HW6

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This function takes pdb files (files from the protien data bank that contain information about the 3D structure of protiens) and renders a plot of B-factor values

```r
# Load the bio3d library
library(bio3d)

# Here is the function that will turn pdb protein structure files into B-factor plots
  Analyze_proteins <- function(pdb_file) {

# Read the PDB file. The pdb file is the input for this function.
  pdb <- read.pdb(pdb_file)

# Trim to the specified chain
  pdb.chainA <- trim.pdb(pdb, chain = "A", elety = "CA")

# Identify B-factors
  pdb.b <- pdb.chainA$atom$b

# Plot B-factors. This is the output of the function
  plotb3(pdb.b, sse=pdb.chainA, typ="l", ylab="Bfactor")

}
```

```r
# Test out the function on a pdb file
  Analyze_proteins("4AKE")
```

Note: Accessing on-line PDB file