

FAST NON-RIGID 2-DE GEL IMAGE REGISTRATION

Rogers, M.^{*}, Graham, J., Tonge, R.P.

Imaging Science and Biomedical Engineering, University of Manchester

Large-scale proteomics research requires the production of sets of 2 Dimensional Electrophoresis (2-DE) gels, often containing many duplicates. The analysis and comparison of these large gel sets remains a bottleneck in the proteomics workflow process despite advances in commercially available software. The ability to define an exact correspondence between gel images is central to accurate gel comparison. Recently, there has been much interest in applying non-rigid image registration techniques to determine this correspondence. Many commercial gel analysis systems (Z3/Z4000, Progenesis and others) implement proprietary image registration algorithms, some of which have been published; however, little work has been done to compare the performance of these algorithms with other methods published in the machine vision literature. In this work, we propose a novel method for fast non-rigid registration of 2-DE gel images. Our method is similar to Thirion's 'demons' (Medical Image Analysis 2:3, pp. 243-260, 1980) but is driven by an image force determined by the differential structure of protein spots. A regularisation stage ensures transformations are smooth and diffeomorphic. We have carried out an objective evaluation of our algorithm using realistic synthetic gel images with precisely known deformations, and validated with real data. We have compared our results to those achieved with our own implementation of the Z3 registration algorithm (Electrophoresis 22, pp 1616-1626, 2001). Our algorithm is shown to be more robust and to produce more realistic deformation fields. The study demonstrates the necessity of considering both accuracy (the intensity differences between the post-registered images) and the form of the estimated deformation field when evaluating 2-DE gel registration algorithms.