

HW06

Danika

```
# Can you improve this analysis code?  
library(bio3d)  
s1 <- read.pdb("4AKE") # kinase with drug
```

Note: Accessing on-line PDB file

```
s2 <- read.pdb("1AKE") # kinase no drug
```

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

```
s3 <- read.pdb("1E4Y") # kinase with drug
```

Note: Accessing on-line PDB file

```
# This is the input code  
x <- "4AKE"  
a <- read.pdb(x)
```

Note: Accessing on-line PDB file

```
Warning in get.pdb(file, path = tempdir(), verbose =  
FALSE): /var/folders/x9/r3h9zqcq9533g921wcjbjvh480000gn/T//RtmpAKXRT0/4AKE.pdb  
exists. Skipping download
```

```

s1.chainA <- trim.pdb(s1, chain="A", elety="CA")
s2.chainA <- trim.pdb(s2, chain="A", elety="CA")
s3.chainA <- trim.pdb(s3, chain="A", elety="CA")

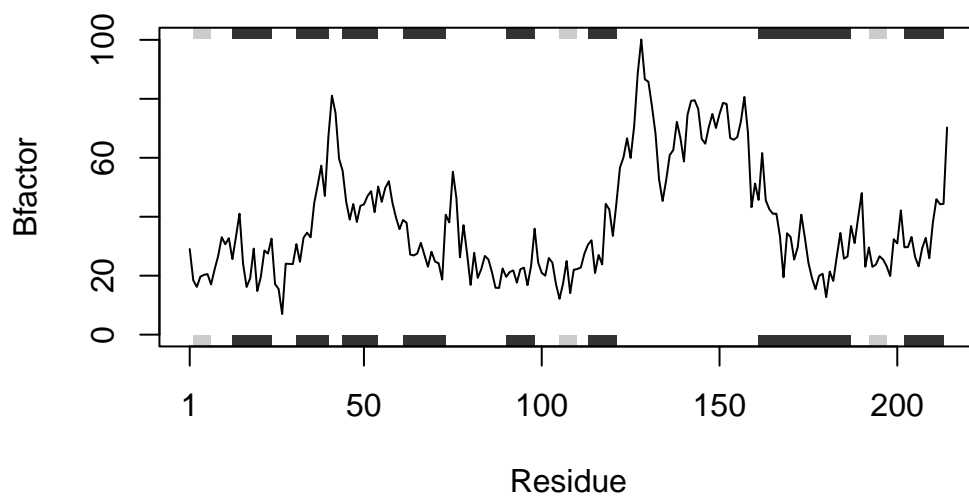
a.chainA <- trim.pdb(a, chain="A", elety="CA")

s1.b <- s1.chainA$atom$b
s2.b <- s2.chainA$atom$b
s3.b <- s3.chainA$atom$b

a.b <- a.chainA$atom$b

plotb3(s1.b, sse=s1.chainA, typ="l", ylab="Bfactor")

```



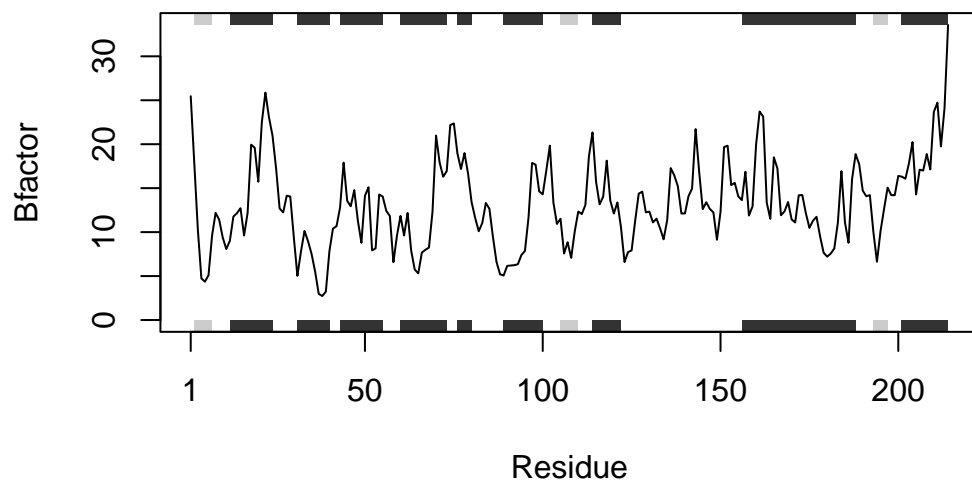
```

plotb3(s2.b, sse=s2.chainA, typ="l", ylab="Bfactor")

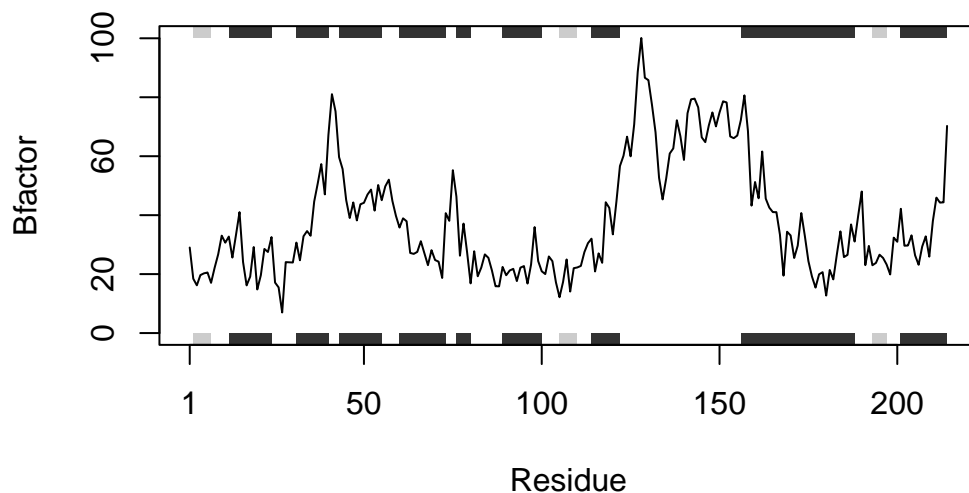
```



```
plotb3(s3.b, sse=s3.chainA, typ="l", ylab="Bfactor")
```



```
plotb3(a.b, sse=s3.chainA, typ="l", ylab="Bfactor")
```



Should read any protein PDB data and outputs a plot

```
library(bio3d)
x <- "4AKE"

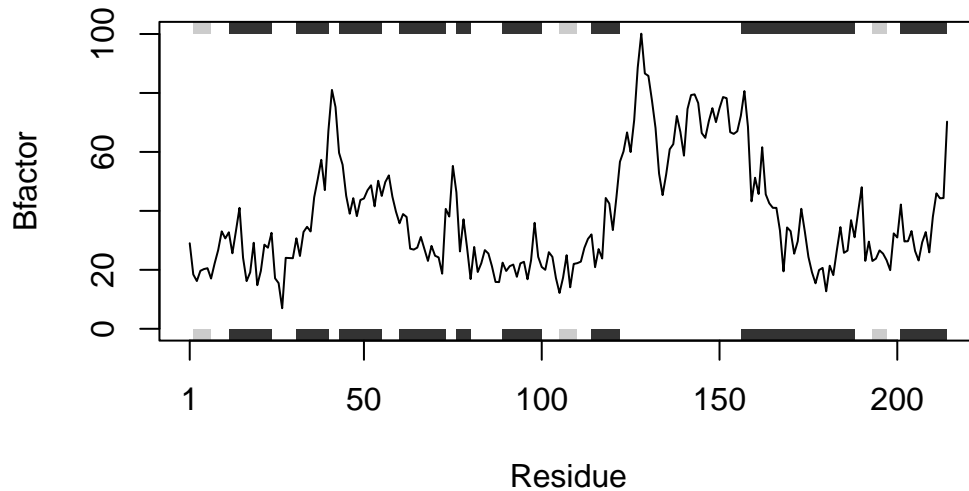
newfunction <- function(x){
  a <- read.pdb(x)
  a.chainA <- trim.pdb(a, chain="A", elety="CA")
  a.b <- a.chainA$atom$b
  plotb3(a.b, sse=s3.chainA, typ="l", ylab="Bfactor")
}

newfunction(x)
```

Note: Accessing on-line PDB file

Warning in get.pdb(file, path = tempdir(), verbose =

```
FALSE): /var/folders/x9/r3h9zcq9533g921wcjbjvh480000gn/T//RtmpAKXRT0/4AKE.pdb  
exists. Skipping download
```

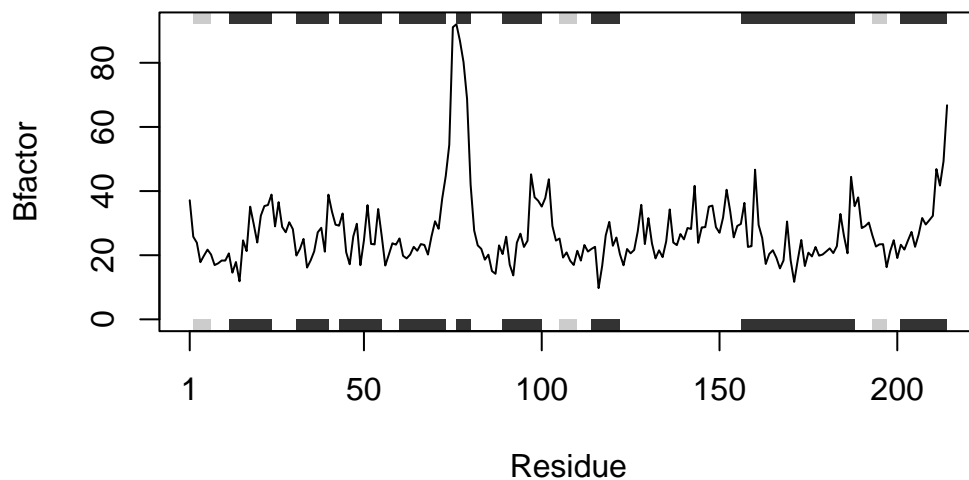


```
newfunction("1AKE")
```

Note: Accessing on-line PDB file

```
Warning in get.pdb(file, path = tempdir(), verbose =  
FALSE): /var/folders/x9/r3h9zcq9533g921wcjbjvh480000gn/T//RtmpAKXRT0/1AKE.pdb  
exists. Skipping download
```

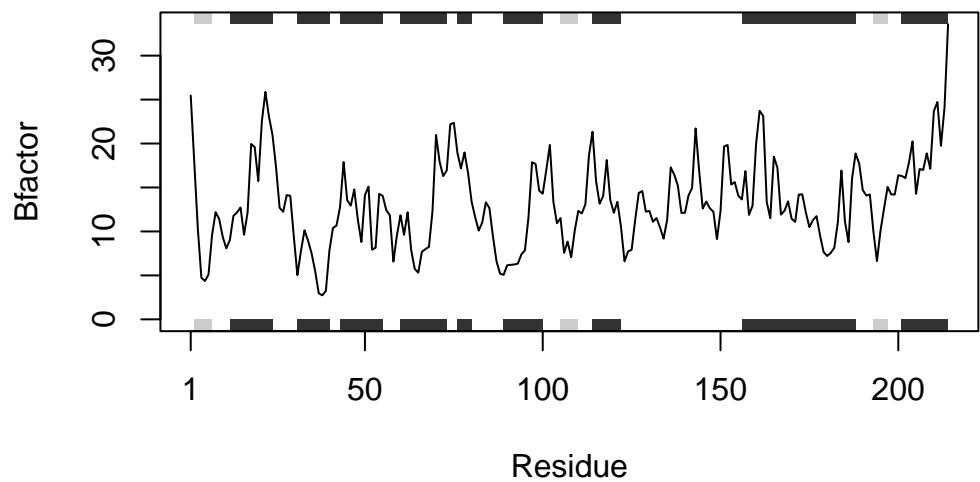
PDB has ALT records, taking A only, rm.alt=TRUE



```
newfunction("1E4Y")
```

Note: Accessing on-line PDB file

```
Warning in get.pdb(file, path = tempdir(), verbose =  
FALSE): /var/folders/x9/r3h9zcq9533g921wcjbjvh480000gn/T//RtmpAKXRT0/1E4Y.pdb  
exists. Skipping download
```



The graphs are the output