**Analytical codes of RNA-seq**

#Combine Fastq files of the same sample

$ cat E19.5\_oil-1\_CAGATC\_L001\_R1\_001.fastq E19.5\_oil-1\_CAGATC\_L002\_R1\_001.fastq > E19.5\_O-1.fastq

#Fastqc

$ fastqc E19.5\_O-1.fastq -o Fastqc

#Mapping

$ tophat2 -p 4 -G /home/common/xbio/db/iGenomes/Mus\_musculus/UCSC/mm10/Annotation/Genes/genes.

gtf -o Tophat\_result\_ E19.5\_O-1 /home/common/xbio/db/iGenomes/Mus\_musculus/UCSC/mm10/

Sequence/Bowtie2Index/genome E19.5\_O-1.fastq

#Count data

$ featureCounts -t exon -g gene\_id -a /home/common/xbio/db/iGenomes/Mus\_musculus/UCSC/mm10/Annotation/Genes/genes.gtf -o counts.txt Tophat\_result\_1/accepted\_hits\_E19.5\_O-1.bam Tophat\_result\_2/accepted\_hits\_E19.5\_O-2.bam Tophat\_result\_3/accepted\_hits\_E19.5\_D-1.bam Tophat\_result\_5/accepted\_hits\_SPG\_O-1.bam Tophat\_result\_6/accepted\_hits\_SPG\_O-2.bam Tophat\_result\_7/accepted\_hits\_SPG\_D-1.bam Tophat\_result\_8/accepted\_hits\_SPG\_D-2.bam Tophat\_result\_9/accepted\_hits\_SPC\_O-1.bam Tophat\_result\_10/accepted\_hits\_SPC\_O-2.bam Tophat\_result\_11/accepted\_hits\_SPC\_D-1.bam Tophat\_result\_12/accepted\_hits\_SPC\_D-2.bam Tophat\_result\_13/accepted\_hits\_RS\_O-1.bam Tophat\_result\_14/accepted\_hits\_RS\_O-1.bam Tophat\_result\_15/accepted\_hits\_RS\_D-1.bam Tophat\_result\_16/accepted\_hits\_ RS\_D-2.bam

#TMM normalization (R in windows)

$ library(edgeR)

$ count<-read.table("E19.5 germ counts.txt",sep="\t",header=T,row.names=1)

$ count <- as.matrix(count)

$ group <- factor(c("Oil", "Oil", "DEHP", "DEHP"))

$ d <- DGEList(counts = count, group = group)

$ d <- calcNormFactors(d)

$ d <- estimateCommonDisp(d)

$ d <- estimateTagwiseDisp(d)

$ result <- exactTest(d)

$ table <- as.data.frame(topTags(result, n = nrow(count)))

$ write.table(table, file = "result.txt", col.names = T, row.names = T, sep = ",")