Class 06 Function Homework

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What is the function input? The function input is a character string that specifies the PDB ID of a specific protein structure.

What does the function do and how do we use it? The function reads a protein structure, trims the structure to chain A and alpha carbon atoms, extracts the B-factor values, and plots the B-factor along the protein sequence. It can be used to visualize B-factor variation along the protein sequence

What is the function output? The function output is a line plot of B-factor values for alpha carbon atons in chain A of the protein.

```
library(bio3d)
```

```
# Name the function
protein_analysis <- function(pdb_id) {

  # Read the protein structure
  pdb <- read.pdb(pdb_id)

  # Trim to specified chain A and alpha carbon atom
  pdb_chain <- trim.pdb(pdb, chain = "A", elety = "CA")

  # Extract B-factor
  b_factors <- pdb_chain$atom$b

  # Plot the B-factor
```

```
    plotb3(b_factors, sse=pdb_chain, typ="l", ylab="Bfactor")

}
```

```
protein_analysis("4AKE")
```

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