CIC biomaGUNE
CENTER FOR COOPERATIVE RESEARCH IN BIOMATERIALS

seminar

Friday, 14th September, 12.30 pm, Seminar Room

Host: Dr. Ivan Coluzza

Exploring the Energy Landscape for Protein Folding and Function: The Convergences of Structural Models and Sequence Coevolution Information

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Energy landscape theory has been a powerful approach to study protein folding dynamics and function. The discovery that an accurate estimate of the joint probability distribution of amino acid occupancies in protein families provides insights about residue-residue coevolution and concrete details about protein folding landscapes has also advanced structural biophysics. Our realization that the collection of couplings and local fields as parameters of such distribution is inherently connected with the thermodynamics of sequence selection towards folding and function demonstrates the importance of coevolutionary methods to understand stability and function of biomolecules. The synergy between structure based models and coevolutionary information has spearheaded the field of structure prediction, including protein and RNA, as well as accelerating the discovery of functional structural states and the prediction of protein complexes. Coevolution signals can also be used to create protein recognition metrics, which led to successful experimental efforts, and the uncovering of novel molecular interactions. This idea has opened the door to encode recognition in protein pairs. Coevolved interfaces can also be combined with small molecule hot spot estimation methods to improve the discovery of druggable interfaces. Finally, we show that biophysical modeling via statistical inference approaches can shed light on structural properties of chromosomes. We demonstrate that it is possible to reconstruct with fidelity experimental maps of interacting genomic regions for particular chromosomal types by learning only generic properties of single chromosomes. We provide evidence of the depth and coverage of energy landscape theory approaches linked with coevolutionary methods and their impact in our goal to understand biological function at the molecular level.