## data\_analysis.R

*sayaneshome* 2020-06-04

```
library(bio3d)
setwd('/Users/sayaneshome/Desktop/New Folder With Items/prelims_stuffs/data/data_analysis_dip1/')
f117r_dipl <- read.table('f117r_dipl_smd01.dat')</pre>
f541r_dipl <- read.table('f541r_dipl_smd01.dat')</pre>
148f_dipl <- read.table('148f_dipl_smd01.dat')</pre>
1826f_dipl <- read.table('1826f_Dipl_smd01.dat')</pre>
native_dipl <- read.table('smd01_native.dat')</pre>
#force-position graph
plot(f117r_dipl$V2,f117r_dipl$V3,type = 'line')
## Warning in plot.xy(xy, type, ...): plot type 'line' will be truncated to
## first character
lines(f541r_dipl$V2,f541r_dipl$V3,col = "red")
lines(1826f_dipl$V2,1826f_dipl$V3,col = "green")
lines(native_dipl$V2,native_dipl$V3,col = "purple")
     1000
f117r_dipl$V3
      500
      0
                    20
                                  40
                                                 60
                                                               80
                                                                             100
                                          f117r dipl$V2
#time-position graph; get the frames from this graph specially native one
```

```
plot((native_dipl$V1)/100000, smooth(native_dipl$V3), type = 'line', ylab="Force", xlab="Time(ns)", xlim =
## Warning in plot.xy(xy, type, ...): plot type 'line' will be truncated to
## first character
lines((f117r_dipl$V1)/100000, smooth(f117r_dipl$V3), col = "purple")
lines((f541r_dipl$V1)/100000, smooth(f541r_dipl$V3), col = "red")
```

```
lines((1826f_dipl$V1)/100000,smooth(1826f_dipl$V3),col = "green")
```

```
9203

0 0001

0 2 4 6 8 10

Time(ns)
```

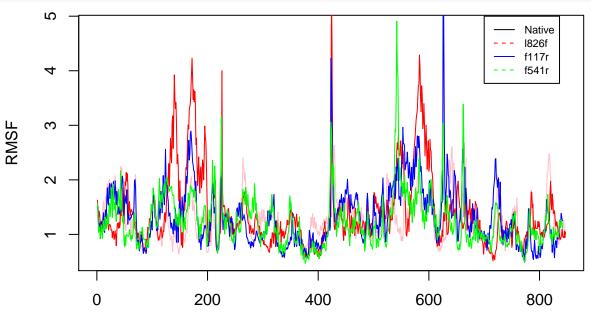
```
#diploptene pdbs
f117r_dipl_pdb <- read.pdb('f117r_dipl_stride100_full.pdb',multi = TRUE)</pre>
native_dipl_pdb <- read.pdb('hpnn_dipl_stride100_full.pdb',multi = TRUE)</pre>
1826f dipl pdb <- read.pdb('1826f dipl stride100 full.pdb',multi = TRUE)
f541r_dipl_pdb <- read.pdb('f541r_dipl_stride100_full.pdb',multi = TRUE)
ca.inds_native <- atom.select(native_dipl_pdb, elety="CA")</pre>
xyz_native <- fit.xyz(fixed=native_dipl_pdb$xyz[1,], mobile=native_dipl_pdb$xyz[2:11,])</pre>
## Warning in fit.xyz(fixed = native_dipl_pdb$xyz[1, ], mobile = native_dipl_pdb$xyz[2:11, : No fitting
rd_native <- rmsd(xyz_native[1,ca.inds_native$xyz]), xyz_native[,ca.inds_native$xyz])
ca.inds_1826f <- atom.select(1826f_dipl_pdb, elety="CA")</pre>
xyz_1826f <- fit.xyz(fixed=1826f_dipl_pdb$xyz[1,], mobile=1826f_dipl_pdb$xyz[2:11,])</pre>
## Warning in fit.xyz(fixed = 1826f_dipl_pdb$xyz[1, ], mobile = 1826f_dipl_pdb$xyz[2:11, : No fitting in
rd_1826f <- rmsd(xyz_1826f[1,ca.inds_1826f$xyz], xyz_1826f[,ca.inds_1826f$xyz])
ca.inds_f117r <- atom.select(f117r_dipl_pdb, elety="CA")</pre>
xyz_f117r <- fit.xyz(fixed=f117r_dipl_pdb$xyz[1,], mobile=f117r_dipl_pdb$xyz[2:11,])</pre>
## Warning in fit.xyz(fixed = f117r_dipl_pdb$xyz[1, ], mobile = f117r_dipl_pdb$xyz[2:11, : No fitting in
rd_f117r <- rmsd(xyz_f117r[1,ca.inds_f117r\$xyz], xyz_f117r[,ca.inds_f117r\$xyz])
ca.inds_f541r <- atom.select(f541r_dipl_pdb, elety="CA")</pre>
xyz_f541r <- fit.xyz(fixed=f541r_dipl_pdb$xyz[1,], mobile=f541r_dipl_pdb$xyz[2:11,])</pre>
## Warning in fit.xyz(fixed = f541r_dipl_pdb$xyz[1, ], mobile = f541r_dipl_pdb$xyz[2:11, : No fitting in
```

rd\_f541r <- rmsd(xyz\_f541r[1,ca.inds\_f541r\\$xyz], xyz\_f541r[,ca.inds\_f541r\\$xyz])

```
rf_native <- rmsf(xyz_native[,ca.inds_native$xyz])
plot(rf_native, ylab="RMSF", xlab="Residue Position", typ="l",col="pink")
rf_l826f <- rmsf(xyz_l826f[,ca.inds_l826f$xyz])
lines(rf_l826f, ylab="RMSF", xlab="Residue Position", typ="l",col="red")
rf_f117r <- rmsf(xyz_f117r[,ca.inds_f117r$xyz])
lines(rf_f117r, ylab="RMSF", xlab="Residue Position", typ="l",col="blue")
rf_f541r <- rmsf(xyz_f541r[,ca.inds_f541r$xyz])
lines(rf_f541r, ylab="RMSF", xlab="Residue Position", typ="l",col="green")
rf_dipl <- data.frame(cbind(rf_f117r,rf_native,rf_f541r,rf_l826f))</pre>
```

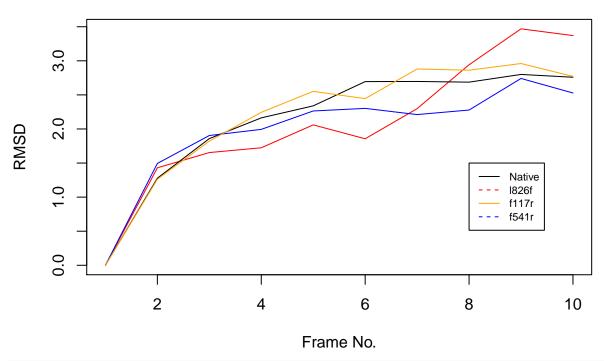
## Warning in cbind(rf\_f117r, rf\_native, rf\_f541r, rf\_1826f): number of rows
## of result is not a multiple of vector length (arg 1)

legend(700,5,legend=c("Native","1826f","f117r","f541r"),col=c("black","red","blue","green"), lty=1:2, c



## Residue Position

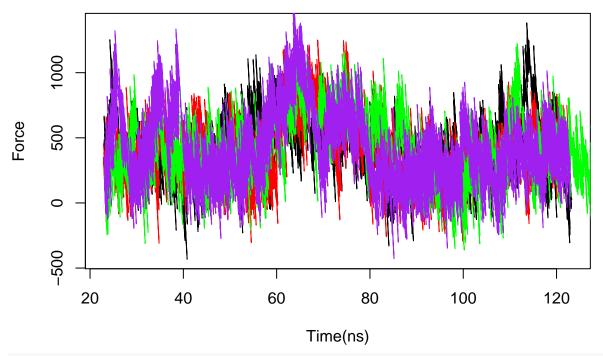
```
plot(rd_1826f, typ="1", ylab="RMSD", xlab="Frame No.",col="red")
#points(lowess(rd_1826f), typ="l", col="red", lty=2, lwd=2)
lines(rd_native, typ="1", ylab="RMSD", xlab="Frame No.")
#points(lowess(rd_native), typ="l", col="black", lty=2, lwd=2)
lines(rd_f541r, typ="1", ylab="RMSD", xlab="Frame No.",col="blue")
#points(lowess(rd_f541r), typ="l", col="blue", lty=2, lwd=2)
lines(rd_f117r, typ="1", ylab="RMSD", xlab="Frame No.",col="orange")
#points(lowess(rd_f117r), typ="l", col="orange", lty=2, lwd=2)
legend(8,1.5,legend=c("Native", "l826f","f117r","f541r"),col=c("black","red","orange","blue"), lty=1:2,
```



```
setwd('/Users/sayaneshome/Desktop/New Folder With Items/prelims_stuffs/data/data_analysis_tauro/')
native_tauro <- read.table('hpnn_t_native_phase2_trial2.dat')
f117r_tauro <- read.table('f117r_smd_tauro.dat')
f541r_tauro <- read.table('f541r_tauro_smd.dat')
l826f_tauro <- read.table('l826f_smd_tauro.dat')

#force-position graph
plot(f117r_tauro$V2,f117r_tauro$V3,type = 'line', ylab="Force", xlab="Time(ns)")

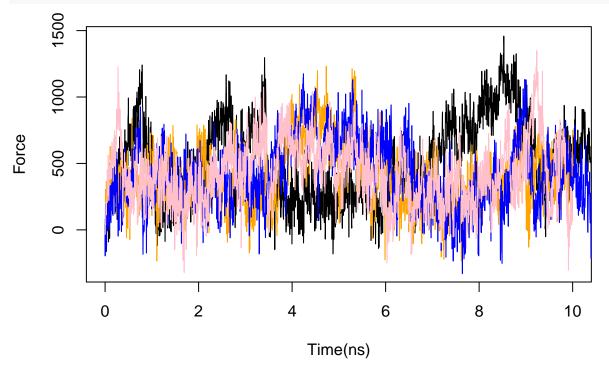
## Warning in plot.xy(xy, type, ...): plot type 'line' will be truncated to
## first character
lines(f541r_tauro$V2,f541r_tauro$V3,col = "red")
lines(l826f_tauro$V2,l826f_tauro$V3,col = "green")
lines(native_tauro$V2,native_tauro$V3,col = "purple")</pre>
```



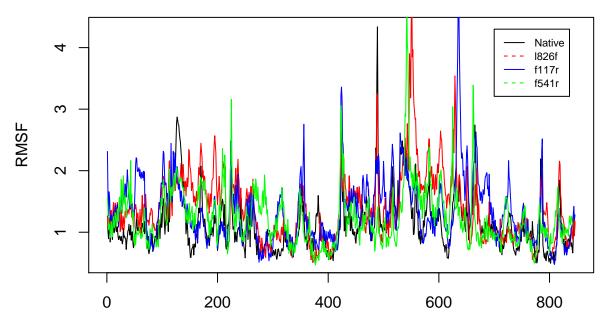
#time-position graph;get the frames from this graph specially native one
plot(native\_tauro\$V1/100000,smooth(native\_tauro\$V3),type = 'line',ylab="Force", xlab="Time(ns)",xlim =

## Warning in plot.xy(xy, type,  $\dots$ ): plot type 'line' will be truncated to ## first character

```
lines((f541r_tauro$V1)/100000,smooth(f541r_tauro$V3),col = "orange")
lines((1826f_tauro$V1)/100000,smooth(1826f_tauro$V3),col = "blue")
lines((f117r_tauro$V1)/100000,smooth(f117r_tauro$V3),col = "pink")
```



```
f117r_tauro_pdb <- read.pdb('hpnn_f117r_tauro_stride100_full.pdb',multi = TRUE)
native_tauro_pdb <- read.pdb('hpnn_tauro_phase2_trial2_stride100_full.pdb',multi = TRUE)</pre>
1826f_tauro_pdb <- read.pdb('hpnn_1826f_tauro_stride100_full.pdb',multi = TRUE)
f541r_tauro_pdb <- read.pdb('hpnn_f541r_tauro_stride100_full.pdb',multi = TRUE)
ca.inds native <- atom.select(native tauro pdb, elety="CA")</pre>
xyz_native <- fit.xyz(fixed=native_tauro_pdb$xyz[1,], mobile=native_tauro_pdb$xyz[2:11,])</pre>
## Warning in fit.xyz(fixed = native_tauro_pdb$xyz[1, ], mobile = native_tauro_pdb$xyz[2:11, : No fitti
rd_native <- rmsd(xyz_native[1,ca.inds_native$xyz]), xyz_native[,ca.inds_native$xyz])
ca.inds 1826f <- atom.select(1826f tauro pdb, elety="CA")
xyz_1826f <- fit.xyz(fixed=1826f_tauro_pdb$xyz[1,], mobile=1826f_tauro_pdb$xyz[2:11,])</pre>
## Warning in fit.xyz(fixed = 1826f_tauro_pdb$xyz[1, ], mobile = 1826f_tauro_pdb$xyz[2:11, : No fitting
rd 1826f <- rmsd(xyz 1826f[1,ca.inds 1826f$xyz], xyz 1826f[,ca.inds 1826f$xyz])
ca.inds_f117r <- atom.select(f117r_tauro_pdb, elety="CA")</pre>
xyz_f117r <- fit.xyz(fixed=f117r_tauro_pdb$xyz[1,], mobile=f117r_tauro_pdb$xyz[2:11,])</pre>
## Warning in fit.xyz(fixed = f117r_tauro_pdb$xyz[1, ], mobile = f117r_tauro_pdb$xyz[2:11, : No fitting
rd_f117r <- rmsd(xyz_f117r[1,ca.inds_f117r\$xyz], xyz_f117r[,ca.inds_f117r\$xyz])
rf native <- rmsf(xyz native[,ca.inds native$xyz])</pre>
plot(rf_native, ylab="RMSF", xlab="Residue Position", typ="l",col="black")
rf_1826f <- rmsf(xyz_1826f[,ca.inds_1826f$xyz])
lines(rf_1826f, ylab="RMSF", xlab="Residue Position", typ="1",col="red")
rf_f117r <- rmsf(xyz_f117r[,ca.inds_f117r$xyz])</pre>
lines(rf_f117r, ylab="RMSF", xlab="Residue Position", typ="l",col="blue")
rf_f541r <- rmsf(xyz_f541r[,ca.inds_f541r$xyz])
lines(rf_f541r, ylab="RMSF", xlab="Residue Position", typ="l",col="green")
rf_tauro <- data.frame(cbind(rf_f117r,rf_native,rf_f541r,rf_1826f))</pre>
## Warning in cbind(rf_f117r, rf_native, rf_f541r, rf_1826f): number of rows
## of result is not a multiple of vector length (arg 3)
legend(700,4.3,legend=c("Native","1826f","f117r","f541r"),col=c("black","red","blue","green"), lty=1:2,
```



## **Residue Position**

```
plot(rd_1826f, typ="1", ylab="RMSD", xlab="Frame No.",col="red")
#points(lowess(rd_l826f), typ="l", col="red", lty=2, lwd=2)
lines(rd_native, typ="1", ylab="RMSD", xlab="Frame No.")
#points(lowess(rd_native), typ="l", col="black", lty=2, lwd=2)
lines(rd_f541r, typ="1", ylab="RMSD", xlab="Frame No.",col="blue")
#points(lowess(rd_f541r), typ="l", col="blue", lty=2, lwd=2)
lines(rd_f117r, typ="1", ylab="RMSD", xlab="Frame No.",col="orange")
#points(lowess(rd_f117r), typ="l", col="orange", lty=2, lwd=2)
legend(8,1.5,legend=c("Native","l826f","f117r","f541r"),col=c("black","red","orange","blue"), lty=1:2,
```

