***Abstract –*** In recent years the omics disciplines have made their way across a wider spectrum of research groups, thus leading to the generation of multi-omics data sets in a great number of studies. While traditional omics studies only focused on a single biological level, the multi-omics approach has the potential of studying systems in further detail. However, along with this great potential comes the challenge of integrating and analyzing data far more complex in nature than that of a single omic discipline.

One of such multi-omics data integration challenges is exemplified by the EU-funded DENAMIC project, which investigated neurotoxic effects of low-concentration mixtures of pesticides and a number of common environmental pollutants in children using a *Rattus norvegicus* animal model. To meet this feat, several omics platforms were employed using brain tissue samples from rats treated with the aforementioned pollutants: proteomics, metabolomics and transcriptomics (RNA-seq and miRNA-seq). Clinical data in the form of learning tests was obtained prior to brain tissue sample extraction as well.

This project aimed to develop a strategy for the integration of multi-omics and clinical data for the DENAMIC experimental set up by means of creating multi-omic models regarding the neural response to toxic compounds, as well as to confirm previous conclusions of the DENAMIC project and to obtain new information about the global effect of pesticide developmental exposure at both molecular and physiological levels from a multi-omic point of view.

The strategy presented here tackles the different challenges of integrative analysis: First, the pre-processing of multi-omic data and the treatment of missing values; second, the establishment of potential associations between mRNAs, miRNAs, proteins and metabolites, while trying to filter out spurious associations to increase the mapping specificity; third, the visualization of these associations by mapping onto KEGG pathways, which allows the identification and study of relevant pathways and components for the various omics studied as well as their interactions; and finally, the association of molecular changes to phenotypic changes, as represented by the clinical data. The results obtained could potentially help locate markers of neurotoxicity and explain the molecular basis of impaired neurodevelopment.

***Keywords –*** multi-omic data integration, multivariate statistics, transcriptomics, proteomics, metabolomics, bioinformatics, neurobiology, pesticide exposure