Compression of Mass Spectral Imaging Data Using Discrete Wavelet Analysis with Incorporated Spatial Information

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The presented method reduces the size of MSI data sets considerably while still achieving excellent reconstruction of the original mass spectra. This is done by retaining only a limited number of wavelet coefficients that express spatial structure.

Motivation
Mass Spectral Imaging is a relatively new molecular imaging technology that makes it possible to detect thousands of molecules throughout tissue simultaneously, ranging from low-mass metabolites to high-mass proteins. This technology is of prime interest for the molecular characterization of tissue in biomedical studies.

In recent years, MSI data sets have grown in size to such extent that it becomes more and more infeasible to computationally analyze them in their raw form due to both memory and calculation time constraints.

Methods
Previous research at ESAT by Van de Plas et al. has shown solid results using Discrete Wavelet Transform (DWT) on mass spectra to perform feature selection, thus reducing data size, dimensionality and noise. Our newest method further improves on this approach by incorporating one of the key aspects of MSI, spatial information, to better understand what part of the data can truly be considered noise. By using this information, we can selectively remove only those details that do not exhibit a spatial structure.

Results
We demonstrate the performance of this new compression method on a sagittal section of mouse brain and compare the results to the Van de Plas et al. method and to direct analysis of the raw measurements. The presented study focuses on neurodegenerative diseases that show spatially specific behaviour. Examples of such diseases include Parkinson's disease, where dopamine producing brain nuclei such as the amygdala are affected, and amyotrophic lateral sclerosis, where motor neuron regions in the brain are affected.

Conclusions

By retaining a small number of detail coefficients that express spatial structure we can strongly improve reconstruction of the mass spectra while still achieving considerable compression.