

# lab 6 homework

Nicholas Pacia

prerequisites for running example

```
library("bio3d")
```

creating function that accepts a string for the filename, will take a set of data from the file, and output a plot of the selected data.

```
plotchain <- function(name = "file"){  
  data <- read.pdb(name)  
  data_chain <- trim.pdb(data, chain = "A", elety = "CA")  
  data_new <- data_chain$atom$b  
  plotb3(data_new, sse = data_chain, typ = "l", ylab = "Bfactor")  
}
```

running example

```
plotchain("4AKE")
```

Note: Accessing on-line PDB file

