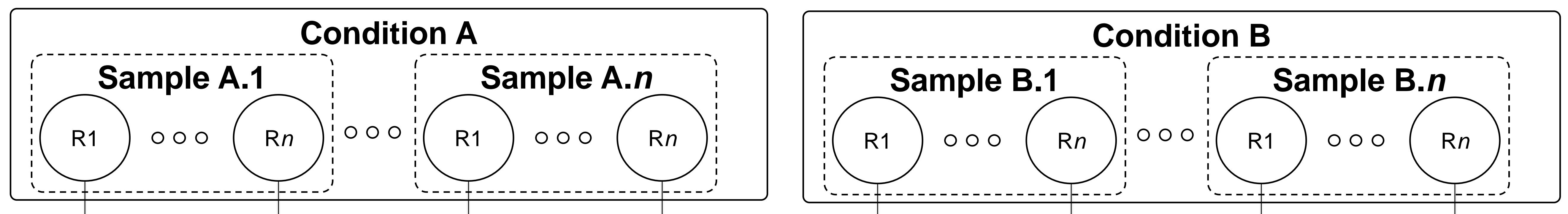# Using S2P to process emPAI quantitation results obtained from MS/MS Mascot searches

H. López-Fernández[1,2,3], J.E. Araújo[3], H.M. Santos[3], A. Fernández-Lodeiro[3], C. Fernández-Lodeiro[3], J. Djafari[3], J. Coelho[3], G. Pinto[3], N. Morais[3], G. Marcelo[3], J. Machado[3], S. Jorge[3], J. Prates[3], E. Oliveira[3], J. Fernández-Lodeiro[3], C. Lodeiro-Espiño[3], J. L. Capelo-Martínez[3]

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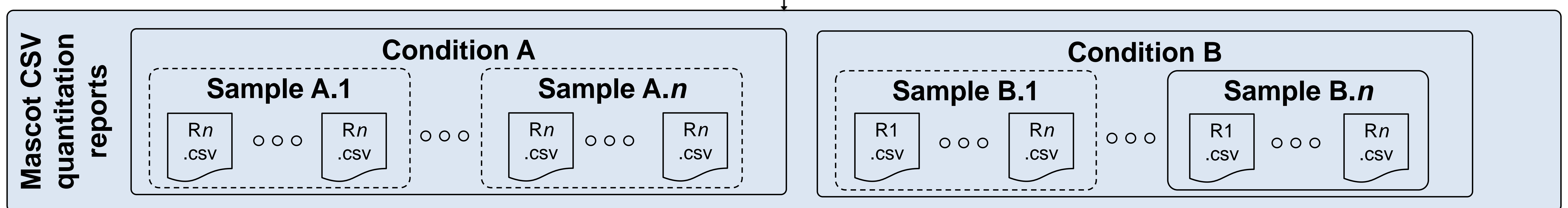
The Mascot search engine creates one CSV report file for each experiment replicate, containing the protein identifications along with their corresponding emPAI quantitation values.

S2P is used to process the Mascot CSV reports, allowing users to normalize the emPAI quantification values, and creating the three different visualizations shown bellow.

Replicates table: a table with one row by each single protein quantitation in the whole dataset. This is the raw quantification data arranged as a table.

Replicates (by protein) table: a table where replicates can be compared by protein identification.

Conditions table: a table where experimental conditions can be compared by protein identification using the quantitation values. In this table, the t-test results of the comparison between each pair of experimental conditions are provided in order to detect differences in the average quantitation values.

Try S2P now!
S2P is freely available at
http://www.sing-group.org/s2p