**Abstract**

**Objectives:**

The objective of this study was to introduce and evaluate advanced statistical tools for the analysis of 2D gel electrophoresis (2DGE) data. We aimed to improve the detection of differentially expressed proteins and provide a comprehensive view of protein expression patterns.

**Methods:**

We developed a suite of advanced statistical tools, including multivariate analysis methods such as Principal Component Analysis (PCA) and Correlation Analysis, and hierarchical clustering algorithms. These tools were applied to a set of 2DGE data from a biological study. The data were preprocessed using standard normalization techniques and analyzed using a combination of visual inspection and statistical testing.

**Results:**

The results showed a significant improvement in the detection of differentially expressed proteins compared to conventional methods. The advanced tools allowed for the identification of complex expression patterns that were not apparent with traditional approaches. Furthermore, the hierarchical clustering algorithms provided a comprehensive overview of the data, allowing for the visualization of clusters of proteins with similar expression profiles.

**Conclusion:**

The advanced statistical tools developed in this study provide a powerful framework for the analysis of 2DGE data. They allow for the detection of complex expression patterns and provide a comprehensive view of protein expression profiles. The tools are freely available for download and can be used by researchers in the field of proteomics.

**Keywords:** 2DGE, Protein Expression, Multivariate Analysis, Hierarchical Clustering, Advanced Statistical Tools.