



Exercise 7 notes

- no need to check in *data* to your assignment (GitHub) repo
- (for working on renku, it may make sense to upload data to a repo)
- remember ```\${r message=FALSE} ...` to avoid all the startup messages

Exercise 7 notes

```
> (samples <- read.table("samples.txt", header=TRUE,
+                          row.names=5, stringsAsFactors=FALSE))

      rep condition libtype shortname      countfile
CG8144_RNAi-1.bam  T1        T      SE      T1.SE CG8144_RNAi-1.count
CG8144_RNAi-3.bam  T3        T      PE      T3.PE CG8144_RNAi-3.count
CG8144_RNAi-4.bam  T4        T      PE      T4.PE CG8144_RNAi-4.count
Untreated-1.bam    C1        C      SE      C1.SE  Untreated-1.count
Untreated-6.bam    C6        C      SE      C6.SE  Untreated-6.count
Untreated-3.bam    C3        C      PE      C3.PE  Untreated-3.count
Untreated-4.bam    C4        C      PE      C4.PE  Untreated-4.count

> (mm <- model.matrix(~condition, data=samples))
      (Intercept) conditionT
CG8144_RNAi-1.bam      1      1
CG8144_RNAi-3.bam      1      1
CG8144_RNAi-4.bam      1      1
Untreated-1.bam        1      0
Untreated-6.bam        1      0
Untreated-3.bam        1      0
Untreated-4.bam        1      0
attr(,"assign")
[1] 0 1
attr(,"contrasts")
attr(,"contrasts")$condition
[1] "contr.treatment"
```

- can use a data.frame in `model.matrix`

- note the use of metadata, instead of manually making a vector

