

A day in the life of intrinsically disordered proteins: from computation to experiments – Oct 26th 2015

Disorder flavors explored using Hydrophobic Cluster Analysis

Isabelle Callebaut

IMPMC, UMR7590, CNRS-Université Pierre et Marie Curie-MNHN-IRD

A significant part of protein sequences does not match any known domain, as stored in dedicated databases. These “orphan” sequences include globular domains, which do not share any obvious sequence similarity with already known domain families, but also disordered regions, which play key roles in regulatory and signaling processes. Many efforts have been directed during the last years at the prediction of these disordered regions in proteins.

Here, I will describe a tool we have developed for delineating, in a comprehensive and automated way, foldable regions, where order can be predicted. This tool is based on the Hydrophobic Cluster Analysis methodology and uses only the information of a single amino acid sequence, without the prior knowledge of homologs. It gives insightful information not only for characterizing the function and evolution of globular domains, but also for investigating disordered regions, especially when combined with other disorder predictors (e.g. IUPRED). Hence, different flavors of disorder can be discriminated, from fully disordered states to segments able to undergo disorder to order transitions.