Homework 6

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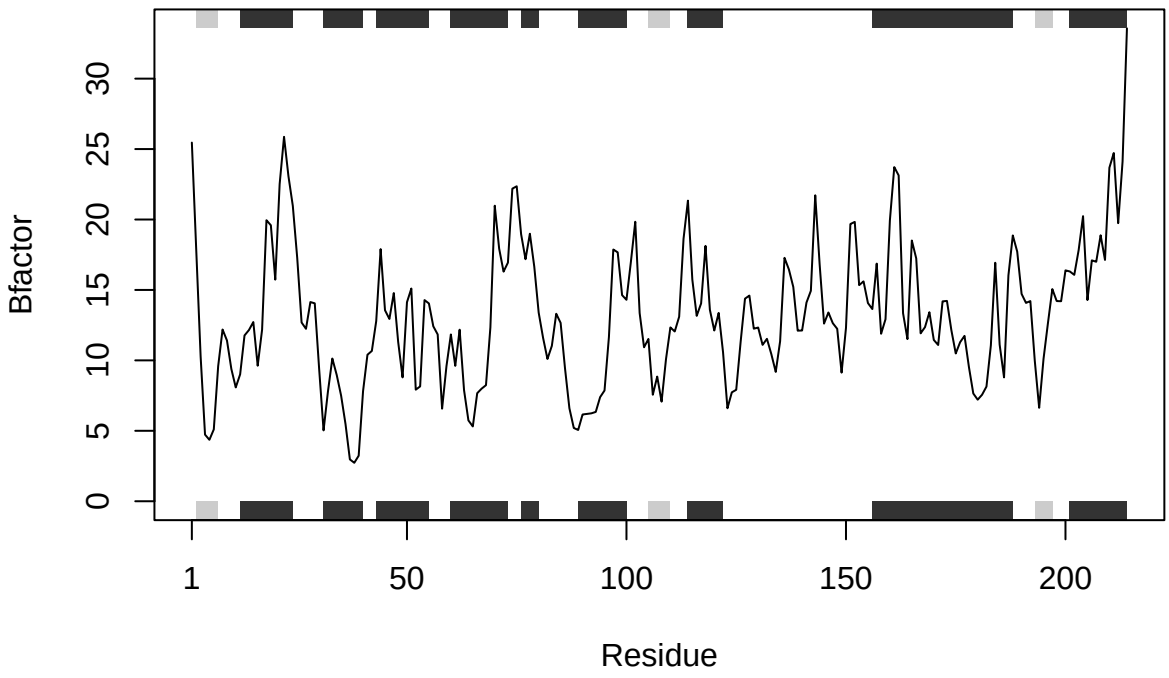
#Question 6:

```
#Load bio3d

library(bio3d)

#Create code that works with any input of protein structures

protein_plot <- function(pdb_file, chain_id = "A") {

  # Read.pdb will provide information of the PDB file used to read in the function
  protein <- read.pdb(pdb_file)

  #Trim.pdb will extract subset from protein such as the specifc chains
  protein_chain <- trim.pdb(protein, chain = chain_id, elety = "CA")

  #Make b_factors into a vector that has B_factor values for each atom in the specified chain
  b_factors <- protein_chain$atom$b

  #Generate line plot with b_factors vector with Bfactor as the y-axis
  plotb3(b_factors, sse = protein_chain, typ = "l", ylab = "Bfactor")
}
```

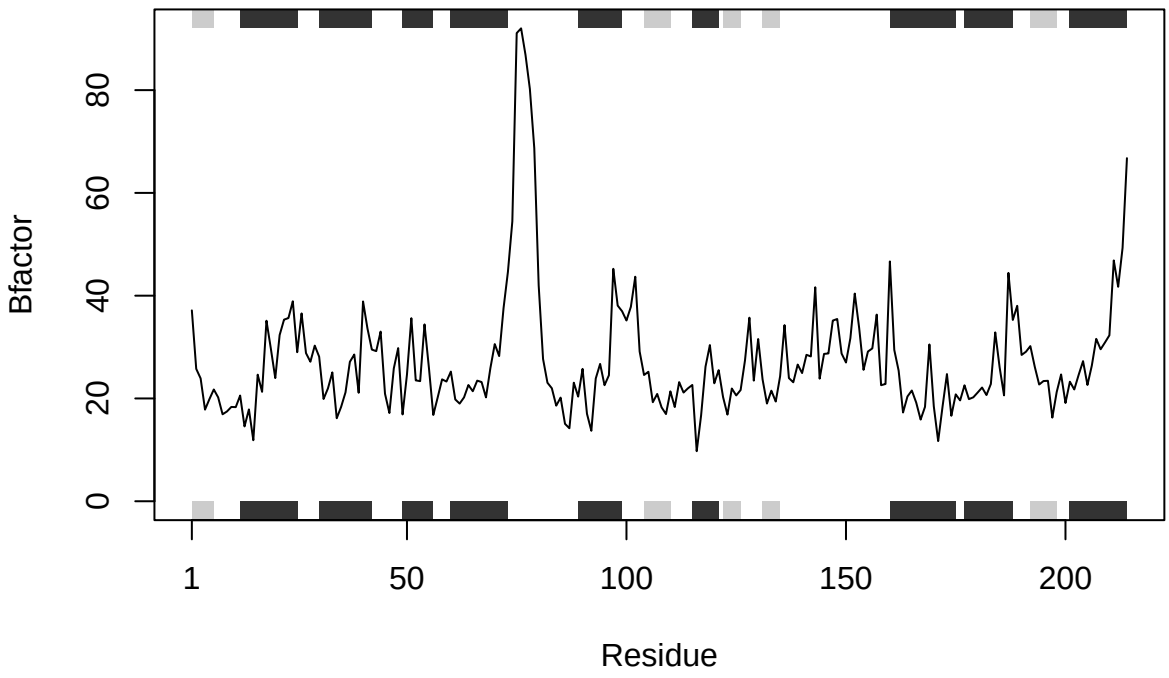
```
#Test code with different proteins
protein_plot("1E4Y")
```

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



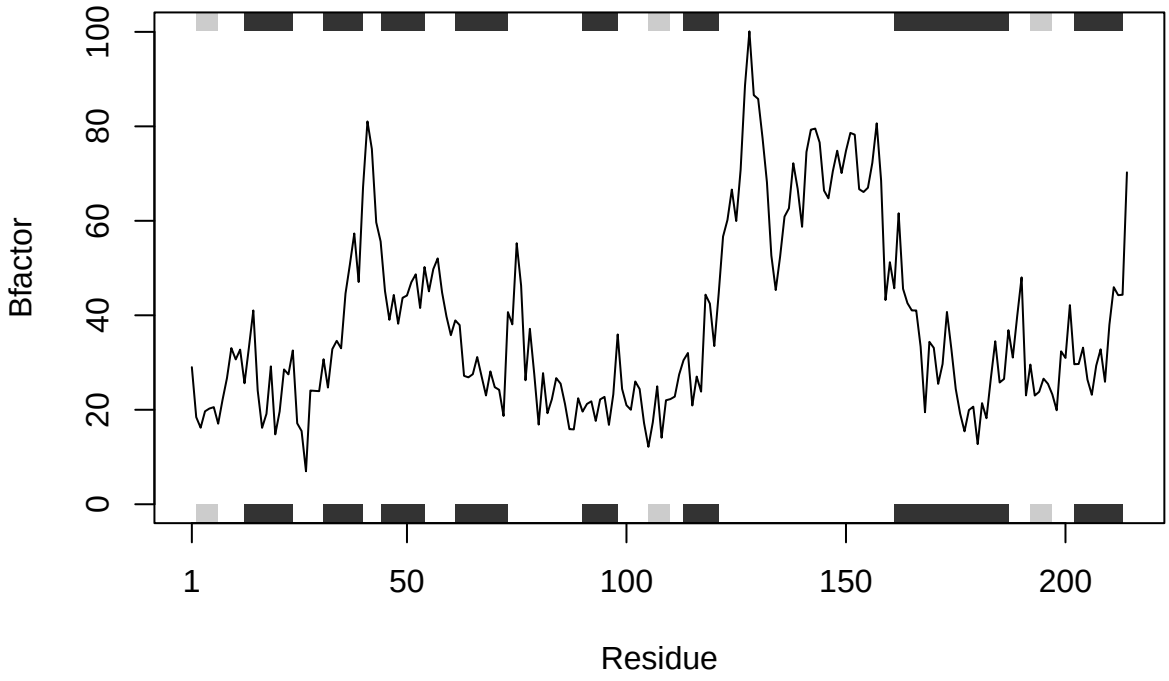

```
#Test code with different proteins
protein_plot("1AKE")
```

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




```
#Test code with different proteins
protein_plot("4AKE")
```

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


Bfactor
0
20
40
60
80
100
1
50
100
150
200
Residue