

Class 9: Structural Bioinformatics pt.1

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The PDB database

The main repository for biomolecular structure data is the Protein Data Bank (PDB)
<https://www.rcsb.org>

Let's have a quick look at the composition of this database:

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

	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			

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

```
as.numeric( sub(", ", "", stats$X.ray) )
```

```
[1] 176378 10284 9007 3077 174 11
```

This is annoying lets try a different import function from the `readr` package.

```
library(readr)
#or readr::read_csv()
stats <- 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.

```
stats
```

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>

Percent X-ray:

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

round( n.xray/n.total * 100, 2 )
```

```
[1] 81.43
```

Percent EM:

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

round( n.em/n.total * 100, 2 )
```

```
[1] 12.27
```

```
81.43 + 12.27
```

```
[1] 93.7
```

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

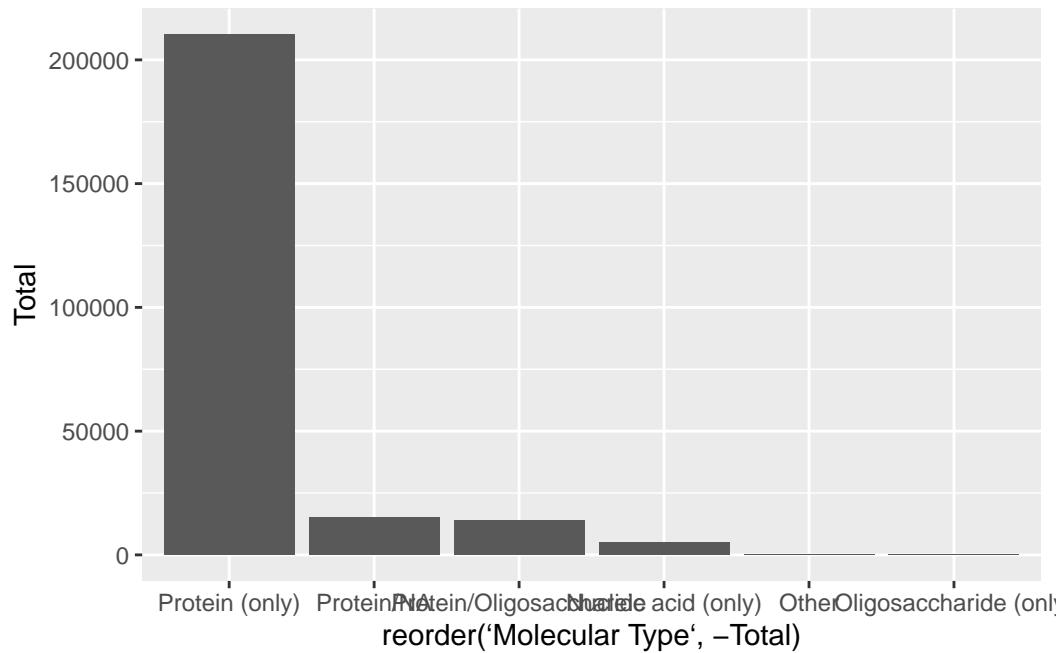
```
round(stats$Total[1] / n.total, 2)
```

```
[1] 0.86
```

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? Make a bar plot overview of Molecular type composition using ggplot

```
library(ggplot2)

ggplot(stats) +
  aes(reorder(`Molecular Type`, -Total), Total) +
  geom_col()
```



Visualizing structure data

The Mol* viewer is embedded in many bioinformatics websites. The homepage is <https://molstar.org>.

I can insert any figure or image file using markdown format

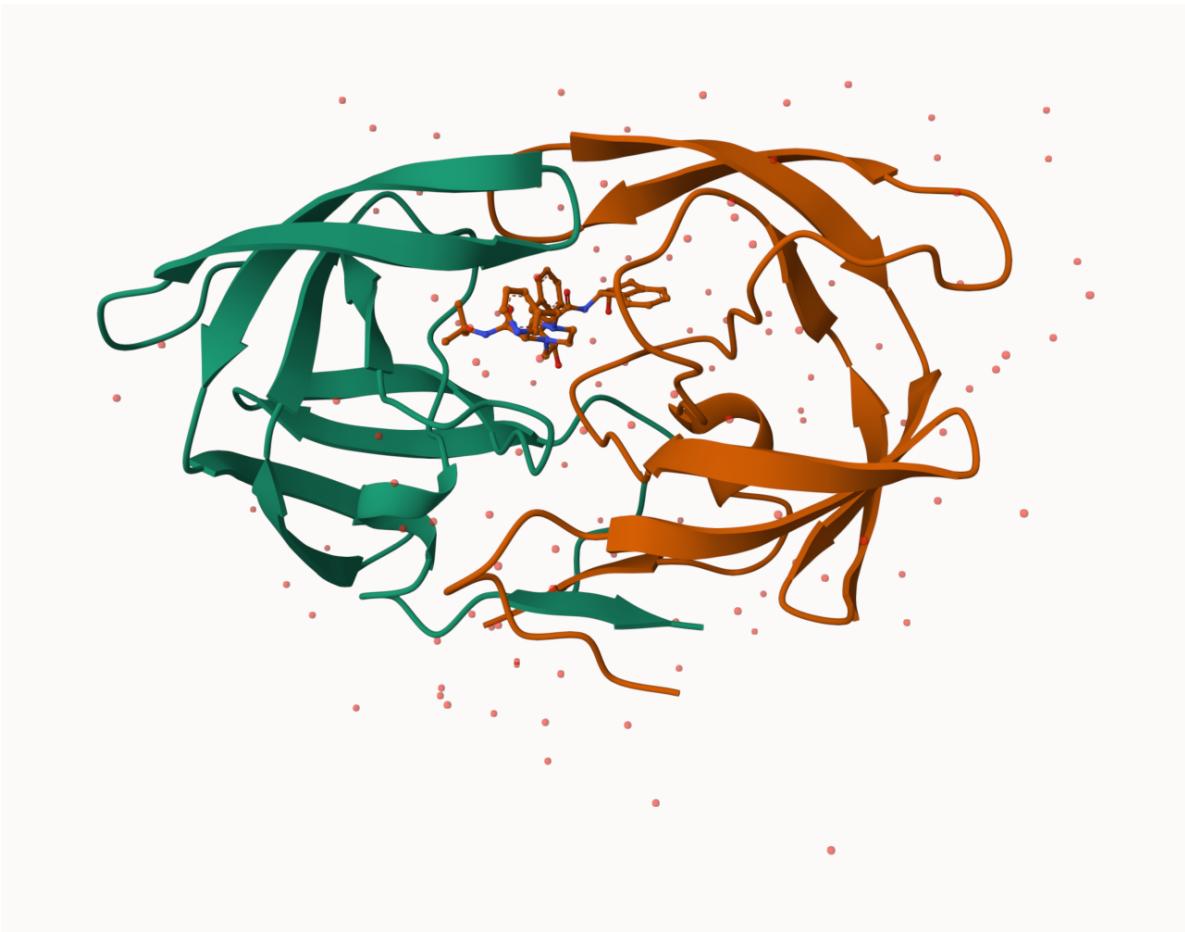


Figure 1: The HIV-Pr dimer with bound inhibitor

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

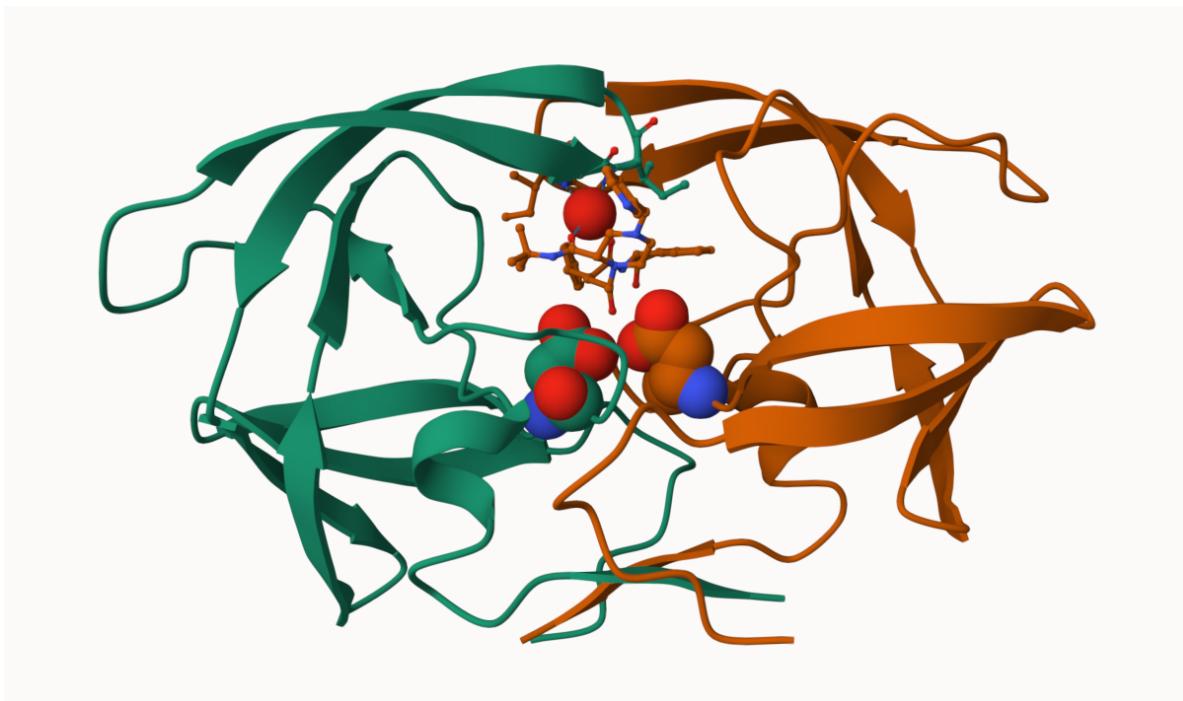
Only the oxygen atom is visible for each water molecule.

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



Bio3D package for structural bioinformatics

We can use the bio3d package to read and analyze biomolecular data in R:

```
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:

```
PQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWPKMIGGIGGFIKVRQYD
QILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFPQITLWQRPLVTIKIGGQLKE
ALLDTGADDTVLEEMSLPGRWPKMIGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTP
VNIIGRNLLTQIGCTLNF
```

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

```
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>										

Lets get 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" "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"

```

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

99 per chain.

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

HOH or MK1.

Q9: How many protein chains are in this structure?

Two chains.

```

chainA <- trim.pdb(hiv, chain="A")
chainA.seq <- pdbseq(chainA)

```

Let's blast

```

blast <- blast.pdb(chainA.seq)

```

```

Searching ... please wait (updates every 5 seconds) RID = G570D9AV014
....
Reporting 249 hits

```

```

head(blast$hit.tbl)

```

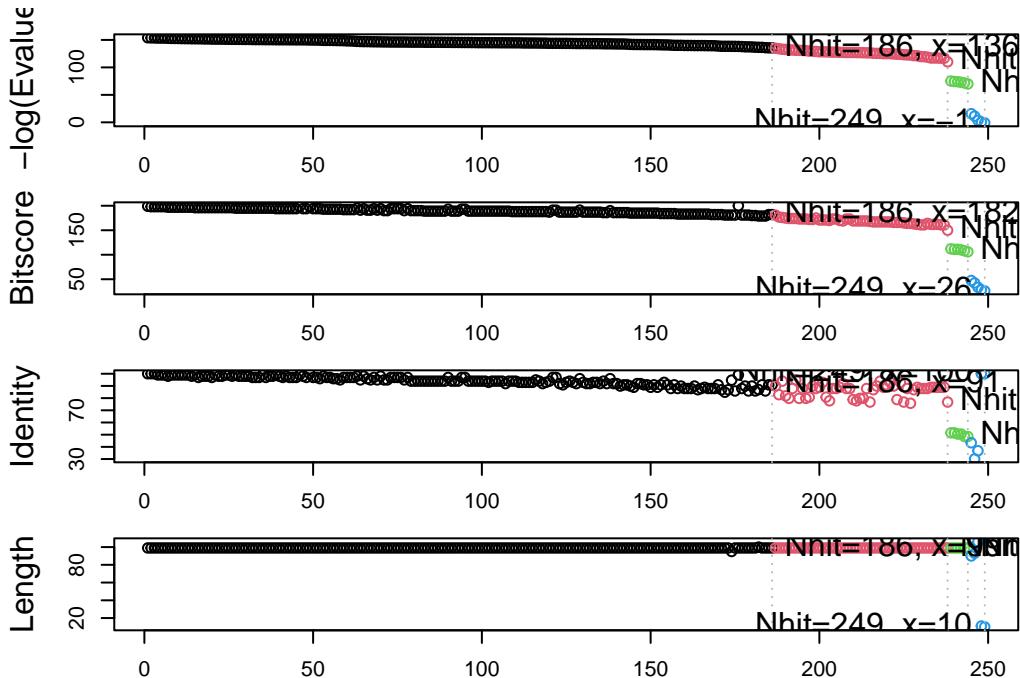
	queryid	subjectids	identity	alignmentlength	mismatches	gapopens	q.start	q.end	s.start	s.end	evalue	bitscore	positives	mlog.evalue	pdb.id	acc	
1	Query_2910643	1W5V_A	100.00		99	0	0		99	12	110	1.38e-67	199	100	153.9511	1W5V_A	1W5V_A
2	Query_2910643	2FDE_A	100.00		99	0	0		99	2	100	1.70e-67	198	100	153.7426	2FDE_A	2FDE_A
3	Query_2910643	1AJV_A	100.00		99	0	0		99	1	99	1.99e-67	198	100	153.5851	1AJV_A	1AJV_A
4	Query_2910643	2R38_A	98.99		99	1	0		99	1	99	2.50e-67	198	100	153.3569	2R38_A	2R38_A
5	Query_2910643	2R3T_A	98.99		99	1	0		99	1	99	2.50e-67	198	100	153.3569	2R3T_A	2R3T_A
6	Query_2910643	1HXB_A	98.99		99	1	0		99	1	99	2.50e-67	198	100	153.3569	1HXB_A	1HXB_A

Plot a quick overview of our blast results

```
hits <- plot(blast)

* Possible cutoff values:    135 110 69 -2
Yielding Nhits:          186 238 244 249

* Chosen cutoff value of:   69
Yielding Nhits:          244
```



```
hits$pdb.id
```

```
[1] "1W5V_A" "2FDE_A" "1AJV_A" "2R38_A" "2R3T_A" "1HXB_A" "1BV9_A" "1AAQ_A"
[9] "1AXA_A" "1HVS_A" "1ZP8_A" "2QHC_A" "1A8G_A" "204L_A" "5COK_A" "1TCX_A"
[17] "2Z54_A" "1D4S_A" "1BV7_A" "1BWA_A" "1A9M_A" "2FLE_A" "1ODY_A" "1GNN_A"
[25] "1GNM_A" "5YRS_B" "1HEF_E" "10DX_A" "4QGI_A" "1BVE_A" "2AZ8_A" "1A30_A"
[33] "6DH6_A" "6DHO_A" "2I4D_A" "600S_A" "1RL8_A" "5YRS_A" "1ZSF_A" "2Q64_A"
[41] "6DH3_A" "2NPH_A" "2Q63_A" "1LZQ_A" "1FB7_A" "1G6L_A" "1HIV_A" "600U_A"
[49] "1HVC_A" "2I4V_A" "2AZ9_A" "600T_A" "2P3B_B" "5KAO_A" "2WLO_A" "6OPT_A"
[57] "1IZI_A" "1MRX_A" "2PYM_A" "2PYN_A" "1DMP_A" "4K4P_A" "1LV1_A" "1AID_A"
[65] "1LV1_A" "1ZBG_A" "3TKG_A" "1HVC_A" "5YOK_A" "1G6L_A" "1FGC_C" "3K4V_A"
[73] "3KT5_A" "3KT5_A" "4QLH_A" "4QLH_A" "2F3K_A" "4Q5M_A" "2AOC_A" "3B80_A"
[81] "3VF5_A" "2AVQ_A" "1DW6_C" "1KZK_A" "2HS1_A" "1K6C_A" "1MTB_A" "4Q1X_A"
[89] "4Q1W_A" "4Q5M_A" "3D1X_A" "2AVM_A" "3PWM_A" "3KT2_A" "3KT2_A" "1SDV_A"
[97] "3JWV_A" "3OY4_A" "1A94_A" "2HS2_A" "4EJ8_A" "2FGU_A" "2AVV_A" "3JW2_A"
[105] "3BVA_A" "1FFF_C" "3S43_B" "2NXD_A" "1FG6_C" "1EBK_C" "4Q1Y_A" "3EL4_A"
[113] "1F7A_A" "1K2B_A" "2FGV_A" "1Z8C_A" "2G69_A" "3EL9_A" "30XV_A" "1BDR_A"
[121] "3N3I_A" "3N3I_A" "30XW_A" "3S43_A" "3EM3_A" "3CYW_A" "5KQX_A" "2B60_A"
[129] "7DOZ_A" "1K2C_A" "1MT7_A" "3EM4_A" "4QJ9_A" "1BDL_A" "3LZS_A" "5T84_A"
[137] "4DQB_A" "7DOZ_A" "4QJ2_A" "3LZV_A" "1SGU_A" "2FXE_A" "1BDQ_A" "3U71_A"
[145] "2R5P_A" "4OBD_A" "7MAS_A" "3IXO_A" "3D3T_A" "5YOJ_A" "3LZU_A" "4NJS_A"
[153] "3EKP_A" "1B6J_A" "3EKQ_A" "2RKF_A" "1C6X_A" "7MAR_A" "4DQF_A" "1RPI_A"
```

```
[161] "3OU1_B" "3PJ6_A" "2P3A_A" "60GQ_A" "30Q7_A" "5KR1_A" "30QD_A" "4RVI_A"
[169] "30QA_A" "1B6K_A" "30UD_B" "6MK9_A" "3S09_A" "1Q9P_A" "6I45_A" "7SEP_A"
[177] "4NJT_A" "3BXR_A" "4YOA_A" "4DQC_A" "2FDD_A" "2RKG_A" "4DQH_A" "2P3C_A"
[185] "4EP2_A" "4EP2_A" "4EQO_A" "4NPT_A" "6OPU_A" "4NPU_A" "3U7S_A" "3HAW_A"
[193] "2AZB_A" "3TTP_A" "3HBO_A" "3GGU_A" "7N6T_A" "60PV_A" "4EQO_A" "60PX_A"
[201] "204N_A" "5T2E_A" "3UCB_A" "3KA2_A" "3FSM_A" "60PW_A" "2AZC_A" "3FSM_A"
[209] "3HLO_A" "2P3D_A" "3T3C_A" "7MYP_A" "6054_X" "60PY_A" "4Z4X_A" "60PZ_A"
[217] "2JE4_A" "1DAZ_C" "7MAP_A" "7MAQ_A" "1K1U_A" "2B7Z_A" "3MWS_A" "1K1T_A"
[225] "8DCH_A" "3I2L_A" "6P9A_A" "2FXD_A" "2J9J_A" "3DCK_A" "2J9J_B" "3NXE_A"
[233] "2040_A" "2040_A" "3NXE_A" "3KA2_A" "3HLO_A" "5B18_A" "1SIP_A" "2SAM_A"
[241] "1AZ5_A" "1SIV_A" "1HII_A" "1IVP_A"
```

Prediction of functional motions

We can run an Normal Mode Analysis (NMA) to predict large scale motions/flexibility/dynamics of any biomolecule that we can read into R.

Let's look at ADK

```
adk <- read.pdb("1AKE")
```

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

```
adk_A <- trim.pdb(adk, chain="A")
adk_A
```

```
Call: trim.pdb(pdb = adk, chain = "A")

Total Models#: 1
Total Atoms#: 1954, XYZs#: 5862 Chains#: 1 (values: A)

Protein Atoms#: 1656 (residues/Calpha atoms#: 214)
Nucleic acid Atoms#: 0 (residues/phosphate atoms#: 0)

Non-protein/nucleic Atoms#: 298 (residues: 242)
Non-protein/nucleic resid values: [ AP5 (1), HOH (241) ]

Protein sequence:
MRIILLGAPGAGKGTQAQFIMEKYGIPQISTGDMRLRAAVKSGSELGKQAKDIMDAGKLVT
```

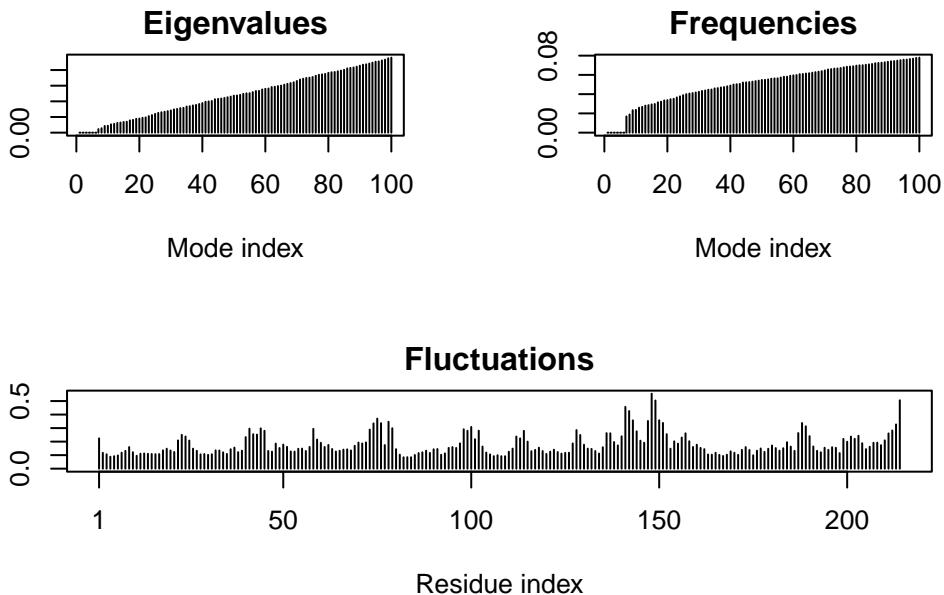
```
DELVIALVKERIAQEDCRNGFLLDGFPR TIPQADAMKEAGINV D YVLEFDVPDELIVDRI  
VGRRVHAPSGRVYHVKFNPPKVEGKDDVTGEELTRKDDQEETVRKRLVEYHQMTAPLIG  
YY SKEAEAGNTKYAKVDGTPVAEVRA D LEKILG
```

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

```
m <- nma(adk_A)
```

```
Building Hessian...      Done in 0.014 seconds.  
Diagonalizing Hessian... Done in 0.275 seconds.
```

```
plot(m)
```



Let's write out a “trajectory” of predicted motion

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

Play with 3D viewing in R

We can use the new **bio3dview** package, which is not yet on CRAN, to render interactive 3D views in R and HTML quarto output reports.

To install from GitHub we can use the **pak** package.

Q10. Which of the packages above is found only on BioConductor and not CRAN?

Bio3dview.

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

rpdb.

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

True.

Comparative analysis protein structures

Starting with a sequence or structure ID (accession number) let's run a complete analysis plan.

```
library(bio3d)

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

Warning in get.seq(id): Removing existing file: seqs.fasta

Fetching... Please wait. Done.

```
aa
```

	1	60
pdb 1AKE A	MRIILLGAPGAGKGTQAQFIMEKYGIPQISTGMLRAAVKGSELGKQAKDIMDAGKLVT	
	1	60
	61	120
pdb 1AKE A	DELVIALVKERIAQEDCRNGFLLDGFPRTRIPQADAMKEAGINVVDYVLEFDVPDELIVDRI	
	61	120
	121	180
pdb 1AKE A	VGRRVHAPSGRKYHVKFNPPKVEGKDDVTGEELTTRKDDQEETVRKRLVEYHQMTAPLIG	
	121	180

```
    181      .      .      .      214  
pdb|1AKE|A  YYSKAEAGNTKYAKVVDGTPVAEVRADEKILG  
    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
```

```
blast <- blast.pdb(aa)
```

```
Searching ... please wait (updates every 5 seconds) RID = GRKG4GBV014
```

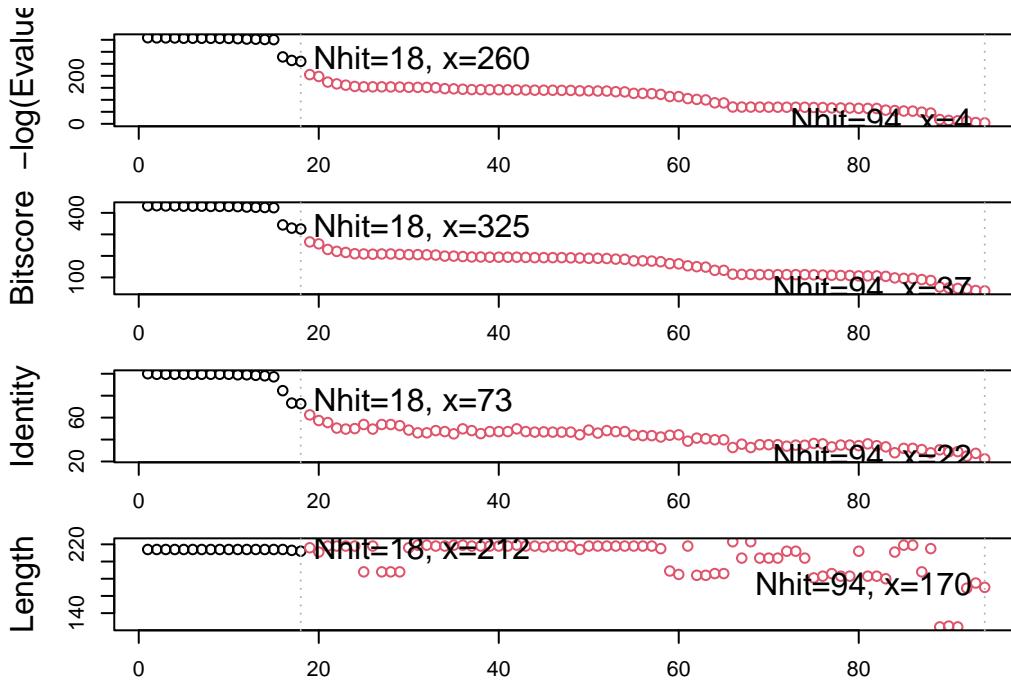
```
.....
```

```
Reporting 94 hits
```

```
hits <- plot(blast)
```

```
* Possible cutoff values: 260 3  
  Yielding Nhits: 18 94
```

```
* Chosen cutoff value of: 260  
  Yielding Nhits: 18
```



```
hits$pdb.id
```

```
[1] "1AKE_A" "8BQF_A" "4X8M_A" "6S36_A" "8Q2B_A" "8RJ9_A" "6RZE_A" "4X8H_A"
[9] "3HPR_A" "1E4V_A" "5EJE_A" "1E4Y_A" "3X2S_A" "6HAP_A" "6HAM_A" "8PVW_A"
[17] "4K46_A" "4NP6_A"
```

Download all these “hits” that are similar to our starting id sequence.

```
# Download released PDB files
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/8BQF.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/8Q2B.pdb.gz exists. Skipping download

Warning in get.pdb(hits\$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/8RJ9.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

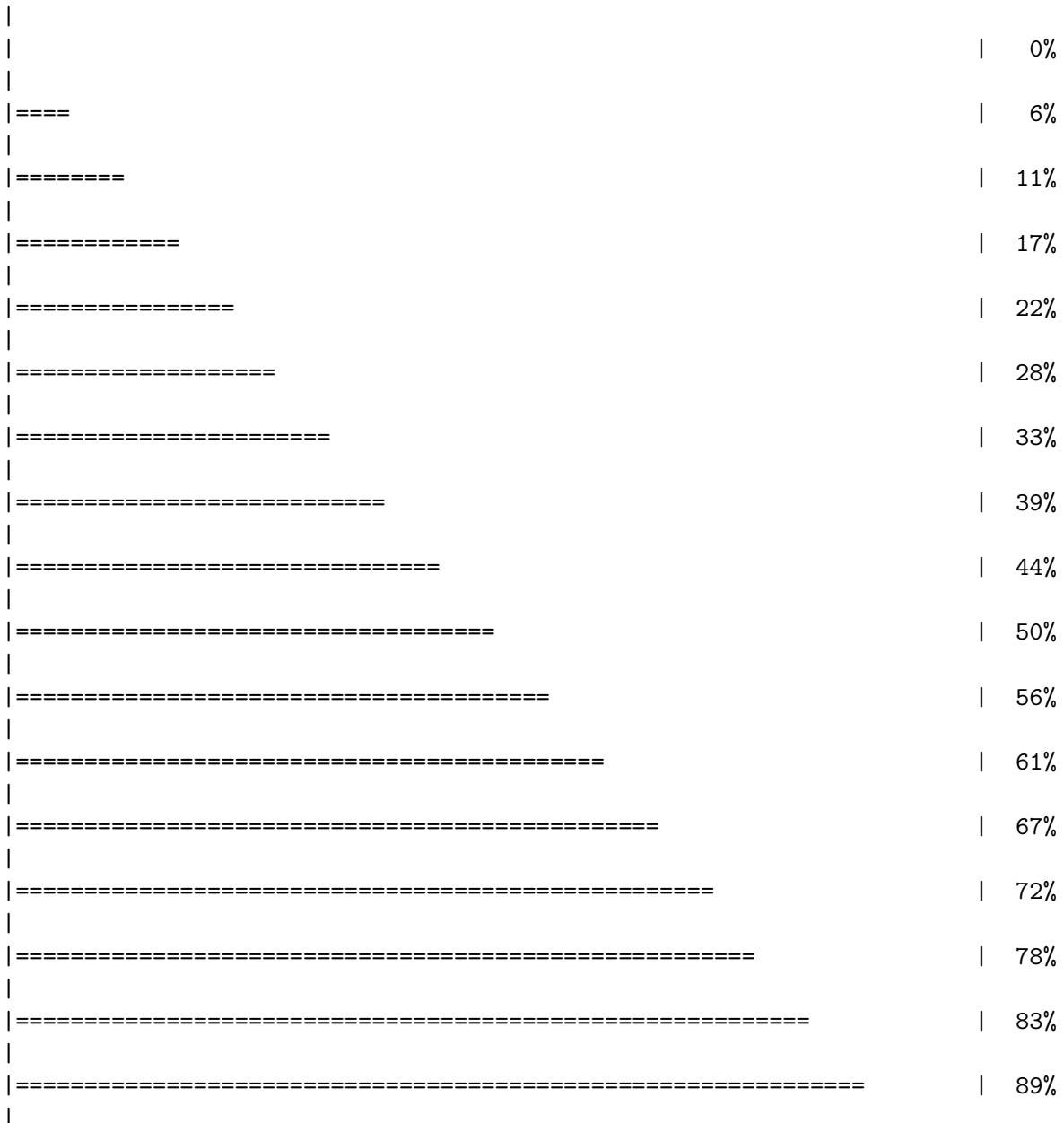
Warning in get.pdb(hits\$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/6HAP.pdb.gz exists. Skipping download

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/8PWV.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
```



```
|=====| 94%  
|  
|=====| 100%
```

```
pdbaln <- pdbaln(files, fit = TRUE, exefile="msa")
```

Reading PDB files:
pdbs/split_chain/1AKE_A.pdb
pdbs/split_chain/8BQF_A.pdb
pdbs/split_chain/4X8M_A.pdb
pdbs/split_chain/6S36_A.pdb
pdbs/split_chain/8Q2B_A.pdb
pdbs/split_chain/8RJ9_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/8PVW_A.pdb
pdbs/split_chain/4K46_A.pdb
pdbs/split_chain/4NP6_A.pdb

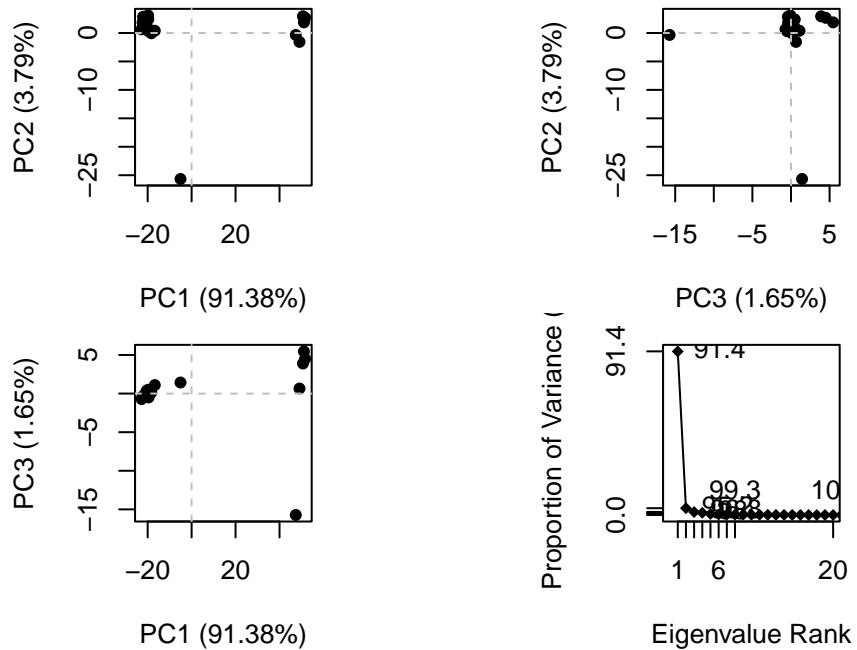
PDB has ALT records, taking A only, rm.alt=TRUE
.. PDB has ALT records, taking A only, rm.alt=TRUE
.. PDB has ALT records, taking A only, rm.alt=TRUE
.. PDB has ALT records, taking A only, rm.alt=TRUE
.. PDB has ALT records, taking A only, rm.alt=TRUE
.. PDB has ALT records, taking A only, rm.alt=TRUE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

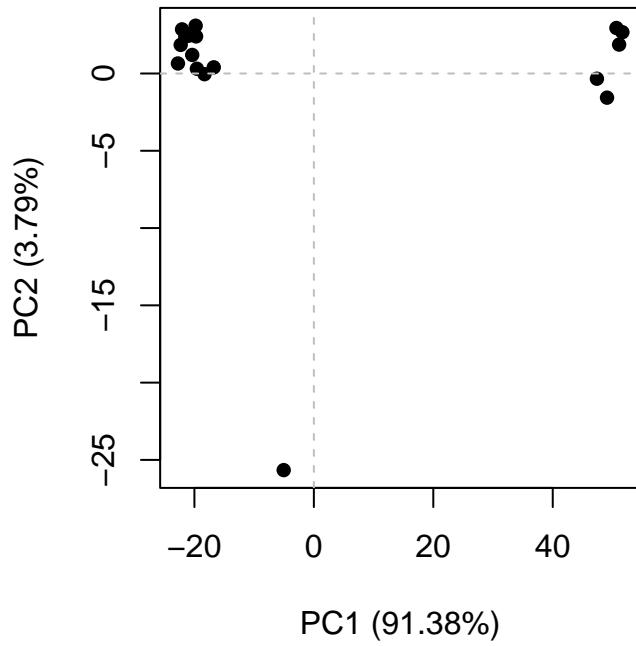
pdb/seq: 1 name: pdbs/split_chain/1AKE_A.pdb
 PDB has ALT records, taking A only, rm.alt=TRUE

```
pdb/seq: 2    name: pdbs/split_chain/8BQF_A.pdb
  PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 3    name: pdbs/split_chain/4X8M_A.pdb
pdb/seq: 4    name: pdbs/split_chain/6S36_A.pdb
  PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 5    name: pdbs/split_chain/8Q2B_A.pdb
  PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 6    name: pdbs/split_chain/8RJ9_A.pdb
  PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 7    name: pdbs/split_chain/6RZE_A.pdb
  PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 8    name: pdbs/split_chain/4X8H_A.pdb
pdb/seq: 9    name: pdbs/split_chain/3HPR_A.pdb
  PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 10   name: pdbs/split_chain/1E4V_A.pdb
pdb/seq: 11   name: pdbs/split_chain/5EJE_A.pdb
  PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 12   name: pdbs/split_chain/1E4Y_A.pdb
pdb/seq: 13   name: pdbs/split_chain/3X2S_A.pdb
pdb/seq: 14   name: pdbs/split_chain/6HAP_A.pdb
pdb/seq: 15   name: pdbs/split_chain/6HAM_A.pdb
  PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 16   name: pdbs/split_chain/8PVW_A.pdb
  PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 17   name: pdbs/split_chain/4K46_A.pdb
  PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 18   name: pdbs/split_chain/4NP6_A.pdb
```

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



```
plot(pc.xray, 1:2)
```



```
mktrj(pc.xray, file = "pca_results.pdb")
```

```
#library(bio3dview)
#view.pca(pc.xray)
```