Class 11 AlphaFold

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Table of contents

First part of Class: Structural Bionformatics 2

Load up the packages we will need for analysis of protein structure sets.

```
library(bio3d)
```

install.packages("BiocManager") BiocManager::install("msa") These above packages were already previously installed.

We will analyze the ADK family with a single ADK database accession code: "1ake_A"

```
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
```

We can search the PDB database to find all related entries.

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

```
 Searching ... please wait (updates every 5 seconds) RID = 21TMK759013
 .
 Reporting 90 hits
```

```
attributes(blast)
```

```
$names
```

```
[1] "hit.tbl" "raw"     "url"

$class
[1] "blast"
```

```
head(blast$hit.tbl)
```

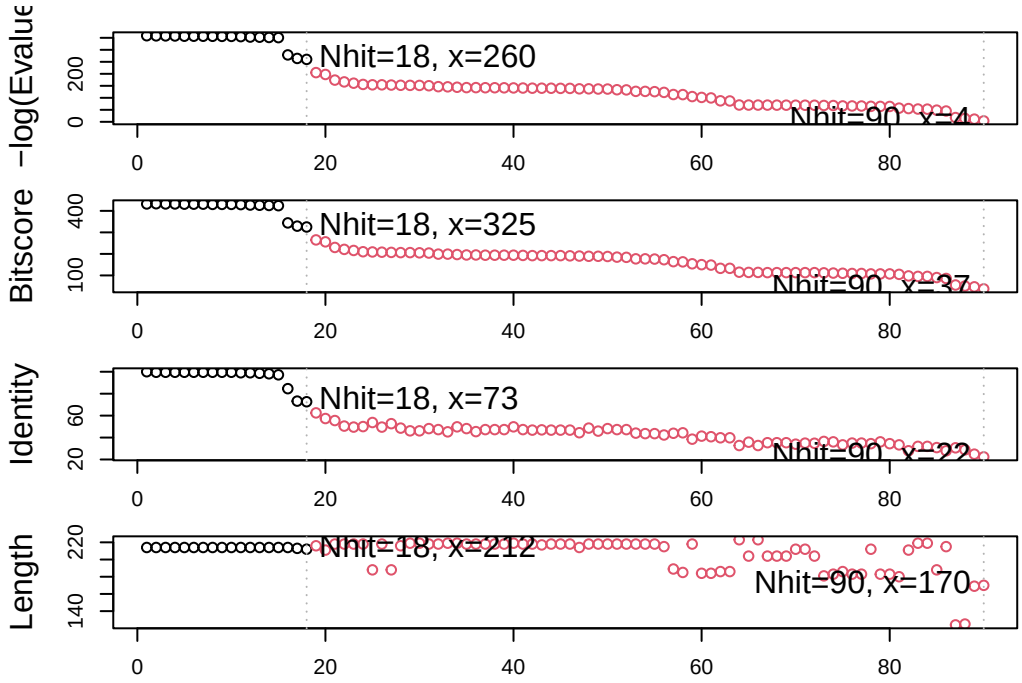
```
        queryid subjectids identity alignmentlength mismatches gapopens q.start
1 Query_3163241     1AKE_A  100.000             214          0        0       1
2 Query_3163241     8BQF_A   99.533             214          1        0       1
3 Query_3163241     4X8M_A   99.533             214          1        0       1
4 Query_3163241     6S36_A   99.533             214          1        0       1
5 Query_3163241     8Q2B_A   99.533             214          1        0       1
6 Query_3163241     8RJ9_A   99.533             214          1        0       1
  q.end s.start s.end    evalue bitscore positives mlog.evalue pdb.id    acc
1   214       1   214 1.66e-156      432    100.00    358.6965 1AKE_A 1AKE_A
2   214      21   234 2.71e-156      433    100.00    358.2063 8BQF_A 8BQF_A
3   214       1   214 2.96e-156      432    100.00    358.1181 4X8M_A 4X8M_A
4   214       1   214 4.35e-156      432    100.00    357.7331 6S36_A 6S36_A
5   214       1   214 1.15e-155      431     99.53    356.7609 8Q2B_A 8Q2B_A
6   214       1   214 1.15e-155      431     99.53    356.7609 8RJ9_A 8RJ9_A
```

Make a little summary figure of these results:

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

```
  * Possible cutoff values:    260 3
            Yielding Nhits:    18 90

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



Our "top hits" i.e the most similar entries in the database are:

```
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"
```

```
#Downoload related 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/8PVW.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
```

```
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```

```
# Align releated PDBs
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/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
.   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
```

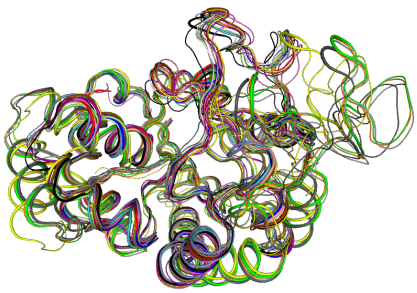
Align and superimpose all these structures:

Sidenote:

```
library(bio3dview)

view.pdbs(pdbs)
```

```
PhantomJS not found. You can install it with webshot::install_phantomjs(). If it is installe
```

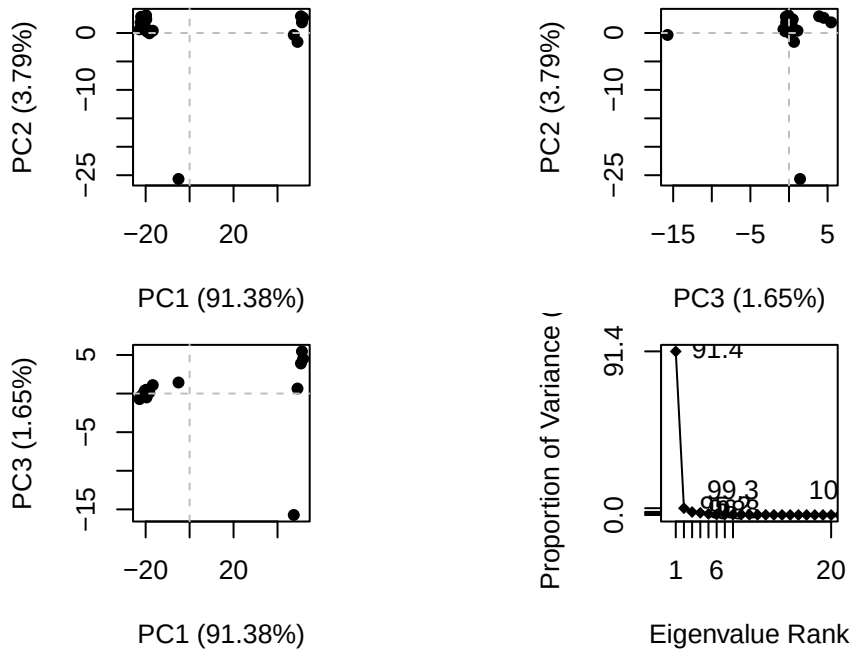
```
file:////private/var/folders/m8/ndytkmz55395lwskyz8gkrsh0000gn/T/RtmpKqLNxC/file57733fbacf71/
```



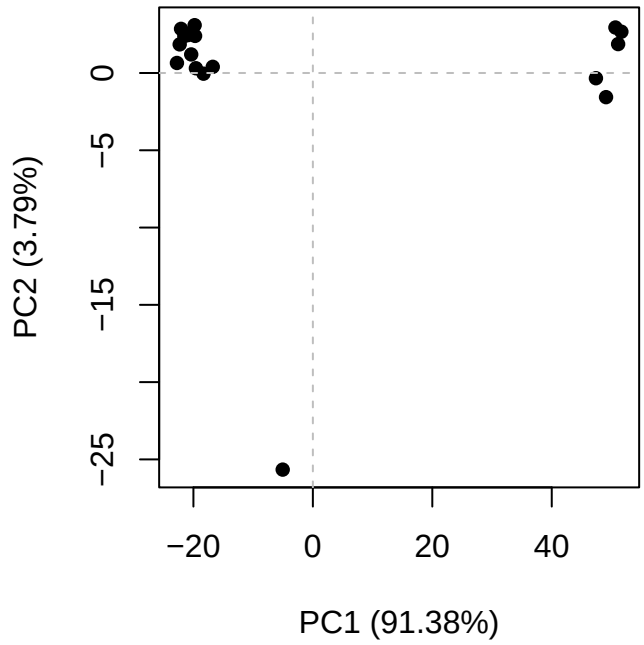
This is better but still difficult to see what is similar and different in all these structures or indeed learn much about how this family works.

Let's try PCA:

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

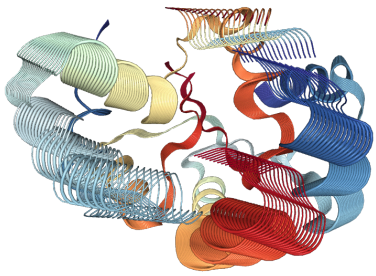



```
plot(pc, pc.axes=1:2)
```




```
view.pca(pc)
```

```
file:////private/var/folders/m8/ndytkmz55395lwskyz8gkrsh0000gn/T/RtmpKqLNxC/file5773219fc4a2/
```



Write a PDB "trajectory" for mol-star

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

Allow for downloading of results

Beginning of Alpha Fold for Dimer Protein

```
library(bio3d)

pth <- "dimer_23119_1/"
pdb.files <- list.files(path=pth, full.names=TRUE, pattern= ".pdb")
```

Align and superimpose all these models.

```
file.exists(pdb.files)
```

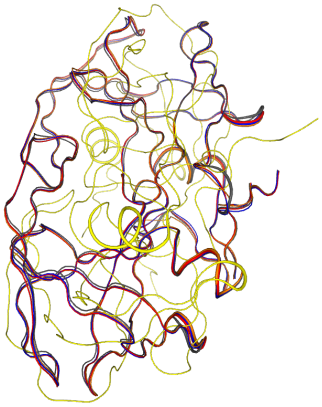
```
[1] TRUE TRUE TRUE TRUE TRUE
```

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

```
Reading PDB files:
dimer_23119_1//dimer_23119_1_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb
dimer_23119_1//dimer_23119_1_unrelaxed_rank_002_alphafold2_multimer_v3_model_5_seed_000.pdb
dimer_23119_1//dimer_23119_1_unrelaxed_rank_003_alphafold2_multimer_v3_model_4_seed_000.pdb
dimer_23119_1//dimer_23119_1_unrelaxed_rank_004_alphafold2_multimer_v3_model_1_seed_000.pdb
dimer_23119_1//dimer_23119_1_unrelaxed_rank_005_alphafold2_multimer_v3_model_3_seed_000.pdb
.....

Extracting sequences

pdb/seq: 1   name: dimer_23119_1//dimer_23119_1_unrelaxed_rank_001_alphafold2_multimer_v3_mod
pdb/seq: 2   name: dimer_23119_1//dimer_23119_1_unrelaxed_rank_002_alphafold2_multimer_v3_mod
pdb/seq: 3   name: dimer_23119_1//dimer_23119_1_unrelaxed_rank_003_alphafold2_multimer_v3_mod
pdb/seq: 4   name: dimer_23119_1//dimer_23119_1_unrelaxed_rank_004_alphafold2_multimer_v3_mod
pdb/seq: 5   name: dimer_23119_1//dimer_23119_1_unrelaxed_rank_005_alphafold2_multimer_v3_mod
```

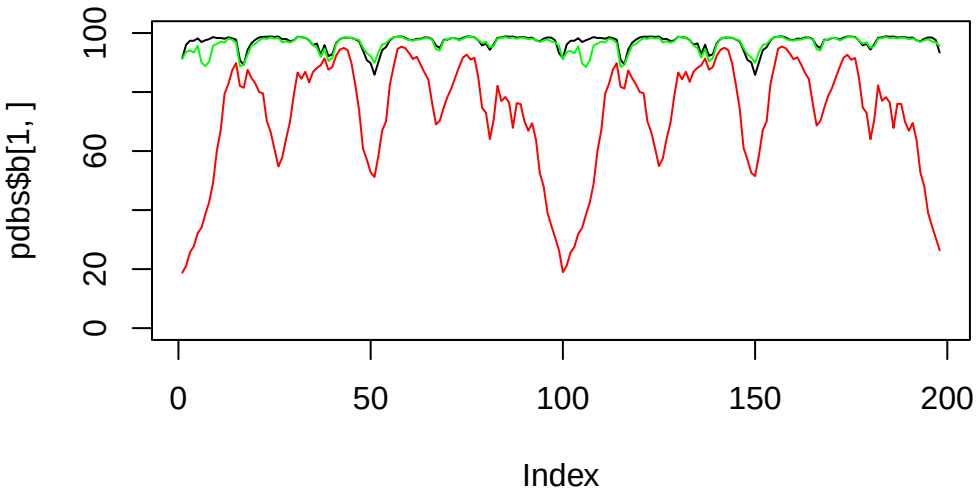
```
library(bio3dview)
view.pdbs(pdbs)
```

file:////private/var/folders/m8/ndytkmz55395lwskyz8gkrsh0000gn/T/RtmpKqLNxC/file577359c3c3b9/



High pldt scores above 70 are good. y-axis is pldt score x-axis is amino acid. Low paes plots are good.

```
plot(pdbs$b[1,], typ="l", ylim=c(0,100))
lines(pdbs$b[5,], typ="l", col="red")
lines(pdbs$b[3,], typ="l", col="green")
```




```
core <- core.find(pdbs)
```

```
 core size 197 of 198  vol = 32.323
 core size 196 of 198  vol = 28.916
 core size 195 of 198  vol = 27.276
 core size 194 of 198  vol = 25.733
 core size 193 of 198  vol = 24.724
 core size 192 of 198  vol = 23.805
 core size 191 of 198  vol = 23.128
 core size 190 of 198  vol = 22.502
 core size 189 of 198  vol = 21.867
 core size 188 of 198  vol = 21.293
 core size 187 of 198  vol = 20.774
 core size 186 of 198  vol = 20.305
 core size 185 of 198  vol = 19.783
```

```
core size 184 of 198  vol = 19.353
core size 183 of 198  vol = 18.94
core size 182 of 198  vol = 18.539
core size 181 of 198  vol = 18.097
core size 180 of 198  vol = 17.694
core size 179 of 198  vol = 17.257
core size 178 of 198  vol = 16.867
core size 177 of 198  vol = 16.519
core size 176 of 198  vol = 16.237
core size 175 of 198  vol = 15.978
core size 174 of 198  vol = 15.693
core size 173 of 198  vol = 15.412
core size 172 of 198  vol = 15.174
core size 171 of 198  vol = 14.957
core size 170 of 198  vol = 14.733
core size 169 of 198  vol = 14.532
core size 168 of 198  vol = 14.363
core size 167 of 198  vol = 14.222
core size 166 of 198  vol = 13.981
core size 165 of 198  vol = 13.885
core size 164 of 198  vol = 13.822
core size 163 of 198  vol = 13.736
core size 162 of 198  vol = 13.646
core size 161 of 198  vol = 13.58
core size 160 of 198  vol = 13.46
core size 159 of 198  vol = 13.261
core size 158 of 198  vol = 13.076
core size 157 of 198  vol = 12.91
core size 156 of 198  vol = 12.971
core size 155 of 198  vol = 12.926
core size 154 of 198  vol = 12.892
core size 153 of 198  vol = 12.769
core size 152 of 198  vol = 12.648
core size 151 of 198  vol = 12.53
core size 150 of 198  vol = 12.326
core size 149 of 198  vol = 12.104
core size 148 of 198  vol = 11.905
core size 147 of 198  vol = 11.473
core size 146 of 198  vol = 11.155
core size 145 of 198  vol = 10.956
core size 144 of 198  vol = 10.755
core size 143 of 198  vol = 10.546
core size 142 of 198  vol = 10.276
```

```
core size 141 of 198  vol = 10.066
core size 140 of 198  vol = 9.835
core size 139 of 198  vol = 9.619
core size 138 of 198  vol = 9.405
core size 137 of 198  vol = 9.142
core size 136 of 198  vol = 8.863
core size 135 of 198  vol = 8.526
core size 134 of 198  vol = 8.229
core size 133 of 198  vol = 7.998
core size 132 of 198  vol = 7.809
core size 131 of 198  vol = 7.509
core size 130 of 198  vol = 7.288
core size 129 of 198  vol = 7.084
core size 128 of 198  vol = 6.88
core size 127 of 198  vol = 6.59
core size 126 of 198  vol = 6.38
core size 125 of 198  vol = 6.197
core size 124 of 198  vol = 5.976
core size 123 of 198  vol = 5.764
core size 122 of 198  vol = 5.568
core size 121 of 198  vol = 5.312
core size 120 of 198  vol = 5.021
core size 119 of 198  vol = 4.758
core size 118 of 198  vol = 4.501
core size 117 of 198  vol = 4.218
core size 116 of 198  vol = 4.031
core size 115 of 198  vol = 3.801
core size 114 of 198  vol = 3.604
core size 113 of 198  vol = 3.379
core size 112 of 198  vol = 3.183
core size 111 of 198  vol = 3.002
core size 110 of 198  vol = 2.79
core size 109 of 198  vol = 2.603
core size 108 of 198  vol = 2.508
core size 107 of 198  vol = 2.421
core size 106 of 198  vol = 2.24
core size 105 of 198  vol = 2.084
core size 104 of 198  vol = 1.945
core size 103 of 198  vol = 1.832
core size 102 of 198  vol = 1.659
core size 101 of 198  vol = 1.582
core size 100 of 198  vol = 1.483
core size 99 of 198  vol = 1.382
```

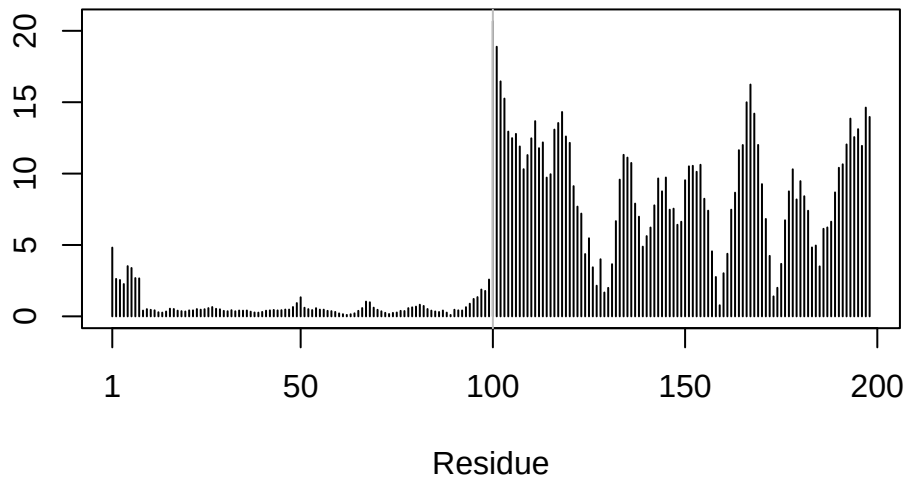
```
 core size 98 of 198  vol = 1.331
 core size 97 of 198  vol = 1.264
 core size 96 of 198  vol = 1.137
 core size 95 of 198  vol = 1.043
 core size 94 of 198  vol = 0.957
 core size 93 of 198  vol = 0.885
 core size 92 of 198  vol = 0.803
 core size 91 of 198  vol = 0.73
 core size 90 of 198  vol = 0.637
 core size 89 of 198  vol = 0.56
 core size 88 of 198  vol = 0.489
 FINISHED: Min vol ( 0.5 ) reached
```

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

```
# 89 positions (cumulative volume <= 0.5 Angstrom^3)
  start end length
1    10  42     33
2    44  50      7
3    52  66     15
4    69  77      9
5    80  98     19
```

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

```
rf <- rmsf(xyz)

plotb3(rf,)
abline(v=100, col="gray", ylab="RMSF")
```



Custom Analysis for Resulting Domains

```
results_dir <- "dimer_23119_1"
```

```
pdb_files <- list.files(path=results_dir,
                        pattern="*.pdb",
                        full.names = TRUE)
basename(pdb.files)
```

```
[1] "dimer_23119_1_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb"
[2] "dimer_23119_1_unrelaxed_rank_002_alphafold2_multimer_v3_model_5_seed_000.pdb"
[3] "dimer_23119_1_unrelaxed_rank_003_alphafold2_multimer_v3_model_4_seed_000.pdb"
[4] "dimer_23119_1_unrelaxed_rank_004_alphafold2_multimer_v3_model_1_seed_000.pdb"
[5] "dimer_23119_1_unrelaxed_rank_005_alphafold2_multimer_v3_model_3_seed_000.pdb"
```

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

```
Reading PDB files:
```

```
dimer_23119_1/dimer_23119_1_unrelaxed_rank_001_alphafold2_multimer_v3_model_2_seed_000.pdb
dimer_23119_1/dimer_23119_1_unrelaxed_rank_002_alphafold2_multimer_v3_model_5_seed_000.pdb
dimer_23119_1/dimer_23119_1_unrelaxed_rank_003_alphafold2_multimer_v3_model_4_seed_000.pdb
dimer_23119_1/dimer_23119_1_unrelaxed_rank_004_alphafold2_multimer_v3_model_1_seed_000.pdb
dimer_23119_1/dimer_23119_1_unrelaxed_rank_005_alphafold2_multimer_v3_model_3_seed_000.pdb
.....

Extracting sequences

pdb/seq: 1   name: dimer_23119_1/dimer_23119_1_unrelaxed_rank_001_alphafold2_multimer_v3_mode
pdb/seq: 2   name: dimer_23119_1/dimer_23119_1_unrelaxed_rank_002_alphafold2_multimer_v3_mode
pdb/seq: 3   name: dimer_23119_1/dimer_23119_1_unrelaxed_rank_003_alphafold2_multimer_v3_mode
pdb/seq: 4   name: dimer_23119_1/dimer_23119_1_unrelaxed_rank_004_alphafold2_multimer_v3_mode
pdb/seq: 5   name: dimer_23119_1/dimer_23119_1_unrelaxed_rank_005_alphafold2_multimer_v3_mode
```

```
pdbs
```

```
                              1        .         .         .         .         50
[Truncated_Name:1]dimer_2311  PQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGI
[Truncated_Name:2]dimer_2311  PQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGI
[Truncated_Name:3]dimer_2311  PQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGI
[Truncated_Name:4]dimer_2311  PQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGI
[Truncated_Name:5]dimer_2311  PQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGI
                              **************************************************
                              1        .         .         .         .         50

                             51        .         .         .         .         100
[Truncated_Name:1]dimer_2311  GGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFP
[Truncated_Name:2]dimer_2311  GGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFP
[Truncated_Name:3]dimer_2311  GGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFP
[Truncated_Name:4]dimer_2311  GGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFP
[Truncated_Name:5]dimer_2311  GGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFP
                              **************************************************
                             51        .         .         .         .         100

                            101        .         .         .         .         150
[Truncated_Name:1]dimer_2311  QITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGIG
[Truncated_Name:2]dimer_2311  QITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGIG
[Truncated_Name:3]dimer_2311  QITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGIG
[Truncated_Name:4]dimer_2311  QITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGIG
[Truncated_Name:5]dimer_2311  QITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGIG
                              **************************************************
```

```
                            101       .         .         .         .         150

                            151       .         .         .         .       198
[Truncated_Name:1]dimer_2311   GFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF
[Truncated_Name:2]dimer_2311   GFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF
[Truncated_Name:3]dimer_2311   GFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF
[Truncated_Name:4]dimer_2311   GFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF
[Truncated_Name:5]dimer_2311   GFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF
                               ******************************************************
                            151       .         .         .         .       198

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

Class:
  pdbs, fasta

Alignment dimensions:
  5 sequence rows; 198 position columns (198 non-gap, 0 gap)

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

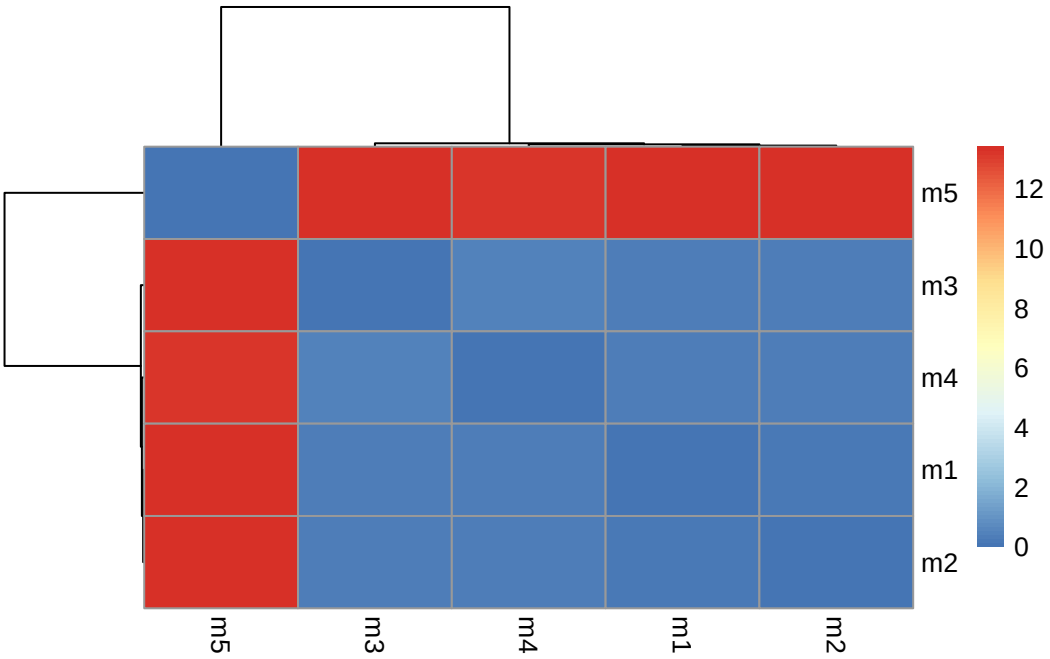
```
rd <- rmsd(pdbs, fit=T)
```

```
Warning in rmsd(pdbs, fit = T): No indices provided, using the 198 non NA positions
```

```
range(rd)
```

```
[1]  0.000 13.406
```

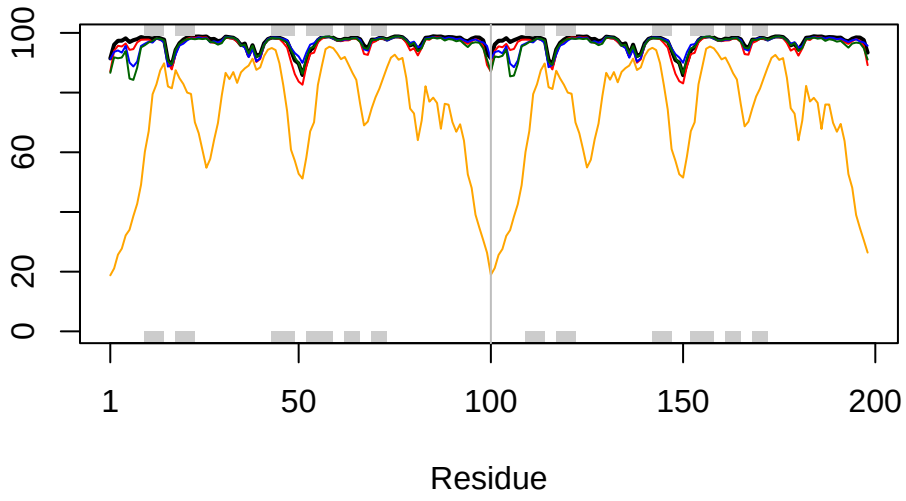
```
library(pheatmap)

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




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

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

```
plotb3(pdbs$b[1,], typ="l", lwd=2, sse=pdb)
points(pdbs$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 197 of 198  vol = 32.323
 core size 196 of 198  vol = 28.916
 core size 195 of 198  vol = 27.276
 core size 194 of 198  vol = 25.733
 core size 193 of 198  vol = 24.724
 core size 192 of 198  vol = 23.805
 core size 191 of 198  vol = 23.128
 core size 190 of 198  vol = 22.502
 core size 189 of 198  vol = 21.867
 core size 188 of 198  vol = 21.293
 core size 187 of 198  vol = 20.774
 core size 186 of 198  vol = 20.305
 core size 185 of 198  vol = 19.783
 core size 184 of 198  vol = 19.353
 core size 183 of 198  vol = 18.94
 core size 182 of 198  vol = 18.539
 core size 181 of 198  vol = 18.097
 core size 180 of 198  vol = 17.694
 core size 179 of 198  vol = 17.257
 core size 178 of 198  vol = 16.867
```

```
core size 177 of 198  vol = 16.519
core size 176 of 198  vol = 16.237
core size 175 of 198  vol = 15.978
core size 174 of 198  vol = 15.693
core size 173 of 198  vol = 15.412
core size 172 of 198  vol = 15.174
core size 171 of 198  vol = 14.957
core size 170 of 198  vol = 14.733
core size 169 of 198  vol = 14.532
core size 168 of 198  vol = 14.363
core size 167 of 198  vol = 14.222
core size 166 of 198  vol = 13.981
core size 165 of 198  vol = 13.885
core size 164 of 198  vol = 13.822
core size 163 of 198  vol = 13.736
core size 162 of 198  vol = 13.646
core size 161 of 198  vol = 13.58
core size 160 of 198  vol = 13.46
core size 159 of 198  vol = 13.261
core size 158 of 198  vol = 13.076
core size 157 of 198  vol = 12.91
core size 156 of 198  vol = 12.971
core size 155 of 198  vol = 12.926
core size 154 of 198  vol = 12.892
core size 153 of 198  vol = 12.769
core size 152 of 198  vol = 12.648
core size 151 of 198  vol = 12.53
core size 150 of 198  vol = 12.326
core size 149 of 198  vol = 12.104
core size 148 of 198  vol = 11.905
core size 147 of 198  vol = 11.473
core size 146 of 198  vol = 11.155
core size 145 of 198  vol = 10.956
core size 144 of 198  vol = 10.755
core size 143 of 198  vol = 10.546
core size 142 of 198  vol = 10.276
core size 141 of 198  vol = 10.066
core size 140 of 198  vol = 9.835
core size 139 of 198  vol = 9.619
core size 138 of 198  vol = 9.405
core size 137 of 198  vol = 9.142
core size 136 of 198  vol = 8.863
core size 135 of 198  vol = 8.526
```

```
core size 134 of 198  vol = 8.229
core size 133 of 198  vol = 7.998
core size 132 of 198  vol = 7.809
core size 131 of 198  vol = 7.509
core size 130 of 198  vol = 7.288
core size 129 of 198  vol = 7.084
core size 128 of 198  vol = 6.88
core size 127 of 198  vol = 6.59
core size 126 of 198  vol = 6.38
core size 125 of 198  vol = 6.197
core size 124 of 198  vol = 5.976
core size 123 of 198  vol = 5.764
core size 122 of 198  vol = 5.568
core size 121 of 198  vol = 5.312
core size 120 of 198  vol = 5.021
core size 119 of 198  vol = 4.758
core size 118 of 198  vol = 4.501
core size 117 of 198  vol = 4.218
core size 116 of 198  vol = 4.031
core size 115 of 198  vol = 3.801
core size 114 of 198  vol = 3.604
core size 113 of 198  vol = 3.379
core size 112 of 198  vol = 3.183
core size 111 of 198  vol = 3.002
core size 110 of 198  vol = 2.79
core size 109 of 198  vol = 2.603
core size 108 of 198  vol = 2.508
core size 107 of 198  vol = 2.421
core size 106 of 198  vol = 2.24
core size 105 of 198  vol = 2.084
core size 104 of 198  vol = 1.945
core size 103 of 198  vol = 1.832
core size 102 of 198  vol = 1.659
core size 101 of 198  vol = 1.582
core size 100 of 198  vol = 1.483
core size 99 of 198  vol = 1.382
core size 98 of 198  vol = 1.331
core size 97 of 198  vol = 1.264
core size 96 of 198  vol = 1.137
core size 95 of 198  vol = 1.043
core size 94 of 198  vol = 0.957
core size 93 of 198  vol = 0.885
core size 92 of 198  vol = 0.803
```

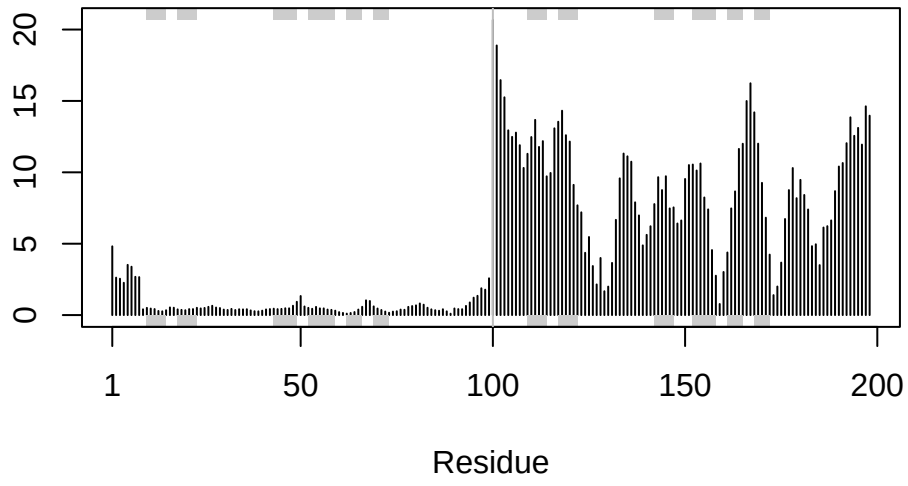
```
 core size 91 of 198  vol = 0.73
 core size 90 of 198  vol = 0.637
 core size 89 of 198  vol = 0.56
 core size 88 of 198  vol = 0.489
 FINISHED: Min vol ( 0.5 ) reached
```

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

```
# 89 positions (cumulative volume <= 0.5 Angstrom^3)
  start end length
1    10  42     33
2    44  50      7
3    52  66     15
4    69  77      9
5    80  98     19
```

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

```
rf <- rmsf(xyz)

plotb3(rf, sse=pdb)
abline(v=100, col="gray", ylab="RMSF")
```



Predicted Alignment Error for Domains

```
library(jsonlite)
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"     "iptm"
```

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

```
[1] 91.44 96.06 97.38 97.38 98.19 96.94
```

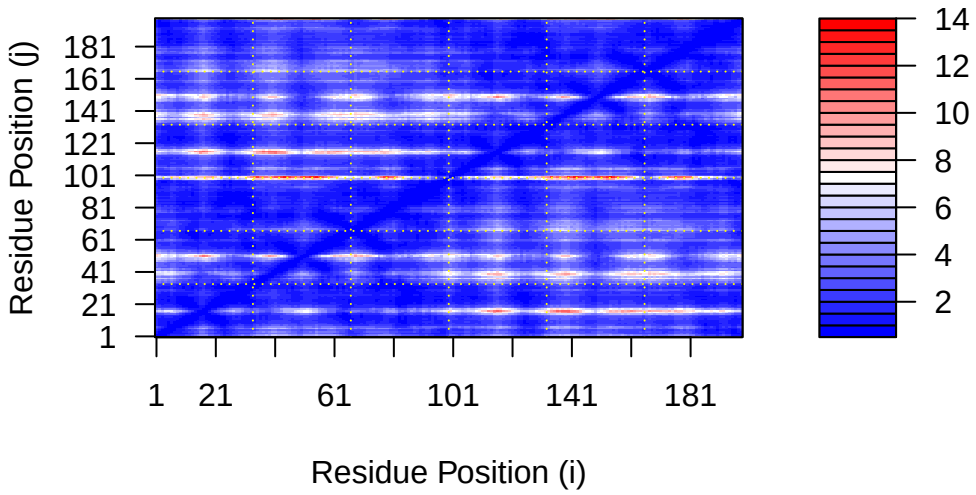
```
pae5$max_pae
```

```
[1] 29.85938
```

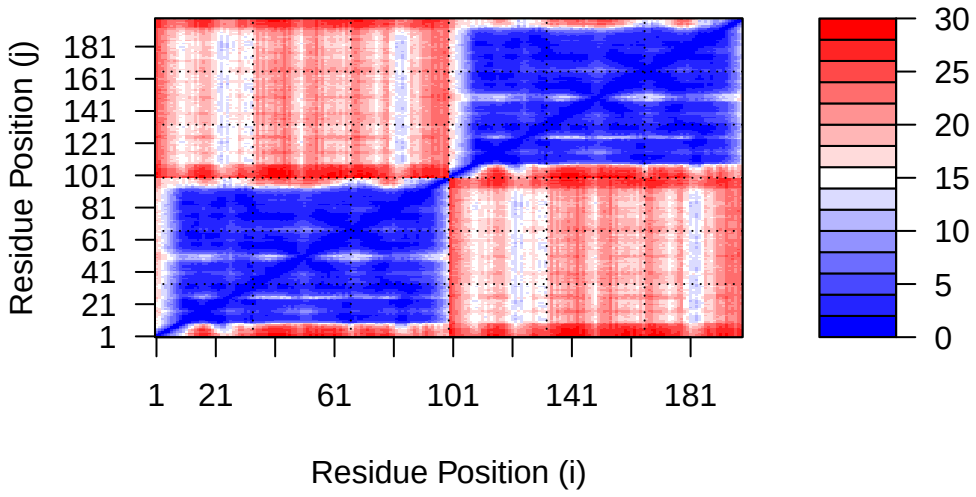
```
pae1$max_pae
```

```
[1] 13.57812
```

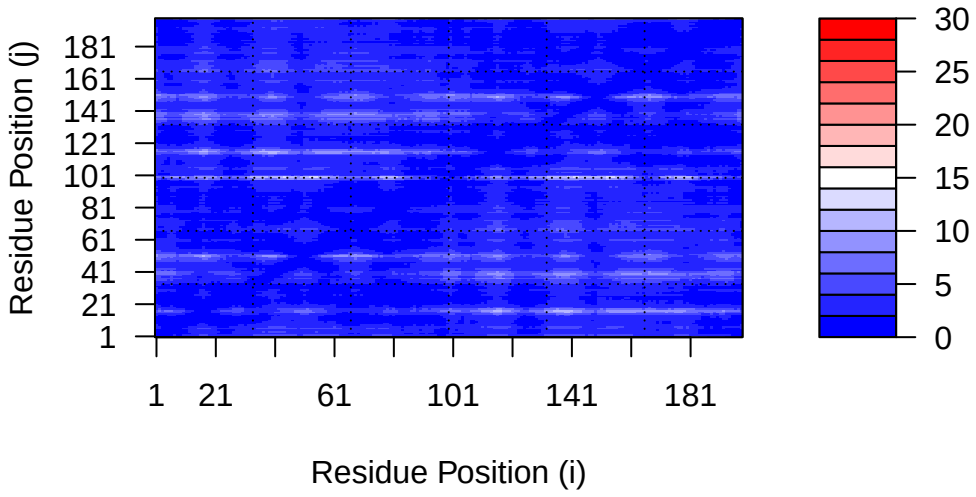
```
plot.dmat(pae1$pae,
          xlab="Residue Position (i)",
          ylab="Residue Position (j)")
```




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




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



Score Residue Conservation from alignment file

Alpha-fold returns it's large alignment file used for analysis. Here we read this rile and score conservation per position.

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

```
[1] "dimer_23119_1//dimer_23119_1.a3m"
```

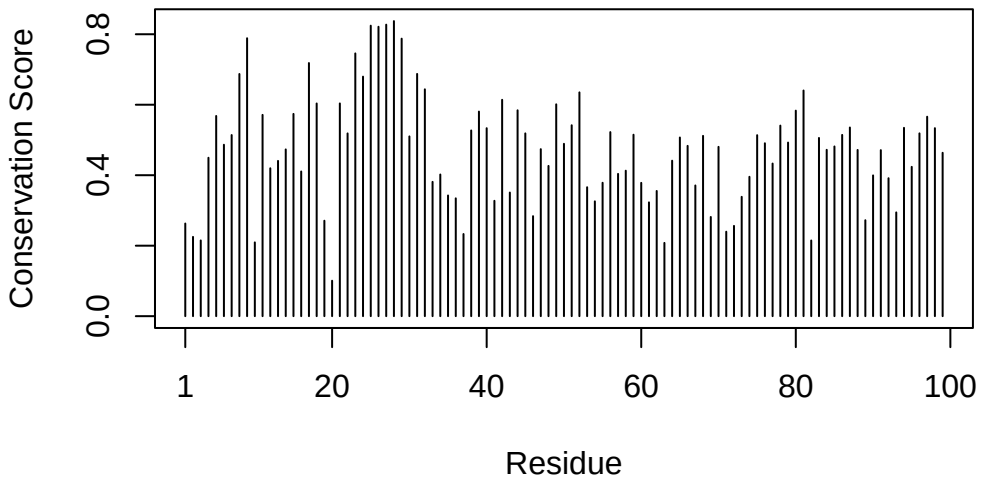
```
aln <- read.fasta(aln_file[1], to.upper = TRUE)
```

```
[1] " ** Duplicated sequence id's: 101 **"
[2] " ** Duplicated sequence id's: 101 **"
```

```
dim(aln$ali)
```

```
[1] 5378  132
```

```
sim <- conserv(aln)

plotb3(sim[1:99],
       ylab="Conservation Score")
```



Residue Conservation for Alignment File

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

```
[1] "dimer_23119_1/dimer_23119_1.a3m"
```

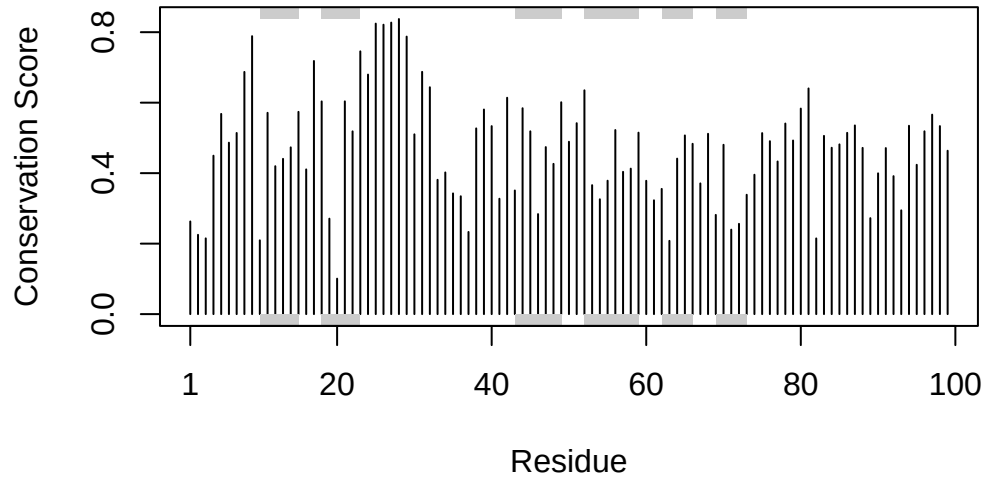
```
aln <- read.fasta(aln_file[1], to.upper = TRUE)
```

```
[1] " ** Duplicated sequence id's: 101 **"
[2] " ** Duplicated sequence id's: 101 **"
```

```
dim(aln$ali)
```

```
[1] 5378  132
```

```
sim <- conserv(aln)

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




```
con <- consensus(aln, cutoff = 0.9)
con$seq
```

```
  [1] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
 [19] "-" "-" "-" "-" "-" "-" "D" "T" "G" "A" "-" "-" "-" "-" "-" "-" "-" "-" "-"
 [37] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
 [55] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
 [73] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
 [91] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[109] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[127] "-" "-" "-" "-" "-" "-"
```

```
m1.pdb <- read.pdb(pdb_files[1])
occ <- vec2resno(c(sim[1:99], sim[1:99]), m1.pdb$atom$resno)
write.pdb(m1.pdb, o=occ, file="m1_conserv.pdb")
```

Find a gene project alpha fold continuation

```
library(bio3d)

pth <- "novel_d48c6"
pdb.file <- list.files(path=pth, full.names=TRUE, pattern= ".pdb")
```

```
file.exists(pdb.file)
```

```
[1] TRUE TRUE TRUE TRUE TRUE
```

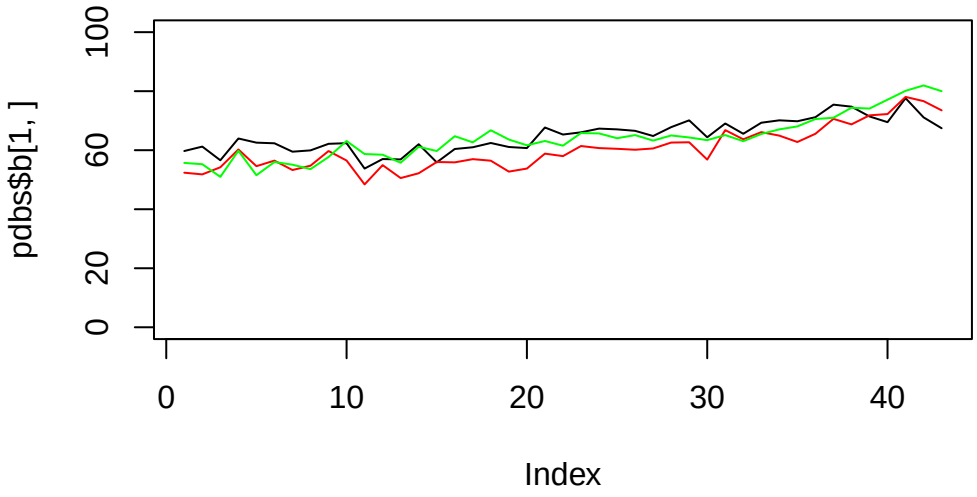
```
pdbs <- pdbaln(pdb.file, fit=TRUE, exefile="msa")
```

```
Reading PDB files:
novel_d48c6/novel_d48c6_unrelaxed_rank_001_alphafold2_ptm_model_5_seed_000.pdb
novel_d48c6/novel_d48c6_unrelaxed_rank_002_alphafold2_ptm_model_2_seed_000.pdb
novel_d48c6/novel_d48c6_unrelaxed_rank_003_alphafold2_ptm_model_1_seed_000.pdb
novel_d48c6/novel_d48c6_unrelaxed_rank_004_alphafold2_ptm_model_3_seed_000.pdb
novel_d48c6/novel_d48c6_unrelaxed_rank_005_alphafold2_ptm_model_4_seed_000.pdb
.....

Extracting sequences

pdb/seq: 1   name: novel_d48c6/novel_d48c6_unrelaxed_rank_001_alphafold2_ptm_model_5_seed_00
pdb/seq: 2   name: novel_d48c6/novel_d48c6_unrelaxed_rank_002_alphafold2_ptm_model_2_seed_00
pdb/seq: 3   name: novel_d48c6/novel_d48c6_unrelaxed_rank_003_alphafold2_ptm_model_1_seed_00
pdb/seq: 4   name: novel_d48c6/novel_d48c6_unrelaxed_rank_004_alphafold2_ptm_model_3_seed_00
pdb/seq: 5   name: novel_d48c6/novel_d48c6_unrelaxed_rank_005_alphafold2_ptm_model_4_seed_00
```

```
library(bio3dview)
view.pdbs(pdbs)
```

```
file:////private/var/folders/m8/ndytkmz55395lwskyz8gkrsh0000gn/T/RtmpKqLNxC/file5773487075f5,
```

```
plot(pdbs$b[1,], typ="l", ylim=c(0,100))
lines(pdbs$b[5,], typ="l", col="red")
lines(pdbs$b[3,], typ="l", col="green")
```




```
core <- core.find(pdbs)
```

```
 core size 42 of 43  vol = 1205.189
 core size 41 of 43  vol = 1041.769
 core size 40 of 43  vol = 868
 core size 39 of 43  vol = 784.033
 core size 38 of 43  vol = 684.46
 core size 37 of 43  vol = 514.588
 core size 36 of 43  vol = 327.276
 core size 35 of 43  vol = 285.479
 core size 34 of 43  vol = 245.102
 core size 33 of 43  vol = 183.967
 core size 32 of 43  vol = 137.695
 core size 31 of 43  vol = 99.102
 core size 30 of 43  vol = 74.297
 core size 29 of 43  vol = 64.473
 core size 28 of 43  vol = 51.949
 core size 27 of 43  vol = 28.907
```

```
 core size 26 of 43  vol = 15.468
 core size 25 of 43  vol = 11.956
 core size 24 of 43  vol = 10.347
 core size 23 of 43  vol = 7.155
 core size 22 of 43  vol = 4.509
 core size 21 of 43  vol = 2.792
 core size 20 of 43  vol = 2.391
 core size 19 of 43  vol = 1.709
 core size 18 of 43  vol = 1.197
 core size 17 of 43  vol = 0.912
 core size 16 of 43  vol = 0.774
 core size 15 of 43  vol = 0.638
```

Custom Analysis of Resulting Models: Find a Gene Project

```
results_dir <- "novel_d48c6"
```

```
pdb_files <- list.files(path=results_dir,
                        pattern="*.pdb",
                        full.names = TRUE)
basename(pdb_files)
```

```
[1] "novel_d48c6_unrelaxed_rank_001_alphafold2_ptm_model_5_seed_000.pdb"
[2] "novel_d48c6_unrelaxed_rank_002_alphafold2_ptm_model_2_seed_000.pdb"
[3] "novel_d48c6_unrelaxed_rank_003_alphafold2_ptm_model_1_seed_000.pdb"
[4] "novel_d48c6_unrelaxed_rank_004_alphafold2_ptm_model_3_seed_000.pdb"
[5] "novel_d48c6_unrelaxed_rank_005_alphafold2_ptm_model_4_seed_000.pdb"
```

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

```
Reading PDB files:
novel_d48c6/novel_d48c6_unrelaxed_rank_001_alphafold2_ptm_model_5_seed_000.pdb
novel_d48c6/novel_d48c6_unrelaxed_rank_002_alphafold2_ptm_model_2_seed_000.pdb
novel_d48c6/novel_d48c6_unrelaxed_rank_003_alphafold2_ptm_model_1_seed_000.pdb
novel_d48c6/novel_d48c6_unrelaxed_rank_004_alphafold2_ptm_model_3_seed_000.pdb
novel_d48c6/novel_d48c6_unrelaxed_rank_005_alphafold2_ptm_model_4_seed_000.pdb
.....
```

```
Extracting sequences

pdb/seq: 1   name: novel_d48c6/novel_d48c6_unrelaxed_rank_001_alphafold2_ptm_model_5_seed_000
pdb/seq: 2   name: novel_d48c6/novel_d48c6_unrelaxed_rank_002_alphafold2_ptm_model_2_seed_000
pdb/seq: 3   name: novel_d48c6/novel_d48c6_unrelaxed_rank_003_alphafold2_ptm_model_1_seed_000
pdb/seq: 4   name: novel_d48c6/novel_d48c6_unrelaxed_rank_004_alphafold2_ptm_model_3_seed_000
pdb/seq: 5   name: novel_d48c6/novel_d48c6_unrelaxed_rank_005_alphafold2_ptm_model_4_seed_000
```

```
pdbs
```

```
                              1        .         .         .         .  43
[Truncated_Name:1]novel_d48c  MLPRLVSNSWPQVTLPPQPPKVLGLQARAMVPGHTYTLINILS
[Truncated_Name:2]novel_d48c  MLPRLVSNSWPQVTLPPQPPKVLGLQARAMVPGHTYTLINILS
[Truncated_Name:3]novel_d48c  MLPRLVSNSWPQVTLPPQPPKVLGLQARAMVPGHTYTLINILS
[Truncated_Name:4]novel_d48c  MLPRLVSNSWPQVTLPPQPPKVLGLQARAMVPGHTYTLINILS
[Truncated_Name:5]novel_d48c  MLPRLVSNSWPQVTLPPQPPKVLGLQARAMVPGHTYTLINILS
                              *******************************************
                              1        .         .         .         .  43

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

Class:
  pdbs, fasta

Alignment dimensions:
  5 sequence rows; 43 position columns (43 non-gap, 0 gap)

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

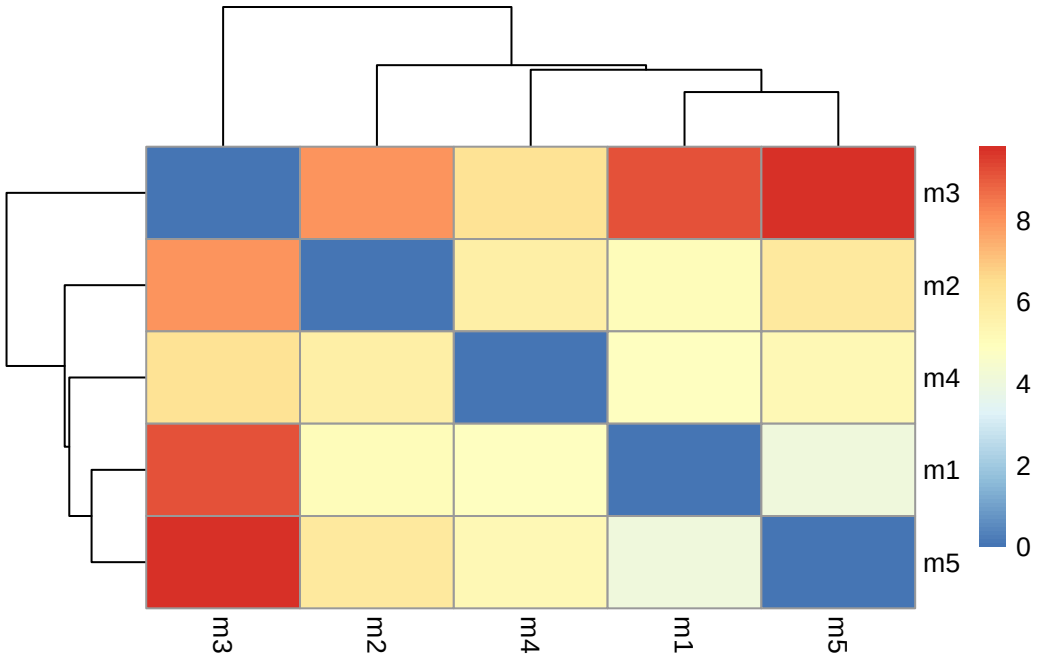
```
rd <- rmsd(pdbs, fit=T)
```

```
Warning in rmsd(pdbs, fit = T): No indices provided, using the 43 non NA positions
```

```
range(rd)
```

```
[1] 0.000 9.803
```

```
library(pheatmap)

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




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

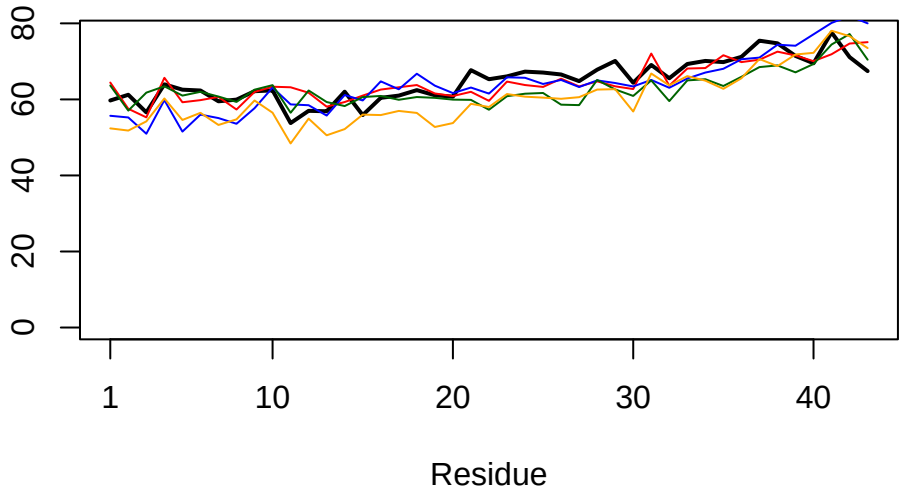
```
  Note: Accessing on-line PDB file
```

```
Warning in get.pdb(file, path = tempdir(), verbose = FALSE):
/var/folders/m8/ndytkmz55395lwskyz8gkrsh0000gn/T//RtmpKqLNxC/1hsg.pdb exists.
Skipping download
```

```
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.inds <- core.find(pdbs, thresh = 0.9)
```

```
 core size 42 of 43  vol = 1205.189
 core size 41 of 43  vol = 1041.769
 core size 40 of 43  vol = 868
 core size 39 of 43  vol = 784.033
 core size 38 of 43  vol = 684.46
 core size 37 of 43  vol = 514.588
 core size 36 of 43  vol = 327.276
 core size 35 of 43  vol = 285.479
 core size 34 of 43  vol = 245.102
 core size 33 of 43  vol = 183.967
 core size 32 of 43  vol = 137.695
 core size 31 of 43  vol = 99.102
 core size 30 of 43  vol = 74.297
 core size 29 of 43  vol = 64.473
```

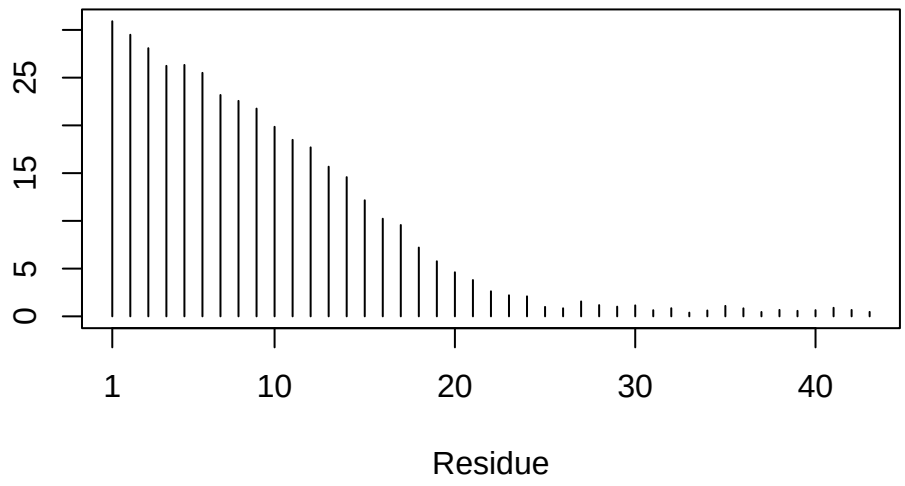
```
 core size 28 of 43  vol = 51.949
 core size 27 of 43  vol = 28.907
 core size 26 of 43  vol = 15.468
 core size 25 of 43  vol = 11.956
 core size 24 of 43  vol = 10.347
 core size 23 of 43  vol = 7.155
 core size 22 of 43  vol = 4.509
 core size 21 of 43  vol = 2.792
 core size 20 of 43  vol = 2.391
 core size 19 of 43  vol = 1.709
 core size 18 of 43  vol = 1.197
 core size 17 of 43  vol = 0.912
 core size 16 of 43  vol = 0.774
 core size 15 of 43  vol = 0.638
```

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

```
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")
```




```
library(jsonlite)
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] 59.72 61.22 56.59 63.97 62.56 62.34
```

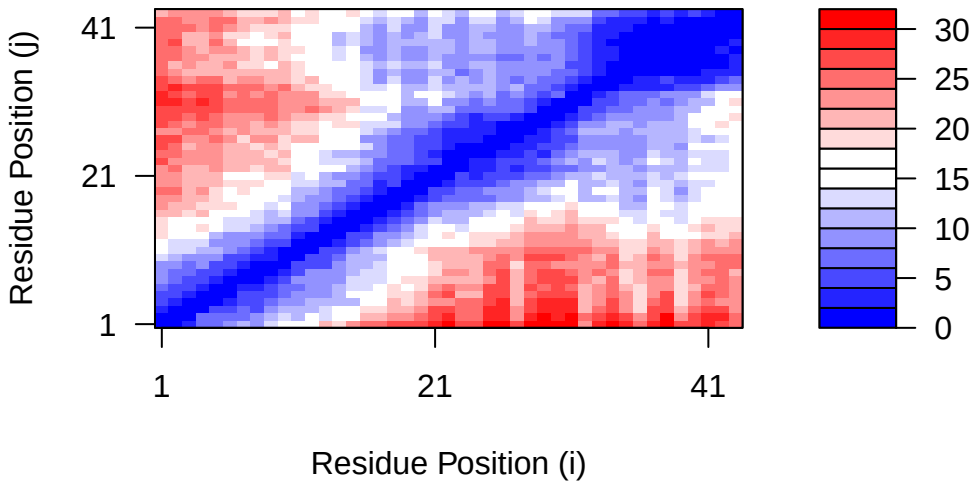
```
pae1$max_pae
```

```
[1] 30.09375
```

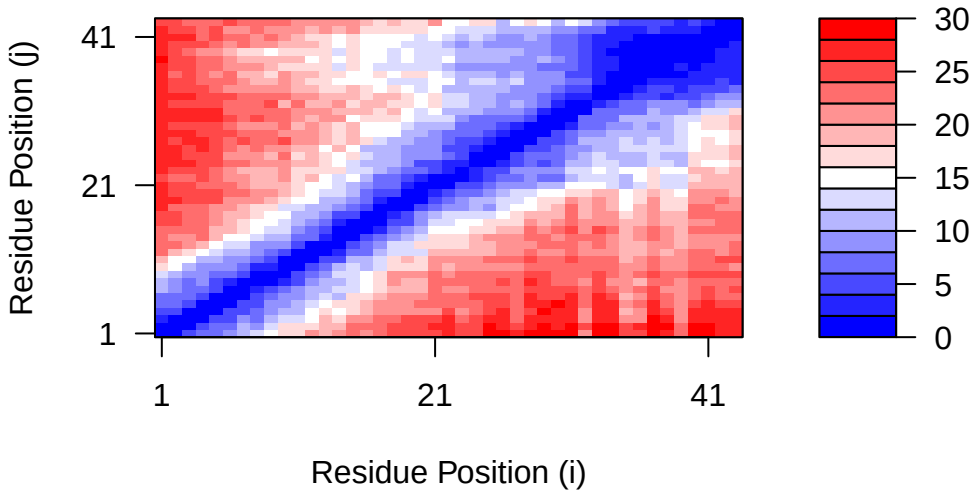
```
pae5$max_pae
```

```
[1] 29.92188
```

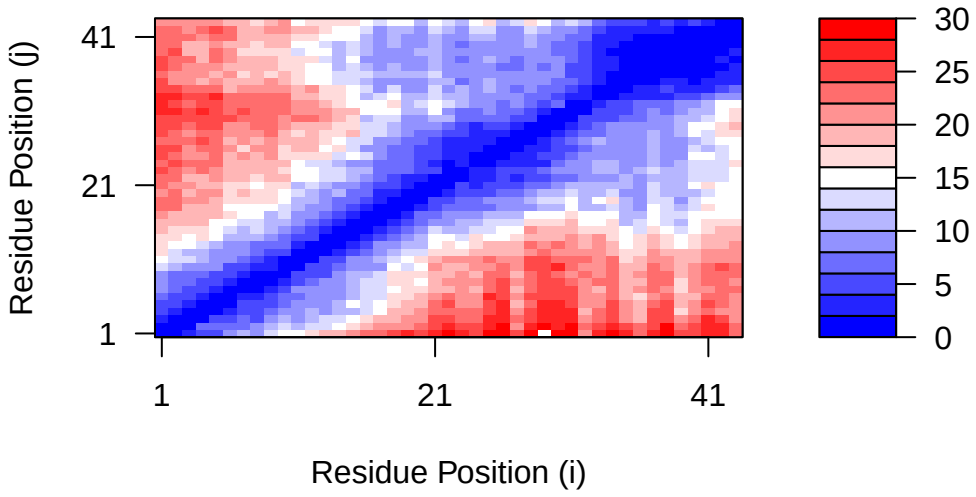
```
plot.dmat(pae1$pae,
          xlab="Residue Position (i)",
          ylab="Residue Position (j)")
```




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




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




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

```
[1] "novel_d48c6/novel_d48c6.a3m"
```

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

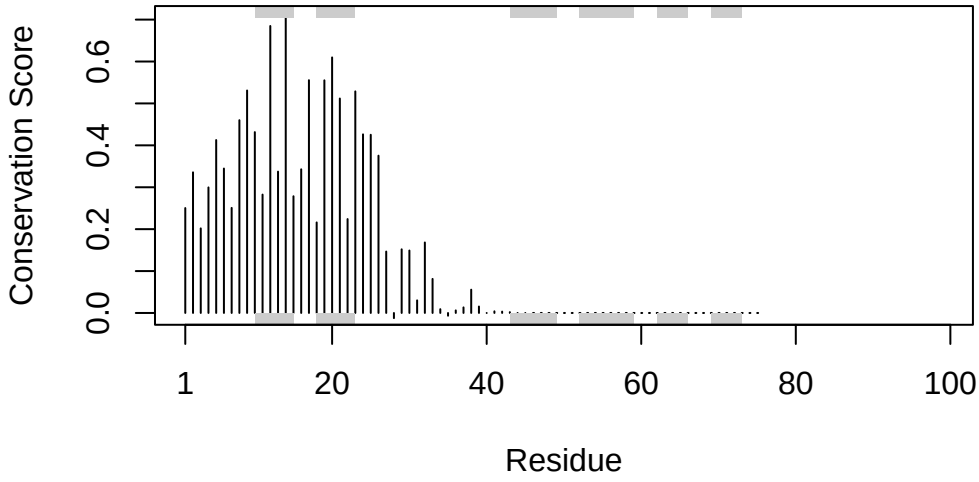
```
[1] " ** Duplicated sequence id's: 101 **"
```

```
dim(aln$ali)
```

```
[1] 6234   75
```

```
sim <- conserv(aln)

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

```
Warning in tmp.sse[!is.na(x)] <- sse: number of items to replace is not a
multiple of replacement length
```




```
con <- consensus(aln, cutoff = 0.9)
con$seq
```

```
 [1] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[20] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[39] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
[58] "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-" "-"
```