How to use LORIS?

LOgistic Regression based Interaction Sites predictor

Step 0) In the folder LORIS, 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 'download results'. Download the *.prsa file and copy it into the folder input_prsa.



Step 2) PSSM: Upload your fasta file on <u>PSI-BLAST server</u> or your locally installed server. Take 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.



Step 4) Execute the code: Go to Terminal. And then execute the loris.py file in python by typing: python <space> (path of directory)/LORIS/codes/loris.py

L1 logistic regression based classifier source: http://www.stanford.edu/~boyd/l1_logreg/

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



Note:

- (i) You can also use **LORIS** for prediction of multiple proteins by placing multiple files in the **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.
- (ii) Before you run your protein files, it is suggested to run the three example files that have been supplemented.
- (iii) LORIS is suited for UNIX based Operating Systems.

Copyright © LORIS version 1.0 2013 Kaustubh Dhole, Gurdeep Singh & Sukanta Mondal

Department of Biological Sciences, BITS Pilani, K.K. Birla Goa Campus, India

For more information on LORIS or to report any bugs, feel free to mail at suku@goa.bits-pilani.ac.in

