

Attempt2.R

Noah

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```
library(bio3d)
aa <- get.seq("1ake_A")
```

```
## Warning in get.seq("1ake_A"): Removing existing file: seqs.fasta
```

```
## Fetching... Please wait. Done.
```

```
aa
```

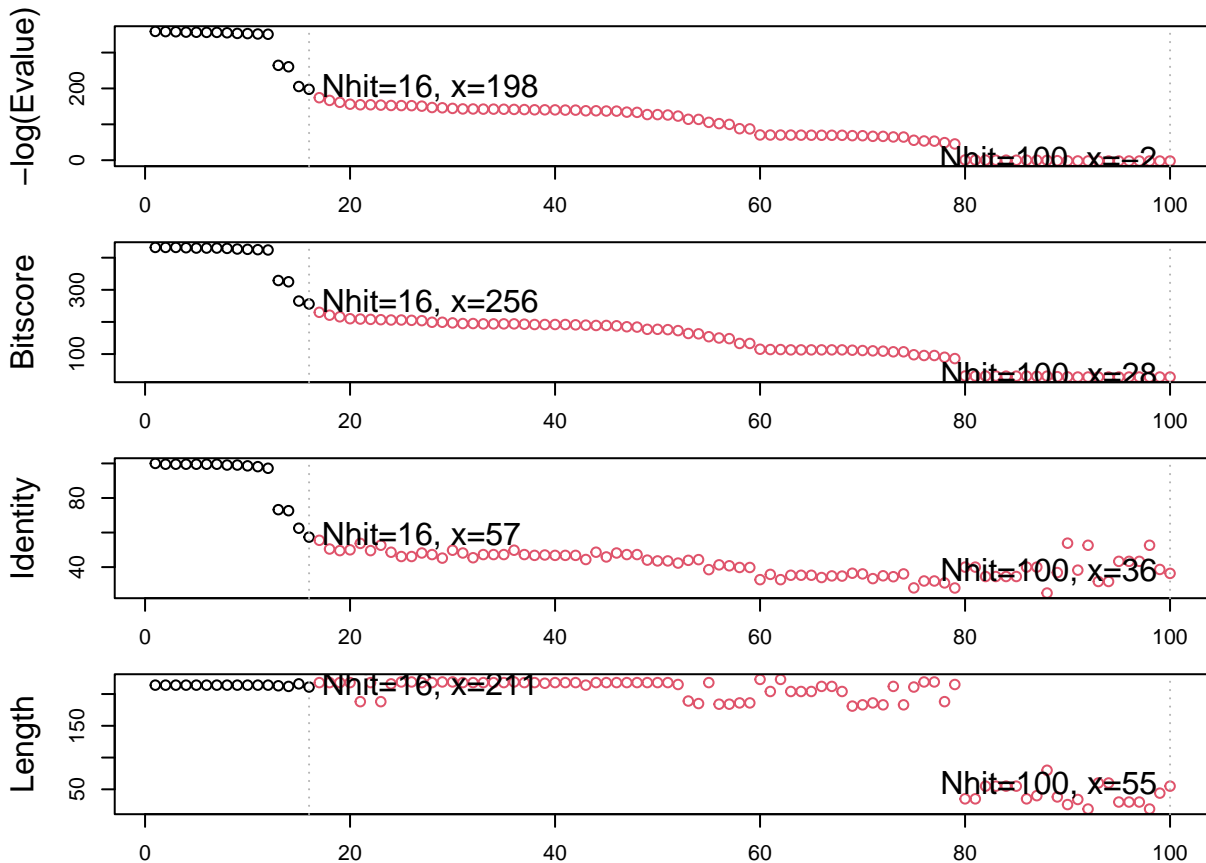
```
##           1           .           .           .           .           .           60
## pdb|1AKE|A  MRIILLGAPGAGKGTQAQFIMEKYGIPQISTGDMLRAAVKSGSELGKQAKDIMDAGKLV
##           1           .           .           .           .           .           60
##
##           61           .           .           .           .           .           120
## pdb|1AKE|A  DELVIALVKERIAQEDCRNGFLLDGFPRTIPQADAMKEAGINVDYVLEFDVPDELIVDRI
##           61           .           .           .           .           .           120
##
##           121          .           .           .           .           .           180
## pdb|1AKE|A  VGRRVHAPSGRVYHVKFNPPKVEGKDDVTGEELTTRKDDQEETVRKRLVEYHQMTAPLIG
##           121          .           .           .           .           .           180
##
##           181          .           .           .           214
## pdb|1AKE|A  YYSKEAEAGNTKYAKVDGTPVAEVRADLEKILG
##           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
```

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

```
## Searching ... please wait (updates every 5 seconds) RID = 2809ESXB016
## .
## Reporting 100 hits
```

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

```
## * Possible cutoff values: 197 -3
##      Yielding Nhits: 16 100
##
## * Chosen cutoff value of: 197
##      Yielding Nhits: 16
```



```
head(hits$ pdb.id)
```

```
## [1] "1AKE_A" "4X8M_A" "6S36_A" "6RZE_A" "4X8H_A" "3HPR_A"
```

```
hits <- NULL
```

```
hits$ pdb.id <- c('1AKE_A', '6S36_A', '6RZE_A', '3HPR_A', '1E4V_A', '5EJE_A', '1E4Y_A', '3X2S_A', '6HAP_A', '6HAM_A')
```

```
files <- get.pdb(hits$ pdb.id, path="pdb", split=TRUE, gzip=TRUE)
```

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

```
## Warning in get.pdb(hits$ pdb.id, path = "pdb", split = TRUE, gzip = TRUE): pdbs/
## 6S36.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/
## 3HPR.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/
## 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/
## 3GMT.pdb exists. Skipping download

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

##      |

```