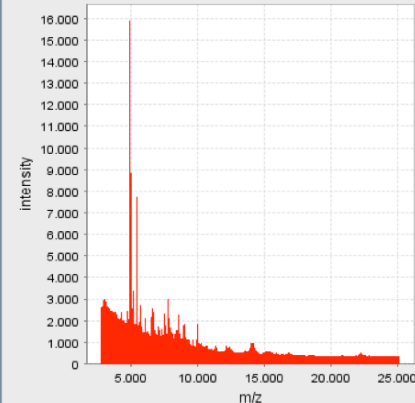
- Data export
 - ↳ Computational & statistical analysis
- Image export
- Data exploration
- Real-scale representation
- Ion image generation
- Overlay with different modalities (e.g. microscopy)



Mass spectrum at x = 8450.0 μm, y = 2650.0 μm



Mass spectrum at x = 7200.0 μm, y = 2700.0 μm



Mass Spectrum

size: 6490 entries
 m/z-range: 2,800.0718 to 25,115.6289 Th
 min intensity (mass spec): 262.0
 max intensity (mass spec): 15880.0
 position:

min intensity (collection): 0.0
 max intensity (collection): 0.0

page 1 [next] [last]

m/z	intensity	%intensity (in mass spec)	%intensity (in collection)	entry
2,800.0718	2491.0	15.95 %	∞ %	0
2,801.7937	2493.0	15.96 %	∞ %	1
2,803.5161	2487.0	15.92 %	∞ %	2
2,805.2393	2492.0	15.96 %	∞ %	3
2,806.9626	2413.0	15.45 %	∞ %	4
2,808.6868	2445.0	15.66 %	∞ %	5
2,810.4114	2498.0	15.99 %	∞ %	6
2,812.1356	2510.0	16.10 %	∞ %	7

Viewport navigation

Translation Zoom Ind. Zoom Rotation Po

Center

Autofit

Viewport navigation

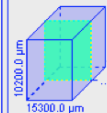
Translation Zoom Ind. Zoom Rotation Positioning Background Color mapping

Open Image file: cropped_mousebrain2.jpg

X (μm): -200,00 Y (μm): -250,00 Ratio (μm/pixel): 33,00

Rot (deg): 0,00 Flip x Flip y

Data explorer



m/z intensity m/z-indices intensity-indices TIC & extrema entry-indices

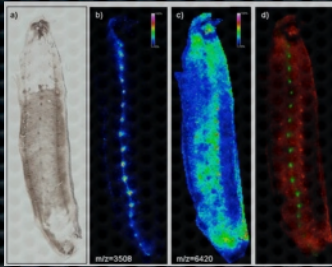
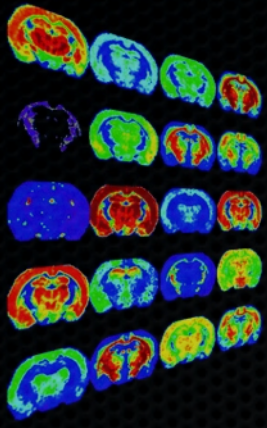
m/z-value: 14140,00 ± 2,00 Go

Flatten by Max

Live update

Mass Spectral Imaging

Experiencing rapid growth...



MALDI

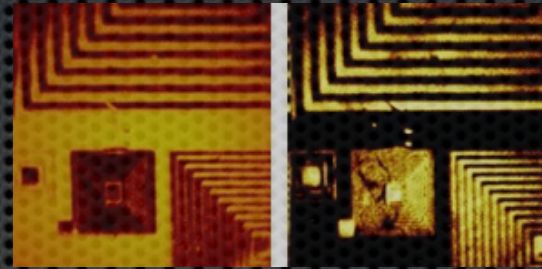
organic, biomacromolecules

Caprioli, Vanderbilt University

McDonnell, Leiden University

Fournier & Salzet, University of Lille

K.U.Leuven



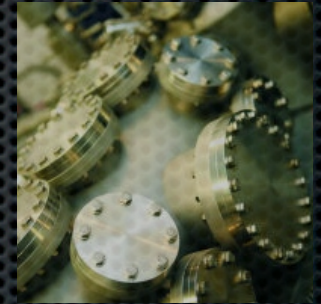
SIMS

anorganic, small molecules

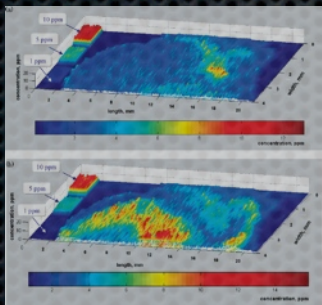
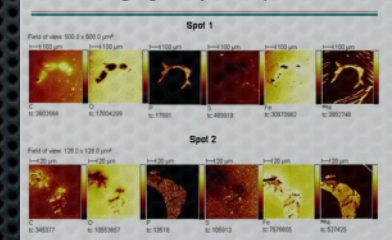
Heeren, AMOLF Amsterdam

Vickerman, University of Manchester

Winograd, Penn State University



SIMS imaging: Mayerthorpe meteorite



LA-ICP

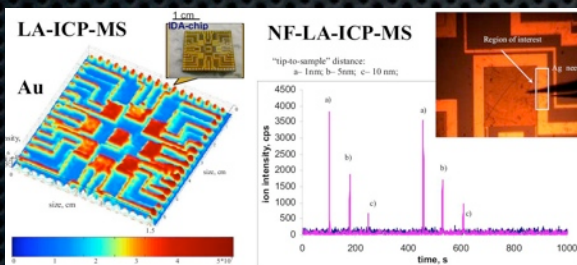
anorganic, material science

Becker, Juelich Research Centre

LA-ESI

organic, ambient pressure

Vertes, George Washington University



DESI

forensic apps, latent fingerprints,...

Cooks, Purdue University

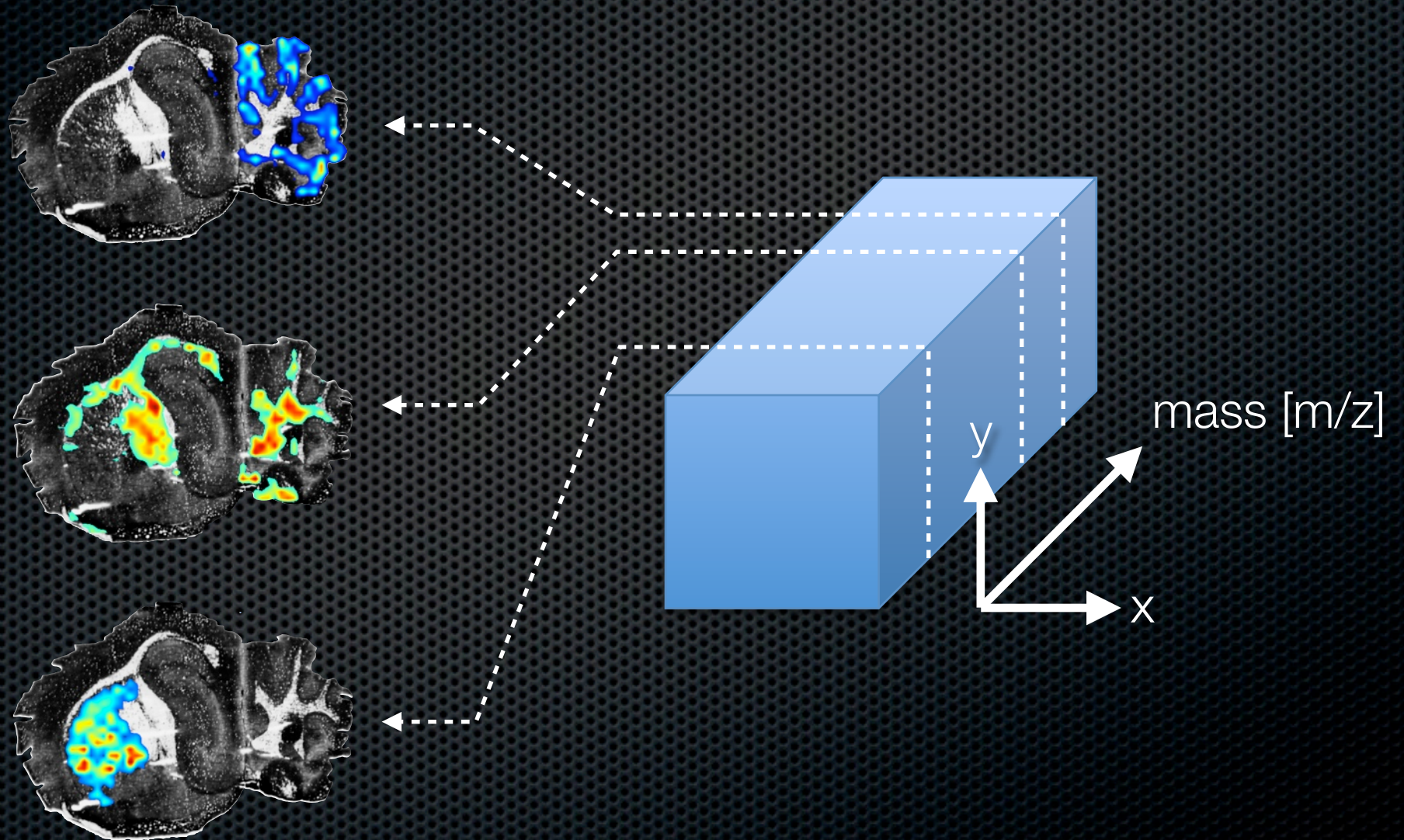


Computational Analysis of MSI Data

Contributions of this thesis

Mass Spectral Imaging

MSI data



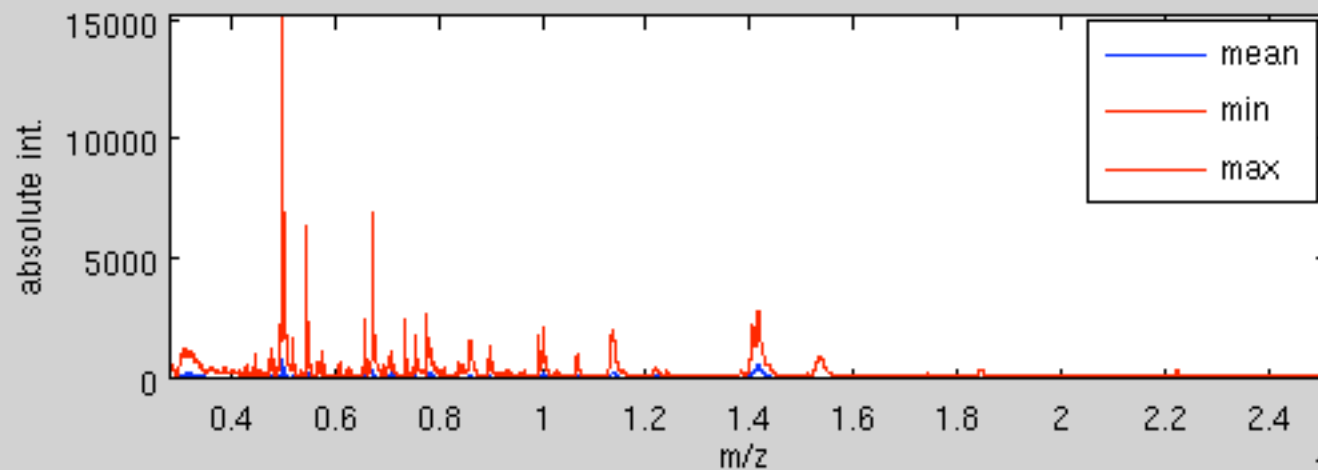
Mass Spectral Imaging

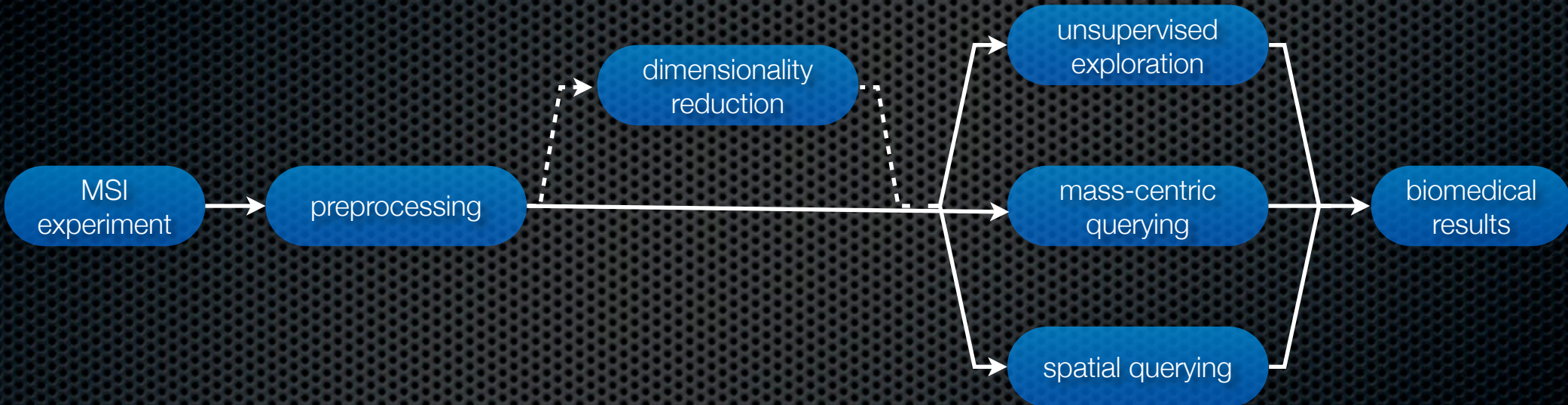
MSI data

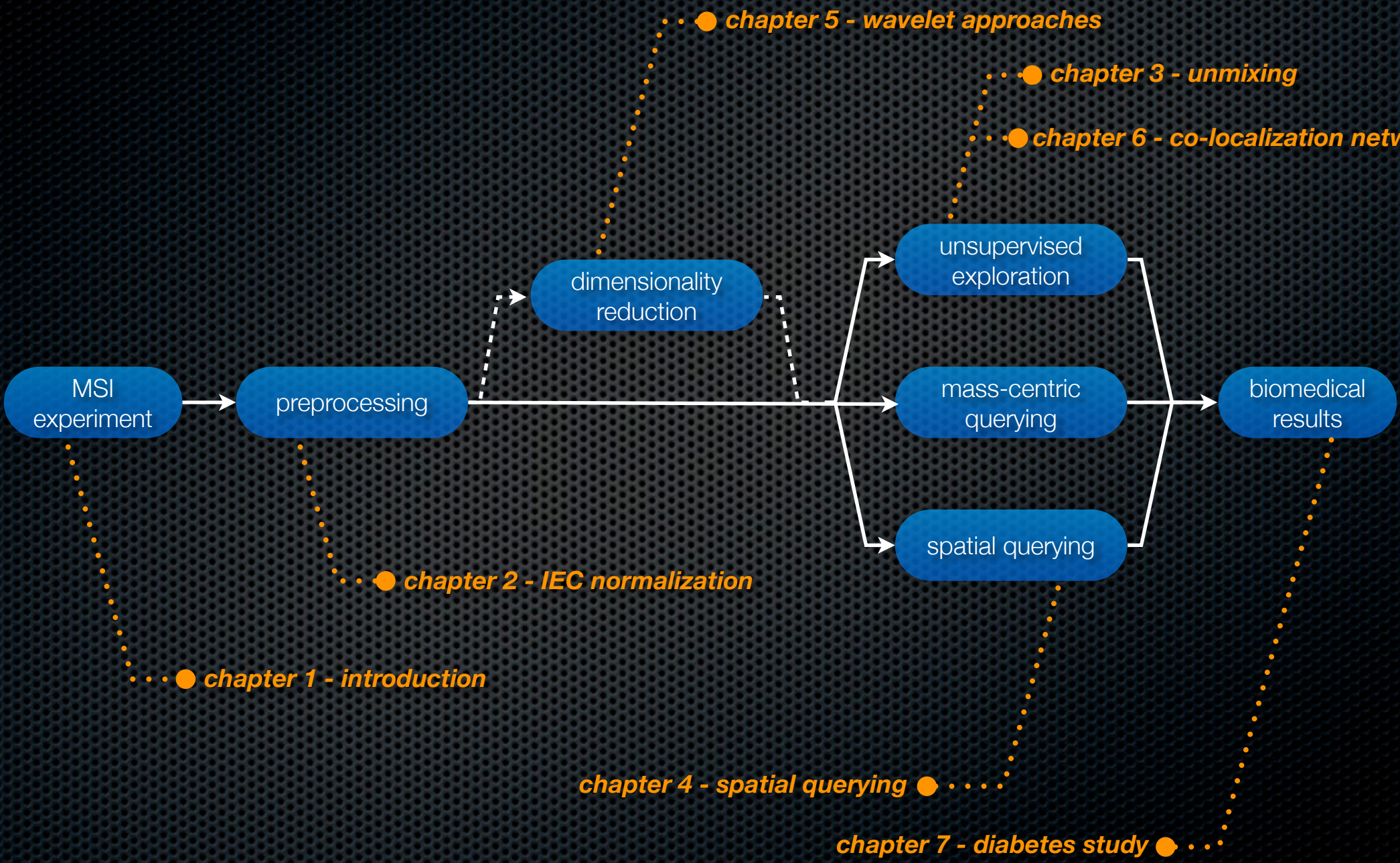
Measurement locations (51 × 34)

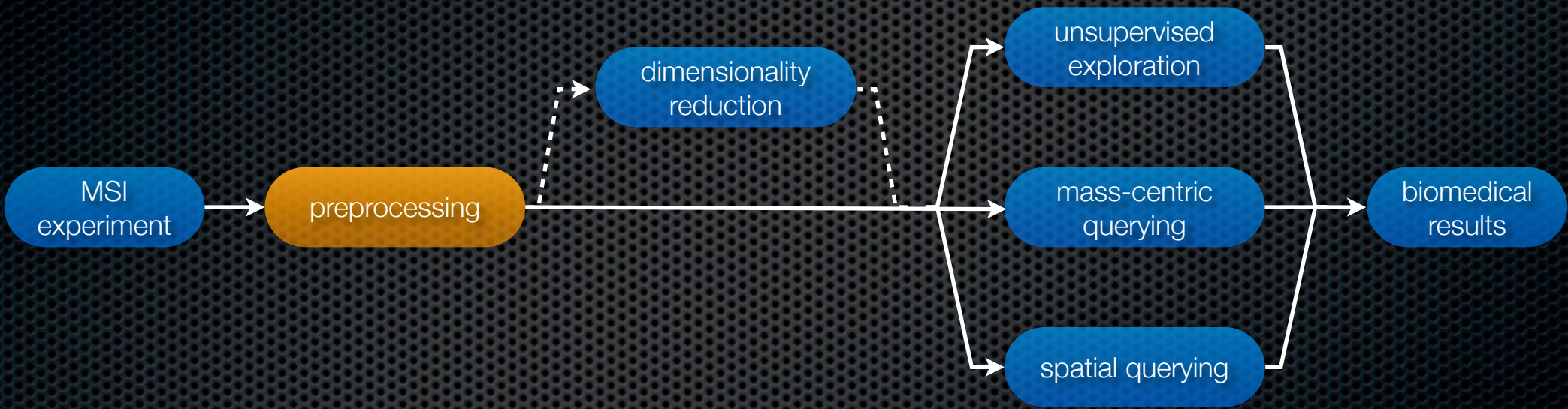


Mass spectra









Preprocessing - Normalization

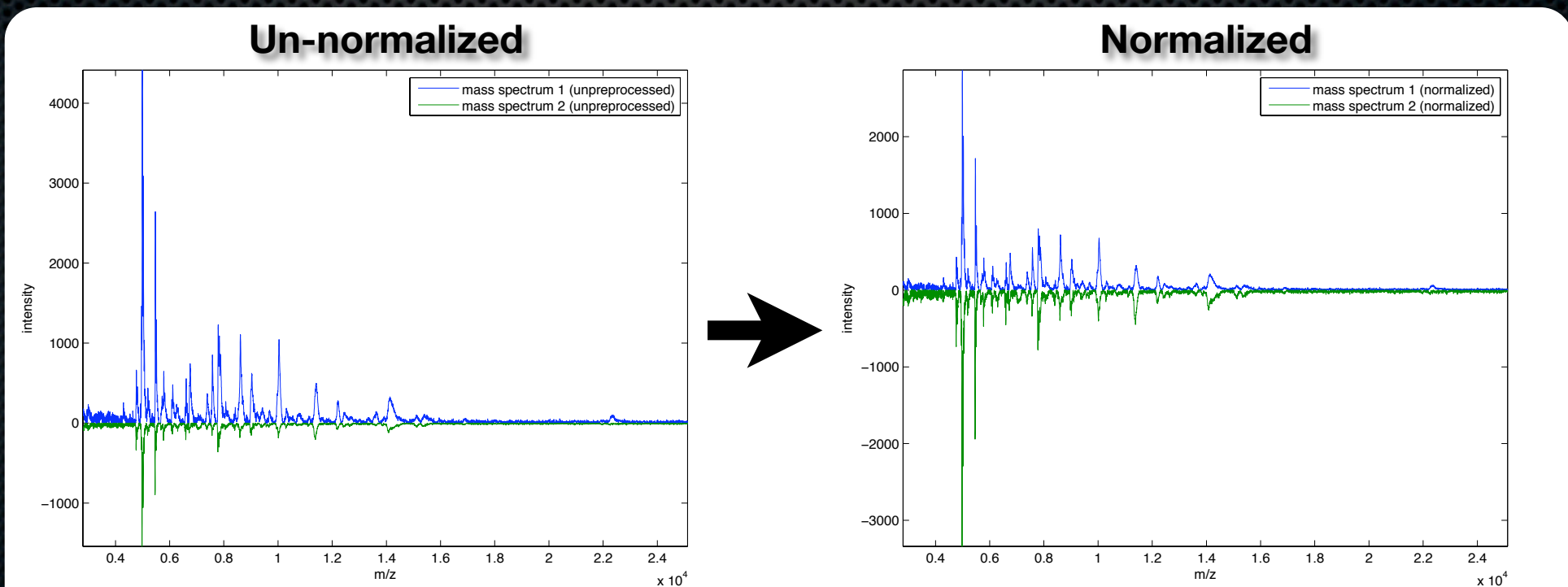
Problem definition

Problem

SNR differs from spectrum to spectrum due to wet lab sample prep and instrumental noise. → Non-biological variation

Goal

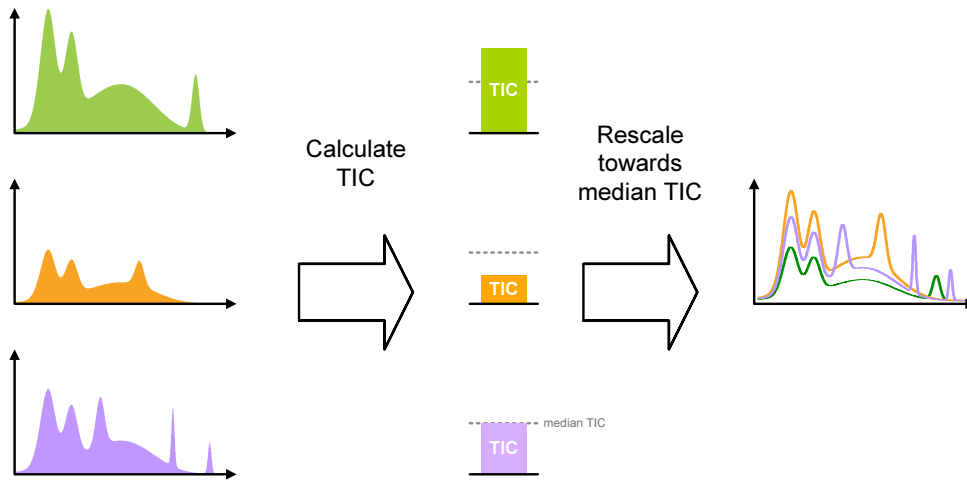
Project peak heights from several spectra onto common intensity scale.



Preprocessing - Normalization

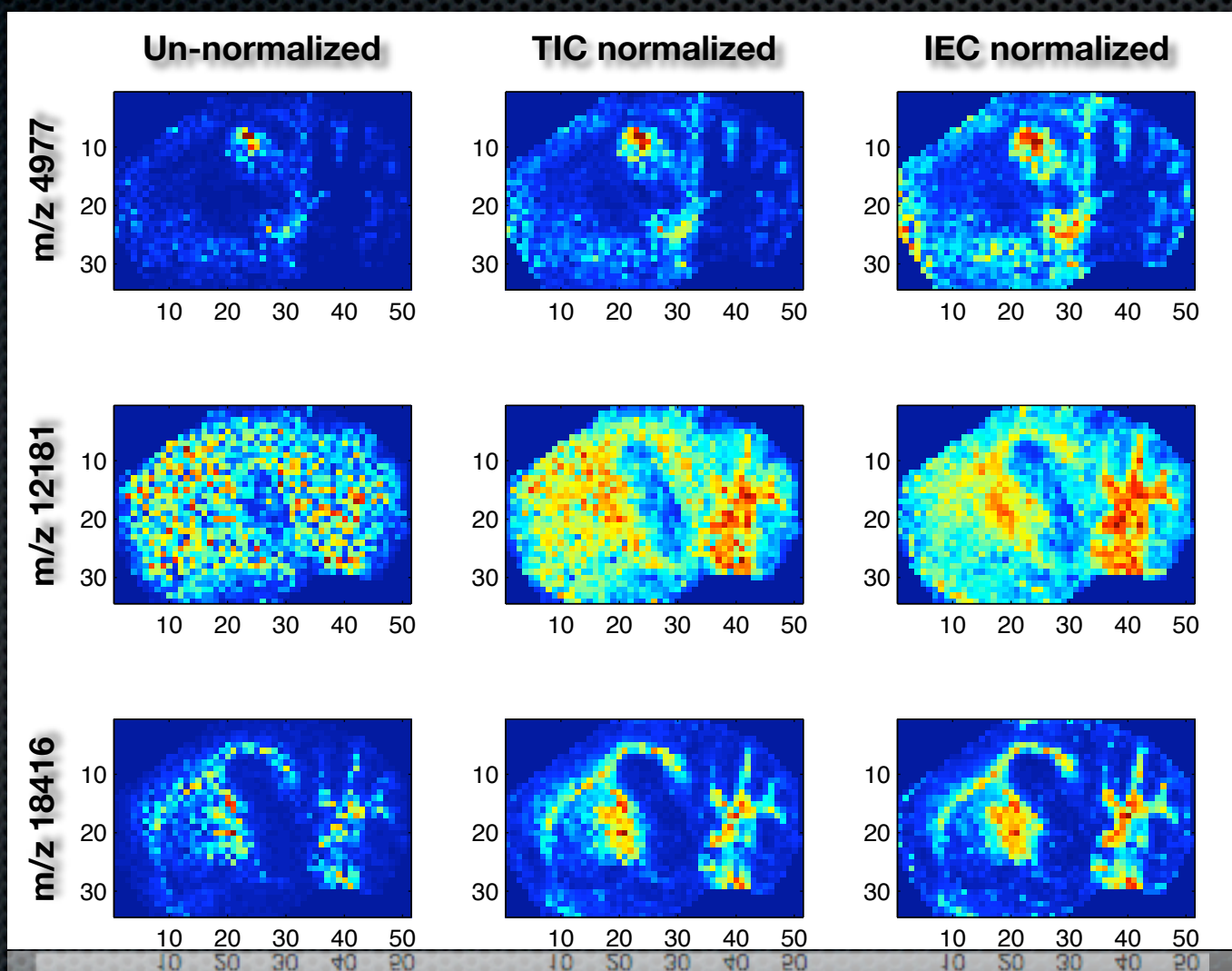
Contribution: Ionization Efficiency Correction

TIC based normalization:



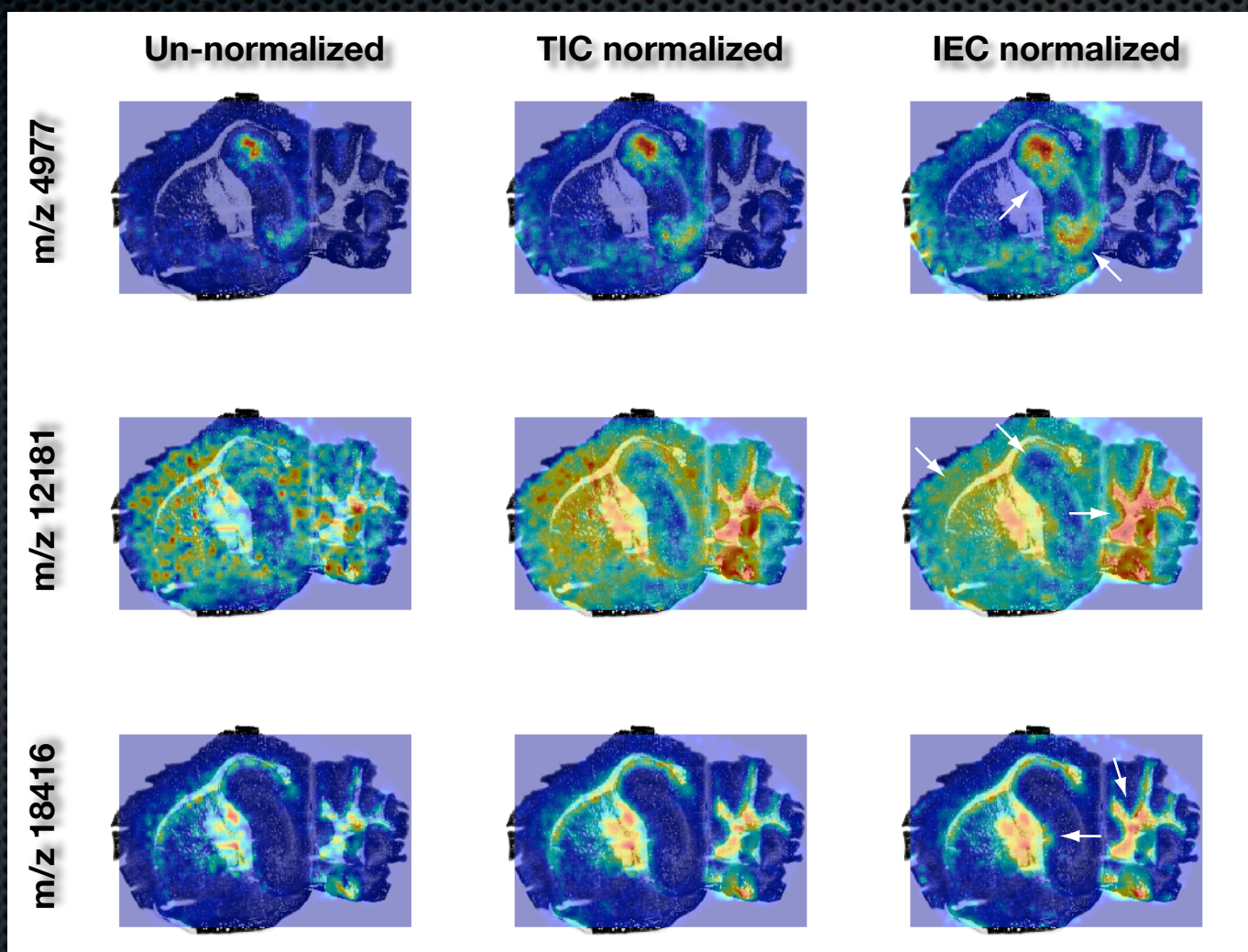
Preprocessing - Normalization

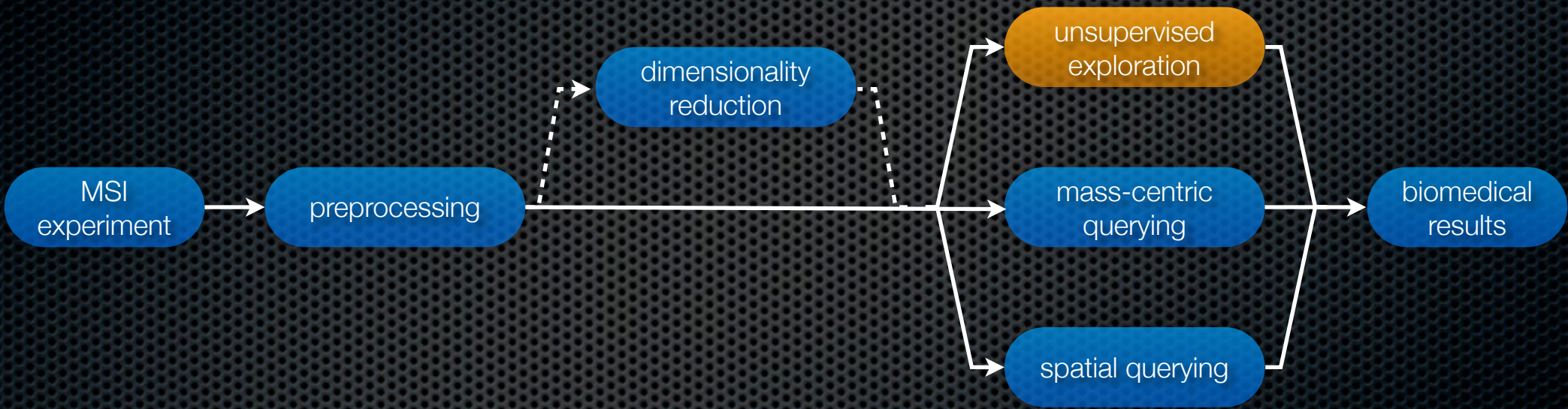
Contribution: Ionization Efficiency Correction



Preprocessing - Normalization

Contribution: Ionization Efficiency Correction





Unmixing

Problem definition

Problem

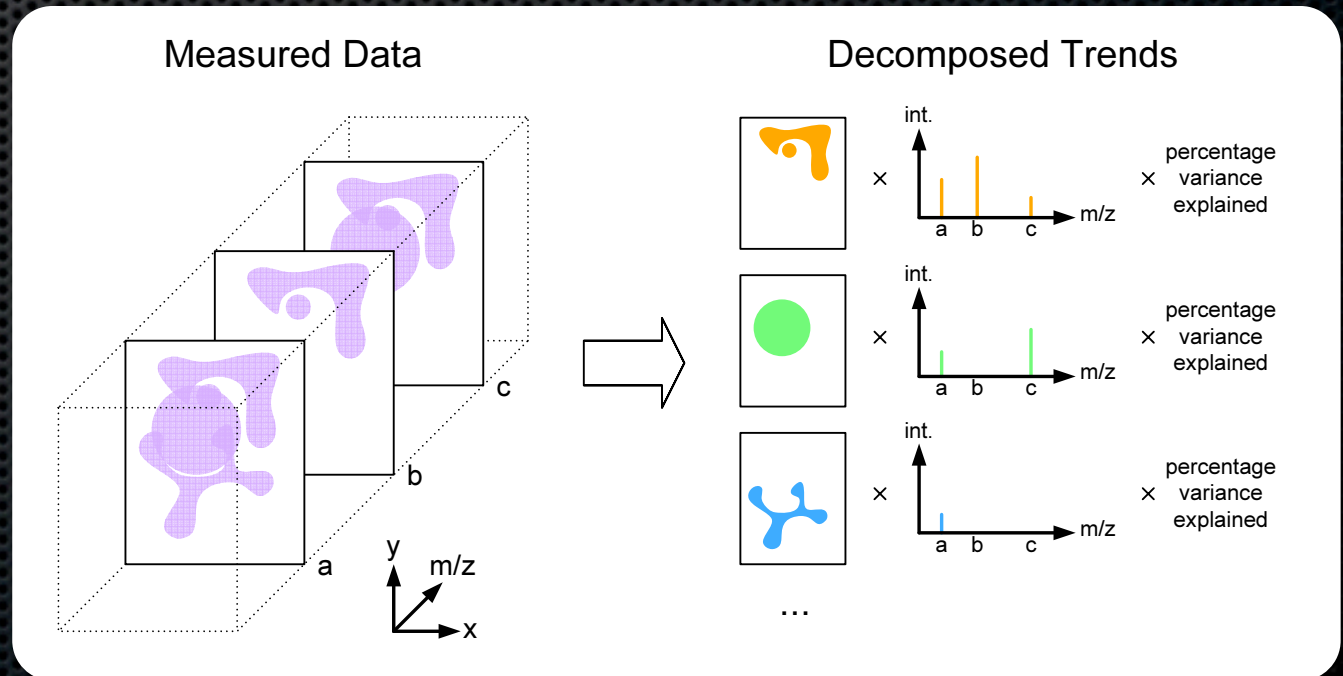
Organic tissue is a complex mixture of chemical content signatures due to biological, wet lab, and instrumental effects.

Goal

To reverse the mixing process and disassemble the measurements into underlying components.

Applications

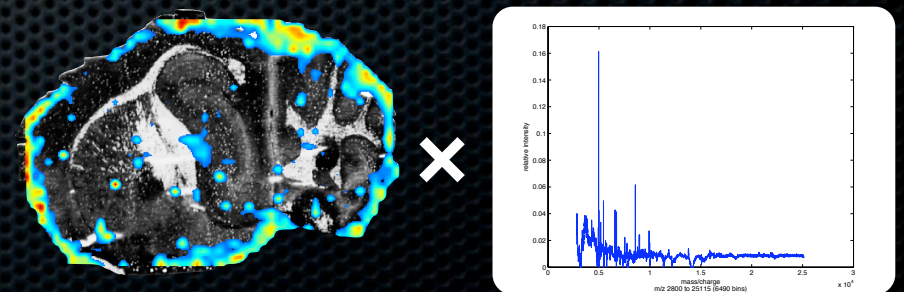
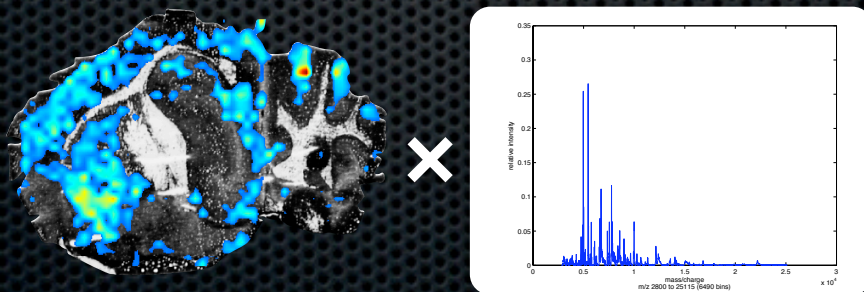
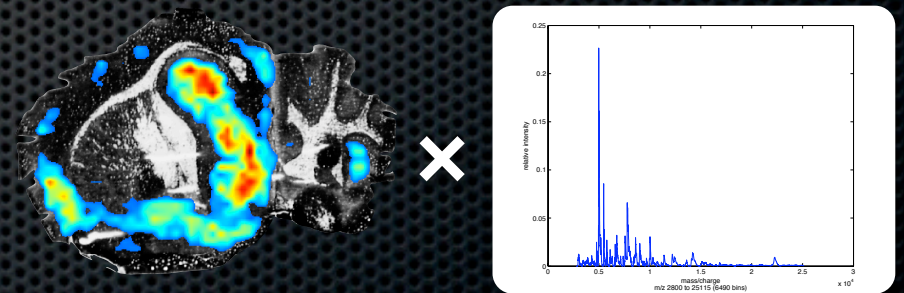
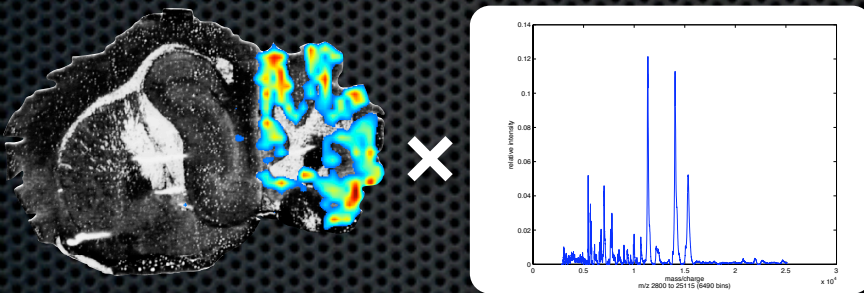
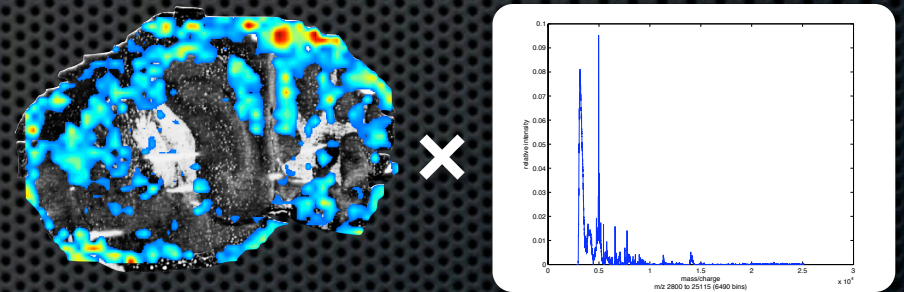
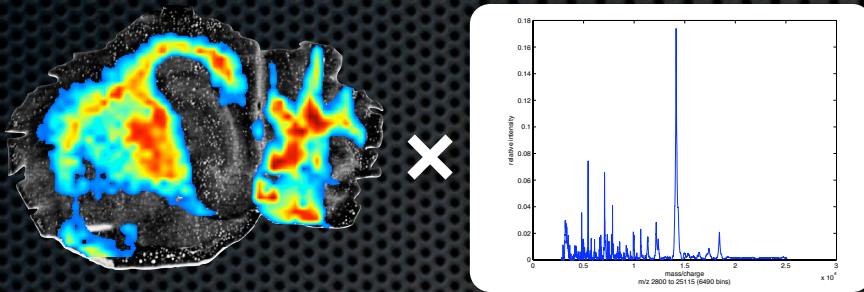
- Aid interpretation
- Filtering
- Dimensionality reduction
- Denoising



Unmixing Contributions

- Principal Component Analysis (PCA)
- Peak Intensity Weighted PCA (PIW-PCA)
- Non-negative matrix factorization (NMF)

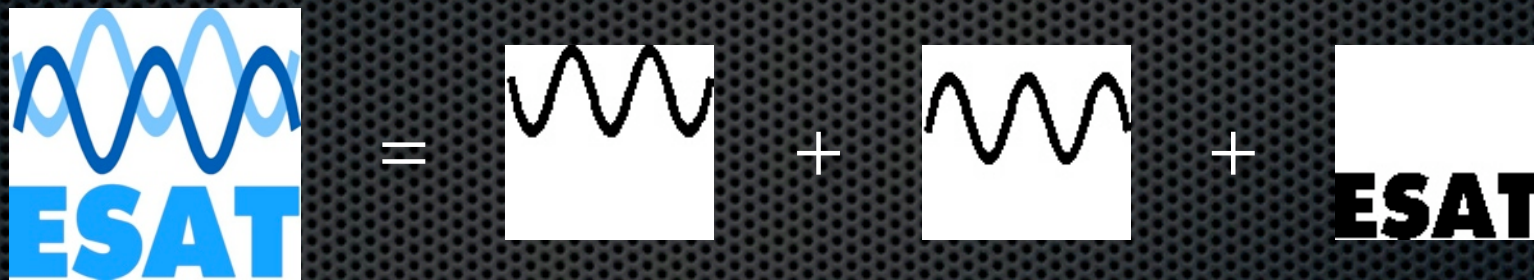
$$X \approx \sum_{a=1}^r w_a h_a^T = W'H'^T$$



Unmixing

Algorithm comparison

The ESAT logo at micrometer scale
divided in 3 distinct subzones

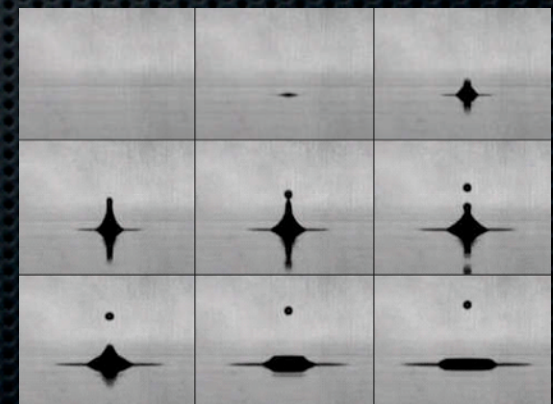


How?



Using the Labcyte Portrait
P630 chemical spotter

Principle: Acoustic Droplet
Ejection for "Touchless"
Liquid Transfer

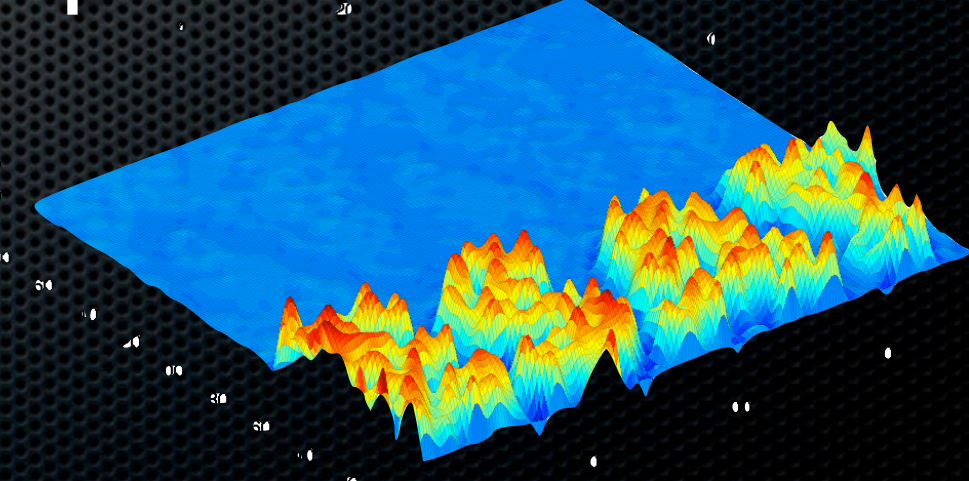
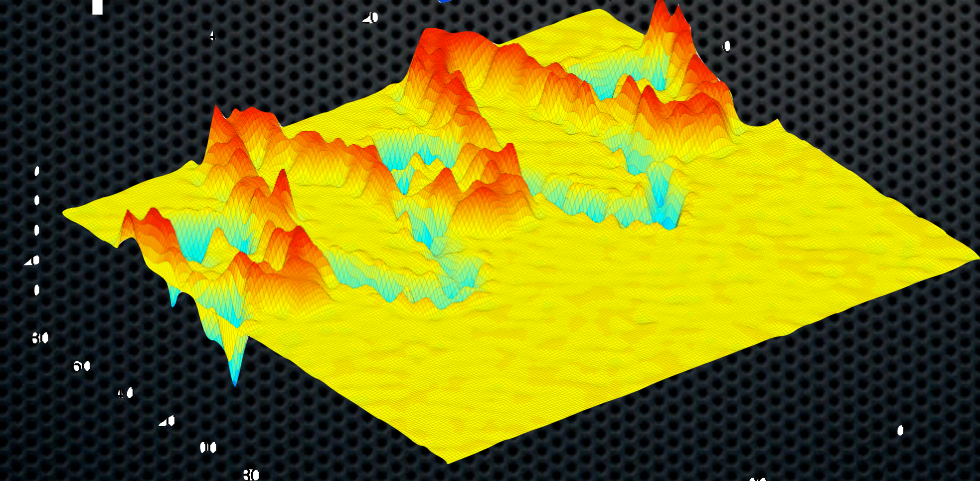
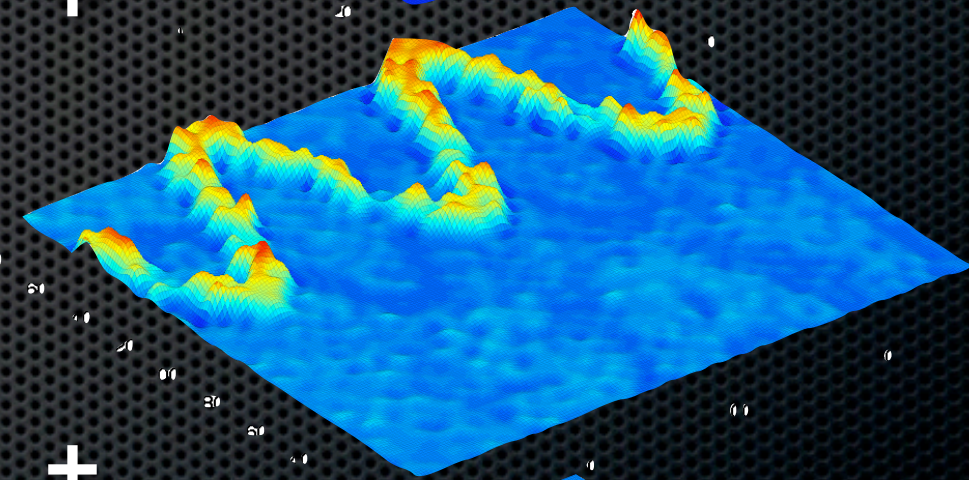
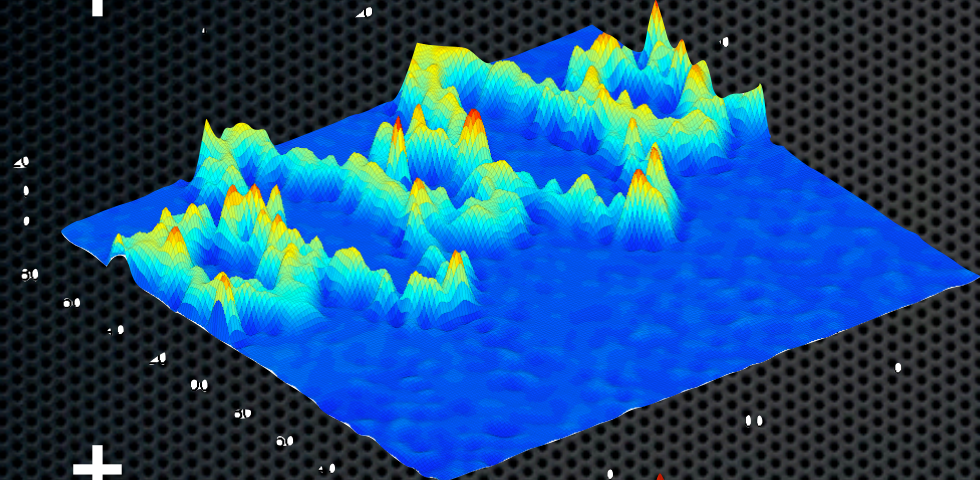
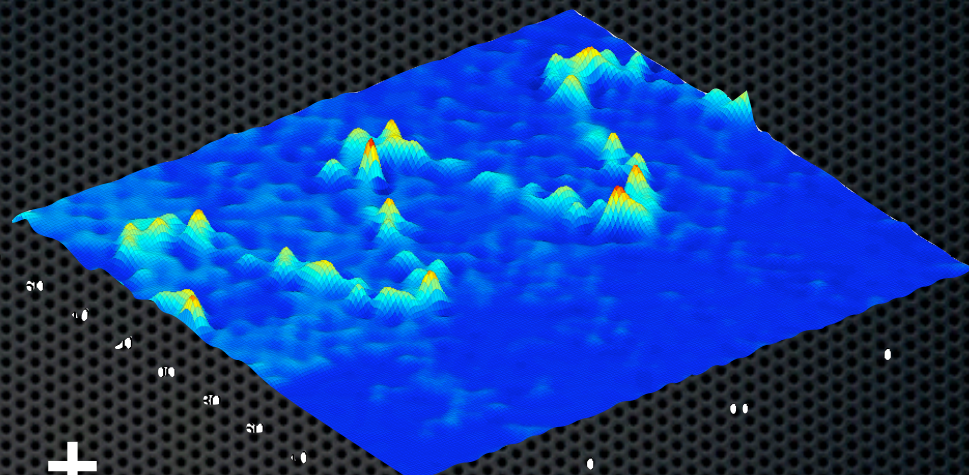
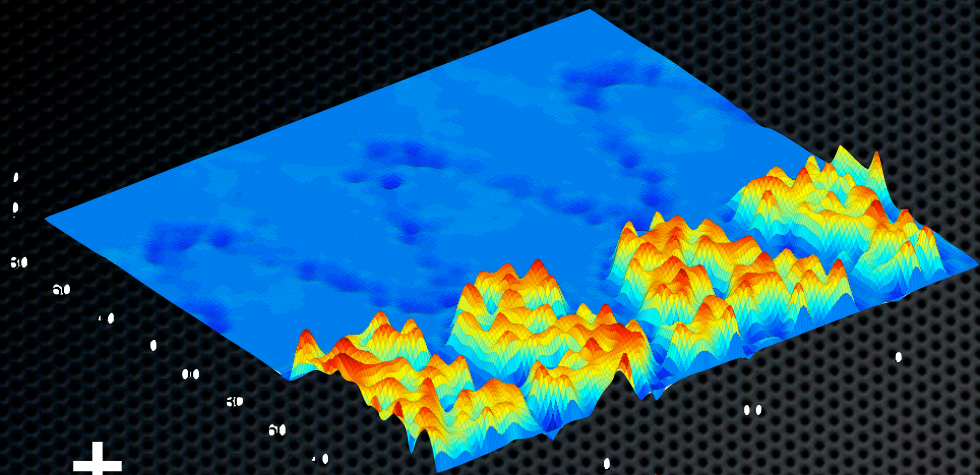


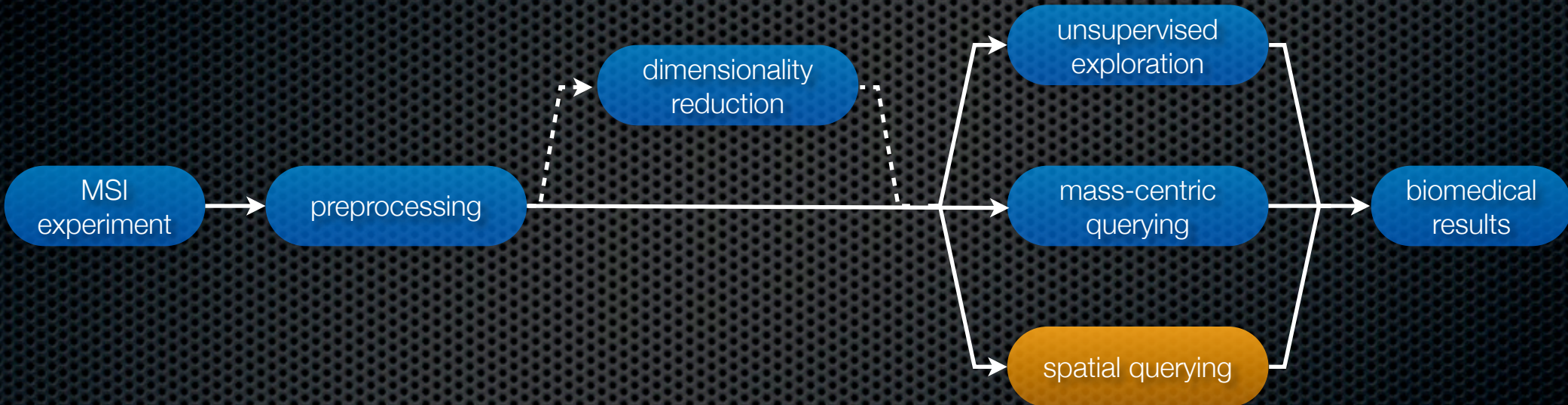
We kindly acknowledge Siobhan Pickett, Jovica Pavlović, and Elaine Heron from Labcyte Inc.

PCA

versus

NMF





Spatial Querying

Problem definition

Problem

Need method to interrogate MSI data for molecules that exhibit a spatial expression pattern of interest. Many disease cases have spatial prior information available.

Goal

The ability to ask a biological question using a spatial expression pattern of interest (= spatial query). A spatial query

- is a hypothesis-testing question **formulated in the spatial domain**.
- arises from scientific questions that **focus on a particular area in the tissue**.
- retrieves the **chemical signatures and relationships specific to that area**.

A method for spatial querying of MSI data is currently lacking, although there are many opportunities:

- Parkinson's disease - amygdala and putamen in the brain
- Huntington's disease - striatum in the brain
- Amyotrophic Lateral Sclerosis - motor neurons in spinal cord
- ...

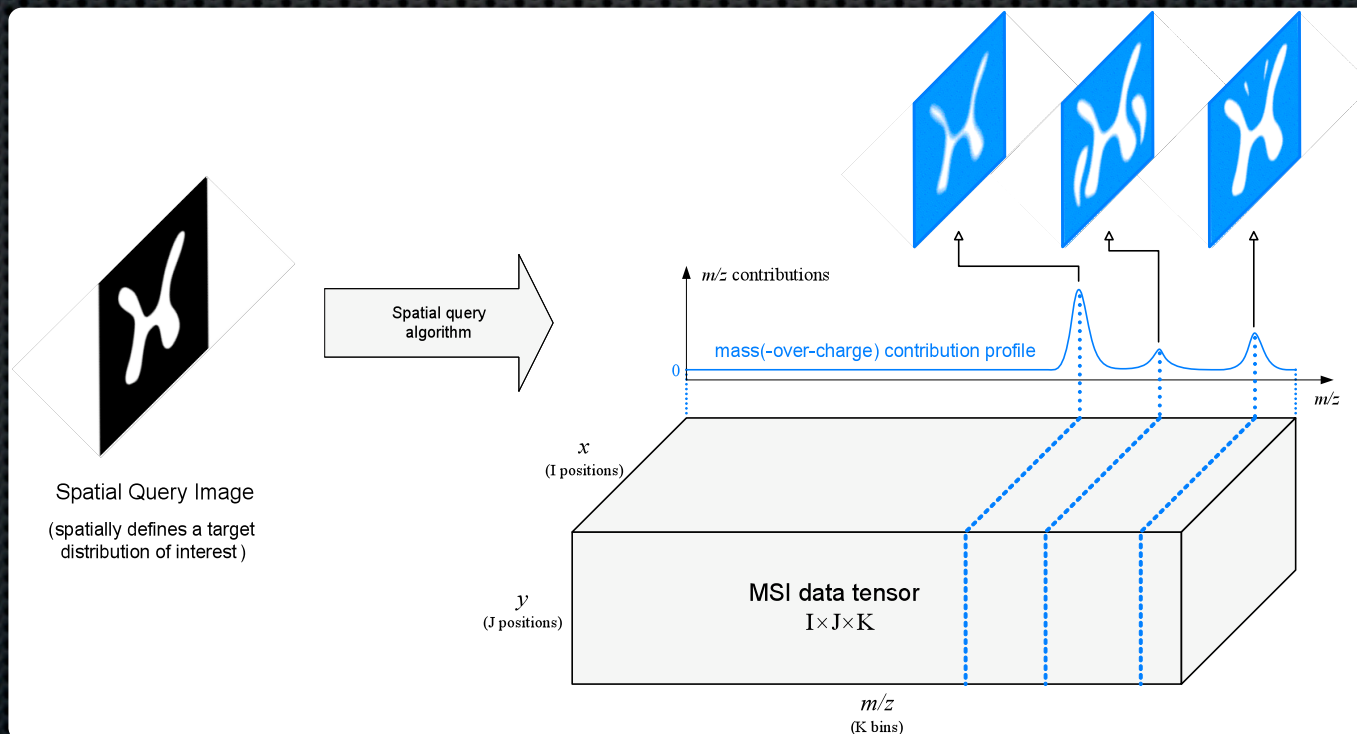
Spatial Querying

Contribution: non-negative least squares approach

The query q is considered a weighted sum of all features (ion images, m/z bins).

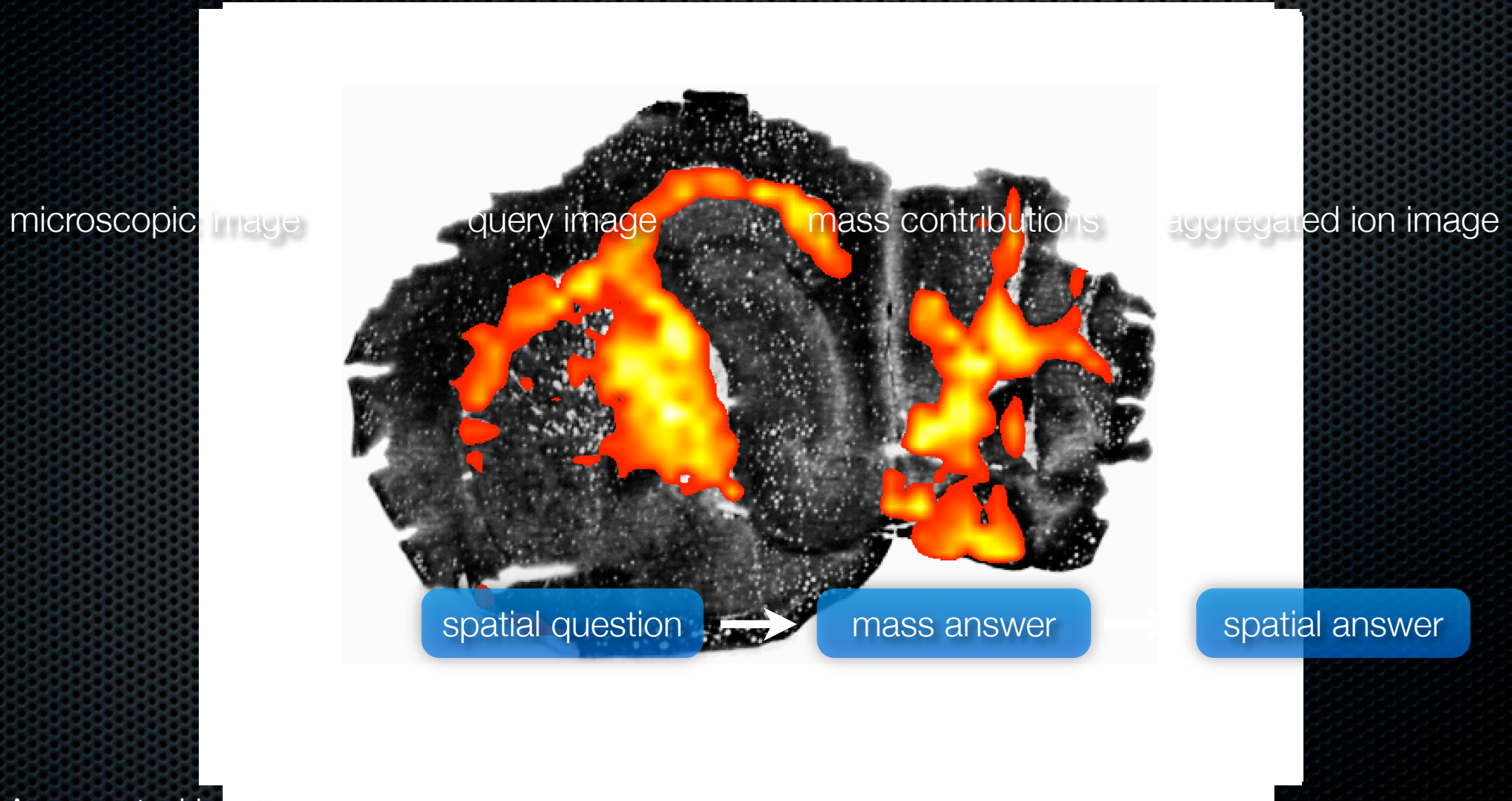
A linear model is adopted: $q_k = \sum_{m=1}^M \phi_k^m p_m + \epsilon_k, \quad \forall k = 1, \dots, K$

Goal - To find mass contribution coefficients: $p = (p_1, \dots, p_M)^T$



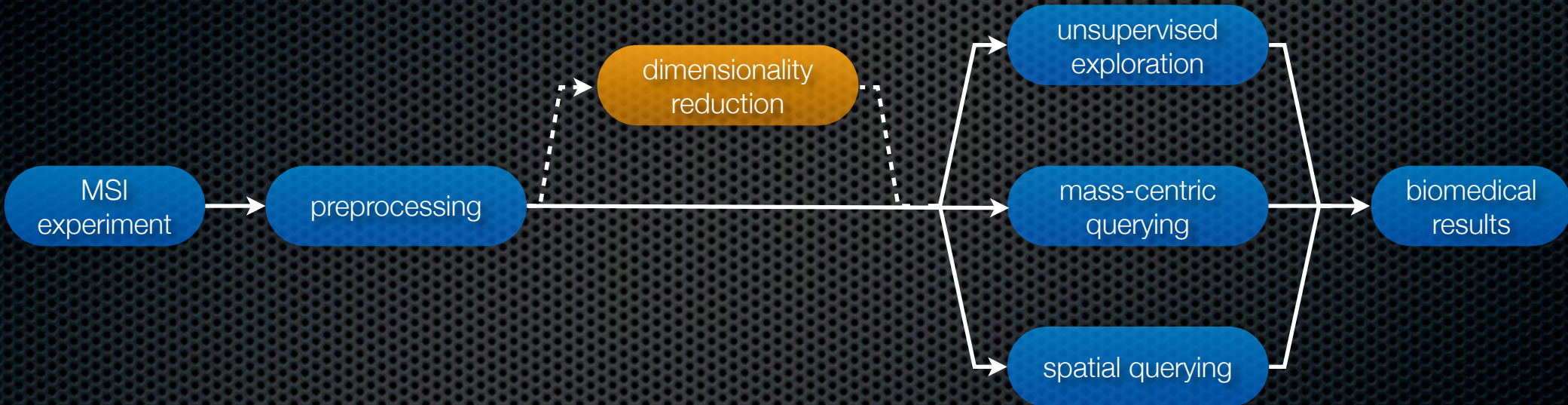
Spatial Querying

Contribution: non-negative least squares approach



Aggregated ion image:

Pulls in other areas in the tissue that exhibit a similar chemical signature to the queried area.



Wavelet approaches

Problem definition

Problem

MSI commonly become very large, making computational analysis from a computational and memory standpoint increasingly difficult. Size is influenced by:

- covered tissue surface area
- spatial resolution
- extent of mass range
- mass resolution

Goal

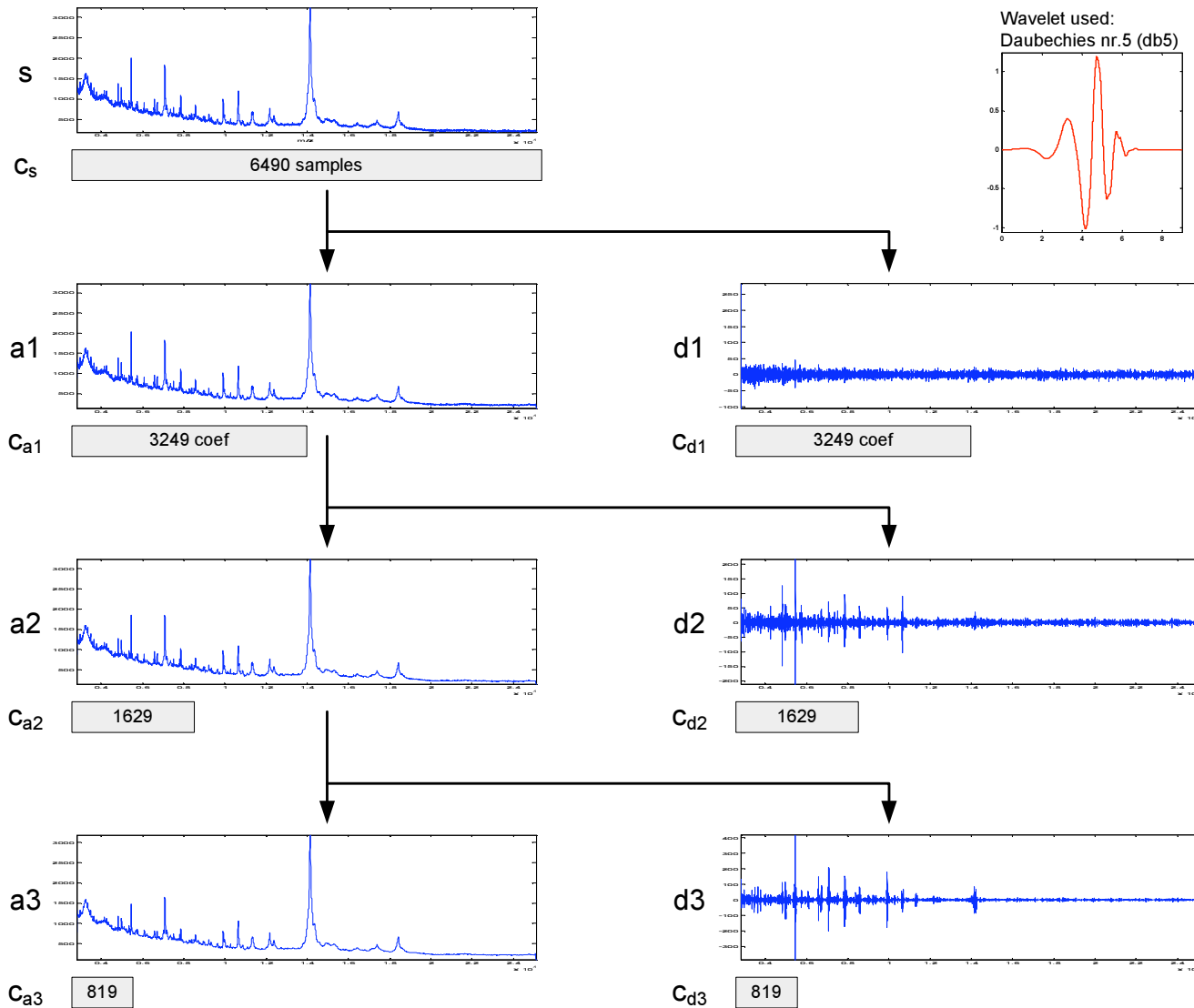
Provide a strategy for those situations where the multivariate analysis of a MSI data set becomes either

- infeasible due to memory constraints;
- impractical due to exorbitant calculation times or scalability of the algorithm;
- unreliable due to the 'curse of dimensionality'.

Wavelet approaches

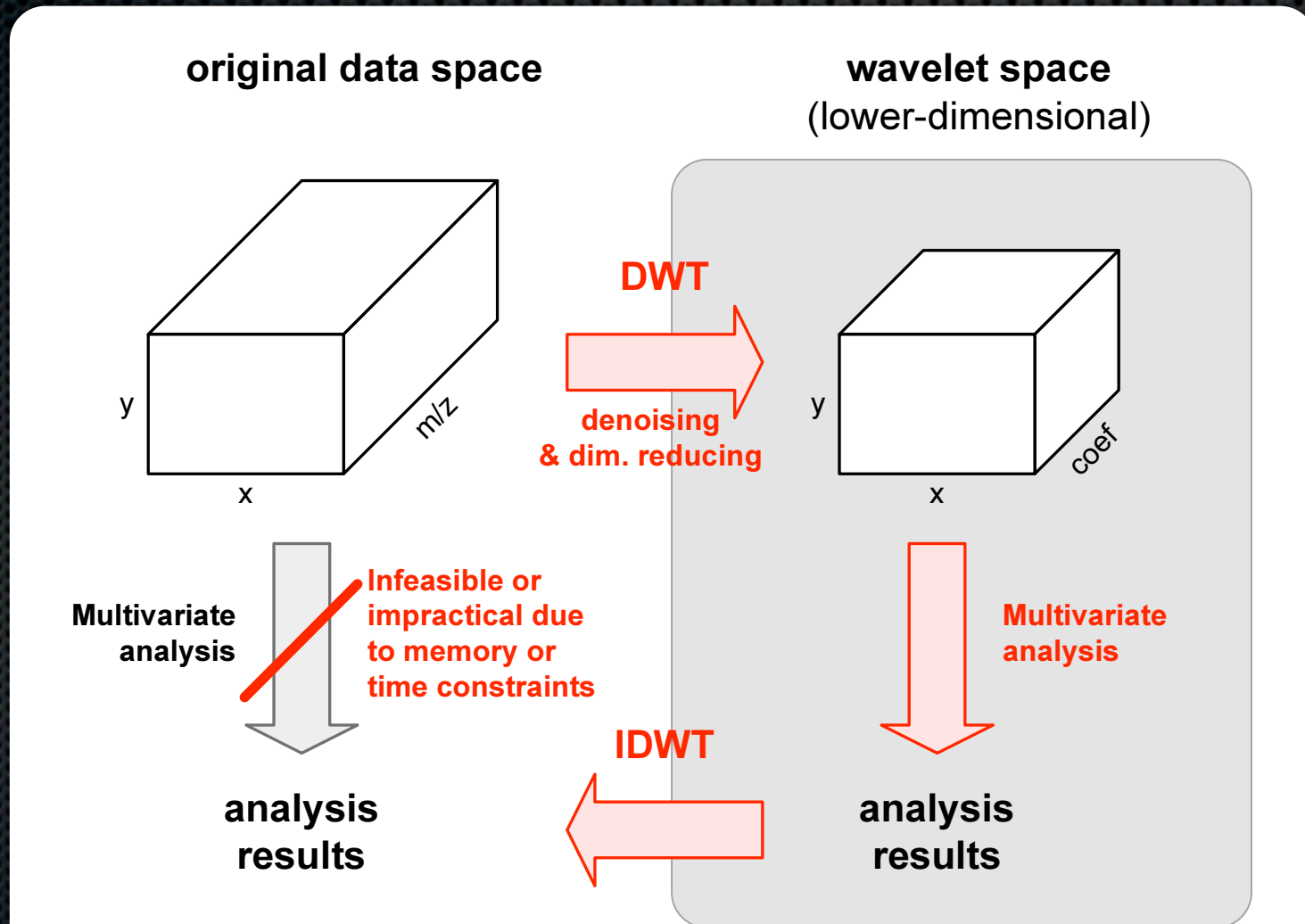
Contribution: multivariate analysis in DWT space

Discrete Wavelet Transform on a single mass spectrum



Wavelet approaches

Contribution: multivariate analysis in DWT space

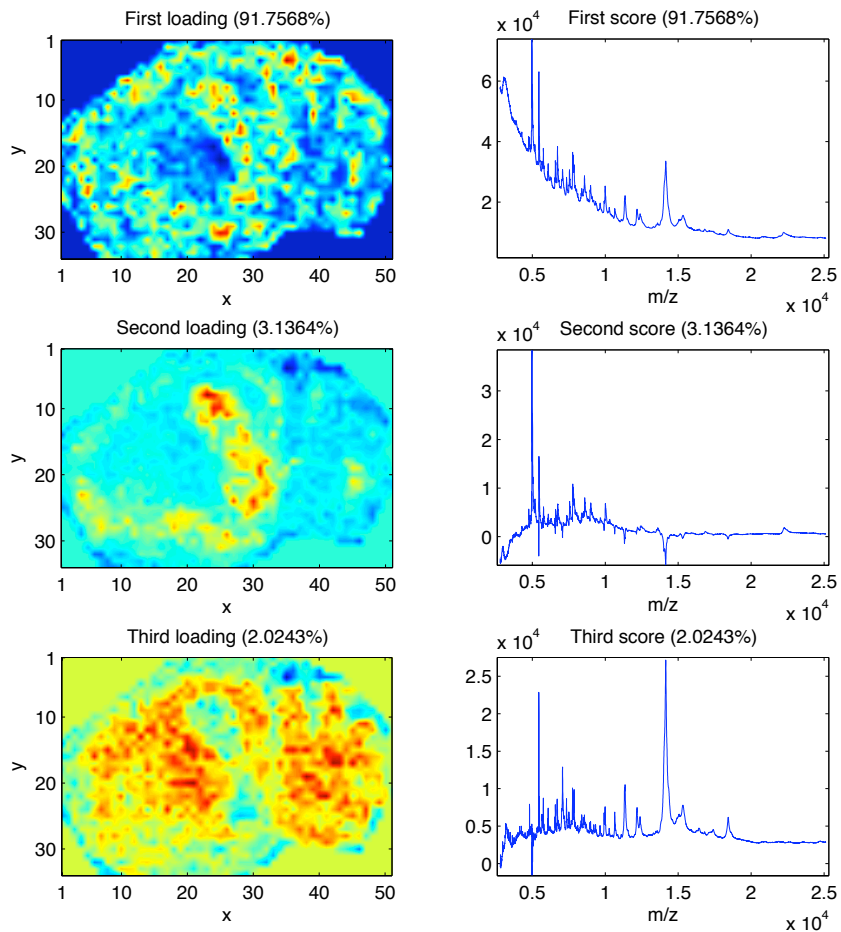


Wavelet approaches

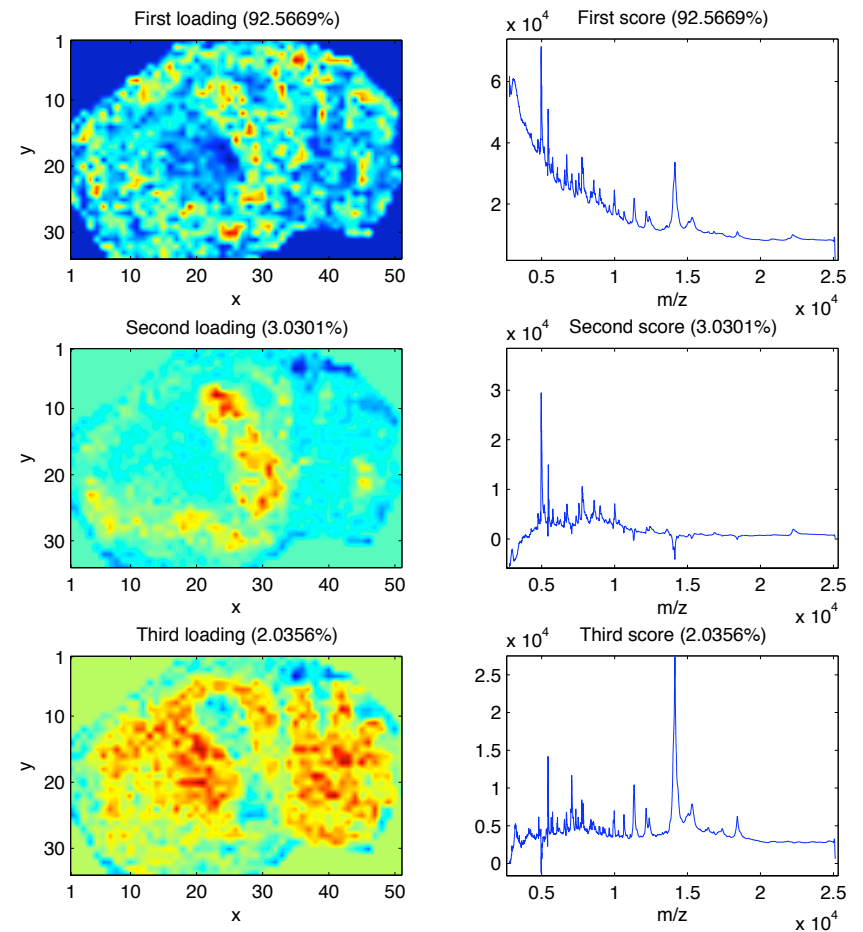
Contribution: multivariate analysis in DWT space

visually indiscernible results

PCA on raw data



PCA on in wavelet space



Wavelet approaches

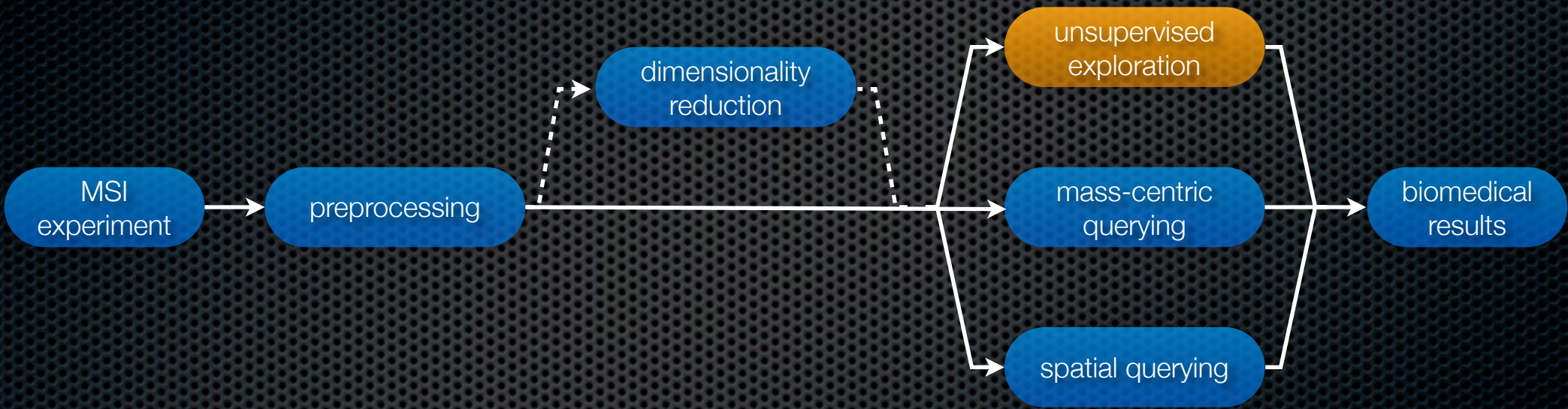
Contribution: multivariate analysis in DWT space

	Non-DWT PCA	DWT PCA
size cov. matrix	m/z bins \times m/z bins	coef \times coef
required memory	6490 \times 6490 (337MB)	819 \times 819 (5.3MB)
contrib./cov. entry	# pixels	# pixels

... 63-fold reduction in memory requirements

	Non-DWT PCA	DWT PCA
size cov. matrix	pixels \times pixels	pixels \times pixels
required memory	1734 \times 1734 (24MB)	1734 \times 1734 (24MB)
contrib./cov. entry	# m/z bins	# coefficients
required calc. time	158.3 s	13.2+75.6 s = 88.8 s
	(PCA)	(DWT) + (PCA)

... 44% reduction in calculation time



Co-localization networks

Problem definition

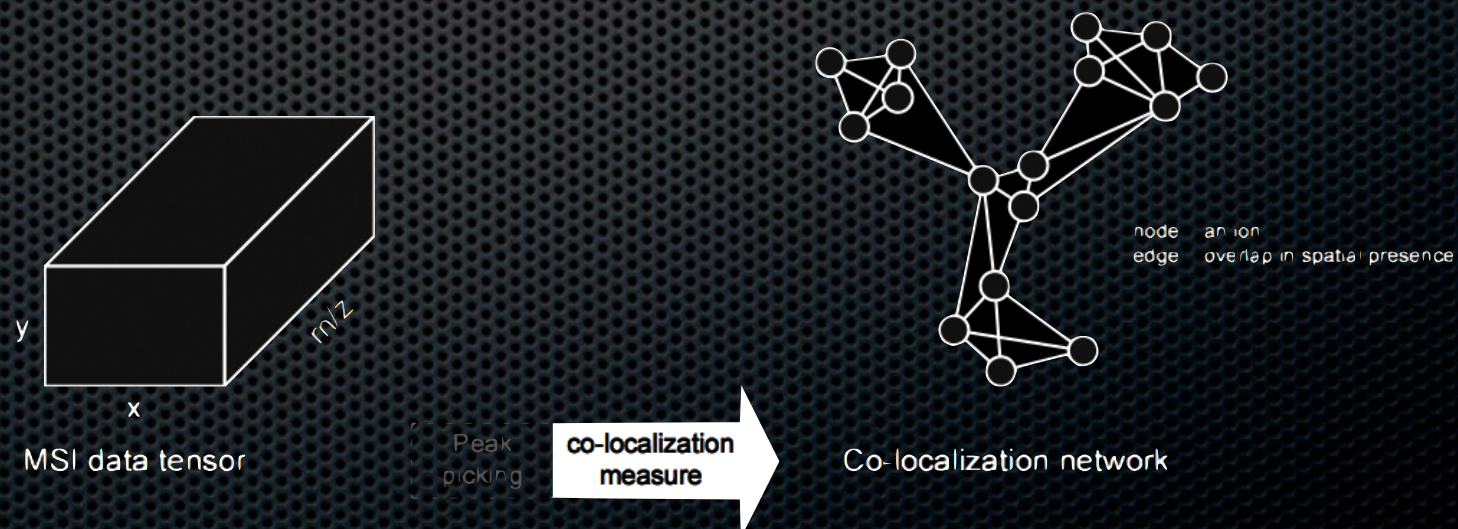
Problem

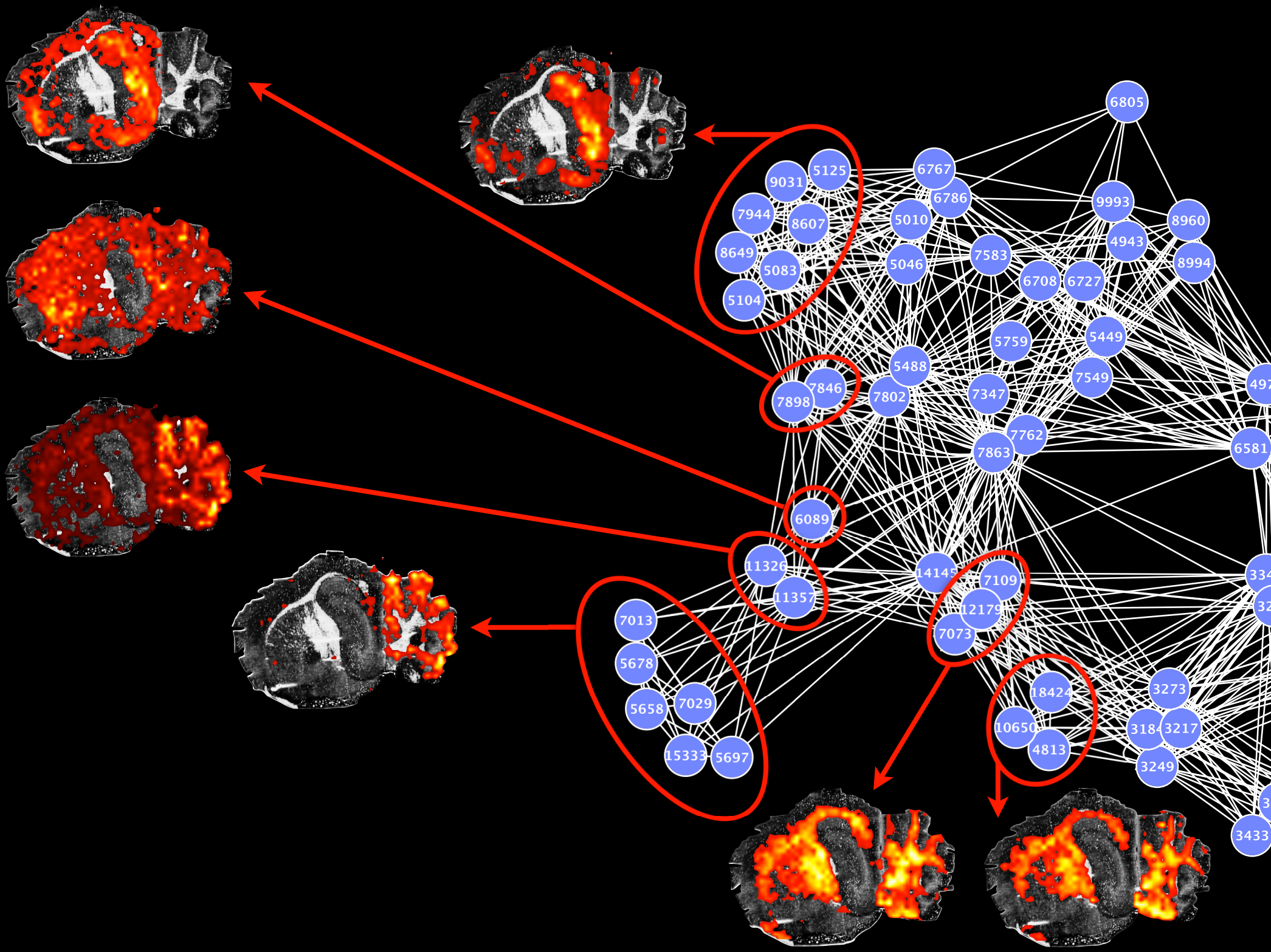
Most MSI analysis has focused on the imaging aspect of the data. MSI, however, has a dual spatio-biochemical nature due to its strong mass resolution.

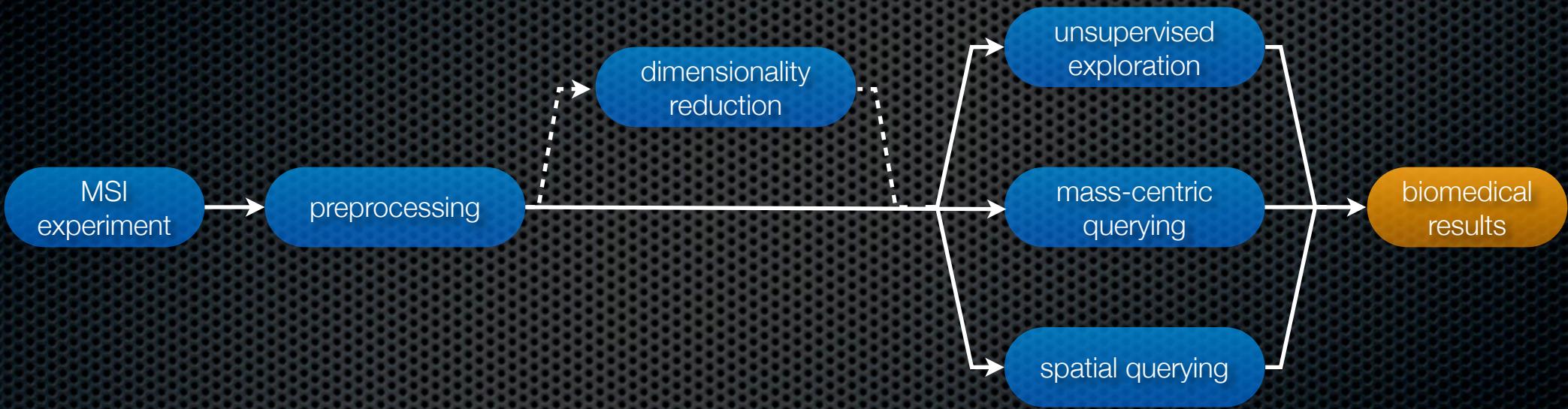
Goal

Construct a network representation of the inter-molecule relationships present in a MSI experiment, such as co-localization and correlated expression.

Such a co-localization network can provide **insight into both biological and instrumentally induced relationships between ions.**







Diabetes Case Study

Problem Definition

Problem

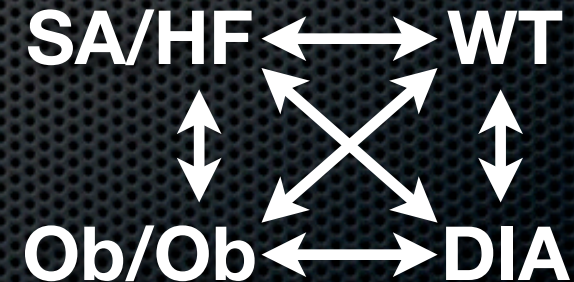
Is it possible to detect where diseased metabolic pathways start deviating from normal metabolic function straight from tissue?

Goal

To construct a **metabolic screening method straight from tissue** by combination of MSI and computational multivariate analysis techniques.

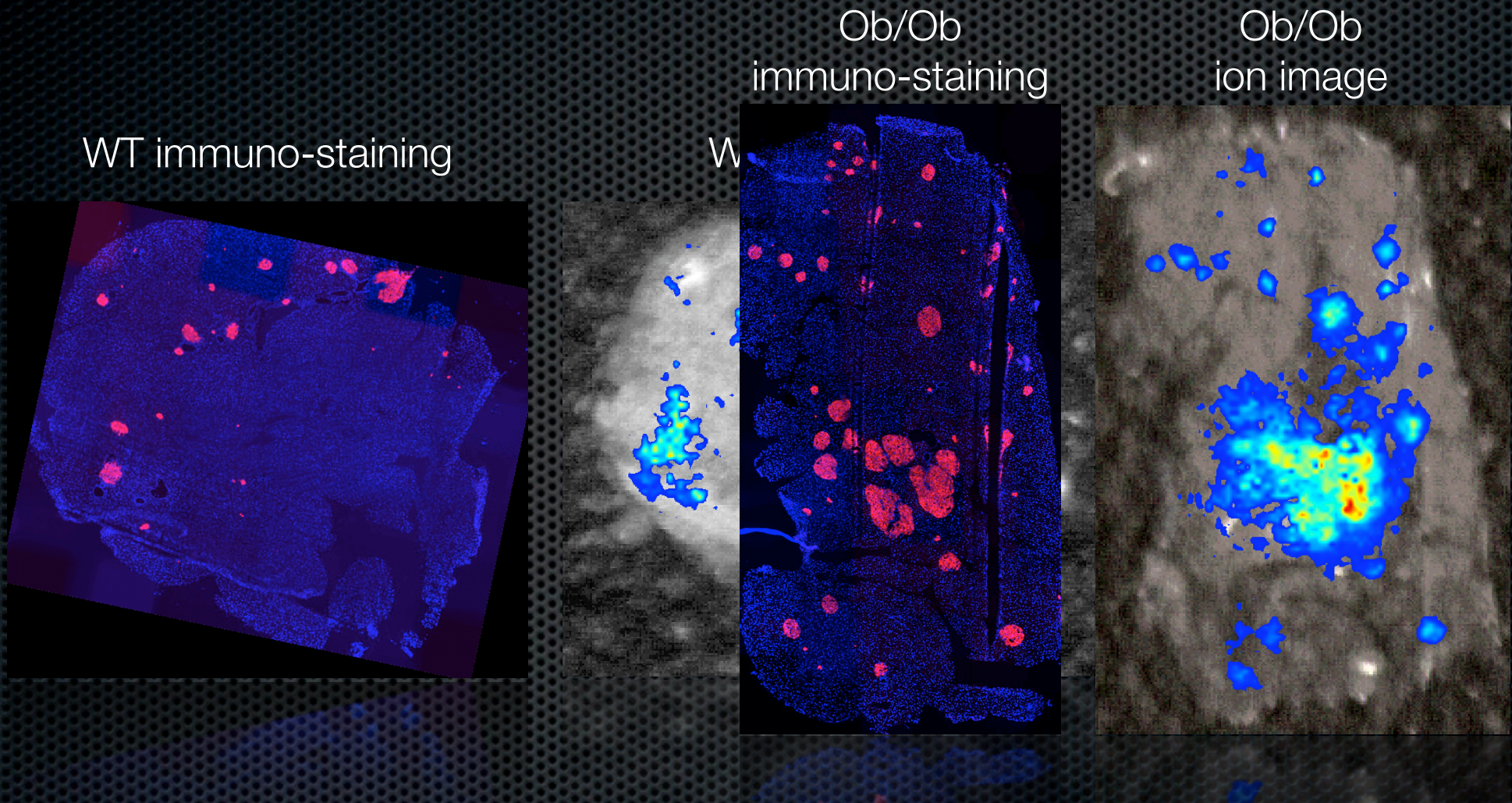
Sub-goals

1. Label-free *in situ* imaging of insulin in tissue;
2. Relative quantification of insulin;
3. Extract multi-molecular content signature for the islets of Langerhans;
4. Differential comparison of islet content;
5. Mapping to metabolic pathways.



Diabetes Case Study

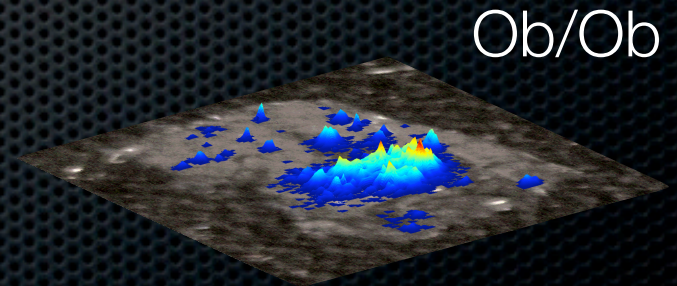
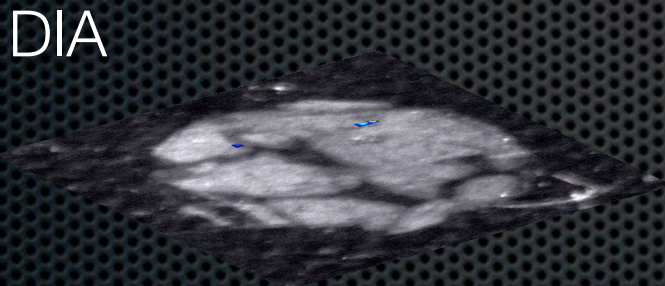
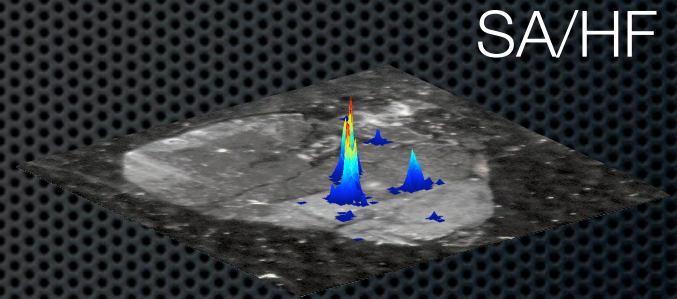
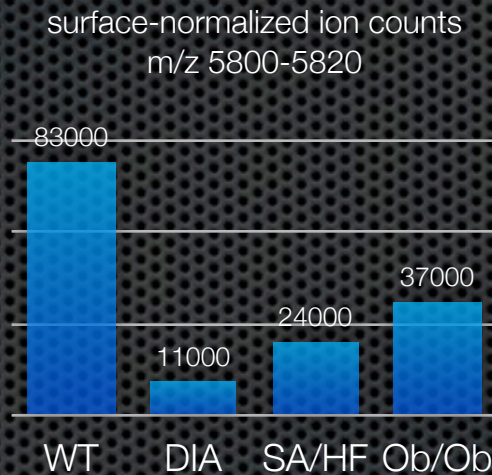
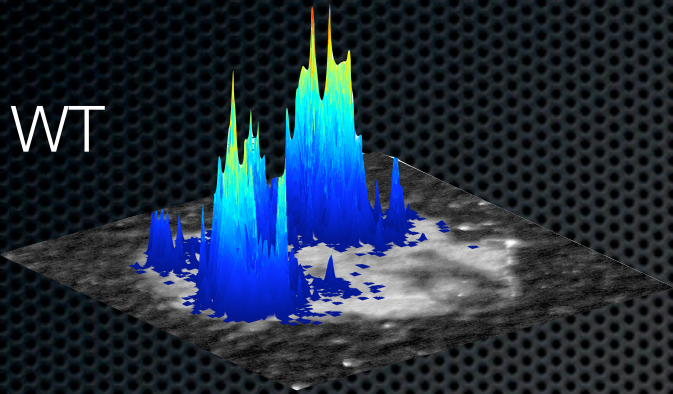
Metabolic screening straight from tissue



1. Label-free *in situ* imaging of insulin in tissue

Diabetes Case Study

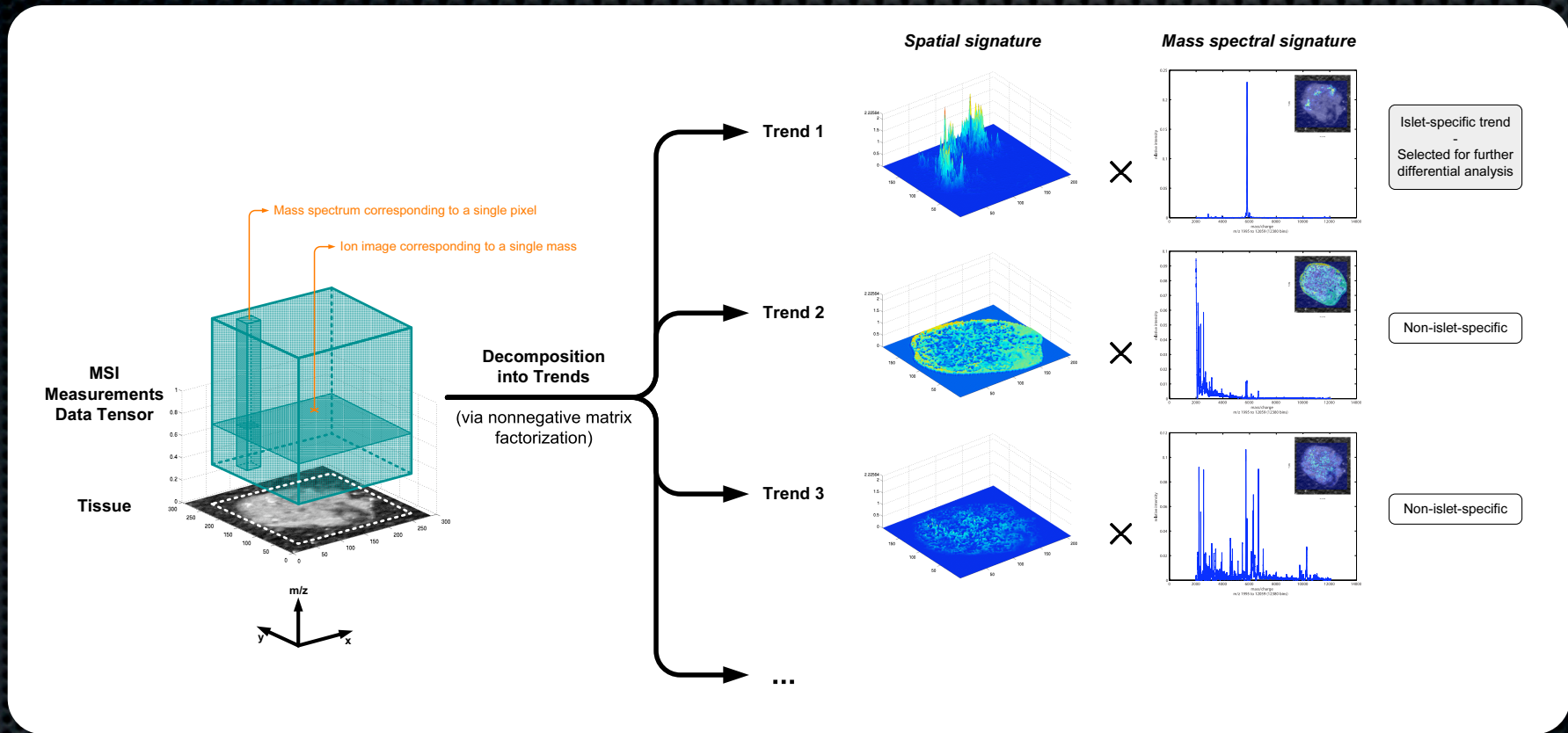
Metabolic screening straight from tissue



2. Relative quantification of insulin

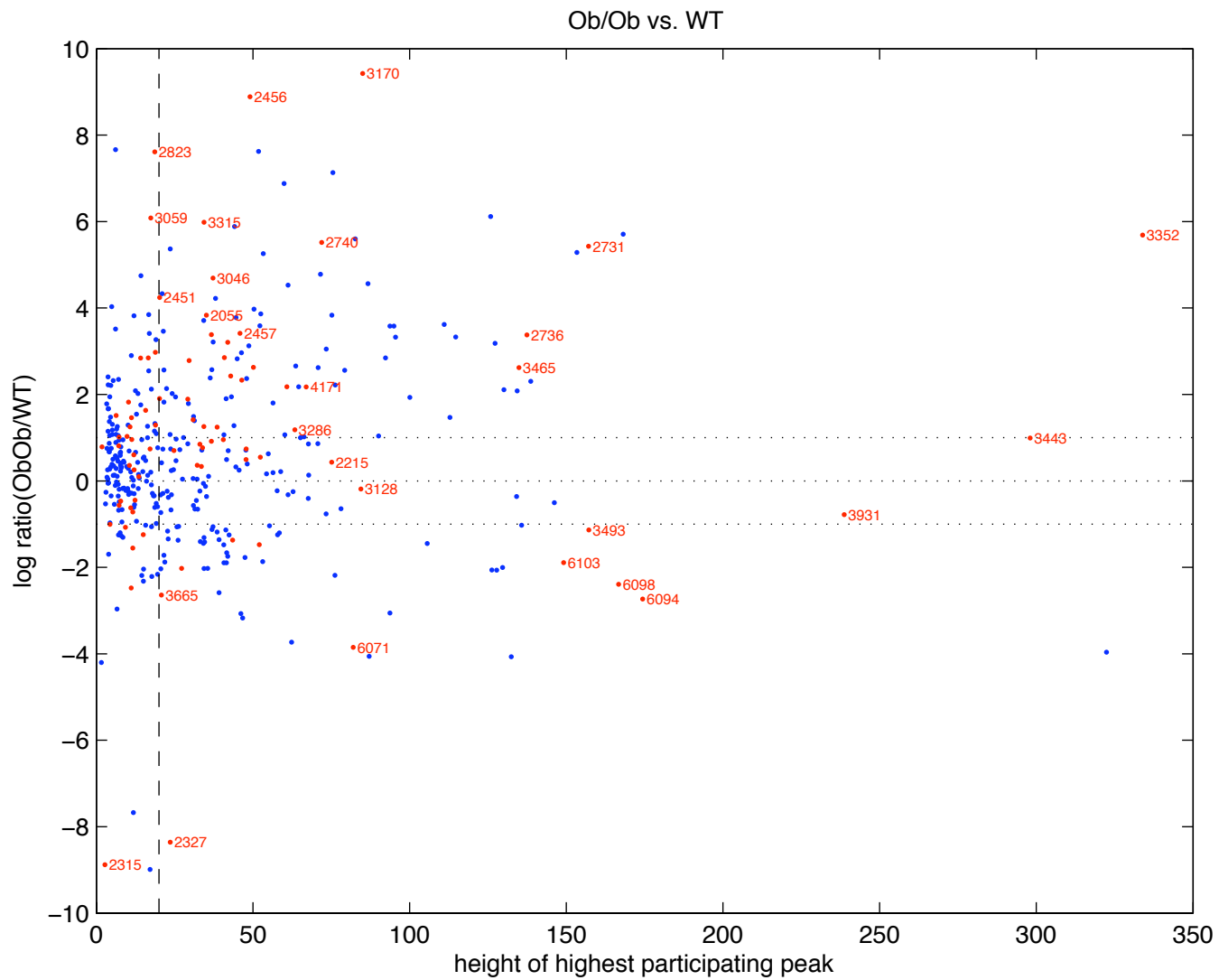
Diabetes Case Study

Metabolic screening straight from tissue



3. Extract multi-molecular content signature for the islets of Langerhans

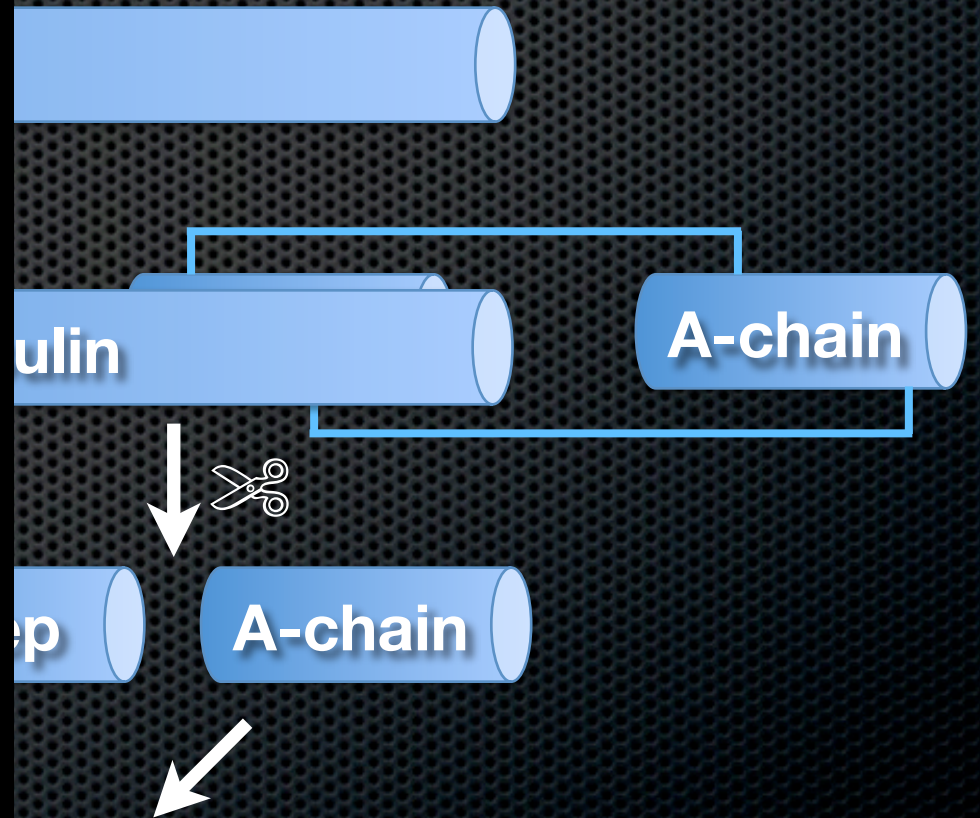
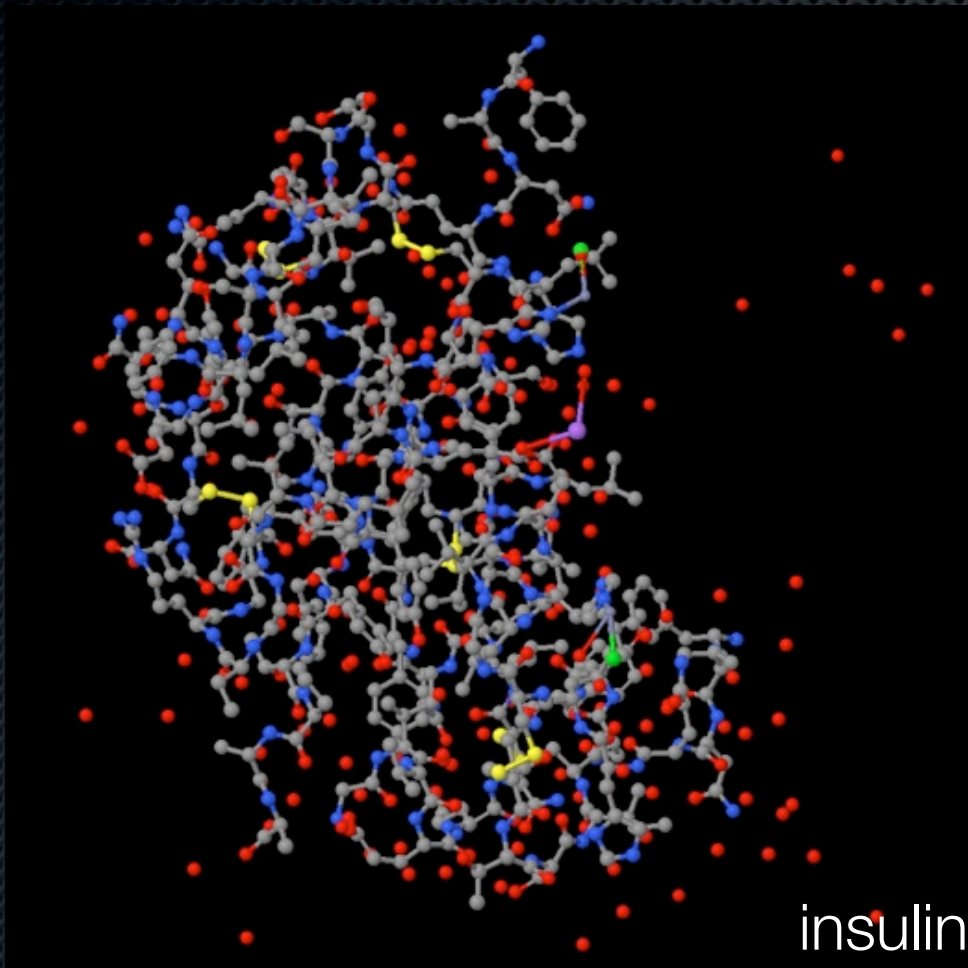
Diabetes Case Meta



4. Differential comparison of islet content

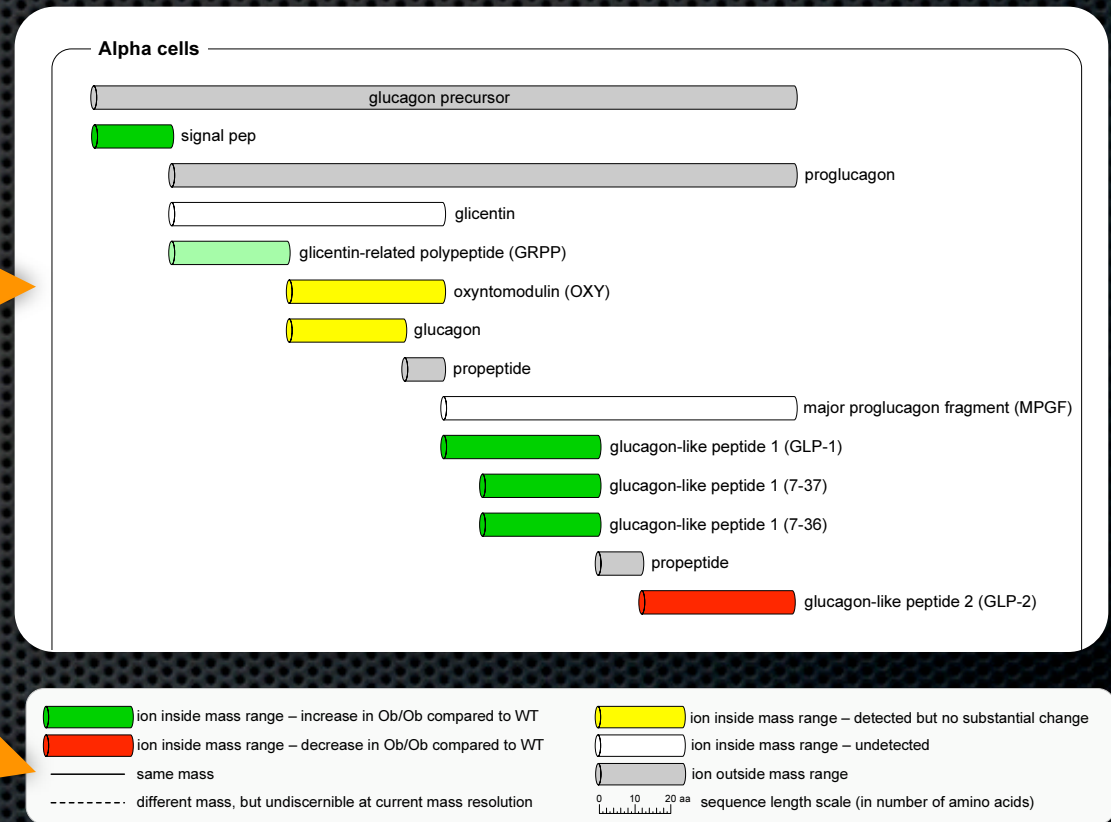
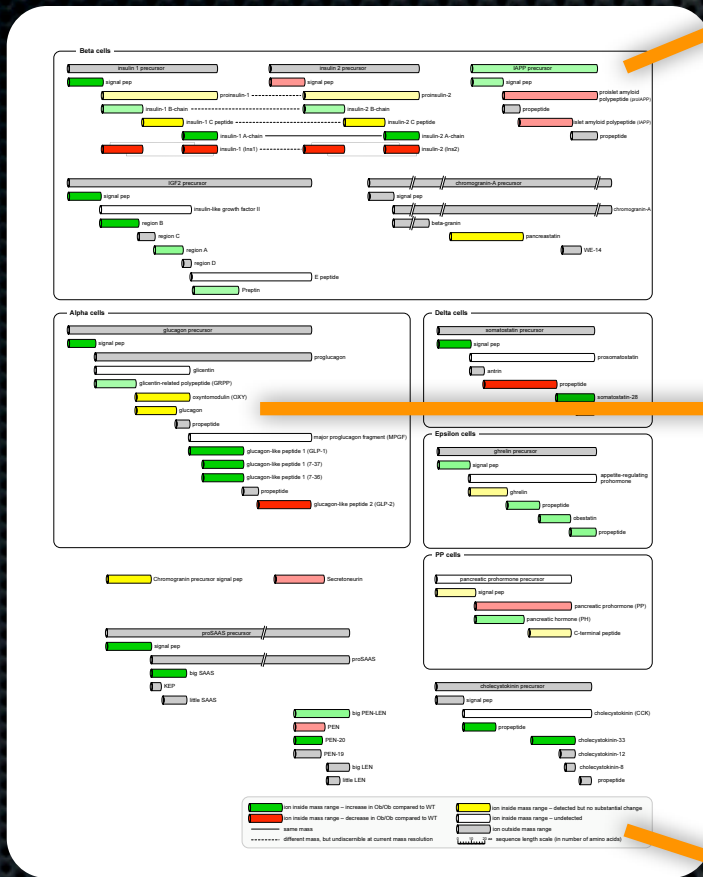
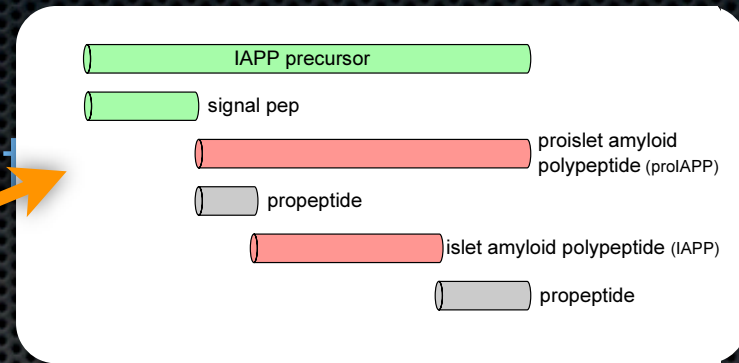
Diabetes Case Study

Metabolic screening straight from tissue

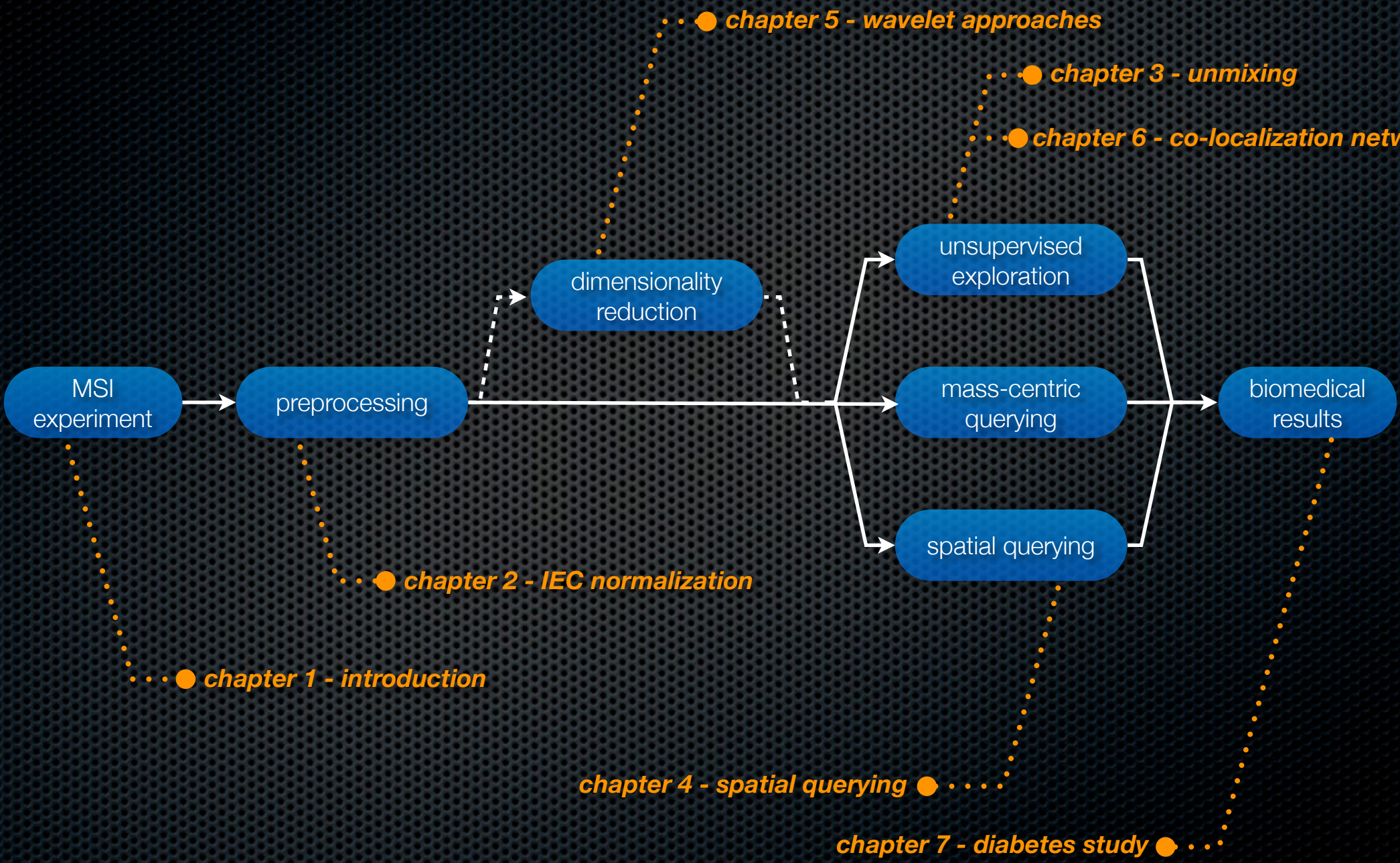


Diabetes Case Study

Metabolic screening straight



5. Mapping to metabolic pathways



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