Class 09

Dahlia Loomis

5/3/23

1. Introduction to RCSB Protein Data Bank (PDB)

First, we need to read the data using the command `read.csv`:

```
read.csv('Data Export Summary.csv')
```

```
           Molecular.Type   X.ray     EM    NMR Multiple.methods Neutron Other
1          Protein (only) 154,766 10,155 12,187              191      72    32
2 Protein/Oligosaccharide   9,083  1,802     32                7       1     0
3              Protein/NA   8,110  3,176    283                6       0     0
4     Nucleic acid (only)   2,664     94  1,450               12       2     1
5                   Other     163      9     32                0       0     0
6  Oligosaccharide (only)      11      0      6                1       0     4
    Total
1 177,403
2  10,925
3  11,575
4   4,223
5     204
6      22
```

```
PDB.data <- read.csv('Data Export Summary.csv', row.names = 1)
```

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

I need to sum all the elements of the X.ray column, but R does not read the values as numbers since they have commas.

```
#with commas, R does not understand that these are numbers
PDB.data$X.ray
```

```
[1] "154,766" "9,083"   "8,110"   "2,664"   "163"     "11"
```

In order to remove the commas, we will use the `gsub` function. We also need to read the numbers as a numeric using the `as.numeric()` function

```
as.numeric(gsub(',', '', PDB.data$X.ray))
```

```
[1] 154766   9083   8110   2664    163     11
```

Now, we can take the sum:

```
n.Xray <- sum(as.numeric(gsub(',', '', PDB.data$X.ray)))

n.EM <- sum(as.numeric(gsub(',', '', PDB.data$EM)))

n.total <- sum(as.numeric(gsub(',', '', PDB.data$Total)))

p_xray_em <- ((n.Xray + n.EM)/ n.total) *100

p_xray_em
```

```
[1] 92.99297
```

The answer is 93 percent.

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

```
n.proteins <- sum(as.numeric(gsub(',', '', PDB.data[1,7])))
n.proteins
```

```
[1] 177403
```

```
prop_proteins <- n.proteins/n.total
```

```
prop_proteins
```

```
[1] 0.8681246
```

0.868

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?

We found 2,003 protease structures in the current PDB, but it was difficult to find the actual number of structures.

2. Visualizing the HIV-1 Protease Structure

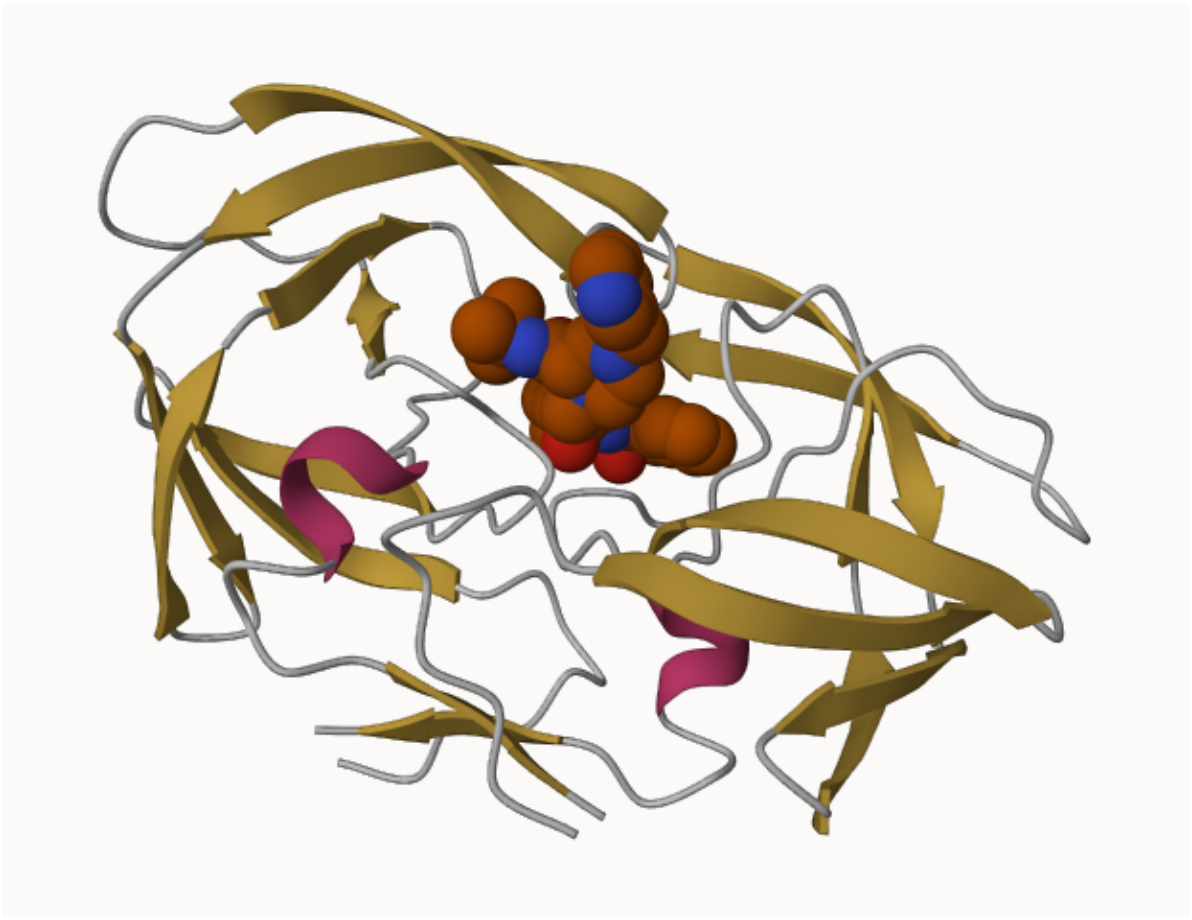
Q4: Water molecules normally have 3 atoms. Why do we see just one atom per water molecule in this structure?

It simplifies it to one atom. If you hover over a water molecule, it says it is an O atom. It only shows the main molecule to avoid complexity and allow the structure to be viewed more easily in a more organized way.

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

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.



Discussion Topic: Can you think of a way in which indinavir, or even larger ligands and substrates, could enter the binding site?

3. Introduction to Bio3D in R

```
library(bio3d)

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

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

```
pdb
```

```
 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
```

```
attributes(pdb)
```

```
$names
[1] "atom"   "xyz"    "seqres" "helix"  "sheet"  "calpha" "remark" "call"

$class
[1] "pdb" "sse"
```

Q7. How many animal acid residues are there in this pdb object?

There are 198 residues

Q8. Name one of the two non-protein residues.

HOH and MK1

Q9. How many protein chains are in this structure?

There are two protein chains

```
head(pdb$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 Function Motions of a Single Structure by NMA

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

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

```
adk
```

```
Call:  read.pdb(file = "6s36")

  Total Models#: 1
    Total Atoms#: 1898,  XYZs#: 5694  Chains#: 1  (values: A)

    Protein Atoms#: 1654  (residues/Calpha atoms#: 214)
    Nucleic acid Atoms#: 0  (residues/phosphate atoms#: 0)

    Non-protein/nucleic Atoms#: 244  (residues: 244)
    Non-protein/nucleic resid values: [ CL (3), HOH (238), MG (2), NA (1) ]
```

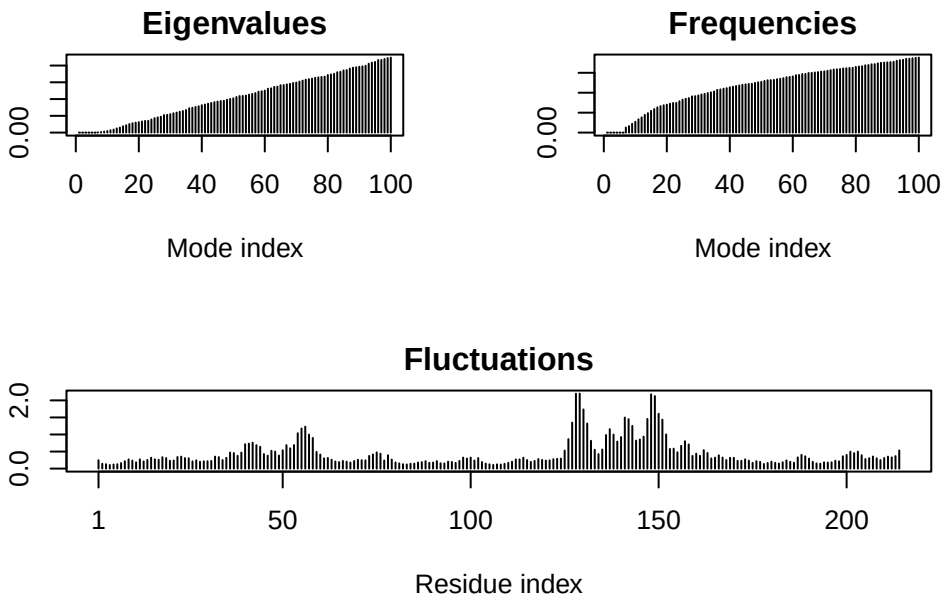
```
   Protein sequence:
      MRIILLGAPGAGKGTQAQFIMEKYGIPQISTGDMLRAAVKSGSELGKQAKDIMDAGKLVT
      DELVIALVKERIAQEDCRNGFLLDGFPRTIPQADAMKEAGINVDYVLEFDVPDELIVDKI
      VGRRVHAPSGRVYHVKFNPPKVEGKDDVTGEELTTRKDDQEETVRKRLVEYHQMTAPLIG
      YYSKEAEAGNTKYAKVDGTKPVAEVRADLEKILG

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

Now, we will perform normal mode analysis (NMA) to predict protein flexibility and potential functional motions

```
m <- nma(adk)
```

```
 Building Hessian...        Done in 0.034 seconds.
 Diagonalizing Hessian...   Done in 0.431 seconds.
```

```
plot(m)
```



```
#fluctuations are the amounts of flexibility
#corresponding to particular amino acids.
```

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