Integrative Analysis of Omics Data with Biological Knowledge in Translational Medicine

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Abstract (wip)

Over the past decade, advancements in omics technologies have facilitated the high-throughput monitoring of molecular and organism processes. These techniques have been widely applied to identify biological agents and to characterize biochemical systems, often focusing on the discovery of therapeutic targets and biomarkers related with specific diseases (Cisek et al., 2016),(K. Wang et al., 2014),(F. Wang et al., 2014). While many single-omic approaches target comprehensive analysis of genes (genomics), mRNA (transcriptomics), proteins (proteomics), and metabolites (metabolomics) among other, there is still field to improve omics data analyses through integrative methods (Wanichthanarak et al., 2015),(Gomez-Cabrero et al., 2014). In this sense, the integrative point of view defined in the paragraph above, applied to multi-omics data, is a promising approach to achieve better biomarker development in biomedical research projects, and this is the core idea of this work.

As the field of omics has evolved from analyzing a unique type of data to multiple types, it has been natural to extend the previous use of multivariate techniques to this new situation. With this aim classical and new multivariate techniques have been applied to the analysis of multi-omics datasets. Many of these techniques are dimension reduction methods that aim at finding main sources of variability in the data while maximizing some information characteristic such as the variance of each dataset, the correlation between groups of variables or other. Examples of such techniques are well consolidated methods such as Principal Component Analysis (PCA), Singular Value Decomposition (SVD), Correspondence Analysis (CA), and Partial Least Squares (PLS). Besides these more "novel" approaches have been used such as: Principal Components Regression, Coinertia and Multiple Coinertia Analysis, Generalized SVD, Sparse PLS, Multiple Factor Analysis (MFA), or combined versions of them (M. Wheelock & E. Wheelock, 2013),(Lê Cao et al., 2009),(Culhane et al., 2003). Publications such as (Meng et al., 2016), (Cavill et al., 2016), (Wu et al., 2019), (Subramanian et al., 2020), (Krassowski et al., 2020), and (Cantini et al., 2021), are good reviews of the state of the art of using multivariate and joint reduction methods for Integrative Multi-Omics Analysis.

Dimension reduction methods, especially those that are able to deal with situations that are typical from the omics context (with many more variables than samples, or possibly sparse matrices with many missing values), have been of

great help in visualizing datasets or even for performing variable selection to find biomarkers for a given situation (Wu et al., 2019). There is however one point where they underperform other approaches, that is, the difficulty in interpreting results from a biological point of view. This is relatively reasonable, because the most of these methods work by creating new variables that are some type of linear combination from the original ones. While this is useful, for example, for removing redundancy, this does not provide any clues on what these new dimensions may mean from a biological point of view.

This problem has been known since the beginning of using multivariate methods with omics data, but only a few approaches have been taken to deal with this. The first attempts to introduce biological information in the analyses consisted of using the most well-known database of biological functions, the Gene Ontology (GO) (Ashburner et al., 2000). Fellenberg (Busold et al., 2005) introduces a way to integrate Gene Ontology information with Correspondence Analysis to facilitate the interpretation of microarray data. De Tayrac et al. (Tayrac et al., 2009) applies multiple factor analysis to the integrative analysis of microarray and DNA copy number data. They apply GO Terms on data visualizations by treating these terms as supplemental information. In recent years the representation of biological knowledge has shifted from Gene Ontology to using Gene Sets (Huang et al., 2009). Meng and Culhane (Meng et al., 2016) have introduced the Integrative Clustering with Gene Set Analysis where gene set expression analysis is performed based on multiple omics data; and Tyekucheva et al. (Tyekucheva et al., 2011), go one step further and use the results of Gene Set Expression Analysis (GSEA) to integrate different omics data.

The previous approaches show several things: Although the idea that integrating quantitative data with biological knowledge may increase interpretability, the number of successful attempts to do this is still small. In this thesis, the use of either classical GO Terms or more flexible annotations (Gene Sets or custom annotations), will be combined with different approaches, and combinations of them if needed, to guide integrative analysis and to improve its biological interpretability from the point of view of the biomedical researchers.

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List of Abbreviations

1-D, 2-D . . .   One- or two-dimensional, referring **in this thesis** to spatial dimensions in an image.

Otter . . . . .   One of the finest of water mammals.

Hedgehog . . .   Quite a nice prickly friend.

1

Introduction

Contents

1.1 Content of the introductory text

The general concept of Data Integration can be defined as the combination of data from different sources to provide users with a unified view of the data (Lenzerini, 2002). However, the practical meaning of the term Integration may vary from, for instance, the computational combination of data to the combination of studies performed independently, the simultaneous analysis of multiple variables on multi-

ple datasets, or any possible approach for homogeneously querying heterogeneous data sources. Therefore, in many cases, integrative analysis may be preferable to a simple combination of data from distinct sources. Integrative analysis allows not only the combination of heterogeneous data but also the combined use of these data to obtain the most relevant information and, what is better, to be able to extract some information that could not be unveiled by the separate analysis of each of the original data types.

Over the past decade, advancements in omics technologies have facilitated high-throughput monitoring of molecular and organism processes. These techniques have been widely applied to identify biological agents and characterize biochemical systems, often focusing on the discovery of therapeutic targets and biomarkers related to specific diseases (Cisek et al., 2016),(K. Wang et al., 2014), and (F. Wang et al., 2014). Although many single-omic approaches target comprehensive analysis of genes (genomics), mRNA (transcriptomics), proteins (proteomics), and metabolites (metabolomics), among others, there is still a need to improve omics data analyses through integrative methods (Wanichthanarak et al., 2015),(Gomez-Cabrero et al., 2014). In this sense, the integrative point of view defined in the paragraph above, applied to multi-omics data, is a promising approach to achieving better biomarker development in biomedical research projects, and this is the core idea of this work.

As the field of omics has evolved from analyzing unique types of data to multiple types, it is natural to extend the previous use of multivariate techniques to this new situation. With this aim, classical and new multivariate techniques have been applied for the analysis of multi-omics datasets. Many of these techniques are dimension reduction methods that aim to find the main sources of variability in the data while maximizing some information characteristics, such as the variance of each dataset and the correlation between groups of variables. Examples of such techniques are well-consolidated methods such as Principal Component Analysis (PCA), Singular Value Decomposition (SVD), Correspondence Analysis (CA), and Partial Least Squares (PLS). Besides these more "novel" approaches have been

used such as: Principal Components Regression, Coinertia and Multiple Coinertia Analysis, Generalized SVD, Sparse PLS, Multiple Factor Analysis (MFA), or combined versions of them (M. Wheelock & E. Wheelock, 2013),(Lê Cao et al., 2009),(Culhane et al., 2003). Publications such as (Meng et al., 2016), (Cavill et al., 2016), (Wu et al., 2019), (Subramanian et al., 2020), (Krassowski et al., 2020), and (Cantini et al., 2021), are good reviews of the state of the art of using multivariate and joint reduction methods for Integrative Multi-Omics Analysis.

Dimension reduction methods, especially those that are able to deal with situations that are typical of the omics context (with many more variables than samples, or possibly sparse matrices with many missing values), have been of great help in visualizing datasets or even in performing variable selection to find biomarkers for a given situation (Wu et al., 2019). However, there is one point where they underperform other approaches: the difficulty in interpreting results from a biological point of view. This is relatively reasonable because most of these methods work by creating new variables that are a type of linear combination from the original ones. While this is useful, for example, for removing redundancy, it does not provide any clues on what these new dimensions may mean from a biological point of view.

This problem has been known since the introduction of multivariate methods with omics data, but only a few approaches have been taken to deal with this problem. The first attempts to introduce biological information in the analyses consisted of using the most well-known database of biological functions, the Gene Ontology (GO) (Ashburner et al., 2000). Fellenberg (Busold et al., 2005) introduces a way to integrate Gene Ontology information with Correspondence Analysis to facilitate the interpretation of microarray data. De Tayrac et al. (Tayrac et al., 2009) applies multiple factor analysis to the integrative analysis of microarray and DNA copy number data. They applied GO Terms on data visualizations by treating these terms as supplemental information. In recent years, the representation of biological knowledge has shifted from Gene Ontology to Gene Sets (Huang et al., 2009). Meng and Culhane (Meng et al., 2016) have introduced the Integrative

Clustering with Gene Set Analysis where gene set expression analysis is performed based on multiple omics data; and Tyekucheva et al. ([Tyekucheva et al., 2011](#)), go one step further and use the results of Gene Set Expression Analysis (GSEA) to integrate different omics data.

Altogether, the previous approaches show several things: Although the idea that integrating quantitative data with biological knowledge may increase interpretability, the number of successful attempts to do this is still small. In this thesis, the use of either classical GO Terms or more flexible annotations (Gene Sets or custom annotations) will be combined with different approaches, and combinations of them, if needed, to guide integrative analysis and improve its biological interpretability from the point of view of biomedical researchers.

1.2 Background/State of the Art

FALTA DESENVOLUPAR PUNTS

1.2.1 Omics data analyses

Omics data encompasses comprehensive information about a biological system, encompassing its entirety. The term "omics" originates from the Greek word "oma," meaning "a collection" or "a mass." Omics data is generated through high-throughput analysis technologies that enable the measurement of gene expression, protein composition, DNA structure, metabolism, and more.

Among the primary omics data types one can highlight the following:

- Genomics: The study of the genome, which comprises the complete set of genes within an organism.
- Transcriptomics: The investigation of gene expression, focusing on the amount of messenger RNA (mRNA) produced from each gene.
- Proteomics: The examination of proteins, the molecules that carry out the majority of biological functions.

- Metabolomics: The study of metabolism, the ensemble of chemical reactions occurring within an organism.

- Epigenomics: The exploration of changes in gene expression that are not attributed to alterations in DNA sequence.

Omics data integration stands as a complex endeavor requiring advanced statistical and computational methods. It is employed for a range of biomedical applications, such as identifying novel genes and proteins linked to diseases, developing new drugs, and enhancing diagnostic accuracy.

3 PROBLEMES ESENCIALS (veure projecte recerca Alex):

- **Omics data may be partly incomplete**, especially in multiomics studies, where not all types of data are usually available for all individuals.

- **The results of these analyses are difficult to interpret**. If we agree that the ultimate goal of many analyzes is a better understanding of the underlying biological processes, for example, in a disease study context, it should be possible to establish a clear relationship between the outcome of an analysis and what this means biologically. And this is not always so.

- **These kind of data analytics are difficult to standardize**, as it is not easy to make complex pipelines of multi-omics analyses, which integrate multiple processes with multiple sources, easy to reproduce or communicate.

MES EL TEMA DE LA p»n (Dimensionallity Reduction Techniques; The p»n situation)

1.2.2   The problem of having partly incomplete data

Having partly incomplete data is a common challenge in biomedical multi-omics data analyses, where not all omics layers or samples have complete measurements for all variables of interest. This problem, known as missing data, can hinder the integrative analysis and interpretation of multi-omics datasets.

1. Introduction

Missing Data Types: Missing data can occur in various forms in multi-omics datasets. For example, some omics layers may have missing values for certain variables (e.g., genes, proteins, metabolites), or specific samples may be missing data for certain omics layers. This can result from technical limitations, experimental design, or inherent biological variability.(Flores et al., 2023)

Impact on Analysis: Incomplete data can introduce biases and distort the results of multi-omics analyses. It can affect downstream statistical analyses, clustering, network inference, and machine learning algorithms, leading to inaccurate or unreliable findings. Addressing missing data appropriately is crucial for obtaining valid and meaningful results. Reference:

Missing Data Mechanisms: Understanding the underlying mechanisms of missing data is essential for selecting appropriate imputation methods. Missing data can occur due to different mechanisms, such as missing completely at random (MCAR), missing at random (MAR), or missing not at random (MNAR). These mechanisms influence the choice of imputation techniques and the assumptions made during data analysis.(Little & Rubin, 2002)

Imputation Methods: Imputation techniques are employed to estimate missing values in multi-omics datasets. Various imputation methods, including mean imputation, regression imputation, multiple imputation, and machine learning-based approaches, have been proposed to handle missing data in different omics layers. Each method has its assumptions, strengths, and limitations, and the choice of imputation strategy should be carefully considered. Reference: Buuren, S. V., & Groothuis-Oudshoorn, K. (2011). mice: Multivariate imputation by chained equations in R. Journal of Statistical Software, 45(3), 1-67.

Uncertainty and Sensitivity Analysis: Dealing with missing data introduces uncertainty in the imputed values and subsequent analyses. Sensitivity analyses, such as multiple imputation and bootstrapping, can help assess the robustness of the results to missing data assumptions and imputation methods. Reference: Sterne, J. A., et al. (2009). Multiple imputation for missing data in epidemiological and clinical research: Potential and pitfalls. BMJ, 338, b2393.

Addressing the issue of incomplete data in multi-omics analyses is crucial to avoid biased or misleading results. By utilizing appropriate imputation methods and understanding the missing data mechanisms, researchers can mitigate the impact of missing data and enhance the accuracy and reliability of their analyses.

PENDENT REVISAR TOT

1.2.3 Results interpretation in the context of integrative multi-omics data analyses

Interpretation of results in integrative multi-omics data analyses is a critical challenge due to the complexity and high dimensionality of the data, as well as the need to integrate information from multiple omics layers. Here, I will explain the problem of result interpretation in this context and provide relevant bibliographic references.

Data Integration Challenges: Integrating multi-omics data involves combining information from different molecular layers such as genomics, transcriptomics, proteomics, and metabolomics. Each omics layer provides a unique perspective on biological processes, and integrating these layers can reveal comprehensive insights. However, interpreting the integrated results becomes challenging due to the heterogeneity and scale differences among the omics data. Reference: Wang, X., & Zhang, B. (2018). Integrating multiple 'omics' data for biomarker discovery and clinical assessment. Molecular & Cellular Proteomics, 17(6), 991-1003.

Dimensionality and Complexity: Multi-omics data analyses often result in high-dimensional datasets with numerous features, making it difficult to interpret the results directly. The challenge lies in identifying the most relevant features or patterns and extracting meaningful biological insights from the vast amount of data. Reference: Nguyen, T. M., et al. (2019). Integrative analysis of multi-omics data for discovery and functional studies of complex human diseases. Advances in Genetics, 103, 143-175.

Contextual Interpretation: Interpreting multi-omics results requires considering the biological context, such as pathways, networks, and regulatory interactions. Understanding how different omics layers interact and influence each other

within biological systems is crucial for accurate interpretation. Reference: Mei, H., et al. (2017). The road beyond omics: Integration of multi-omics data for the inference of regulatory networks and precision medicine. Computational and Structural Biotechnology Journal, 15, 359-366.

Validation and Biological Significance: Integrative multi-omics analyses often generate numerous associations, correlations, or biomarkers. However, validating and determining the biological significance of these findings is a key challenge. Experimental validation, functional enrichment analysis, and comparison with existing knowledge are essential for confirming the biological relevance of the results. Reference: Sun, H., et al. (2020). Strategies for interpreting multiomics studies in schizophrenia and other neuropsychiatric disorders. Journal of Psychiatric Research, 129, 121-133.

Visualization and Interactive Tools: Visualizing and exploring multi-omics data can aid in result interpretation. Interactive visualization tools that integrate different omics layers, provide network views, and enable user-driven exploration can facilitate the interpretation process. Reference: Swatloski, T., & et al. (2020). Multi-Omics Data Integration, Interpretation, and Its Application. Genes, 11(10), 1162.

In summary, the problem of result interpretation in integrative multi-omics data analyses stems from the challenges of data integration, high dimensionality, contextual understanding, validation, and visual exploration. Addressing these challenges requires a combination of statistical methods, biological knowledge, and interactive tools to extract meaningful insights from the integrated data.

PENDENT REVISAR REFS ANTERIORS

1.2.4 Approaches for the biological and clinical interpretation

The biological and clinical interpretation of multi-omics data analysis results is crucial for gaining insights into the underlying molecular mechanisms, identifying biomarkers, and understanding disease processes.

1. Introduction

1. **Pathway and Functional Enrichment Analysis**: Pathway and functional enrichment analysis aim to identify overrepresented biological pathways, gene sets, or functional categories that are significantly associated with the differentially expressed genes or other omics features. These analyses help in understanding the biological processes, molecular functions, and cellular components that are affected in a particular condition or disease. Citation: Khatri, P., et al. (2012). Ten years of pathway analysis: Current approaches and outstanding challenges. PLoS Computational Biology, 8(2), e1002375.

2. **Network Analysis**: Network analysis involves the construction and analysis of biological networks, such as gene regulatory networks or protein-protein interaction networks, using multi-omics data. Network-based approaches help in identifying key hub genes, modules, or subnetworks that play important roles in disease progression or phenotype. Citation: Barabási, A. L., et al. (2011). Network medicine: A network-based approach to human disease. Nature Reviews Genetics, 12(1), 56-68.

3. **Machine Learning and Predictive Modeling**: Machine learning algorithms, such as random forests, support vector machines, or deep learning models, can be applied to multi-omics data to develop predictive models for disease diagnosis, prognosis, or treatment response. These models can uncover potential biomarkers or patterns in multi-omics data and provide insights into disease classification and personalized medicine. Citation: Alizadeh, A. A., et al. (2000). Prediction of survival in diffuse large-B-cell lymphoma based on the expression of six genes. New England Journal of Medicine, 344(14), 1031-1037.

4. **Integration of Multi-Omics Data**: Integrative analysis methods aim to combine and analyze different omics datasets, such as transcriptomics, proteomics, and epigenomics, to identify molecular interactions and relationships across different layers of biological information. These methods enable a more comprehensive understanding of the molecular mechanisms underlying

complex diseases or biological processes. Citation: Liu, Y., et al. (2014). A survey of integrative analysis methods for multi-omics data. Statistical Methods in Medical Research, 27(11), 3061-3077.

5. **Data Visualization**: Data visualization techniques, such as heatmaps, scatter plots, or network visualizations, play a crucial role in the interpretation of multi-omics data analysis results. Visualizations help in identifying patterns, clusters, and relationships between variables, enabling researchers to generate hypotheses and communicate findings effectively. Citation: Gehlenborg, N., et al. (2010). Visualization of omics data for systems biology. Nature Methods, 7(3), S56-S68.

These methods, among others, contribute to the biological and clinical interpretation of multi-omics data analysis results, providing insights into disease mechanisms, biomarker discovery, and potential therapeutic targets.

PENDENT REVISAR REFS ANTERIORS

1.2.5 Data processing and standarization

Data processing and standardization are critical steps in biomedical multi-omics data analyses to ensure data quality, comparability, and compatibility across different omics layers and studies. In this context, I will explain the problem of data processing and standardization and provide relevant bibliographic references.

Data Preprocessing: Raw multi-omics data often require preprocessing steps to handle technical variations, correct systematic biases, and remove noise. This may involve background correction, normalization, batch effect removal, and quality control measures to ensure data quality and comparability. Reference: Tarazona, S., et al. (2015). Data quality aware analysis of differential expression in RNA-seq with NOISeq R/Bioc package. Nucleic Acids Research, 43(21), e140.

Integration Challenges: Integrating multi-omics data involves combining information from different omics layers, which may have distinct measurement scales, dynamic ranges, and data distributions. Harmonizing the data across omics layers

is necessary to enable meaningful comparisons and integrative analyses. Reference: Meng, C., et al. (2014). Dimension reduction techniques for the integrative analysis of multi-omics data. Briefings in Bioinformatics, 17(4), 628-641.

Missing Data Handling: In multi-omics datasets, missing data can be present due to technical limitations or experimental designs. Proper handling of missing data, such as imputation or exclusion strategies, is crucial to avoid biases and ensure accurate analyses. Reference: Zhou, Y., et al. (2021). Missing data imputation in single-cell RNA sequencing and its implications in integrative multi-omics analysis. Briefings in Bioinformatics, 22(5), bbaa212.

Standardization and Metadata: Standardization of data formats, annotation, and metadata is vital for data sharing, reproducibility, and cross-study comparisons. The use of common data standards and ontologies facilitates data integration and harmonization efforts. Reference: Sansone, S. A., et al. (2012). Toward interoperable bioscience data. Nature Genetics, 44(2), 121-126.

Quality Control: Implementing quality control measures is essential to identify and remove low-quality or unreliable data points. Quality control procedures can include outlier detection, sample exclusion criteria, and identifying technical artifacts or batch effects. Reference: Leek, J. T., et al. (2010). Tackling the widespread and critical impact of batch effects in high-throughput data. Nature Reviews Genetics, 11(10), 733-739.

Effective data processing and standardization in multi-omics analyses are crucial for accurate and meaningful interpretations. These steps ensure data quality, comparability, and compatibility, enabling integrative analyses and cross-study comparisons.

PENDENT REVISAR REFS ANTERIORS

1.2.6 Tools for the development of bioinformatics pipelines in biomedical multi-omics data integration

PENDENT DE PRIMERES NOTES

1.2.7   Motivation for Integrative analysis

The fable of the blind men and the elephant (https://en.wikipedia.org/wik
i/Blind_men_and_an_elephant) is a metaphorical story that can be applied to
various contexts, including the motivation behind using distinct omics data types
in biomedical integrative data analyses. In this fable, several blind men touch
different parts of an elephant and form their own interpretations based on the
limited information they gather from their individual experiences. See Figure 1.1.
In the parable, several blind men touch different parts of an elephant, but each one
perceives only a small aspect of the whole animal. As a result, they form vastly
different and often conflicting impressions of what an elephant is. Each blind man,
based on his limited sense of touch, describes the elephant differently. One might
touch the tail and think the elephant is like a rope, while another feeling the leg
believes it's like a tree trunk. Yet another touching the ear might think it's like a fan.
None of them, however, comprehends the entirety of the elephant. See Figure 1.2.

The parable is often interpreted to convey the idea that individuals may have
partial, subjective truths based on their limited experiences and perspectives. It's
a metaphor for the limitations of perception and the importance of considering
multiple viewpoints to arrive at a more complete understanding of a complex
reality. Similarly, in biomedical research, different omics data types provide distinct
perspectives on biological processes, and no single omics layer can fully capture the
complexity of the underlying system. Each omics layer, such as genomics, tran-
scriptomics, proteomics, and metabolomics, provides specific insights into different
molecular components and interactions. By integrating these diverse data types, we
aim to create a more comprehensive and accurate understanding of the biological
system, similar to how the blind men can form a more complete understanding of
the elephant by sharing and integrating their individual observations.

Each omics data type reveals a specific aspect of biological information. For
example, genomics focuses on the DNA sequence, providing insights into genetic
variations and potential disease-causing mutations. Transcriptomics examines gene
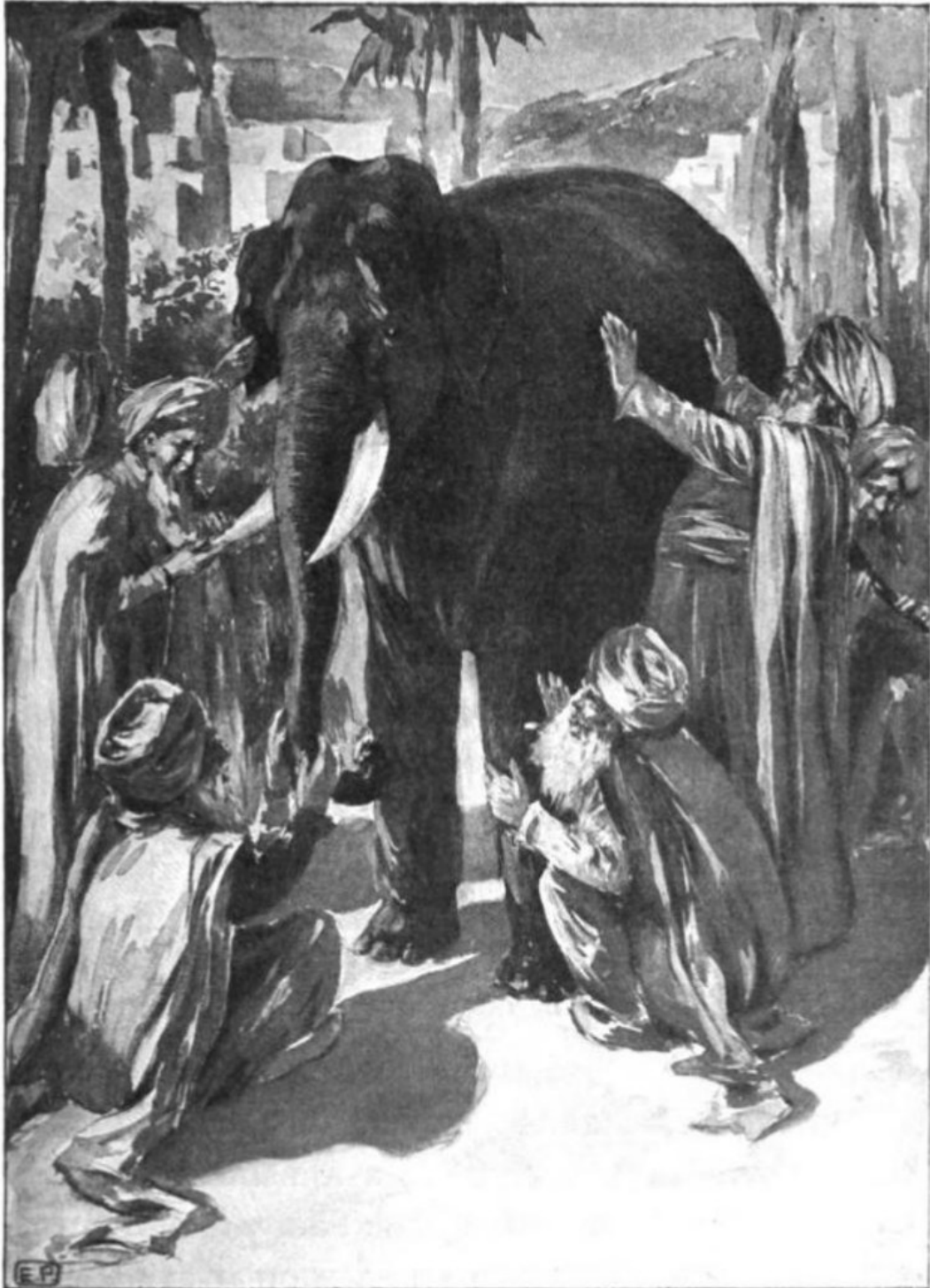
Figure 1.1: The blind men and the elephant. By Illustrator unknown - From The Heath readers by grades, D.C. Heath and Company (Boston), p. 69., Public Domain, https://commons.wikimedia.org/w/index.php?curid=4581263
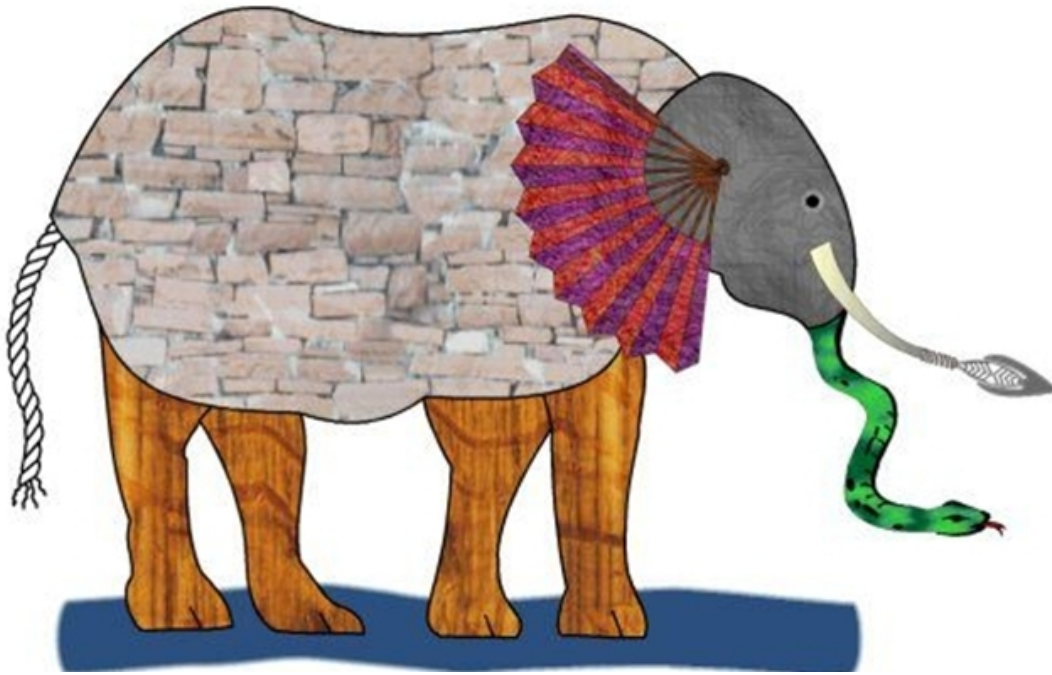
Figure 1.2: Reconstruction of the elephant as the blind men perceive it. Image source: http://doug-johnson.squarespace.com/blue-skunk-blog/2012/12/8/the-blind-men-and-the-elephant.html;jsessionid=30DE43866E1B453471B75CB39688E2CB.v5-web003

expression levels, helping us understand which genes are active in a given condition. Proteomics investigates the expression and abundance of proteins, shedding light on protein-protein interactions and signaling pathways. Metabolomics analyzes small molecules, providing insights into metabolic pathways and cellular processes.

By integrating these different omics layers, we can overcome the limitations of each individual data type and gain a more holistic understanding of biological phenomena. Integrative multi-omics data analyses enable us to uncover complex relationships, identify key biological pathways, discover biomarkers, and generate more accurate predictions for diseases and therapeutic interventions.

Just as the blind men needed to collaborate and share their individual perceptions to form a complete understanding of the elephant, biomedical researchers can leverage the strengths of different omics data types and integrate their findings to reveal a more comprehensive picture of biological systems. Integrative approaches allow us to move beyond isolated observations and capture the intricate interplay among genes, proteins, metabolites, and other molecular entities.

In conclusion, the fable of the blind men and the elephant serves as an analogy for the motivation behind using distinct omics data types in biomedical integrative data analyses. Just as the blind men's individual perceptions were limited, focusing on a single omics data type can lead to an incomplete understanding of complex biological processes. Integration of diverse omics data types enables us to overcome these limitations and gain a more comprehensive understanding of the intricacies of living systems.

Interpretability is a weak point of most multi omics approaches

La reducció ve més motivada per la necessitat de destacar els aspectes més rellevants i de que aquests siguin més fàcilment interpretables

Methods focus much more on feature selection discovery and interaction highlighting measurement than on clinical or biological interpretability.

1.2.8 Existing approaches for multi-omics data integration

Maneres de reduir dimensió amb finalitat integració òmiques

MCIA, RGCCA, MFA... ...(Culhane et al., 2003) ...(Cavill et al., 2016) ...(Vahabi & Michailidis, 2022) ...(Wekesa & Kimwele, 2023) ...(Athieniti & Spyrou, 2023)

1.2.9 Revisió de mètodes de creació de pipelines

PENDENT INCLOURE PRIMERES NOTES

2
Objectives

Contents

2.1 Working phases (modificar titols)

The motivation for this thesis stems from my work and research experience at Vall d'Hebron Research Institute in Barcelona, where, with the aim of providing a useful tool for the interpretation of omics data in the field of biomedical research, the following phases of work were proposed:

1. Application of integrative multi-omics methods to (I) the analysis of specific data sets provided by research units from our former affiliation center, VHIR, and other research institutions that we collaborate with (Rodríguez-Hernández et al., 2016), (Rodriguez-Fernandez et al., 2018), (Simats et al., 2020) and (II) to the integrative analysis of larger data sets from public data bases, such as Breast Cancer samples from the TCGA project [TCGA

Research Network: http://cancergenome.nih.gov/], [TCGA-BRCA Project: https://portal.gdc.cancer.gov/projects/TCGA-BRCA].

2. Development of methods, either in terms of new algorithms or in terms of combinative workflows, which will be able to improve, and facilitate, the analysis and biological interpretation of those data sets to be integrated.

3. Implementation of the methods developed for this study in the appropriate bioinformatics tools, such as an R package or a web-based application, to facilitate their use in the context of biomedical research projects.

REVISAR i POTSER REESCRIURE AQUESTS PUNTS COM A UN SOL BLOC?

Here is a brief description of the main activities that derived from the initially proposed phases, the methods on which they were based, the objectives with which they were related, as well as some of their results, which will be discussed in more detail in subsequent chapters.

1. Application of some state-of-the-art methods for integrative multi-omics data analysis to the study of human brain tissue samples, collected by the Neurovascular Diseases Laboratory at Vall d'Hebron Research Institute. This part is already finished, and led to publications in 2018 and 2021 (Simats et al., 2020), (Ramiro et al., 2021). Researchers obtained different omics data from necropsies, which had been processed to obtain mRNA, microRNA and protein expression values. Each dataset had been first analyzed independently using standard bioinformatics protocols [R Development Core Team. 2008]. These analyses allowed selecting subsets of relevant features, for each type of data, to be used in the integrative analysis. Among all available options, we decided to use two distinct and complementary approaches: (I) Multiple Co-inertia Analysis implemented in Bioconductor packages made4 (Culhane et al., 2005) and mogsa (Singh et al., 2016), and (II) Regularized Canonical Correlation Analysis with Sparse Partial Least Squares regression

(sPLS), provided by mixomics R package (Rohart et al., 2017). This work had been presented at some meetings (Briansó et al., 2016a), (Briansó et al., 2016b), (García-Berrocoso et al., 2016), (García-Berrocoso et al., 2017) and in an already published extended abstract's series book (Briansó et al., 2017). This step had been obviously useful for the achievement of the objective number 3 explained in the previous section, which aims on the study of the regulome's response to ischemic stroke, but also useful for detecting the advantages and drawbacks of the methods applied, thus setting the basis for the work regarding to objective number 2.

2. Reproduction of the same analyses steps performed in point 1) above with publicly available databases, such as distinct omics data from 150 samples from the TCGA-BRCA collection. This data set contains the expression or abundance of mRNA, miRNA and proteomics for 150 breast cancer samples previously prefiltered, as explained in Rohart et al. (Rohart et al., 2017), and allows identifying a good multi-omics signature to discriminate between Basal, Her2 and Luminal A breast cancer subtypes. This work is already finished, and complies with objectives 3 and 2.

3. Use of all the data sets analyzed up to this point to make a comparison of results between the main implemented methods, and eventually some others, which is the aim of objective 1. This is based on quantitative and qualitative comparison and visualization methods, such as those explained by Thallinger (Pucher et al., 2019) and Martin (Martin et al., 2010), going from simple Venn diagrams to more complex, network analysis, software such as some specific R packages (R Core Team, 2022) or Cytoscape (Cline et al., 2007). The focus here is to use graphical visualization elements to compare the results of the analyses with and without the addition of biological information.

4. Development of new methods and/or workflows in order to improve and/or combine the benefits from the selected approaches, with focus in those allowing the addition of biological significance to the integration process. Here

follows an overview of the methods developed to expand the original datasets (X, Y) with annotations (Ax, Ay) to obtain new blocks of data (Nx, Ny,and Nxy). And the workflow has been implemented adapting the integrative pipelines applied so far to the R targets package (Landau, 2021), a pipeline toolkit that improves reproducibility, skipping unnecessary steps already up to date and showing tangible evidence that the results match the underlying code and data. The development of this targets workflow is intended to comply with the objective number 2 of this working plan.

5. Implementation of the methods resulting from 4) as a new R package to be submitted to Bioconductor repository (Huber et al., 2015), and, finally, to complete objective 4 of this thesis plan, as a web application (Chang et al., 2021) to be used in further steps of the current biomedical research projects in which our collaborators are implied, as well as in future studies.

2.2 Main objectives of this work

In light of the challenges presented in the previous point, the main objectives of this thesis were established as follows:

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.

Ein Mann, der recht zu wirken denkt,

Muß auf das beste Werkzeug halten

The man who seeks to be approved,

must stick to the best tools for it

— Goethe's *Faust. Eine Tragödie* (1808).

3
Methodology

Contents

In the context of multi-omics data integration, our proposal relies on the idea that incorporating biological annotations into datasets before integrative analysis enriches outcomes and enhances their biological interpretability. Therefore, augmenting quantitative omics data with contextual biological knowledge will deepen our understanding of complex biological phenomena. To do so, we begin with meticulous data quality assessment and standardization, laying the foundation for reliable analyses. We then infuse biological knowledge using standard biological annotations, creating "Expanded Datasets" that provide context for comprehensive analysis. Advanced dimension-reduction techniques can be applied to illuminate hidden patterns and relationships between data sources or blocks, and the semi-

automation capabilities of the Targets R package allow us to build an easy-to-use implementation of the process.

3.1   Data Quality Assessment and Format Review

Before initiating the integrative analysis, a meticulous evaluation of data quality and format compatibility was conducted to ensure the reliability of the input datasets. This crucial step aimed to identify and rectify discrepancies, inconsistencies, or errors that could potentially impact subsequent analyses. During this process, datasets spanning various omics technologies, including transcriptomics and proteomics, are selectively acquired from reputable sources and repositories. Emphasis was placed on meticulous source selection to guarantee consistency and adherence to standardized formats. Subsequently, the raw omics data underwent a comprehensive preprocessing phase, addressing issues such as missing values, outliers, and normalization. This preprocessing step was indispensable for enhancing data quality and enabling comparability across diverse datasets. Additionally, a thorough review of data formats encompassing file types, column naming conventions, and units of measurement was conducted. Non-standardized data were systematically transformed into a uniform format to streamline the downstream integration processes. Through these procedures, a robust foundation was established for subsequent integrative omics analysis, ensuring coherence and validity of the synthesized biomedical insights.

FALTA DETALLAR AQUI COM SHAN VALIDAT ELS DATASETS DE TCGA (ELS DE STROKE ANIRAN A BANDA, pero fer-hi mencio breu).

Explicar aquí els requeriments de format dels data sets d'entrada

Mostrar Figure 3.1 i Figure 3.2 PERO POTSER MILLOR COM A TAULES INTEGRADES AMB MARKDOWN?

Data loaded from files **data/mrna.csv** and **data/prots.csv**

Samples in rows; Features in columns

```
## # A tibble: 150 x 201
##    sample RTN2 NDRG2 CCDC113 FAM63A ACADS  GMDS HLA.H SEMA4A  ETS2 LIMD2  NME3  ZEB1 CDCP1 GIYD2 RTKN2 MANSC1
##    <chr> <dbl> <dbl>   <dbl>  <dbl> <dbl> <dbl> <dbl>  <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>  <dbl>
##  1 A0FJ   4.36  7.53    3.96   4.46  2.26  6.02  5.01   3.22  4.73  5.10  4.56  3.99  6.42  2.47  4.58   8.08
##  2 A13E   1.98  7.46    5.43   5.44  4.03  4.34  6.18   2.86  5.41  4.21  5.14  3.76  6.61  4.98  5.17   7.30
##  3 A0G0   1.73  8.08    2.23   5.54  2.63  6.36  6.04   5.95  5.65  3.30  4.45  3.85  6.41  3.20  4.24   7.99
##  4 A0SX   4.36  5.79    3.54   4.74  4.27  4.00  7.09   5.01  5.90  5.48  3.76  5.23  6.02  4.30  4.25   5.41
##  5 A143   2.45  7.16    4.69   4.81  2.44  7.03  5.94   5.90  6.64  5.51  4.24  3.54  7.09  5.71  3.96   8.49
##  6 A0DA   4.77  8.75    4.31   5.31  3.24  4.24  6.91   6.59  5.86  3.77  4.26  4.80  6.05  4.01  2.07   5.90
##  7 A0B3   3.35  5.10   0.593   5.22  3.89  5.92  8.04   6.53  6.31  4.11  4.79  4.26  7.27  4.64  3.53   5.03
##  8 A0I2   1.81  3.79    2.72   4.36  4.20  4.83  9.13   4.98  5.30  5.15  5.76  2.46  3.79  6.90  1.91   6.39
##  9 A0RT   2.09  6.33    2.36   4.04  4.13  4.29  7.59   5.94  6.57  7.07  5.13  5.55  3.85  5.66  4.27   3.71
## 10 A131   4.34  4.70    3.64   4.03  3.14  5.25  6.35   6.06  6.32  4.89  5.73  4.52  6.57  5.42  3.36   5.74
## # ... with 140 more rows, and 184 more variables: TAGLN <dbl>, IFIT3 <dbl>, ARL4C <dbl>, HTRA1 <dbl>,
## #   KIF13B <dbl>, CPPED1 <dbl>, SKAP2 <dbl>, ASPM <dbl>, KDM4B <dbl>, TBXAS1 <dbl>, MT1X <dbl>, MED13L <dbl>,
## #   SNORA8 <dbl>, RGS1 <dbl>, CBX6 <dbl>, WWC2 <dbl>, TNFRSF12A <dbl>, ZNF552 <dbl>, MAPRE2 <dbl>,
## #   SEMA5A <dbl>, STAT5A <dbl>, FLI1 <dbl>, COL15A1 <dbl>, C7orf55 <dbl>, ASF1B <dbl>, FUT8 <dbl>,
## #   LASS4 <dbl>, SQLE <dbl>, GPC4 <dbl>, AKAP12 <dbl>, AGL <dbl>, ADAMTS4 <dbl>, EPHB3 <dbl>, MAP3K1 <dbl>,
## #   PRNP <dbl>, PROM2 <dbl>, SLCO3A1 <dbl>, SNHG1 <dbl>, PRKCDBP <dbl>, MXI1 <dbl>, CSF1R <dbl>, TANC2 <dbl>,
## #   SLC19A2 <dbl>, RHOU <dbl>, C4orf34 <dbl>, LRIG1 <dbl>, DOCK8 <dbl>, BOC <dbl>, C11orf52 <dbl>, ...
```

```
## # A tibble: 150 x 112
##    sample  YWHAE EIF4EBP1 TP53BP1    ARAF   ACACA    ACCB  PRKAA1    ANLN     AR ARID1A   ASNS     ATM
##    <chr>   <dbl>    <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>  <dbl>  <dbl>  <dbl>   <dbl>
##  1 A0FJ   0.0491    0.447   0.918  0.0227 -0.0863  -0.417   0.285   0.172  -1.31  0.505  0.811 -0.496
##  2 A13E  -0.0800    0.605  0.0591  -0.460  -0.593 -0.0623  -0.275   0.222  -1.62  0.340   1.18 -0.276
##  3 A0G0  -0.0328    0.895   0.517  -0.192   0.411   0.826  0.0677   0.122  -1.08  0.227   1.95  0.771
##  4 A0SX   -0.205   -0.141  -0.314 -0.0748  -0.851  -0.663  0.0296    1.05  -1.27  0.355  0.607  0.781
##  5 A143   0.0602    0.132   0.331 -0.0244   0.770   0.873  -0.217  0.0138 -0.601  0.544  0.539 0.0139
##  6 A0DA   0.0308   0.0330  -0.220   0.419  -0.714  -0.218 -0.0631  0.0603  -1.21 -0.111  0.312 0.0717
##  7 A0B3   -0.108  -0.0371  -0.545   0.431  -0.363  -0.269 -0.0776 0.00887  -1.02 -0.233   1.14 -0.210
##  8 A0I2    0.650   -0.521   -1.60  -0.187    1.08    1.59 -0.0775 -0.0519 -0.421 -0.355 -0.633 -0.924
##  9 A0RT  -0.0137   -0.635  -0.721  -0.375   -1.25  -0.901 -0.0419 -0.0419 -0.952 -0.179  0.145  0.834
## 10 A131    0.431     1.05  -0.811   0.353  -0.883  -0.681   0.261 -0.00213 -0.180 -0.475  0.573  -1.44
## # ... with 140 more rows, and 99 more variables: AKT1 <dbl>, ANXA1 <dbl>, BRAF <dbl>, BAK1 <dbl>, BAX <dbl>,
## #   BCL2 <dbl>, BCLX <dbl>, BECN1 <dbl>, BID <dbl>, BCL2L11 <dbl>, RAF1 <dbl>, PECAM1 <dbl>, ITGA2 <dbl>,
## #   CDK1 <dbl>, CASP7 <dbl>, CAV1 <dbl>, CHEK1 <dbl>, CHEK2 <dbl>, CLDN7 <dbl>, COL6A1 <dbl>, CCNB1 <dbl>,
## #   CCND1 <dbl>, CCNE1 <dbl>, PARK7 <dbl>, DVL3 <dbl>, CDH1 <dbl>, EGFR <dbl>, ESR1 <dbl>, MAPK1 <dbl>,
## #   FOXO3 <dbl>, FN1 <dbl>, GAB2 <dbl>, GATA3 <dbl>, GSK3A <dbl>, ERBB2 <dbl>, ERBB3 <dbl>, HSPA1A <dbl>,
## #   IGFBP2 <dbl>, INPP4B <dbl>, IRS1 <dbl>, MAPK9 <dbl>, MAPK8 <dbl>, KRAS <dbl>, XRCC5 <dbl>, LCK <dbl>,
## #   MAPK1_1 <dbl>, MAP2K1 <dbl>, ERRFI1 <dbl>, MRE11 <dbl>, CDH2 <dbl>, NF2 <dbl>, NOTCH1 <dbl>, ...
```

Figure 3.1: Example of gene expression and protein quantification data as loaded in R

	A0FJ	A13E	A0G0	A0SX	A143	A0DA	A0B3	A0I2	A0RT
YWHAE	0.049130778	-0.079982106	-0.032849886	-0.205329492	0.060190211	0.030761714	-0.107861537	0.64984396	-0.013650441
EIF4EBP1	0.447486231	0.605218418	0.894609732	-0.141322924	0.131768992	0.032996799	-0.037124691	-0.52148657	-0.634850633
TP53BP1	0.917834192	0.059101206	0.517044530	-0.313728669	0.330912383	-0.220271002	-0.544743061	-1.60203535	-0.720723295
ARAF	0.022741468	-0.459852981	-0.191821916	-0.074823472	-0.024357467	0.418616650	0.430503500	-0.18714658	-0.374882996
ACACA	-0.086267822	-0.592691835	0.411171898	-0.851480596	0.769751430	-0.714308701	-0.363474049	1.07761482	-1.254491083
ACCB	-0.416624416	-0.062268404	0.825828592	-0.663410436	0.873478702	-0.217526770	-0.269313837	1.58998239	-0.901353585
PRKAA1	0.285270389	-0.275233600	0.067741840	0.029563729	-0.216531821	-0.063065064	-0.077581092	-0.07753959	-0.177636653
ANLN	0.172311102	0.222105981	0.121993985	1.054948103	0.013784220	0.060256895	0.008872461	-0.05187936	-0.041880238
AR	-1.307605693	-1.620475956	-1.077894436	-1.267054694	-0.601327437	-1.208038484	-1.016297633	-0.42122691	-0.952324860
ARID1A	0.505094485	0.339581595	0.227180664	0.355297672	0.544125136	-0.110944799	-0.233223615	-0.35537533	-0.179195256
ASNS	0.811462882	1.181015791	1.950922363	0.607423831	0.538762877	0.311949453	1.138875941	-0.63275876	0.145464752
ATM	-0.495944728	-0.275533386	0.770857796	0.781328690	0.013854306	0.071748319	-0.209624373	-0.92406461	0.833870191
AKT1	-0.001377255	-0.755547887	-0.067397666	0.056726701	0.238114357	0.193712038	-0.301495924	-0.47402849	-0.367759411
ANXA1	-0.092909287	0.194749839	1.252992383	0.575274185	-1.557003586	0.491015188	0.533878400	1.21076392	0.424004827
BRAF	0.476309798	0.143257789	0.224891925	-0.221859607	0.248234872	-0.195445933	-0.036284702	-1.07351919	-0.711215072
BAK1	0.112201063	0.111310840	-0.069962738	-0.036546549	-0.124839115	-0.257300059	-0.115681609	0.87744695	0.183770057
BAX	-0.156538756	-0.205462637	-0.047604780	0.085173319	0.151544397	-0.090041106	-0.041475148	-0.54119284	0.146947246
BCL2	1.060203513	-0.160826453	-1.771917375	0.345023494	-1.588878871	-0.782913123	-1.041432134	0.41442932	0.531749294
BCLX	-0.100950513	-0.171629248	-0.056202128	-0.096473309	-0.140526557	-0.099476757	-0.037510164	0.74769887	-0.275295151
BECN1	-0.019449441	-0.041253352	-0.076969142	0.963238561	-0.219198072	-0.208762350	-0.219048417	-0.65145061	-0.165614955
BID	-0.034821157	-0.298426931	0.073740813	-0.203558523	-0.147058902	-0.035583612	-0.166370155	0.94513564	0.310251463
BCL2L11	0.408337983	-0.442249202	-1.244877548	0.163042908	0.051760204	-0.434277577	-0.290144108	-0.52809090	0.227648621
RAF1	0.108839334	0.403923023	-0.157470172	0.037683828	0.219029836	0.120775889	0.149760561	-0.42642058	-0.284617195
PECAM1	0.096913816	-0.135688779	-0.229473098	0.073040655	-0.037514094	-0.172646324	-0.003427764	-0.57845063	0.081700778
ITGA2	0.056953664	-0.369652041	0.225919578	-0.377061206	0.032209215	-0.279859151	0.064025012	0.20592716	-0.132198583
CDK1	0.391893475	0.431874216	0.170553859	0.487608500	0.356320675	0.057826839	0.201249969	0.15530981	0.238982271
CASP7	-0.209648791	-0.442253479	-0.027768363	0.619517693	-0.113207256	-0.533360022	1.021124691	0.62764170	1.765265466
CAV1	0.533755894	-1.310081134	-2.024819193	-0.105724014	-1.723398601	-1.761346920	-0.396679637	2.68650874	1.696473472
CHEK1	0.160404592	0.223441176	0.376873438	0.004513815	0.227372000	-0.069237193	0.204323902	0.48476037	0.190864987
CHEK2	1.056926875	0.651510308	0.881431094	0.222821482	0.425296288	-0.258980977	0.163256893	-0.70436969	0.476877281
CLDN7	-0.620225952	0.780008039	-0.343776287	0.228050453	0.233078487	0.040042353	-0.287622816	-1.39960030	-1.606562159
COL6A1	-0.869405130	-0.262350291	-0.425013922	-0.159521178	-0.805978550	-0.535507295	-0.513767940	0.97852799	0.835688459
CCNB1	1.516735476	1.025776946	0.977360144	0.569273220	1.368956673	0.071681473	1.237889430	-1.32406936	0.245716912
CCND1	-0.310524605	-0.434476563	-0.226412035	-0.512848244	-0.875023630	0.099692628	-0.359145590	1.01357985	0.247347773
CCNE1	0.987850528	0.249589732	-0.329458663	1.425506793	1.406639282	-0.042159529	0.516007883	0.38413664	0.193681101

Figure 3.2: Example of proteomics input data

3.2 Preprocessing for Integration of Biological Knowledge: Generating the "Expanded Datasets"

The integration of biological knowledge into omics datasets can be achieved through a preprocessing step aimed at expanding the original data matrices with annotations accessed from specialized R libraries, which provided direct access to curated biological databases such as Gene Ontology (GO(Ashburner et al., 2000)) and biochemical pathways information (e.g., KEGG(Kanehisa & Goto, 2000)). This process, that combines the annotation of the most significant biological entities with the quantification and integration of their annotation values to the data matrices, ends up with what we term "Expanded Data Sets", which include the original biological features (e.g., gene expression or protein quantification values) as well as new variables coming from the annotation of biological terms. The following steps explain this preprocessing procedure in more detail:

- Selected biological annotations: Specialized R libraries, dedicated to biological knowledge integration, are employed to access and retrieve up-to-date annotations from databases such as GO and KEGG.

- Data-Annotation Mapping: Each omics dataset are mapped to the retrieved biological annotations based on identifiers (e.g., gene or protein names) using the capabilities of the R libraries. This step facilitates the linking of omics data to biological knowledge.

- Annotation Integration: The annotated information is integrated, implementing new R functions, into the starting omics datasets, resulting in expanded data matrices that combined the original quantitative omics measurements with new quantified features associated with the given biological annotations.

3.2.1 Selecció de les fonts d'anotacions biològiques

PENDENT DE DETALLAR com escullo les fonts de les anotacions per defecte. Apuntar que es poden facilitar ja anotacions disponibles prèviament, sempre que

compleixin amb el format que s'explica al següent apartat. Aquestes poden ser estàndard o bé personalitzades a mida de l'usuari (tot i que si es aixi hi ha certes funcionalitats posteriors que no es podran aprofitar).

```
  [1] "RTN2"    "NDRG2"    "CCDC113"  "FAM63A"   "ACADS"    "GMDS"     "HLA.H"     "SEMA4A"   "ETS2"     "LIMD2"    "NME3"
 [12] "ZEB1"    "CDCP1"    "GIYD2"    "RTKN2"    "MANSC1"   "TAGLN"    "IFIT3"     "ARL4C"    "HTRA1"    "KIF13B"   "CPPED1"
 [23] "SKAP2"   "ASPM"     "KDM4B"    "TBXAS1"   "MT1X"     "MED13L"   "SNORA8"    "RGS1"     "CBX6"     "WWC2"     "TNFRSF12A"
 [34] "ZNF552"  "MAPRE2"   "SEMA5A"   "STAT5A"   "FLI1"     "COL15A1"  "C7orf55"   "ASF1B"    "FUT8"     "LASS4"    "SQLE"
 [45] "GPC4"    "AKAP12"   "AGL"      "ADAMTS4"  "EPHB3"    "MAP3K1"   "PRNP"      "PROM2"    "SLCO3A1"  "SNHG1"    "PRKCDBP"
 [56] "MXI1"    "CSF1R"    "TANC2"    "SLC19A2"  "RHOU"     "C4orf34"  "LRIG1"     "DOCK8"    "BOC"      "C11orf52" "S100A16"
 [67] "NRARP"   "TTC23"    "TBC1D4"   "DEPDC6"   "ILDR1"    "SDC1"     "STC2"      "DTWD2"    "TCF4"     "ITPR2"    "DPYD"
 [78] "NME1"    "EGLN3"    "CD302"    "AHR"      "LAPTM4B"  "OCLN"     "HIST1H2BK" "HDAC11"   "C18orf1"  "C6orf192" "AMPD3"
 [89] "COL6A1"  "RAB3IL1"  "APBB1IP"  "PSIP1"    "EIF2AK2"  "CSRP2"    "EIF4EBP3"  "LYN"      "WDR76"    "SAMD9L"   "ASPH"
[100] "RBL1"    "SLC43A3"  "HN1"      "TTC39A"   "MTL5"     "NES"      "APOD"      "RIN3"     "ALCAM"    "C1orf38"  "PLCD3"
[111] "BSPRY"   "NTN4"     "IL1R1"    "EMP3"     "ZKSCAN1"  "FMNL2"    "OGFRL1"    "IRF5"     "IGSF3"    "DBP"      "CNN2"
[122] "CAMK2D"  "SIGIRR"   "AKAP9"    "ICA1"     "FGD5"     "DSG2"     "E2F1"      "QSOX1"    "TOB1"     "CSF3R"    "SHROOM3"
[133] "CCDC80"  "FRMD6"    "CXCL12"   "CCNA2"    "TIGD5"    "ALDH6A1"  "POSTN"     "FZD4"     "NCAPG2"   "SDC4"     "SNED1"
[144] "PLEKHA4" "KCNAB2"   "SH3KBP1"  "IGSF9"    "DNLZ"     "S1PR3"    "PTPRE"     "FLJ23867" "PLSCR1"   "LMO4"     "IFITM2"
[155] "LRRC25"  "TST"      "NCF4"     "NCOA7"    "IL4R"     "CCDC64B"  "SGPP1"     "RUNX3"    "SLC5A6"   "IFIH1"    "PREX1"
[166] "PLAUR"   "CDK18"    "SLC43A2"  "GK"       "ICAM2"    "YPEL2"    "CBR1"      "MEX3A"    "ZNRF3"    "PTPRM"    "C1orf162"
[177] "GAS6"    "C1QB"     "PVRL4"    "CTSK"     "MRVI1"    "LEF1"     "PLCD4"     "ZNF37B"   "MEGF9"    "GINS2"    "FAM13A"
[188] "CPT1A"   "SNX10"    "TRIM45"   "ELP2"     "ALOX5"    "AMN1"     "CERCAM"    "SEMA3C"   "KRT8"     "TP53INP2" "JAM3"
[199] "ZNF680"  "PBX1"
```

Figure 3.3: List of gene symbols used as example

3.2.2 Anotació de la info biològica

COM VAM PLANTEJAR fer l'anotació biologica. Quines opcions i amb quins metodes estadístics/bioinformatics... DUBTO SI LO QUE SEGUEIX NO ANIRIA A RESULTATS

For each input data set, if annotations are not already provided, two distinct basic annotation methods can be performed:

 (i) a basic GO mapping, returning annotations to those GO entities for which we find more than a certain number of features (gene ids coming from our data set, see Figure 3.3 for an example) annotated to them,

(ii) a Gene Enrichment Analysis (based on Hypergeometric tests against all GO categories, with FDR correction) is performed in order to retrieve the most relevant annotations to that set of genes/features.(Yu et al., 2012)

[mostrar exemple de llista de gens]

[punt de millora, que l'anotacio basica pugui ser tb a KEGG]

[mostrar formula]

es mostra exemple en Figure 3.4 POSSIBLE INTEGRAT EN MARKDOWN?

[comentar aquí l'opció d'afegir les anotacions com a individus suplementaris enlloc de variables Figure 3.6 is an example.]

Annotated Matrix

Gene Ontology used: **BP**

Min. number of genes required to pass the filter: **8**

Annotated categories: **13** (for *data/mrna.csv*)

Annotated categories: **61** (for *data/prots.csv*)

Shared annotated categories: GO:0000122, GO:0006357, GO:0007155, GO:0007165, GO:0007411, GO:0008285, GO:0019221, GO:0030335, GO:0045893, GO:0045944

(Showing only partial output)

```
tar_read(categ_sums1)
```

```
## GO:0000122 GO:0006357 GO:0007155 GO:0007165 GO:0007411 GO:0008285 GO:0016477 GO:0019221 GO:0030335 GO:0043312
##         11         14         11         21         10          9         10         10          8          8
## GO:0045893 GO:0045944 GO:0055114
##         11         14         10
```

```
tar_read(categ_sums2)
```

```
## GO:0000082 GO:0000122 GO:0000165 GO:0000187 GO:0001525 GO:0001666 GO:0001701 GO:0001934 GO:0006357 GO:0006367
##          8         19         17          8         11          9         10         10         13         10
## GO:0006468 GO:0006915 GO:0006974 GO:0006977 GO:0007050 GO:0007155 GO:0007165 GO:0007169 GO:0007411 GO:0007507
##         24         17         14          8         10         11         30         11          8         12
## GO:0007568 GO:0008283 GO:0008284 GO:0008285 GO:0010468 GO:0010628 GO:0010629 GO:0016032 GO:0016579 GO:0018105
##         10         12         20         16          8         29         12         19         11         16
## GO:0018107 GO:0018108 GO:0019221 GO:0030154 GO:0030335 GO:0032355 GO:0032869 GO:0033138 GO:0033674 GO:0035556
##         11         11         15         11         11         10          9          9          8         17
## GO:0042060 GO:0042127 GO:0042493 GO:0042981 GO:0043065 GO:0043066 GO:0045471 GO:0045892 GO:0045893 GO:0045944
##          9          9         23         10         11         31          8         11         23         30
## GO:0046777 GO:0048538 GO:0050821 GO:0051091 GO:0051897 GO:0070374 GO:0071456 GO:0090090 GO:0098609 GO:1901796
##         10          8          8          8         12          9         11          8          9          9
## GO:2001244
##          8
```

Figure 3.4: Example of basic Go annotation by raw count against GO Biological Processes, setting 8 as minimum number of genes included in the BP entity. Annotation performed separately for gene expression and protein quantification input files
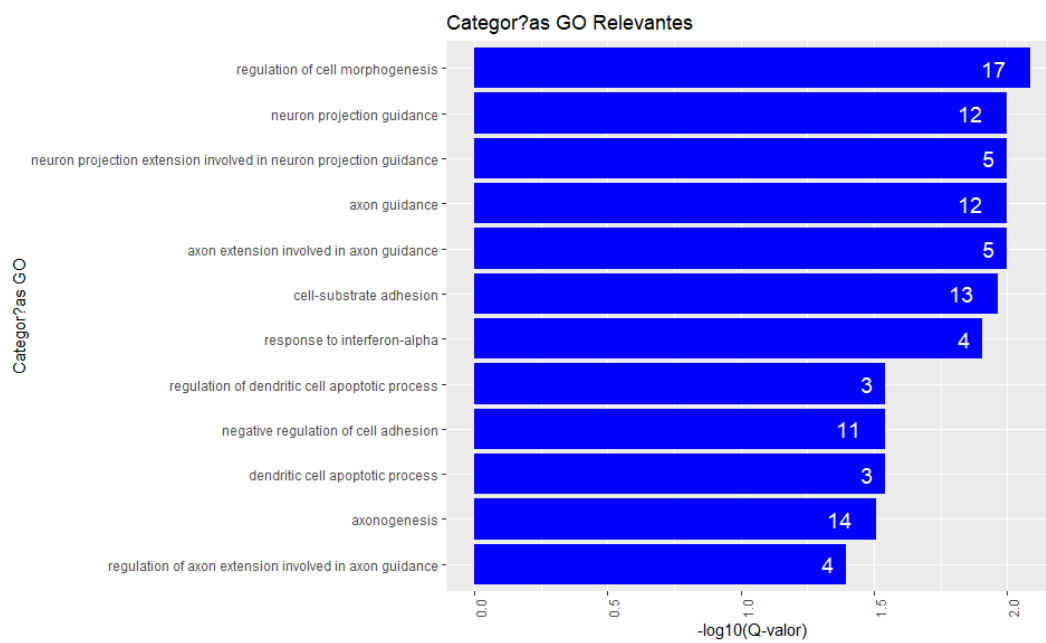
Figure 3.5: Example of results from GO annotation. Results of the biological significance analysis performed with the lists of genes against GO through clusterProfiler
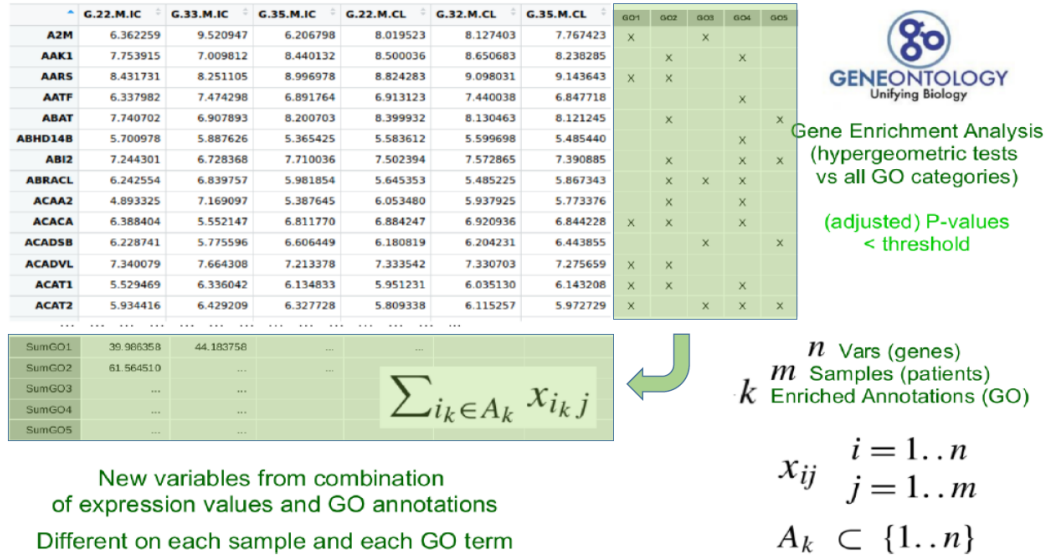
Figure 3.6: Addition of GO terms

Alternatively, manual annotations can be provided (eg. GO terms, canonical pathways, or even annotation to custom entities) as an optional input file.

[mostrar el format requerit].

Other annotation methods can be implemented, as functions to be used by the main pipeline, if more complex methods for biological information addition are required.

[Mostrar el format final de les anotacions, com a matrius dels data sets amb anotacions binàries 1/0 com a columnes extra]

EXPANSIO DE LES MATRIUS (numeritzar anotacions, creació de noves vars a partir de les anotacions)

The process starts already having a couple of data sets from distinct 'omics sources [punt de millora: admetre 3 o + inputs, comentar més tard a Discussion], mapped to gene ids (in the default case, where GO annotation have been performed), containing the results from a selection of differentially expressed genes or most relevant proteins analysis, or similar.
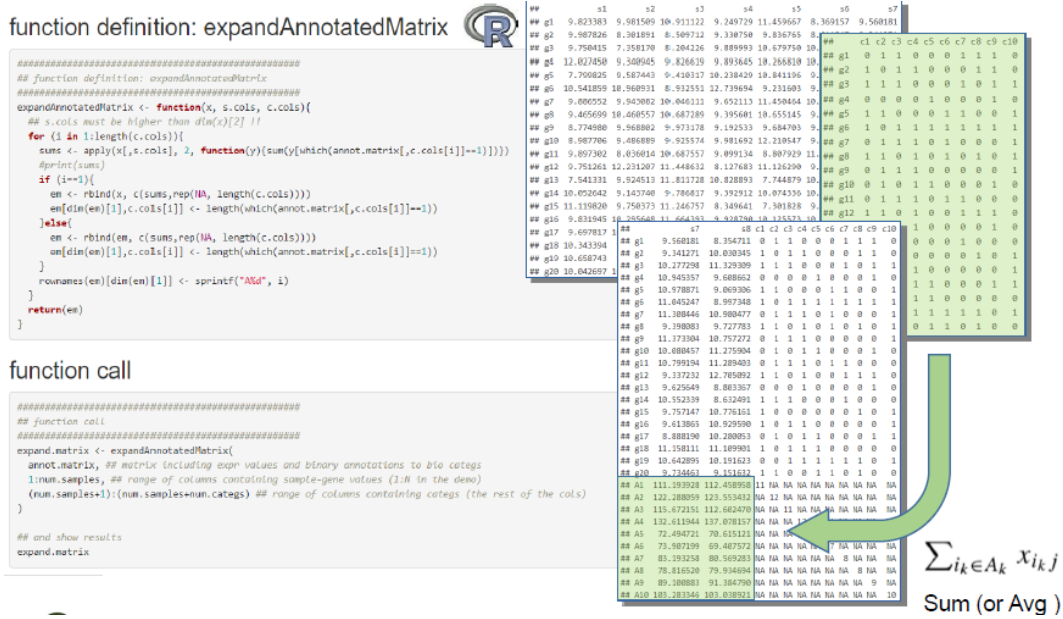
Figure 3.7: Addition of news feats
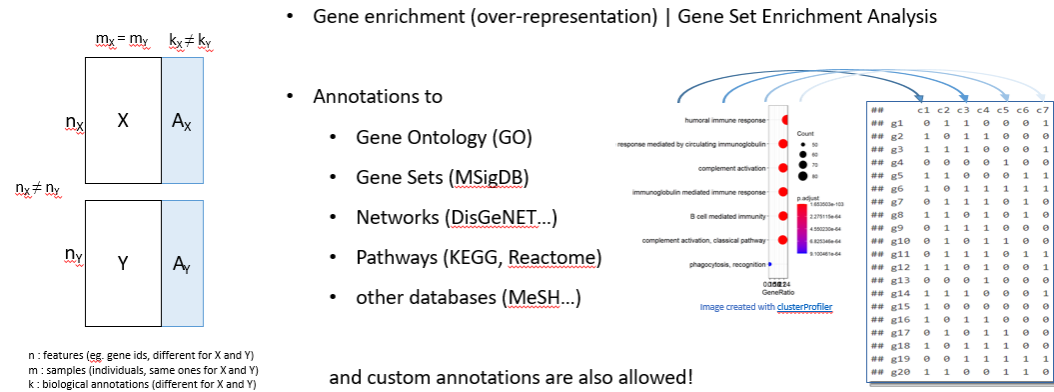
Figure 3.8: Gene enrichment diagram

3.2.3 Annotation Integration

Once the annotations are already computed, mapping each feature of the input data set to the corresponding biological entity, they can be used to generate new features (as new rows), computing the average value [punt de millora: funció de ponderació] of the expression/intensity values from all original features being mapped to the annotated biological entities.

Once we have the annotated matrices (Figure 3.9, highlighted in blue) we proceed to generate the Expanded matrices (in green) by casting these annotations
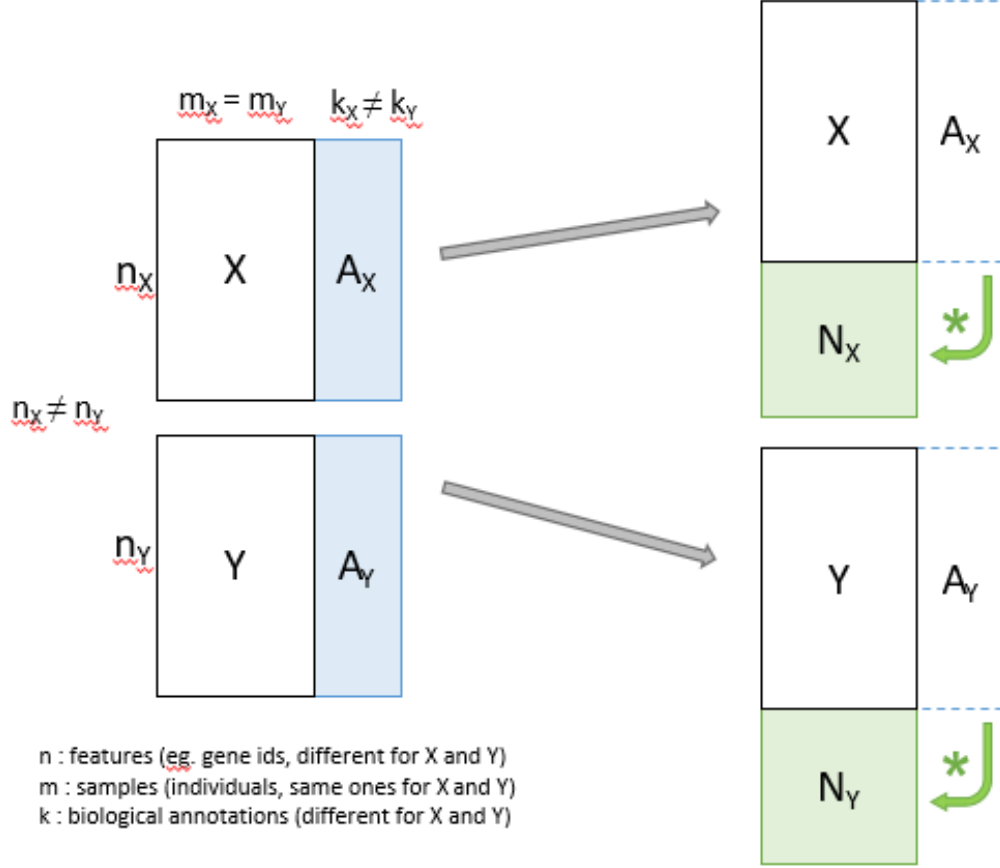
Figure 3.9: Matrix expansion diagram

as numerical values, that is, calculating the average of the numerical expressions of each individual for the variables annotated to each category. This is done with the matrix product of the initial numerical values (expression, proteins...) with the transposed matrices of their annotations, and then with the inverse matrix of a diagonal matrix of the count of how many annotations each category or entity annotated has had.

3.3   Integrative Analysis with Joint Dimension Reduction Techniques

To uncover meaningful insights from the expanded data sets and extract relevant information from the integrated omics and biological knowledge, contrasted joint dimension reduction techniques were employed. These techniques enable the si-

$$N_G = \phi(G, A_G), \quad G \in X, Y, \dots,$$

$$N_X = \frac{1}{r_X}(X \times A'_X),$$

$$N_Y = \frac{1}{r_Y}(Y \times A'_Y),$$

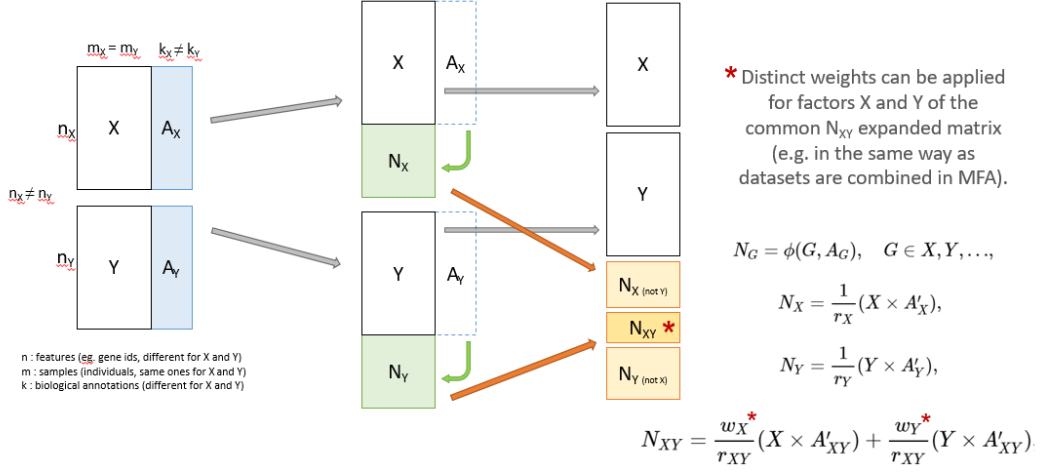**Figure 3.10:** Addition of new feats (2)

Figure 3.11: Matrix expansion diagram (2)

multaneous analysis of multiple data types and facilitate the identification of key patterns and relationships. The following methods were applied:

- Multiple Factor Analysis (MFA): MFA, adapted for multi-omics data, was utilized to identify sources of variability in the integrated dataset while considering both quantitative omics data and biological annotations. MFA aims to maximize relevant information within the data while accounting for the hierarchical structure of the biological knowledge.

- Multiple Co-Inertia Analysis (MCIA): MCIA, a technique that aligns the covariance structures of multiple datasets, was employed to explore relationships between omics measurements and biological annotations. MCIA seeks to identify common patterns and associations between these data sources.

- Regularized Generalized Canonical Correlation Analysis (RGCCA): RGCCA was used to identify latent variables that capture joint information from omics data and biological annotations. RGCCA extends canonical correlation analysis to handle multi-view data integration and helps reveal correlated features across datasets.

PUNTS A INCLOURE:

- Reducció de dimensió. Anàlisi factorial en detall (MFA), + MCIA + RGCCA

- incloure aquí % variabilitat explicat segons la estructura de la intersecció de les 2 taules (article Lovino 2022)

- avantatge del MFA és que podem definir blocs de variables!

- no mirem unicament si guanyem variabilitat, sino tambe si millorem interpretabilitat biologica

3.4 Semi-Automation using the Targets R Package

The semi-automation of the integrative analysis process was facilitated by leveraging the Targets R package, which provides an efficient and user-friendly framework for building and managing complex analysis pipelines. In the development of the Targets pipeline, careful management of functions and parameters was essential to ensure a systematic and reproducible workflow. The following principles were applied:

- Function Modularity: Functions within the Targets pipeline were designed to be modular, focusing on specific tasks or analyses. This modularity enhanced code readability and maintainability.

- Parameterization: Parameters for each function and analysis step were carefully defined, allowing for flexibility and adaptability in the pipeline. This parameterization enabled the adjustment of analysis settings without modifying the underlying code.

- Dependency Management: Dependencies between different analysis steps were explicitly defined within the pipeline. This ensured that each step was executed in the correct order, and dependencies were automatically managed by the Targets package.

- Error Handling: Error handling procedures were implemented to capture and address potential issues during pipeline execution. This included the ability to handle errors, retries, and reporting of errors for troubleshooting. (NO APLICAT ARA PER ARA!)

PENDENT A AMPLIAR:

- Introduccio al paquet Targets en general i de les seves caracteristiques. . .

The R 'targets' package is a powerful tool for building and managing data science and data analysis pipelines. It is primarily designed for workflow automation, dependency management, and parallel processing in R projects. This package is useful for the following purposes:

1. Define and Manage Workflows: You can create a directed acyclic graph (DAG) that represents the workflow of your data analysis or machine learning project. Each node in the graph corresponds to a target, which can be a data file, an R script, or any other computational task.

2. Manage Dependencies: 'targets' allows you to specify dependencies between targets, ensuring that tasks are executed in the correct order. If a target depends on another target, it won't be executed until its dependencies are up-to-date.

3. Parallel Processing: One of the strengths of 'targets' is its ability to parallelize tasks. It can automatically determine which targets can be executed concurrently, improving the efficiency of your workflows, especially when working with large datasets or computationally intensive tasks.

4. Incremental Builds: When you make changes to your code or data, 'targets' can identify the minimal set of targets that need to be recomputed, saving time and computational resources. This is particularly useful for iterative development and experimentation.
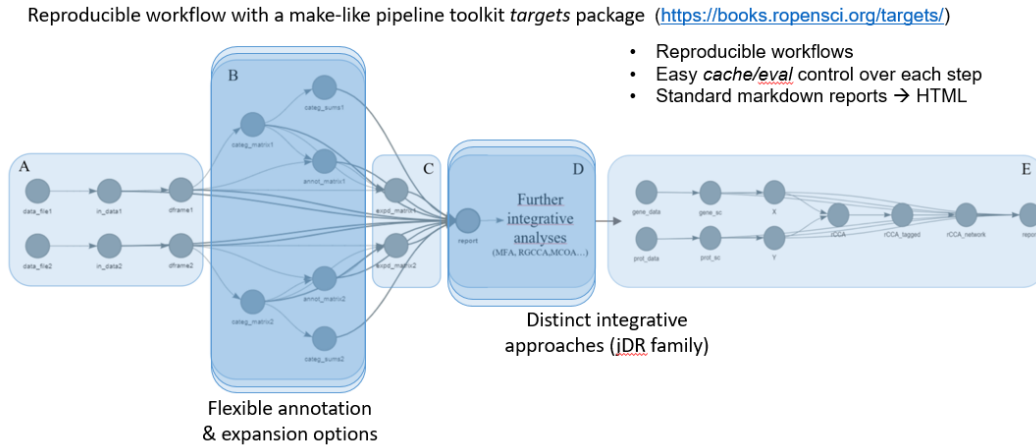
Figure 3.12: Workflow overview

5. Reports and Logging: 'targets' provides tools for generating reports and logging the progress of your workflow, making it easier to track and document your work.

6. Integration: It can be seamlessly integrated with other R packages and tools, such as 'drake' for more advanced data workflow management.

So, the 'targets' package is especially valuable for projects where data processing is a significant component, and you need a structured way to manage the various steps of your analysis or modeling pipeline. It helps ensure that your analyses are reproducible, efficient, and well-documented.

- Sistema que hem aplicat per crear el pipeline amb Targets. . .

Targets workflow diagram (Figure 3.12) showing the steps corresponding with the complete process: The pipeline starts from (A) a couple of 'omics-derived input data sets (e.g. pre-processed gene expression and protein abundance matrices). These are converted to R data frames with features in rows and samples in columns. Then, a data frame containing related annotations (B) is created, or loaded, for each given input matrix, and used to expand these original data, in order to end up with a pair of data frames (C) containing the original values plus the average expression/abundance values of the features related to each annotation as new

features in additional rows. After that, distinct Dimension Reduction Methods are applied to perform the integrative analysis (D), and finally, an R markdown report (E) is rendered to show steps and main results of the full process.

4

Results

Contents

Text de presentacio dels resultats. . .

Fer que 4.1 sigui l'actual 4.2 (tota la info d'aplicar el mètode)

ESTRUCTURA DELS RESULTATS:

4.1 Implementació dels algos i les funcions en R

4.2 Pipeline d'anàlisi en amb el paquet 'targets'

4.3 Exemples i aplicacions 4.3.1 Results from the analysis of human brain tissue samples 4.3.2 Results from the expansion of omics data with biological annotations 4.3.3 Results from the analysis of 150 TCGA-BRCA samples 4.3.4 Results from the application of MFA on TCGA-BRCA data with, and without, expanded data 4.3.5 . . .
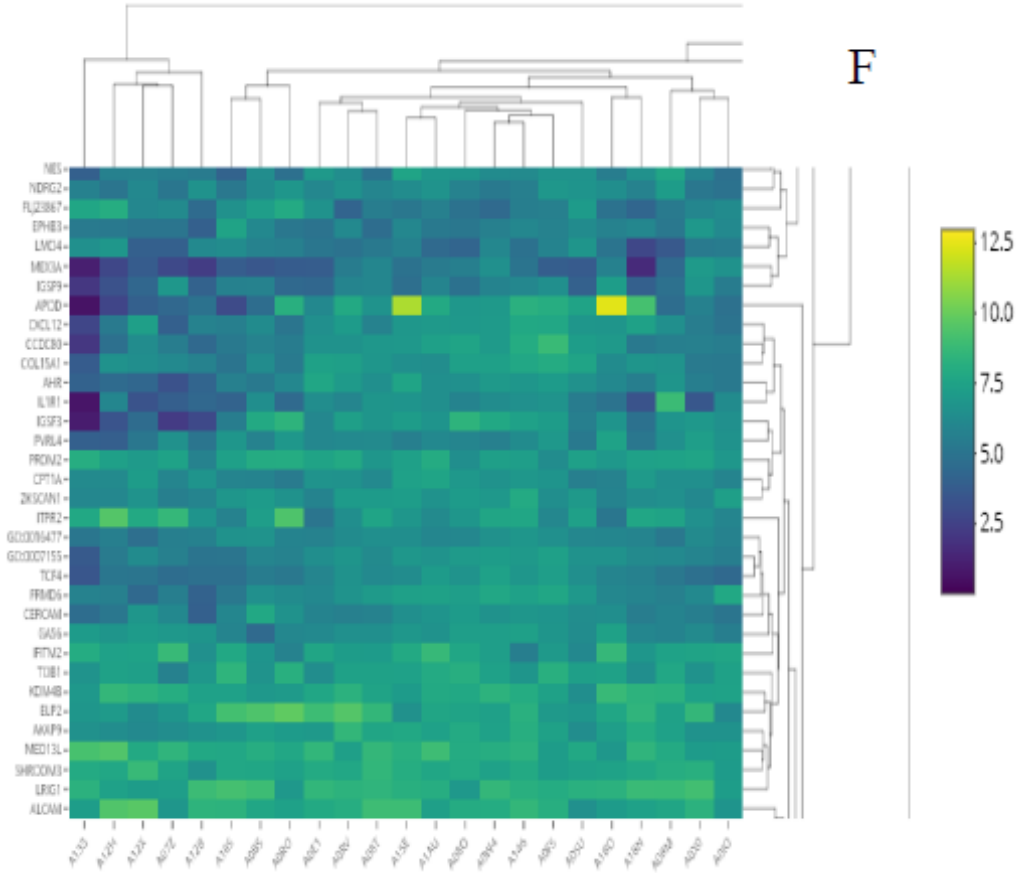
Figure 4.1: Heapmap of an expanded matrix

4.1   Results from the analysis of human brain tissue samples

4.2   Results from the expansion of omics data with biological annotations

Figure 4.1 is an snapshot (F) of one of the heat maps created to show the expanded

matrices obtained in (Figures 3.9 i 3.10 prèvies, de Methods).
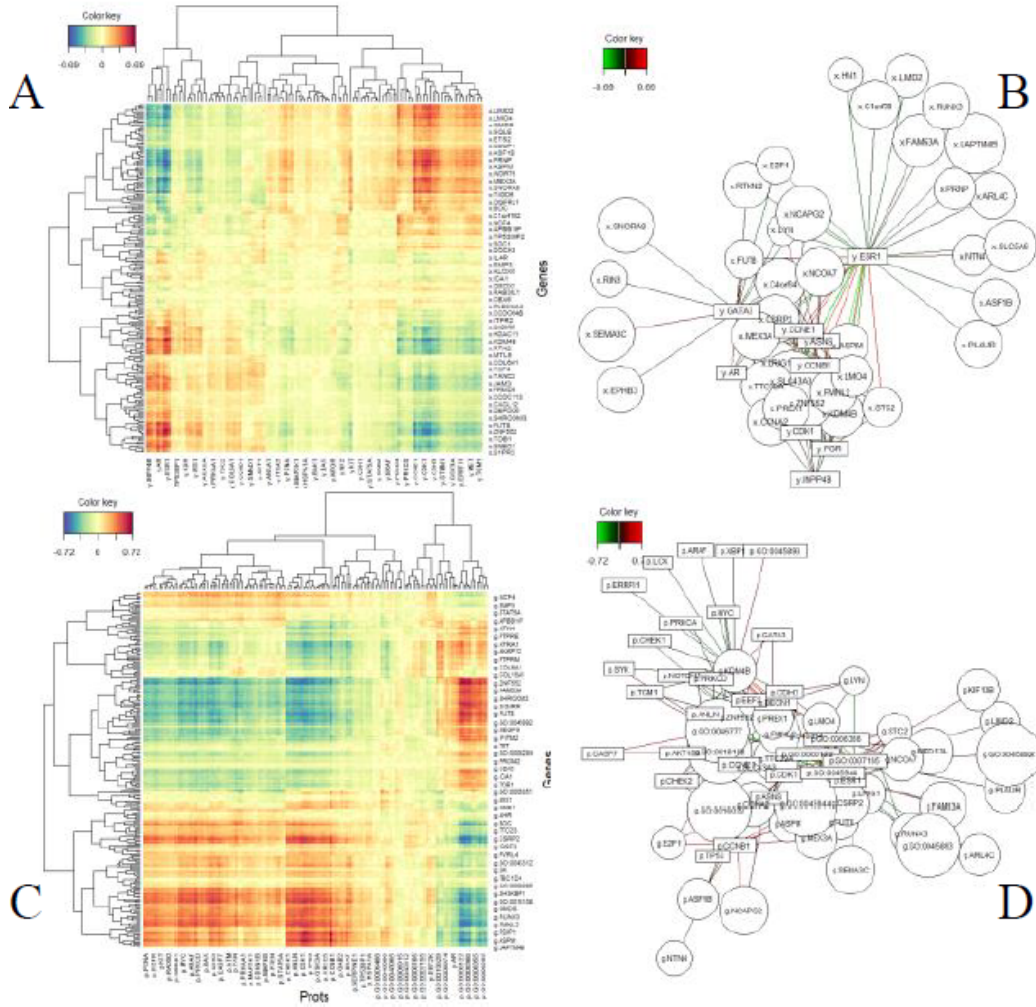
Figure 4.2: BRCA results overview

4.3 Results from the analysis of 150 TCGA-BRCA samples

Figure 4.2 contains some of the graphical results of the analysis of the 150 samples from TCGA-BRCA: Heat maps (A, C) and association networks (B, D) resulting from the integration by Regularized Canonical Correlations Analysis with mixomics R package. Performed with the original data sets (A, B) or using data expanded with biological annotations to Gene Ontology (C, D), so adding some GO terms to the features from each source, where the outputs contain higher level of information (higher density in both type of plots).
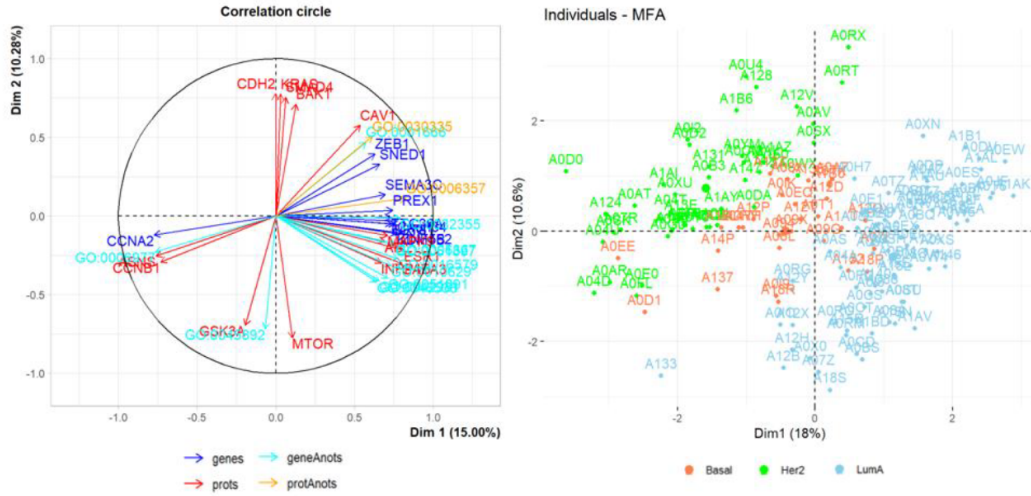
Figure 4.3: BRCA results with MFA

4.4 Results from the application of MFA on TCGA-BRCA data with, and without, expanded data

Figure 4.3 includes a Correlation Circle (left), with most relevant genes, proteins and added GO annotations. Distribution of samples (right) along the first two plotted dimensions. Both results coming from the application of Multiple Factor Analysis (FactoMineR and factoextra R packages) performed on the same 150 samples (Basal, Her2 and LuminalA conditions) from TCGA-BRCA.

4.5 Resultats de la creacio del paquet amb Targets. . .

5
Discussion

Potser no cal posar la TOC aqui?

Resum de l'article. Apuntant a les conclusions. Comentant problemes i limitacions (emprar combinacions lineals de variables per crear-ne de noves).

Principals problemes i limitacions de la nostra proposta: * Pendent d'apuntar. . . * . . .

Possibles extensions i punts de millora. Comentar i descriure cadascun d'ells:

- Poder fer servir 3 o més conjunts de dades òmiques
- que l'anotacio basica pugui ser tb a KEGG i no sols a GO
- opció d'afegir les anotacions com a individus suplementaris enlloc de variables
- Poder ponderar els pesos de les anotacions, segons tipus, data set d'origen, etc.
- Permetre treballar amb dades faltants o, fins i tot, blocs de dades faltants.
- Millorar les opcions del paquet: mètodes d'anotació bio, mètodes d'integració, tipus de gràfics resultants. . .

There is grandeur in this view of life, with its several powers, having been originally breathed into a few forms or into one; and that, whilst this planet has gone cycling on according to the fixed law of gravity, from so simple a beginning endless forms most beautiful and most wonderful have been, and are being, evolved.

— Darwin's *On the Origin of Species* (1859).

6
Conclusions

If we don't want Conclusion to have a chapter number next to it, we can add the `{-}` attribute.

Conclusion 1

The need for a better biological interpretation of multi-omics integrative methods let us to consider the inclusion of biological information during (not after) the analysis process

Conclusion 2

We propose a method focused on the expansion of the starting omics datasets, by adding new annotation-derived features to those matrices, before applying the integrative analysis

Conclusion 3

This approach allows the inclusion of relevant information from the main biological annotation tools, as well as any custom annotation, combined with the use our preferred Dimension Reduction techniques

Conclusion 4

We have implemented a pipeline for reproducible and easy-to-use execution, that facilitates the control of each step, the visualization of results and their reporting to PDF/HTML formats.

Appendices

A
The First Appendix

This first appendix includes an R chunk that was hidden in the document (using `echo = FALSE`) to help with readibility:

In 02-rmd-basics-code.Rmd

And here's another one from the same chapter, i.e. Chapter ??:

B
The Second Appendix, for Fun

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