

Class 09: Structural Bioinformatics

AUTHOR

Suraj Sidhu (A18512793)

The PDB Database

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

##PDB objects in R

```
library(readr)
stats <- read_csv("Data Export Summary.csv")
stats
```

Molecular Type	X-ray	EM	NMR	Integrative	Multiple methods	Neutron
<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1 Protein (only)	176204	20299	12708	342	218	83
2 Protein/Oligosacch...	10279	3385	34	8	11	1
3 Protein/NA	9007	5897	287	24	7	0
4 Nucleic acid (only)	3066	200	1553	2	15	3
5 Other	173	13	33	3	0	0
6 Oligosaccharide (o...	11	0	6	0	1	0
# i 2 more variables: Other <dbl>, Total <dbl>						

```
n.total <- sum(stats$Total)
n.total
```

[1] 243910

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

```
n.xray <- sum(stats$`X-ray`)
percent.xray <- n.xray / n.total * 100
percent.xray
```

[1] 81.48087

There are 81.48 percent xray structures in the PDB

```
n.em <- sum(stats$EM)
percent.em <- n.em / n.total * 100
percent.em
```

[1] 12.21516

There are 12.22 percent xray structures in the PDB

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

```
round(stats$Total[1]/n.total *100,2)
```

[1] 86.05

Exploring PDB Structures

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:

PQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWPKMIGGIGGF IKVRQYD
 QILIEICGHKAIGTQLVGPTPVNIIGRNLLTQIGCTLNFPQITLWQRPLVTIKIGGQLKE
 ALLDTGADDTVLEEMSLPGRWPKMIGGIGGF IKVRQYDQILIEICGHKAIGTQLVGPTP
 VNIIGRNLLTQIGCTLNF

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

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



My first view of HIV-Pr

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?

As of October 2025, there are approximately 400 HIV-1 protease structures.

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

Water molecules appear as single atoms in PDB structures because only the oxygen atom is visible in electron density maps; hydrogens are too small to detect at typical resolution and are not modeled explicitly.

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

The conserved water molecule is residue HOH 50, which bridges the two catalytic Asp25 residues in the HIV-1 protease active site.

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.

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

There are 198 amino acid residues in total (99 residues per chain A and B).

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

One of the non-protein residues is the ligand XK2 (an inhibitor molecule). Another is HOH (water).

Q9: How many protein chains are in this structure?

The structure contains two protein chains (A and B).

```
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)
```

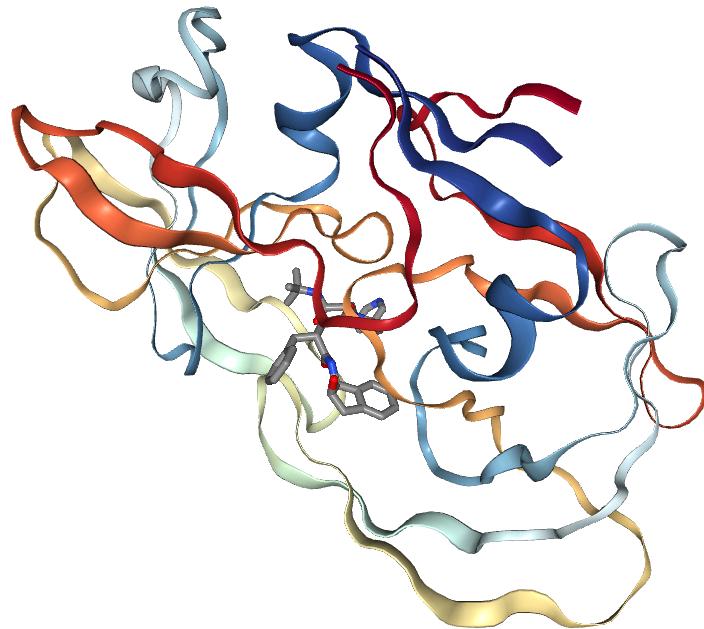
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
"P"	"Q"	"I"	"T"	"L"	"W"	"Q"	"R"	"P"	"L"	"V"	"T"	"I"	"K"	"I"	"G"	"G"	"Q"	"L"	"K"
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
"E"	"A"	"L"	"L"	"D"	"T"	"G"	"A"	"D"	"D"	"T"	"V"	"L"	"E"	"E"	"M"	"S"	"L"	"P"	"G"
41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
"R"	"W"	"K"	"P"	"K"	"M"	"I"	"G"	"G"	"I"	"G"	"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"))
```

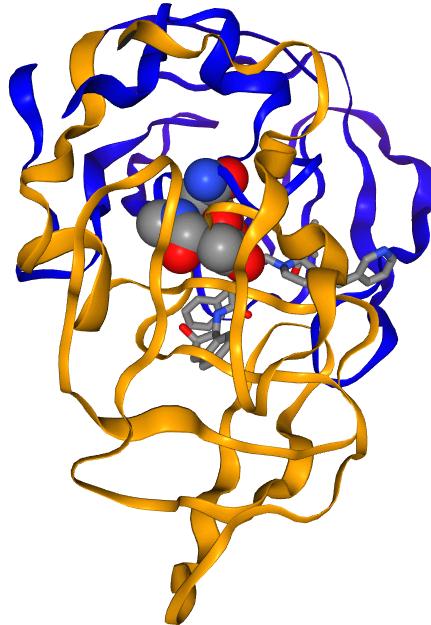
```
library(bio3dview)
library(NGLVieweR)

view.pdb(hiv) |>
  setSpin()
```



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

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



```
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:
MRIILLGAPGAGKGTQAQFIMEKYGIPQISTGDMRLAAVKSGSELGKQAKDIMDAGKLVT
DELVIALVKERIAQEDCRNGFLLDGFPRTIPQADAMKEAGINVDYVLEFDVPDELIVDKI
VGRRVHAPSGRVYHVKFNPPKVEGKDDVTGEELTRKDDQEETVRKRLVEYHQMTAPLIG
YYSKAEAGNTKYAKVDGTPVAEVRADLEKILG

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

Q10: From which three sources can we install the bio3d package?

`bio3d` can be installed from CRAN, Bioconductor, or GitHub.

Q11. Which of the above packages is not found on Bioconductor or CRAN?

NGLVieweR is not found on Bioconductor or CRAN — it must be installed from GitHub.

Q12. True or False? Functions from the pak package can be used to install packages from GitHub and BitBucket?

TRUE

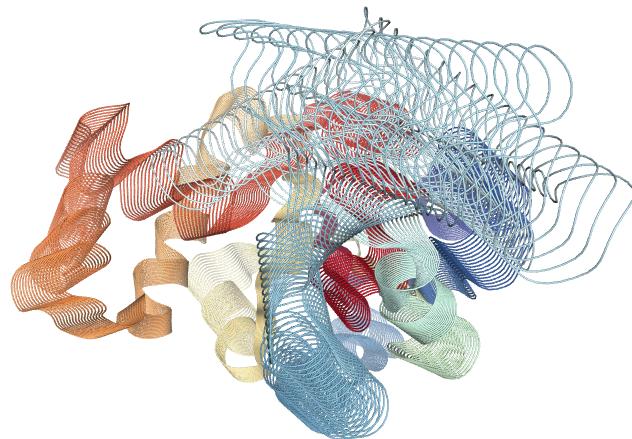
```
m <- nma(adk)
```

```
Building Hessian...      Done in 0.06 seconds.  
Diagonalizing Hessian... Done in 0.56 seconds.
```

Generate a "trajectory" of predicted motion

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

```
view.nma(m)
```



Q13. How many amino acid residues are there in Adenylate Kinase (6s36)?

Adenylate Kinase (PDB: 6S36) has 214 amino acid residues.

Q14. Briefly describe what you observe in the normal mode visualization.

The normal mode trajectory shows a large-scale opening and closing motion of the LID and NMP-binding domains relative to the CORE domain.