Class 10 Structural Bioinformatics pt 1 BIMM 143

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The PDB Database

Here we examine the size and compostion of the main database of biomolecular structures - the PDB.

Get a CSV file from the PDB databse and read it into R.

```
pdbstats <- read.csv("pdb_stats.csv", row.names=1)
head(pdbstats)
```

```
                          X.ray     EM    NMR Multiple.methods Neutron Other
Protein (only)          161,663 12,592 12,337              200      74    32
Protein/Oligosaccharide   9,348  2,167     34                8       2     0
Protein/NA                8,404  3,924    286                7       0     0
Nucleic acid (only)       2,758    125  1,477               14       3     1
Other                       164      9     33                0       0     0
Oligosaccharide (only)       11      0      6                1       0     4
                          Total
Protein (only)          186,898
Protein/Oligosaccharide  11,559
Protein/NA               12,621
Nucleic acid (only)       4,378
Other                       206
Oligosaccharide (only)       22
```

> Q1: What percentage of structures in the PDB are solved by X-Ray and Electron Microscopy.

My pdbstats data frame has numbers with commas in them. This may cause us problems. Let's see:

```
pdbstats$X.ray
```

```
[1] "161,663" "9,348"   "8,404"   "2,758"   "164"     "11"
```

```
x <- "2.22"
as.numeric(x) +1
```

```
[1] 3.22
```

WE are going to use a function called **`gsub()`** which stands for global substitution. This is going to replace all the commas with an empty space in the list.

```
as.numeric(gsub(",","",pdbstats$X.ray))
```

```
[1] 161663   9348   8404   2758    164     11
```

I can turn this snipet into a function that I can use for every column in the table.

```
commasum <- function(x) {
  sum(as.numeric(gsub(",","",x)))
}
commasum(pdbstats$X.ray)
```

```
[1] 182348
```

Now let's try to *APPLY* this to all of the columns.

```
totals <- apply(pdbstats, 2, commasum)
totals
```

```
           X.ray               EM              NMR Multiple.methods 
          182348            18817            14173              230 
         Neutron            Other            Total 
              79               37           215684 
```

Now to answer the question: From the table below, the answer is 8.72 is solved by EM.

```
round((totals / totals["Total"]) * 100,2)
```

```
          X.ray                EM               NMR Multiple.methods 
          84.54              8.72              6.57              0.11 
        Neutron             Other             Total 
           0.04              0.02            100.00 
```

> Q2: What proportion of structures in the PDB are protein?

```
round(commasum(pdbstats[1,7])/ totals["Total"] * 100, 2)
```

```
Total 
86.65 
```

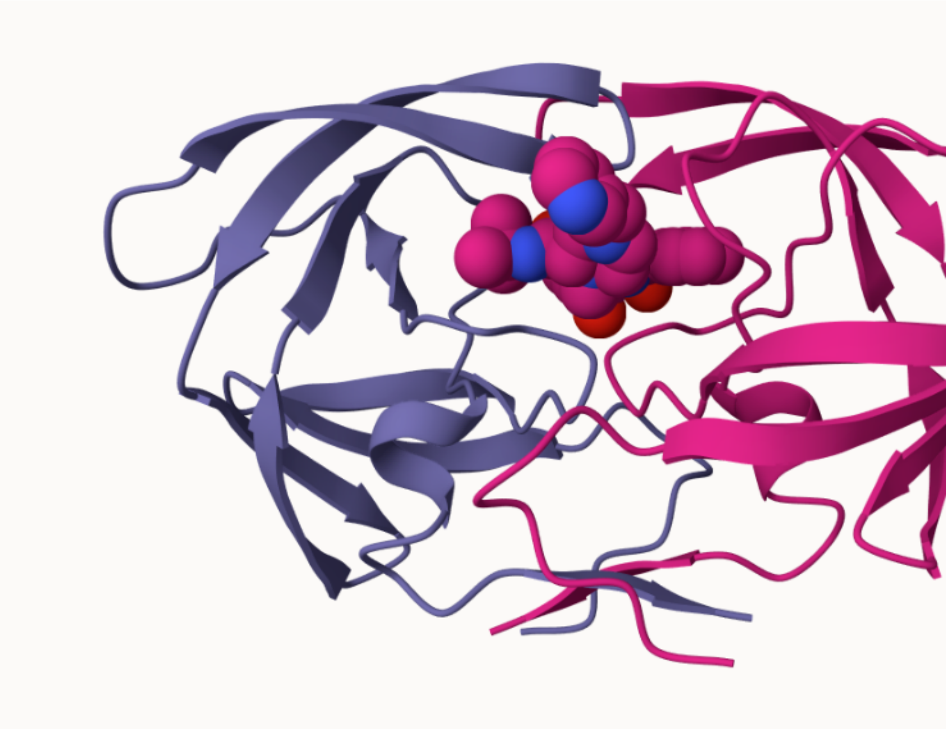
> Q3: Type HIV in the PDB website search box on the home page and determine how many HIV-1 protease structures are in the current PDB?

PROF SAID we are going to skip this question.

2. Viualizing Protein Strucutre

We will learn the basics of Mol* (mol-star). https://molstar.org/viewer/

We will play with PDB code 1HSG

This is general photo of the structure 

Show the ASP 25 Amino acids: These are really important so I highlighted them in green!

Back to R and working with PDB structures

Predict the dynamic (flexibility) of an important protein:

(We are jumping down to 3 (predicting dynamics))

```
library(bio3d)

hiv <- read.pdb("1hsg")
```

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

```
hiv
```

```
 Call:  read.pdb(file = "1hsg")
```

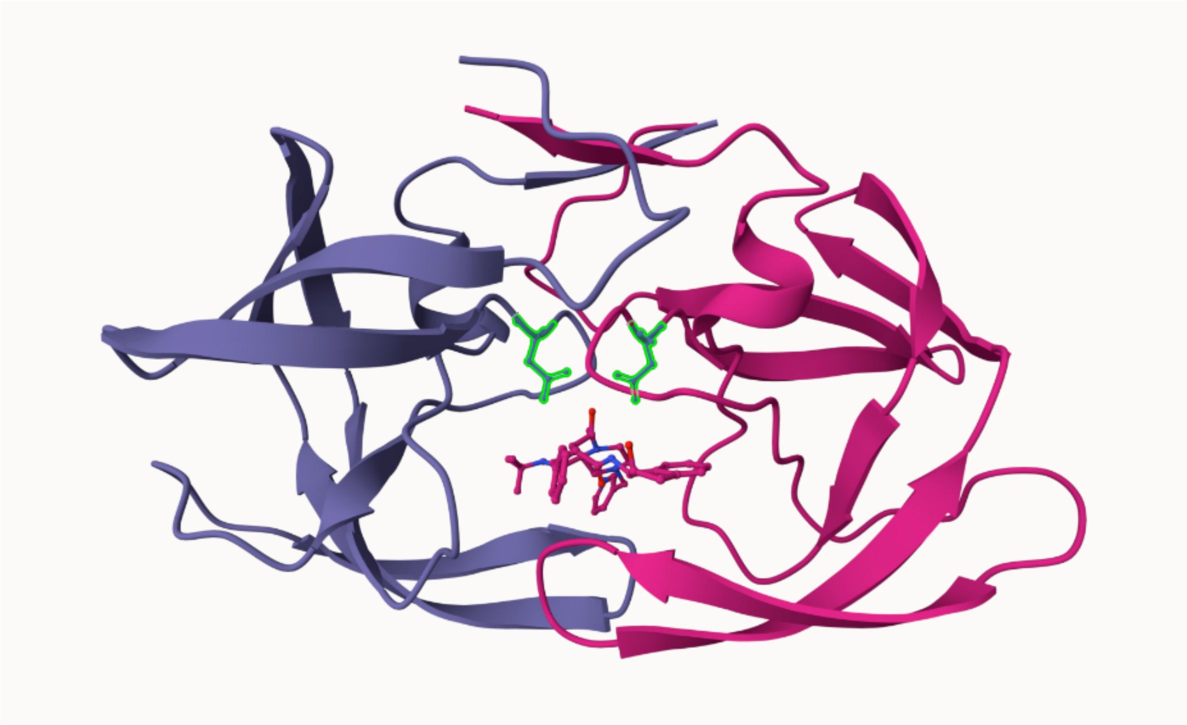


Figure 1: HIV-Pr with a bound inhibitor showing the two important ASP-25 amino acids

```
   Total Models#: 1
     Total Atoms#: 1686,  XYZs#: 5058  Chains#: 2  (values: A B)

     Protein Atoms#: 1514  (residues/Calpha atoms#: 198)
     Nucleic acid Atoms#: 0  (residues/phosphate atoms#: 0)

     Non-protein/nucleic Atoms#: 172  (residues: 128)
     Non-protein/nucleic resid values: [ HOH (127), MK1 (1) ]

   Protein sequence:
      PQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGIGGFIKVRQYD
      QILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFPQITLWQRPLVTIKIGGQLKE
      ALLDTGADDTVLEEMSLPGRWKPKMIGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTP
      VNIIGRNLLTQIGCTLNF

+ attr: atom, xyz, seqres, helix, sheet,
        calpha, remark, call
```

This the first atoms of the 1HSG protein! We saw this same file in the PDB website!

```
head(hiv$atom)
```

```
  type eleno elety  alt resid chain resno insert      x      y     z o     b
1 ATOM     1     N <NA>   PRO     A     1   <NA> 29.361 39.686 5.862 1 38.10
2 ATOM     2    CA <NA>   PRO     A     1   <NA> 30.307 38.663 5.319 1 40.62
3 ATOM     3     C <NA>   PRO     A     1   <NA> 29.760 38.071 4.022 1 42.64
4 ATOM     4     O <NA>   PRO     A     1   <NA> 28.600 38.302 3.676 1 43.40
5 ATOM     5    CB <NA>   PRO     A     1   <NA> 30.508 37.541 6.342 1 37.87
6 ATOM     6    CG <NA>   PRO     A     1   <NA> 29.296 37.591 7.162 1 38.40
  segid elesy charge
1  <NA>     N   <NA>
2  <NA>     C   <NA>
3  <NA>     C   <NA>
4  <NA>     O   <NA>
5  <NA>     C   <NA>
6  <NA>     C   <NA>
```

```
pdbseq(hiv)
```

```
  1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18  19  20
```

```
"P" "Q" "I" "T" "L" "W" "Q" "R" "P" "L" "V" "T" "I" "K" "I" "G" "G" "Q" "L" "K" 
 21  22  23  24  25  26  27  28  29  30  31  32  33  34  35  36  37  38  39  40 
"E" "A" "L" "L" "D" "T" "G" "A" "D" "D" "T" "V" "L" "E" "E" "M" "S" "L" "P" "G" 
 41  42  43  44  45  46  47  48  49  50  51  52  53  54  55  56  57  58  59  60 
"R" "W" "K" "P" "K" "M" "I" "G" "G" "I" "G" "G" "F" "I" "K" "V" "R" "Q" "Y" "D" 
 61  62  63  64  65  66  67  68  69  70  71  72  73  74  75  76  77  78  79  80 
"Q" "I" "L" "I" "E" "I" "C" "G" "H" "K" "A" "I" "G" "T" "V" "L" "V" "G" "P" "T" 
 81  82  83  84  85  86  87  88  89  90  91  92  93  94  95  96  97  98  99   1 
"P" "V" "N" "I" "I" "G" "R" "N" "L" "L" "T" "Q" "I" "G" "C" "T" "L" "N" "F" "P" 
  2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18  19  20  21 
"Q" "I" "T" "L" "W" "Q" "R" "P" "L" "V" "T" "I" "K" "I" "G" "G" "Q" "L" "K" "E" 
 22  23  24  25  26  27  28  29  30  31  32  33  34  35  36  37  38  39  40  41 
"A" "L" "L" "D" "T" "G" "A" "D" "D" "T" "V" "L" "E" "E" "M" "S" "L" "P" "G" "R" 
 42  43  44  45  46  47  48  49  50  51  52  53  54  55  56  57  58  59  60  61 
"W" "K" "P" "K" "M" "I" "G" "G" "I" "G" "G" "F" "I" "K" "V" "R" "Q" "Y" "D" "Q" 
 62  63  64  65  66  67  68  69  70  71  72  73  74  75  76  77  78  79  80  81 
"I" "L" "I" "E" "I" "C" "G" "H" "K" "A" "I" "G" "T" "V" "L" "V" "G" "P" "T" "P" 
 82  83  84  85  86  87  88  89  90  91  92  93  94  95  96  97  98  99 
"V" "N" "I" "I" "G" "R" "N" "L" "L" "T" "Q" "I" "G" "C" "T" "L" "N" "F" 
```

Here we will doa Normal Mode Analysis (NMA) to predict functional motions of a kinase protein.

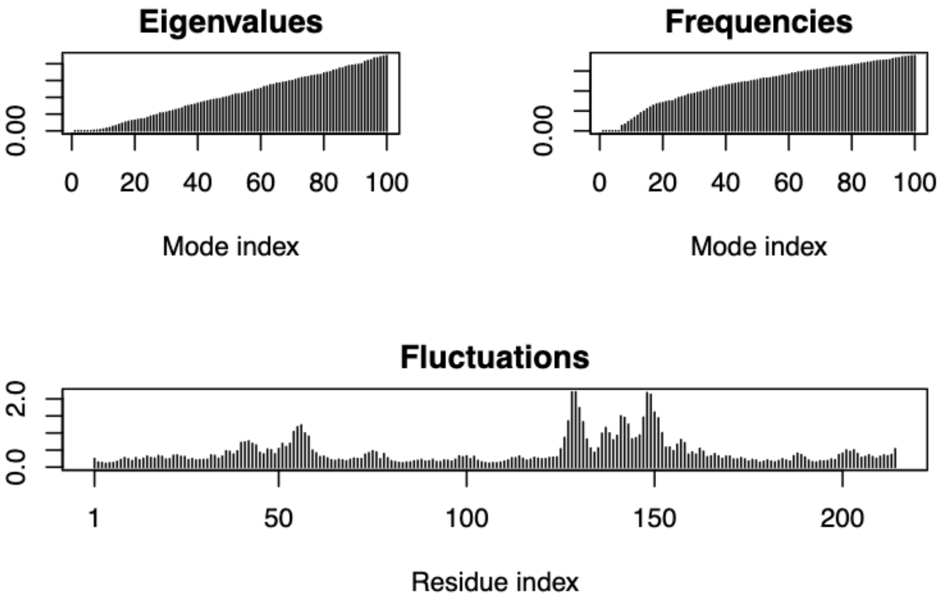
```r
library("bio3d")
adk <- read.pdb("6s36")
```

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

```r
modes <- nma(adk)
```

```
 Building Hessian...        Done in 0.028 seconds.
 Diagonalizing Hessian...   Done in 0.37 seconds.
```

```r
plot(modes)
```



Make a “movie” called a trajectory of the predicted motions:

```
mktrj(modes, file="adk_m7.pdb")
```

Then I can open this file in Mol*