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| **PROTOCOL CODING IN “R”** |

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| **PROJECT ID** | **18 Bwanya** |
| **Title:** | **Gene Expression Analysis and Visualization of Lung Cancer Pathways Using R and Bioinformatics Pipelines** |
| **Version:** | **01** |
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Contents

[1. INTRODUCTION 2](#_Toc119389311)

[2. EQUIPEMENT / MATERIAL / SOFTWARE / DATA / SAMPLES (select what is applicable) 2](#_Toc119389312)

[3. HEALTH AND SAFETY (if applicable) 2](#_Toc119389313)

[4. SPECIFIC RECOMMENDATIONS / WARNING (if applicable) 2](#_Toc119389314)

[5. PROCEDURE TO FOLLOW 2](#_Toc119389315)

[6. DATA ANALYSIS AND STATISTICS (if applicable) 3](#_Toc119389316)

[7. LITERATURE 4](#_Toc119389317)

[8. APPENDIX (if required) 4](#_Toc119389318)

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| 1. INTRODUCTION |

This protocol describes the steps involved in analyzing differentially expressed genes (DEGs) in lung cancer using RNA-seq data. In the project, we focus on analyzing the publicly available dataset GSE1089 to identify significant DEGs between tumor and healthy tissues. We aim to gain more insight into biological pathways and genes relevant to lung cancer. We try to look at risk factors and characteristics of non-small lung cancer to identify differential gene expression and consequently guide future interventions.

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| 2. SOFTWARE / DATA |

Various programs and databanks were employed to work in and aid the project’s progress:

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| **Name** | **Description** | **Version / (Main) Developer** |
| *Computer* | A computer with at least 16 GB RAM available. This is recommended so running the code is a smooth and efficient endeavour. | - |
| *Github* | GitHub is an online and desktop application. The program is employed to create a global location to share and work on files collectively. It is primarily used to work on the code, but can also be used to work on other files of interest which are non-code related. | Version 3.4.16 (x64) |
| *R* | R is a programming language primarily employed for statistical computing and data visualization. To use this programming language, the “R” package first must be fetched online. | 4.2.2. |
| *Rstudio* | Rstudio is a program that uses the R programming language to develop a working code. | 4.2.2. |
| *NCBI* | The GSE81089 dataset comprises RNA sequencing (RNA-seq) data from 199 non-small cell lung cancer (NSCLC) tissue samples, along with paired normal lung tissues from 19 patients. Each sample includes 63129 gene expression readings recorded by Ensembl IDs. | - |
| *Rstudio packages* | **Biocmanager**: The BiocManager package, as the modern successor package to BiocInstaller, allows users to install and manage packages from the Bioconductor project. Bioconductor focuses on the statistical analysis and comprehension of high-throughput genomic data. | 1.30.25 / Martin Morgan |
|  | **DESeq2**: Package from the Bioconductor project. Allows estimate variance-mean dependence in count data from high-throughput sequencing assays and tests for differential expression based on a model using the negative binomial distribution. | 3.20 / Michael Love |
|  | **ggplot2**: A system for 'declaratively' creating graphics, based on "The Grammar of Graphics". ggplot2 helps with mapping variables by offering freedom in aesthetics, graphical primitives, and other details. | 3.5.1 / Hadley Wickham |
|  | **dplyr**: A fast, consistent tool for working with data frame-like objects, both in and out of memory. | 1.1.4 / Hadley Wickam |
|  | **pheatmap**: Allows implementation of heatmaps and offers more control over dimensions and appearance. | 1.0.12 / Raivo Kolde |
|  | **clusterProfiler**: Package from the Bioconductor project. This package supports functional characteristics of both coding and non-coding genomics data for thousands of species with up-to-date gene annotation. It provides a universal interface for gene functional annotation from various sources. It provides a tidy interface to access, manipulate, and visualize enrichment results to aid in efficient data interpretation. | 3.20 / Guanchuang Yu |
|  | **org.Hs.eg.db**: Package from the Bioconductor project. Helps with genome-wide annotation for Humans, primarily based on mapping using Entrez Gene identifiers. | 3.20 / Marc Carlson |
|  | **GEOquery**: Package from the Bioconductor project. The NCBI Gene Expression Omnibus (GEO) is a public repository of microarray data. GEOquery is the bridge between GEO and BioConductor and thus integrates GEO into Rstudio. | 3.20 / Sean Davis |

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| 3. HEALTH AND SAFETY |

We will be working entirely with computers thus this section is not applicable

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| 4. SPECIFIC RECOMMENDATIONS / WARNING |

We are using GitHub, so we have to take caution with working on our code together. If we work individually, we have to push our code not together otherwise the GitHub will not accept multiple edits at once and some of the code will be lost.

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| 5. PROCEDURE TO FOLLOW |

These are the procedure to follow to get results

1. Download the lung cancer data from GEO database​ to perform the analysis of the data
2. Install and require libraries in R, the libraries we will be using are DESeq2, ggplot2, dplyr, pheatmap, clusterProfiler, org.HS.eg.db and GEOquery.
3. Load the count matrix, it has the data from step 1
4. Load metadata, this can be required from the R library GEOquery
5. Create a DESeq2 dataset in R to create a statistical model
6. Perform Quality control
7. Get results and sort by pValue
8. Filter significant genes with adjusted p-value < 0.05
9. Visualize results such as volcano plot, heatmap, MA plot
10. Functional enrichment analysis using GO, KEGG

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| 6. DATA ANALYSIS AND STATISTICS |

For the analysis of the normalized gene expression data (GSE81089\_FPKM\_cufflinks.tsv), we used R and the DESeq2 package. DESeq2 applies a statistical model to assess differences in gene expression between two or more sample groups. In our case, it assessed the difference between the people with NSCLC and normal lung tissue. To identify differentially expressed genes (DEGs), DESeq2 calculated a p-value for each gene. We used a threshold of p< 0.05 to determine statistically significant DEGs. To visualize the results, we used R to generate volcano plots to highlight significant DEGs.

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| 7. LITERATURE |

Indicate any literature if needed, or reference to other documents needed to understand / complement this protocol. That includes scientific papers, websites, databases or books.

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| 8. APPENDIX (if required) |

Add here any materials or information that are needed to understand/reproduce the protocol, but are too extensive to add to the main text.