

# Class 11: Structural Bioinformatics pt2.

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We saw last day that the PDB has 209,886 entries (Oct/Nov 2025). UniProtKB (i.e. protein sequence database) has 199,579,901 entries

```
100 * 209886/199579901
```

```
[1] 0.1051639
```

So the PDB has 0.1% coverage of the main sequence database

Enter AlphaFold data base (AFDB) <https://alphafold.ebi.ac.uk/> that attempts to provide computed models for all sequences in UniProt.

## AlphaFold

AlphaFold has 3 main outputs

- the predicted coordinates (PDB files)
- A local quality score called **pLDDT** (one for each amino-acid)
- A second quality score **PAE** Predicted Aligned Error (for each pair of amino-acid)

We can run alphaFold ourselves if we are not happy with afdb (i.e. no coverage or poor model)

## Interpreting/ Analyzing AF results in R

```
# Change this for YOUR results dir name
results_dir <- "HIVPR_dimer_23119/"
```

```
# File names for all PDB models
pdb_files <- list.files(path=results_dir,
                         pattern="*.pdb",
                         full.names = TRUE)

# Print our PDB file names
basename(pdb_files)
```

```
[1] "HIVPR_dimer_23119_unrelaxed_rank_001_alphaFold2_multimer_v3_model_2_seed_000.pdb"
[2] "HIVPR_dimer_23119_unrelaxed_rank_002_alphaFold2_multimer_v3_model_4_seed_000.pdb"
[3] "HIVPR_dimer_23119_unrelaxed_rank_003_alphaFold2_multimer_v3_model_1_seed_000.pdb"
[4] "HIVPR_dimer_23119_unrelaxed_rank_004_alphaFold2_multimer_v3_model_5_seed_000.pdb"
[5] "HIVPR_dimer_23119_unrelaxed_rank_005_alphaFold2_multimer_v3_model_3_seed_000.pdb"
```

```
library(bio3d)
library(bio3dview)

# Read all data from Models
# and superpose/fit coords
pdbs <- pdbaln(pdb_files, fit=TRUE, exefile="msa")
```

Reading PDB files:

```
HIVPR_dimer_23119//HIVPR_dimer_23119_unrelaxed_rank_001_alphaFold2_multimer_v3_model_2_seed_000
HIVPR_dimer_23119//HIVPR_dimer_23119_unrelaxed_rank_002_alphaFold2_multimer_v3_model_4_seed_000
HIVPR_dimer_23119//HIVPR_dimer_23119_unrelaxed_rank_003_alphaFold2_multimer_v3_model_1_seed_000
HIVPR_dimer_23119//HIVPR_dimer_23119_unrelaxed_rank_004_alphaFold2_multimer_v3_model_5_seed_000
HIVPR_dimer_23119//HIVPR_dimer_23119_unrelaxed_rank_005_alphaFold2_multimer_v3_model_3_seed_000
....
```

Extracting sequences

```
pdb/seq: 1 name: HIVPR_dimer_23119//HIVPR_dimer_23119_unrelaxed_rank_001_alphaFold2_multimer_v3_model_2_seed_000
pdb/seq: 2 name: HIVPR_dimer_23119//HIVPR_dimer_23119_unrelaxed_rank_002_alphaFold2_multimer_v3_model_4_seed_000
pdb/seq: 3 name: HIVPR_dimer_23119//HIVPR_dimer_23119_unrelaxed_rank_003_alphaFold2_multimer_v3_model_1_seed_000
pdb/seq: 4 name: HIVPR_dimer_23119//HIVPR_dimer_23119_unrelaxed_rank_004_alphaFold2_multimer_v3_model_5_seed_000
pdb/seq: 5 name: HIVPR_dimer_23119//HIVPR_dimer_23119_unrelaxed_rank_005_alphaFold2_multimer_v3_model_3_seed_000
```

```
view.pdbs(pdbs)
```

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

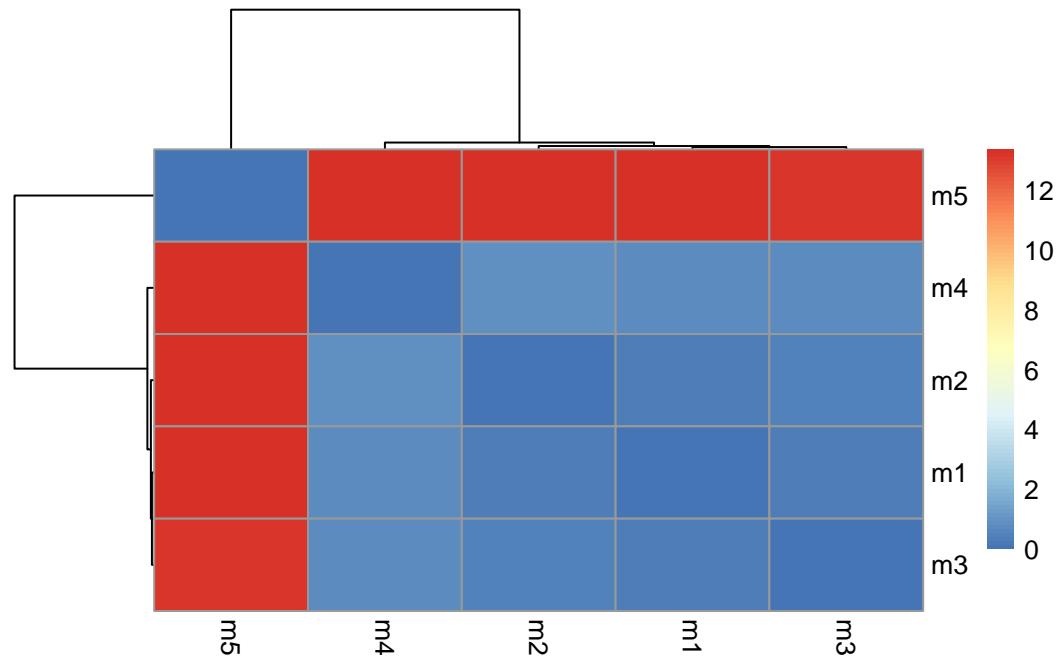
Warning in rmsd(pdfs, fit = T): No indices provided, using the 198 non NA positions

```
range(rd)
```

```
[1] 0.000 13.383
```

```
library(pheatmap)
```

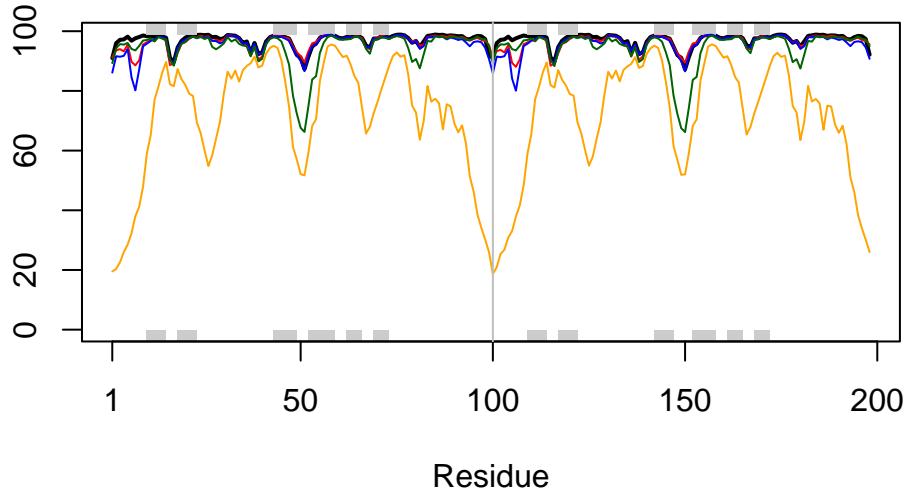
```
colnames(rd) <- paste0("m", 1:5)
rownames(rd) <- paste0("m", 1:5)
pheatmap(rd)
```



```
# Read a reference PDB structure
pdb <- read.pdb("1hsg")
```

Note: Accessing on-line PDB file

```
plotb3(pdb$b[1,], typ="l", lwd=2, sse=pdb)
points(pdb$b[2,], typ="l", col="red")
points(pdb$b[3,], typ="l", col="blue")
points(pdb$b[4,], typ="l", col="darkgreen")
points(pdb$b[5,], typ="l", col="orange")
abline(v=100, col="gray")
```



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

```
core size 197 of 198  vol = 76.955
core size 196 of 198  vol = 71.565
core size 195 of 198  vol = 67.163
core size 194 of 198  vol = 63.383
core size 193 of 198  vol = 61.543
core size 192 of 198  vol = 59.997
core size 191 of 198  vol = 58.48
core size 190 of 198  vol = 57.075
core size 189 of 198  vol = 55.366
core size 188 of 198  vol = 53.694
core size 187 of 198  vol = 52.261
core size 186 of 198  vol = 50.655
core size 185 of 198  vol = 49.378
```

```
core size 184 of 198 vol = 48.108
core size 183 of 198 vol = 47.022
core size 182 of 198 vol = 45.974
core size 181 of 198 vol = 45.167
core size 180 of 198 vol = 44.387
core size 179 of 198 vol = 43.45
core size 178 of 198 vol = 42.652
core size 177 of 198 vol = 42.015
core size 176 of 198 vol = 41.433
core size 175 of 198 vol = 41.139
core size 174 of 198 vol = 41.106
core size 173 of 198 vol = 40.986
core size 172 of 198 vol = 41.329
core size 171 of 198 vol = 41.389
core size 170 of 198 vol = 41.233
core size 169 of 198 vol = 40.957
core size 168 of 198 vol = 40.842
core size 167 of 198 vol = 40.889
core size 166 of 198 vol = 40.764
core size 165 of 198 vol = 40.562
core size 164 of 198 vol = 40.107
core size 163 of 198 vol = 39.511
core size 162 of 198 vol = 38.759
core size 161 of 198 vol = 38.179
core size 160 of 198 vol = 37.378
core size 159 of 198 vol = 36.853
core size 158 of 198 vol = 36.146
core size 157 of 198 vol = 35.636
core size 156 of 198 vol = 34.62
core size 155 of 198 vol = 34.129
core size 154 of 198 vol = 33.759
core size 153 of 198 vol = 33.278
core size 152 of 198 vol = 32.798
core size 151 of 198 vol = 32.638
core size 150 of 198 vol = 31.411
core size 149 of 198 vol = 30.726
core size 148 of 198 vol = 30.463
core size 147 of 198 vol = 29.999
core size 146 of 198 vol = 29.513
core size 145 of 198 vol = 29.003
core size 144 of 198 vol = 28.605
core size 143 of 198 vol = 28.047
core size 142 of 198 vol = 27.45
```

```
core size 141 of 198  vol = 26.83
core size 140 of 198  vol = 26.296
core size 139 of 198  vol = 25.027
core size 138 of 198  vol = 24.308
core size 137 of 198  vol = 23.425
core size 136 of 198  vol = 22.808
core size 135 of 198  vol = 22.055
core size 134 of 198  vol = 20.741
core size 133 of 198  vol = 19.848
core size 132 of 198  vol = 18.924
core size 131 of 198  vol = 18.311
core size 130 of 198  vol = 17.908
core size 129 of 198  vol = 17.148
core size 128 of 198  vol = 16.295
core size 127 of 198  vol = 15.711
core size 126 of 198  vol = 14.902
core size 125 of 198  vol = 14.213
core size 124 of 198  vol = 13.223
core size 123 of 198  vol = 12.44
core size 122 of 198  vol = 11.527
core size 121 of 198  vol = 10.655
core size 120 of 198  vol = 10.118
core size 119 of 198  vol = 9.486
core size 118 of 198  vol = 8.841
core size 117 of 198  vol = 8.175
core size 116 of 198  vol = 7.599
core size 115 of 198  vol = 7.251
core size 114 of 198  vol = 6.921
core size 113 of 198  vol = 6.668
core size 112 of 198  vol = 6.375
core size 111 of 198  vol = 5.942
core size 110 of 198  vol = 5.733
core size 109 of 198  vol = 5.308
core size 108 of 198  vol = 4.945
core size 107 of 198  vol = 4.534
core size 106 of 198  vol = 4.347
core size 105 of 198  vol = 4.215
core size 104 of 198  vol = 4.058
core size 103 of 198  vol = 3.879
core size 102 of 198  vol = 3.772
core size 101 of 198  vol = 3.523
core size 100 of 198  vol = 3.257
core size 99 of 198  vol = 2.949
```

```
core size 98 of 198  vol = 2.579
core size 97 of 198  vol = 2.298
core size 96 of 198  vol = 1.967
core size 95 of 198  vol = 1.773
core size 94 of 198  vol = 1.643
core size 93 of 198  vol = 1.454
core size 92 of 198  vol = 1.29
core size 91 of 198  vol = 1.247
core size 90 of 198  vol = 1.088
core size 89 of 198  vol = 0.982
core size 88 of 198  vol = 0.921
core size 87 of 198  vol = 0.831
core size 86 of 198  vol = 0.509
core size 85 of 198  vol = 0.344
FINISHED: Min vol ( 0.5 ) reached
```

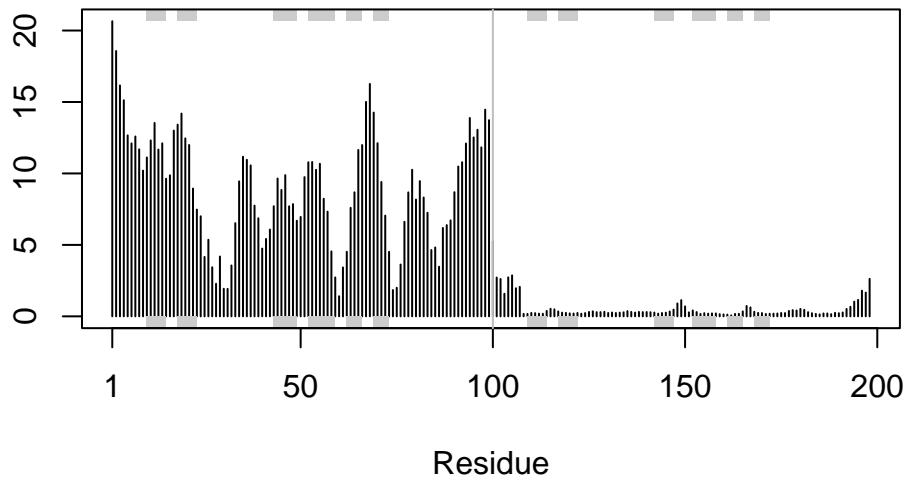
```
core inds <- print(core, vol=0.5)
```

```
# 86 positions (cumulative volume <= 0.5 Angstrom^3)
  start end length
1      9   47     39
2     52   78     27
3     80   97     18
```

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

```
rf <- rmsf(xyz)

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



```
library(jsonlite)

# Listing of all PAE JSON files
pae_files <- list.files(path=results_dir,
                        pattern=".*model.*\\.json",
                        full.names = TRUE)
```