HW6 Arman Farahani A17497672

Quarto

Quarto enables you to weave together content and executable code into a finished document. To learn more about Quarto see https://quarto.org.

```r
#The data library is loaded
library(bio3d)

#This variable is assigned a reading and matching function
generalize <- function(pdb_data) {

  #The variable is made to read the PDB data files
  pdbread <- read.pdb(pdb_data)

  #This variable trims the data to be within chain A and CA
  chaintrim <- trim.pdb(pdbread, chain="A", elety="CA")

  #The B-factor is taken from chain A
  factorb <- chaintrim$atom$b

  #The B-factors are plotted
  plotb3(factorb, typ="l", ylab="B-factor", main=paste("B-factor for", pdb_data))
}

#The IDs of the pdb data are compiled into this variable
sets <- c("4AKE", "1AKE", "1E4Y")

#Create a plot for each data point
for(pdb_data in sets) {
  generalize(pdb_data)
}
```
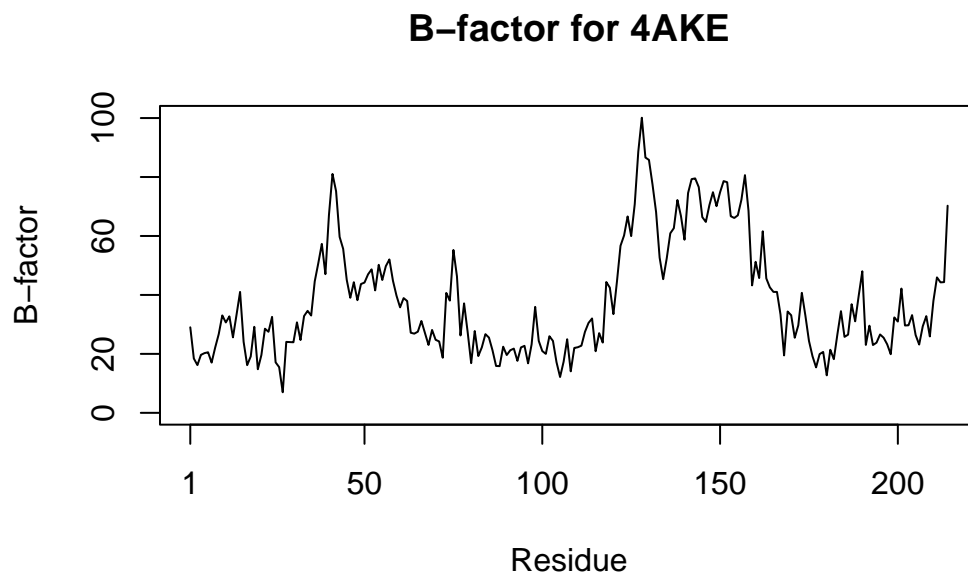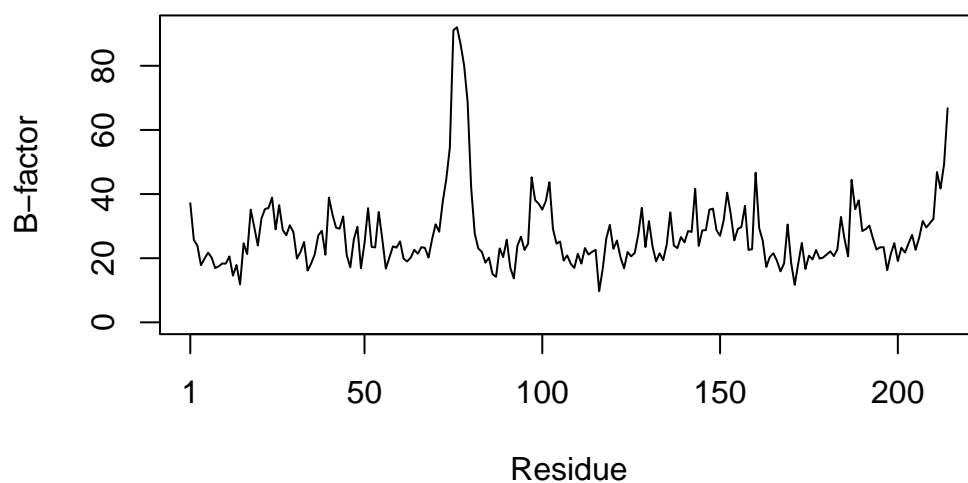
Note: Accessing on-line PDB file

B-factor for 4AKE
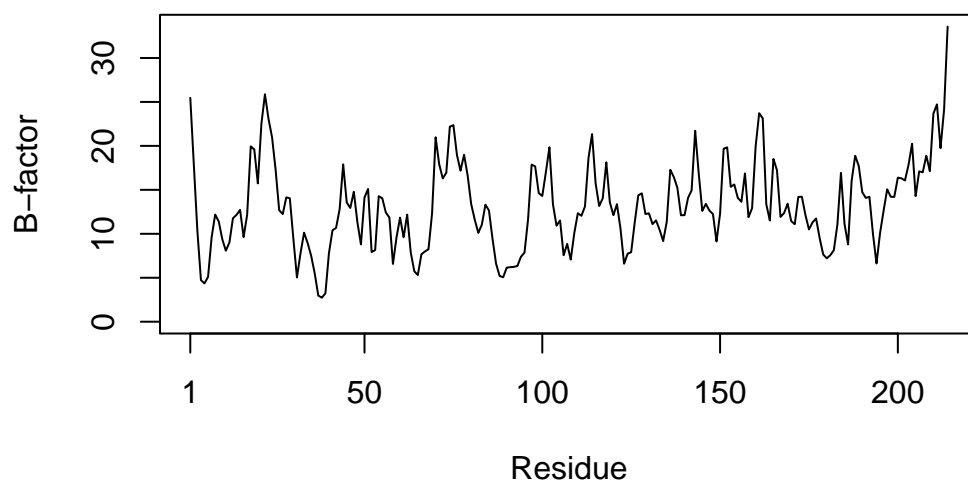

Note: Accessing on-line PDB file
 PDB has ALT records, taking A only, rm.alt=TRUE

B−factor for 1AKE

Note: Accessing on-line PDB file

B−factor for 1E4Y

Running Code

When you click the **Render** button a document will be generated that includes both content and the output of embedded code. You can embed code like this:

```
1 + 1
```

```
[1] 2
```

You can add options to executable code like this

```
[1] 4
```

The `echo: false` option disables the printing of code (only output is displayed).