How to use SPRINGS?

Sequence Based Predictor of **PR**otein-protein Interact**ING S**ites

Step 0) In the folder **SPRINGS,** you should see four folders along with this **README** file.

1) **codes**
2) **input_prsa**
3) **input_pssm**
4) **Output**

Step 1) Solvent Accessibility: Upload your fasta file on <u>SANN</u>. Then once SANN completes running the job, go to '<u>download results</u>'. Download the ***.prsa** file and copy it into the folder **input_prsa**.

Step 2) PSSM: Upload your fasta file on PSI-BLAST server or your locally installed server. Download the ***.pssm** file and copy it into the folder **input_pssm**.

Step 3) Ensure that the filenames (i.e. 'file_name' in the pictures) of both the files (the .prsa and the .pssm files) are the same for a particular protein.

Eg. 1acb_I.prsa and 1acb_I.pssm ✔

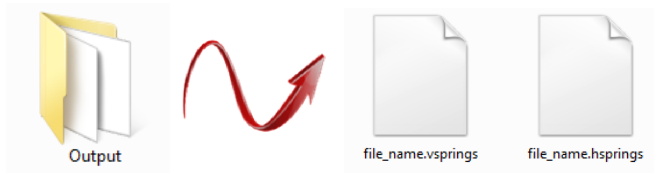1acb_I.prsa and 3h4s_A.pssm ✘

1acb_I.prsa and 1acbI.pssm ✘

1acb_I.prsa and 1Acb_I.pssm ✘

Step 4) Executing the code: Go to your Terminal. And then execute the **springs.py** file in python by typing: **python <space> (path of directory)/SPRINGS/codes/springs.py**

Step 5) You should get an output like this. Go to the folder **Output** to get your output file in ***.vsprings** (vertically aligned) format and ***.hsprings** (horizontally aligned) format.

Go to the folder **output** to get your output file in ***.springs** format.

Note:

    (i)   Ensure that GNU Octave is installed. Works best for versions 3.6.4 and above.

    (ii)   You can also use **SPRINGS** for prediction of multiple proteins by placing multiple files in **input_prsa** and **input_pssm** folders. You just need to ensure that two files representing the same protein should have the same name i.e. they follow the above given format.

    (iii)   Before you run your protein files, it is suggested to run the three example files that have been supplemented.

    (iv)   SPRINGS is suited for UNIX based Operating Systems.

★★★★★