A Visual Encoding System for Comparative Exploration of Magnetic Resonance Spectroscopy Data

Laura Garrison [1,2]
Jakub Vašíček [3]
Renate Grüner [2,4]
Noeska Smit [1,2]
Stefan Bruckner [1,2]

[1] Dept. of Informatics, Univ. of Bergen, Bergen, Norway
[2] Mohn Medical Imaging and Visualization Centre, Haukeland Univ. Hospital, Bergen, Norway
[3] Dept. of Informatics, Masaryk University, Brno, Czech Republic
[4] Dept. of Physics and Technology, Univ. of Bergen, Bergen, Norway

Presenting a novel visualization system for the exploratory analysis of MRS data

Introduction

What is MRS? Magnetic resonance spectroscopy (MRS) is an *in vivo* non-invasive biochemical imaging technique utilized for tissue metabolite characterization used often for early detection and treatment of tumors and neuropsychiatric conditions. [2,3]

Why is this data difficult to visualize? MRS data output is inherently abstract, with a steep learning curve to successful interpretation. Data often have poor signal to noise ratio, making comparison difficult. [2,3]

What are the current toolset limitations?

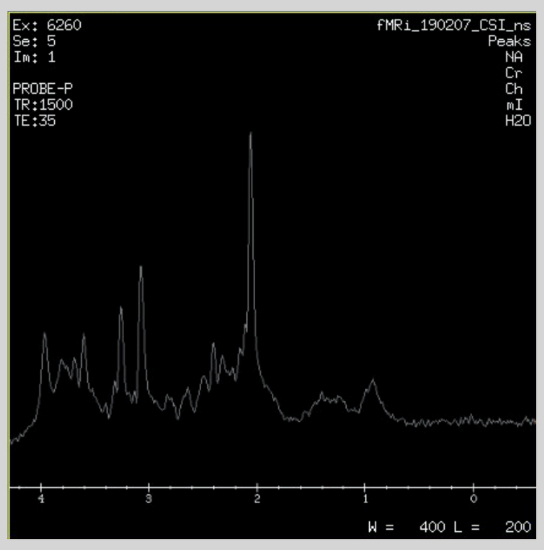
- Qualitative comparison between voxel samples is difficult or impossible
- Limited capabilities to compare all permutations of spectral metabolite ratios[1]
- Limited tools for correlating spectral peaks to corresponding metabolites and spatial sample location

Data & Tasks

Tier 1 — Spectral metabolite samples

Tier 2 — Key attributes: Time, Patient, State, Voxel

Tier 3 — Hidden but retained attributes



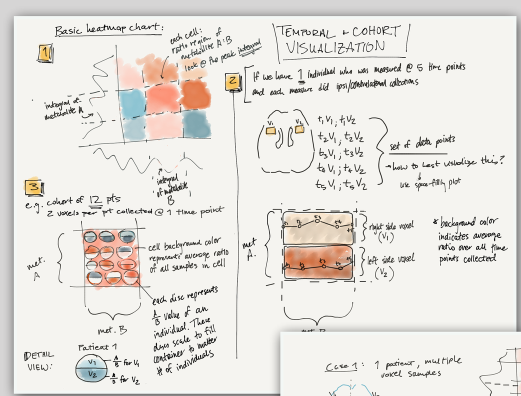
Typical MRS output

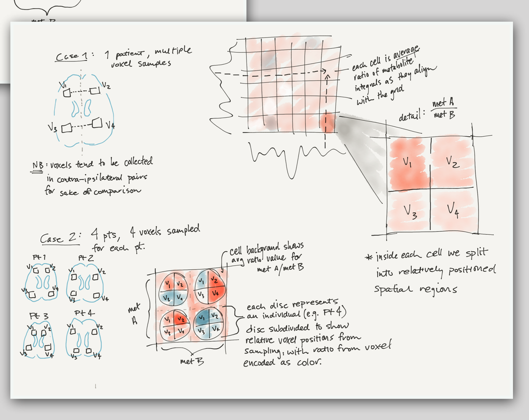
Core Tasks

1. Correlate spectral peaks with corresponding metabolites
2. Match voxel sample to spectral output
3. Determine the ratio of metabolites in a sample(s) by calculating the ratio of their peak integrals
4. Select a subset of spectral acquisitions from a single group for further analysis
5. Discover outliers in spectral output
6. Compare spectral metabolite concentrations within and across voxel samples

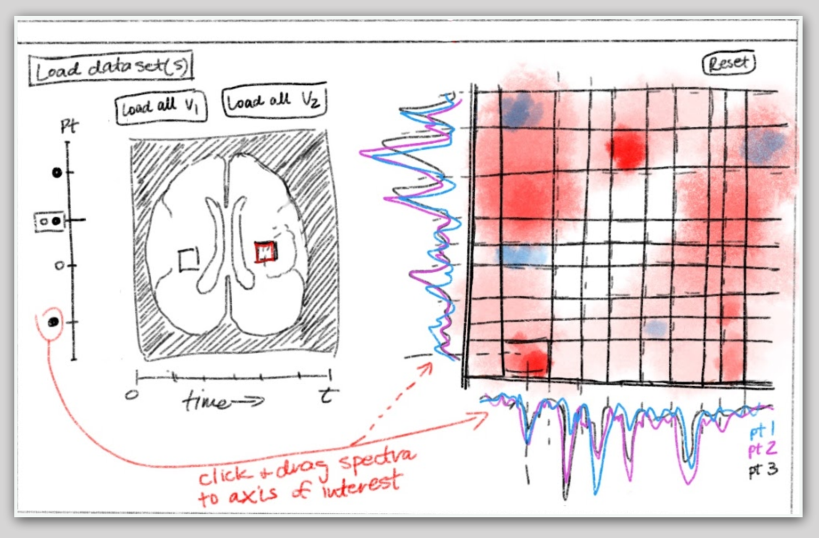
Design Requirements

1. Web application
2. Spectral peak identification
3. Linking between data sources
4. Support comparison of spectral metabolite concentrations as ratios
5. Layered design: overview vs. detail





We then developed a **taxonomy of visual encodings** to represent the range of different **metabolite concentration ratios** at different dimensional tiers.



Results

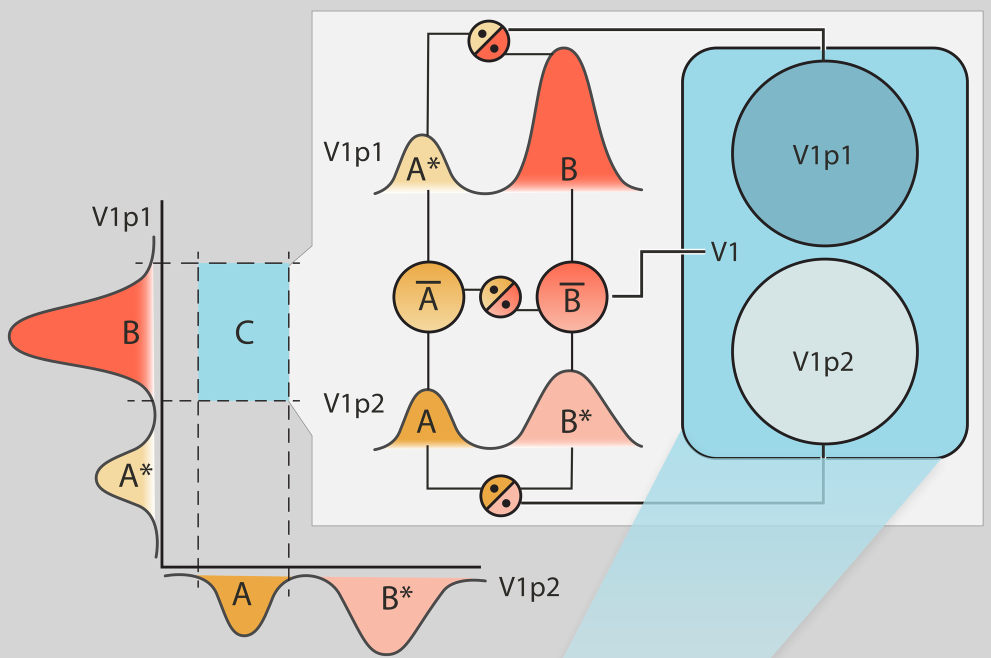
Visual Encodings

Case	patient	voxel	time pt	state	encoding
1	single	single	single	single	
2	single	single	single	dual	
3	single	single	multiple	single	
4	single	single	multiple	dual	
5	single	multiple	single	single	
6	single	multiple	single	dual	
7	single	multiple	multiple	single	
8	single	multiple	multiple	dual	
9	multiple	single	single	single	
10	multiple	single	single	dual	
11	multiple	single	multiple	single	
12	multiple	single	multiple	dual	
13	multiple	multiple	single	single	
14	multiple	multiple	single	dual	
15	multiple	multiple	multiple	single	
16	multiple	multiple	multiple	dual	

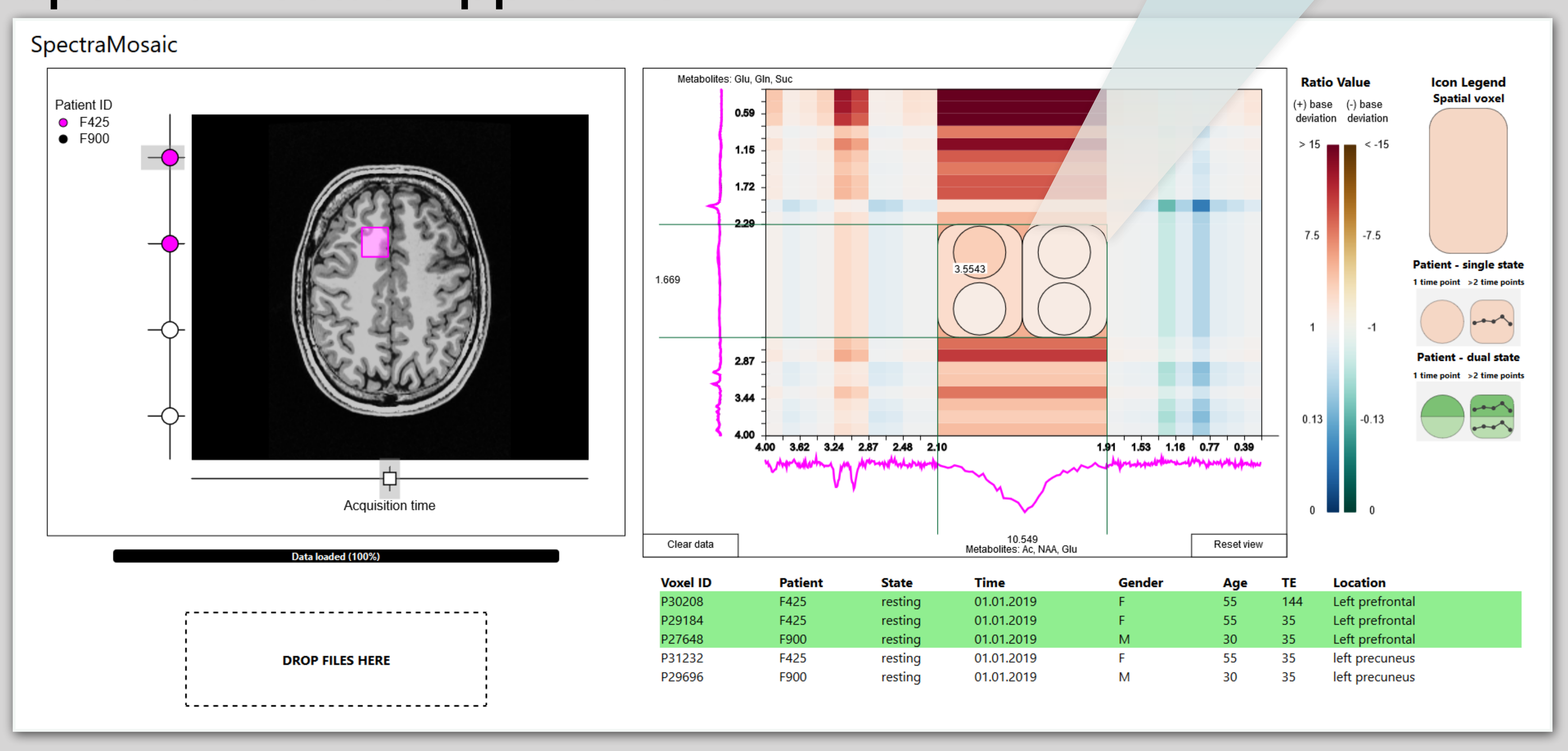
Glyphs encoded to each Tier 2 attribute (individual, voxel, time point, state) permute to 16 possible MRS case scenarios.

Calculations

We perform 2 different metabolite ratio calculations based on peak integrals, one for the overview layer and one for the detail layer.



SpectraMosaic Application



We realized this visual encoding system as part of an **interactive insight-generation tool** for rapid exploration and comparison of metabolite ratio variation for deeper insights to these complex data.

Conclusions

We have developed a novel visual encoding system for selected MRS data attributes using simple glyph shapes with diverging color maps to represent variation. We have implemented this system in a spectral visual analysis tool, and plan to continue working with domain experts to extend our visual system to manage groups and uncertainty.

References

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