An open-source software for fast and automatic processing of 2D-gel and MALDI-based mass spectrometry protein data

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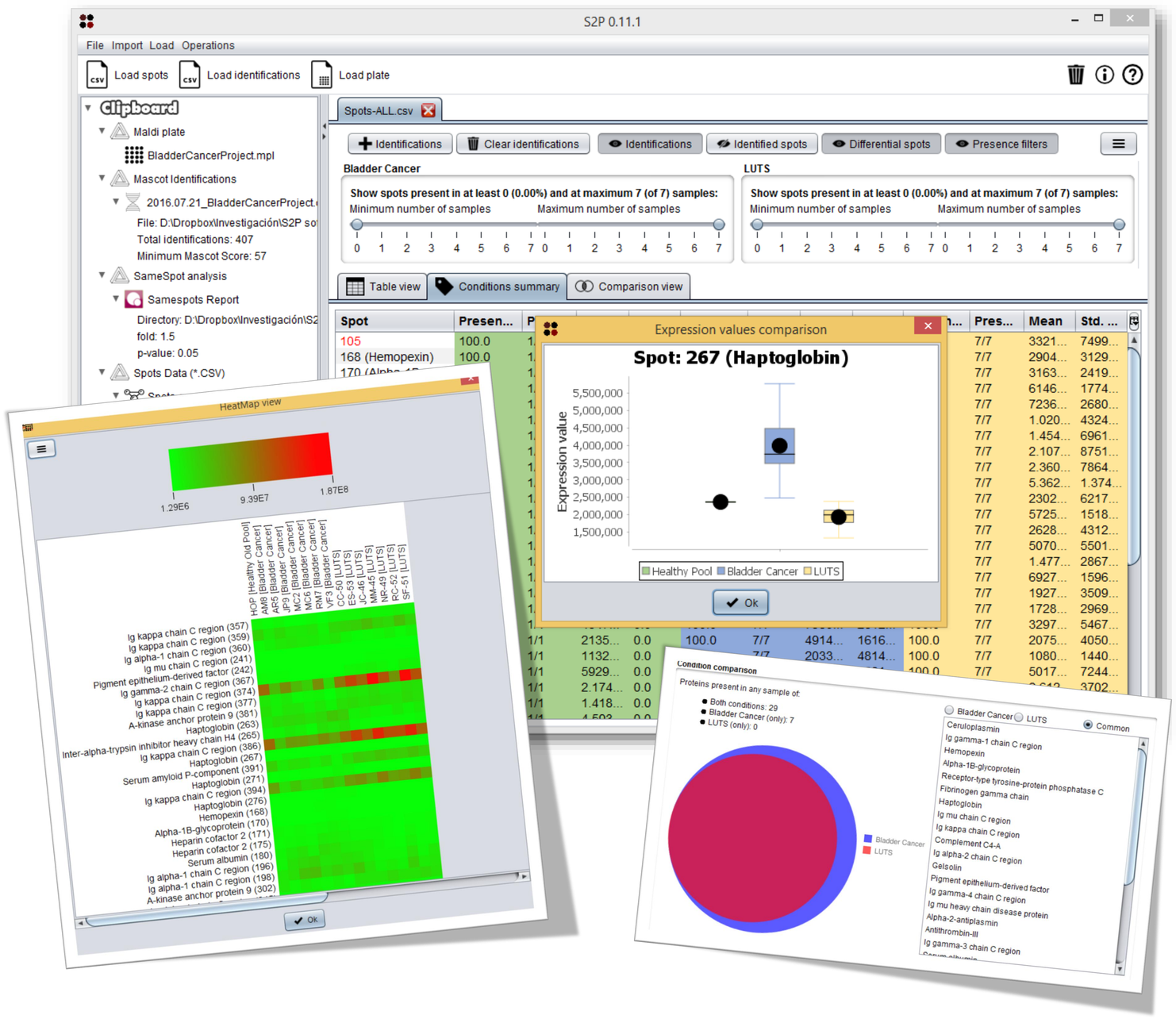
Introduction

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 (***www.sing-group.org/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 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).



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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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