ACLS Seminar
情報生命博士教育院セミナー

日時：2015年3月30日（月）13:30～15:00
場所：大岡山西8号館E棟5階コラボレーション室（W8-E509）

演題： Computational methods for understanding and predicting the folding rates of proteins and mutants

演者：Prof. M. Michael Gromiha , Department of Biotechnology, Indian Institute of Technology (IIT) Madras

Protein folding rate is a measure of slow/fast folding of proteins from the unfolded state to its native three-dimensional structure. Prediction of protein folding rates from amino acid sequences is one of the most important challenging tasks, similar to protein folding problem (1). In this talk, I will briefly introduce the concept of protein folding rates and their relationship with structural parameters such as contact order, long-range order and multiple contact index obtained from protein three-dimensional structures (2-4). Although these structure based parameters are highly correlated with experimental folding rates their role in predicting the folding rates upon mutations is limited. Hence, we have developed novel statistical methods for discriminating the accelerating and decelerating mutants upon amino acid mutations (5) and predicting the folding rates upon mutations (6). Recently, we have explored the importance of classifying the mutants based on the location of mutants, which enhanced the correlation significantly (7). The salient features of the results will be discussed.

References:

(1) M.M. Gromiha and L-T. Huang (2011) Curr. Prot. Pept. Sci. 12:490-502
(2) M.M. Gromiha (2010) Protein Bioinformatics: From Sequence to Function, Elsevier/Academic Press.
(3) M.M. Gromiha and S. Selvaraj (2001) J. Mol. Biol. 310, 27-32.
(4) M.M. Gromiha (2009) J. Chem. Inf. Model. 49:1130-1135.
(5) L-T. Huang and M.M. Gromiha (2010) Bioinformatics 26: 2121-2127.
(6) L-T. Huang and M.M. Gromiha (2012) J. Comp. Aid. Mol. Des. 26, 339-347.
(7) P. Chaudry, A. Naganathan and M.M. Gromiha (2015) Bioinformatics (in press).

«問い合せ先» 情報生命博士教育院
大岡山事務室 内線3755