Homework 6 Q6

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

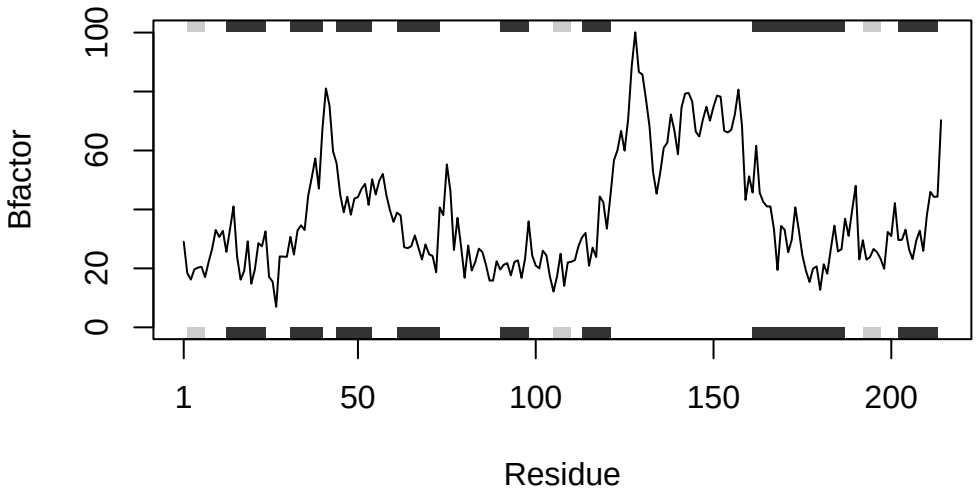
Below is the `analysis` function, which takes in a single protein string as input and outputs a plot of the protein's Bfactor in respect to its residue amount. To use the `analysis` function, pass in a protein name (formatted as "PROTEIN") to the analysis function.

```
# How to use: analysis("PROTEIN")
analysis <- function(protein) {
  library(bio3d)
  s <- read.pdb(protein)
  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")
}
```

Here are some example uses of the `analysis` function.

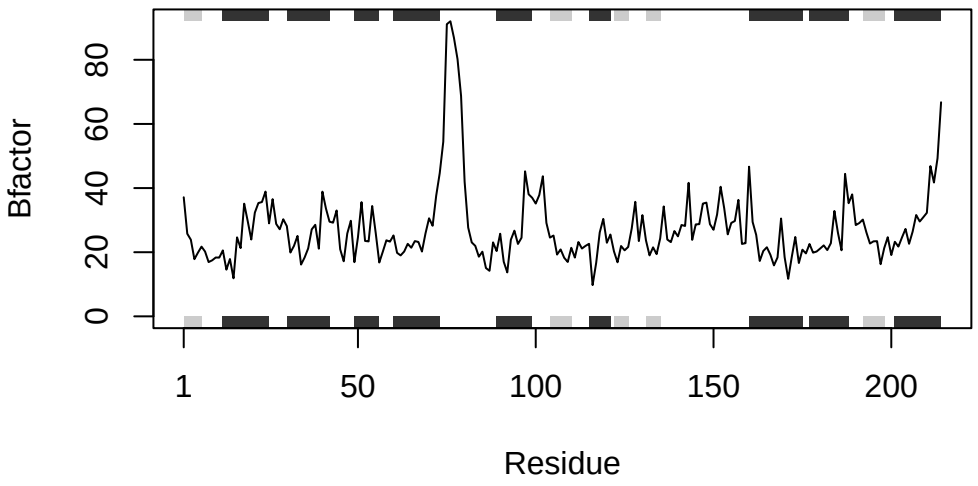
```
# Example use of analysis function
protein <- "4AKE"
analysis(protein)
```

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



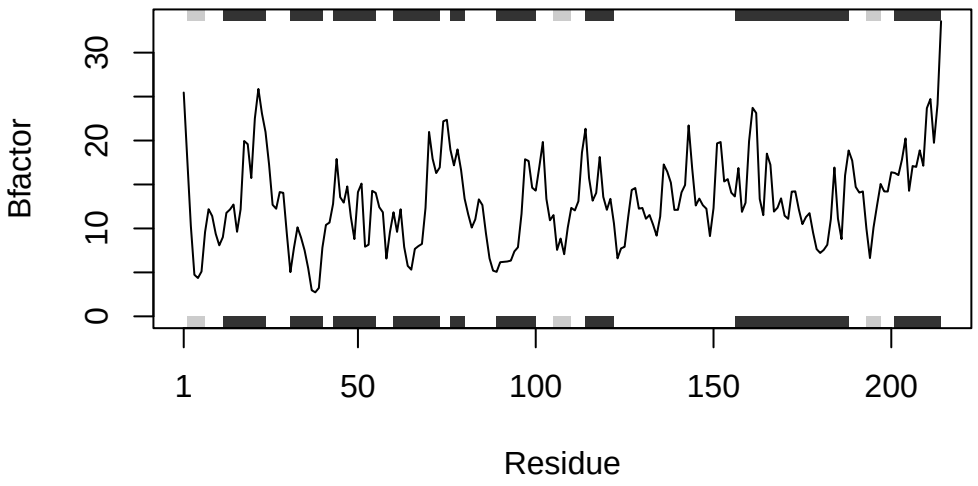

```
# Example use of analysis function
protein <- "1AKE"
analysis(protein)
```

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




```
protein <- "1E4Y"
analysis(protein)
```

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


Bfactor
0
10
20
30
1
50
100
150
200
Residue