Bioinformatics Master Student Course "Structural Bioinformatics"

Syllabus

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Lectures	**Seminars (synced with lecture topics)**
1. Methods of experimental structure elucidation • X-ray crystallography and interpretation of structure quality • NMR • Various other methods (SAXS, CD, cryo-EM) 2. Principles of protein structures • Properties of amino acids, Peptide bond, main degrees of freedom/ main chain dihedral angles • Hierarchies of protein structure, secondary structure assignments (DSSP), • Packing constraints, cavities 3. Fold classification and structure comparison • Folding topologies, term "topology", fold databases • Structure comparison (RMSD, contact map overlap) 4. Protein folding • Thermodynamic hypothesis • Detailed discussion of enthalpic/entropic contributions to delta-G (bonds, angles, electrostatics, van-der Waals, solvation etc.), • Levinthal paradox, folding funnel, folding pathways, concepts of folding (two-state, framework model) • "lattice"-proteins 5. Molecular dynamics • Force fields (AMBER, ECEPP-2, CHARMM) • Newtonian equations of motion, Taylor expansion, Verlet algorithm, boundary conditions, time step, neighbor lists 6. Energy minimization • Search problem (global vs. local	1. Introduction to the PDB (protein databank, search, structure stats), 2. Molecular geometry (distances, angles, dihedral angle, plane normals etc.) • **Exercise/ homework:** dihedral angle calculation (Ramachandran plot) 3. Molecular graphics • Types of structure renderings, visualization software (Pymol) side-by-side stereo, contact maps, cartoons, surfaces, marching cube algorithm 4. Structural superposition and selected aspects of polymer physics relevant to structural biology (Rotation matrix, Radius of gyration, Inertia matrix, Moments of inertia) • **Exercise/ homework:** superposition of two helices 5. Molecular dynamics: analytical solution of the harmonic oscillator (2nd order differential equ.) 6. Derivation of the Boltzmann distribution 7. Introduction to MD software (Abalone) • **Exercise/ homework:** MD and energy minimization of two poly-peptides 8. Branch-and-bound (homology modelling, sidechain placement) **Student presentations:** As part of the seminar, every student is given an article on relevant subjects that expand on the material covered in the lectures (e.g. methods of structure comparison) and are both classical "landmark" papers as well as contemporary contributions. For the latter, focus if placed on approaches that bridge between different themes, e.g. network analysis approaches towards structure analysis

minima) • Steepest descent, conjugate gradient, ensemble properties, Monte Carlo simulation, simulated annealing. 7. Database-derived potentials • Inverse Boltzmann statistic, pairwise potentials of mean force, solvent exposure interactions, fold quality assessment 8. Docking • Protein-protein interaction and docking • Small-molecule docking, binding pocket identification, geometric hashing • Intro to cheminformatics (descriptors of small molecules, comparison) 9. Secondary structure prediction • Chou-Fasman, GOR, neural networks, ab-initio methods, Deep Learning methods 10. Homology modeling • Profile methods, true homology modeling (incl. loop modelling with dead-end elimination) • Public resources for Homol. Modelling 11. Threading • Optimal threading (branch-and-bound) • Structure quality assessment • CASP competition 12. DeepLearning methods/ AlphaFold 13. Principles of DNA/RNA structure • Principles governing nucleic acid structures • Descriptors of RNA structures • Concept of isostericity 14. RNA structure prediction • RNA secondary structure prediction (Nussinov algorithm, energy minimization)	