



CHEM 422

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 COURSE NAME / NUMBER
 

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**LEARNING OBJECTIVES / GOALS / OUTCOMES/ LEARNING OUTCOMES:**

Students will become familiar with molecular mechanics, molecular dynamics and Monte Carlo techniques in their application to the conformational analysis, and will get practical experience with molecular mechanics calculations.

**METHODS:**

Lectures, computer lab, problem solving.

**PRIOR LEARNING ASSESSMENT RECOGNITION (PLAR):**

Credit can be awarded for this course through PLAR      YES \_\_\_\_\_      NO   X  

**METHODS OF OBTAINING PLAR:****TEXTBOOKS, REFERENCES, MATERIALS:**

N/A - Lecture notes and recommended reading.

**SUPPLIES / MATERIALS:****STUDENT EVALUATION:**

Assignments	10%
Midterms (2)	30%
Final	30%
Lab	30%

**COURSE CONTENT:****Introduction**

Molecular geometry. Internal and Cartesian coordinates. Bond length. Bond angle. Torsion angle.

**Conformational analysis of simple systems**

Ethane, butane, ethylene, butene, cyclohexane.

**Force fields**

Stretching and bending energy. Harmonic approximation. Anharmonicity. Torsion energy. Rotation around single and double bond. Van-der-Waals interactions. Exp-6 and Lennard-Jones potentials. Parametrization.

**Energy minimization**

Potential energy surface. Stationary points: minima, maxima, saddle points. Minimization procedures.

**Computer program packages**

ECEPP, MM2/MM3, AMBER, CHARMM.

**Conformations of large molecules**

Multiple minima problem. Global minimum. Relative importance of conformations. Experimental sources of the molecular conformation data.

**COURSE CONTENT: (contd.)****Molecular dynamics and Monte Carlo techniques**

Introduction to techniques.

**Proteins**

Primary, secondary, tertiary, and quaternary structures. Protein conformations. Protein data base (PDB).

**Introduction to computer-aided drug design**

Basics of the molecular mechanism of drug action. Guest-host interactions. Specific and nonspecific interactions. Hydrophobic interactions. Docking. Rigid-molecules approximation. Conformational change upon complexation.

**COMPUTER LABS**

1. Introduction to UNIX environment.
2. Input files: internal and Cartesian coordinates.
3. Simple MM3 calculations.
- 4-5. Conformational analysis of medium-sized rings.
- 6-7. Effect of solvent on molecular conformations.
8. Comparative analysis of the potential functions in MM3 and AMBER.
- 9-10. Protein Data Base.
- 11-12. Docking.

**SELECTED REFERENCES:**

1. U. Burkert, N.L. Allinger, *Molecular Mechanics*, ACS, Washington, 1982.
2. *Molecular Modelling and Drug Design*, J.G. Vinter and M. Gardner, eds., CRC Press, Boca Raton, FL, 1994.
3. T. Clark, *A Handbook of Computational Chemistry*, Wiley, N.Y., 1985.
4. P. Comba, T.W. Hambley, *Molecular Modeling of Inorganic Compounds*, VCH, Weinheim, FRG, 1995.
5. K. Rasmussen, *Potential Energy Functions in Conformational Analysis*.
6. J.M. Haile, *Molecular Dynamics Simulations: Elementary Methods*, Wiley, N.Y., 1992.
7. A.C. Norris, *Computational Chemistry. An Introduction to Numerical Methods*, Wiley, N.Y., 1981.
8. W.H. Press et al., *Numerical Recipes. The Art of Scientific Computing*, Cambridge University Press, Cambridge, 1989.
9. *Prediction of Protein Structure and the Principles of Protein Conformation*, G.D. Fasman, ed., Plenum Press, N.Y., 1989.
10. C. Branden, J. Tooze, *Introduction to Protein Structure*, Garland Publishing, N.Y., 1991.
11. *Applications of NMR Spectroscopy to Problems in Stereochemistry and Conformational Analysis*, Y. Takeuchi and A.P. Marchand, eds., VCH Publishers, Deerfield Beach, FL, 1986.