

Make sure you download DISOPRED3 and sequence debases. You need to change the directory path in <run_disopred.pl>. Also, make sure you have human unaligned sequence files. E.g. <human_genename.fasta>

You can use <extract_human_unalignedseq.py> to extract human sequence from <all_seqs_with_latin_names\$genename.fasta> files. Then, you have to change the name of human sequence file using <change_names.py> in order to run DISOPRED.

```
[xiao@es-3095m-tp-moses run_DISOPRED_testing]$ python run_DISP.py /home/xiao/run_DISOPRED_testing/human_seqfiles/ /home/xiao/DISOPRED/run_disopred.pl
/home/xiao/DISOPRED/run_disopred.pl /home/xiao/run_DISOPRED_testing/human_seqfiles/human_CCNB1.fasta
/home/xiao/run_DISOPRED_testing/human_seqfiles/human_CCNB1.fastaRunning PSI-BLAST search ...
}

/home/xiao/blast-2.2.26/bin/blastpgp -i /home/xiao/run_DISOPRED_testing/human_seqfiles/human_CCNB1.fasta -d /home/xiao/blastdb/uniref90/uniref90.fasta -a 1 -b 0 -j 3 -h 0.001 -C /home/xiao/run_DISOPRED_testing/human_seqfiles/human_CCNB1_1
30754_968eSed6.chk -o /home/xiao/run_DISOPRED_testing/human_seqfiles/human_CCNB1_130754_968eSed6.blast
```