# Lecture 6 Lab Homework

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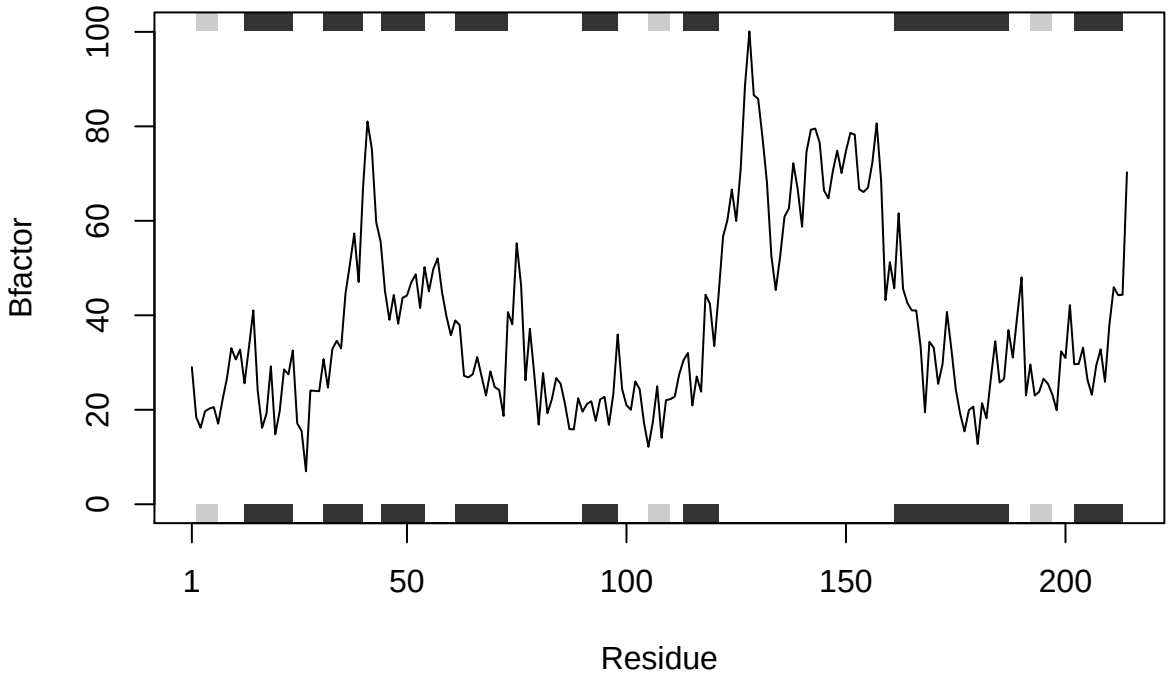
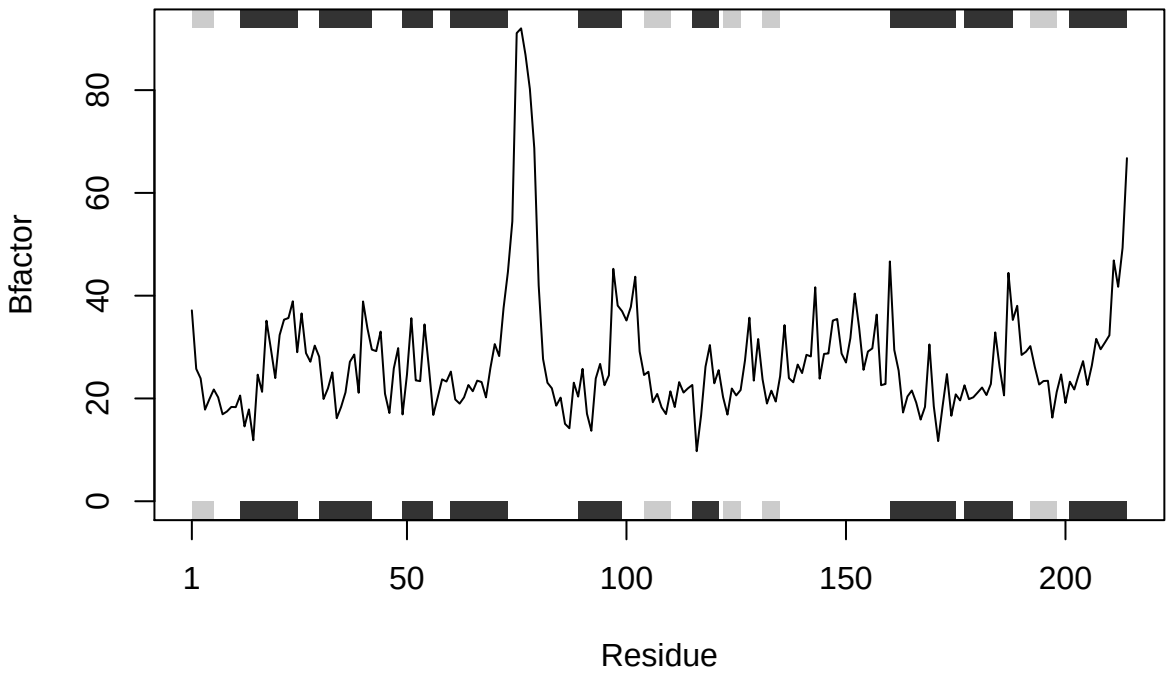
```
#Load bio3d package into RStudio
library(bio3d)

#Create function that can be applied to any protein in PDB
#input for the function is protein identifier name
#output for function is a line plot for protein atomic chain data
protein_plot <- function(x){

  #read pdb file of input protein from protein database
  protein_file <- read.pdb(x)

  #produce a smaller pdb file with subset of specified atom chain
  subset_chain <- trim.pdb(protein_file, chain="A", elety="CA")

  #Assign specified atom values in subset chain to variable
  atom_values <- subset_chain$atom$b

  #Plot the specified atom values in line graph
  plotb3(atom_values, sse=subset_chain, typ="l", ylab="Bfactor")
}

#examples for protein_plot() function
protein_plot("4AKE") #kinase with drug
```

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



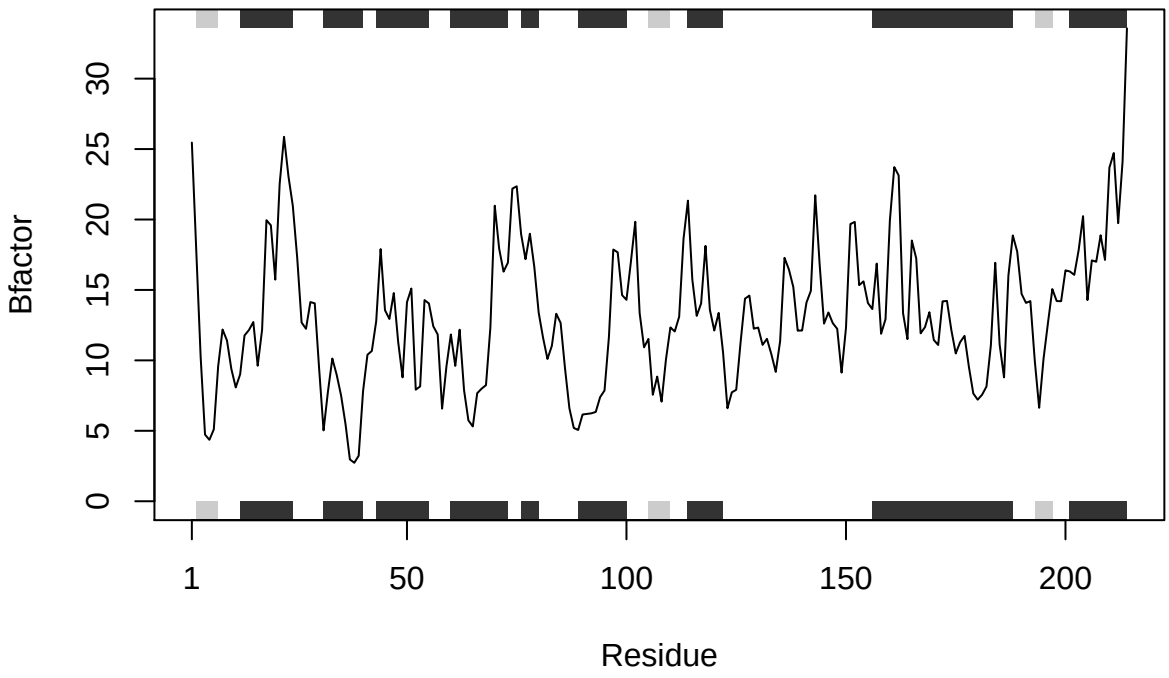

```
protein_plot("1AKE") #kinase with no drug
```

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




```
protein_plot("1E4Y") #kinase with drug
```

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


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