**Abstract**

Bioinformatics is an interdisciplinary field that combines biology, computer science, and statistics to analyze large-scale biological data, such as genomics. Genes, as sequences of DNA, carry instructions for cellular functions, and differential gene expression refers to how these genes are expressed at varying levels under different conditions or across groups, including between males and females. Sex-based differences at the gene level, influenced by sex chromosomes and hormones, are thought to shape various biological pathways—complex sequences of molecular interactions that lead to specific cellular outcomes.

This research aims to explore how gender differences influence gene expression across multiple tissues, using data from the Genotype-Tissue Expression (GTEx) project. By applying advanced bioinformatics techniques, we expect to identify genes and biological pathways that may exhibit sex-biased expression patterns. Through the analysis of gene regulatory networks (GRNs) and the application of machine learning models, such as XGBoost and SVM, we aim to investigate the roles of transcription factors and their potential contribution to these differences.

While the specific regulatory mechanisms remain to be uncovered, we anticipate revealing insights into how gender-specific factors might influence key biological processes. This study ultimately seeks to understand how gender impacts biological pathways, providing a foundation for the development of more precise, individualized medical interventions that take gender-related genetic differences into account.