

On the characterization of proteomic maps by a novel similarity/diversity measure

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Summary

A new distance measure derived from the partial ordering approach is proposed for evaluating the similarity/diversity among proteomic maps. This distance – weighted standardized Hasse distance - is evaluated between pairs of Hasse matrices derived from the classical partial ordering rules. Therefore, this distance is particularly indicated to detect similarity/diversity into sequential data, i.e. data where a quantitative variable is ordered by a ranking variable. Examples are IR, NMR, mass spectra as well as DNA sequences and proteomic maps.

This distance measure can be naturally standardized, thus allowing the interpretation of the distances as absolute values (e.g. percentage) and deriving simple similarity and correlation indices. The proposed measure has been evaluated on some proteomic maps taken from literature. A sensitivity analysis has been also performed showing the high capability of this measure to taking into account small modifications of the proteomic maps. Finally, a comparison with results obtained from literature is given, together with a comparison with matrix invariants derived from the Hasse matrix.