Multiresolution Analysis of Proteomics Images using Contourlets.

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2D gel electrophoresis (2DGE) is the most commonly used method for protein separation. After gel scanning, images with a plethora of spot features are generated. Proper preprocessing of 2DGE images is essential to suppress noise without distorting the signal and extract reliable spot features in proteomics workflows for biomarkers discovery. We have introduced the use of the Contourlet Transform (CT) for 2D gels image analysis and compare it to the well known Wavelet Transform (WT). We will show that Contourlets not only achieve better average signal-to-noise ratio, but also preserve better, relatively to wavelets, the spot boundaries and alter less the intensities of significant spot features. Work in progress includes investigating CT-based methods for multiplicative and impulsive noise removal from gel images. Furthermore, we are working on developing multiresolution spot matching algorithms and effective 3D visualization schemes for feature vectors extracted at different stages of a differential proteomics workflow for biomarkers discovery (based on either 2DE gels or LC-MS datasets).