Lecture 6 hw: Improving R Code

```r
# s1.chainA <- trim.pdb(s1, chain="A", elety="CA")
# s1.b <- s1.chainA$atom$b
# plotb3(s1.b, sse=s1.chainA, typ="l", ylab="Bfactor")

hw <- function(input) {
  # this function takes any input kinase we choose from the "bio3d" package, trims it, sel
  require(bio3d)
  # import kinase
  x <- read.pdb(input)

  #trim.pdb trims input x
  x.a <- trim.pdb(x, chain="A", elety="CA")

  #selects atom b from x.a
  x.b <- x.a$atom$b

  #plots x.b
  plotb3(x.b, sse=x.a, typ="l", ylab="Bfactor")
}
hw("4AKE")
```

```
Loading required package: bio3d
```

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