Exploratory data analysis through computational methods has been widely used in the Life Sciences and Medical field in order to reveal intrinsic information that is pertinent for elucidating biological processes involved in diseases. Moreover, clustering is a classic technique used to group sets of elements that share similarities among each other and it has been actively studied and improved through the years.

In this study we perform gene expression analysis of microarray data from Type-1 Diabetes (T1D) through a particular class of clustering algorithms called biclustering. With biclustering, the task of grouping entities is done in two dimensions and in the case of microarray gene expression data these entities are genes and conditions. However, most of the classic biclustering algorithms focus on datasets with single time point measurements. For this project, we choose EDISA (Extended Dimension Iterative Signature Algorithm) as our choice of algorithm as it has the capability of performing on multi time-series data.

The project is aimed at finding groups of genes and conditions from our T1D dataset that together can be related to a biological process for the disease. This is achieved through an analysis pipeline that undergoes different steps: filtering, clustering, mining and Gene Set Enrichment Analysis (GSEA). In addition, we implement modifications on EDISA in order to be able to find coherent patterns on datasets with different number of measurements between conditions (which was not possible initially) and also to account for that difference on its metric for calculating the distance between the genes and conditions.

After GSEA was performed on the final clusters discovered by the algorithm, we found gene sets that were either related to studies on diabetes or at least contained genes that were previously showed to be related with diabetes. Now, with these hypotheses in hands, further investigation needs to be done for these particular genes to attest whether they play a role on the development of T1D or not.

**Keywords** Clustering, Gene Expression Analysis, Biclustering, Diabetes, T1D, Microarray dataset, Time-Series Data, Gene Ontology, GSEA, Data Mining.