Structural Bioinformatics pt 2

Emily Hendrickson (PID: A69034780)

First, finish last week's stuff.

```
library(bio3d)
```

```
Warning: package 'bio3d' was built under R version 4.3.3
```

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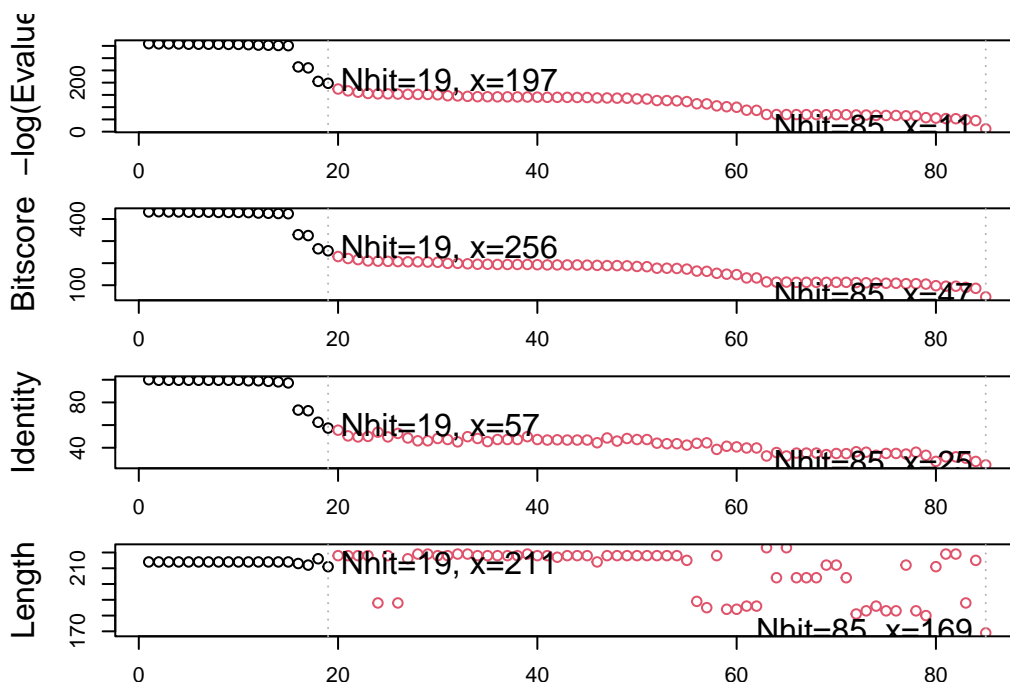
```r
b <- blast.pdb(aa)
```

```
 Searching ... please wait (updates every 5 seconds) RID = K2YC6TB2016
 ................................................
 Reporting 85 hits
```

```r
hits <- plot(b)
```

```
  * Possible cutoff values:    197 11
           Yielding Nhits:    19 85

  * Chosen cutoff value of:    197
           Yielding Nhits:    19
```

```r
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/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
```
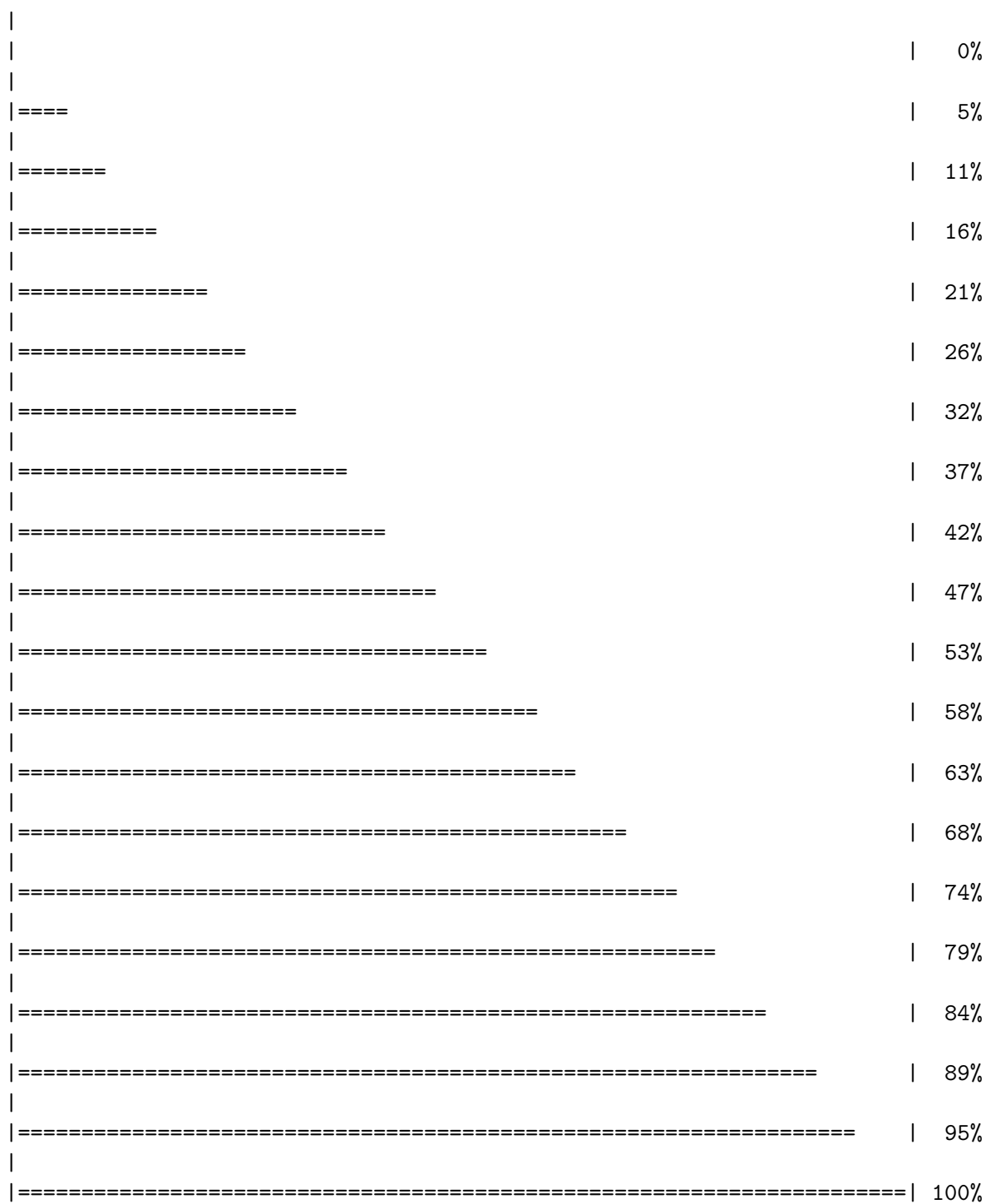
```
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|
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```

I have now downloaded the all the ADK structures in the PDB database but viewing them is

challenging. They need to be aligned and superposed. I already had BiocManager installed and installed the pdbaln package using BiocManager::install()

```
pdbs <- 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/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
....     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/4K46_A.pdb
    PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 17   name: pdbs/split_chain/4NP6_A.pdb
pdb/seq: 18   name: pdbs/split_chain/3GMT_A.pdb
pdb/seq: 19   name: pdbs/split_chain/4PZL_A.pdb
```
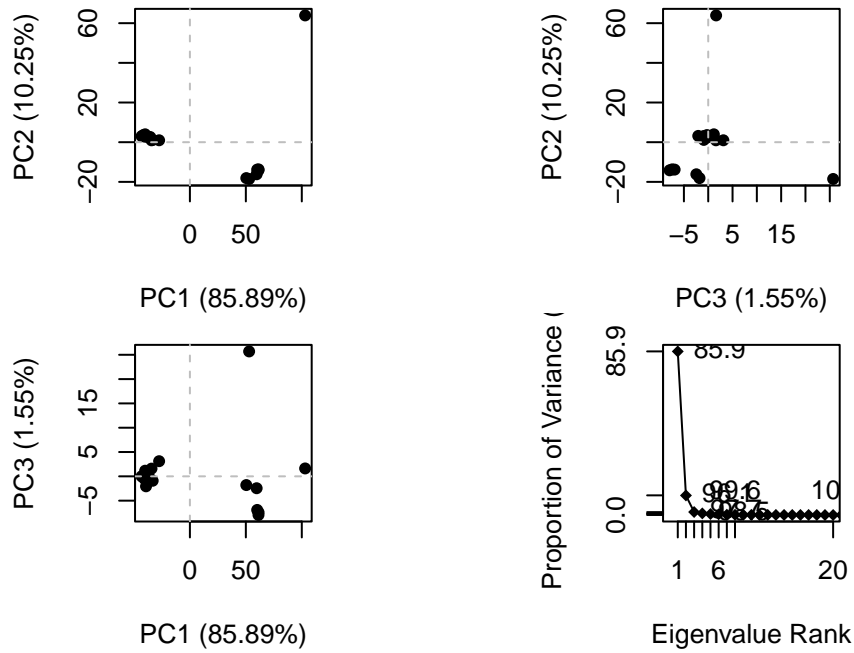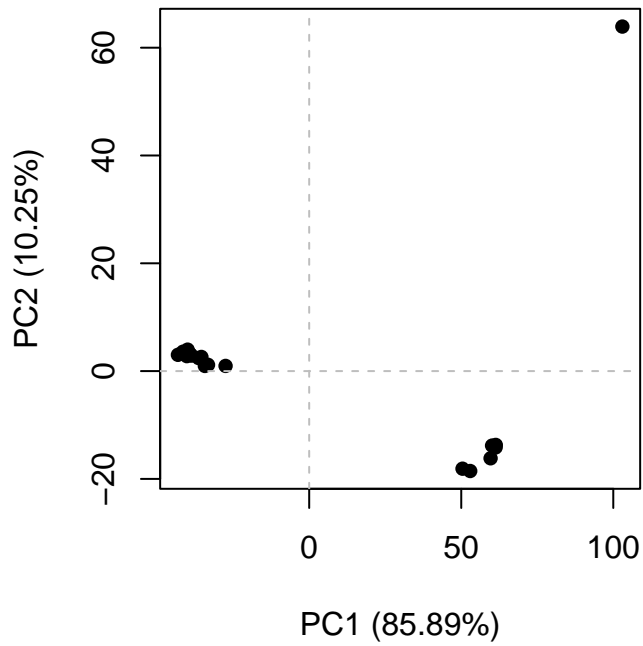
##Principal Component Analysis

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

```r
plot(pc, pc.axes = c(1:2))
```


visualize the structural components of the variation in xray structures that is described by PC1.

```
pc1 <- mktrj(pc, pc=1, file="pc_1.pdb")
```

AlphaFold

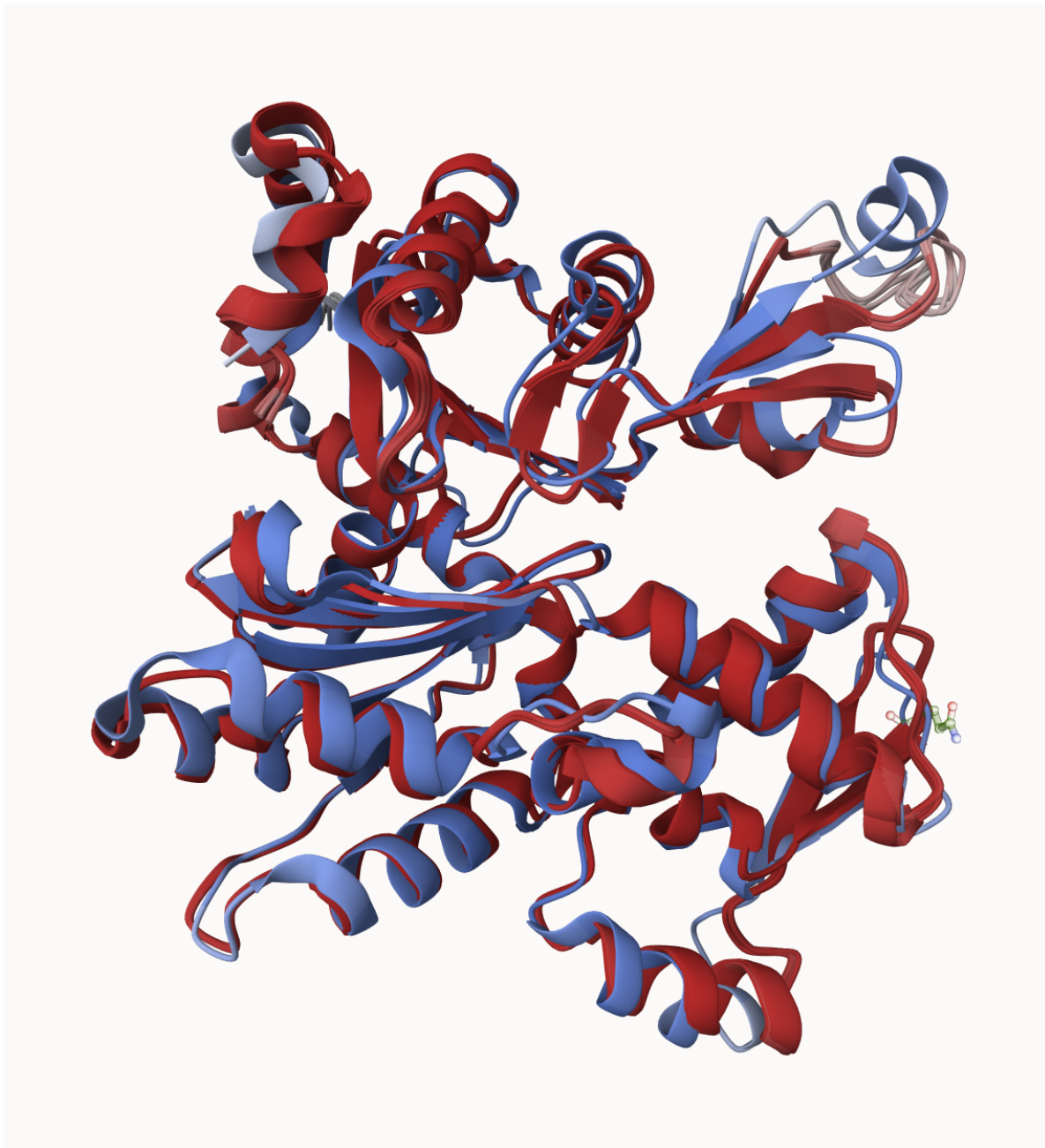I used the predicted protein sequence from my find a gene project.

Figure 1: My predicted protein structures with the reference actin PDB structure

```
results_dir <- "test_3910f/"
pdb_files <- list.files(path=results_dir,
                        pattern="*.pdb",
```

```
                            full.names = TRUE)
basename(pdb_files)
```

```
[1] "test_3910f_unrelaxed_rank_001_alphafold2_ptm_model_4_seed_000.pdb"
[2] "test_3910f_unrelaxed_rank_002_alphafold2_ptm_model_1_seed_000.pdb"
[3] "test_3910f_unrelaxed_rank_003_alphafold2_ptm_model_5_seed_000.pdb"
[4] "test_3910f_unrelaxed_rank_004_alphafold2_ptm_model_3_seed_000.pdb"
[5] "test_3910f_unrelaxed_rank_005_alphafold2_ptm_model_2_seed_000.pdb"
```

```
library(bio3d)
pdbs <- pdbaln(pdb_files, fit=TRUE, exefile="msa")
```

```
Reading PDB files:
test_3910f//test_3910f_unrelaxed_rank_001_alphafold2_ptm_model_4_seed_000.pdb
test_3910f//test_3910f_unrelaxed_rank_002_alphafold2_ptm_model_1_seed_000.pdb
test_3910f//test_3910f_unrelaxed_rank_003_alphafold2_ptm_model_5_seed_000.pdb
test_3910f//test_3910f_unrelaxed_rank_004_alphafold2_ptm_model_3_seed_000.pdb
test_3910f//test_3910f_unrelaxed_rank_005_alphafold2_ptm_model_2_seed_000.pdb
.....

Extracting sequences

pdb/seq: 1   name: test_3910f//test_3910f_unrelaxed_rank_001_alphafold2_ptm_model_4_seed_000
pdb/seq: 2   name: test_3910f//test_3910f_unrelaxed_rank_002_alphafold2_ptm_model_1_seed_000
pdb/seq: 3   name: test_3910f//test_3910f_unrelaxed_rank_003_alphafold2_ptm_model_5_seed_000
pdb/seq: 4   name: test_3910f//test_3910f_unrelaxed_rank_004_alphafold2_ptm_model_3_seed_000
pdb/seq: 5   name: test_3910f//test_3910f_unrelaxed_rank_005_alphafold2_ptm_model_2_seed_000
```

```
pdbs
```

```
                                   1        .         .         .         .        50
[Truncated_Name:1]test_3910f    CDEEVAALVVDNGSGMCKAGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK
[Truncated_Name:2]test_3910f    CDEEVAALVVDNGSGMCKAGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK
[Truncated_Name:3]test_3910f    CDEEVAALVVDNGSGMCKAGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK
[Truncated_Name:4]test_3910f    CDEEVAALVVDNGSGMCKAGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK
[Truncated_Name:5]test_3910f    CDEEVAALVVDNGSGMCKAGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQK
                                **************************************************
                                   1        .         .         .         .        50

                                  51        .         .         .         .       100
```

11

```
[Truncated_Name:1]test_3910f     DSYVGDEAQSKRGILTLKYPIEHGIVTNWDDMEKIWHHTFYNELRVAPEE
[Truncated_Name:2]test_3910f     DSYVGDEAQSKRGILTLKYPIEHGIVTNWDDMEKIWHHTFYNELRVAPEE
[Truncated_Name:3]test_3910f     DSYVGDEAQSKRGILTLKYPIEHGIVTNWDDMEKIWHHTFYNELRVAPEE
[Truncated_Name:4]test_3910f     DSYVGDEAQSKRGILTLKYPIEHGIVTNWDDMEKIWHHTFYNELRVAPEE
[Truncated_Name:5]test_3910f     DSYVGDEAQSKRGILTLKYPIEHGIVTNWDDMEKIWHHTFYNELRVAPEE
                                 **************************************************
                            51          .         .         .         .        100


                            101         .         .         .         .        150
[Truncated_Name:1]test_3910f     HPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQAVLSLYASGRTTG
[Truncated_Name:2]test_3910f     HPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQAVLSLYASGRTTG
[Truncated_Name:3]test_3910f     HPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQAVLSLYASGRTTG
[Truncated_Name:4]test_3910f     HPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQAVLSLYASGRTTG
[Truncated_Name:5]test_3910f     HPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQAVLSLYASGRTTG
                                 **************************************************
                            101         .         .         .         .        150


                            151         .         .         .         .        200
[Truncated_Name:1]test_3910f     IVLDSGDGVSHTVPIYEGYALPHAILRLDLAGRDLTDYLMKILTERGYSF
[Truncated_Name:2]test_3910f     IVLDSGDGVSHTVPIYEGYALPHAILRLDLAGRDLTDYLMKILTERGYSF
[Truncated_Name:3]test_3910f     IVLDSGDGVSHTVPIYEGYALPHAILRLDLAGRDLTDYLMKILTERGYSF
[Truncated_Name:4]test_3910f     IVLDSGDGVSHTVPIYEGYALPHAILRLDLAGRDLTDYLMKILTERGYSF
[Truncated_Name:5]test_3910f     IVLDSGDGVSHTVPIYEGYALPHAILRLDLAGRDLTDYLMKILTERGYSF
                                 **************************************************
                            151         .         .         .         .        200


                            201         .         .         .         .        250
[Truncated_Name:1]test_3910f     TTTAEREIVRDIKEKLCYVALDFEQEMATAASSSSLEKSYELPDGQVITI
[Truncated_Name:2]test_3910f     TTTAEREIVRDIKEKLCYVALDFEQEMATAASSSSLEKSYELPDGQVITI
[Truncated_Name:3]test_3910f     TTTAEREIVRDIKEKLCYVALDFEQEMATAASSSSLEKSYELPDGQVITI
[Truncated_Name:4]test_3910f     TTTAEREIVRDIKEKLCYVALDFEQEMATAASSSSLEKSYELPDGQVITI
[Truncated_Name:5]test_3910f     TTTAEREIVRDIKEKLCYVALDFEQEMATAASSSSLEKSYELPDGQVITI
                                 **************************************************
                            201         .         .         .         .        250


                            251         .         .         .         .        300
[Truncated_Name:1]test_3910f     GNERFRCPEALFQPSFLGMEACGIHETTYNSIMKCDVDIRKDLYANTVLS
[Truncated_Name:2]test_3910f     GNERFRCPEALFQPSFLGMEACGIHETTYNSIMKCDVDIRKDLYANTVLS
[Truncated_Name:3]test_3910f     GNERFRCPEALFQPSFLGMEACGIHETTYNSIMKCDVDIRKDLYANTVLS
[Truncated_Name:4]test_3910f     GNERFRCPEALFQPSFLGMEACGIHETTYNSIMKCDVDIRKDLYANTVLS
[Truncated_Name:5]test_3910f     GNERFRCPEALFQPSFLGMEACGIHETTYNSIMKCDVDIRKDLYANTVLS
                                 **************************************************
                            251         .         .         .         .        300
```

```
                            301        .         .         .         .        350
[Truncated_Name:1]test_3910f   GGTTMYPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWIGGSILASLS
[Truncated_Name:2]test_3910f   GGTTMYPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWIGGSILASLS
[Truncated_Name:3]test_3910f   GGTTMYPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWIGGSILASLS
[Truncated_Name:4]test_3910f   GGTTMYPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWIGGSILASLS
[Truncated_Name:5]test_3910f   GGTTMYPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWIGGSILASLS
                               **************************************************
                            301        .         .         .         .        350

                            351        .         .       375
[Truncated_Name:1]test_3910f   TFQQMWISKQEYDESGPSIVHRKCF
[Truncated_Name:2]test_3910f   TFQQMWISKQEYDESGPSIVHRKCF
[Truncated_Name:3]test_3910f   TFQQMWISKQEYDESGPSIVHRKCF
[Truncated_Name:4]test_3910f   TFQQMWISKQEYDESGPSIVHRKCF
[Truncated_Name:5]test_3910f   TFQQMWISKQEYDESGPSIVHRKCF
                               ************************
                            351        .         .       375
```

Call:
```
  pdbaln(files = pdb_files, fit = TRUE, exefile = "msa")
```

Class:
```
  pdbs, fasta
```

Alignment dimensions:
```
  5 sequence rows; 375 position columns (375 non-gap, 0 gap)
```

+ attr: xyz, resno, b, chain, id, ali, resid, sse, call

```r
rd <- rmsd(pdbs, fit=T)
```

Warning in rmsd(pdbs, fit = T): No indices provided, using the 375 non NA positions

```r
range(rd)
```

```
[1] 0.000 0.398
```

```r
library(pheatmap)
```

```
colnames(rd) <- paste0("m",1:5)
rownames(rd) <- paste0("m",1:5)
pheatmap(rd)
```
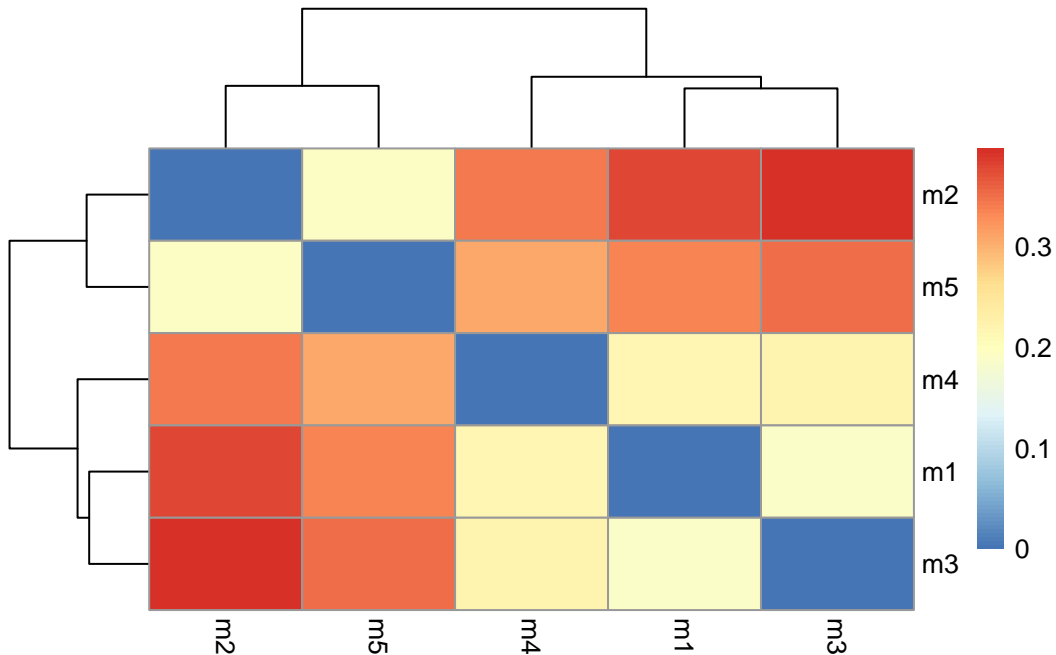


```
pdb <- read.pdb("1j6z")
```

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

```
plotb3(pdbs$b[1,], typ="l", lwd=2, sse=pdb)
```

```
Warning in plotb3(pdbs$b[1, ], typ = "l", lwd = 2, sse = pdb): Length of input
'sse' does not equal the length of input 'x'; Ignoring 'sse'
```

```
points(pdbs$b[2,], typ="l", col="red")
points(pdbs$b[3,], typ="l", col="blue")
points(pdbs$b[4,], typ="l", col="darkgreen")
points(pdbs$b[5,], typ="l", col="orange")
abline(v=100, col="gray")
```

```
core <- core.find(pdbs)
```
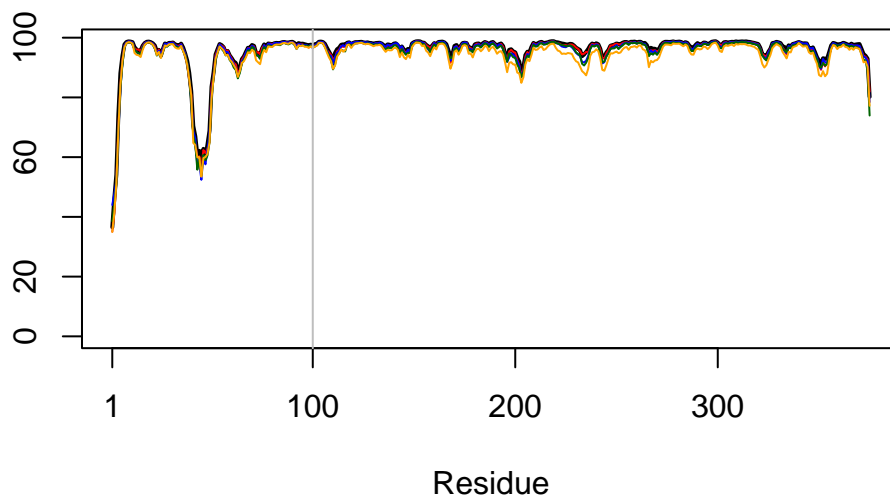
```
 core size 374 of 375  vol = 0.973
 core size 373 of 375  vol = 0.841
 core size 372 of 375  vol = 0.774
 core size 371 of 375  vol = 0.72
 core size 370 of 375  vol = 0.664
 core size 369 of 375  vol = 0.629
 core size 368 of 375  vol = 0.592
 core size 367 of 375  vol = 0.567
 core size 366 of 375  vol = 0.55
 core size 365 of 375  vol = 0.536
 core size 364 of 375  vol = 0.519
 core size 363 of 375  vol = 0.506
 core size 362 of 375  vol = 0.493
 FINISHED: Min vol ( 0.5 ) reached
```

```
core.inds <- print(core, vol=0.5)
```

```
# 363 positions (cumulative volume <= 0.5 Angstrom^3)
  start end length
```

```
1      3  41     39
2     49 194    146
3    198 375    178
```

```
xyz <- pdbfit(pdbs, core.inds, outpath="corefit_structures")
```
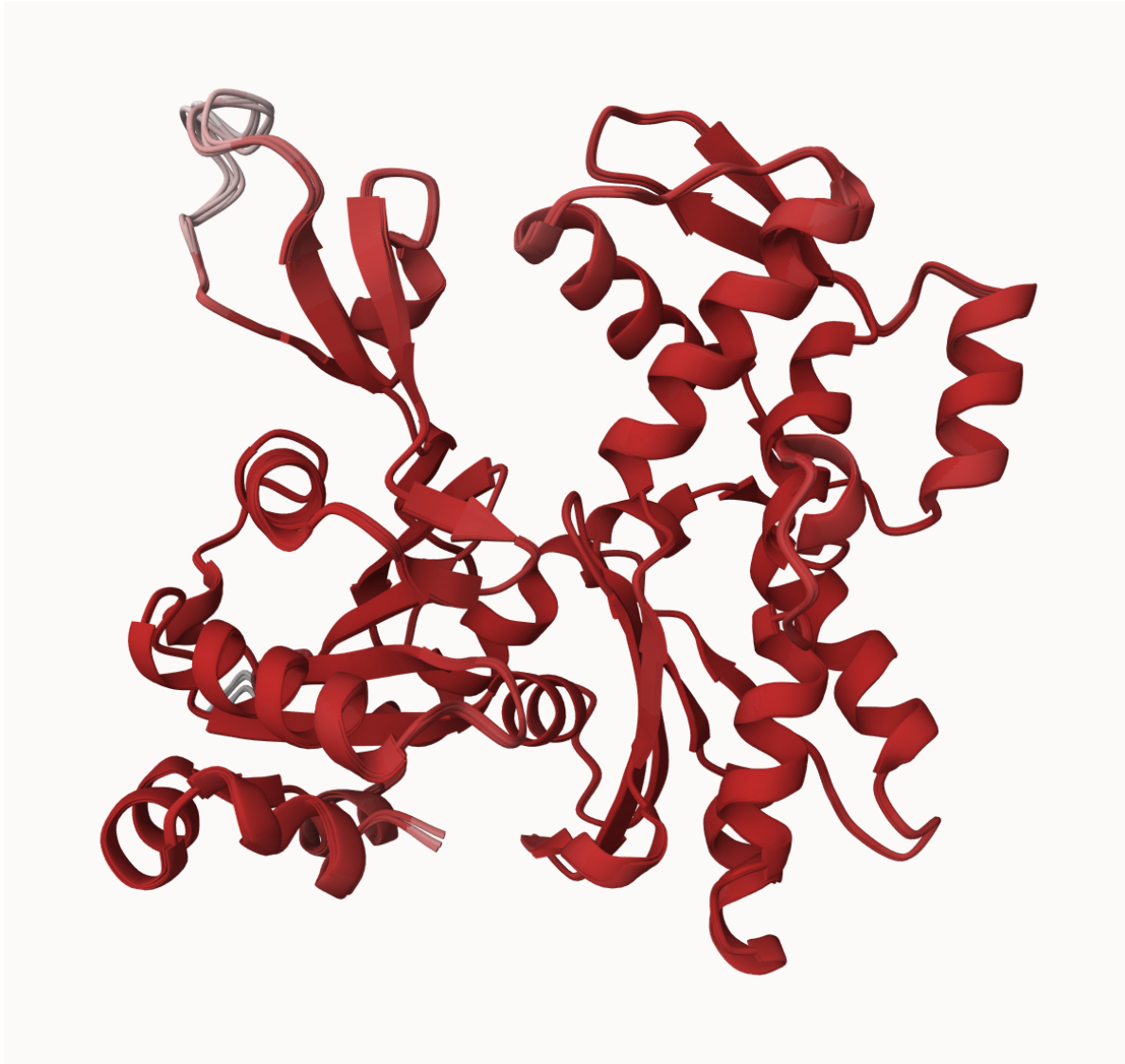

Figure 2: Core superposed structures colored by B-factor

```
rf <- rmsf(xyz)

plotb3(rf, sse=pdb)
```

Warning in plotb3(rf, sse = pdb): Length of input 'sse' does not equal the
length of input 'x'; Ignoring 'sse'

```
abline(v=100, col="gray", ylab="RMSF")
```
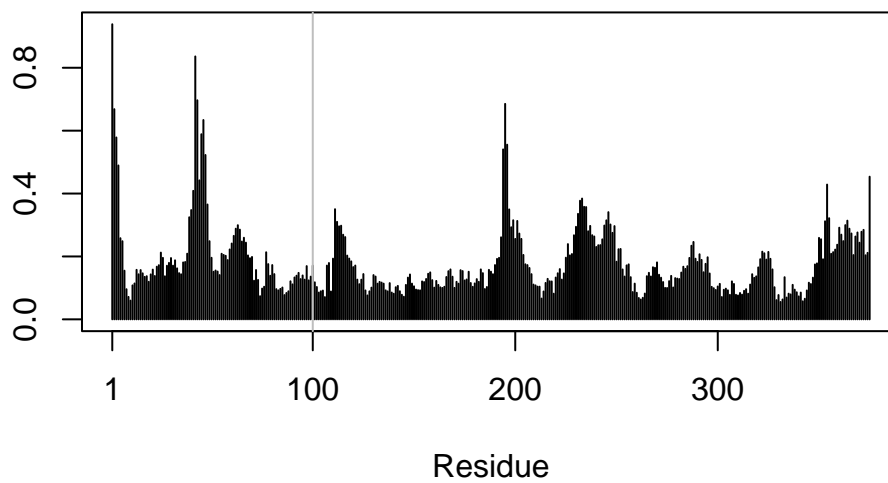

Predicted Alignment Error for domains

```
library(jsonlite)
```

Warning: package 'jsonlite' was built under R version 4.3.3

```
pae_files <- list.files(path=results_dir,
                        pattern=".*model.*\\.json",
                        full.names = TRUE)
pae1 <- read_json(pae_files[1],simplifyVector = TRUE)
pae5 <- read_json(pae_files[5],simplifyVector = TRUE)

attributes(pae1)
```

```
$names
[1] "plddt"   "max_pae" "pae"      "ptm"
```

```
head(pae1$plddt)
```

```
[1] 36.53 46.22 54.09 74.19 88.12 93.88
```
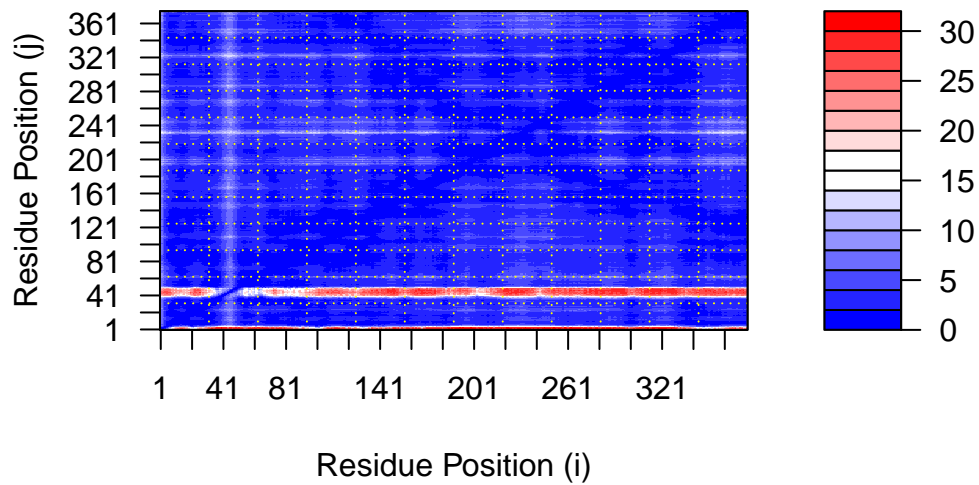
Max pae scores

```
pae1$max_pae
```

```
[1] 31.09375
```
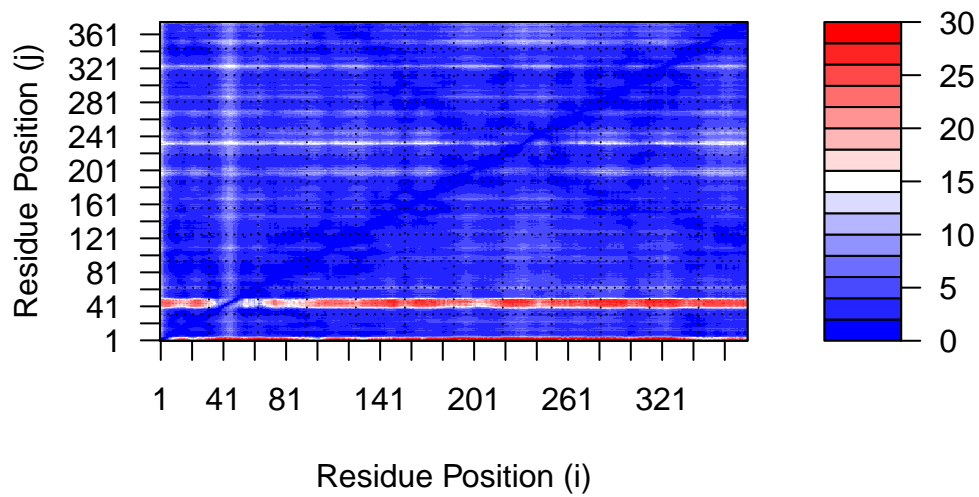
```
pae5$max_pae
```

```
[1] 30.9375
```

Plotted residue-by-residue pae scores for model 1 and 5

```
plot.dmat(pae1$pae,
          xlab="Residue Position (i)",
          ylab="Residue Position (j)")
```
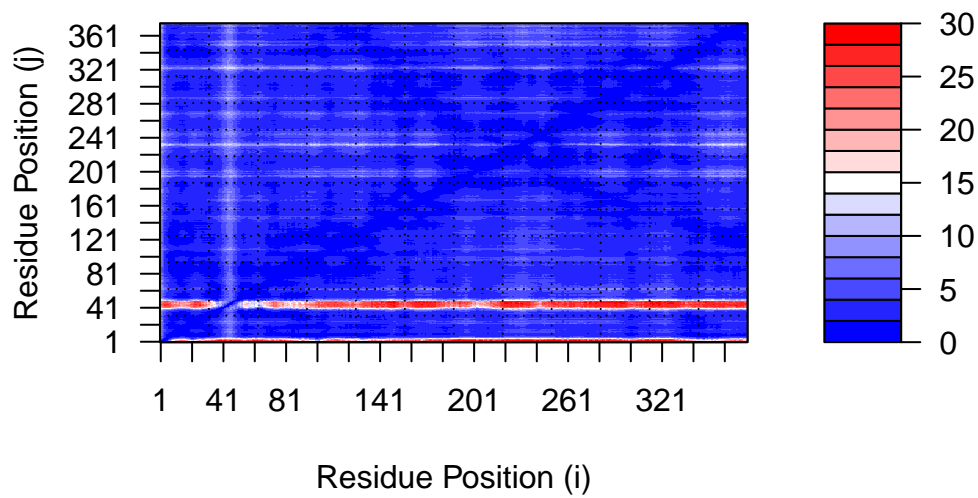
```
plot.dmat(pae5$pae,
          xlab="Residue Position (i)",
          ylab="Residue Position (j)",
          grid.col = "black",
          zlim=c(0,30))
```


model 1 with range of 0-30

```
plot.dmat(pae1$pae,
          xlab="Residue Position (i)",
          ylab="Residue Position (j)",
          grid.col = "black",
          zlim=c(0,30))
```

Residue conservation from alignment file

```r
aln_file <- list.files(path=results_dir,
                       pattern=".a3m$",
                        full.names = TRUE)
aln_file
```

```
[1] "test_3910f//test_3910f.a3m"
```

```r
aln <- read.fasta(aln_file[1], to.upper = TRUE)
```

```
[1] " ** Duplicated sequence id's: 101 **"
```
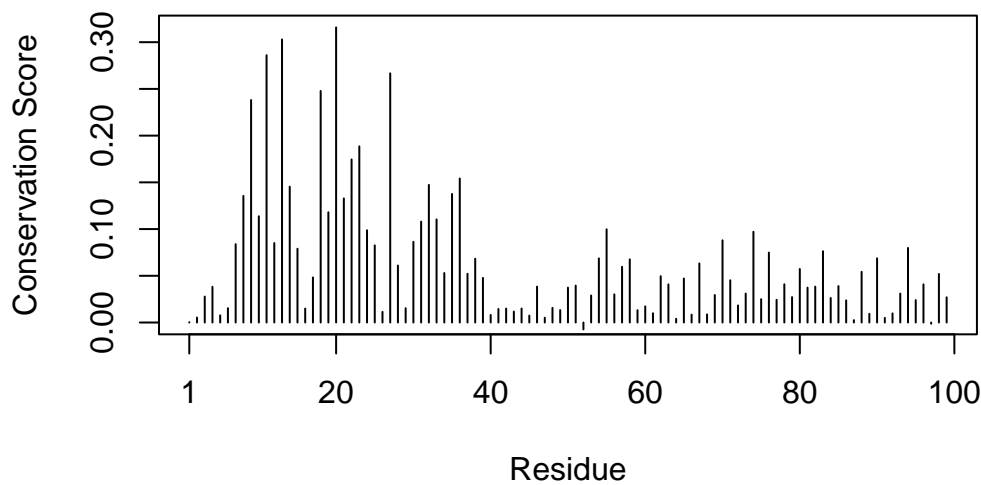
```r
# number of sequences
dim(aln$ali)
```

```
[1] 21157   757
```

Socring residue conservation

```
sim <- conserv(aln)
plotb3(sim[1:99], sse=trim.pdb(pdb, chain="A"),
       ylab="Conservation Score")
```

Warning in plotb3(sim[1:99], sse = trim.pdb(pdb, chain = "A"), ylab =
"Conservation Score"): Length of input 'sse' does not equal the length of input
'x'; Ignoring 'sse'


```
con <- consensus(aln, cutoff = 0.25)
con$seq
```

```
  [1] "-" "-" "-" "-" "-" "-" "-" "-" "V" "-" "D" "N" "G" "S" "G" "-" "-" "K"
 [19] "A" "G" "F" "A" "G" "-" "D" "-" "P" "-" "-" "V" "F" "P" "S" "-" "V" "G"
 [37] "-" "P" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
 [55] "G" "-" "-" "A" "-" "-" "-" "-" "-" "-" "L" "-" "L" "-" "-" "P" "-" "-"
 [73] "-" "G" "-" "-" "-" "-" "W" "D" "D" "M" "E" "-" "-" "W" "-" "H" "-" "F"
 [91] "-" "-" "-" "L" "-" "-" "-" "P" "-" "E" "-" "-" "-" "L" "L" "T" "E" "-"
[109] "P" "L" "N" "P" "-" "-" "N" "R" "E" "-" "-" "-" "-" "-" "M" "F" "E" "-"
[127] "F" "-" "-" "P" "A" "-" "Y" "-" "-" "-" "Q" "A" "V" "L" "S" "L" "Y" "A"
[145] "S" "G" "R" "T" "T" "G" "-" "V" "-" "D" "S" "G" "D" "G" "V" "-" "H" "-"
[163] "V" "P" "I" "Y" "E" "G" "Y" "-" "L" "P" "H" "A" "-" "-" "R" "L" "D" "L"
```

```
[181] "A" "G" "R" "D" "L" "T" "-" "Y" "L" "-" "-" "L" "L" "-" "E" "-" "G" "-"
[199] "-" "F" "-" "T" "-" "A" "E" "-" "E" "I" "V" "R" "D" "I" "K" "E" "K" "-"
[217] "C" "Y" "V" "A" "-" "D" "-" "-" "-" "E" "-" "-" "-" "-" "-" "-" "-" "-"
[235] "-" "-" "-" "-" "-" "Y" "-" "L" "P" "D" "G" "-" "-" "-" "-" "-" "G" "-"
[253] "E" "R" "F" "-" "-" "P" "E" "-" "L" "F" "-" "P" "-" "-" "-" "G" "-" "-"
[271] "-" "-" "G" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[289] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "L" "-" "G" "G" "-" "-" "-" "-"
[307] "-" "G" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[325] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[343] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[361] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[379] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[397] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[415] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[433] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[451] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[469] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[487] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[505] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[523] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[541] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[559] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[577] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[595] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[613] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[631] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[649] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[667] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[685] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[703] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[721] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[739] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[757] "-"
```