

Example: Analysis of SRS3173555 1000SEGs

Preparation:

- ✓ **Documents:** cluster.txt SRS3173555_clusters.txt SRS3173555.mat
- ✓ **Programs:** ex_bo.bat bootstrap_random.exe extract_file.exe
 - Three programs should be placed in one folder

Double click to open ex_bo.bat



```
C:\WINDOWS\system32\cmd.exe
input the last cluster who exceed 100:
```

- ✓ Follow the instruction and input the last cluster in cluster.txt that exceeds 100

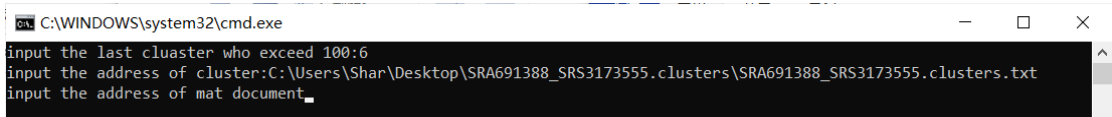
```
0 1147 Ductal cells
1 813 Basal cells
2 582 Ductal cells
3 431 Cholangiocytes
4 418 Unknown
5 255 Ductal cells
6 253 Basal cells
7 93 Luminal epithelial cells
8 73 Cholangiocytes
9 47 Fibroblasts
10 40 Ductal cells
11 21 Unknown
12 13 Ductal cells
```

- ✓ Input 6 in this case



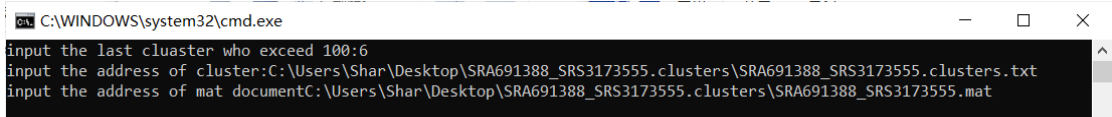
```
C:\WINDOWS\system32\cmd.exe
input the last cluster who exceed 100:6
input the address of cluster:
```

- ✓ Input the full path of SRS3173555_clusters.txt



```
C:\WINDOWS\system32\cmd.exe
input the last cluster who exceed 100:6
input the address of cluster:C:\Users\Shar\Desktop\SRA691388_SRS3173555_clusters\SRA691388_SRS3173555_clusters.txt
input the address of mat document_
```

- ✓ Input the full path of SRS3173555.mat



```
C:\WINDOWS\system32\cmd.exe
input the last cluster who exceed 100:6
input the address of cluster:C:\Users\Shar\Desktop\SRA691388_SRS3173555_clusters\SRA691388_SRS3173555_clusters.txt
input the address of mat documentC:\Users\Shar\Desktop\SRA691388_SRS3173555_clusters\SRA691388_SRS3173555.mat
```

- ✓ A folder named "out" will be produced after 3 steps

Create a new folder named "1000SEGs" and copy all the files ended with bin. txt to the "1000SEGs" folder

- ✓ Open R and run the following code

```
dir <- "the full path of 1000SEGs "
filename <- list.files(dir,full.names = T)
for (i in 1:length(filename)){
```

```

data=read.table(filename[i],sep="\t",header=TRUE)
data$gene <- gsub("_EN.*$", "", data$gene)
data <- data[,-length(data)]#remove the last col
data = data[!duplicated(data$gene),]
newdata<-data[,-1]
row.names(newdata)<-data$gene
newdata<-newdata[,]*1000000
dim(newdata)
newdata<-newdata[,]/colSums(newdata)
dim(newdata)
newdata<-newdata[which(rowSums(newdata) > 0),]
dim(newdata)
newdata<-newdata[,]+1
newdata<-log(newdata[,],base=2)
Mean<-apply(newdata,1,mean)
SD<-apply(newdata,1,sd)
x<-data.frame(Mean,SD)
GESI<-1/(1+x$SD/x$Mean)
y<-data.frame(x,GESI)
y<-y[order(-y$GESI),]
y<-y[c(1:1000),]
write.csv(y,"data.csv")
data<-read.csv("data.csv",header=T)
names(data)[1]<- "GENE"
write.table(data,file=paste(dir,"/",i-1,"_cell_1000_SEGs.txt",sep
""),sep="\t",quote=F,row.names = F)
}

```

- ✓ The final results will be produced in the folder