class09

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1. Protein data bank

```
pdb_df = read.csv("Data Export Summary.csv")
pdb_df
```

```
          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.

```
library(stringr)
pdb_df <- as.data.frame(lapply(pdb_df, str_remove, ","))
pdb_df[,-1] <- as.data.frame(lapply(pdb_df[,-1], strtoi))
```

```
pdb_df
```

```
           Molecular.Type  X.ray   EM   NMR Multiple.methods Neutron Other
1          Protein (only) 152809 9421 12117               191      72    32
2 Protein/Oligosaccharide   9008 1654    32                 7       1     0
3              Protein/NA   8061 2944   281                 6       0     0
4     Nucleic acid (only)   2602   77  1433                12       2     1
5                   Other    163    9    31                 0       0     0
6  Oligosaccharide (only)     11    0     6                 1       0     4
   Total
1 174642
2  10702
3  11292
4   4127
5    203
6     22
```

```
print(paste(round(sum(pdb_df$X.ray)/sum(pdb_df$Total) * 100, 2), "% by X-Ray"))
```

```
[1] "85.9 % by X-Ray"
```

```
print(paste(round(sum(pdb_df$EM)/sum(pdb_df$Total) * 100, 2), "% by EM"))
```

```
[1] "7.02 % by EM"
```

Q2.

```
print(paste(round(sum(pdb_df[(pdb_df$Molecular.Type=="Protein (only)" | pdb_df$Molecular.T
```

```
[1] "92.22 %"
```

Q3.

Plain text search "HIV" doesn't give us a straight answer. We can maybe try restrict the search term to protease and hoping it catch all the answers.

2. Visualizing HIV-1 protease structure

Q4.

Only the oxygen is visible, because the resolution is not enough for the hydrogen to be see. It's too small.

Q5.

Choose "ligand", and we can find a water molecular in the center of the ligand. It's HOH 308, having 4 bonds that connect to both the ligand and the backbone chain.

Q6

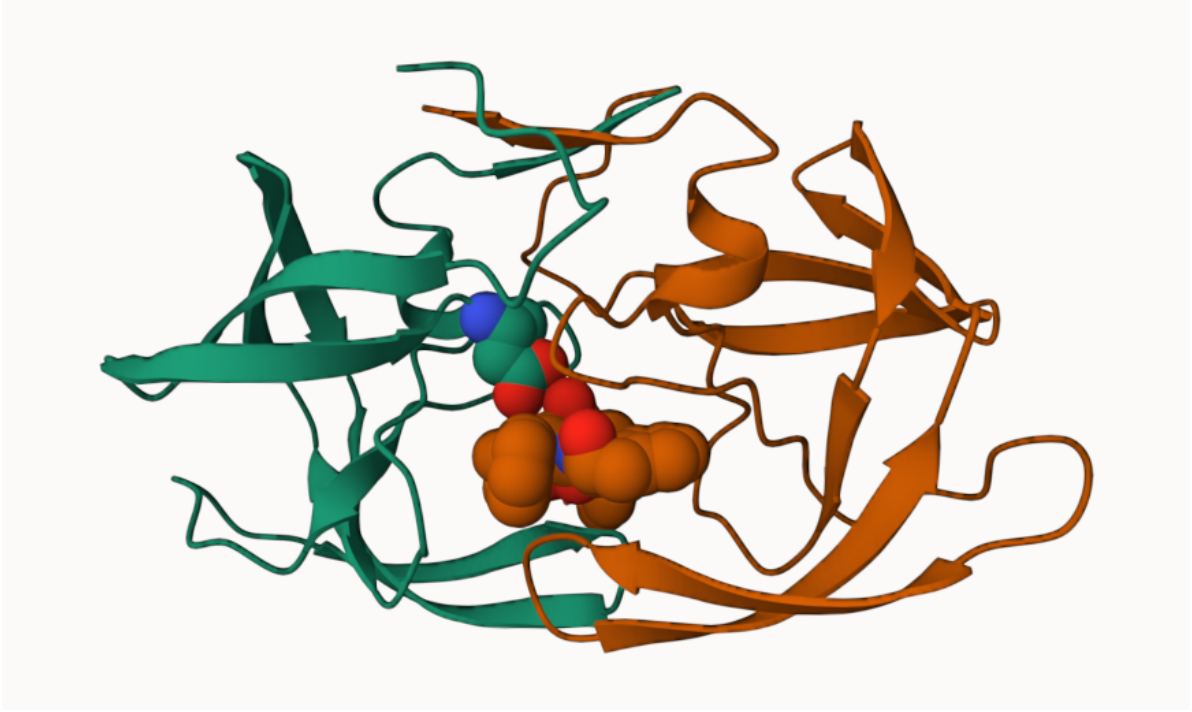


Figure 1: "HIV-Pr"

3. PDB data in R

Q7. 198

Q8. HOH

Q9. 2

```
library(bio3d)
pdb <- read.pdb("1hsg")
```

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

```
attributes(pdb)
```

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

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

```
head(pdb$atom$resid[1])
```

```
[1] "PRO"
```

Normal mode analysis (NMA) is a structural bioinformatics method to predict protein flexibility and potential functional motions (a.k.a. conformational changes).

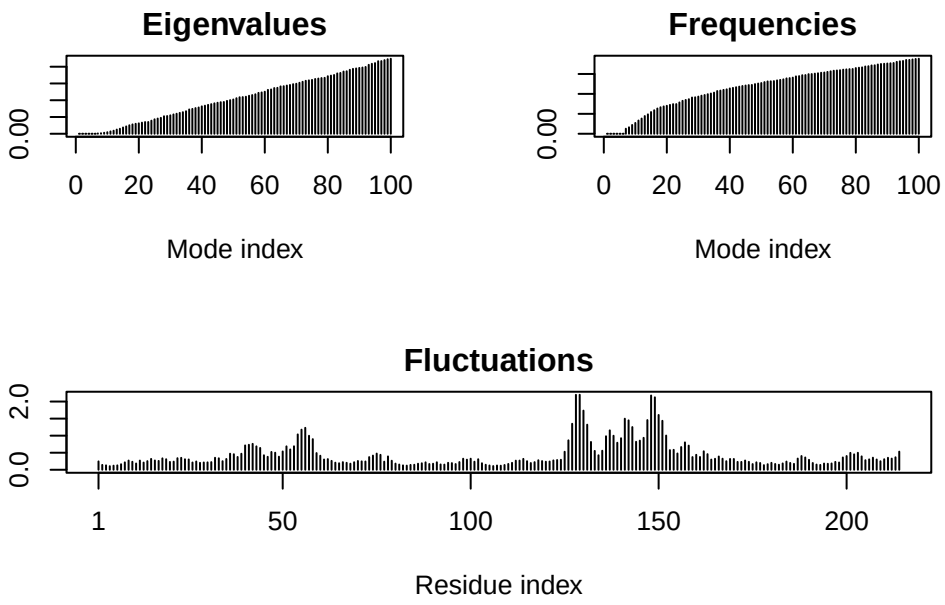
```
adk <- read.pdb("6s36")
```

```
  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 0.014 seconds.
 Diagonalizing Hessian...   Done in 0.271 seconds.
```

```
plot(m)
```




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

import this file into pdb and see the movement.

```
# get the sequence by identifier
#get.seq()
#blast.pdb()
#get.pdb()
#pdbaln() # align and superpose all structure

# pca()
# plot()
```

Section 4/ Comparative structure analysis

Q10. msa

Q11. bio3d-view

12. TRUE

```
library(bio3d)
aa <- get.seq("1ake_A")
```

```
Warning in get.seq("1ake_A"): Removing existing file: seqs.fasta

Fetching... Please wait. Done.
```

```
aa
```

```
             1        .         .         .         .         .         60
pdb|1AKE|A   MRIILLGAPGAGKGTQAQFIMEKYGIPQISTGDMLRAAVKSGSELGKQAKDIMDAGKLVT
             1        .         .         .         .         .         60

            61        .         .         .         .         .         120
pdb|1AKE|A   DELVIALVKERIAQEDCRNGFLLDGFPRTIPQADAMKEAGINVDYVLEFDVPDELIVDRI
            61        .         .         .         .         .         120

           121        .         .         .         .         .         180
pdb|1AKE|A   VGRRVHAPSGRVYHVKFNPPKVEGKDDVTGEELTTRKDDQEETVRKRLVEYHQMTAPLIG
           121        .         .         .         .         .         180

           181        .         .         .   214
pdb|1AKE|A   YYSKEAEAGNTKYAKVDGTKPVAEVRADLEKILG
           181        .         .         .   214

Call:
  read.fasta(file = outfile)

Class:
  fasta

Alignment dimensions:
  1 sequence rows; 214 position columns (214 non-gap, 0 gap)

+ attr: id, ali, call
```

Q13. 214

```
# Blast or hmmer search
#b <- blast.pdb(aa)
```

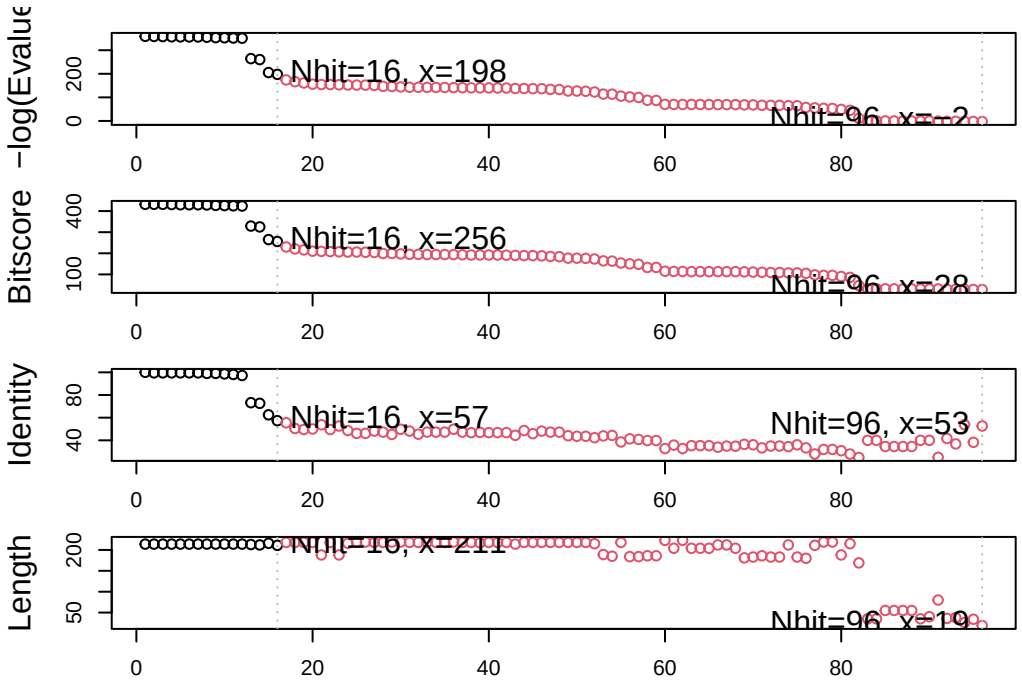
To render it without running blast each time but still have the "b" object, we can save the b object and load it next time.

```
# saveRDS(b, file = "blast_1ake_A.RDS")
b <- readRDS("blast_1ake_A.RDS")
```

```
# Plot a summary of search results
hits <- plot(b)
```

```
* Possible cutoff values:    197 -3
          Yielding Nhits:    16 96

* Chosen cutoff value of:    197
          Yielding Nhits:    16
```




```
# List out some 'top hits'
head(hits$pdb.id)
```

```
[1] "1AKE_A" "4X8M_A" "6S36_A" "6RZE_A" "4X8H_A" "3HPR_A"
```

```
# if blast doesn't work, we can download the above ids directly from the database.

#hits <- NULL
#hits$pdb.id <- c('1AKE_A','6S36_A','6RZE_A','3HPR_A','1E4V_A','5EJE_A','1E4Y_A','3X2S_A',
```

```
# Download releated PDB files
# the path argument make a new folder called "pdbs" and store the downloads in it.
# split by genes
# gzip make the file smaller
files <- get.pdb(hits$pdb.id, path="pdbs", split=TRUE, gzip=TRUE)
```

```
Warning in get.pdb(hits$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/1AKE.pdb.gz exists. Skipping download

Warning in get.pdb(hits$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/4X8M.pdb.gz exists. Skipping download

Warning in get.pdb(hits$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/6S36.pdb.gz exists. Skipping download

Warning in get.pdb(hits$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/6RZE.pdb.gz exists. Skipping download

Warning in get.pdb(hits$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/4X8H.pdb.gz exists. Skipping download

Warning in get.pdb(hits$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/3HPR.pdb.gz exists. Skipping download

Warning in get.pdb(hits$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/1E4V.pdb.gz exists. Skipping download

Warning in get.pdb(hits$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/5EJE.pdb.gz exists. Skipping download

Warning in get.pdb(hits$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/1E4Y.pdb.gz exists. Skipping download
```

```
Warning in get.pdb(hits$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/3X2S.pdb.gz exists. Skipping download

Warning in get.pdb(hits$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/6HAP.pdb.gz exists. Skipping download

Warning in get.pdb(hits$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/6HAM.pdb.gz exists. Skipping download

Warning in get.pdb(hits$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/4K46.pdb.gz exists. Skipping download

Warning in get.pdb(hits$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/4NP6.pdb.gz exists. Skipping download

Warning in get.pdb(hits$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/3GMT.pdb.gz exists. Skipping download

Warning in get.pdb(hits$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/4PZL.pdb.gz exists. Skipping download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```

```
# Align PDBs downloaded before
pdbs <- pdbaln(files, fit = TRUE, exefile="msa")
```

```
Reading PDB files:
pdbs/split_chain/1AKE_A.pdb
pdbs/split_chain/4X8M_A.pdb
pdbs/split_chain/6S36_A.pdb
pdbs/split_chain/6RZE_A.pdb
pdbs/split_chain/4X8H_A.pdb
pdbs/split_chain/3HPR_A.pdb
pdbs/split_chain/1E4V_A.pdb
pdbs/split_chain/5EJE_A.pdb
pdbs/split_chain/1E4Y_A.pdb
pdbs/split_chain/3X2S_A.pdb
pdbs/split_chain/6HAP_A.pdb
pdbs/split_chain/6HAM_A.pdb
pdbs/split_chain/4K46_A.pdb
pdbs/split_chain/4NP6_A.pdb
pdbs/split_chain/3GMT_A.pdb
pdbs/split_chain/4PZL_A.pdb
   PDB has ALT records, taking A only, rm.alt=TRUE
..   PDB has ALT records, taking A only, rm.alt=TRUE
.   PDB has ALT records, taking A only, rm.alt=TRUE
..   PDB has ALT records, taking A only, rm.alt=TRUE
```

```
..   PDB has ALT records, taking A only, rm.alt=TRUE
....   PDB has ALT records, taking A only, rm.alt=TRUE
.   PDB has ALT records, taking A only, rm.alt=TRUE
....

Extracting sequences

pdb/seq: 1   name: pdbs/split_chain/1AKE_A.pdb
   PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 2   name: pdbs/split_chain/4X8M_A.pdb
pdb/seq: 3   name: pdbs/split_chain/6S36_A.pdb
   PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 4   name: pdbs/split_chain/6RZE_A.pdb
   PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 5   name: pdbs/split_chain/4X8H_A.pdb
pdb/seq: 6   name: pdbs/split_chain/3HPR_A.pdb
   PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 7   name: pdbs/split_chain/1E4V_A.pdb
pdb/seq: 8   name: pdbs/split_chain/5EJE_A.pdb
   PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 9   name: pdbs/split_chain/1E4Y_A.pdb
pdb/seq: 10   name: pdbs/split_chain/3X2S_A.pdb
pdb/seq: 11   name: pdbs/split_chain/6HAP_A.pdb
pdb/seq: 12   name: pdbs/split_chain/6HAM_A.pdb
   PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 13   name: pdbs/split_chain/4K46_A.pdb
   PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 14   name: pdbs/split_chain/4NP6_A.pdb
pdb/seq: 15   name: pdbs/split_chain/3GMT_A.pdb
pdb/seq: 16   name: pdbs/split_chain/4PZL_A.pdb
```

```
head(pdbs$id)
```

```
[1] "pdbs/split_chain/1AKE_A.pdb" "pdbs/split_chain/4X8M_A.pdb"
[3] "pdbs/split_chain/6S36_A.pdb" "pdbs/split_chain/6RZE_A.pdb"
[5] "pdbs/split_chain/4X8H_A.pdb" "pdbs/split_chain/3HPR_A.pdb"
```

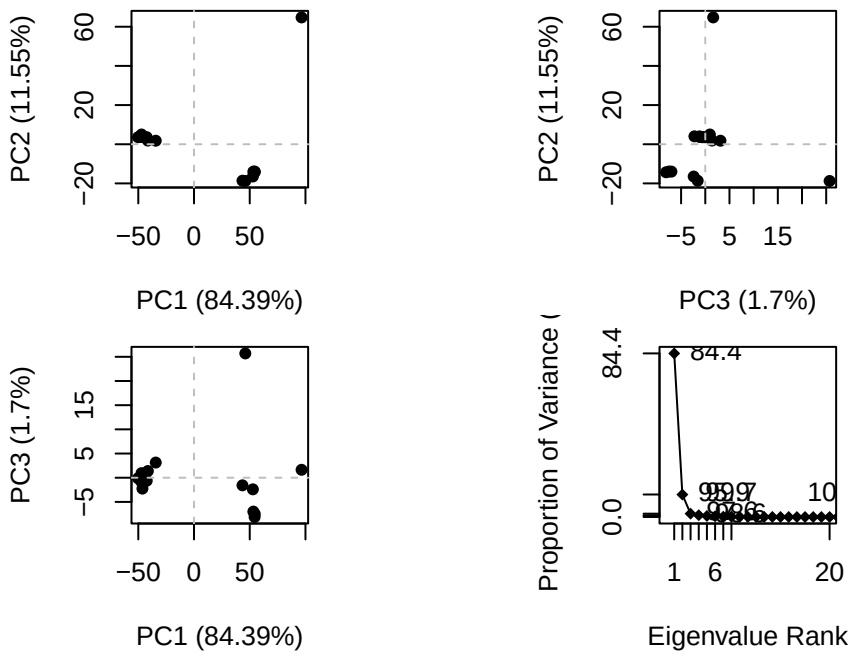
```
# Vector containing PDB codes for figure axis, the basename function strip the id name out
ids <- basename.pdb(pdbs$id)
```

```
# Draw schematic alignment

# plot(pdbs, labels=ids)
```

```
# anotate collected PDB structures
# basically expand description of the ids
anno <- pdb.annotate(ids)
unique(anno$source)
```

```
[1] "Escherichia coli"
[2] "Escherichia coli K-12"
[3] "Escherichia coli O139:H28 str. E24377A"
[4] "Escherichia coli str. K-12 substr. MDS42"
[5] "Photobacterium profundum"
[6] "Vibrio cholerae O1 biovar El Tor str. N16961"
[7] "Burkholderia pseudomallei 1710b"
[8] "Francisella tularensis subsp. tularensis SCHU S4"
```

```
# pca

pc.xray <- pca(pdbs)
plot(pc.xray)
```



Each of the dots represent one PDB structure.

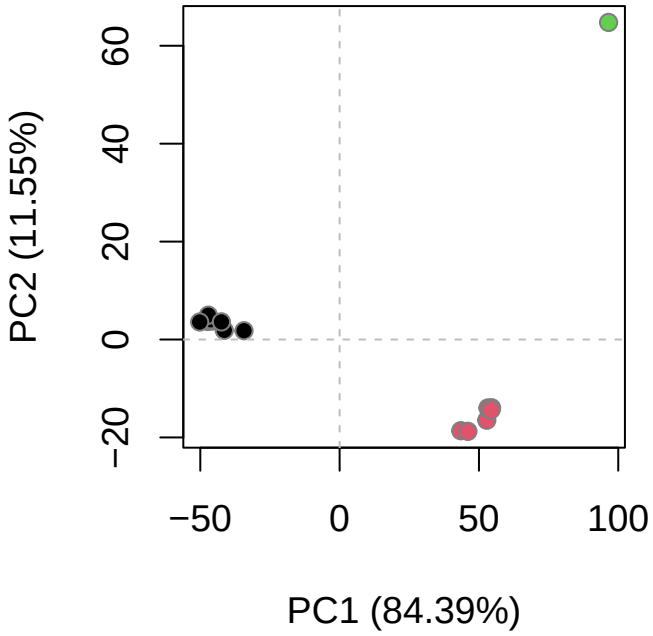
PMSD is the pairwise RMSD values of the structural ensemble. It represent the "distance" of each pdb structure pair. It could be used as distance matrix for clustering.

The clustering assigned a "label" to each class. It's sort of confirm the points that are clustered together in pca are indeed also close by rmsd distance.

```
# Calculate RMSD
rd <- rmsd(pdbs)
```

```
Warning in rmsd(pdbs): No indices provided, using the 204 non NA positions
```

```
# Structure-based clustering
hc.rd <- hclust(dist(rd))
grps.rd <- cutree(hc.rd, k=3)


# bg = plot background color
plot(pc.xray, 1:2, col="grey50", bg=grps.rd, pch=21, cex=1)
```



Visualization

```
# Visualize first principal component
pc1 <- mktrj(pc.xray, pc=1, file="pc_1.pdb")
```