

1

Objectives

The main objectives of this work are the following:

1. To make an empirical comparison of some of the currently available dimension reduction techniques applied for the integration of omics data, focused on their ability to include biological annotations,
2. To develop methods and workflows able to apply these techniques, focusing on the matching of distinct omics datasets relying on biological knowledge,
3. To apply these methods to specific translational biomedical research cases, such as an integrative analysis of transcriptomics and proteomics data to study ischemic stroke, as well as to public datasets, which can be easily shared and are not as restricted by sample sizes as other projects.
4. To implement the knowledge acquired with this work into the appropriate bioinformatics tools, e.g. R packages or web-based tools, that will be used in future biomedical research projects for providing a better interpretation of this kind of studies.

All these objectives are in agreement with the tasks defined within a project partially supported by Grant MTM2015-64465-C2-1-R (MINECO/FEDER) from

the Ministerio de Economía y Competitividad (Spain), to which the PhD Thesis proposed here is related.