LORIS User Guide

L1-regularized **LO**gistic **R**egression based protein-protein **I**nteraction **S**ites predictor

LORIS is a novel method that identifies protein-protein interaction residues, using sequence features and is implemented via the L1-logreg classifier. This standalone package could be useful for facilitating drug-design and targeted mutation related studies, which require a deeper knowledge of protein interactions sites.

Before you begin) 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) Predicted Relative Solvent Accessibility (PRSA): Upload query protein sequence on the SANN web-server (http://lee.kias.re.kr/~newton/sann/). Then download **query.prsa** file (PRSA for the query protein) and copy it into the folder **input_prsa**.

Step 2) Position Specific Scoring Matrix (PSSM): Generate **query.pssm** file for the query protein and copy it into the folder **input_pssm**.

For example: *1acb_I.prsa and 1acb_I.pssm* (correct format)
1acb_I.prsa and 3h4s_A.pssm
1acb_I.prsa and 1acbI.pssm
1acb_I.prsa and 1Acb_I.pssm

Step 3) Execute code: Go to terminal and then execute **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) Output/Prediction: Go to the folder Output.

query.vloris *(vertically aligned) format and* ***query.hloris*** *(horizontally aligned) format*

Note:
(i) One can also use LORIS for prediction of multiple proteins by placing multiple files in the **input_prsa** and **input_pssm** folders. One just needs to ensure that two files representing the same protein should have the same name.

(ii) LORIS is suited for UNIX based Operating Systems.

Happy computing!