

Documentation of PreDisorder

PreDisorder 1.1: Prediction of disordered regions from protein sequences

PreDisorder was ranked among the best during and Eighth Critical Assessment of Techniques for Protein Structure Prediction (CASP7 and 8), 2008.

References:

X. Deng, J. Eickholt, and J. Cheng. PreDisorder: Ab Initio Sequence-Based Prediction of Protein Disordered Regions. *BMC Bioinformatics*, 10:436, 2009.

J. Hecker, J. Yang, and J. Cheng. Protein Disorder Prediction at Multiple Levels of Sensitivity and Specificity. *BMC Genomics*. 9(S1):S9, 2008.

J. Cheng, M. Sweredoski, and P. Baldi. Accurate Prediction of Protein Disordered Regions by Mining Protein Structure Data, *Data Mining and Knowledge Discovery*, vol. 11, no. 3, pp. 213-222, 2005.

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Installation (Linux Version):

0. Install PSpro package (PSpro1.1 or PSpro2.0) first. Get it from:
http://sysbio.rnet.missouri.edu/multicom_toolbox/. Very easy to install.

1.unzip predisorder1.1.tar.gz

e.g. tar xzf predisorder1.1.tar.gz

2.change directory into predisorder1.1

e.g. cd predisorder1.1

3. edit configure.pl

set PreDisorder path (\$install_dir) and PSpro path (\$spro_dir) to their installation directories.

4. run configure.pl

e.g. ./configure.pl

Installation is done.

Check the integrity of installation

cd test

../bin/predict_diso.sh seq.fasta test.out

The result in test.out should be the same as that in seq.diso.

Output format:

line 1: sequence

line 2: D -> disorder, O -> order

line 3: probability of disorder. You can set different

thresholds to make your own disorder/order predictions.

line 2 are generated by setting threshold to 0.5.

Scripts in bin subdirectory:

predict_diso.sh: predict disordered residues

Enjoy it!