

Fast processing of 2D-gel and MALDI-based mass spectrometry protein data

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Introduction

2D-gel electrophoresis and MALDI-TOF-MS (mass spectrometry using matrix assisted laser desorption ionization coupled to time of flight analysers) are usually employed together in experimental workflows. While 2D-gel electrophoresis allows obtaining a set of differentially expressed spots, MALDI-TOF-MS allows identifying the proteins associated with such spots. Such processes involve large data processing in order: (i) to analyze 2D-gels across samples to obtain the differentially expressed spots using Progenesis SameSpots software, (ii) to excise such spots and to treat them for protein identification and (iii) to bind those protein identifications to the 2D-gel spots. Such procedure is done in an intensive handling and time consuming way. Moreover, doing this repetitive process in a non-automated manner is error-prone, threatening study reliability and reproducibility.

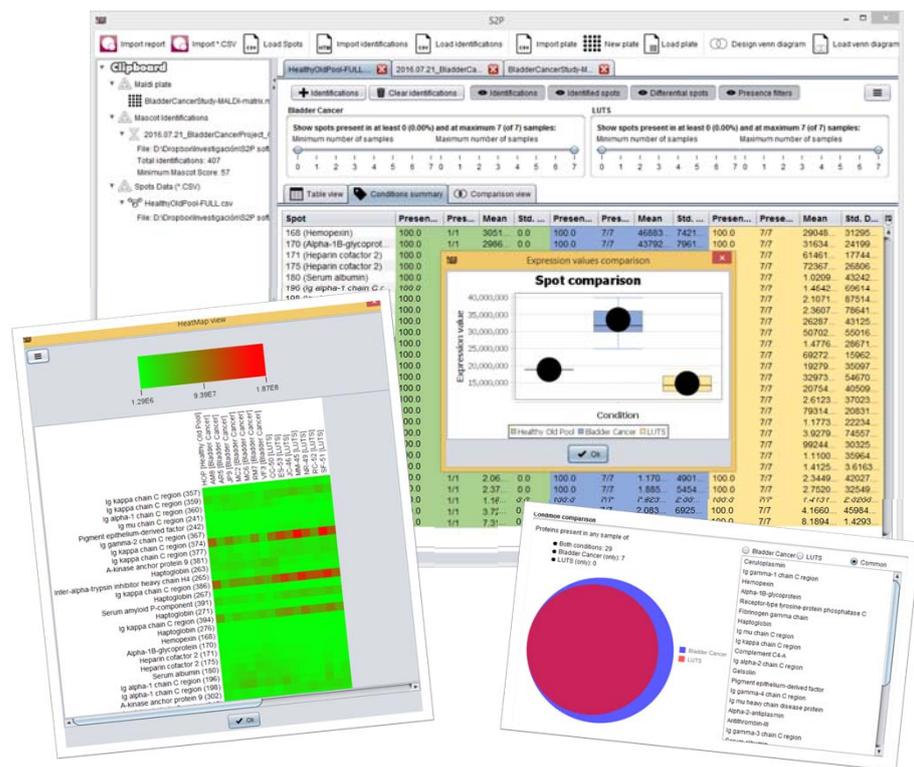
In order to fast and automatically perform these tasks we are developing the **S2P** software application (<http://sing.ei.uvigo.es/s2p/>), to help researchers to overcome this tedious but necessary data processing. The purpose of this work is to present this open software.

Results: S2P

S2P (*Spot to Proteomics*) is a desktop application specifically created to perform fast processing of 2D-gel and MALDI-based mass spectrometry protein identification-based data. Currently, S2P allows researchers: (i) to collect Progenesis SameSpots reports into a full table where all samples can be compared and analyzed, (ii) to link spots to protein identifications obtained with Mascot, and (iii) to export and explore data in different ways (such as heatmaps or Venn Diagrams).

Try S2P now!

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Conclusions

S2P is completely free, distributed under license GPLv3, and provide a friendly graphical user interface designed to allow researchers saving time in data processing tasks related to 2D and MALDI mass spectrometry protein identification-based data.

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