class06_hw

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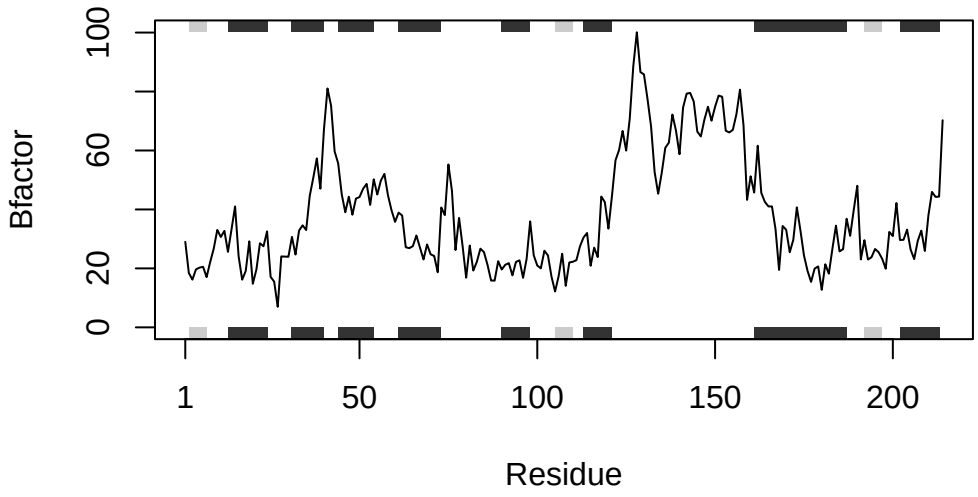
> Q6 How would you generalize the original code above to work with any set of input protein structures?

To do this question I will make a function using some of the tools found in the `bio3d` library

```
#import tools from the bio3d library
library(bio3d)

#Creates the function named 'ploot', with argument 'input'
Ploot <- function(input) {

  #uses read.pdb on the input and stores the protein information in 'S0"
  S0 <- read.pdb(input)

  #Creates a smaller PDB object with a subset of atoms
  S0.chainA <- trim.pdb(S0, chain="A", elety="CA")

  #Stores specific column of values within S0.b to be graphed
  S0.b <- S0.chainA$atom$b

  #Plots the data, outputs a graph comparing residue (x) and Bfactor (Y)
  plotb3(S0.b, sse=S0.chainA, typ="l", ylab="Bfactor")
}

#Calls the function with `Ploot()`,
#The argument is the protein accession number for your protein of interest
#Protein 4AKE has been used as an example
Ploot("4AKE")
```

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


Bfactor
0
20
60
100
1
50
100
150
200
Residue