# Computer Simulation of Molecular Systems A Practical Guide

# (D530)

# PREFACE

## 1. Introduction

- 1. The many-particle problem
- 2. Equations of motion
  - 1. Schrödinger
  - 2. Newton
  - 3. Langevin
  - 4. Lagrange
  - 5. Hamilton
- 3. Statistical mechanics
- 4. Molecular models
- 5. Simulation methods
- 6. Computing effort
- 7. Assumptions, approximations and limitations
- 8. Experimental validation
- 9. Historical development
- 10. Applications in chemistry
- 11. Is computer simulation useful ?

#### 2. Molecular models and force fields

- 1. Molecular models
- 2. Force field representations
- 3. Special forces
- 4. Virtual atoms or sites
- 5. Potentials of mean force
- 6. Determination of force field parameters
- 7. Examples of force fields
- 8. Tests of force fields

#### **3.** Treatment of boundaries

- 1. No wall (vacuo)
- 2. Hard wall
- 3. Extended wall region boundary conditions
- 4. Periodic boundary conditions
- 5. Physical effects

#### 4. Polarisation

- 1. Many-body interactions
- 2. Models
- 3. Algorithms
- 4. Choice of parameters
- 5. Examples of polarisable molecular models

# 5. Treatment of long-range forces

- 1. Long-range forces
- 2. Distance dependent dielectric constant
- 3. Cut-off radius and variations
  - 1. Switching functions
  - 2. Shifted potential
  - 3. Charge group concept
  - 4. Multipole expansion
  - 5. Twin-range method
- 4. Continuum approximation to the reaction field
  - 1. Uniform (dipolar) reaction field in sphere
  - 2. Image charge approximation to the reaction field in sphere
  - 3. Exact reaction field in sphere, PB outside
  - 4. Series expansion to the reaction field
  - 5. Three-dimensional finite difference techniques
  - 6. Two-dimensional boundary element techniques
- 5. Langevin dipole model
- 6. Periodic lattice summation methods
  - 1. Ewald sum
  - 2. Fourier methods
- 7. Treatment of solvent around solutes

## 6. Energy minimisation

- 1. Methods
- 2. Steepest descents
- 3. Conjugate gradients
- 4. Application of energy minimisation techniques

## 7. Normal mode analysis

- 1. Method
- 2. Physical assumptions
- 3. Applications

## 8. Monte Carlo simulation

- 1. Metropolis MC algorithm
- 2. Reptation MC algorithm for polymers
- 3. Other MC algorithms
- 4. Applications of MC

## 9. Varieties of molecular dynamics

- 1. Microcanonical MD
- 2. Constant temperature MD
  - 1. Calculation of the temperature
  - 2. Constraint methods
  - 3. Extended system methods
  - 4. Weak coupling methods
  - 5. Stochastic methods
- 3. Constant pressure MD

- 1. Calculation of virial and pressure
- 2. Constraint methods
- 3. Extended system methods
- 4. Weak coupling methods
- 5. Stochastic methods
- 4. MD at constant chemical potential

#### **10.** Varieties of stochastic dynamics

- 1. Brownian dynamics
- 2. Generalised Langevin dynamics
- 3. Brownian dynamics with hydrodynamic interactions
- 4. Choice of frictional parameters
- 5. Applications of SD

## 11. Algorithms for MD and SD

- 1. Types of algorithms
- 2. Leap-frog scheme for MD
- 3. Equivalence of algorithms
- 4. Accuracy of algorithms
- 5. Leap-frog scheme for SD
- 6. Multiple time step algorithms
- 7. Choice of the parameters

#### **12.** Application of constraints

- 1. Type of constraints
- 2. Methods for application of distance constraints
- 3. Constraint forces
- 4. Constrained EM
- 5. Constrained MC
- 6. Constrained MD
- 7. Metric tensor effects
- 8. Physical implications
- 9. Application of other constraints

#### **13.** Searching configuration space

- 1. Systematic search methods
- 2. Random search methods
- 3. Search by dynamical simulation
- 4. Other search methods
- 5. Comparison of search techniques

#### 14. Initial conditions and equilibration

- 1. Initial configuration
- 2. Initial velocities
- 3. Equilibration

#### 15. Analysis of trajectories

- 1. Averages and fluctuations
- 2. Estimation of errors
- 3. Harmonic approximation
- 4. Correlation functions
- 5. Frequency filtering of trajectories
- 6. Expressions for various physical quantities
- 7. Use of graphics display facilities

#### 16. Determination of entropy, free energy and potentials of mean force

- 1. Energy versus free energy
- 2. Methods
- 3. Particle-insertion method and variations
- 4. Entropy by direct integration
- 5. Free energy by thermodynamic integration
  - 1. Perturbation method
  - 2. Continuous integration
  - 3. Integration by numerical quadrature
  - 4. Entropy by thermodynamic integration
- 6. Free energy as a function of a reaction coordinate
  - 1. Unrestricted sampling
  - 2. Umbrella sampling
  - 3. Sampling with a constrained reaction coordinate
- 7. Thermodynamic cycles
- 8. Free energy and constraints
- 9. Creation and annihilation of atoms
- 10. Calculation of the chemical potential
- 11. Quantum corrections
- 12. Approximations and choices to be made in practical calculations
  - 1. Choice of pathway and coupling parameter
  - 2. Extent of sampling: system relaxation time
  - 3. Effect of long-range interactions
  - 4. Effect of boundary conditions
  - 5. Sensitivity to force field parameters

## **17.** Treatment of quantum effects

- 1. Quantum mechanics and quantum effects
- 2. Incorporation of quantum effects in simulation
- 3. Quantum corrections to a classical simulation
- 4. Semi-classical trajectory simulation
  - 1. Zero-point energy model
  - 2. Tunneling model
  - 3. Gaussian wave packet method
- 5. Quantum mechanical treatment of a few degrees of freedom in a classical system
  - 1. Path-integral method
  - 2. Parallel classical dynamics in quantum and classical degrees of freedom

- 3. Quantum molecular dynamics method
- 6. Combination of quantum and classical methods
- 7. Simulation methods in quantum chemistry
  - 1. Variational quantum Monte Carlo
  - 2. Diffusive quantum Monte Carlo
  - 3. Greens function quantum Monte Carlo

#### 18. Non-equilibrium molecular dynamics

- 1. Rheology
- 2. Calculation of transport coefficients
- 3. Generalisation of Newton's equations of motion
- 4. Methods for non-equilibrium MD (NEMD)
- 5. Algorithms for NEMD
- 6. Application of NEMD
  - 1. Thermal conductivity
  - 2. Viscosity
  - 3. Diffusion

## **19.** Use of MD in structure refinement based on crystallographic or NMR data

- 1. MD and NMR refinement
- 2. MD and crystallographic refinement
- 3. Time-dependent restraints

#### 20. Simulation of long time scale events: time-saving techniques

- 1. Reduction of number of degrees of freedom
- 2. Short range forces: search for neighbours
- 3. Long integration time steps
- 4. Efficient search of configuration space
- 5. Reduction of energy barriers: choice of pathway
- 6. Scaling of system parameters

## 21. Applications of molecular simulation in chemistry and physics

- 1. Types of systems
  - 1. Liquids
    - 2. Solutions
    - 3. Electrolytes
    - 4. Polymers
      - 1. Proteins
        - 2. DNA and RNA
      - 3. Sugars
      - 4. Other polymers
      - 5. Membranes
    - 6. Micelles and colloids
    - 7. Liquid crystals
    - 8. Crystals
    - 9. Glasses
    - 10. Zeolites
    - 11. Metals

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- 2. Types of properties
  - 1. Structural properties
  - 2. Mechanical properties
  - 3. Mobility
  - 4. Dynamical properties
  - 5. Thermodynamic properties
  - 6. Transport coefficients
- 3. Types of processes
  - 1. Melting
  - 2. Adsorption
  - 3. Segregation
  - 4. Complex formation
  - 5. Protein folding
  - 6. Order-disorder transitions
  - 7. Crystallisation

## 22. On testing theoretical models by comparison of calculated with experimental data

## 23. Computational details

- 1. Transformation of coordinates
- 2. Searching neighbours
- 3. Switching functions
- 4. Avoiding a square root when computing bond forces
- 5. Bond-angle and torsional angle forces
- 6. Random number generation

## 24. Use of vector, parallel or special purpose computers

- 1. Computational effort required by simulation
- 2. Vector computers
- 3. Parallel computers
- 4. Special purpose computers

# 25. Future developments

## APPENDICES

#### A. Reduced units

## B. A program library for dynamical simulation of molecular systems: GROMOS

- 1. Philosophy underlying GROMOS structure
- 2. Overview and architecture of GROMOS