

CHAPTER 1

INTRODUCTION



1.1 Liquid State and Computer Simulations

Liquid state, including liquid solutions, plays an essential role in most chemical processes in nature. Many chemical operations, for example, synthesis, mixing, purification and separation are carried out in liquid solution, involving the structure and energetic and dynamic characteristics of solute-solvent interactions at the molecular level. The study of liquid state of matter has a long and rich history, from both theoretical and experimental approaches, for example, based on the theoretical method by Bernal and Fowler [1], water was considered as individual molecules.

The characteristic of solvation is often used in general to describe the structure of the solution where the geometrical arrangements are significantly different from the bulk structure of the solvent itself. The dynamical stability depends on the combination of forces acting between homogeneous or heterogeneous molecules of which the solution consists. On one hand, a discrete solvation shell can be based on the solute-solvent interaction which is so strong that the exchange rate is much lower in the first solvation shell than that among solvent molecules. On the other hand, a shell structure can also be detected even when the interaction between solute and solvent is weaker than the solvent-solvent interaction.

Some decades ago, investigation of solution structure was mainly a domain of spectroscopical methods such as X-ray, neutron diffraction and NMR etc. They encounter, however, some difficulties to produce data when the sample is very

dilute, or when solvent exchange takes place very fast, or when the interaction is so weak that the input energy from the spectroscopic apparatus exceeds that of the interaction which should be measured. In addition, the measurements concern mostly the study of a one-component solvent, while preferential solvation in mixed solvents is acceptably important phenomena, for which theoretical studies are also still quite rare, mostly due to the relatively high computational effort needs for the simulation of multicomponent systems.

Quantum chemical investigations, which still have strong limits in the size of molecular system and the related computational time, have been a useful tool for predicting configurations of molecules, stabilization energies, excitation energies, force constants, and other physical data. Although they often produce data in good agreement with experiment, this approach can not reflect all properties of a condensed system with large amounts of particles.

The availability of electronic computers with high processing capacities has changed the situation most favourably within the past twenty years. Numerical calculations for n -electron systems have become feasible at ever increasing levels of accuracy and complexity. Statistical mechanics has made a remarkable progress with the help of computer technology, and can be applied by simulations of Monte Carlo or molecular dynamics types, originally introduced by Metropolis et al. [2] and Adler et al. [3], respectively. These methods have overcome some limitations of first approaches and made it possible to simulate the statistical and dynamical behaviors of rather large ensembles of molecules based on accurate potentials derived from quantum chemical calculations. Therefore, theoretical investigations of the liquid state and solutions have rapidly developed and numerous studies based on these methods for solution have been published [for examples, 4-8].

Monte Carlo simulation allows not only to evaluate solvation numbers and solute-solvent distances from computed radial distribution functions, but gives also access to data not available from any experimental technique so far, as for example an analysis of the percentual contribution of various coordination numbers to the average solvation number of ions or solvent molecules. The access to the angular distribution of neighbour molecules is also an important means of these methods for the evaluation of structural data in solution.

1.2 What and Why is Glucosamine?

β -D-glucosamine is a unit cell of poly- β (1,4)-2-amino-deoxy-D-glucose, normally known as chitosan. The sketches of the β -D-glucosamine ($C_6H_{13}NO_5$) and chitosan molecules are shown in Figures 1.1 and 1.2, respectively.

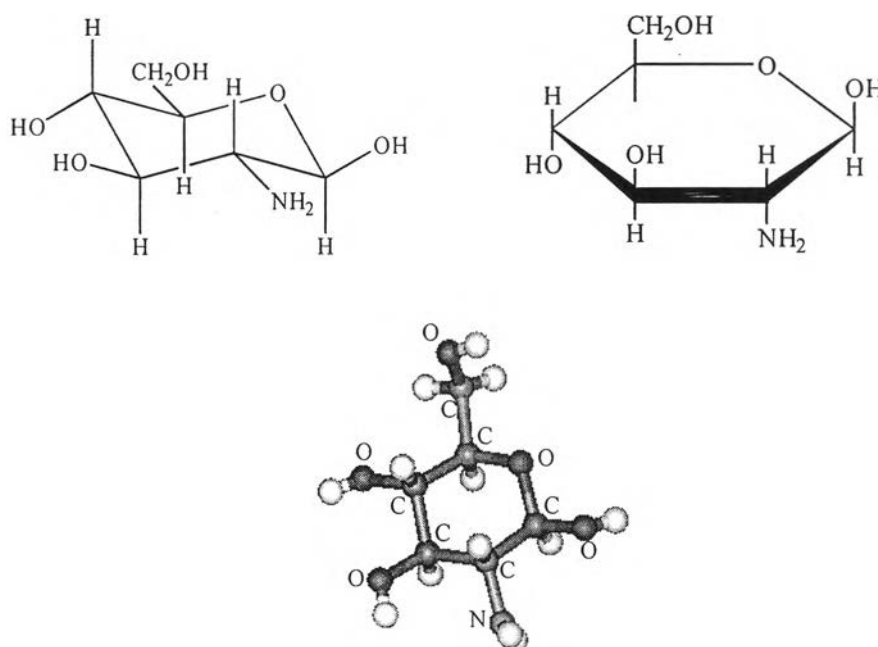


Figure 1.1 The β -D-glucosamine molecules in each form.

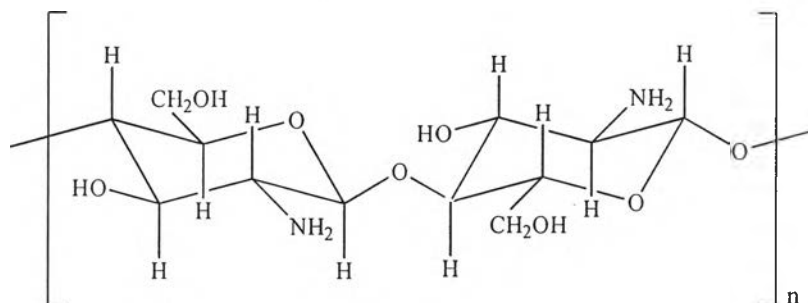


Figure 1.2 The chitosan molecule.

This polymer is widely used for biomedical treatment [9-10], such as to reduce cholesterol levels [11-12], as well as to control drug release and drug delivery [13-16]. Efficiency of such applications depends strongly on molecular weight, structure, crosslinking percentage, and porous size of the chitosan [17-25]. These factors are surely controlled, in molecular level, by the interactions between chitosan, drug and solvent molecules. This relates directly to the solvation and desolvation of all species in the solution [26-28]. Understanding of this behaviour would help directly to the development and the wide applications of chitosan.

The above statement convinces us to investigate the solvation structure of chitosan. Metropolis Monte Carlo procedure [2] with conventional pair potentials has been applied to examine the solvation structure of its unit cell, β -D-glucosamine, in water. According to our best knowledge, such data is not yet available, neither by means of experimental nor theoretical investigations.

After brief review of computer simulations of liquid and the role and application of glucosamine in Chapter 1, theoretical background of quantum mechanics, analytic forms of intermolecular potential functions, and Monte Carlo

simulations are presented in Chapter 1, 2, 3, and 4, respectively. Then specific information concerning glucosamine, namely detail of calculations, results and discussion, and conclusion are given in Chapter 5, 6, and 7, respectively.