**********INTRODUCTION**********
This tool is designed for predicting the distance of unknown structure from its native without using its native form in terms of RMSD, GDT and TM, therefore it named as D2N.Principle of prediction is based on universal properties of protein structure such as area, energy, and secondary structure and CB arrangement. User has to submit a protein file in PDB format and D2N gives score of RMSD, GDT and TM.

********INSTALLATION**********

======STEP 1. Prerequisite tools and software=======
a) This tool can run oonly on linux machine.
b) Naccess: http://www.bioinf.manchester.ac.uk/naccess/
c) Psipred: http://bioinf.cs.ucl.ac.uk/software_downloads/
d) AMBER: http://ambermd.org/
e) Stride: http://webclu.bio.wzw.tum.de/stride/
f) R statistical software

==========STEP 2. Download D2N==========
a) Download tool (FILE: web_donloadable_D2N.tar.gz) from
http://www.scfbio-iitd.res.in/software/d2n.jsp
b) Uncompressed file in home directory
c) Place following directories/file/executable/scripts in home directory
all_Model energy_minimization_short_step
CB_CB.exe first_resi.exe sequencenumber.exe
d2n.sh final_result.sh run_energy.sh
run_merge_features.sh run_polar_area.sh run_residue_length.sh
tleap1.sh
exseq.sh run_area.sh run_euclidian_distance.sh run_pair_number.sh
run_process_pdb.sh run_secondary_structure.sh trial.sh
run_merge_features_area.sh
one_file.pl s1.cmd tleap1.sh
singlecode test-result-4.RData testUsingRandomForest_new_area.R
testUsingRandomForest.R

==========STEP 3. Set Path==========
a) Set the path of Naccess in run_area.sh
a) Set the path of Naccess in run_polar_area.sh
b) Set the path of runpsipred in run_secondary_structure.sh
c) Set the path of Stride in run_secondary_structure.sh

**********STEP3. RUN D2N**********
a) Make a sub directory (ex:TEST) in directory web_donloadable_D2N
(extracted in step 2(a) & (b))
b) Copy a query protein model in TEST
c) Remove multiple chain entry, HETATM record, HEADERS from protein file
c) run d2n script:
sh d2n.sh TEST

**********STEP 4. RESULT**********
Result File: patch_result
Result File (HTML): result_d2n.html (open in browser)