



Proteomics Gel Matching

A leading biotech company specializes in proteomics, the comprehensive study of proteins, as a foundation for the discovery of new drugs and ways of diagnosing disease. They operate a sophisticated combined proteomics and genomics data factory generating very large quantities of data. Effective IT systems are a vital part of this operation.

Business Problem

This company compares the proteins from different subjects, looking for those which are different in healthy and unhealthy subjects.

One of the key stages in this investigation is the production of 2D electrophoresis gels which “map” the protein peptides according to mass and acidity.

It is vital that the gels from different samples can be compared accurately with each other. Unfortunately, the production of the gels is an inexact art, and so the correct aligning of the map images, and the correct matching of peptides from one map to another, is a complex problem. To solve the problem manually involves many man-hours of painstaking work so an automated approach was clearly required.

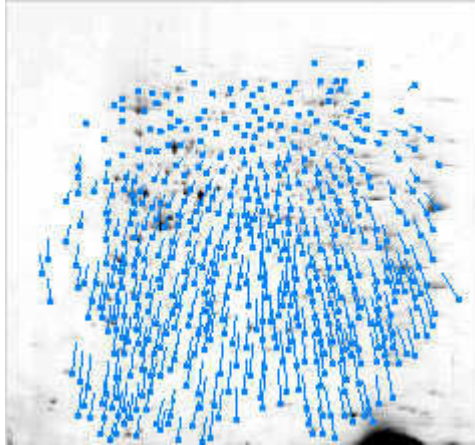
Tessella Solution

The solution involved state-of-the-art image processing techniques, developed in collaboration with Professor Wilson of Warwick University, and new statistical methods formulated by the Tessella developer.

The image analysis involved pre-processing of the map images, and then a multi-resolution approach, which aligns the maps at successively increasing levels of detail.

Once the image maps are aligned, the statistical work begins. Using a Bayesian model, drawing prior assumptions from theoretical modelling and existing databases of manually matched peptides, the statistical algorithm matches the peptides from one map to the corresponding peptides in the other map.

The CPU-intensive application program was written in C++, with the advantages of high efficiency and an object-oriented approach.



The dark blobs in the above “map” correspond to protein peptides, and some artefacts. The blue vectors show how those peptides need to be translated to align them with their corresponding peptides in a second map.

Results and Benefits

The development of this state-of-the-art application has been critical for the growth of the customer’s proteomics operations.

The application has been continuously improved and is now regarded as highly accurate. This accuracy means that the amount of manual work involved in identifying potential drug targets is much smaller. In turn, this allows for a much higher throughput of studies and, therefore, an increase in the rate at which drugs can be brought to market.

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