

系統生物學概論 R之基因表現量分析

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R – 簡介

- 一種常用於統計分析、繪圖、資料探勘的程式語言
- 主要以命令列、圖形用戶介面進行操作
- 常見的開發環境為RStudio
- 特色：高階語言、統計繪圖函數豐富、在生資界有一定權威性
- R語言基礎教學：<https://blog.gtwang.org/programming/r/>

GEO - GENE EXPRESSION OMNIBUS

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Gene Expression Omnibus

GEO is a public functional genomics data repository supporting MIAME-compliant data submissions. Array- and sequence-based data are accepted. Tools are provided to help users query and download experiments and curated gene expression profiles.


Gene Expression Omnibus

GSE111803

Keyword or GEO Accession

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Tools

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Repository Browser	
DataSets:	4348
Series:	112132
Platforms:	19667
Samples:	3005597



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<https://www.ncbi.nlm.nih.gov/geo/>

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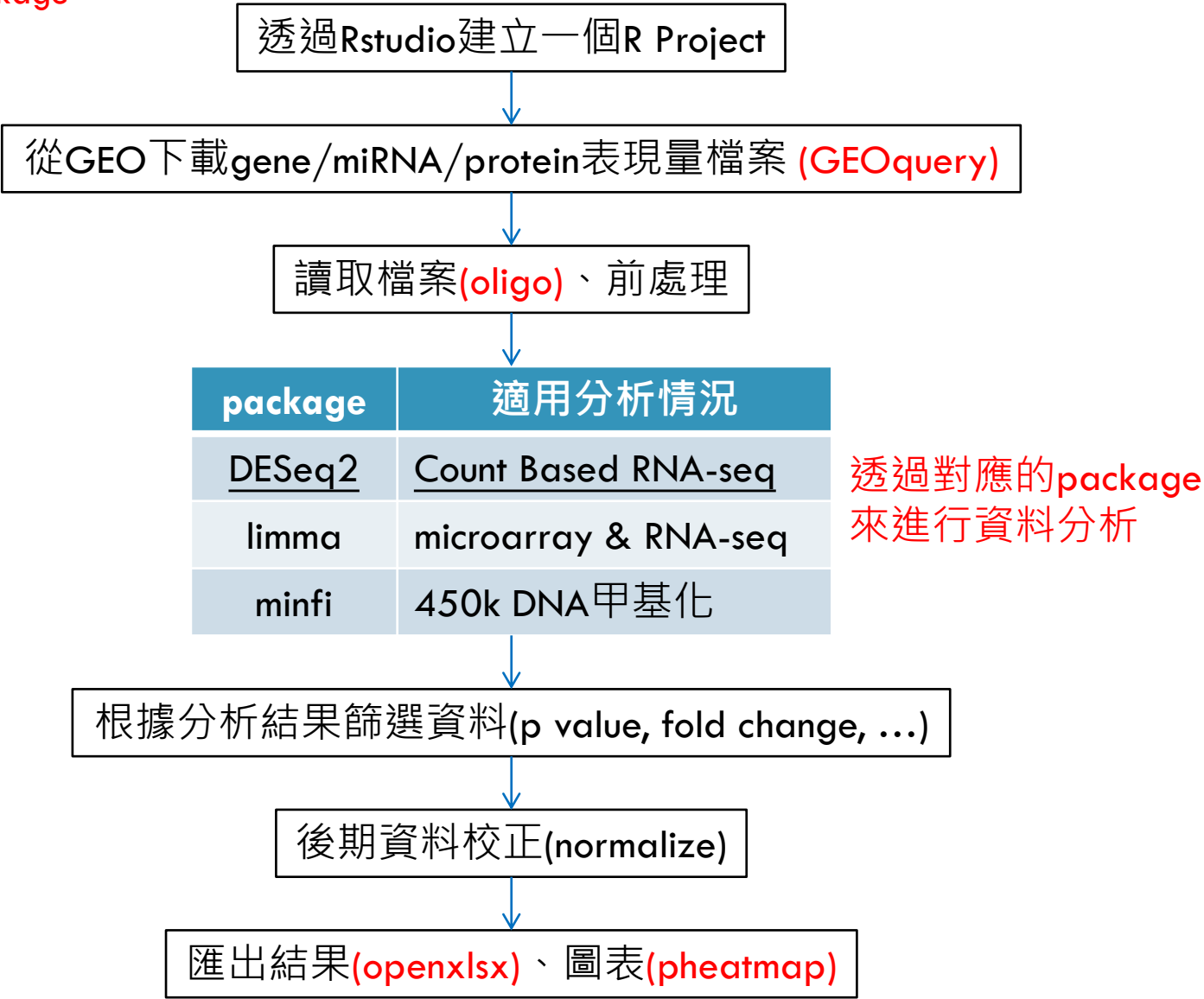
Scope: Format: Amount: GEO accession:

Series GSE111803 [Query DataSets for GSE111803](#)

Status	Public on Mar 14, 2019
Title	High throughput sequencing analyzes small RNA profile alteration in the exosomes from lung cancer patients and healthy controls
Organism	Homo sapiens
Experiment type	Non-coding RNA profiling by high throughput sequencing
Summary	<p>Purpose: The goals of this study are to compare the small RNA expression profiles in the peripheral exosomes and try to find biomarkers for early diagnosis of lung adenocarcinoma</p> <p>Methods: Exosome was extracted from peripheral blood samples from 5 patients with lung adenocarcinoma and 5 healthy controls. RNA was extracted and microRNA profile was analyzed by high throughput sequencing.</p> <p>Results: The expression of 5 microRNAs was found significantly altered in patients with lung adenocarcinoma</p>
Overall design	Examination of peripheral blood exosome microRNAs from 5 patients with lung adenocarcinoma and 5 healthy controls

https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE111803&fbclid=IwAR3cxRWdm6XLcMiYnWwjhKsy_d6YWtUdXEh9X1bsjDS18rR4ET_mrxuEnt8

*紅色括弧內為
對應功能的R package



參考資料：http://kasperdanielhansen.github.io/genbioconductor/?fbclid=IwAR3ckldU6IrvCQHIXO0-e7qZck1iknmdmLK5tRQWxYZLn3nSKmlwjBzi_g