class 10

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what is in the PDB?

dowload a csv with current commposition data

```
pdbstats <- read.csv('pdbsummaru.csv', row.names=1)
```

```
head(pdbstats)
```

	X.ray	EM	NMR	Multiple.methods	Neutron	Other	Total
Protein (only)	161,663	12,592	12,337	200	74	32	186,898
Protein/Oligosaccharide	9,348	2,167	34	8	2	0	11,559
Protein/NA	8,404	3,924	286	7	0	0	12,621
Nucleic acid (only)	2,758	125	1,477	14	3	1	4,378
Other	164	9	33	0	0	0	206
Oligosaccharide (only)	11	0	6	1	0	4	22

testing method

```
x <- '2,222'
as.numeric(gsub(',','', x))
```

```
[1] 2222
```

creating into a function to remove comma, convert to numeric and sum the values

```
sumnum <- function(x){
  sum(as.numeric(gsub(',','', x)))
}
```

```
sumnum(pdbstats$X.ray)
```

```
[1] 182348
```

```
sumnum(pdbstats$EM)
```

```
[1] 18817
```

apply the function to the entrie table and divide by total to get the percentages

```
apply(pdbstats,2,sumnum) / sumnum(pdbstats$Total)
```

```
        X.ray                EM               NMR Multiple.methods
0.8454405519     0.0872433746     0.0657118748     0.0010663749
     Neutron            Other            Total
0.0003662766     0.0001715473     1.0000000000
```

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

84.54% is done using x-ray and 8.7% is done using EM

```
apply(pdbstats,1,sumnum) / sum(apply(pdbstats,1,sumnum))
```

```
      Protein (only) Protein/Oligosaccharide              Protein/NA
        0.8665362289           0.0535922924           0.0585161625
Nucleic acid (only)                  Other Oligosaccharide (only)
        0.0202982141           0.0009551010           0.0001020011
```

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

86% is protien only

Q3: How does the total number of protein structires in the PDB relate to the total number of protein sequences in UniProt?

the PDB database only accounts of 0.0746% of the data avaliable in Uniprot

```
186898/250322721 *100
```

```
[1] 0.07466282
```

Using Mol*

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

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

25

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

working with structures in R

```
library(bio3d)
```

```
Warning: package 'bio3d' was built under R version 4.2.3
```

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

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

```
hiv
```

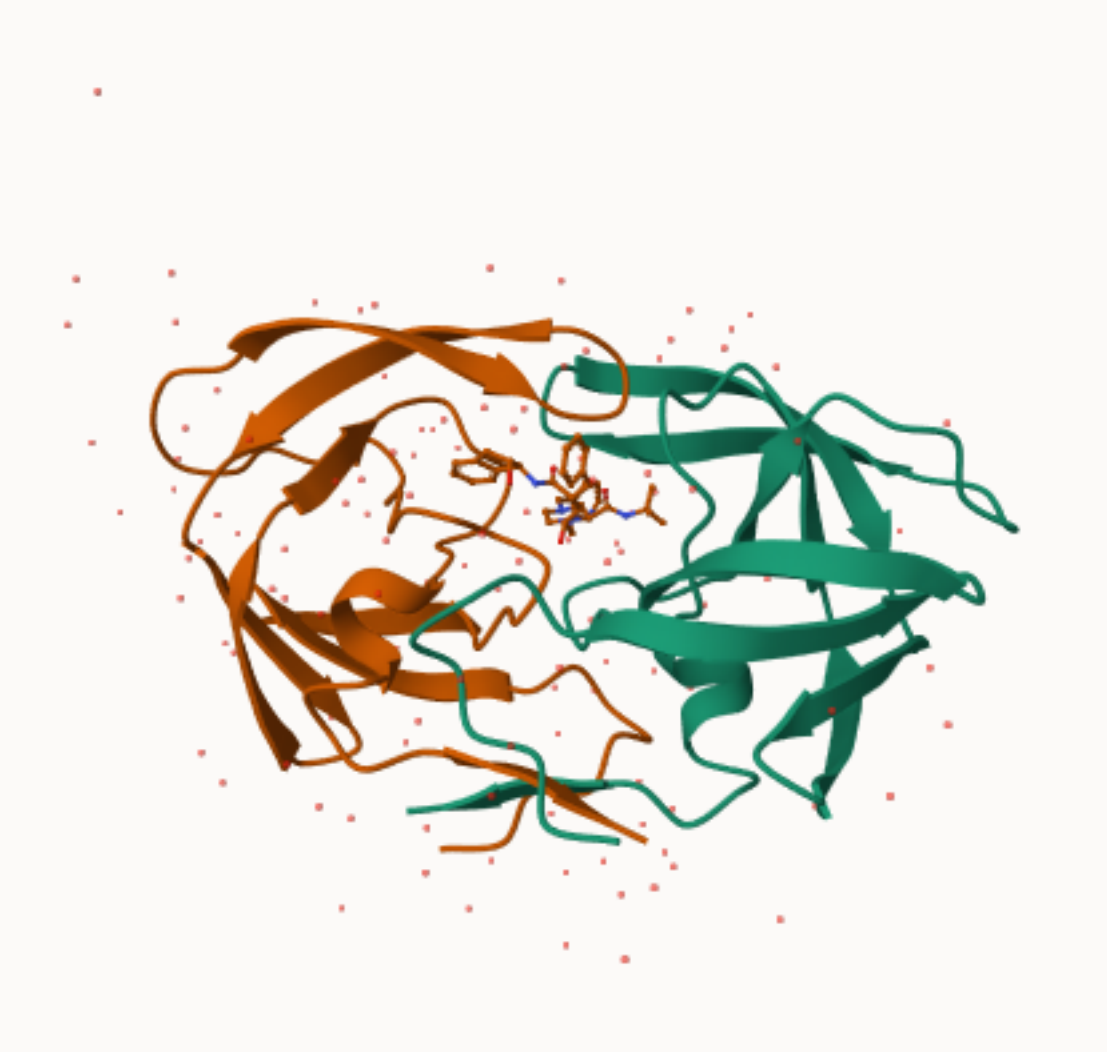


Figure 1: 1HSG structure

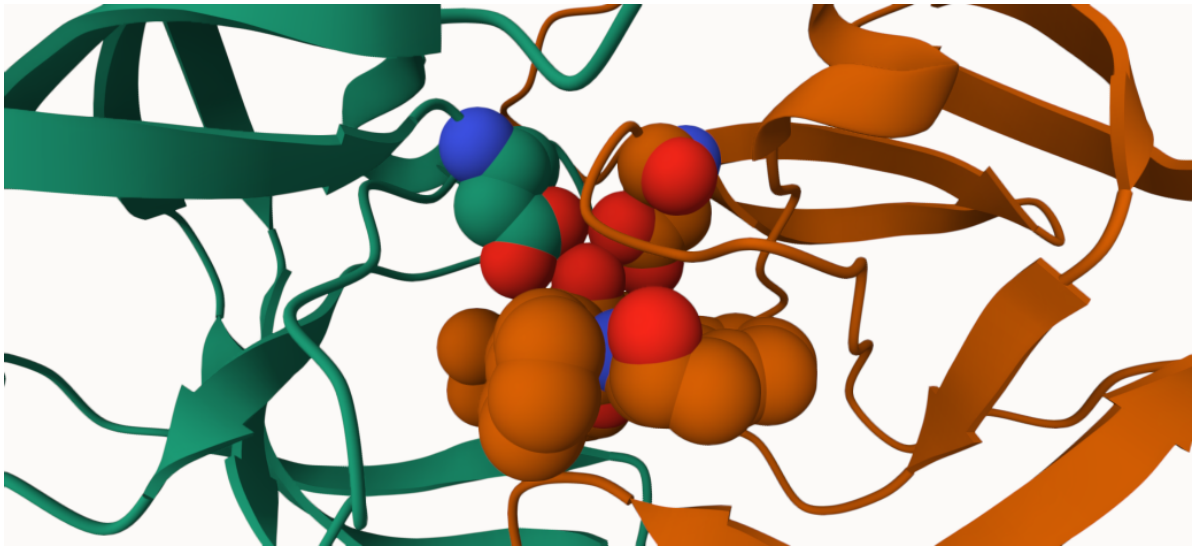


Figure 2: 1HSG structure displaying the MK1 ligand and the Asp 25 catalytic residues

```
 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
```

```
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>
```

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

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

MK1

Q9: How many protein chains are in this structure?

2

Predicting functional motions of a single structure

```
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:
      MRIILLGAPGAGKGTQAQFIMEKYGIPQISTGDMLRAAVKSGSELGKQAKDIMDAGKLVT
      DELVIALVKERIAQEDCRNGFLLDGFPRTIPQADAMKEAGINVDYVLEFDVPDELIVDKI
      VGRRVHAPSGRVYHVKFNPPKVEGKDDVTGEELTTRKDDQEETVRKRLVEYHQMTAPLIG
      YYSKEAEAGNTKYAKVDGTKPVAEVRADLEKILG

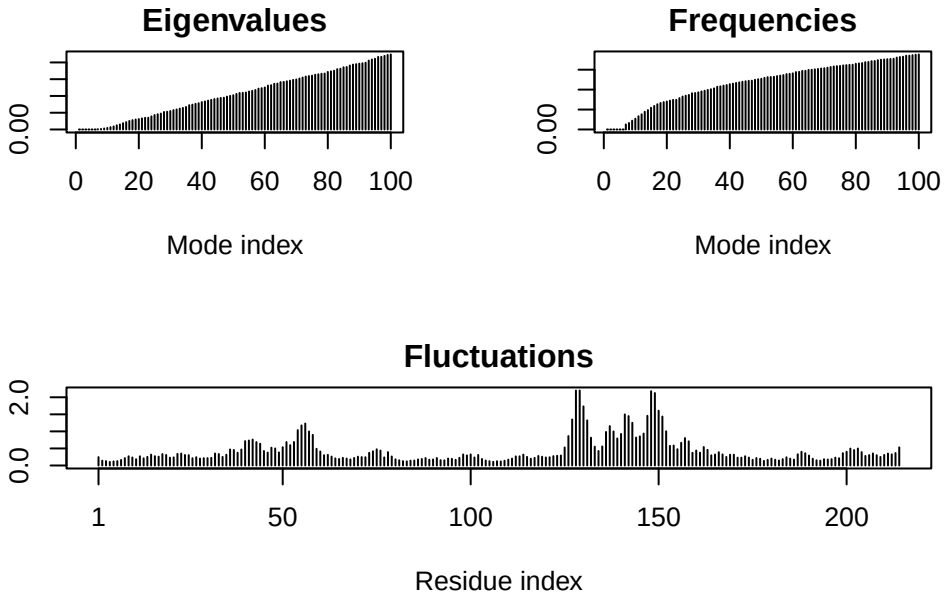
+ attr: atom, xyz, seqres, helix, sheet,
        calpha, remark, call
```

Normal mode analysis (nma) - predicts functional motions and large-scale stucture changes

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

```
 Building Hessian...        Done in 0.04 seconds.
 Diagonalizing Hessian...   Done in 0.59 seconds.
```

```
plot(m)
```



make a movie (a.k.a trajectory) of the predicted motion

```
mktrj(m, file='adk_movie.pdb')
```

Quick comparitice analysis of structures

extract sequence and runa BLAST search

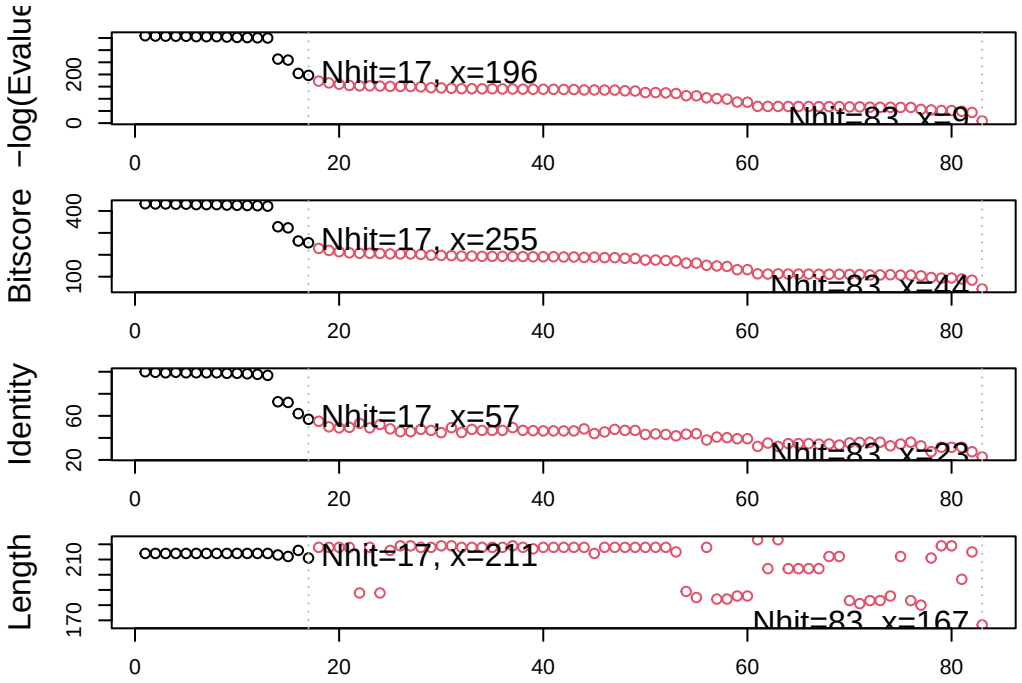
```
s <- pdbseq(adk)
blast <- blast.pdb(s)
```

```
Searching ... please wait (updates every 5 seconds) RID = WJDC3EW301N
.
Reporting 83 hits
```

```
plot(blast)
```

```
 * Possible cutoff values:    196 9
           Yielding Nhits:    17 83

 * Chosen cutoff value of:    196
           Yielding Nhits:    17
```

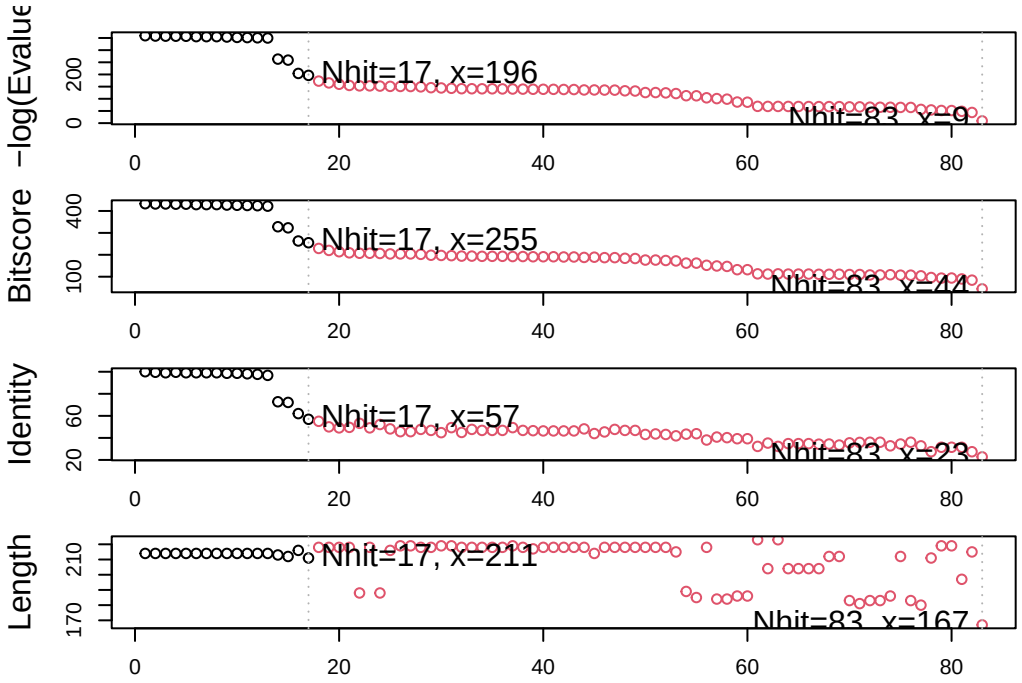


Get the ruslts from BLAST and download all the top hits

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

```
* Possible cutoff values:    196 9
          Yielding Nhits:    17 83

* Chosen cutoff value of:    196
          Yielding Nhits:    17
```



accession numbers of all the significant blasts to the database

```
hits$pdb.id
```

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

download all the blast result 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/6S36.pdb exists. Skipping download
```

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

```
Warning in get.pdb(hits$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE):
pdbs/8BQF.pdb exists. Skipping download
```

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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```

Align and superimpose the structures

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

```
Reading PDB files:
pdbs/split_chain/6S36_A.pdb
pdbs/split_chain/1AKE_A.pdb
pdbs/split_chain/8BQF_A.pdb
pdbs/split_chain/6RZE_A.pdb
pdbs/split_chain/4X8M_A.pdb
pdbs/split_chain/4X8H_A.pdb
pdbs/split_chain/1E4V_A.pdb
pdbs/split_chain/3HPR_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
.   PDB has ALT records, taking A only, rm.alt=TRUE
....

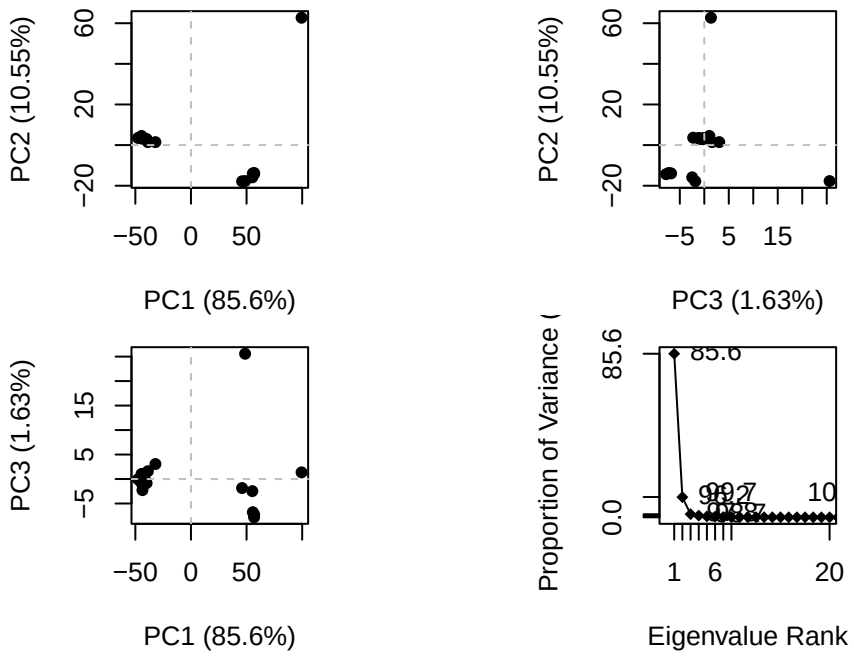
Extracting sequences

pdb/seq: 1   name: pdbs/split_chain/6S36_A.pdb
   PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 2   name: pdbs/split_chain/1AKE_A.pdb
   PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 3   name: pdbs/split_chain/8BQF_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/4X8M_A.pdb
pdb/seq: 6   name: pdbs/split_chain/4X8H_A.pdb
```

```
pdb/seq: 7   name: pdbs/split_chain/1E4V_A.pdb
pdb/seq: 8   name: pdbs/split_chain/3HPR_A.pdb
   PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 9   name: pdbs/split_chain/5EJE_A.pdb
   PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 10   name: pdbs/split_chain/1E4Y_A.pdb
pdb/seq: 11   name: pdbs/split_chain/3X2S_A.pdb
pdb/seq: 12   name: pdbs/split_chain/6HAP_A.pdb
pdb/seq: 13   name: pdbs/split_chain/6HAM_A.pdb
   PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 14   name: pdbs/split_chain/4K46_A.pdb
   PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 15   name: pdbs/split_chain/4NP6_A.pdb
pdb/seq: 16   name: pdbs/split_chain/3GMT_A.pdb
pdb/seq: 17   name: pdbs/split_chain/4PZL_A.pdb
```

PCA of all the adk structures

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



```
mktrj(pc.xray, file='pca_movie.pdb')
```