Class 6 Homework

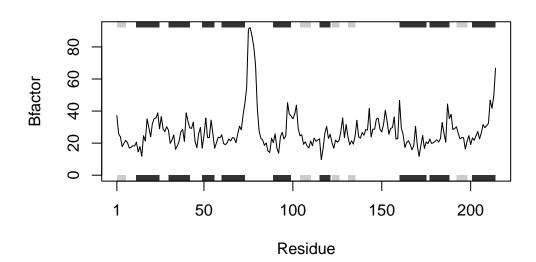
Jason Hsiao (PID: A15871650)

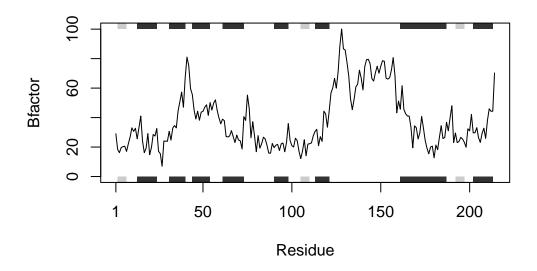
Original Code:

```
# Can you improve this analysis code?
library(bio3d)
s1 <- read.pdb("4AKE") # kinase with drug</pre>
Note: Accessing on-line PDB file
s2 <- read.pdb("1AKE") # kinase no drug</pre>
Note: Accessing on-line PDB file
PDB has ALT records, taking A only, rm.alt=TRUE
s3 <- read.pdb("1E4Y") # kinase with drug
Note: Accessing on-line PDB file
s1.chainA <- trim.pdb(s1, chain="A", elety="CA")</pre>
s2.chainA <- trim.pdb(s2, chain="A", elety="CA")</pre>
s3.chainA <- trim.pdb(s1, chain="A", elety="CA")
s1.b <- s1.chainA$atom$b</pre>
s2.b <- s2.chainA$atom$b</pre>
s3.b <- s3.chainA$atom$b
plotb3(s1.b, sse=s1.chainA, typ="1", ylab="Bfactor")
```



plotb3(s2.b, sse=s2.chainA, typ="1", ylab="Bfactor")





Writing the Function

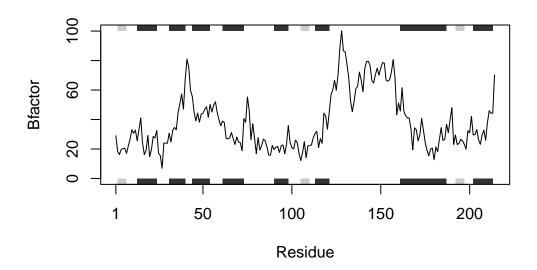
```
#Compressing the original code to a function called 'visualize()', which iterates
#pdb accession files through the functions defined below
visualize <- function(x) {
  pdb <- read.pdb(x) #reading pdb file
  trim <- trim.pdb(pdb, chain = "A", elety = "CA") #removing metadata
  atomb <- trim$atom$b #accessing atom level data
  plotb3(atomb, sse = trim, typ = "l", ylab = "Bfactor") #plotting bfactor
}</pre>
```

Testing, Testing, 1, 2, 3...

#Output of the function, inputting pdb accession codes into function visualize("4AKE")

Note: Accessing on-line PDB file

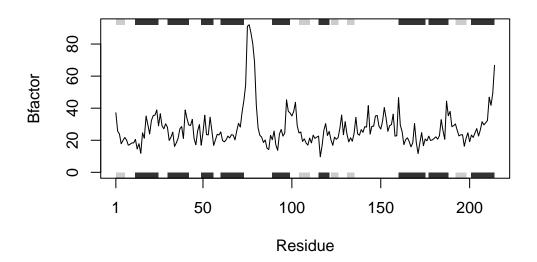
Warning in get.pdb(file, path = tempdir(), verbose = FALSE):
/var/folders/wd/9lxssr4x6qj8knq0ng53tgqw0000gn/T//Rtmpx6Euod/4AKE.pdb exists.
Skipping download



visualize("1AKE")

Note: Accessing on-line PDB file

Warning in get.pdb(file, path = tempdir(), verbose = FALSE):
/var/folders/wd/9lxssr4x6qj8knq0ng53tgqw0000gn/T//Rtmpx6Euod/1AKE.pdb exists.
Skipping download



visualize("1E4Y")

Note: Accessing on-line PDB file

Warning in get.pdb(file, path = tempdir(), verbose = FALSE):
/var/folders/wd/9lxssr4x6qj8knq0ng53tgqw0000gn/T//Rtmpx6Euod/1E4Y.pdb exists.
Skipping download

