class06\_Worsheet\_Hw\_.proj

# Install R package "bio3d" to easily visualize data and analyze through plots  
install.packages("bio3d", repos = "http://cran.us.r-project.org")

## Installing package into 'C:/Users/kanew/Documents/R/win-library/3.6'  
## (as 'lib' is unspecified)

## package 'bio3d' successfully unpacked and MD5 sums checked  
##   
## The downloaded binary packages are in  
## C:\Users\kanew\AppData\Local\Temp\RtmpO6ymFg\downloaded\_packages

# Load the package into the console so that it can be used  
library(bio3d)  
# Create function and access data   
pdb\_data <-function(x) {  
 p\_struct <- read.pdb(x)  
   
# Extract desired data on protein strucutre read and organized by read.pdb(x)  
 p\_struct.chain <- trim.pdb(p\_struct,chain="A",elety="CA")  
   
# Isolate data on atomic information  
 p\_struct.b <- p\_struct.chain$atom$b  
   
# Plot the two variables to determine the protein structure's stability  
 plot.bio3d(p\_struct.b,sse <- p\_struct.chain,type = "l",ylab="Bfactor", sse = sse)  
   
  
}  
  
# Example of functionality  
pdb\_data("4AKE")

## Note: Accessing on-line PDB file

