

2-DE Gel Analysis

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In this talk I discuss three elements of 2-DE gel analysis:

1. Protein spot modeling for quantification and analysis
2. Gel image registration
3. Novel methods of differential analysis.

Modeling: In image analysis of two dimensional electrophoresis (2-DE) gels, individual spots need to be identified and quantified. I describe a parametric representation of spot shape that is both general enough to represent unusual spots, and specific enough to introduce constraints on the interpretation of complex images. Our method uses an automatically constructed, robust model of shape based on the statistics of an annotated training set and has been applied to spot quantification and algorithm evaluation.

Gel Registration: I present a robust and accurate 2-DE gel alignment algorithm which combines point matching and local image-based refinement. The algorithm uses a novel combination of Euclidian, shape context, image and feature based attributes to produce a point distance measure. Correspondence is determined using this measure and is further improved using an iterative M-estimation approach, and shown to be robust in the presence of large image distortions.

Differential Analysis: I present an alternative to the traditional method of spot volume differential analysis, using a single, consistent spot detection based on a registered image set. The idea can be extended to a fully pixel-wise differential analysis and has shown promise on an initial dataset.