1. **Linux上如何安裝軟體**
2. # wget download\_file\_url
3. 解壓縮，參考<http://note.drx.tw/2008/04/command.html>
4. 加入PATH
5. **下載RSEM(v1.3.0) : (quantifying transcript abundances from RNA-Seq data)**

<https://deweylab.github.io/RSEM/>

# wget <https://github.com/deweylab/RSEM/archive/v1.3.0.tar.gz>

# tar zxvf v1.3.0.tar.gz

# cd ~/RSEM/RSEM-1.3.0

# make

# PATH="$HOME/bio\_tool/RSEM/RSEM-1.3.0:$PATH"

# source ~/.profile

1. **下載bowtie(v1.0.0) : (align to reference)**

**(RSEM1.3.0與bowtie1.2在reads 為paired-end時不相容,故不安裝最新版)**

[https://sourceforge.net/projects/bowtie-bio/files/bowtie/1.0.0/](https://sourceforge.net/projects/bowtie-bio/files/bowtie/1.0.0/%20)

# unzip

# PATH="$HOME/bio\_tool/bowtie/bowtie-1.0.0:$PATH"

# source ~/.profile

要使用bowtie需有libtbb套件

# sudo apt-get update

# sudo apt-get install libtbb-dev (or #sudo apt-get install libtbb2)

1. **下載FastQC(v0.11.5) : (quality control checks on raw sequence data)**

[http://www.bioinformatics.babraham.ac.uk/projects/download.html#fastqc](http://www.bioinformatics.babraham.ac.uk/projects/download.html" \l "fastqc)

# wget <http://www.bioinformatics.babraham.ac.uk/projects/fastqc/fastqc_v0.11.5.zip>

# unzip fastqc\_v0.11.5.zip

# chmod 755 fastqc

# PATH="$HOME/bio\_tool/FastQC/FastQC:$PATH"

# source ~/.profile

1. **下載cutadapt(v1.13) : (修剪fastq軟體)**

<http://cutadapt.readthedocs.io/en/stable/installation.html>

# sudo pip install cutadapt (請管理員安裝)

1. **下載samtools(v0.1.19) : (bam轉sam檔)**

# sudo apt-get install samtools (請管理員安裝)

**使用**

# samtools view file.bam > file.sam

1. **下載sratoolkit(2.8.2) : (sra 轉 fastq , 下載sra 資料)**

<https://trace.ncbi.nlm.nih.gov/Traces/sra/sra.cgi?view=software>

# wget <https://ftp-trace.ncbi.nlm.nih.gov/sra/sdk/2.8.2-1/sratoolkit.2.8.2-1-ubuntu64.tar.gz>

# tar zxf sratoolkit.2.8.2-1-ubuntu64.tar.gz

# PATH="$HOME/bio\_tool/sratoolkit/sratoolkit.2.8.2-1-ubuntu64/bin:$PATH"

# source ~/.profile

**使用**

# prefetch SRR975551 SRR975552 SRR975553 (download sra file)

# fastq-dump file.sra (sra to fastq) (single-end)

# fastq-dump –split-3 file.sra (sra to \_1.fastq and \_2.fastq) (paired-end)

1. **下載edgeR(v3.16.5) : (Differential expression analysis of RNA-seq expression profiles)**

<https://bioconductor.org/packages/release/bioc/html/edgeR.html>

start R

# source("https://bioconductor.org/biocLite.R")

# biocLite("edgeR") (安裝在個人帳號)

# biocLite("edgeR",lib="/usr/local/lib/R/site-library") (安裝在server上)