General-purpose Coarse-grained

Molecular Dynamics Program



(<u>COarse-Grained molecular dynamics program by NAgoya Cooperation</u>)

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Coarse-grained model

A set of atoms are represented by one dynamical unit

- United atom model
 - A methylene (CH₂) unit is represented by single mass point



 A rigid part of molecule is represented by single ellipsoid

- Bead-spring model
 - Several monomer units are represented by single bead (mass point)







General-purpose

- General computational models and potential functions
- General objectives
 - < Features and functions of COGNAC >
- Basic function of molecular dynamics/mechanics
- Potential functions for coarse-grained model
- Flexible modeling
- Extended functions and tools for analysis
- New functions for zooming
- Extensibility of the program
- User interface



Molecular Dynamics/Molecular Mechanics

- Molecular dynamics (MD)
 - Ensembles
 - » NVE
 - » NVT,NPH,NPT

(loose-coupling / extended Hamiltonian methods)

- Langevin dynamics
- Molecular mechanics (MM)
 - Steepest descent / conjugate gradient methods



Potential Functions for Coarse-grained Models

- Bonding
 - 2-body(bond):Harmonic,Morse,FENE,Gaussian, Polynomial,Table
 - 3-body(angle):Theta harmonic,Cosine harmonic
 Theta polynomial,Table
 - 4-body(torsion):Cosine polynomial,Table
- Non-bonding pair interaction
 - Lennard-Jones, Gay-Berne, LJ-GB, Table
- Electrostatic
 - Coulomb interaction(Ewald,Reaction field)
 - Dipole-dipole interaction (Reaction field)



Example of Application: Gay-Berne - Lennard-Jones hybrid potential



Smectic phase(non-polar model)



Nematic phase(polar model)



Modeling molecular architectures using SILK (1)

- SILK is a tool to generate molecular architectures for COGNAC
- ◆ **SILK** is written in **Python** and used on GOURMET
- **SILK** has basic functions and template functions.
 - Basic functions define atoms, bonds, angles, torsions.
 They are used to generate molecules with complex architectures
 - Template functions are used to generate simple polymer molecules such as homopolymers and blockcopolymers

Modeling molecular architectures using SILK (2)

• An example of the usage of the basic functions

```
name="mol"
 numMol=10
 self.engine.createMolecule(name)
 for i in range(0, 4):
    self.engine.addAtoms(name, "UA", "UA_PE")
 for i in range(0, 3):
    self.engine.addBonds(name, i, i+1, "BOND_PE")
 for i in range(0, 2):
    self.engine.addAngles(name, i, i+1, i+2, "ANGLE_PE")
 for i in range(0, 1):
    self.engine.addTorsions(name, i, i+1, i+2, i+3, "TORSION_PE")
 for i in range(0, 4):
    self.engine.addInteractionSites(name, [i], "NB_PE", "PAIR")
 self.engine.setSystem(name, numMol)
```



Modeling molecular architectures using SILK (3)

An example of the usage of the template functions

```
name="A20B40A20"

numMol=50

key="LINEAR"

sequence=[("A",20),("B",40),("A",20)]

atomType={"A":"atom1", "B":"atom2"}

bondType={"A_A":"bond1", "A_B":"bond3", "B_B":"bond2"}

interactionSiteType={"A":"siteType1", "B":"siteType2"}

self.engine.makeBeadSpringPolym(name, numMol, key, sequence, atomType,

bondType, interactionSiteType)
```



Modeling molecular architectures using "Action" SILK

• Running SILK by "Action" on GOUMET

UDF P	ath: Set_of_Molecules				
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	Simulation_Conditions		SILK_CREATE_LinearPolyr	ner_Bead_Spring_2_Di_Block Ar… 🗙	
] Initial_Structure		Names	Values	
	J Molecular_Attributes		name	linear_di	
	Interactions		numMol	1	
	React_Conditions		atom0_name	A	
	DOST FILE CONVERT Check Bonding Detential		atom0_num	10	
			atom1_name	B	
	SILK_CONVERT_REDUCED_CHARGE_TO_VALENCE		atoml_num	10	
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	SILK_CREATE_CombPolymer_Bead_Spring_2_branched	Delection	bond type in 0		
	SILK_CREATE_CombPolymer_Bead_Spring_X_branched	of diblock /	bond_type in 1	bondBB	
	SILK CREATE LinearPolymer Bead Spring 1 Homo		bond_type_0_to_1	bondAB	
	SILK CREATE LinearDolymor Read Spring 2 Di Block	·	interactionSite_Type_0	siteTypeA	
	SILK_CREATE_LinearPolymer_Dead_Spring_2_DI_Diock		interactionSite_Type_1	siteTypeB	
	SILK_CREATE_LINEarPolymer_Bead_Spring_3_Tri_Block				
	SILK_CREATE_LinearPolymer_Bead_Spring_X_Multi_Block			Cancel OK	
1.15	SILK_CREATE_LinearPolymer_Semiatomistic			Cancer	
	SILK_CREATE_StarPolymer_Bead_Spring_3				
	SILK_MOLECULE_HANDLE_CLEAR				
	SILK_MOLECULE_HANDLE_DELETE	0			
Pyd	SILK_MOLECULE_HANDLE_PRINT				
Pyt	SILK_OUT_SYSTEM_to_Set_of_Molecules	Notes: Thi	s function is re	eleased	

as a gift without documents

Analysis tools

- Python scripts for the analysis of COGNAC output
 - Basic analysis
 - » Distance, angle, torsion
 - » Radius of gyration, etc.
 - Geometry analysis
 - » Pair distribution functions
 - » Orientation order parameters etc.
 - Trajectory analysis
 - » Mean square displacements
 - » Correlation function of normal coordinates etc.



Example of Application : Topological gel



Snapshot structure during elongation

Repeat: ONCE

Time:20550.000000 Boundary:PERIODIC Repeat: ONCE

Generation of initial coordinates

- Generation by COGNAC
 - Random: Amorphous like structures
 - Helix: Helical structures at regular lattice points
 - Crystal: Crystal structures defined by crystal data, i.e. unit lattice, symmetric operation and fractional coordinates
 - Semi-crystalline lamella: Semi-crystalline lamella structures consisting of a crystal phase and an amorphous phase
 - Multi phase structure: Micro/macro phase-separeted structures of block copolymer/polymer blend obtained by SUSHI



Data conversion of molecular structure from other file formats

Conversion from mol/PDB format file to UDF file



mol format file displayed by WebLab ViewerLite^(TM)



Converted data to UDF displayed by GOURMET



Data conversion of molecular structure to other file formats

Conversion from UDF file to PDB/car/XYZ format file



UDF file displayed by GOURMET



Additional functions for studying mechanical properties of materials

- External field and deformation
 - Homogeneous field, e.g. electric fields
 - Shear flow by the Lees-Edwards boundary conditions
 - Unit cell deformation
- Solid wall
 - Flat wall
 - Structured wall
- Bond creation/scission
 - Simple model for chemical reaction



Example of Application : Clay(laponite) - Polymer(PEO) composite

Network structure of clay-polymer is observed in water. Clay plates order under shear flow.









Example of Application: Confined polymer melts under shear flow

Polymer melts confined between walls. Apply shear flow by sliding the walls.



Example of Application: Network formation



Reaction among two and three functional monomers



New Functions for Zooming

- Density biased Monte Carlo (DBMC)
- Density biased potential (DBP)
 - Embedding polymer chain into multiphase structures obtained by SUSHI
- Staggered reflective boundary condition (SRBC)
 Boundary conditions for simulating interfacial structure of polymer blends
- Lamella builder
 - Generation of semi-crystalline lamella structures



Example of Application: ABA triblock copolymer

A lamella structure of ABA triblock copolymer.

Loop/bridge ratio obtained by the SCF calculation(SUSHI) is reproduced. View - test.udf [F:¥home¥COGNAC3¥sample¥block] File View Display Options Tool Window Help

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Example of Application: Elastic behavior of ABA triblock copolymer



300% Strain

Example of Application: Interface of Polymer Blend

Interfacial structure of A/B polymer blend



Elongation by deforming the unit cell

Example of Application: Semi-crystalline lamella

- A semi-crystalline lamella structure of the united atom model of alkane
- The distribution of the length and loop/bridge ratio in amorphous phase are determined by mean field theory
- A snapshot during elongation

User defined potential functions

- ◆ COGNAC is written in C++
- COGNAC has classes for the templates of user defined potentials
- Users can define

 a functional form
 and parameters in
 a template function

double r,delR,ene,tmp;

r=dr.length(); delR=r-r0; tmp=kconst*delR; ftmp=dr*(tmp/r); ene=0.5*tmp*delR; return ene;

Example of user defined dynamics and potential functions: DPD

• Equations of motion and potential functions of dissipative particle dynamics (DPD)

$$\frac{d\mathbf{r}_{i}}{dt} = \mathbf{v}_{i}, \frac{d\mathbf{v}_{i}}{dt} = \mathbf{f}_{i}$$
$$\mathbf{f}_{i} = \sum_{i \neq j} \left(\mathbf{F}_{ij}^{\mathrm{C}} + \mathbf{F}_{ij}^{\mathrm{D}} + \mathbf{F}_{ij}^{\mathrm{R}} \right)$$

$$\mathbf{F}_{ij}^{C} = \begin{cases} a_{ij} (1 - r_{ij}) \hat{\mathbf{r}}_{ij} & (r_{ij} < 1), \\ 0 & (r_{ij} \ge 1) \end{cases}$$

$$\mathbf{F}_{ij}^{\mathrm{D}} = - w^{\mathrm{D}} \left(r_{ij} \right) \left(\hat{\mathbf{r}}_{ij} \cdot \mathbf{v}_{ij} \right) \hat{\mathbf{r}}_{ij}, \quad \mathbf{F}_{ij}^{\mathrm{R}} = w^{\mathrm{R}} \left(r_{ij} \right)_{ij} \hat{\mathbf{r}}_{ij}$$

Display of molecular structures

- Molecuar structures can be displayed by using "Action" tools or Python scripts
 - Arbitrary set of molecules/atoms/bonds can be displayed

Displaying all molecules of ABA triblock copolymers in a lamella phase

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Displaying only A type atoms and single bridge chain.

Analysis using "Action" on GOURMET

 Some of the analysis tools can be launched by "Action" on GOURMET

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PLOT_data	100000					
SILK UDF CREATE						
MEWER show						
R		Save	Save Lib			
Run import libsushi_show_field						
if \$SUSHIOutput != None :						
dimension = sizeof(\$SUSHIInput.mesh.axes[])						
Clear Log						
9			Initial #1			
1 1 2 3 4 5	6 7 9	 R Q 1	0 /1			

Plot of the results : Density profiles

 O_{CT} A

Plot of the results : Stress-strain curve

 Q_{CT} A

Help

 Brief comments on each UDF structure and parameter are displayed

HELP

Unit conversion

- Unit of each parameter can be converted to arbitrary units
- if COGNAC UDF has unit parameters, i.e.

reduced mass in [amu] reduced energy in [kJ/mol] reduced length in [nm].

float

SvmMat3x3

f Pressure

• 🗂 Stress

15.131034 [MPa]

COGNAC: Linking to other layers

Summary

- COGNAC has following functions:
 - Basic functions for MD/MM
 - Versatile functions for molecular modeling
 - Various potential functions and ensembles for coarse-grained models
 - Various functions and tools for material design
 - New functions for zooming
 - Extensibility of program

Developers of COGNAC

- T.Aoyagi, F.Sawa, T.Shoji, H.Fukunaga (JCII, Doi project)
- Prof. J.Takimoto (Nagoya Univ.)