Question 6

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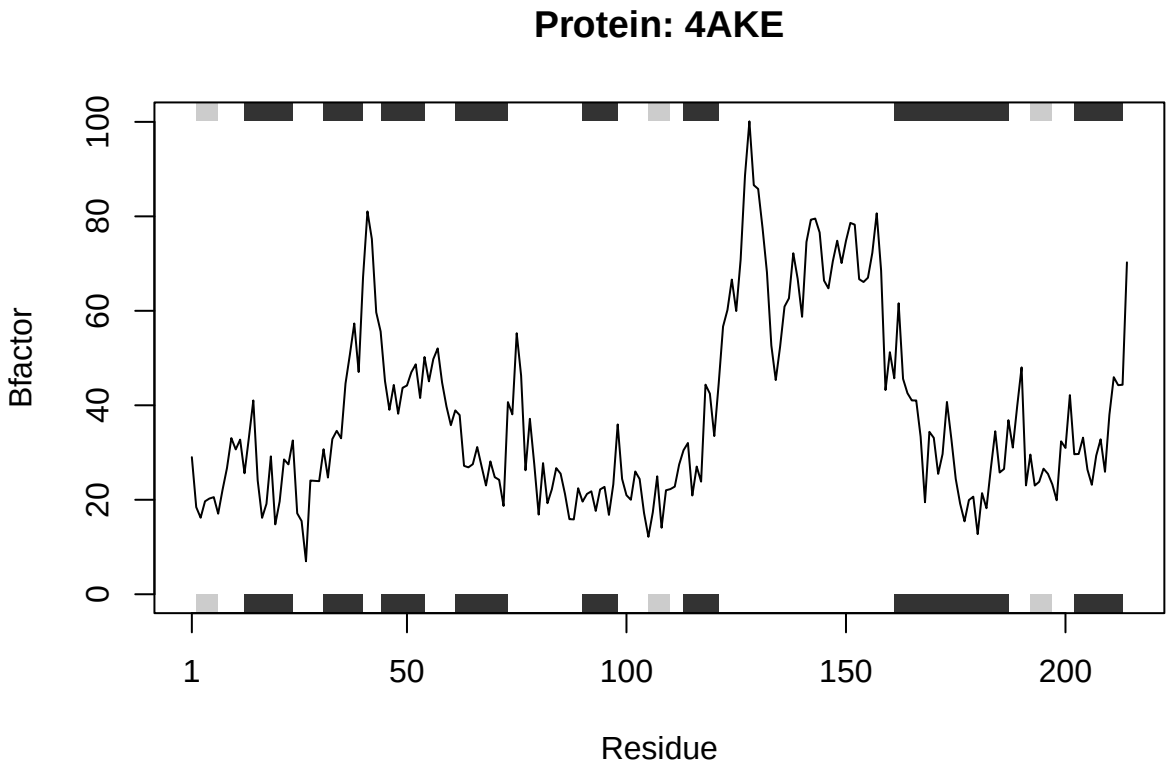
Q6. How would you generalize the original code above to work with any set of input protein structures?

```
library(bio3d)
```

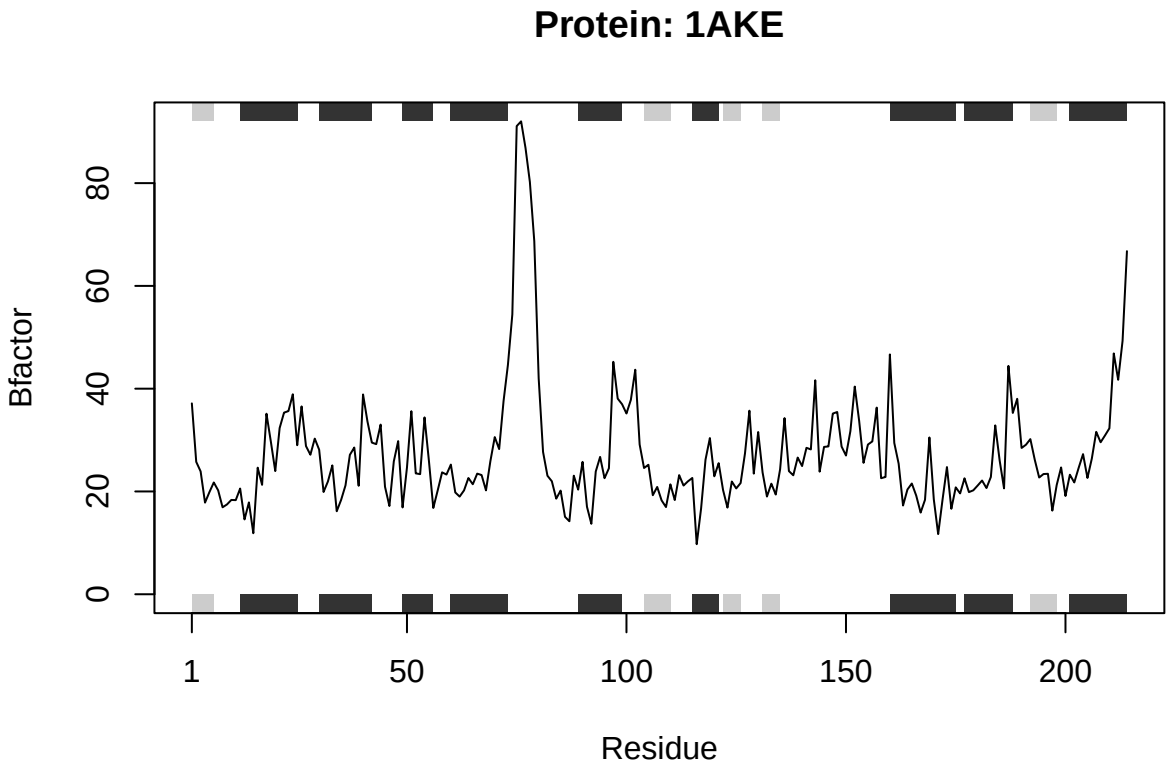
```
   #my function
 analyze_protein_interactions <- function(pdb_files) {
  #ensures "bio3d" package is loaded
   require(bio3d)
  #apply specified function - function(file) - to each element of the input
 #list - pdb_files, want to read each PDB file separately and apply the function to each specific file
 lapply(pdb_files, function(file) {
  #first returns class of protein structure data in PDB format (three dimentional structures)
    pdb <- read.pdb(file)
  #trim protein data to only include chain A and alpha carbon atoms
    pdb_trimmed <- trim.pdb(pdb, chain="A", elety="CA")
  #extract b-factor values
    b_factors <- pdb_trimmed$atom$b
  #output of function, list of plots
    plotb3(b_factors, sse=pdb_trimmed, typ="l", ylab="Bfactor", main=paste("Protein:", file))
  })
}
```

```
# Example usage
 pdb_files <- c("4AKE", "1AKE", "1E4Y")
analyze_protein_interactions(pdb_files)
```

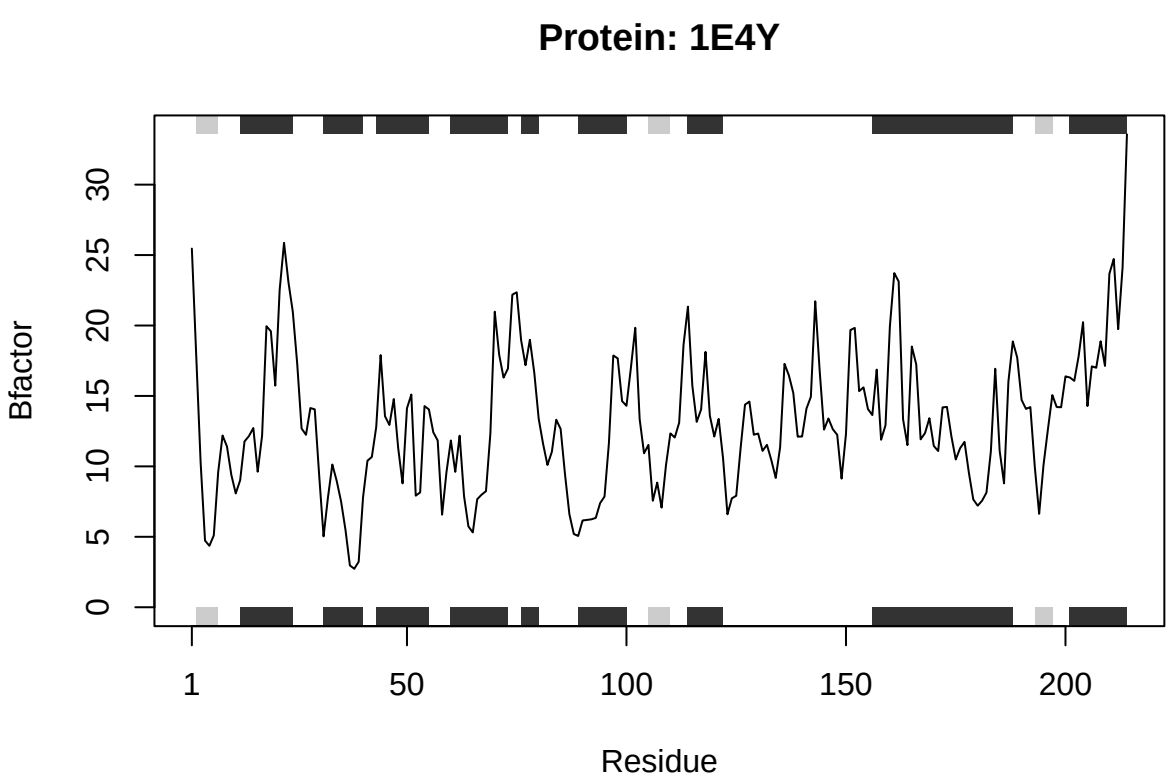
```
##   Note: Accessing on-line PDB file
```




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




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




```
## [[1]]
## NULL
##
## [[2]]
## NULL
##
## [[3]]
## NULL
```