Class 10: Structural Bioinformatics (Pt. 1)

Lena (A16420052)

The PDB database

First let's see what is in the PDB database- the main repository of protein structures.

Downloaded composition stats from: https://www.rcsb.org

```
pdb <- "Data Export Summary.csv"
stats <- read.csv(pdb, row.names = 1)
stats
```

```
                         X.ray     EM    NMR Multiple.methods Neutron Other
Protein (only)         158,844 11,759 12,296              197      73    32
Protein/Oligosaccharide  9,260  2,054     34                8       1     0
Protein/NA               8,307  3,667    284                7       0     0
Nucleic acid (only)      2,730    113  1,467               13       3     1
Other                      164      9     32                0       0     0
Oligosaccharide (only)      11      0      6                1       0     4
                         Total
Protein (only)         183,201
Protein/Oligosaccharide  11,357
Protein/NA               12,265
Nucleic acid (only)       4,327
Other                       205
Oligosaccharide (only)       22
```

```
x <- stats$X.ray
x
```

```
[1] "158,844" "9,260"   "8,307"   "2,730"   "164"     "11"
```

There is a problem here due to the commas in the numbers. This causes R to treat them as characters.

Substitute without commas `gsub()`

```
gsub(",", "", x)
```

```
[1] "158844" "9260"   "8307"   "2730"   "164"    "11"
```

```
rm.comma <- function(x){
  as.numeric(gsub(",", "", x))
}
```

```
rm.comma(stats$EM)
```

```
[1] 11759  2054  3667   113     9     0
```

I can also use `apply()` to fix the whole table...

```
pdbstats <- apply(stats, MARGIN = 2, FUN= rm.comma)
rownames(pdbstats) <- rownames(stats)
head(stats)
```

```
                         X.ray     EM    NMR Multiple.methods Neutron Other
Protein (only)         158,844 11,759 12,296              197      73    32
Protein/Oligosaccharide  9,260  2,054     34                8       1     0
Protein/NA               8,307  3,667    284                7       0     0
Nucleic acid (only)      2,730    113  1,467               13       3     1
Other                      164      9     32                0       0     0
Oligosaccharide (only)      11      0      6                1       0     4
                         Total
Protein (only)         183,201
Protein/Oligosaccharide 11,357
Protein/NA              12,265
Nucleic acid (only)      4,327
Other                      205
Oligosaccharide (only)      22
```

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

```
totals <- apply(pdbstats, 2, sum)
round(totals/totals["Total"]*100,2)
```

```
        X.ray            EM           NMR Multiple.methods
        84.83          8.33          6.68             0.11
      Neutron         Other         Total
         0.04          0.02        100.00
```

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

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

```
      Protein (only) Protein/Oligosaccharide             Protein/NA
               86.67                    5.37                   5.80
Nucleic acid (only)                   Other Oligosaccharide (only)
                2.05                    0.10                   0.01
```

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?

SKIPPED for time!!!

Protein structures in PDB as a fraction of UniProt sequences

```
round((pdbstats[1, "Total"]/251600768)*100, 2)
```

```
[1] 0.07
```

Visualizing the HIV-1 protease structure

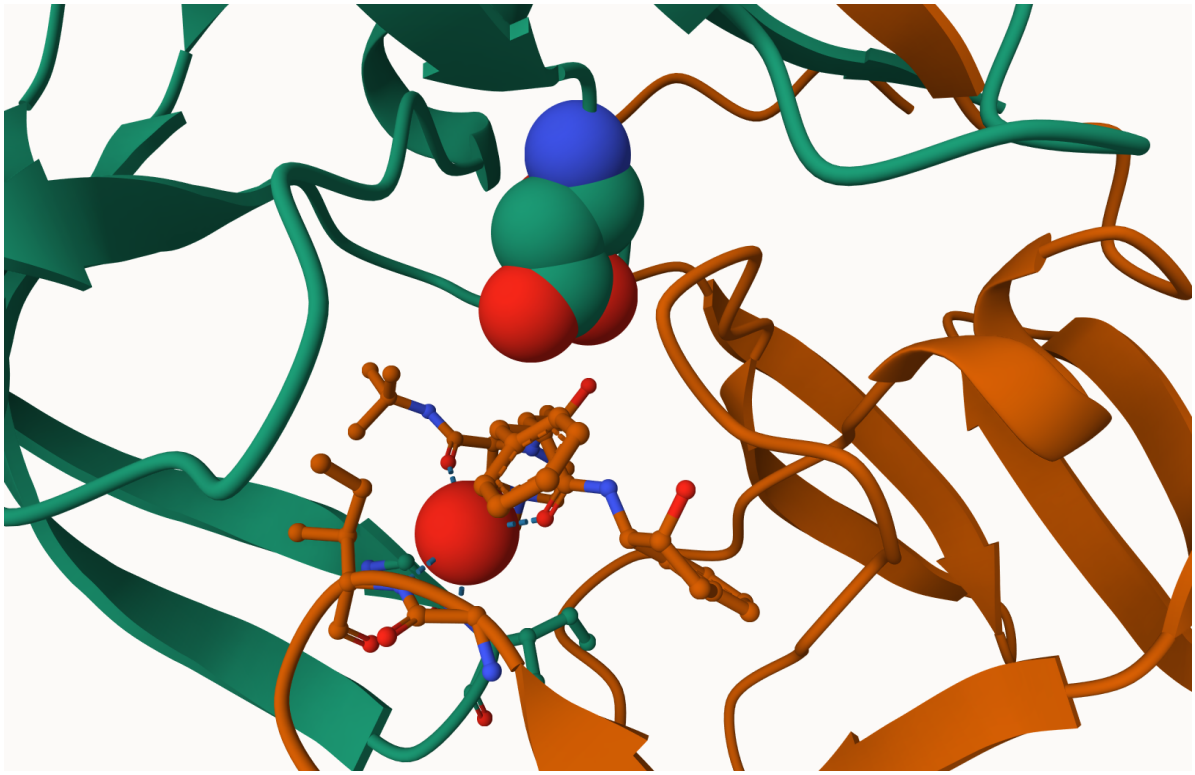
Q4: Water molecules normally have 3 atoms. Why do we see just one atom per water molecule in this structure?

This is a 2 angstrom structure and hydrogen is not visible at this resolution. You need 1 angstrom or better to be able to see small atoms like hydrogen

Q5: There is a critical "conserved" water molecule in the binding site. Can you identify this water molecule? What residue number does this water molecule have

Water HOH 308

Q6: Generate and save a figure clearly showing the two distinct chains of HIV-protease along with the ligand. You might also consider showing the catalytic residues ASP 25 in each chain and the critical water (we recommend "Ball & Stick" for these side-chains). Add this figure to your Quarto document.



The bio3d package for structural bioinformatics

```
library(bio3d)

pdb1 <- read.pdb("1hsg")
```

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

```
pdb1
```

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

```
   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
```

```
head(pdb1$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>
```

Predicting functional motions of a single structure

Let's finish today with a bioinformatics calculation to predict the functional motions of a PDB structure

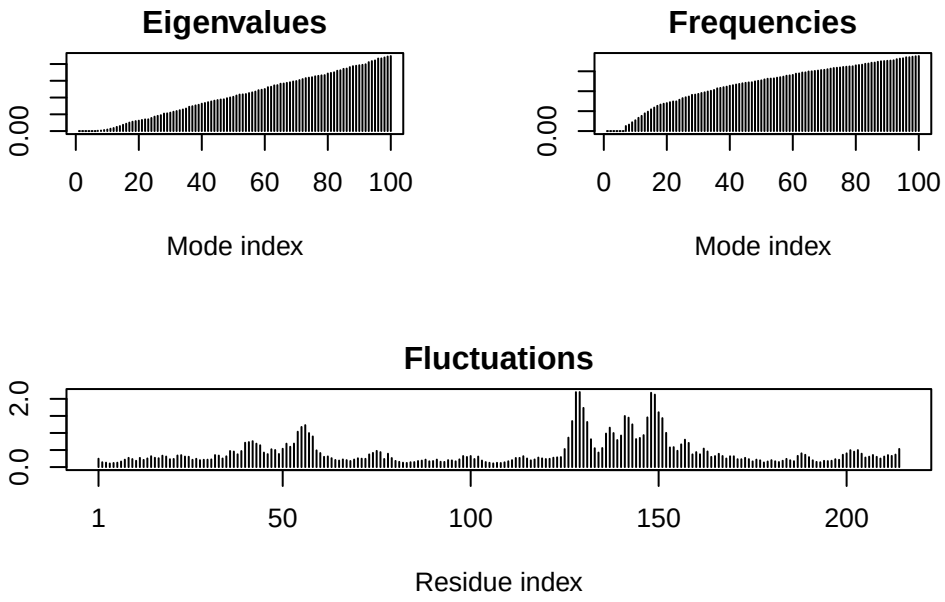
```
adk <- read.pdb("6s36")
```

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

```
# Perform flexiblity prediction
m <- nma(adk)
```

```
Building Hessian...        Done in 0.044 seconds.
Diagonalizing Hessian...   Done in 0.499 seconds.
```

```
plot(m)
```




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