accessory secondary structures in some cases. We found that the atomic fluctuations of each of the beta-strands have a high correlation with its immediate beta-strand neighbour in the core. Compared to the beta strands, the alpha helices have less correlation with each other and almost none with the strands. We also defined rotation and translation vectors to decompose the type of movements to which the normal modes of these TIMs correspond. We relate differences in the mobility of the individual secondary structure elements to the differences in function and structure of the five different enzymes.

1168-Pos Board B60

Comparing Normal Modes of Protein Structures using Webnm@ 2.0

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Normal modes analysis (NMA) has been shown to be an effective computational method to study the movements of proteins, especially at the domain level. WEBnm@ (http://apps.cbu.uib.no/webnma/home) is a web-tool which provides access to calculations of these modes on C-alpha atoms of protein structures and various analyses with output as images, plots or raw data points. We have improved the efficiency for input processing and have added new functionality that interprets the normal modes calculated. In the Single Analysis section, we have included an interactive visualisation of the lowest six mode vectors, the calculation of the correlation matrix based on all the modes vectors and the overlap analysis with another conformation of the same structure. The newest section, Comparative Analysis, calculates and compares the normal modes of a set of aligned protein structures, which is currently not available in any other tool. It includes comparative analyses such as fluctuations profiles, deformation energies and comparison of modes calculated on the input structures using the root mean square inner product (RMSIP) . For this part, more than one structure can be submitted along with a FASTA file of their alignment. In addition to the updates, we have also provided a SOAP web-service for a more programmable interface for both of these sections.

1169-Pos Board B61

A Quantitative Measure of Protein Flexibility

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Protein flexibility plays an important role in the proper structure and function of proteins. It also dominate complex phenomenon such as protein-ligand interactions, protein-protein interactions. A quantitative measure of protein flexibility would be valuable in many applications such as docking and modeling problems. In this work we provide a quantitative measure of protein flexibility based on side-chain conformational analysis and hydropathy pattern for all possible tripeptide strings in the protein sequence. We used 5730 PDB structures culled by PISCES server based on sequence identity, resolution and R-factor. We used the chi-1-3CPD (chi-1 three (3) conformational propensity diversion) parameter defined as the standard deviation of RFs (relative frequencies) in 3 possible conformations of central residue in each tripeptide. Chi-1-3CPD = 0 means RFs in G+, G- and Trans are exactly equal. We used chi-1-3CPD index in sliding window method to get flexibility predicted values. Our analysis showed a strong correlation between chi-1-3CPD and backbone flexibility indicated by the B-factor. We then analyzed the hydropathy pattern from all possible tripeptides we have had used in these studies. Our findings illustrated, those tripeptides with non-homogeneous hydropathy pattern for all their three residues have small values of chi-1-3CPD. For instance, tripeptides with hydrophilic central residue and hydrophobic marginal residues had minimum chi-1-3CPDs value (less chi-1-3CPD means central residue has nearly equal propensity for three possible conformations and more like for conformational switching). It is suggested that the hydropathy pattern of residues play a major role in the flexibility of proteins. The knowledge-based flexibility prediction method presented here is a simple and non-expensive method comparable to previously sophisticated methods used for flexibility analysis of proteins.

1170-Pos Board B62

Structural Dynamics Flexibility Informs Function and Evolution at a Proteome Scale

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Abstract: Protein structures are dynamic entities with a myriad of atomic fluctuations, side chain rotations, and collective domain movements. While the importance of these dynamics to proper functioning of some proteins is emerging, there is a lack of broad evidence for the critical role of protein dynamics in shaping the biological functions and protein evolution for a large number of proteins in a proteome. To this aim, we develop novel dynamic flexibility index (*dfi*) to quantify the dynamic properties of individual residues in any protein using perturbation response scanning that couples elastic network models with linear response theory. Then, we use *dfi* to assess the importance of protein dynamics in over 100 human proteins. Our analyses involving functionally critical positions, disease-associated and benign population variations, and the rate of interspecific substitutions per residue produce concordant patterns and establish that the preservation of dynamic properties of residues in a protein structure are critical for maintaining the protein/biological function at a proteome scale. Therefore, structural dynamics needs to become a major component of the analysis of protein function and evolution.

Protein Structure Prediction

1171-Pos Board B63

De Novo Protein Structure Determination from Incomplete Experimental Data

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The problem of theoretical *de novo* protein structure prediction has been already investigated for a few decades. Throughout those years numerous different algorithms have been proposed to solve this problem. The most successful ones are capable of predicting the structure for small-size globular proteins (up to 80 amino acids). Recent years have also witnessed improvement in experimental structure determination methods, which became throughput and highly automated. Several steps however still have to be done manually. Combination of *de novo* prediction methods with fragmentary experimental data can be used to alleviate some of these bottlenecks.

In our work we combined one of the most successful approaches for protein structure modeling: fragment recombination (ROSETTA method[1]) into a single protocol that employs fragmentary NMR data: Chemical Shifts, J-couplings as well as TEDOR and VEANS obtained in Solid State NMR experiments. The protocol, managed by BioShell[2,3] software is very general and can utilize a wide variety of other than NMR types of data. The experimental restraints are applied on various stages of the procedure: to derive distance restraints, to select matching protein fragments from a structural database, to guide the conformational search and finally to score the obtained models. Our results show that in several cases it is possible to calculate a high-resolution protein structure without long-range experimental restraints i.e. solely from local backbone information. Moreover, the use of high-resolution lattice model greatly improves computational efficiency of the whole protocol.

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1172-Pos Board B64

Large Scale Structure Sampling for Protein Fold Prediction using the Generalized Simulated Annealing

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Proteins are the building blocks of cells and the executioners of nearly all cellular functions. Their structure is of paramount importance to understand their dynamics and function, as well as the interactions with other molecules.

In this work, we apply the Generalized Simulated Annealing (GSA) to guide the exploration of the energy hyper surface of the protein folding process, looking for the global minimum and, hence, the native fold of the protein. The GSA is a stochastic search algorithm employed in energy minimization and used in global optimization problems, such as gravity models, fitting of numerical data and conformation optimization of small molecules. Our software applies the analytical inverse of the probability distribution from GSA, a new method to apply rotations to the phi and psi angles of the peptide bonds and side chains, faster connection with NAMD for potential energy calculation and the possibility of parallel execution, granting a new take on ab-initio protein structure prediction. The new design also allows for an easier inclusion of knowledge derived potentials, based on experimentally determined protein structures.

We present results for the 14 amino acid protein mastoparan-X. The chain folds with RMSD of 3,0 angstroms after 500.000 GSA steps. Currently, for this