

Class06 Homework

Dora Deng (A17445600)

Can you improve this analysis code?

Explanation for this function:

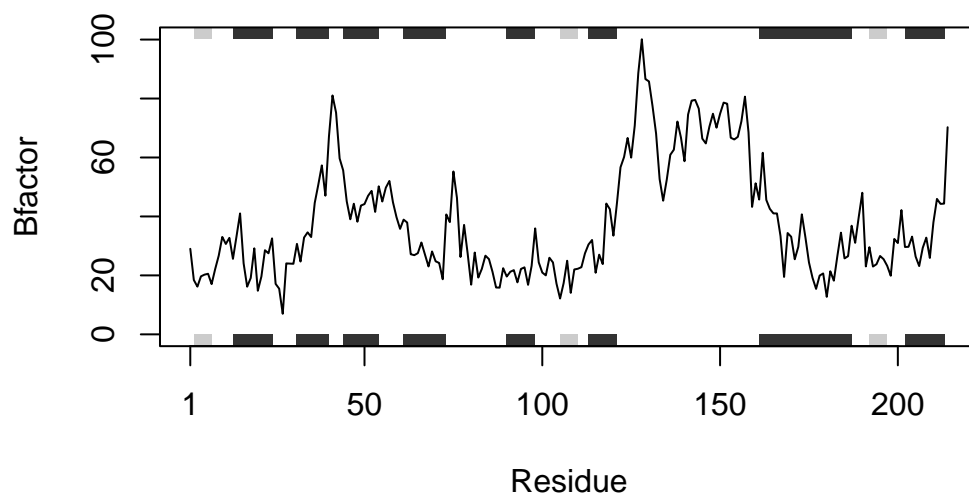
This function that I created take the input string, which is the protein code, and it reads the PDB file of the input string. Then, we use the trim.pdb function to create a smaller PDB object. After that, it will take the output of s.chainA and accessing the atom column and b element. Finally, the function creates a plot of the output from s.b and label x as Bfactor and y as residue.

```
library(bio3d)

analysis_fun <- function(string){
  s.name <- read.pdb(string)
  s.chainA <- trim.pdb(s.name, chain="A", elety="CA")
  s.b <- s.chainA$atom$b
  plotb3(s.b, sse=s.chainA, typ="l", ylab="Bfactor")
}

analysis_fun("4AKE")
```

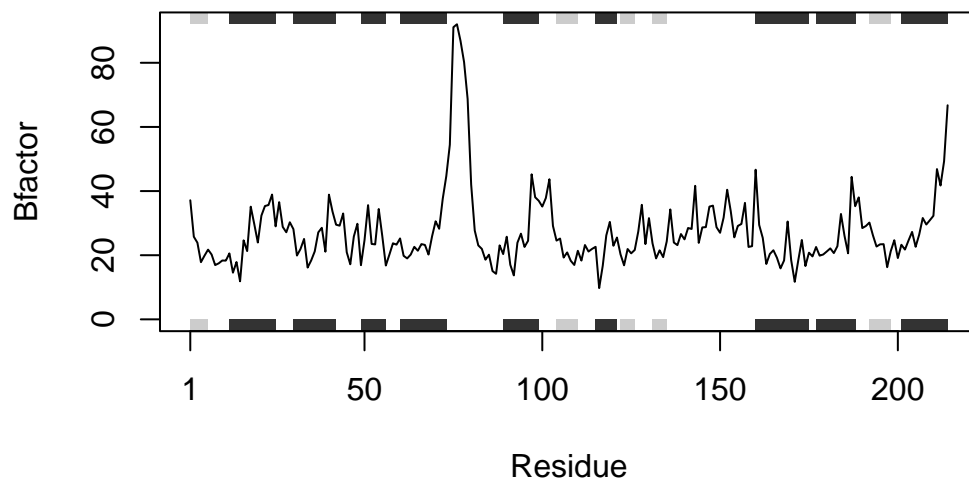
Note: Accessing on-line PDB file



```
analysis_fun("1AKE")
```

Note: Accessing on-line PDB file

PDB has ALT records, taking A only, rm.alt=TRUE



```
analysis_fun("1E4Y")
```

Note: Accessing on-line PDB file

