This exercise practices sequence subsetting.

```
> # Load the yeast genome
> library(BSgenome.Scerevisiae.UCSC.sacCer3)
>
> # Assign data to the yeastGenome object
> yeastGenome <- BSgenome.Scerevisiae.UCSC.sacCer3
>
> # Get the head of seqnames and tail of seqlengths for yeastGenome
> head(seqnames(yeastGenome))
[1] "chrI"   "chrII" "chrIII" "chrIV" "chrV"   "chrVI"

> tail(seqlengths(yeastGenome))
 chrXII chrXIII  chrXIV   chrXV  chrXVI     chrM
1078177  924431  784333 1091291  948066   85779
>
> # Select chromosome M, alias chrM
getSeq(yeastGenome, "chrM")
> chrM = yeastGenome$chrM
> # Count characters of the chrM sequence
> chrM = yeastGenome$chrM
> nchar(chrM)
[1] 85779
```