Class06HW

Tim

```r
library(bio3d)
s1 <- read.pdb("4AKE") # kinase with drug
```

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

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

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

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

```
  Note: Accessing on-line PDB file
```
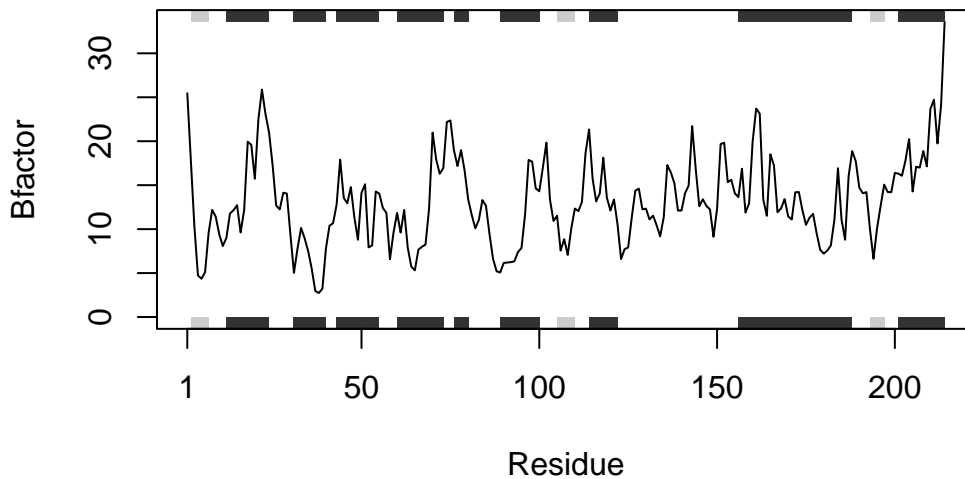
```r
s1.chainA <- trim.pdb(s1, chain="A", elety="CA")
s2.chainA <- trim.pdb(s2, chain="A", elety="CA")
s3.chainA <- trim.pdb(s3, chain="A", elety="CA")
s1.b <- s1.chainA$atom$b
s2.b <- s2.chainA$atom$b
s3.b <- s3.chainA$atom$b
plotb3(s1.b, sse=s1.chainA, typ="l", ylab="Bfactor")
```

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


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



```
generate_pdb <- function(Tim) {
  t <- read.pdb(Tim)
  t.chainA <- trim.pdb(t, chain="A", elety="CA")
t.b <- t.chainA$atom$b
plotb3(t.b, sse=t.chainA, typ="l", ylab="Bfactor")}
```

```
#example
generate_pdb("4AKE")
```

  Note: Accessing on-line PDB file

Warning in get.pdb(file, path = tempdir(), verbose = FALSE):
C:\Users\timha\AppData\Local\Temp\RtmpGm6BBG/4AKE.pdb exists. Skipping download