

## Software Components

Functions	QMMM plus
MD Automatic Simulator	SOLUTION
MD Analysis	AMBINFO GMXINFO TRJ2GJF
QC Tools	GAUEDIT GAURUN GJOB
QC Analysis	GAUINFO GAUCUBE

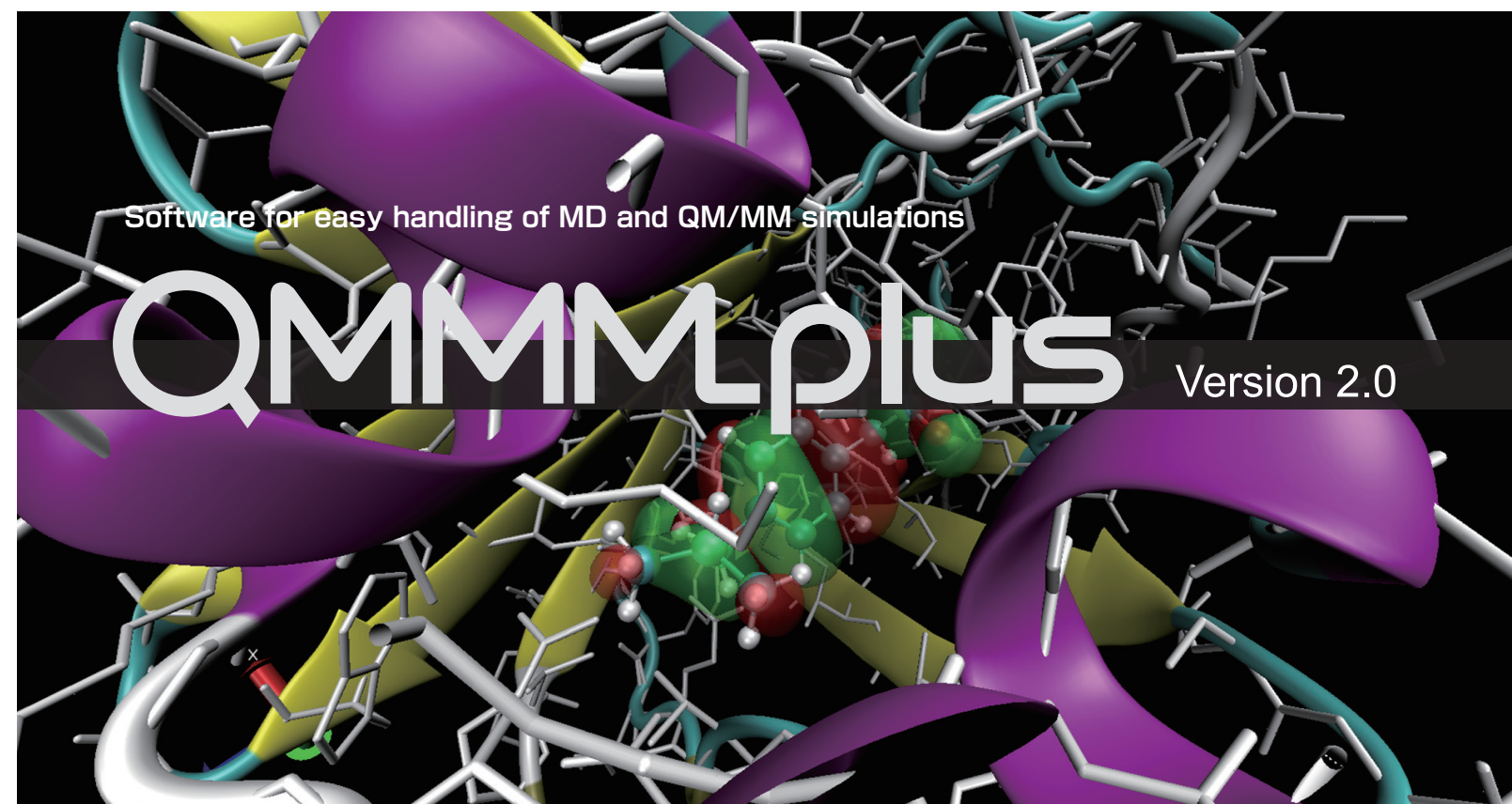
SOLUTION	Automatic simulator of MD and QC for liquid solution
AMBINFO	Analyzer for MD outputs of AMBER
GMXINFO	Analyzer for MD outputs of GROMACS
GAUINFO	Analyzer for QC outputs of Gaussian
GAUCUBE	Analyzer for Gaussian Cube files
GAUEDIT	Editing tool for Gaussian input files
GAURUN/GJOB	Job controller for multiple Gaussian calculations
TRJ2GJF	AMBER trajectory to Gaussian input converter

\*MD : Molecular Dynamics, QC : Quantum Chemistry

## System Requirements

Requirements	QMMM plus
◎ : necessary ○ : recommended	
Python 2.6	◎
LSF, LAVA or Grid Engine	○
Gaussian09	○
AMBER14	○
AmberTools 14	◎
GROMACS 4.6 or 5.0	◎
acpype.py	◎
Open Babel 2.x	◎
Gnuplot	○
Image Magick	○

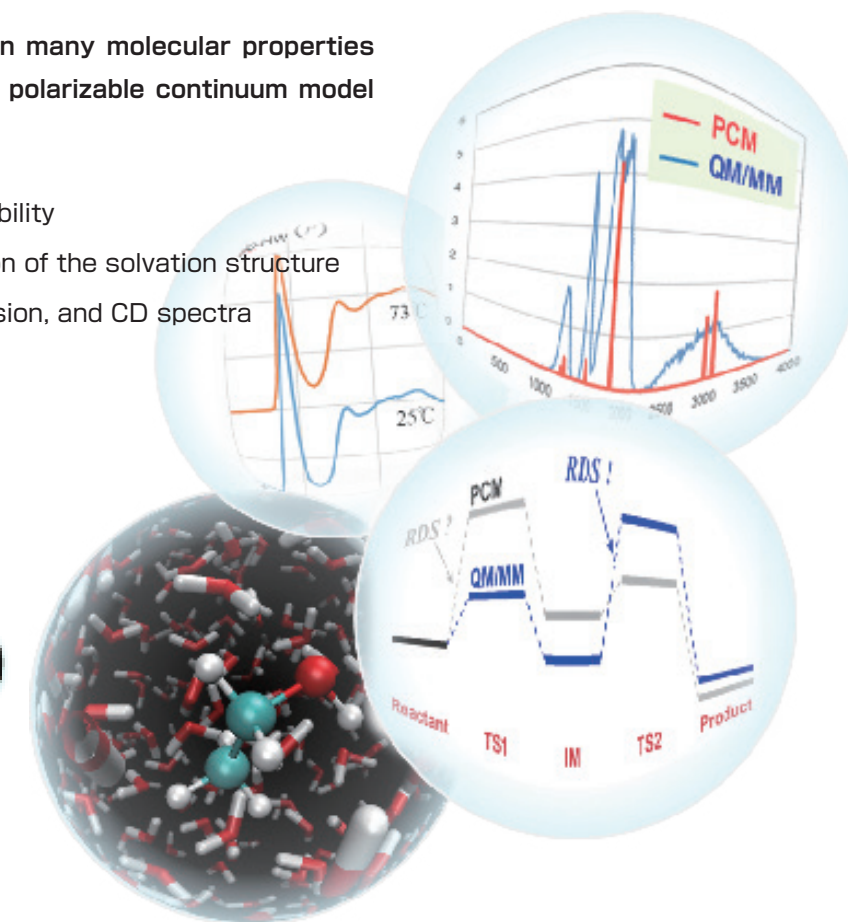
## Software



You can easily and automatically obtain many molecular properties in mixed solvent beyond the traditional polarizable continuum model (PCM), for example,

- Solvent dependence of the isomer stability
- Spectral band shape due to fluctuation of the solvation structure
- Solvatochromism for absorption, emission, and CD spectra
- Radial distribution functions
- Temperature effects

even if you know only Gaussian usage.



## HPC Systems Inc.

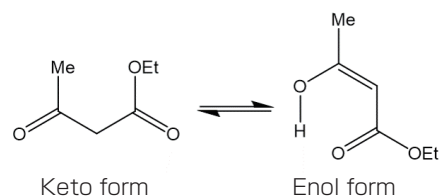
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## Overview

### Tautomerism in Different Solvents

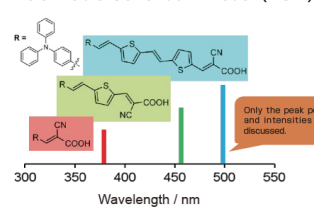


#### Prediction of stable isomer in solution

Solvents	Experiment population (keto:enol)	Calculation (PCM) relative energy (keto-enol)	Calculation (QM/MM) relative energy (keto-enol)
Cyclohexane	enol (38% : 62%)	○ enol (+4.3kcal/mol)	○ enol (+3.8kcal/mol)
Acetone	keto (99.9% : 0.13%)	× enol (+2.4kcal/mol)	○ keto (-3.2kcal/mol)
Water	keto (93.9% : 6.5%)	× enol (+0.9kcal/mol)	○ keto (-10.4kcal/mol)

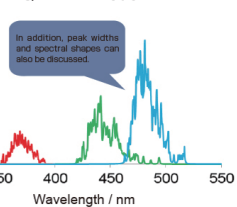
### Spectrum Width and Shift in Different Solvents

#### Polarizable Continuum Model (PCM)

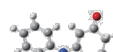


Only the peak positions and intensities can be discussed.

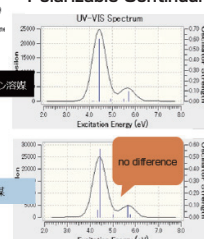
#### QM/MM model



In addition, peak widths and spectral shapes can also be discussed.

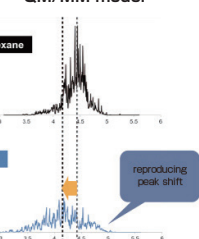


#### Polarizable Continuum Model (PCM)



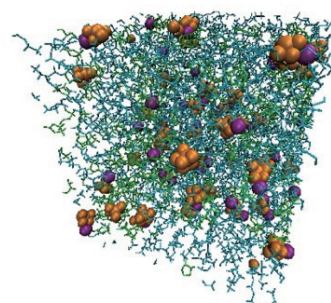
no difference

#### QM/MM model

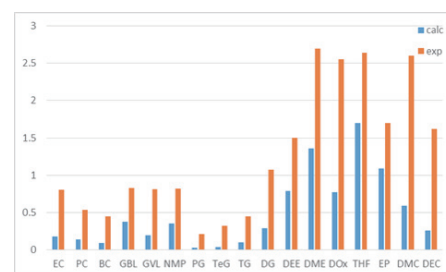


reproducing peak shift

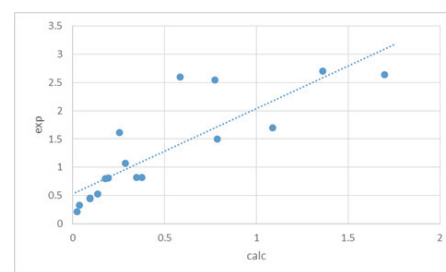
### Efficient Evaluation of Many Materials



Electrolyte consisting of four molecular (ionic) species. Concentration can be set easily.



Diffusion coefficients for many electrolytes. One material can be evaluated in only 30 minutes, hence 480 materials per a day using ten computers (16 core).



## How to Use

### 1 Create the input file

Set only molecule files, number of molecules, temperature and pressure conditions, and so on. User also can modify details of MD calculation processes.

### 2 Run

Just a single command. All simulation processes are automatically performed.

```
$ solution mer.input
```

```
[control]
n_core      = 16      parallel number and
style       = normal  calculation style

[molecule]
molecule01 = 1, BMC, input/merocyanine.gjf
molecule02 = 1000, AC, input/acetone.mol2
              number of molecules and molecule files
              (merocyanine : 1 molecule + acetone: 1000 molecules)

[md_default]
qmcondition = PM6 conditions for QM/MM calculation
temperature = 298.15 temperature
t            = 0.1    time
dt_output   = 0.001

[analysis]
n_data      = 64 chemistry analysis
gjf_template = input/template-td.gjf
```

Input file

## Functions

### 1. Molecular Dynamics Automatic Simulator

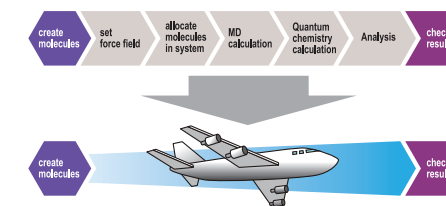
#### Automatic Calculation

Simulation for liquid solution have ever required many procedures such as creation of molecule, set of force field, allocation of molecules in system using many programs.

QMMM plus automates all these procedures. Only molecular structure files as well as conditions for temperature and pressure are required. No action required. Energy and spectra in liquid solution can be automatically calculated.

#### Restart

Available for restarting in middle of procedures.



Everyone can easily perform MD calculations even that experts have ever examined after a day.

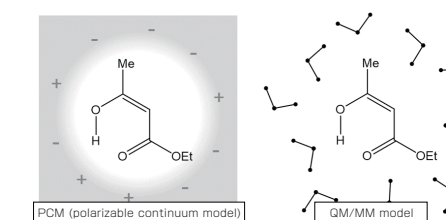
### 2. Molecular Dynamics Analysis

#### Time Evolution and Statistics of Energy and Temperature

Time evolution and statistics of energy, temperature, density, and interaction energy between a solute molecule and solvent molecules can be calculated.

#### Distribution and Diffusion of Molecules

RDF (radial distribution function) and diffusion behavior can be calculated.



Available also for QM/MM model.

### 3. Quantum Chemistry Tools

#### Bulk Editor

Many Gaussian input files can be edited at once.

#### Bulk Execution

Many Gaussian jobs can be executed under limited number of CPU cores.

### 4. Quantum Chemistry Analysis

#### Statistics of Energy, Dipole, Atomic charges

Statistical analysis is available from many Gaussian output files. Energy, dipole moments and atomic charges are represented as values with standard deviations. Therefore, a new perspective such as softness of molecular structure as is proposed.

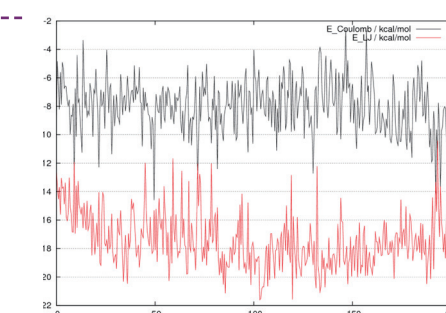
#### Spectrum in Liquid Solution (IR, Raman, UV-Vis, CD, NMR)

Since QMMM plus collects statistics from quantum chemistry calculations of many molecular structures in liquid solution, it provides continuous spectra with width and shape, whereas traditional quantum chemistry have ever provided line spectra.

### 5. Report

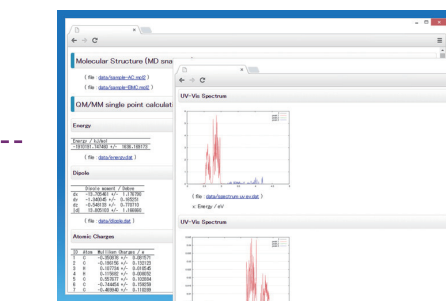
#### HTML-formatted Report

Calculation results are available in HTML format which can be viewed in a Internet browser. Tab-delimited output files are stored in "data" directory.



Property	Value
Total Energy / kcal/mol	15377.917632 +/- 382.471834
Kinetic Energy / kcal/mol	8030.652062 +/- 68.383889
Potential / kcal/mol	7347.265524 +/- 370.218350
Temperature / K	298.053425 +/- 2.538403
Pressure / bar	17.234825 +/- 1060.386258
Volume / Angstrom <sup>3</sup>	106493.393877 +/- 3004.786844
Density / g/cm <sup>3</sup>	1.370276 +/- 0.035797
E_Doulob(V_FIRST) / kcal/mol	-7.295341 +/- 1.887728
E_UJ(V_FIRST) / kcal/mol	-10.714645 +/- 1.886958
E_Doulob(GE_FIRST) / kcal/mol	-7.985198 +/- 1.821891
E_UJ(GE_FIRST) / kcal/mol	-17.422890 +/- 1.949266
E_Doulob(LI+ FIRST) / kcal/mol	-115.589843 +/- 7.138112
E_UJ(LI+ FIRST) / kcal/mol	4.273472 +/- 2.158720
E_Doulob(PF8_FIRST) / kcal/mol	-21.788988 +/- 2.832948
E_UJ(PF8_FIRST) / kcal/mol	-11.523351 +/- 1.801136

Time evolution and statistics of many properties.



Calculation results are available from a browser.