

California State University San Bernardino
School of Computer Science and Engineering

CSE 595 Independent Study Presentation

Date

June 12, 2014

Time

1:00 pm

Place

JB 359

Title

Analyzing gene expression data using Bioconductor

Student

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Advisor

Dr. Qiao

Abstract

A field of bioinformatics is the analysis of gene expression data in order to study the cause of many genetic diseases. Bioconductor via the R programming language is a program that is able to process gene expression data. With the use of multiple libraries, Bioconductor will be able to preprocess, isolate significant genes, and graph the results of the experiment. Also, because of the integration of the R language, one can also perform statistical analysis on gene expression data. This specific study analyzes the ApoAI gene (responsible for fat metabolism) and determines the differentially expressed genes in the liver.