# Class 9: Structural Bioinformatics (Pt. 1)

Emily Rodriguez

## PDB Statistics

The PDB is the main database for structural information on biomolecules. Let's see what it contains:

Download a CSV file from the PDB site (accessible from "Analyze" > "PDB Statistics" > "by Experimental Method and Molecular Type". Move this CSV file into your RStudio project and use it to answer the following questions:

```r
db <- read.csv("DataExportSummary.csv")
db
```

```
           Molecular.Type   X.ray    EM    NMR Multiple.methods Neutron Other
1          Protein (only) 152,809 9,421 12,117              191      72    32
2 Protein/Oligosaccharide   9,008 1,654     32                7       1     0
3              Protein/NA   8,061 2,944    281                6       0     0
4     Nucleic acid (only)   2,602    77  1,433               12       2     1
5                   Other     163     9     31                0       0     0
6  Oligosaccharide (only)      11     0      6                1       0     4
    Total
1 174,642
2  10,702
3  11,292
4   4,127
5     203
6      22
```

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

```
xray.total <- sum(as.numeric(gsub(",", "", db$X.ray)))
em.total <- sum(as.numeric(gsub(",", "", db$EM)))
```

```
# I will work with `x` as input.

sum_comma <- function(x) {
  # Substitute the comma and convert to numeric
  sum(as.numeric(gsub(",", "", x)))

}
```

For X-ray:

```
sum_comma(db$X.ray) / sum_comma(db$Total)
```

```
[1] 0.8590264
```

For EM:

```
round(sum_comma(db$EM) / sum_comma(db$Total), 2)
```

```
[1] 0.07
```

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

```
round(sum_comma(db$Total[1]) / sum_comma(db$Total), 2)
```

```
[1] 0.87
```

> 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!!

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

The structure is too low a resolution to see H. You need a sub 1 Angstrom resolution to see 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

HOH308

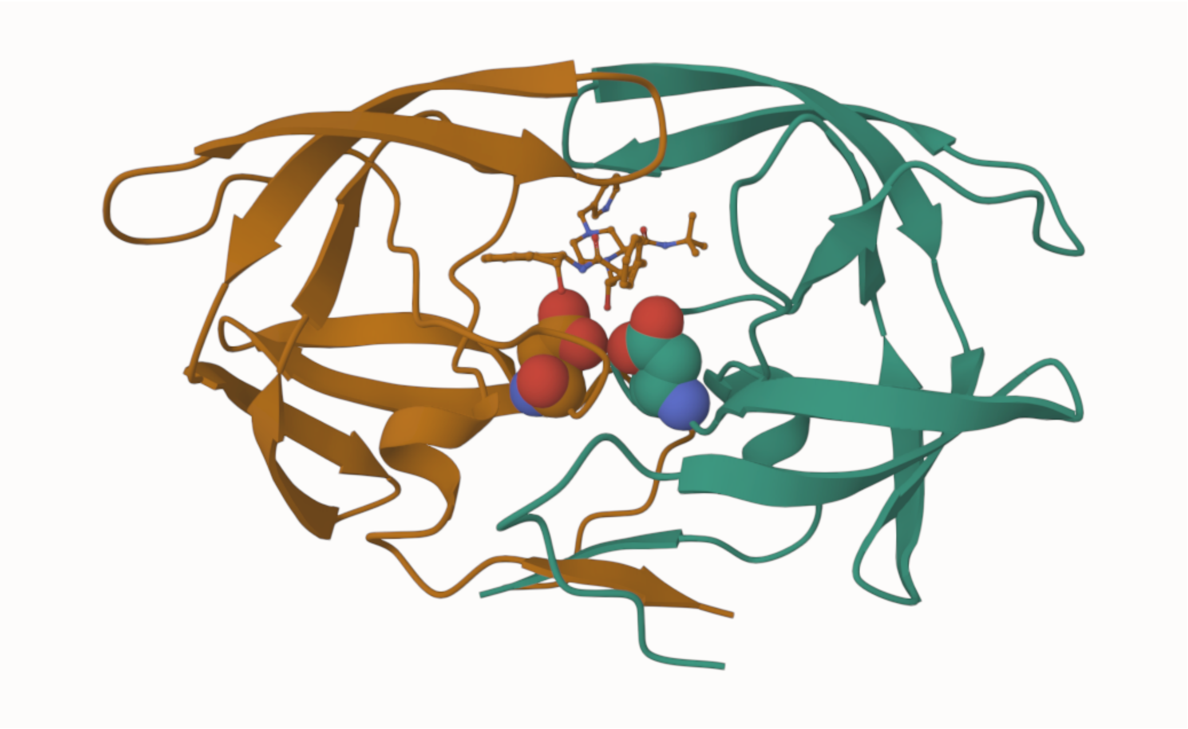


Figure 1: HIV-PR structure from MERK with a bound drug

## Working with Structures in R

we can use the `bio3d` package to read and perform bioinformatics calculations on PDB structures.

```
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"
```

```r
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>
```

Read an ADK structure

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

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

```r
adk
```

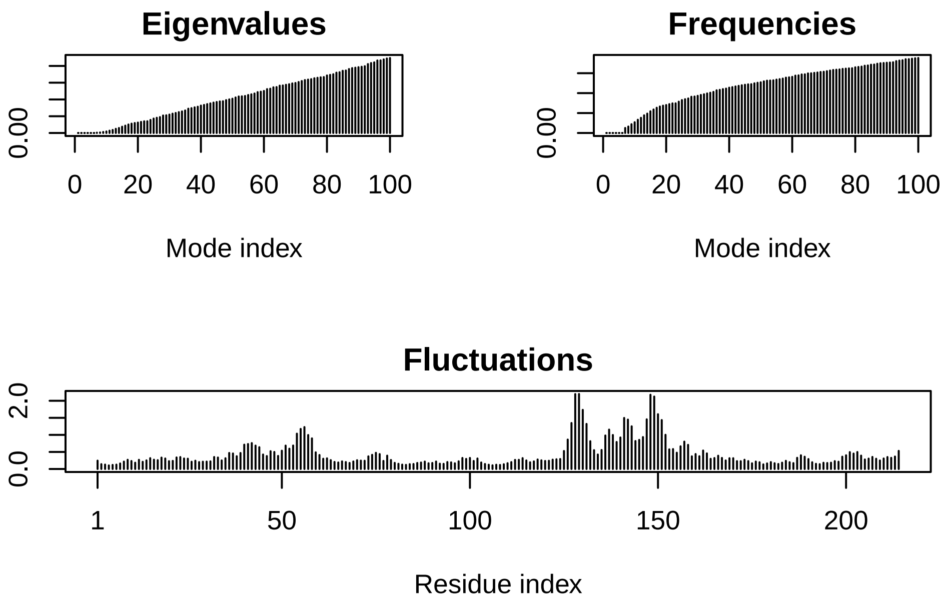
```

 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
```

Perform a prediction of flexibility with a technique called NMA (normal mode analysis)

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

```
 Building Hessian...         Done in 0.053 seconds.
 Diagonalizing Hessian...    Done in 0.418 seconds.
```

```r
plot(m)
```



Write out a “movie” (a.k.a trajectory) of the motion for viewing in MOlstar

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

> Q7: How many amino acid residues are there in this pdb object?

From the output above I can see 198 amino acid residues

> Q8: Name one of the two non-protein residues?

HOH

> Q9: How many protein chains are in this structure?

2 (values: A B)