Class 09: Structural Bioinformatics (pt1)

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PDB statistics

The main database for structural biology is called the PDB. Let's have a look at what it contains:

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

```
data <- read.csv("Data Export Summary.csv")
head(data)
```

```
           Molecular.Type   X.ray     EM    NMR Integrative Multiple.methods
1          Protein (only) 176,378 20,438 12,709         342               221
2 Protein/Oligosaccharide  10,284  3,396     34           8                11
3               Protein/NA   9,007  5,931    287          24                 7
4     Nucleic acid (only)   3,077    200  1,554           2                15
5                   Other     174     13     33           3                 0
6  Oligosaccharide (only)      11      0      6           0                 1
  Neutron Other   Total
1      83    32 210,203
2       1     0  13,734
3       0     0  15,256
4       3     1   4,852
```

```
5       0     0     223
6       0     4      22
```

```
data$Total
```

```
[1] "210,203" "13,734"  "15,256"  "4,852"   "223"     "22"
```

```
data$Neutron
```

```
[1] 83  1  0  3  0  0
```

Some data are not numeric.

```
library(tidyverse)
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.4     v readr     2.1.5
v forcats   1.0.1     v stringr   1.5.2
v ggplot2   4.0.0     v tibble    3.3.0
v lubridate 1.9.4     v tidyr     1.3.1
v purrr     1.1.0
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becor
```

```
pdb <- read_csv("Data Export Summary.csv")
```

```
Rows: 6 Columns: 9
-- Column specification --------------------------------------------------------
Delimiter: ","
chr (1): Molecular Type
dbl (4): Integrative, Multiple methods, Neutron, Other
num (4): X-ray, EM, NMR, Total

i Use `spec()` to retrieve the full column specification for this data.
i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
pdb
```

```
# A tibble: 6 x 9
  `Molecular Type`    `X-ray`    EM   NMR Integrative `Multiple methods` Neutron
  <chr>                 <dbl> <dbl> <dbl>       <dbl>                <dbl>   <dbl>
1 Protein (only)       176378 20438 12709         342                  221      83
2 Protein/Oligosacch~   10284  3396    34           8                   11       1
3 Protein/NA             9007  5931   287          24                    7       0
4 Nucleic acid (only)    3077   200  1554           2                   15       3
5 Other                   174    13    33           3                    0       0
6 Oligosaccharide (o~      11     0     6           0                    1       0
# i 2 more variables: Other <dbl>, Total <dbl>
```

```
pro.xray <- sum(pdb$`X-ray`)/sum(pdb$Total)*100
pro.em <- sum(pdb$EM)/sum(pdb$Total)*100
```

```
round(pro.xray,2)
```

```
[1] 81.43
```

```
round(pro.em,2)
```

```
[1] 12.27
```

81.48% are solved by X-Ray, and 12.22% are solved by Electron Microscopy.

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

```
pro.protein <- sum(pdb[1:3,"Total"])/sum(pdb$Total) * 100
round(pro.protein,2)
```

```
[1] 97.91
```

97.91% are protein.

Exploring PDB Statistics

> 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?

4,866 structures are in PDB.

Package for structural bioinformatics…

```
library(bio3d)

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

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

```
hiv
```

```
 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
```

Let's first use the Mol* viewer to explore this structure.

Figure 1: First view of HIV-pr

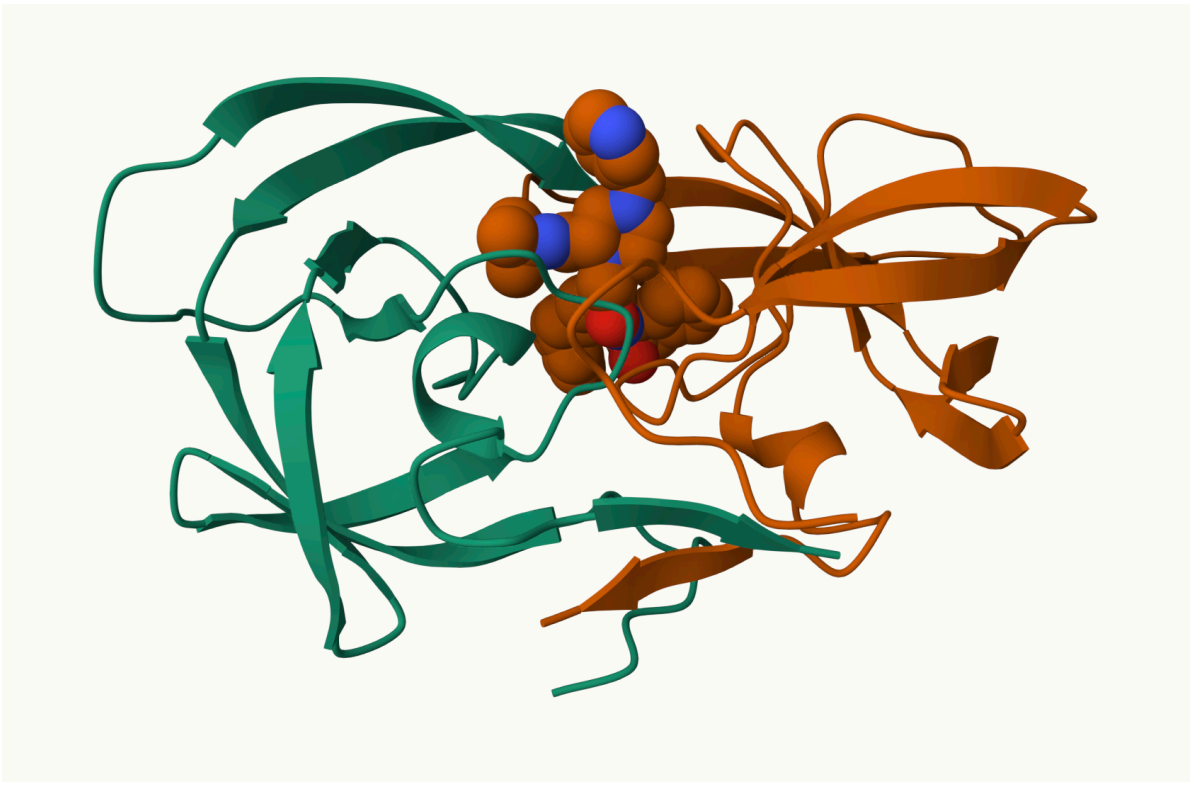


Figure 2: Second view of HIV-pr

PDB objects in R

```
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>
```

Extract the sequence..

```
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"
```

```
chainA_seq <- pdbseq(trim.pdb(hiv, chain="A"))
```

I can interactively view these PDB objects with the **bio3dviewer** package.

```
# install.packages("pak")
# pak::pak("bioboot/bio3dview")
# install.packages("NGLVieweR")
```

```
library(bio3dview)
# view.pdb(hiv)
```

```
# sel <- atom.select(hiv,resno=25)

# view.pdb(hiv, highlight = sel,
#         highlight.style = "spacefill",
#         colorScheme = "chain",
#         col=c("blue","red"),
#         backgroundColor = "grey")
```

Predicting Protein Flexibility

We can also run a bioinformatics calculation to predict protein dynamics (i.e. functional motions).

We will use the nma() function.

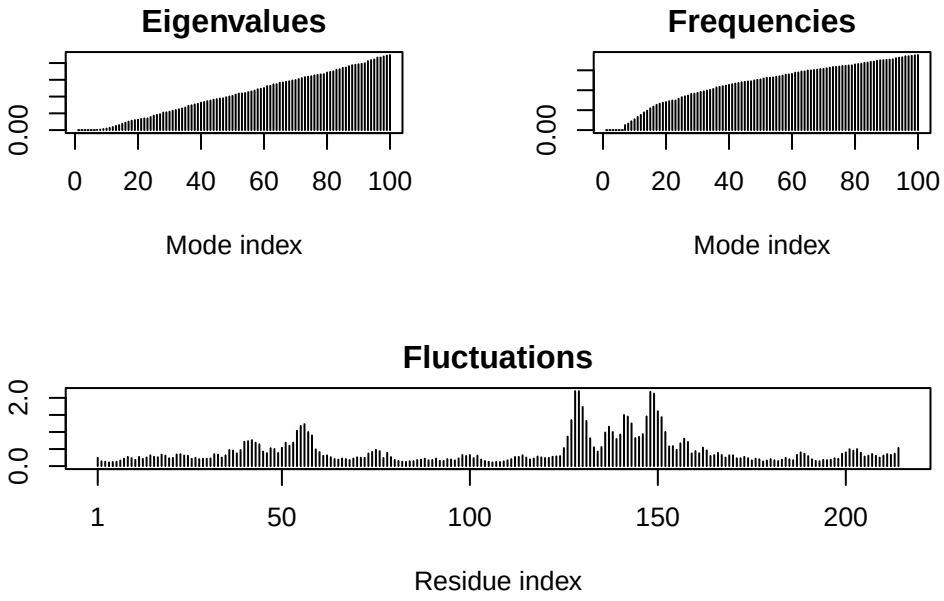
```
adk <- read.pdb("6s36")
```

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

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

```
 Building Hessian...        Done in 0.011 seconds.
 Diagonalizing Hessian...   Done in 0.261 seconds.
```

```
plot(m)
```



Generate a "trajectory" of predicted motion.

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