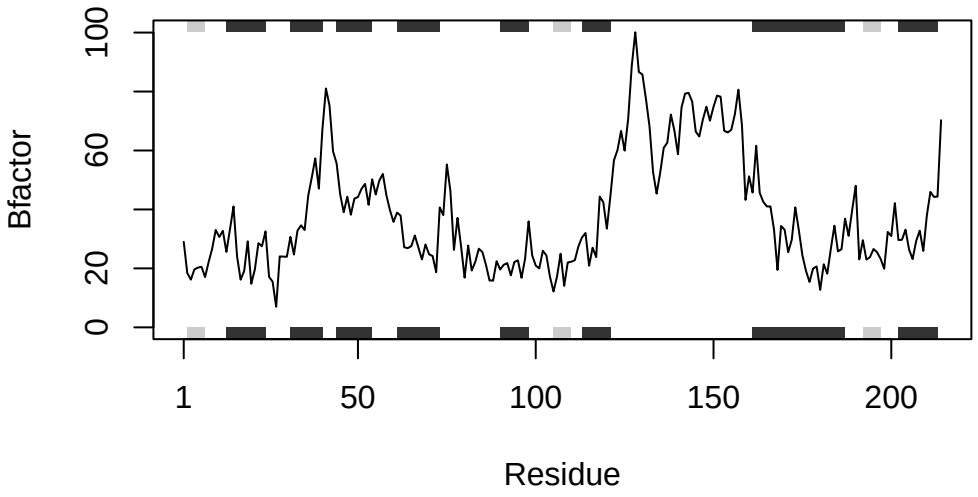
class06homework

hc <- hclust(dist(rbind(s1.b, s2.b, s3.b))) plot(hc)

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

```
library(bio3d)

#input is "p", standing for any protein you are analyzing
#function takes protein p and searches for it in dataset-> finds residue and vfactor value
#output: creates a plot showing Bfactor interactions with residue/amino acid
my_function <- function(p){
  s<-read.pdb(p)

  s.chainA <- trim.pdb(s, chain="A", elety="CA")
  s.b<-s.chainA$atom$b

  plotb3(s.b,sse=s.chainA, typ="l", ylab="Bfactor")

}

my_function("4AKE")
```

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


Bfactor
0
20
60
100
1
50
100
150
200
Residue