

```

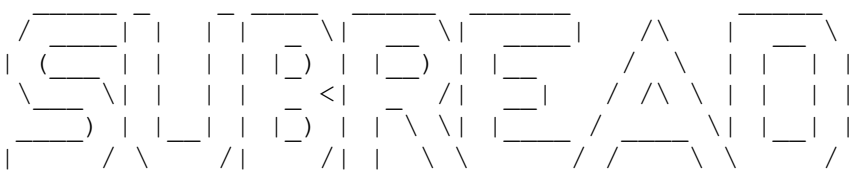
> remove.file <- paste("/home/zhuob/protocol/Rsubread/", file1, sep="")
>
> datafile <- "GSE43073"
>
> setwd("/home/zhuob/protocol/Rsubread")
> read.file <- paste(datafile, "SraRunInfo.csv", sep="" )
> RunInfo <- read.csv(read.file, stringsAsFactors=F)
Error in file(file, "rt") : cannot open the connection
In addition: Warning message:
In file(file, "rt") :
  cannot open file 'GSE43073SraRunInfo.csv': No such file or directory
> id <- which(RunInfo$LibraryStrategy=="RNA-Seq")
> RunInfo <- RunInfo[id, ]
>
>
> (fs <- basename(RunInfo$download_path))
[1] "SRR652150.sra" "SRR652151.sra" "SRR652152.sra"
[4] "SRR652153.sra" "SRR974750.sra" "SRR974751.sra"
[7] "SRR974752.sra" "SRR974753.sra"
> filepath <- RunInfo$download_path
> fsname <- RunInfo$SampleName
> fastq.name <- RunInfo$Run
> layout <- RunInfo$LibraryLayout
> bamfile <- paste(fastq.name, ".bam", sep="")
>
> ## The options for featureCounts are discussed here. see #78
> # http://seqanswers.com/forums/showthread.php?t=30258&page=4-
>
> fc <- featureCounts(files=bamfile,
annot.ext="Arabidopsis_thaliana.TAIR10.22.gtf",
+ isGTFAnnotationFile=T)

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Rsubread 1.14.2

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The logo for Rsubread is a stylized representation of the word 'Rsubread' in a monospace font. The letters are composed of various geometric shapes like rectangles, triangles, and lines, giving it a digital or architectural appearance. The 'R' is particularly large and complex, with many internal lines. The 's' is a simple curve. The 'b' has a large loop. The 'r' is a simple vertical line with a small horizontal bar. The 'e' is a simple oval. The 'a' is a simple vertical line with a small horizontal bar. The 'd' is a simple vertical line with a small horizontal bar. The 'r' is a simple vertical line with a small horizontal bar. The 'e' is a simple oval. The 'a' is a simple vertical line with a small horizontal bar. The 'd' is a simple vertical line with a small horizontal bar.

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//===== featureCounts setting
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||
||
||           Input files : 8 BAM files
||
||           S SRR652150.bam
||
||           S SRR652151.bam
||
||           S SRR652152.bam
||
||           S SRR652153.bam
||
||

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```
| | S SRR974750.bam
| | 
| | S SRR974751.bam
| | 
| | S SRR974752.bam
| | 
| | S SRR974753.bam
| | 
| | 
| | Output file : ../Rsubread_featureCounts_pid2158
| | 
| | Annotations : Arabidopsis_thaliana.TAIR10.22.gtf (GTF)
| | 
| | 
| | Threads : 1
| | 
| | Level : meta-feature level
| | 
| | Paired-end : no
| | 
| | Strand specific : no
| | 
| | Multimapping reads : not counted
| | 
| | Multi-overlapping reads : not counted
| | 
| | 
| | \\\===== http://subread.sourceforge.net/
| | =====//
| | 
| | //===== Running
| | =====\\\
| | 
| | Load annotation file Arabidopsis_thaliana.TAIR10.22.gtf ...
| | 
| | Features : 217183
| | 
| | Meta-features : 33602
| | 
| | Chromosomes : 7
| | 
| | 
| | Process BAM file SRR652150.bam...
| | 
| | Single-end reads are included.
| | 
| | Assign reads to features...
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```
|| Total reads : 60759629
||
|| Successfully assigned reads : 33713477 (55.5%)
||
|| Running time : 3.56 minutes
||
||
|| Process BAM file SRR652151.bam...
||
|| Single-end reads are included.
||
|| Assign reads to features...
||
|| Total reads : 57778356
||
|| Successfully assigned reads : 37016684 (64.1%)
||
|| Running time : 3.61 minutes
||
||
|| Process BAM file SRR652152.bam...
||
|| Single-end reads are included.
||
|| Assign reads to features...
||
|| Total reads : 172442676
||
|| Successfully assigned reads : 40791388 (23.7%)
||
|| Running time : 8.82 minutes
||
||
|| Process BAM file SRR652153.bam...
||
|| Single-end reads are included.
||
|| Assign reads to features...
||
|| Total reads : 149540193
||
|| Successfully assigned reads : 33673854 (22.5%)
||
|| Running time : 7.53 minutes
||
||
|| Process BAM file SRR974750.bam...
||
|| Single-end reads are included.
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```
|| Assign reads to features...
||
|| Total reads : 62469755
||
|| Successfully assigned reads : 42598094 (68.2%)
||
|| Running time : 3.97 minutes
||
||
|| Process BAM file SRR974751.bam...
||
|| Single-end reads are included.
||
|| Assign reads to features...
||
|| Total reads : 69543500
||
|| Successfully assigned reads : 47533065 (68.4%)
||
|| Running time : 4.66 minutes
||
||
|| Process BAM file SRR974752.bam...
||
|| Single-end reads are included.
||
|| Assign reads to features...
||
|| Total reads : 158353479
||
|| Successfully assigned reads : 58651427 (37.0%)
||
|| Running time : 8.59 minutes
||
||
|| Process BAM file SRR974753.bam...
||
|| Single-end reads are included.
||
|| Assign reads to features...
||
|| Total reads : 153191513
||
|| Successfully assigned reads : 71414048 (46.6%)
||
|| Running time : 8.44 minutes
||
||
||
|| Read assignment finished.
```

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||
||
\\===== http://subread.sourceforge.net/
=====//

>
> cun <- fc$counts
> cun <- data.frame(cun[order(row.names(cun)),])
> colnames(cun) <- fsname
>
> dest.path <-
"/home/zhuob/Dropbox/Zhuo/Research/Project2014/Data/arab/Rsubread/"
>
> dest.file <- paste(dest.path, datafile, ".Rsubread.txt", sep="")
> write.table(cun, dest.file)

```