

class06Homework

Hugh Redford

A17067426

Improving the Analysis Code

```
# install.packages("bio3d")
library(bio3d)

# Input "x" is a PDB Entry ID # for a specific protein
proteinPlot <- function(x) {
  temp <- read.pdb(x)
  temp.chainA <- trim.pdb(temp, chain = "A", eley = "CA")
  temp.b <- temp.chainA$atom$b
  plotb3(temp.b, sse = temp.chainA, typ = "l", ylab = "Bfactor")
}
```

Function Description:

The function 'proteinPlot' accepts a PDB entry ID as input, processes the corresponding protein structure, and generates a plot that compares the B-factor values and the corresponding residues of the protein.