hw class 6

Katherine Wong (A16162648)

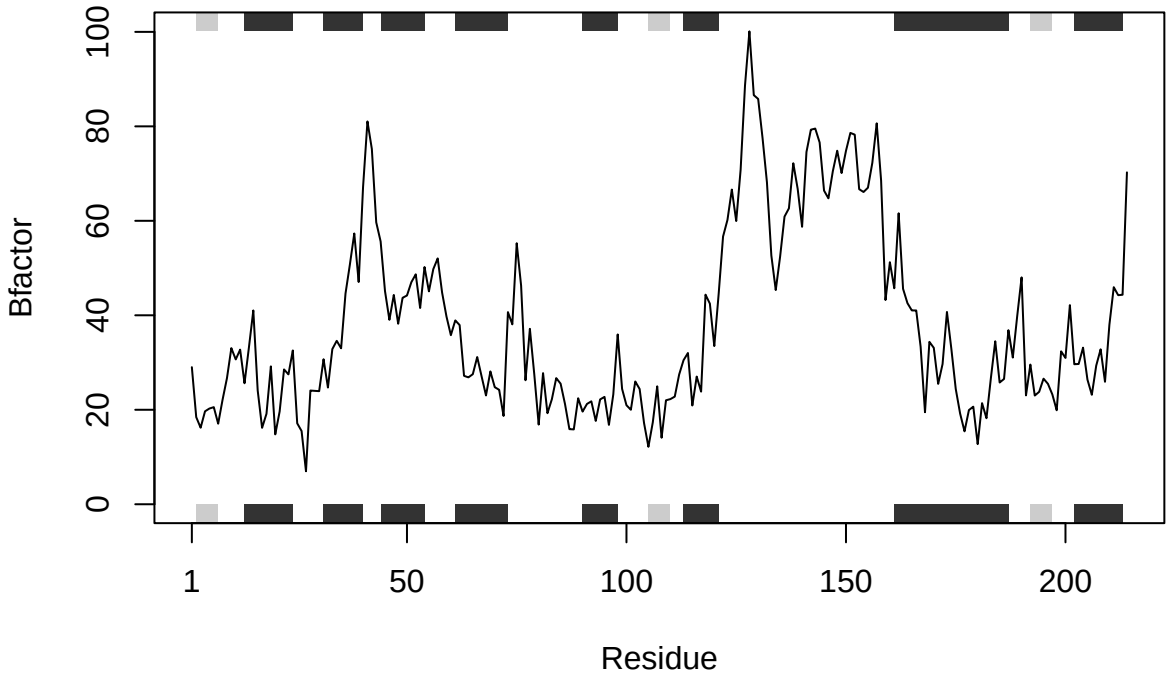
10/23/2021

Write a function

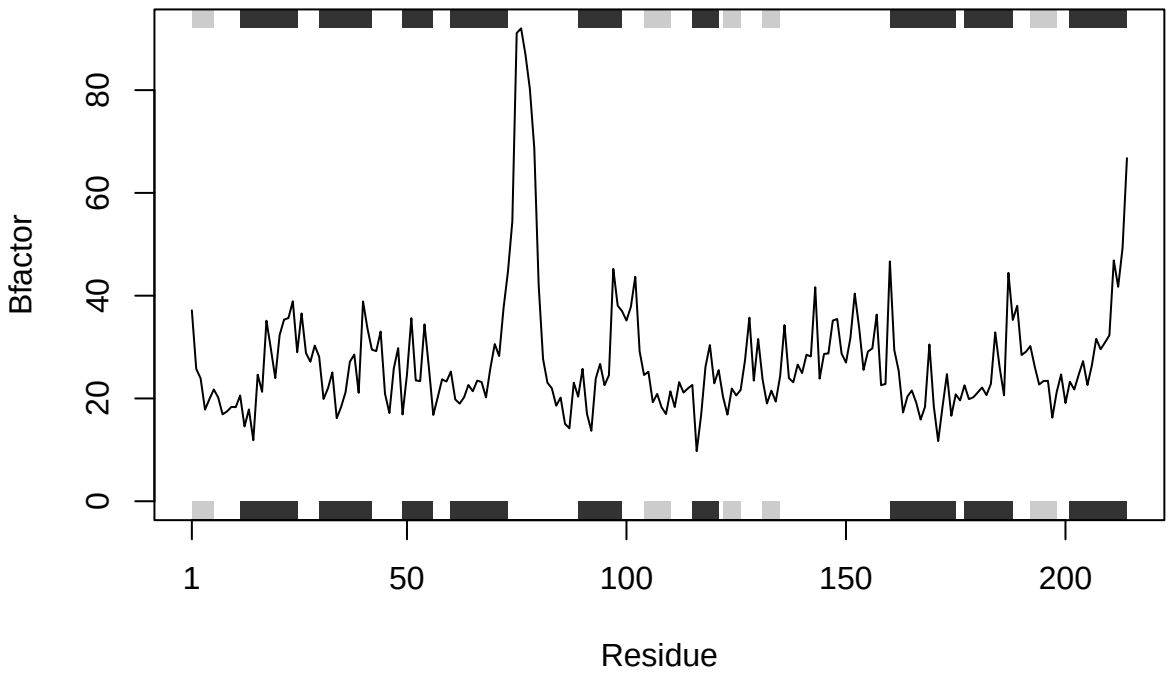
Q6. How would you generalize the original code above to work with any set of input protein structures?

```
# load library
library(bio3d)
# input is a list of 3 proteins
input <- list("4AKE", "1AKE", "1E4Y")
# function that takes an input (list) and iterates through elements of the list to create plots of each
plots <- function(input) {
  # for each element in list
  for (x in input) {
    # read the pdb file
    s <- read.pdb(x)
    # create a smaller pdb object w subset of atoms
    s.chainA <- trim.pdb(s, chain="A", elety="CA")
    s.b <- s.chainA$atom$b
    # plot
    plotb3(s.b, sse=s.chainA, typ="l", ylab="Bfactor")
  }
}
plots(input)
```

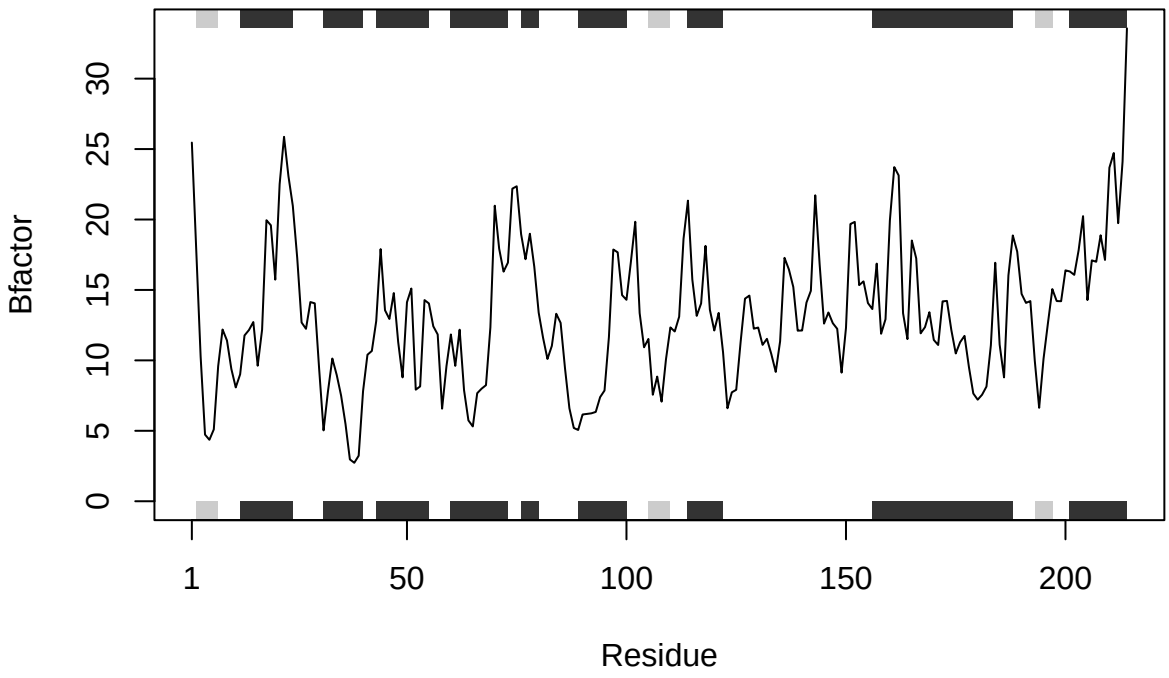
```
##   Note: Accessing on-line PDB file
```




```
##   Note: Accessing on-line PDB file
##    PDB has ALT records, taking A only, rm.alt=TRUE
```




```
##   Note: Accessing on-line PDB file
```


Bfactor
0
5
10
15
20
25
30
1
50
100
150
200
Residue