Predicting lncRNA Expression Levels

Predicting gene expression using known expression levels

In this project, I use Gaussian Process Regression to predict the expression levels of long non-coding RNAs (lncRNAs) based on differential gene expression (DGE) data from studies on conditions like Alzheimer's disease and controls. By integrating these models with expression profiles of known genes, I aim to unravel the regulatory networks that drive lncRNA expression in disease contexts.