# Instruction to use my code

1. Download and put all bam files in folder
2. Run “annotation.R”
   1. Change the path in 8th line to where you put your bam
   2. Change the 16th and 17th line to the database you want to use
      1. TxDb.Hsapiens.UCSC.hg19.knownGene (what we current have)
      2. TxDb.Hsapiens.UCSC.hg19.lincRNAsTranscripts
   3. Type “source(“annotation.R”)”in command line (multiple ways to do this)
3. **Prepare a design matrix file. See example “design.csv”**
   1. Put the design.csv to the folder where the code located
4. Change 8th and 11th line in “main.R”to whatever you like
   1. 8th line is where you put your output files
   2. 11th line is the prefix of output of each comparison.
      1. “outnames”is a vector in the format
      2. c (‘name1’,’name2’,’name3’……)
5. **Change the core part of “Analysis1\_DEG.R”**
   1. After “design=”of “DESeqDataSetFromMatrix”, input your experiment design
      1. Exapmle: ~ subtype + donor. The name should be consistent to “design.csv”
   2. For each question you want to ask under each model
      1. After “contrast=”of“results”, type “c('subtype','Sub1','Sub2')”
      2. The above contrast means we want to know difference between “Sub1” and “Sub2”Expression is decided by subtype and donor.
6. Type “source(“main.R”)”in command line and wait for the results