



# **THE DL\_FIELD USER MANUAL**

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The DL\_FIELD manual assumes readers possess at least a basic knowledge in molecular simulation and potential force fields. It mainly describes the functionality of DL\_FIELD. It does not describe how and when to use the features offer by DL\_FIELD.

DL\_FIELD is a computer program package written in C that primarily serves as a support application software tool for DL\_POLY molecular dynamics simulation package. DL\_FIELD is developed at Daresbury Laboratory by C. W. Yong. The software was developed under the auspices of the Computational Science Centre for Research Communities (CoSeC) in support of several EPSRC-funded communities including Collaborative Computational Project for the Computer Simulation of Condensed Phases (CCP5) and HEC-MCC (High-End Computing for Materials Chemistry Consortium).

If you use DL\_FIELD in your work, please include the following reference in your publication:

***C W Yong, 'Descriptions and Implementations of DL\_F Notation: A Natural Chemical Expression System of Atom Types for Molecular Simulations', J. Chem. Inf. Model. 56, 1405–1409 (2016)***

### **Disclaimer**

While extensive tests have been made to ensure smooth working of DL\_FIELD and the accuracy of the supplied data parameters, neither the UKRI, STFC, EPSRC, CCP5, HEC-MCC nor the author of the DL\_FIELD package or its derivatives guarantee that the software package is free from error. We disclaim any responsibility for any failure, inaccuracy, harm and damage to your projects, theoretical or experimental works as a result of using DL\_FIELD.

## 1 Introduction

DL\_FIELD is intended to serve as an important application tool to enhance the usability of [DL\\_POLY](#) molecular dynamics (MD) simulation package and to facilitate the use of a wide range of advance features included in the MD program suite.

The primary function of DL\_FIELD:

(1) Force field model convertor: DL\_FIELD converts user's atom models, in particular those of large complex biomolecular systems, into file formats that are recognisable and ready to run in DL\_POLY\_2.19, DL\_POLY\_C, DL\_POLY\_3 and DL\_POLY\_4 programs with minimum user's intervention. This basically involves the conversion of a user's atomic configuration in simple xyz coordinates into identifiable atom types base on a particular user-selectable potential schemes and then automatically generate the DL\_POLY configuration file (CONFIG), the force field file (FIELD) and a generic control file (CONTROL).

(2) Force field editor: DL\_FIELD allows user to edit or modify a force field model to produce a customised scheme that is specific to a simulation model. For instance, introduction of pseudo points and rigid body implementation to an otherwise standard potential scheme such as CHARMM, AMBER, etc.

(3) Force field model repertoire: DL\_FIELD has a consistent file structure format for all FF schemes and molecular structure definitions. It also allows user to easily expand the existing standard model library to include user-defined molecular models.

(4) Fully automatic identification of the chemical nature of every atom in a molecule, and from such, to assign a universal atomic expression that is independent of the force field schemes (the [DL F Notation](#)).

### 1.1 File components

The DL\_FIELD program package consists of the following files:

(1) DL\_FIELD programs together with a *Makefile*, in the */source* directory

(2) Data library files located in the */lib* directory. These files are

Molecular structure data files, with filenames end with the extension *.sf*.

Potential parameter data files, with filename end with the extension *.par*.

The DL\_F notation data file, *DLF\_Notation*.

Atom type conversion data file, *dl\_field.atom\_type*.

Atomic chemical and physical data, *dl\_field.atom\_data*.

Other supplementary information specific to a force field scheme such as charge increment, atom equivalence table, etc.

(3) DL\_FIELD control file, of which the name and location is defined in the *dl\_f\_path* file. The control file contains all possible options to tune the force field model setup, including choice of force field schemes and input configuration file.

(5) Solvent templates, in the */solvent* directory.

- (6) A collection of utility program scripts, in the */utility* directory.
- (7) The converted files (such as *dl\_poly.CONFIG*, *dl\_poly.FIELD*), located in the */output* directory. For example, these files can be renamed as CONFIG and FIELD files, respectively for DL\_POLY runs.
- (8) The *dlf\_notation.output* file in the *output/* directory. This file is generated only if the user configuration is in the *xyz* format. It describes the chemical identity of every atom in the system.
- (9) Example files in PDB, *xyz* and *mol2* formats, located in the */Examples* directory.
- (10) The *control\_files/* directory contains a collection of DL\_FIELD's *control* sample files for the structures in the *Examples/* directory.
- (11) The status output file, *dl\_field.output*.
- (12) The *dl\_f\_path* file that specifies the directory paths for various file components, including the DL\_FIELD *control* filename and its location, relative to the DL\_FIELD home directory. The home directory is the directory path where the DL\_FIELD executable and *dl\_f\_path* files are located. The directory paths must be redefined in the *dl\_f\_path* file if they are moved away from the default location.

User must supply a pre-built atomic configuration file for conversion as DL\_FIELD does not include most model building features. However, DL\_FIELD can setup liquids and solution models based on a single molecular template (See [Solution Maker](#)). DL\_FIELD recognises the following input structure files: standard PDB format, a simple *xyz* format and Tripos *mol2* format.

Upon a successful conversion, DL\_FIELD will produce the following output files:

- (1) The CONFIG file, *dl\_poly.CONFIG*, in the */output* directory.
- (2) The FIELD file, *dl\_poly.FIELD*, in the */output* directory.
- (3) The CONTROL file, with the default name *dl\_poly.CONTROL*, in the */output* directory. The location and the name of the file can be changed as specified in the *dl\_f\_path* file.
- (4) The *dl\_field.output* file is created in the home directory, which reports the status of the conversion process.
- (5) An optional PDB output file can be produced and contains the user's configuration with atoms rearranged according to orders specified by the force field files.
- (6) A user-structure file, *dlf\_notation.output* in the *output/* directory, if the user configuration is in the *xyz* or *mol2* formats.

User will have to move the DL\_POLY output files to a directory where DL\_POLY simulations can be run and rename them as CONFIG, FIELD and CONTROL, respectively.

## 1.2 Quick Start Guide

Though not recommended, if you are too impatience, the following instructions show you how to run DL\_FIELD to demonstrate its capabilities.

**Step 1:** Compile DL\_FIELD ([Chapter 1.4](#)) – go to the *source/* directory. Type 'make'. This will produce the *dl\_field.exe* executable file in the DL\_FIELD home directory.

**Step 2:** Open *dl\_f\_path* file. This is the first entry point for DL\_FIELD to correctly locate various file components needed to run the program. Make sure you are using the correct control file. By default, this is pointed to *dl\_field.control*

```
control = dl_field.control
```

**Step 3:** Save (if require) and close *dl\_f\_path* and run DL\_FIELD, by simply typing:

```
./dl_field
```

DL\_FIELD will read the configuration file defined in the *dl\_field.control* file and setup the corresponding FIELD and CONFIG files in the *output/* directory.

**Step 4:** You can run some more example structures described in [Chapter 13](#) of the Manual. You need to make sure it is pointed to the correct control file, pre-defined for each example structure.

Open *dl\_f\_path* and comment out the default *dl\_field.control* file and remove the comment as follows:

```
control = control_files/example_1a.control  
# control = dl_field.control
```

This will run DL\_FIELD and reads the Example 1a structure as described in Chapter 13. All example structures are listed in the *Examples/* folder.

### 1.3 Force field (FF) Schemes

The following potential models are available in *DL\_FIELD*:

- (1) The CHARMM potential parameters are derived from the standard **toppar\_c36\_jul17** directory.
- (2) The united-atom CHARMM19 potential models for protein are derived from the **c35b2\_c36a2** directory.
- (3) The AMBER potential parameters for proteins are derived from the *ff03* force field (Duan *et al.* 2003) including the *frmod.ff03* supplementary file: *all\_amino03.lib*, *all\_aminont03.lib* and *all\_aminoc03.lib*
- (4) The AMBER Glycam potential parameters for carbohydrates and glycoproteins are derived from *Glycam\_06h* files.  
Kirschner, K.N., Yongye, A.B., Tschampel, S.M., Daniels, C.R., Foley, B.L, Woods, R.J. *J. Comput. Chem.* **29**, 622-655 (2008)
- (5) The AMBER's General Amber Force Field (GAFF), Version 2.1, for general organic molecules including small drug molecules.  
Wang, J., Wolf, R. M.; Caldwell, J. W.; Kollman, P. A.; Case, D. A. "Development and testing of a general AMBER force field". *Journal of Computational Chemistry*, 2004 v. 25, 1157-1174.
- (6) DL\_FIELD supports the enhanced version of OPLS, namely, the OPLS\_2005 force field, which covers a larger set of organic functional groups with refitted dihedral parameters.  
J. L. Banks *et. al.*, 'Integrated Modelling Program, Applied Chemical Theory (IMPACT)', *J. Comput. Chem.* **26**, 1752-1780 (2005)

W. Jorgensen, D. Maxwell and J. Tirado-Rives, 'Development and Testing of the OPLS All-Atom Force Field on Conformational Energetics and Properties of Organic Liquids' *J. Am. Chem. Soc.*, **118**, 11225–11236 (1996)

- (7) OPLS AA/M for protein. This is an improvement force field over OPLS AA/L  
M. J. Robertson, J. Tirado-Rives and W. L. Jorgensen, *J. Chem. Theo. Comp.* **11**, 3499-3509 (2015)
- (8) OPLS force field for ionic liquid (CL & P)  
J.N.C. Canongia Lopes and A.A. H. Padua, 'CL&P: A generic and systematic force field for ionic liquids modelling', *Theor. Chem. Acc.* **131**, 1129 (2012).
- (9) OPLS force field for deep-eutectic solvents (OPLS\_DES).  
B. Doherty and O. Acevedo, *J. Phys. Chem. B*, **122**, 9982-9993 (2018).
- (10) DREIDING force field, for general organic molecules.  
S. L. Mayo, B. D. Olafson and W. A. Goddard III, 'DREIDING: A Generic Force Field for Molecular Simulations', *J. Phys. Chem.* **94**, 8897-8909 (1990).
- (11) Polymer Consistent Force Field (PCFF) is based on CFF91 that includes a wide range of parameters for organic polymers, inorganic metals and zeolites. Used of both ab-initio and empirical methods to obtain parameters base on static simulations at 0 K.  
Huai Sun, Stephen J. Mumby, Jon R. Maple, Arnold T. Hagler 'An ab Initio CFF93 All-Atom Force Field for Polycarbonates', *J. Am. Chem. Soc.* **116** 2978–2987 (1994)
- (12) Condensed-phase optimized molecular potentials for atomistic simulation studies (COMPASS). It is a general force field for organic molecules. Based on PCFF, it is re-parametrised for condensed-phase systems.  
H. Sun 'COMPASS: An ab Initio Force-Field Optimized for Condensed-Phase Applications – Overview with Details on Alkane and Benzene Compounds' *J. Phys. Chem. B* **102**, 7338-7364 (1998).

Note: Only a subset of COMPASS parameters was published. The corresponding missing ATOM\_KEYS are still defined in the DL\_FIELD library and are tagged with a remark 'Missing'. During runtime, DL\_FIELD will bypass the check for these missing parameters for COMPASS.

- (13) Consistent valence force field (CVFF). Originally adopted in the Discover program, it is a general force field fit to small organic crystals and gas phase structures. Can handle peptides, proteins and a range of organic systems.
- (14) The united atom model Gromos G54A7.  
N. Schmid, *et. Al.* 'Definition and testing of the GROMOS force-field versions 54A7 and 54B7', *Eur. Phys. J.* **40**, 843-856 (2011)
- (15) Inorganic force fields, classify according to types of materials: binary oxides, ternary oxides, clay, glass, etc.

Note: DL\_FIELD does not implement cross-correlation interactions (such as bond-bond, bond-angle etc) for PCFF, CVFF and COMPASS.

## 1.4 Program Compilation

A standard C compiler must be pre-installed in your operating system. To compile the program, in the */source* directory type and enter the following command:

*make*

A *Makefile* must be included in the directory where source codes are located. The *Makefile* contains a series of instructions to compile and link the codes.

Upon successful compilation, a *dl\_field* executable file will be produced in the *dl\_f\_4.81/* home directory. Type *./dl\_field* to run the program.

## 1.5 DL\_FIELD Features and Release History

The following lists illustrate the development history of DL\_FIELD. The items are, in general accumulative, and they are therefore a complete list of DL\_FIELD features in a timeline order.

DL\_FIELD version 1.0 (released March 2010) contains the following features:

- Convert a PDB structure to CONFIG and FIELD files for DL\_POLY.
- CHARMM force fields for proteins, lipids and carbohydrates.
- Freeze and tether atoms assignment.
- Display additional information (such as protein residues etc) in CONFIG and FIELD files.
- Atom label display in DL\_FIELD (non DL\_F Notation) format or potential-specific format.

DL\_FIELD version 1.1 (released November 2010) contains the following additional features:

- Additional CHARMM force fields for lipids, ethers and other small molecules.
- Assign bond constrain and rigid water.
- Additional water models (TIP3P, TIP3P-PME and SPC).

DL\_FIELD version 2.0 (released May 2011) contains the following additional features:

- AMBER force field for protein (Duan. et. al. 2003).
- MM energy calculation for user's configuration model.
- Able to switch between different potential schemes without any modification to the PDB file.

DL\_FIELD version 2.1 (released October 2011) contains the following additional features:

- OPLS-AA standard force field for protein.
- The user-define force field (udff) file.
- Option to produce a smaller FIELD file size.

DL\_FIELD version 2.2 (released April 2012) contains the following additional features:

- DREIDING force field for general molecules.

- Polymer Consistent Force Field (PCFF) for general organic and polymeric molecules.
- Equivalent atom keys (EQUIVALENCE statement).

DL\_FIELD version 2.3 (released October 2012) contains the following additional features:

- AMBER's Glycam force field for carbohydrates and glycoproteins.
- Rigid atoms assignment to define rigid bodies.
- Pseudo point assignment.
- User-define scaling factors for 1-4 intra-interactions.
- Periodic boundary conditions.

DL\_FIELD version 3.0 (released April 2013) was a major release and contained the following additional features:

- Introduction of inorganic force fields (for simple metal compounds).
- User-selectable energy units (eV, kcal/mol and kJ/mol).
- Random velocity assignment.
- Core-shell models.
- Solvation features with counter-ion insertion.
- Auto-CONNECT features.

DL\_FIELD version 3.1 (released November 2013) contains the following additional features

- Update lipid CHARMM force field (all36\_lipid).
- CHARMM19 united-atom force field for proteins.
- Directives to introduce/remove angles and dihedrals selectively.
- More solvent choices for solvations, TIPnP, where  $n = 3, 4$  and  $5$ .

DL\_FIELD version 3.2 (released June 2014) contains the following additional features

- Inter-conversion of cell vectors and cell parameters
- Automatic determination of periodic boundary conditions (reads CRYST1 statement in PDB files)
- User-selectable mixing rules for vdw LJ12-6 potential (geometric and arithmetic).
- Include methylated and acetylated terminal for CHARMM proteins.
- Improved warning/error reports.

DL\_FIELD version 3.3 (released December 2014) contains the following additional features.

- Improved inorganic force fields including CLAYFF for clay minerals.
- OPLS2005 force field for proteins and general organic molecules.



- Full inclusion of directives to introduce/remove bonds, angles and dihedrals selectively or entirely.
- Miscellaneous improvements on conversion routines and addition of solvent molecules.

DL\_FIELD version 3.4 (released October 2015) contains the following additional features.

- Implementation of the standardised atom typing format, the DL\_F Notation, for PCFF and OPLS2005 force fields.
- Able to read configurations in simple xyz format for PCFF and OPLS2005 force fields, with full automatic assignment of ATOM\_TYPES in the DL\_F notation.
- Additional solvent choices such as SPC and SPC/E water models.

From version 3.4 onwards: ATOM\_KEYS, ATOM\_TYPES, MOLECULE\_TYPES, MOLECULE\_KEYS and element symbols are now case-sensitive. For example, the molecule keys 'ABC' and 'AbC' are distinct keys for different molecules.

DL\_FIELD version 3.5 (released April 2016) contains the following additional features:

- CVFF - Consistent valence force field that implements the DL\_F Notation.
- Addition of new Chemical Groups to OPLS2005 and PCFF for the DL\_F Notation.
- Inclusion of more solvent templates.
- Some improvement on memory usage.

DL\_FIELD version 4.1 (released December 2016) is a major revision and contains the following features:

- Introduction of multiple potentials - can include more than one FF schemes in a system model, such as mixtures of organic force fields or combination of organic/inorganic force fields (PDB input format only).
- Reorganised CHARMM force field into various components with the introduction of additional sets of force fields: CHARMM22\_prot, CHARMM36\_prot, CHARMM36\_lipid and CGenFF (on-going task).
- DL\_F Notation development: Include more new Chemical Groups. Extension of the DL\_F Notation to CHARMM force fields.
- Better memory usage with the storage of selective force field data.

DL\_FIELD version 4.1.1 (released April 2017) is a minor revision mainly to improve certain existing force field schemes as shown below:

- Improvement of INORGANIC force field, with the introduction of three-body term, assignment of freeze and tether atoms (on PDB format only)
- Reorganised INORGANIC force field into various components according to the type of materials: INORGANIC\_binary\_oxide, binary\_halide, ternary\_oxide, glass and clay.
- Inclusion of auto-assignment and correction to scaling due to dihedral degeneration, on PCFF and CVFF.
- DL\_F Notation development: Include more new Chemical Groups.

DL\_FIELD version 4.2 (released January 2018), a revision that contains the following features:

- G54A7 - Gromos united atom force field.
- CHARMM36 force field for carbohydrate (CHARMM36\_carb)
- Inclusion of more solvent templates.
- Introduce *VDW\_FIX* directive. Overrides vdw parameters of an atom pair instead of using parameters derived from some mixing rules.
- DL\_F Notation development: Include more new Chemical Groups.

DL\_FIELD version 4.3 (released July 2018), a revision that contains the following features:

- Solution Maker - automatically setup a disorder system such as liquid or solution (further equilibration require).
- Second-tier *EQUIVALENCE* parameter assignments.
- DL\_F Notation development: More new Chemical Groups, including complex, large fused aromatic systems and pyranose sugar units (in chair conformations).
- Write out *dif\_notation.output* user structure file (for xyz input format only) that contains list of a ATOM\_TYPES in DL\_F Notation.

DL\_FIELD version 4.4 (released January 2019), a revision that contains the following additional features:

- Amber GAFF general force (Amber16 version)
- OPLS-AA/M force field for protein systems.
- DL\_F Notation development: More new Chemical Groups.
- Inorganic system configurations expressed in the xyz input format.
- Improvement on multiple potential features: Allow Molecular Group definitions and multiple potential capability for xyz input format for both organic and inorganic models.
- Custom definition of *control* file and various directory paths (defined in *dl\_f\_path* file).

DL\_FIELD version 4.5 (released June 2019), a revision that contains the following new features:

- User's configuration files in the *mol2* format (for organic systems only).
- Include new vdw mixing rules for multiple-potential systems, which can be independently set for the sigma and epsilon parameters for Lennard-Jones 12-6 functions.
- DL\_F Notation development: Include more new Chemical Groups (small non-aromatic heterocyclic groups)
- Introduce *EXCLUSION\_14* directive to control 1-4 interaction exclusions in MOLECULE templates.

- Run DL\_POLY program via fork process (for Linux/Unix type systems) for single-point calculation and equilibration runs.

DL\_FIELD version 4.6 (released January 2020), a revision that contains the following new features:

- OPLS force field for deep eutectic solvents (OPLS\_DES)
- Inorganic force field library for zeolites (INORGANIC\_ZEOLITE)
- Non-specific, or miscellaneous force field library (MISC\_FF)
- Auto-insertion of core-shell models for inorganic materials.
- Auto-identification of MOLECULE template for template-based force field schemes (for xyz format only).
- DL\_F Notation development: Include more new Chemical Groups (both small and complex heterocyclic groups, some organosilicon groups).

DL\_FIELD version 4.7 (released December 2020), a revision that contains the following new features:

- Improve overall program stability and remove memory leaks.
- New force field for ionic liquids (OPLS\_CL\_P).
- Auto detection of atom types for clay minerals using CLAYFF force field.
- Include new solvent templates.
- DL\_F Notation development: Include more new Chemical Groups (mainly azoles and organic ionic species).

DL\_FIELD version 4.8 (released September 2021), a revision that contains the following new features:

- For PDB file: Auto-detect a residue whether it forms links with neighbouring residues. The linked symbol, -XX-, is no longer needed in PDB files.
- van der Waals (vdw) mixing using Slater-Kirkwood formalism (for multiple potential systems).
- Improvement on auto-identification of MOLECULE template for template-based force field schemes (for xyz format only): some capability to distinguish isomers.
- Force field library update: Include more new Chemical Groups and protein data for CHARMM.
- DL\_F Notation for inorganic systems.

DL\_FIELD version 4.81 (released February 2022) is a minor revision mainly to improve software stability and conversion errors as follows:

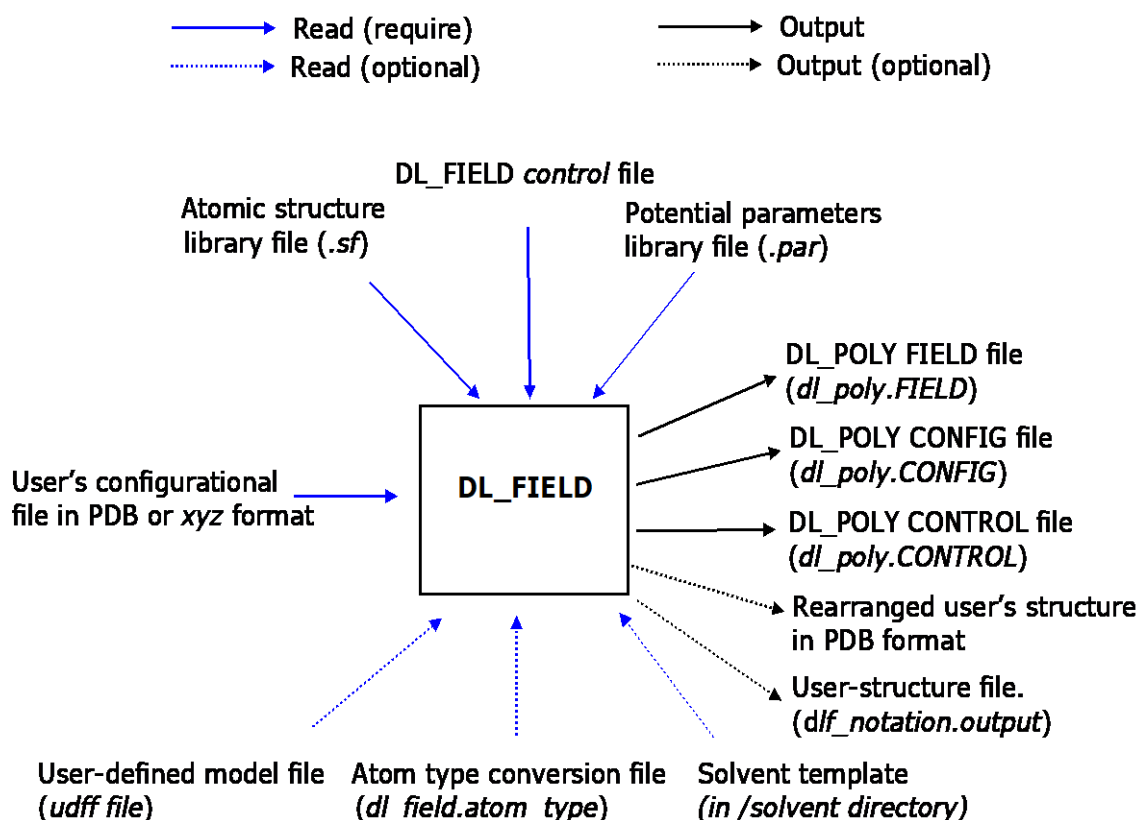
- Removed memory leaks, especially for multiple potential model setup.
- Include a few more Chemical Groups (benzothiophenes and quinazolines) and readjust organosilicon and silica detections.
- Adjust biphenyl detection to ensure correct FF assignment for polyaromatics.

DL\_FIELD version 4.9 (released November 2022), a revision that contains the following new features:

- Enable solvation by using solvent models from different FF schemes, including multiple potential systems.
- COMPASS force field for general molecules in condensed phase.
- CHARMM36 for nucleic acids, CHARMM36\_nucl (in PDB structure format).
- Conversion of Lennard-Jones 9-6 to 12-6 forms and make use of the LJ12-6 vdw mixing schemes in multiple potential systems: Allow mixing of COMPASS and PCFF with other LJ12-6 based FF schemes.
- Improvement on MISC\_FF scheme: Enable vdw mixing between different MOLECULE template models and inclusion of additional vdw functions.

## 1.6 DL\_FIELD Schematic Flowchart

The main thrust behind DL\_FIELD development is to minimise the requirement for users to understand detail knowledge and inner workings of complicated force field descriptions and model preparation procedures. It is intended to be highly agnostic and serve as a user-friendly tool that can process the molecular information with minimum user's intervention. Diagram below shows schematically the functionality of DL\_FIELD.



DL\_FIELD reads several directive commands in the standard library files (the .sf and .par files) and in DL\_FIELD control file. The use of these directives are crucial to properly produce the dl\_poly.CONFIG and dl\_poly.FIELD output files. DL\_FIELD also produces a

generic *dl\_poly.CONTROL* file. These files must be renamed as *CONFIG*, *FIELD* and *CONTROL* respectively for simulation runs in DL\_POLY.

Directive commands in DL\_FIELD will be explained in detail in the following chapters and they appear in capitals as ***BOLD\_ITALICS***. Directives take parameter data will appear as *italics*. Optional directives will be enclosed in the [***SQUARE BRACKET***].

## 1.7 DL\_FIELD Definitions

The following section describes definitions specific to DL\_FIELD. These terms appear as CAPITAL letters in the Manual.

(1) MOLECULE - An entity consists of a collection of ATOMs, which consist of normal atoms, pseudo points and atoms with core-shell components, or even united atoms and coarse-grain particles, that are defined within the **MOLECULE** and **END MOLECULE directives**. It is also called residues, similar those of amino acid components that made up a protein molecule. It can be either a complete molecule or a molecular fragment that can form bonds with other MOLECULEs. It can also refer to as a single atom or ion.

(2) MOLECULE\_TYPE - The name of a MOLECULE, often in a human-readable form.

(3) MOLECULE\_KEY - The corresponding code (up to four characters) for a MOLECULE\_TYPE. This is equivalent to the amino acid residue code as appears in PDB files.

(4) ATOM - An entity or member that made up a MOLECULE. It can be a normal atom, ion, a pseudo point, core and shell part of an atom, united atom or coarse-grain particle etc. They are listed within a **MOLECULE** and **END MOLECULE directives**.

(5) ATOM\_TYPE - The name or identity of an ATOM, often in a human-readable form, distinguishes by its chemical nature or ATOMIC characteristics within a MOLECULE. This is different from an element whereby there can be several ATOM\_TYPES for a given element. An element in different molecules can have different chemical behaviour due to its chemical environment. Different atom definitions are therefore needed and mapped to different sets of potential parameters in order to reflect the differences in chemical behaviour. For instance, an aliphatic carbon would be chemically different than, say, a carbonyl carbon. Two different ATOM\_TYPES will have to define to reflect these differences.

(6) ATOM\_KEY - The abbreviation symbol for an ATOM\_TYPE and is used to map to the corresponding potential parameters. ATOM\_KEYS are defined as 'atoms', or the atom labels that would appear in the *CONFIG* and *FIELD* input files for DL\_POLY.

(7) ATOM\_LABEL - The unique label of an ATOM, visible only within a **MOLECULE** directive. In other words, it is used to distinguish the ATOMs from one another within a MOLECULE.

(8) CONNECT - The way how an ATOM is related to other ATOMs in a MOLECULE. DL\_FIELD recognises three different ways: normal-CONNECT between ATOMs, self-CONNECT and auto-CONNECT. These are distinguished from one another by using the appropriate **CONNECT** directives.

(9) ORGANIC force field - A general reference to a group of force field schemes that is used to model covalent molecules such as amino acids, sugars and other types of organic molecules. Examples of such are CHARMM, AMBER and OPLS-AA etc.

(10) INORGANIC force field - A general reference to a group of force field schemes for inorganic molecules. See Chapter 10 for more information.

(11) Potential (or force field (FF)) Scheme - Refer to a force field data set, which are usually given a name to identify the data set. For example, CHARMM, AMBER and OPLS-AA are three well-known force field schemes to model proteins and organic molecules in the condensed phase simulations.

(12) DL\_F notation - The DL\_FIELD standard ATOM\_TYPE notation for a range of FF scheme including CHARMM, PCFF, CVFF and OPLS force fields. It is the universal atom typing form of which the force fields share the common ATOM\_TYPE and ATOM\_KEY descriptions for a given system.

(13) Directive - A command that is recognisable by DL\_FIELD to perform a function, or as an indication of types of data. Directives mostly appear in the library files but also in the DL\_FIELD's *control* files, as well as in the user's configuration files. Directives are described in ***bold italics***, and in [***square brackets***] for optional directives.

(14) Control Options - The force field model conversions are driven by a set of control Options in the *control* files. The sequence of these Options are fixed and they are expressed as Option **X** in the Manual, where **X** is the unique numerical value for different [controls](#).

## 2 Molecular Structure File (.sf)

The structure file is a standard library file expressed in the ASCII text format where all ATOM\_TYPES and MOLECULEs are defined. It is like the CHARMM's topology file or the Amber's 'prep' file.

The file is free format but each line is restricted to 120 characters in length. It contains several simple directives. Different types of definitions were enclosed within a **DIRECTIVE** and the **END DIRECTIVE** block.

The available **DIRECTIVE**s are shown below:

### 2.1 ATOM\_TYPE and END ATOM\_TYPE

Enclosed within these directives is where all the ATOM\_TYPES of a given potential scheme are defined.

Each entry must take five parameters:

(a) ATOM\_TYPE name - This can be anything up to 30 characters in length (case-sensitive).

(b) ATOM\_KEY - This can be anything up to 15 characters in length (case-sensitive). This is the atom label that will show in the *dl\_poly.CONFIG* and *dl\_poly.FIELD* files. The ATOM\_KEY can be any alphanumeric characters. The exception being the character 'X', which is reserved by the DL\_FIELD to indicate a generic or a representation of 'any-atom' in the parameter (.par) files.

(c) Element - The element symbol (case-sensitive) of an ATOM\_TYPE according to the standard Periodic Table of the Elements. However, DL\_FIELD allows user-define 'element' symbols, such as those for [pseudo points](#) and united atoms.

(d) Relative atomic mass - This value can be shown up to 3-4 significant figures.

(e) Remark - This can be anything and is ignored by DL\_FIELD. It is used to provide brief description to an ATOM\_TYPE.

An example of **ATOM\_TYPE** usage is shown below (extracted from *DLPOLY\_PCFF.sf*)

ATOM_TYPE	key	element	mass	remark (Ver. Ref.)
Ct_alkane	c1	C	12.0115	sp3 carbon -CH (1.0 1) - connect to three C
Cs_alkane	c2	C	12.0115	sp3 carbon -CH2 (1.0 1) - connect to two C
Cp_alkane	c3	C	12.0115	sp3 carbon -CH3 (1.0 1) - connect to one C
...				
...				
END ATOM_TYPE				

The example above defined three different kinds of carbon atoms: ATOM\_TYPES Ct\_alkane, Cs\_alkane and Cp\_alkane, referring to tertiary, secondary and primary alkyl carbon atom, respectively. The corresponding ATOM\_KEYS are c1, c2 and c3 respectively.



Note that each ATOM\_TYPE is unique, whereas the corresponding ATOM\_KEY is not. In other words, more than one ATOM\_TYPES can share a same ATOM\_KEY. DL\_FIELD will flag up an error if more than one identical ATOM\_TYPES are defined.

## 2.2 MOLECULE\_TYPE and END MOLECULE\_TYPE

This directive set displays a list of available MOLECULE templates in the *.sf* file. During the conversion process, DL\_FIELD extracts the MOLECULE\_KEYS from the user configuration (PDB file format) and then look for the corresponding MOLECULE\_TYPES. The latter information is required for DL\_FIELD to look for the correct MOLECULE templates, which are defined by the **MOLECULE** and **END MOLECULE** directives.

The template list is useful for users to look up what MOLECULE templates are available in a structure file. The order of the MOLECULE\_TYPES in the list is not important. They can be grouped according to types of MOLECULEs, for examples, into amino acids and carbohydrates. Alternatively, MOLECULEs can be grouped according to functional groups or molecular weight.

For configurations expressed in *xyz* and *mol2* formats, DL\_FIELD does not need the MOLECULE\_TYPE information or MOLECULE template definition. The exception would be for those template-based FF schemes such as AMBER and CHARMM.

In the case of inorganic systems in *xyz* format, the MOLECULE\_KEY must always be specified. See [Section 6.2](#) for more details.

Each entry within the **MOLECULE\_TYPE** directive must take four parameters (a), (b), (c), and (d) as shown below:

(a) MOLECULE\_TYPE - This can be anything up to 30 characters in length. This is the molecule name (often in a human-readable form) that identifies a MOLECULE.

(b) MOLECULE\_KEY - The unique identity code of the MOLECULE up to four character long. This code is used to identify a MOLECULE in the user's atomic configuration files such as a PDB file. It is equivalent to the protein residue labels in a PDB file. Note that in order to conform to the PDB file format, MOLECULE\_KEYS must have up to 4 characters, though DL\_FIELD allows more than that. In addition, all MOLECULE\_KEYS are case-sensitive. In other words, MOLECULE\_KEYS HIS and HIs are treated as two different keys that corresponds to two different MOLECULEs.

For some MOLECULEs, such as those of carbohydrates, nuclei acids and amino acids, DL\_FIELD will *automatically* determine if they are whole molecules or formed part of linkages as molecular residues. In the latter case, DL\_FIELD will modify the MOLECULE\_KEY to -ABC- where ABC is the original key defined in the user's configuration file.

For instance, in a PDB file, the amino acid residue ALA (alanine) which formed part of a protein, will be recognised by DL\_FIELD as -ALA-. For AMBER's Glycam molecule, the molecule residue 3EA (3- $\alpha$ -D-altropyranose terminal) will be renamed as -3EA-. DL\_FIELD will automatically search and assign additional potential parameters involving bond linkages that straddle across two MOLECULEs.

(c) Relative molecular mass - This can be calculated based on some standard atomic weight. DL\_FIELD need this information for amino acid residues to determine various charge states of some amino acids such as histidine and aspartic acid.

(d) Remark - Brief description of the MOLECULE. This information is ignored by DL\_FIELD.

An example of the **MOLECULE\_TYPE** directive is shown below (extracted from the *DLPOLY\_CHARMM.sf* file):

```

MOLECULE_TYPE    key    mw    remark
ethane           ETHA  30.071 !C2H6
propane          PRPA  44.098 !C3H8
hexane           HEXA  86.181 !C6H14
...
...
END MOLECULE_TYPE

```

DL\_FIELD will always check that there is no repeat of MOLECULE\_TYPE and MOLECULE\_KEY. In other words, each MOLECULE\_TYPE is uniquely referred to a MOLECULE\_KEY. This contrasts with ATOM\_TYPES and ATOM\_KEYS, where different ATOM\_TYPES can share the same ATOM\_KEY.

### 2.3 MOLECULE and END MOLECULE

This directive block is the most commonly encountered in a *.sf* file. This is where a MOLECULE's structure and model states are defined, called a MOLECULE template. Only one MOLECULE template can be defined within the directive set. It is used to match with the user's structure and, from such, to derive the corresponding force field model state.

A MOLECULE definition will always take the following format and sequence order:

```

MOLECULE MOLECULE_TYPE total_atom total_charge
ATOM_LABEL1          ATOM_TYPE1      charge
ATOM_LABEL2          ATOM_TYPE2      charge
...
ATOM_LABELn          ATOM_TYPEn       charge
CONNECT          ATOM_LABEL1 > ATOM_LABEL ...
CONNECT          ATOM_LABEL2 > ATOM_LABEL ...
...
CONNECT          ATOM_LABELn > ATOM_LABEL ...
[RIGID]          ATOM_LABEL1 ATOM_LABEL2 ...
[DIHEDRAL REMOVE/ONLY] ATOM_LABEL1 ATOM_LABEL2 ATOM_LABEL3 ATOM_LABEL4
[ANGLE REMOVE/ONLY]   ATOM_LABEL1 ATOM_LABEL2 ATOM_LABEL3 ATOM_LABEL4
[IMPROPER]        ATOM_LABEL1 ATOM_LABEL2 ATOM_LABEL3 ATOM_LABEL4
[INVERSION]       ATOM_LABEL1 ATOM_LABEL2 ATOM_LABEL3 ATOM_LABEL4
[SHELL]          ATOM_LABEL_core ATOM_LABEL_shell
...
...
END MOLECULE [some information or remark]

```

Each molecular definition must always end with the **END MOLECULE** directive. However, the optional directives can appear in any sequence.

The *total\_atom* indicates the total number of ATOMS in the MOLECULE and each ATOM must be clearly defined. The *total\_charge* is the net charge of the MOLECULE, by summing up all the individual partial charges of ATOMS.

Each ATOM must have the unique ATOM\_LABEL. This is followed by the corresponding ATOM\_TYPE, as defined in the **ATOM\_TYPE** directive. Finally, the *charge* value of the

ATOM must also be defined. If the total charge is set to some 'ridiculously' large value (10.0 or above), then DL\_FIELD will not look for the charge values of the individual ATOMs. Instead, charge values will be determined from the bond charge increment data. This usually applies to force field schemes such as PCFF, CVFF and OPLS2005.

The connectivity information must also be given, immediately after the ATOM definitions. The connectivity of each ATOM must be clearly defined using the directive **CONNECT**. The sequence of **CONNECT** ATOM statements must follow strictly that of ATOM sequence defined earlier. ATOM\_LABELs after the '>' symbol indicate the neighbouring ATOMs that are connected to the ATOM.

### 2.3.1 Bond Connectivity

There are three different types of connections: (1) the normal bond connection between ATOMs, (2) the self-CONNECT and (3) the auto-CONNECT. These different types of connections are distinguished from one another by using the **CONNECT** statement in different formats. This is shown below:

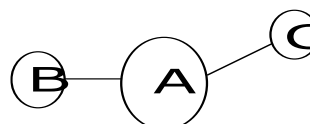
#### (a) Normal CONNECT

The directive **CONNECT** means a physical (covalent) bond is established between two ATOMs when it is defined as follows:

**CONNECT** A > B C

**CONNECT** B > A

**CONNECT** C > A



The directive statements above define bonds A-B and A-C and DL\_FIELD will automatically search for all angles and dihedrals, if any.

#### (b) Self-CONNECT

When an ATOM is defined with this type of connection, DL\_FIELD will assume there is no physical bond connected to this ATOM and, hence, no angle and dihedral. This essentially treats it as an isolated ATOM within the MOLECULE and DL\_FIELD will only assign the charge and vdw parameters to the ATOM:

**CONNECT** A > A

When defining a self-CONNECT ATOM, the correct ATOM\_KEY **must be used** instead of ATOM\_LABELs. The same ATOM\_KEYS must be used also as the atom labels in the user's PDB file.

For ORGANIC force field, self-CONNECT only valid for [pseudo ATOMs](#) and the shell part of a polarisable atom.

For INORGANIC force field, self-CONNECT is normally used since ionic materials are largely interacted via non-bonded interactions. Example below shows how to define a self-CONNECT ATOM. Note that The ATOM\_KEY OP must be used also as the label in the PDB file.

```

ATOM_TYPE
O_phosphate OP O 15.9994 ! Phosphate O
END ATOM_TYPE

MOLECULE an_example 10 0.0
OP O_phosphate -0.3
....
CONNECT OP > OP
...
END MOLECULE

```

## (c) Auto-CONNECT

This type of connection instructs DL\_FIELD to determine the bond connectivity automatically and assign all the necessary 2- (bond), 3- (angle) and 4-bodies (dihedral) interactions accordingly. The general syntax is as follows:

```
CONNECT ATOM_KEY > number_of_neighbours AUTO
```

Note that, similar to the self-CONNECT, ATOM\_KEYS *must be used*, instead of some ATOM\_LABELS in the MOLECULE templates and the user's PDB file.

The directive **AUTO** is required to indicate the **CONNECT** statement is of auto-CONNECT type.

The auto-CONNECT is a powerful feature to construct MOLECULEs consist of many ATOMs, or MOLECULEs with no definite connection order. Examples of such are random polymers, hydrogels, molecules with complex inter-connectivity such as networked polymers and graphenes. While these MOLECULEs can be constructed by using the normal CONNECT feature, use of the auto-CONNECT type is less error-prone, and produced a simpler MOLECULE definition than using the normal CONNECT feature.

The *number\_of\_neighbours* indicates the number of bonds that are expected to connect to the ATOM. DL\_FIELD will flag up an error if the number of neighbours in the user's configuration does not match with what is defined in the **CONNECT** statement.

The *number\_of\_neighbours* can also be replaced with an asterisk, \*, to indicate either an unknown or variable number of neighbours. Example of such use is shown for the CLAYFF in the *DLPOLY\_INORGANIC\_clay.sf* file. Care must be taken when such feature is used, and users must ensure all bond connections are properly accounted for.

The auto-CONNECT feature is also useful for certain ORGANIC force fields to construct a MOLECULE to represent a class of MOLECULEs that share a common functional group. An example is shown below (extracted from *alcohol.udff* in the [Examples/](#) directory):

```

MOLECULE_TYPE
...
aliphatic_alcohol      ROH  999.000  Aliphatic alcohol, CnH2n+1-OH, n is not 1
...
END MOLECULE_TYPE

MOLECULE aliphatic_alcohol 6 -0.22  Any aliphatic alcohol, except methanol
CT3 Cp_alkane  -0.27
CT2 Cs_alkane  0.05      H1 H1 H1
CT1 Ct_alkane  0.14      | | |
HA HC_alkane   0.09      H1-C3-C2-...C2-OH-HO
OH1 O_alcohol  -0.66     | | |
H HO_alcohol   0.43      H1 H1 H1
CONNECT CT3 > 4 AUTO
CONNECT CT2 > 4 AUTO
CONNECT CT1 > 4 AUTO
CONNECT HA > 1 AUTO
CONNECT OH1 > 2 AUTO
CONNECT H > 1 AUTO
END MOLECULE

```

The example above shows that the MOLECULE *aliphatic\_alcohol* represents all types of aliphatic alcohols (all primary, secondary and tertiary) such as ethanol, propanol, pentanol, etc. Unlike the MOLECULEs contain the normal CONNECT type, DL\_FIELD permits the use of a subset number of ATOMs within the MOLECULEs with the auto-CONNECT type. For instance, branched alcohols such as propan-2-ol would need the ATOM\_TYPE *Ct\_alkane*, whereas linear alcohols do not. DL\_FIELD will choose the suitable ATOM\_TYPES according to the user's input structures.

Example uses of the auto-CONNECT feature are illustrated for alcohol structures in the *Examples/* directory (*ethanol\_auto1.pdb*, *ethanol\_auto2.pdb* and *alcohols.pdb* files). Note that they require the *udff* file called *alcohol.udff* for DL\_FIELD to convert these structures. To use the *udff* feature, turn it on by providing the correct *udff* file location, such as *Examples/alcohol.udff*, in the *control* file. Remember to select the CHARMM22\_prot as the FF scheme.

Example uses of the auto-CONNECT feature for inorganic materials can be found in the ternary oxides library such as the MOLECULE *calcium\_carbonate1* template.

### 2.3.2 Optional directives

The following directives can appear in any order within a MOLECULE definition.

(a) [**IMPROPER**] directive

This directive defines improper potentials. It reads four ATOM\_LABELs with three of them linking to a fourth central atom.

(b) [**INVERSION**] directive

This directive indicates the requirement of inversion potentials. It reads four ATOM\_LABELS with three of them linking to a fourth central atom.

(c) [**RIGID**] directive

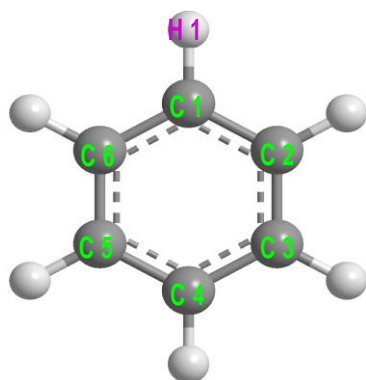
This directive defines rigid ATOMS in a molecule. Each [**RIGID**] statement defines collectively a group of ATOMS as a single rigid body.

For the [**RIGID**] statements defined within a MOLECULE to become active, users must also specify a [**RIGID**] directive to the Molecular Group to which the MOLECULE belongs, in the *control* file. In other words, the [**RIGID**] statements specified within the **MOLECULE** defines the rigid body of the molecule, while the [**RIGID**] directive specified in the *control* file decides whether the rigid body should be implemented for the MOLECULEs that belongs to a Molecular Group.

Consider a MOLECULE benzene with all the carbon ATOM\_LABELS as shown below and let's suppose all six carbon atoms are to be defined as a single rigid body. The [**RIGID**] directive within the MOLECULE is defined as follows:

```
RIGID C1 C3 C2 C6 C4 C5
```

The order of the carbon atoms is not important. The [**RIGID**] directive defines a rigid ring and, except for vdw and coulombic interatomic interactions, all intra-interactions that involve all members of the rigid ATOMS will be excluded in force calculations. The intra-interactions (bonds, angles and dihedrals) among the rigid atoms will not be shown in the *dl\_poly.FIELD* file.



Note that all the hydrogen atoms are still flexible relative to the rigid ring. The following [**RIGID**] directive defines one of the hydrogen atom to form part of the rigid body:

```
RIGID C1 H1 C3 C2 C6 C4 C5
```

DL\_FIELD Limitation:

Each [**RIGID**] statement in DL\_FIELD refers to a single rigid unit within a MOLECULE can only contain up to 15 atoms. This is in contrast to DL\_POLY, which allows more than that but confine to 15 atoms in a statement line in the *FIELD* file.

(d) [**SHELL**] directive

The directive [**SHELL**] introduces core-shell polarisability effect to an ATOM within a MOLECULE. The syntax to define a core-shell model of an ATOM is as follows:

```
SHELL ATOM_LABEL_core ATOM_LABEL_shell
```

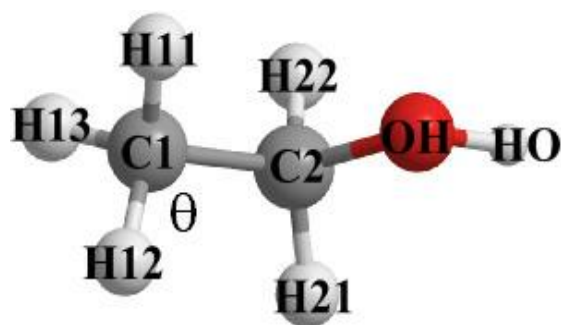
The example above shows DL\_FIELD will consider ATOM\_LABEL\_core and ATOM\_LABEL\_shell as the core and shell component of an atom respectively.

Core-shell models are usually available for inorganic models. However, DL\_FIELD permits core-shell models on all organic potential schemes (see [Section 11.2](#)). For details about core-shell implementations on inorganic materials, please see [Section 11.2](#).

(e) [**ANGLE ONLY**], [**ANGLE REMOVE**] and [**ANGLE OFF**] directives

These are optional angle exclusion directives. Only one of these directives is allowed for a MOLECULE definition. By default, once all ATOMS within a MOLECULE template are matched with the user's configuration, all possible sets of angles contained within a MOLECULE will be identified and assigned with the corresponding potential parameters for the angle interactions.

However, users can selectively remove a specific set of angles by using the [**ANGLE REMOVE**] directive. This directive instructs DL\_FIELD to ignore the assignment of potential parameters to the angle set. Consider a MOLECULE ethanol with ATOM\_LABELS as shown in the sketch below:



By issuing the directive statement, say, [**ANGLE REMOVE**] H12 C1 C2, it tells DL\_FIELD to ignore the angle interaction  $\theta$  (H12-C1-C2) but still consider the rest of the interactions involving all other angles.

If the directive statement [**ANGLE ONLY**] H12 C1 C2 is issued, this instructs DL\_FIELD to assign *only* the angle potential interactions about H12-C1-C2 and ignore the rest.

If the directive statement [**ANGLE OFF**] is issued, then *all* angles will be ignored. Note that this directive does not take any ATOM\_LABEL as the input parameter.

(f) [**DIHEDRAL ONLY**], [**DIHEDRAL REMOVE**] and [**DIHEDRAL OFF**] directives

These optional directives determines dihedral angle exclusions. They function exactly the same way as that of **ANGLE** directives. The syntax is as follows:

```
DIHEDRAL ONLY LABEL1 LABEL2 LABEL3 LABEL4
DIHEDRAL REMOVE LABEL1 LABEL2 LABEL3 LABEL4
Or
DIHEDRAL OFF
```

Note that the 1-4 non-bonded interactions between LABEL1 and LABEL4 still apply, even if the dihedral angle involving these ATOMS is excluded.

(g) [**BOND ONLY**], [**BOND REMOVE**] and [**BOND OFF**] directives

These optional directives determine bond exclusions. They function exactly the same way as that of **ANGLE** directives. The syntax is as follows:

```
BOND ONLY/REMOVE ATOM_LABEL1 ATOM_LABEL2
Or
BOND OFF
```

(h) [**THREE-BODY**] directive

This directive defines three-body interactions with the following syntax

**THREE-BODY** ATOM\_LABEL1 ATOM\_LABEL2 ATOM\_LABEL3

Once a three-body interaction is defined, DL\_FIELD will look for the corresponding parameters in the *.par* file, under the directive **THREE\_BODY**. An example usage of the three-body interactions can be found for MOLECULE *soda-lime\_silicate1* in the *DLPOLY\_INORGANIC\_glass.sf* file.

(i) [**EXCLUSION\_14**] directive

An atom pair that is separated by three bonds will usually be treated with vdw and coulombic interactions, called the 1-4 non-bonded interactions. Quite often, such interactions are also scaled with some [scaling factors](#). With this directive, such interactions can be switched off selectively within a MOLECULE. The syntax is as follows:

**EXCLUSION\_14** ATOM\_LABEL1 ATOM\_LABEL2 ...

Each statement includes a group of ATOM\_LABELS and exclusions will apply if any 1-4 atom pairs were identified within the atom group. By default, up to a maximum number of 15 atoms (set by MAX\_EXCLUSION\_14 in *dl\_field.h*) can be specified in a statement.

More than one **EXCLUSION\_14** statement is allowed within a MOLECULE and they are independent from each other. In other words, the 1-4 exclusions **only** apply to the respective group of atoms defined in each statement.



## 2.4 Example of a Structure File

Below shows a typical example of a *.sf* file composition, extracted from the *CHARMM22\_prot.sf*.

```

ATOM_TYPE
...
...
HC_alkene    HE2    H    1.00797 ! 12 alkene H2C=CR (generic)
C_aldehyde   CD     C    12.0115 ! 24 carbonyl C (top_all22_model)
O_aldehyde   O     O    15.9994 ! 80 carbonyl oxygen
HC_aldehyde  HR1    H    1.00797 ! 46 his he1, (+) his HG,HD2
Np_amine     NH2    N    14.0067 ! 75 amide hydrogen
HN_amine     HC     H    1.00797 ! 42 N-ter H
C_amide      CC     C    12.0115 ! 64 carbonyl C, asn,asp,gln,glu,cter,ct2
Cs_amide     C     C    12.0115 ! 52 carbonyl C, peptide backbone
O_amide      O     O    15.9994 ! 80 carbonyl oxygen
Np_amide     NH2    N    14.0067 ! 75 amide nitrogen
...
END ATOM TYPE
.
.

MOLECULE_TYPE
...
...
acetamide    ACEM    59.068  From CHARMM top_all22_model.inp
...
...
END MOLECULE_TYPE
.
.

MOLECULE acetamide 9 0.0  methyl amide (Acetamide)
C1 Cp_alkane -0.27
H11 HC_alkane 0.09
H12 HC_alkane 0.09      H11 O    H1
H13 HC_alkane 0.09      | ||  /
C C_amide     0.55      H12-C1--C--N
O O_amide     -0.55      |      \
N Np_amide    -0.64      H13     H2
H1 HN_amide   0.32
H2 HN_amide   0.32
CONNECT C1 > H11 H12 H13 C
CONNECT H11 > C1
CONNECT H12 > C1
CONNECT H13 > C1
CONNECT C > C1 O N
CONNECT O > C
CONNECT N > C H1 H2
CONNECT H1 > N
CONNECT H2 > N
IMPROPER C C1 N O
IMPROPER C N C1 O
IMPROPER N C H1 H2
IMPROPER N C H2 H1
END MOLECULE

```

The layout is similar to the CHARMM topology file. A molecule sketch (or any other information) is permitted alongside the ATOM definitions. This information is ignored by DL\_FIELD. However, the **CONNECT** directive must only contain DL\_FIELD readable connectivity information.

Do take extra care when constructing a MOLECULE as it completely defines the state of a molecular model. DL\_FIELD has been programmed to detect many possible typo and syntax errors in the MOLECULE templates. However, it is not able to detect what should (or should not) be included. For instance, no error will flag up if an amide group is defined without the [**IMPROPER**] or [**INVERSION**] directive although this may be needed, to keep the amide functional group in a planar configuration.

All user-defined MOLECULEs can be defined in a separate file called the *udff* file (See [Section 5](#)). Users are strongly recommended to do so since this is the only way to safely include new MOLECULEs without having to tamper with the standard force field library files included in the DL\_FIELD software.

### 3 Parameter File (.par)

The parameter file is a standard force field library file expressed in the standard ASCII text format and contains all atomic interaction parameters. All *.par* files are located in the directory */lib*.

The DL\_FIELD's parameter file is similar to CHARMM's parameter file or AMBER's *.dat* file. Each line is restricted to 120 characters in length. It contains several directives that indicate various types of potential interactions. Each type of potential interaction is grouped into a block and enclosed within the appropriate **DIRECTIVE** and the corresponding **END DIRECTIVE**. Each potential type can only have one set of **DIRECTIVES**. For example, there can be only one set of **BOND** and **END BOND** block within a parameter file. All bond parameters can only be defined within this **DIRECTIVE** block set.

The order of the **DIRECTIVE** block sets is not important. All **DIRECTIVES** have the same functionality for all potential schemes. However, the order and the type of potential parameters appear within each **DIRECTIVE** may vary according to the potential schemes. In addition, some functional forms of a potential type may also be different depending on the potential schemes. Wherever possible, the way the parameters listed in the *.par* file is the same as that of original data library file of a given potential scheme. DL\_FIELD will carry out all the necessary conversion internally to produce equivalent parameter sets in the FIELD file for DL\_POLY.

For example, in DL\_POLY, the spring constant is defined as  $0.5k_b$  and DL\_FIELD will rescale this according to the selected potential scheme, so that the potential parameters for that scheme can be entered 'as is' into the DL\_FIELD's parameter file. For instance, in the CHARMM force field parameter files, the CT3-CT3 bond defines  $k_b = 222.5$  kcal/mol. DL\_FIELD will rescale this as 445.0 in the FIELD file. Internally, DL\_POLY will see this as  $0.5 \times 445.0$  when running the simulation.

The following directives are used in a typical *.par* file.

#### 3.1 UNIT directive

This directive indicates the energy unit that applies to all parameters in the file. It only takes one variable:

**UNIT** *energy\_unit*

The available options are *kcal/mol*, *eV*, *kJ/mol* and *K*. If the energy unit option (Option **2** in the [control](#) file) is specified other than what is defined in the *.par* file, DL\_FIELD will carry out unit conversions automatically for all potential parameters before it is written to the *dl\_poly.FIELD* file.

#### 3.2 POTENTIAL and END POTENTIAL directives

This directive block indicates the type of potential scheme. Enclosed within these directives contain all possible types of interactions for the force field. The directive POTENTIAL only takes one variable, the *potential\_scheme*:

**POTENTIAL** *potential\_scheme*

The available *potential\_scheme* in DL\_FIELD are as follows:

<b>Name of potentials</b>	<b><i>potential_scheme</i></b>
All-atom CHARMM*	CHARMM
CHARMM22 for proteins	CHARMM22_prot
CHARMM36 for proteins	CHARMM36_prot
CHARMM36 for lipids	CHARMM36_lipid
CHARMM36 for carbohydrates	CHARMM36_carb
CHARMM general force field	CHARMM36_cgenff
United-atom for CHARMM	CHARMM19
All-atom Amber	AMBER
AMBER general force field	AMBER16_gaff
OPLS-AA	OPLSAA
OPLS_2005	OPLS2005
OPLS AA/M for proteins	OPLS_AAM
CL&P for ionic liquids	OPLS_CL_P
OPLS for deep eutectic solvent	OPLS_DES
DREIDING	DREIDING
Polymer consistent force field	PCFF
Consistent Valence Force Field	CVFF
Gromos united atom G54A7	G54A7
Inorganic force field**	INORGANIC
Inorganic FF for binary oxides	INORGANIC_binary_oxide
Inorganic FF for ternary oxides	INORGANIC_ternary_oxide
Inorganic FF for binary halides	INORGANIC_binary_halide
Inorganic FF for glass	INORGANIC_glass
Inorganic FF for clay	INORGANIC_clay
Inorganic FF for zeolite	INORGANIC_zeolite
Non-specific, miscellaneous FF	MISC_FF
<a href="#">Multiple potential</a>	multiple

Note that OPLS\_2005 and OPLS-AA essentially share the same potential functional forms. In the following description, anything refers to OPLS-AA also applies to

OPLS\_2005. However, OPLSAA is essentially decrepit within DL\_FIELD since the introduction of the DL\_F Notation.

In general, there are two ways to map a molecular model to a potential scheme: (1) template-base ([MOLECULE](#) template) and (2) topological analysis using [DL\\_F Notation](#). Examples of template-based FF including CHARMM, AMBER, Gromos and some of the OPLS FF components, such as OPLS\_CL\_P. Examples of topological-based FF including OPLS2005, CVFF and PCFF. Depending on the FF schemes and system models, one file formats would be more suited than the other. For instance, the use of PDB file format would be required for system models contain proteins. For more information, please see [Section 6](#).

The MISC\_FF is the most flexible, generic scheme and does not confine to any particular FF models. It is useful to define MOLECULEs and parameters from different sources and with different parameters. It allows definitions of more than one version of identical MOLECULE templates with different sets of FF parameters. For more information, consult the remarks described in the library files, *DLPOLY\_MISC.sf* and *DLPOLY\_MISC.par*.

\*Prior to version 4.1, all CHARMM force fields are collectively included in a single *.sf* file and a single *.par* file. This 'general' set of CHARMM files will be removed in some future DL\_FIELD versions once all individual CHARMM force field components are set up.

\*\*Prior to version 4.1.1, all INORGANIC force fields are collectively included in a single *.sf* file and a single *.par* file. This 'general' set of INORGANIC files has now been removed. All individual force field components are migrated into appropriate library files classified according to the types of inorganic materials.

### 3.3 BOND and END BOND directive

Enclosed within the *BOND* directive is the definition of all two-body bond interactions. The bonds between two atoms are usually represented by a harmonic expression:



Where  $k_b$  is the spring constant and  $b_0$  is the bond equilibrium distance.

Some potential schemes such as PCFF and DREIDING use different functional forms for bonds:

$$U(r) = k_1(r - b_0)^2 + k_2(r - b_0)^3 + k_3(r - b_0)^4$$

$$U(r) = D_e [1 - e^{-\alpha(r - b_0)}]^2$$

$$U(r) = \frac{1}{4} k(r^2 - b_0^2)^2$$

Quartic or expanded harmonic for PCFF

Morse potential for DREIDING

4<sup>th</sup> power harmonic for Gromos G54A7

In DREIDING force field, users are given the option to choose either harmonic or Morse potential for the bond interactions (Option **4** in the *control file*).

In CHARMM, the parameters for two-body Urey-Bradley (UB) terms, which involve 1-3 bonded atoms, are defined in the **ANGLE** directives in the *.par* file. However, UB parameters will be listed under the **bond** directive in the DL\_POLY's *FIELD* file.

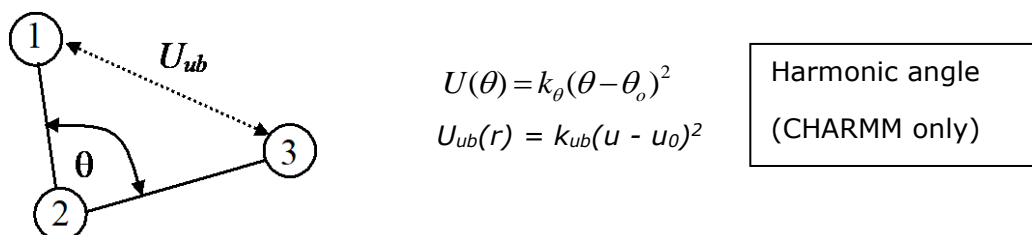
The 4<sup>th</sup> power harmonic form is not available in DL\_POLY. For G54A7, the harmonic function is used, by scaling the force constant

$$k_b = 2k^2b_0^2$$

Where  $k_b$  is the force constant for the usual harmonic function.

### 3.4 *ANGLE* and *END ANGLE* directive

Enclosed within the *ANGLE* directive is the definition of three-body (1-3) angle interactions. In most cases, harmonic angle is being used, given by the equation



Where  $k_\theta$  is the spring constant for the bond angle. For CHARMM, the two-body Urey-Bradley (UB) 1-3 interaction terms,  $U_{ub}$ , is also defined here where  $k_{ub}$  is the corresponding spring constant. If there is no Urey-Bradley term, then  $k_{ub}$  and  $u_0$  must set to zero (0.0). For other potential schemes,  $k_{ub}$  and  $u_0$  must be left out entirely.

Some potential schemes such as DREIDING and PCFF use different functional forms for angles:

$$U(\theta) = k_{\theta_1}(\theta - \theta_0)^2 + k_{\theta_2}(\theta - \theta_0)^3 + k_{\theta_3}(\theta - \theta_0)^4$$

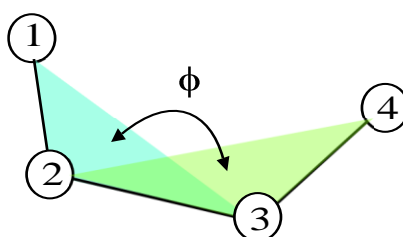
Quartic or expanded harmonic (PCFF)
Harmonic cosine in DREIDING and G54A7

$$U(\theta) = k_c(\cos\theta - \cos\theta_0)^2$$

When using DREIDING force field, users are given options to choose either harmonic or harmonic cosine functions for the angle interactions (Option **5** in the *control* file).

### 3.5 *DIHEDRAL* and *END DIHEDRAL* directives

Enclosed within the *DIHEDRAL* directive contains the four-body (1-4) dihedral interactions.



CHARMM, CVFF, G54A7

$$U(\phi) = k_\phi[1 + \cos(n\phi - \delta)]$$

AMBER	$U(\phi) = \frac{k_\phi}{f} [1 + \cos(n\phi - \delta)]$
OPLS	$U(\phi) = \frac{V_1}{2} [1 + \cos(\phi)] + \frac{V_2}{2} [1 - \cos(2\phi)] + \frac{V_3}{2} [1 + \cos(3\phi)]$
PCFF	$U(\phi) = \sum_{n=1}^3 V_n [1 - \cos(n\phi - \delta)]$
DREIDING	$U(\phi) = V [1 - \cos(n(\phi - \delta))]$

Where  $k_\phi$  and  $V$  are dihedral constants,  $n$  is the periodicity and  $\delta$  is the phase shift in unit angle degree. In AMBER, the quantity  $f$  is the scaling factor to the torsion barrier.

If an atom set contains more than one dihedral term then the multiplicity value,  $n$ , should be set to a negative number  $-n$  with the last term set as the normal positive value  $n$ . Each dihedral term must be defined in separate line of statements in the parameter file. The negative value of  $n$  is just an indication for DL\_FIELD to ensure the 1-4 interaction scale factors (see below) are only applied once for a particular dihedral atom set with more than one dihedral terms.

In addition to the cosine dihedral shown above, the Ryckaert-Belleman dihedral is also implemented for the G54A7 force field:

$$U(\phi) = A[a + b\cos(\phi) + c\cos^2(\phi) + d\cos^3(\phi) + e\cos^4(\phi) + f\cos^5(\phi)]$$

Where the prefactor  $A$  is set to 1.0.

### 3.6 The 1-4 scaling factors

Quite often, the 1-4 electrostatic scaling factor,  $\epsilon_{1-4}$ , and the 1-4 van der Waal's scaling factor,  $v_{1-4}$ , are also included and these values can be different according to the type of potential schemes. DL\_FIELD will set these scaling factors to appropriate values according to the potential scheme in the **dihedral** directive in the DL\_POLY's *FIELD* file.

In CHARMM,  $\epsilon_{1-4} = 1.0$  and  $v_{1-4} = 1.0$ . However, DL\_FIELD will define  $\epsilon_{1-4} = 1.0$  and  $v_{1-4} = 0.0$  in the *FIELD* file since all van der Waals 1-4 interactions will be explicitly defined in the **bond** directive of the *dl\_poly.FIELD* file (see **VDW** directive below for further details).

In AMBER,  $\epsilon_{1-4} = 1.0/1.2$  and  $v_{1-4} = 1.0/2.0$  by default. However, Glycam models use  $\epsilon_{1-4} = v_{1-4} = 1.0$  by default. The variation of scaling factors will be automatically taken care of by DL\_FIELD. If proteins were also present, then the values of 1.0/1.2 and 1.0/2.0 should be used instead. To change the scaling factors, the Glycam's default values can be overridden by user-defined values define in the *dl\_field.control* file. All van der Waals 1-4 interactions share the same potential parameter sets for the non-bonded van der Waals interactions.

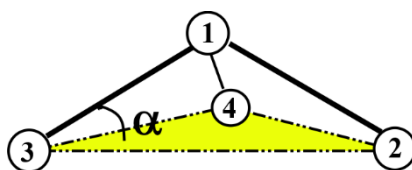
In OPLS force fields,  $\epsilon_{1-4} = 1.0/2.0$  and  $v_{1-4} = 1.0/2.0$ . All van der Waals 1-4 interactions share the same potential parameter sets for the non-bonded van der Waals interactions.

In PCFF, CVFF and DREIDING  $\epsilon_{1-4} = 1.0$  and  $v_{1-4} = 1.0$ . All van der Waals 1-4 interactions share the same potential parameter sets for the non-bonded van der Waals interactions.

In G54A7,  $\epsilon_{1-4} = 1.0$  and  $v_{1-4} = 1.0$ , However, DL\_FIELD will define  $\epsilon_{1-4} = 1.0$  and  $v_{1-4} = 0.0$  in the *dl\_poly.FIELD* file since all van der Waals 1-4 interactions will be explicitly defined in the **bond** directive in the *dl\_poly.FIELD* file.

### 3.7 IMPROPER and END IMPROPER directives

Enclosed within these directives contains all improper terms. These terms are required for molecules that contain certain molecular functional group in order to preserve a particular geometry of three atoms around a central atom. Examples of these functional groups are carbonate and carbonyls.



The improper geometry is preserved by the following expressions:

CHARMM, G54A7: 
$$U(\alpha) = k_{\alpha} (\alpha - \alpha_0)^2$$

AMBER: 
$$U(\alpha) = k_{\alpha} (1 + \cos(n\alpha - \gamma))$$

OPLS: 
$$U(\alpha) = \frac{V_1}{2} [1 + \cos(\alpha)] + \frac{V_2}{2} [1 - \cos(2\alpha)] + \frac{V_3}{2} [1 + \cos(3\alpha)]$$

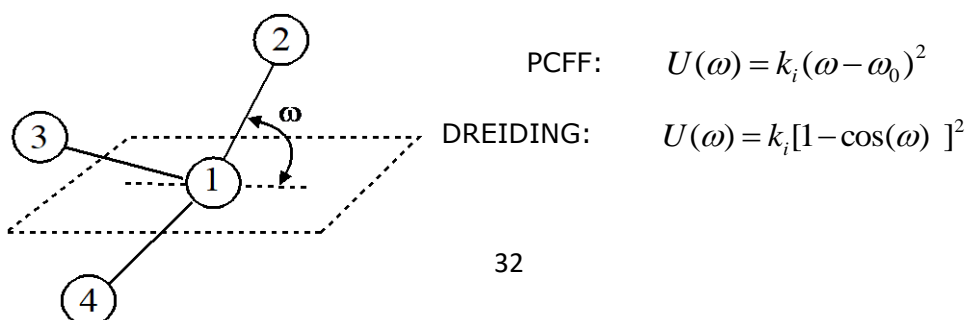
DREIDING and PCFF: similar to CHARMM. CVFF: similar to AMBER.

Where  $\alpha$  is the angle of vector 1-3 relative to the plane consists of atom 2, 3 and 4 and  $k_{\alpha}$  is the corresponding force constant. For AMBER,  $n$  is the periodicity and  $\gamma$  is the phase shift angle. Note that some potential schemes such as DREIDING and PCFF do not use improper torsion to preserve the structure. Instead, these potential schemes use inversion. However, DL\_FIELD does allow improper terms to be described for these potentials and the improper interaction definition would be the same as that of CHARMM.

DL\_FIELD will search for any improper interactions if it is defined in the structure file and will list under the **dihedral** directive in the *dl\_poly.FIELD* file.

### 3.8 INVERSION and END INVERSION directives

Enclosed within these directives contain all inversion terms. These terms are required for molecules that contain certain molecular functional group in order to preserve a particular geometry of three atoms around a central atom. Examples are nitrogen atom surrounded by three hydrogen atoms in the ammonia molecule to form a trigonal pyramid structure. The hydrogen can flip like an inverting umbrella to form another structure. The flipping can be prevented by applying an inversion term.





CHARMM, AMBER, CVFF, OPLS: similar to PCFF.

Note that the inversion angle potential is a sum of the three possible inversion angle terms. The example above shows one of the possible terms with the inversion angle  $w$  due to vector 1-2 relative to the plane consists of atoms 1,3 and 4.

Some potential schemes such as CHARMM, AMBER and OPLSAA do not use inversion torsion to preserve the structure. Instead, these potential schemes use improper functions. However, DL\_FIELD does allow inversion terms to be described for these potentials and the inversion definition would be the same as that of PCFF (harmonic function).

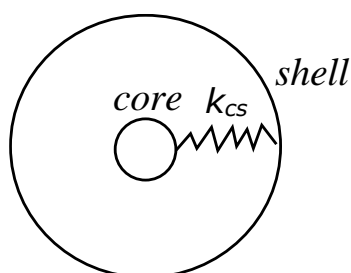
DL\_FIELD will search for any inversion interactions if it is defined in the structure file and will list under the ***inversion*** directive in the *dl\_poly.FIELD* file.

### 3.9 SHELL and END SHELL directives

Enclosed within these directives list the spring constants for all core-shell terms. The core-shell model is usually employed in inorganic materials to simulate polarisability effect of an atom such as oxygen. However, DL\_FIELD also allows core-shell model to be included in any organic force field schemes. For more details, please see [Section 11.2](#). Each core-shell set will have the following format:

ATOM_KEY (or ATOM_LABEL) for core	ATOM_KEY for shell	spring constant	Remark
-----------------------------------	--------------------	-----------------	--------

For the INORGANIC force field, ATOM\_KEYS must be used for both core and shell components. For the ORGANIC force field, an ATOM\_LABEL can be used for the core component and the shell component must always be defined as the [self-CONNECT](#) type.



Schematic diagram showing core-shell component (not to scale) of an atom.

DL\_FIELD considers collectively the core and shell components as a single entity of an atom. Both components are connected to a harmonic spring with a constant  $k_{cs}$ , to mimic the polarisability effect of an atom.

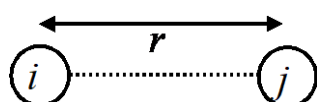
Usually, the net charge of a core-shell atom consists of partial charges from the core and shell components, respectively. For Coulombic calculations, all possible combinations of core and shell charges will be considered, except for the core and the shell belong to a same atom. For vdw calculations, core-core interactions are ignored (assume to be zero) since the 'chemistry' should only occur at shell-component of an atom.

A large proportion of the mass of a core-shell atom is assigned to the core-component. The mass of a shell can be either zero (static shell) or a fraction of the total mass to

permit a dynamic description (adiabatic shell). For more information about the types of shells, please consult the DL\_POLY user manual.

### 3.10 VDW and END VDW directives

Enclosed within these directives define the non-bonded Van-der-Waals (vdw) interactions between atom  $i$  and  $j$ . Except for PCFF, all potential schemes use the Lennard-Jones 12-6 function.



$$V(r_{ij}) = \epsilon \left[ \left( \frac{R}{r_{ij}} \right)^{12} - 2 \left( \frac{R}{r_{ij}} \right)^6 \right]$$

Where  $\epsilon$  and  $R$  are the energy and equilibrium minimum distance terms between two atoms of type  $i$  and  $j$ . If the atoms are of different type ( $i \neq j$ ), then the following mixing rules would be applied, depending on the FF schemes:

For CHARMM and AMBER FF, **half** equilibrium distances are expressed in the data files.

$$R = R_i + R_j \quad \epsilon = \sqrt{\epsilon_i \epsilon_j} \quad (\text{For CHARMM and AMBER})$$

For DREIDING,  $R$  is shown as the equilibrium minimum distance of diatomic  $i$ - $i$ . The mixing rules for atom  $i$ - $j$  of different types are therefore given as:

$$R = \frac{R_i + R_j}{2} \quad \epsilon = \sqrt{\epsilon_i \epsilon_j} \quad (\text{For DREIDING})$$

In CHARMM, CHARMM19 and G54A7, in addition to intermolecular vdw interactions, some atom pairs can have other sets of Lennard-Jones parameters for the *intramolecular* 1-4 interactions. While the intermolecular vdw interactions will be defined under the **vdw** directive in the *dl\_poly.FIELD* file, all intra 1-4 vdw interactions will be defined under the **bond** directive in the *dl\_poly.FIELD* file as excluded atom lists. If the vdw 1-4 parameters are not explicitly defined (set to 0.0 in the *.par* file), then the intermolecular vdw parameters will be used instead.

In OPLS, vdw interactions are usually described in the equivalent 12-6 form of

$$V(r_{ij}) = \epsilon \left[ \left( \frac{\sigma}{r_{ij}} \right)^{12} - \left( \frac{\sigma}{r_{ij}} \right)^6 \right] \quad (\text{OPLS})$$

Where  $\sigma$  is the steric parameter and geometric rules are used to obtain vdw parameters between atom  $i$  and  $j$ :

$$\sigma = \sqrt{\sigma_i \sigma_j} \quad \epsilon = \sqrt{\epsilon_i \epsilon_j} \quad (\text{OPLS and CVFF})$$

In the case of PCFF and COMPASS, the Lennard-Jones 9-3 form is used:

$$V(r_{ij}) = \varepsilon \left[ 2 \left( \frac{R}{r_{ij}} \right)^9 - 3 \left( \frac{R}{r_{ij}} \right)^6 \right] \quad (\text{PCFF, COMPASS})$$

and use the following mixing rules (6<sup>th</sup> order combination rule) for atom  $i$ - $j$  interaction:

$$R = \left[ \frac{(R_i^6 + R_j^6)}{2} \right]^{\frac{1}{6}} \quad \varepsilon = 2\sqrt{\varepsilon_i \varepsilon_j} \left( \frac{R_i^3 R_j^3}{R_i^6 + R_j^6} \right)$$

For G54A7, an equivalent, simplified LJ 12-6 version is used:

$$V(r_{ij}) = \frac{A_{ij}}{r_{ij}^{12}} - \frac{B_{ij}}{r_{ij}^6} \quad (\text{G54A7})$$

with geometric mixing rules to obtain parameters for the atom  $i$ - $j$  interactions:

$$A_{ij} = \sqrt{A_i A_j} \quad B_{ij} = \sqrt{B_i B_j} \quad (\text{G54A7})$$

When the option to calculate energy is switched on, no VDW energy will be calculated for any atom pair distance greater than the cutoff value specified. There is no long-range correction and therefore the energy values obtained are for references only.

The quantity  $v_{1-4}$  is the 1-4 intra-vdw scaling factor. In CHARMM, CHARMM19, PCFF, CVFF, G54A7 and DREIDING, this is 1.0. For AMBER and OPLS, this is 1.0/2.0. However, AMBER's Glycam model sets  $v_{1-4} = 1.0$ . Note that, for some force fields such as CHARMM and G54A7, the  $v_{1-4}$  value is switched to 0.0. This is because, the 1-4 vdw pairs are explicitly defined, which can have different sets of vdw parameters than those of non-bonded ones.

### 3.10.1 Lennard-Jones Mixing Rules in Multiple Potential Systems

If more than one force field schemes are specified (the [multiple potentials](#) scheme), user can specify the mixing equation scheme independently to derive the  $\varepsilon$  and  $\sigma$  for atom pairs  $i$  and  $j$  based on some type of equations expressed in terms of the vdw parameters for pure components  $ii$  and  $jj$ .

The available vdw mixing schemes are shown below:

Mixing rule no	Scheme name	Energy, $\varepsilon_{ij}$	Steric, $\sigma_{ij}$
1	Standard geometric	$\sqrt{\varepsilon_{ii} \varepsilon_{jj}}$	$\sqrt{\sigma_{ii} \sigma_{jj}}$
2	Standard arithmetic	$\frac{\varepsilon_{ii} + \varepsilon_{jj}}{2}$	$\frac{\sigma_{ii} + \sigma_{jj}}{2}$
3	Fender-Halsey	$\frac{2\varepsilon_{ii}\varepsilon_{jj}}{\varepsilon_{ii} + \varepsilon_{jj}}$	$\frac{\sigma_{ii} + \sigma_{jj}}{2}$

4	Halgren HHG	$4 \frac{\varepsilon_{ii}\varepsilon_{jj}}{(\sqrt{\varepsilon_{ii}} + \sqrt{\varepsilon_{jj}})^2}$	$\frac{\sigma_{ii}^3 + \sigma_{jj}^3}{\sigma_{ii}^2 + \sigma_{jj}^2}$
5	Waldman-Hagler	$2\sqrt{\varepsilon_{ii}\varepsilon_{jj}} \frac{(\sigma_{ii}\sigma_{jj})^3}{\sigma_{ii}^6 + \sigma_{jj}^6}$	$\left(\frac{\sigma_{ii}^6 + \sigma_{jj}^6}{2}\right)^{\frac{1}{6}}$
6	Slater-Kirkwood (see below)	$B_{ij} = \frac{3}{2} \frac{\alpha_i\alpha_j}{\sqrt{\frac{\alpha_i}{N_i} + \frac{\alpha_j}{N_j}}}$	$A_{ij} = \frac{1}{2} B_{ij}(w_i + w_j)^6$

Lorentz-Berthelot – specify 1 for energy, 2 for steric

Hogervorst (good hope) – specify 1 for energy, 1 for steric

### 3.10.2 Slater-Kirkwood (SK) combination

Note: SK combination rule only applicable for multiple potential system and [Option 12](#) (ATOM\_KEY display format) in DL\_FIELD control file must select to display DL\_FIELD format (DL\_F Notation). More specifically, it can be used to determine the vdw parameters between atom pairs from two different force field schemes.

The SK combination rule is particularly useful if there is no vdw parameter available in the library. The SK approach uses atomic data such as the atomic polarizability,  $\alpha$  and electron number,  $N$ , to derive the dispersive parameter,  $B$ . Consider two atoms of type  $i$  and  $j$ , by using the Slater-Kirkwood approximation, the dispersive parameter for the atom pair is given as:

$$B_{ij} = \frac{3}{2} \frac{\alpha_i\alpha_j}{\sqrt{\frac{\alpha_i}{N_i} + \frac{\alpha_j}{N_j}}}$$

Although  $N$  can simply be the number of valence electrons of the outer shells of atoms, which is the dominant contributions to the dispersive parameters, this choice is known to overestimate  $B$ . Kiselev *et. al.* [1] treated  $N$  as the complete numbers of electron. If atomic dispersive terms,  $B_{ii}$  and  $B_{jj}$  are known then the SK combination can be rewritten as

$$B_{ij} = \frac{2\alpha_i\alpha_j B_{ii} B_{jj}}{\alpha_i^2 B_{ii} + \alpha_j^2 B_{jj}}$$

where  $N_i$  and  $N_j$  are defined as the *effective* number of electrons [2].

$$N_i = \frac{16B_{ii}^2}{9\alpha_i^3}$$

The repulsive parameter,  $A$ , can be obtained from the sum of atomic radii,  $w$ . For a given atom pair  $i$  and  $j$ ,

$$A_{ij} = \frac{1}{2} B_{ij} (w_i + w_j)^6$$

In order to minimise the use of variable parameters and maximise the use of standard atomic properties, DL\_FIELD will adopt the Kiselev formalism. This leaves  $\alpha$  and  $w$  as the only adjustable parameters. DL\_FIELD will search for the data included in the *dl\_field.atom\_data* file, which contained the atomic polarisabilities, electron numbers and atomic radii data, to determine the corresponding Lennard-Jones parameters.

Most of the atomic polarizability data were extracted from the CRC Handbook [3]. For atoms within a molecule, the polarisabilities of the individual atomic constituents are less well defined. Several sources will be used with the following assumptions taken into consideration [2]: (1) the polarisabilities of atomic constituents are additive to the molecular polarisability. (2) atoms in different chemical environment can share the same polarizability value.

In the case of the atomic radii, it is assumed to be independent of the types of molecules that contain this atom. For atoms and atoms in molecules, the van der Waals radii will be used. For ionic species, the bare ionic radii will be used.

To decide the values of  $\alpha$  and  $w$ , DL\_FIELD will first look for exact match of ATOM\_KEYS (expressed in DL\_F Notation) against the atom list in the library file. If there is no match, DL\_FIELD will look for lists of default entries and, finally, a generic element (X\*) that matches with the ATOM\_KEY. For example, if there is no exact match for, say, a nitrogen atom within a molecule, the generic value for N\* will be used. The values of  $\alpha$  and  $w$  that were chosen for setting up vdw atom pairs will be shown in the *dl\_field.output* file. The *dl\_field.atom\_data* file also contains comments, quoting the sources for each entry.

If any ATOM\_KEYS cannot be matched with the data in the library, the vdw parameters involve the ATOM\_KEYS in question will be set to zero.

Finally, please note that data listed in *dl\_field.atom\_data* library file cannot be overridden by the [udff](#) file. Users would need to change values or add new entries directly in the library file.

## References

- [1] A.V. Kiselev, A.A. Lopatkin and A.A. Shulga, *Zeolites* **5**, 261 (1985).
- [2] T.A. Halgren, *J. Am. Chem. Soc.* **114**, 7827 (1992).
- [3] CRC Handbook for Chemistry and Physics, 95<sup>th</sup> Edition (2014-2015).

### 3.11 VDW\_FIX and END VDW\_FIX directives

Enclosed within these directives are lists of atom pairs with their unique sets of vdw parameters. Usually, the vdw parameters of atom pairs were obtained automatically from some mixing rules (such as the Benoit rules). However, the vdw functional form, as well as the parameters, can be changed by using the **VDW\_FIX** directive.

The syntax for using the directive are as follows (for all force field schemes)

**VDW\_FIX** *potential\_label*

```
atom_1 atom_2 func p1 p2 p3
atom_3 atom_4 func p1 p2 p3
...
END VDW_FIX
```

Where *atom\_1*, *atom\_2* and *atom\_3*, *atom\_4* are two sets of atom pairs of which the vdw parameters will be redefined. These atoms are the ATOM\_KEYS expressed in the standard symbols of a force field scheme (not in [DL F Notation](#)), shown as ATOM\_KEYS in the *.sf* files.

The value 'func' is the vdw functional form, which can be either the 12-6 Lennard-Jones, Morse or buckingham (see the [Inorganic](#) section for the available functional forms). The values p1, p2 and p3 are the parameter values of the functional forms.

The *potential\_label* is the name of a potential scheme. Usually, this would be the same as that where the **VDW\_FIX** directive is located in the *.par* library file. For example, to override the vdw parameters of a pair of atoms, *atom\_1* and *atom\_2* in the AMBER force field, the **VDW\_FIX** directive is issued in the *.par* file, or the *udff* file as follows:

```
POTENTIAL amber
UNIT kj/mol
...
...
VDW_FIX amber
C1 HO lj 5.00 10.000
...
...
END VDW_FIX
```

When AMBER force field is used and assuming the system model contains the ATOM\_KEYS C1 and OH, then instead of using the usual mixing rule (for instance, geometric rule for the  $\epsilon$  parameter) to obtain the vdw parameters for the C1-OH pair, the parameters 5.0 and 10.0 will be chosen instead, and expressed them as the lj functional form in the *dl\_poly.FIELD* file.

The **VDW\_FIX** directive can also be used for models using [multiple-potential](#) force field schemes. Example below shows the use of the directive for a bio-inorganic model.

```
POTENTIAL inorganic_binary_oxide
UNIT eV
...
...
VDW_FIX charmm22_prot
C1 HO lj 5.00 10.000
...
...
END VDW_FIX
...
...
END POTENTIAL
```

Here, the **VDW\_FIX** is located in the **POTENTIAL** inorganic\_binary\_oxide force field, with the potential label charmm22\_prot. This means that for each atom pair that is listed within the **VDW\_FIX** directive, one atom must belong to the inorganic\_binary\_oxide force field and the other atom must belong to the charmm22\_prot force field.

A more generic potential label can also be used. For example, in the case of CHARMM force field, the force field is split into various components (protein, carbohydrates, etc). Example below expresses the potential label as charmm\*, where the asterisk indicates any potential scheme begins with the label 'charmm'.

```

POTENTIAL charmm22_prot
UNIT kcal/mol
...
...
VDW_FIX charmm*
SOD OC buck 124.00 0.34 2.00
CT3 HA mors 111.00 0.01 3.00
...
END VDW_FIX

```

The above example shows the use of the **VDW\_FIX** in the multiple potential schemes, which is in fact the use of more than one CHARMM force field components in the system. One of the components must be the charmm22\_prot, where the **VDW\_FIX** directive is located. The label 'charmm\*' means that DL\_FIELD will look for any matching atom pairs if the second force field is of other CHARMM force field components.

Note that atom [equivalence](#) does not apply to the atoms listed in **VDW\_FIX**. In other words, DL\_FIELD only matches exactly the atoms as shown within the **VDW\_FIX** directives.

### 3.12 Coulombic Energy

The long-range Coulombic energy takes the charge parameters on the atoms. The charges are not listed in .par files. Atomic charge values are usually defined in the [MOLECULE](#) templates in .sf files.

In the case of PCFF, CVFF, and OPLS\_2005, if the charge is not defined in the MOLECULE definition, then charges will be obtained from the special bond increments files (bci) listed in the lib/ directory. DL\_FIELD will determine the total charge on an atom by summing the partial charge contributions from all neighbouring atoms that are directly linked to the atom.

The Coulombic energy takes the following functional form:

$$U(r_{ij}) = k_e \frac{q_i q_j}{|r_{ij}|} \epsilon_{1-4} \quad k_e = \frac{1}{4\pi \epsilon_0}$$

Where  $q_i$  and  $q_j$  are the charges of the ATOM  $i$  and ATOM  $j$ . The quantity  $k_e$  is the Coulombic constant and the exact value is dependent on value definitions for  $\pi$  and the electric constant  $\epsilon_0$ .

The quantity  $\epsilon_{1-4}$  is the 1-4 scaling factor which is included for intra 1-4 Coulombic interactions. In CHARMM, PCFF and DREIDING, this is 1.0. For CHARMM19, this is 0.4. For AMBER, this is 1/1.2. For OPLSAA, this is 1/2.0. However, the AMBER's Glycam model sets  $\epsilon_{1-4} = 1.0$ .

Note that the Coulombic energy calculations in DL\_FIELD is only an approximation that do not include ATOM pairs beyond the cutoff specified. No periodic image or long-range correction such as Ewald summation will be considered. The final value obtained must therefore be treated as a reference only.

### 3.13 *THREE-BODY* and *END THREE-BODY* directives

The three-body interactions are different from the three-body angular (see [Section 3.4](#)) interactions, where the latter describes the bonded 1-3 interactions. For three-body interactions, the atoms are not bonded.

These types of interactions are usually used in inorganic materials such as zeolites and glassy materials. An example is shown in the *DLPOLY\_INORGANIC\_glass.par* file.

### 3.14 *EQUIVALENCE* and *END EQUIVALENCE* directives

Enclosed within these directives contain lists of definitions of equivalent ATOM\_KEYS for a given potential scheme. This feature is especially useful if one were to define a new ATOM\_KEY that shares some common behaviour with the other ATOM\_KEYS. Quite often, the new ATOM\_KEY may share similar potential parameters of other ATOM\_KEYS that are already defined in the parameter file. Instead of redefining a whole new set of parameters for the new ATOM\_KEY, an ***EQUIVALENCE*** directive can be issued for the new ATOM\_KEY. This directive informs DL\_FIELD that, instead of looking for the new ATOM\_KEY, the equivalent ATOM\_KEYS should be used, when searching for the potential parameters that correspond to interactions that contain the new ATOM\_KEY.

Different equivalent ATOM\_KEYS can be assigned for different types of interactions using *interaction components*. The various *interaction components* are shown in the table as follows:

<b>Interaction type</b>	<b><i>Interaction components</i></b>
Bond interactions	<b><i>bond_</i></b>
Angle interaction	<b><i>angle_</i></b>
Dihedral interactions	<b><i>dihedral_</i></b>
Inversion	<b><i>inv_</i></b>
Improper	<b><i>imp_</i></b>
Shell	<b><i>shell_</i></b>
Van-der-Waals	<b><i>vdw_</i></b>
Three-body interactions	<b><i>tbp_</i></b>

The format to define an equivalent atom is as follows:

```
new_atom_key > component1_ATOM_KEY1 component2_ATOM_KEY2 ...
```

For instance, in DREIDING force field, a generic sp<sup>3</sup> hybridised oxygen atom is defined with an ATOM\_KEY *O\_3* (see *DLPOLY\_DREIDING.sf* file). Suppose a user wish to define a new oxygen atom exclusively for molecules containing the -OH alcohol group and assign



a new ATOM\_KEY *OA*. The new key will share the same potential interactions as that of *O\_3*, except the vdw interaction which has a different set of parameters.

The new atom can be defined in the user-define force field (*udff*) file as follows:

```
POTENTIAL DREIDING
ATOM_TYPE
...
...
O_alcohol OA 15.99994 New atom for alcohol -OH only
...
...
END ATOM_TYPE
```

Instead of duplicating all interactions involving *O\_3* for *OA* in the file, the following **EQUIVALENCE** directive can be issued in a *udff* file:

```
EQUIVALENCE
...
...
OA > bond_O_3 angle_O_3 dihedral_O_3 inv_O_3
...
...
END EQUIVALENCE

VDW
...
...
OA 3.5000 0.0957 * New vdw value for OA.
...
END VDW
```

The **EQUIVALENCE** statement shown in the example:

```
OA > bond_O_3 angle_O_3 dihedral_O_3 inv_O_3
```

means any bond, angle, dihedral and inversion components that contain *OA* will be treated as *O\_3*.

For instance, the angle *H-OA-C2* is equivalent to *H-O\_3-C2*, DL\_FIELD will search for the potential parameters correspond to the latter set of angles. Since no equivalence is set for the vdw interactions, DL\_FIELD will therefore look for vdw parameters correspond to *OA*.

DL\_FIELD also allows multiple equivalence definitions such as shown below:

```
OA > bond_O_3 angle_C_2 ...
```

Which means the *OA atom key* is equivalent to *O\_3* for bond interactions but is equivalent to *C\_2* for angle interactions. For instance, the bond *OA - H* is equivalent to *O\_3 - H*, while the angle *H - OA - C\_2* is equivalent to *H - C\_2 - C\_2*. All other interactions (such as vdw and dihedral) involving *OA*, must be explicitly defined.

Once an equivalent ATOM\_KEY is defined for a given interaction, DL\_FIELD will look for data containing the equivalent ATOM\_KEY, ignoring potential parameters involving the original ATOM\_KEY even if they were included in the file.

Note that, the equivalence mentioned so far is also called the *first-tier* equivalence setup. During the conversion processes, DL\_FIELD will look for potential parameters based on the ATOM\_KEYS with the equivalence atom if applicable. If the program fails to locate the parameters, then DL\_FIELD will determine the second set of equivalence atoms, if applicable, and using the modified set of atoms to look for the parameters the second time. This is shown below.

### 3.15 Second-tier Equivalence

This essentially work the same way as that of **EQUIVALENCE** directive mentioned above and allows user to define two different sets of equivalence atoms. When DL\_FIELD fails to find a suitable parameter sets during the first search attempt, it will make a second attempt by using an alternative (second) set of **EQUIVALENCE** atoms, if this is defined. DL\_FIELD will only then report an error if the second attempt also fails to locate a suitable set of parameters. If DL\_FIELD able to locate the parameters in the first attempt, then the second-tier equivalence set will be ignored.

The second-tier equivalence set must be defined within the **EQUIVALENCE** and **END EQUIVALENCE** directives and distinguish from the *first-tier* equivalence set by having the '2' suffix on the interaction components.

Example uses of second-tier equivalence can be found in the OPLS2005 parameter file. For example, consider the equivalence statements below, showing several possible equivalence scenarios:

```
EQUIVALENCE
CDX  > dihedral_CD
CML  > angle_CM imp_CM vdw_CM angle2_CM imp2_CM
C5BB > angle2_CA dihedral2_CA imp2_CA
CTNC > bond_CT angle_CT imp_CT vdw_CT bond2_CT angle2_CT imp2_CT dihedral2_CT
END EQUIVALENCE
```

First, the *dihedral* component for ATOM\_KEY CDX is made equivalent to CD and there is no second-tier equivalence being defined. This means that, during the first search attempt, DL\_FIELD will look for the equivalent dihedral parameter sets involving CD, instead of CDX. If this fails, DL\_FIELD will make a second attempt, looking for the dihedral parameters involving the CDX ATOM\_KEY itself.

In the second equivalence statement, the CML ATOM\_KEY contains the first-tier equivalence to CM ATOM\_KEY for the *angle*, *imp* and *vdw* components. The statement also defines the second-tier equivalence to CM ATOM\_KEY, but only for the *angle* and *imp* components. This means that, when DL\_FIELD make the second search attempts, the equivalence only applies to *angle* and *imp*, but not the *vdw*.

The third equivalence statement only defines second-tier equivalence set for C5BB ATOM\_KEY. This means that, during the first search attempt, DL\_FIELD will look for interaction components involving the original C5BB key itself. When this fails, DL\_FIELD will only then use the equivalent atom CA in the second attempt, for *angle*, *dihedral* and *imp* components.

The fourth equivalence statement stipulates that CTNC is made equivalent to CT in both the first and second search attempts. The exception being the *dihedral* component, which set equivalence to CT only in the second search attempt.

## 4 Control File

The *control* file is read by DL\_FIELD to determine how the *dl\_poly.FIELD* and *dl\_poly.CONFIG* files would be defined. All the available control settings and the number of options available for each setting are shown in the control file.

A typical *control* file is shown below:

```

This is the title line. Put what you want. Reads only 80 columns
1 op1s2005      * Type of force field require.
2 kcal/mol     * Energy unit: kcal/mol, kJ/mol, eV or default
3 normal       * Conversion criteria (strict, normal, loose)
4 1            * Bond type (0=default, 1=harmonic, 2=Morse)
5 2            * Angle type (0=default, 1=harmonic, 2=harmonic cos)
6 none        * Include user-defined information. Put 'none' or a .udff filename
7 0           * Verbosity mode: 1 = on, 0 = off
8 example.pdb * Filename for the user's atomic configuration.
9 None        * Output file in PDB. Put 'none' if not needed.
10 0 1.05 g/cm^3 1.9 * Solution Maker: on/off, density, unit, cutoff)
11 0          * Optimise FIELD output size, if possible? 1=yes 2=no
12 2         * Atom display: 1 = DL_FIELD format. 2 = Standard format
13 1         * Vdw display format: 1 = 12-6 format 2 = LJ format
14 Default   * Epsilon mixing rule (organic FF only) : 1 = geometric 2 = arithmetic or default
15 Default   * Sigma mixing rule (organic FF only) : 1 = geometric 2 = arithmetic or default
16 1         * Epsilon mixing rule (inorganic FF only) : 1 = geometric 2 = arithmetic
17 2         * Sigma mixing rule (inorganic FF only) : 1 = geometric 2 = arithmetic
18 1         * Epsilon mixing rule (between different FF) : 1 = geometric 2 = arithmetic or default
19 1         * Sigma mixing rule (between different FF) : 1 = geometric 2 = arithmetic or default
20 1         * Display additional info. for protein 1=Yes 0=No
21 1         * Freeze atoms? 1 = Yes (see below) 0 = No
22 0         * Tether atoms? 1 = Yes (see below) 0 = No
23 0         * Constrain bonds? 1 = Yes (see below) 0 = No
24 0         * Apply rigid body? 1 = Yes (see below) 0 = No
25 auto      * Periodic condition ? 0=no, other number = type of box (see below)
26 50.00 0.0 0.0 * Cell vector a (x, y, z)
    0.00 50.0 0.0 * Cell vector b (x, y, z)
    0.00 0.0 50.0 * Cell vector c (x, y, z)
27 default    * 1-4 scaling for coulombic (put default or x for scaling=x)
28 default    * 1-4 scaling for vdw (put default or x for scaling=x)
29 0 300      * Include velocity? 1=yes, 0=no and scaling temperature.
30 1         * Position solute at origin 1 = yes, 0 = no
31 tip3p_e 1.7 default * Solvate model? none or specify solvent (see below) and distance criteria.
32 0 20.0     * Add counter ions? 1=yes, 0=no, minimum distance from solute
33 0         * MM energy calculation. 1=Yes, 0=No
34 10.0      * Cut off for electrostatic energy calculation (angstrom)
35 10.0      * Cut off for vdw energy calculation (angstrom)

```

```

#####
FREEZE A all_backbone
FREEZE B all_backbone

TETHER C all_backbone 2390.0
CONSTRAIN F H-bond

RIGID E

#####

```

The order of the control settings is fixed and must not be removed nor rearranged. Do not remove the comments alongside the control settings.

The first line is the title line up to 80 columns in length. The numbers in **red** are the option numbers. They are shown only for illustration purposes in this manual and do not play any role in influencing the outcome of the results output.

The input options are described in more details as follows:

- 1.** Force Field (FF) Scheme. This determines the conversion scheme and the corresponding type of potential parameters for the molecular model. The available choices are shown in the [previous page](#).
- 2.** Energy unit. This is the unit that will be used for the FIELD file. If this unit is different from what is defined in the *.par* file or the *udff* file of the potential scheme, DL\_FIELD will do internal unit conversions and change the parameter values accordingly. The available options are as follows: *kcal/mol*, *kJ/mol*, *eV* and *K*.
- 3.** Conversion criteria. DL\_FIELD determines the bond connections of a molecule based on atomic distance criteria. A bond is identified if two atoms are within a certain minimum distance defined in the header file *dl\_field.h*. User can control the extent of this distance criteria, where the 'strict' option means the minimum distance is reduced by  $-0.01 \text{ \AA}$ . The 'loose' option will increase the distance criteria by  $0.01 \text{ \AA}$ . The 'normal' is the default option and the pre-set minimum distances set in the *dl\_field.h* will remain unchanged.
- 4.** Bond type. If DREIDING potential is selected, users must choose either harmonic bond (value = 1) or Morse bond (value = 2). All other potential schemes will automatically revert to value 0 (default bond type).
- 5.** Angle type. If DREIDING potential is selected, users must choose either harmonic angle (value = 1) or harmonic cos angle (value = 2). All other potential schemes will automatically revert to value 0 (default angle type).
- 6.** Include user-defined information. Once this is activated, DL\_FIELD will read the file with the *.udff* extension specified by the user.
- 7.** Verbosity mode. This setting determines the amount of information to be displayed in *dl\_field.output* file. When this is switched on (1), DL\_FIELD will display detailed conversion process, including the converted atom types.
- 8.** Input filename for the user's atomic configuration. Currently, DL\_FIELD only recognises the configuration file in strict PDB, *xyz* and *mol2* formats.
- 9.** Output file in PDB format. Atom sequence will be rearranged, and atom labels rewritten according to how they are defined in the MOLECULEs. In other words, the atom sequence will be the same as the *dl\_poly.CONFIG* and *dl\_poly.FIELD* files produced by DL\_FIELD. The output file can be used as a PDB model template, along with the HISTORY files produced by the subsequent DL\_POLY runs, in DL\_ANALYSER.

If the output file is not needed, put 'none'. Otherwise, DL\_FIELD will write the PDB structure in that name.

- 10.** Solution Maker. Options to setup disordered system. See [Section 8](#) for more details.
- 11.** FIELD file optimisation. This feature is useful for large molecular models that contain a large number of similar molecules that have to split into different Molecular Groups.

For example, water molecules are usually split into several Molecular Groups in PDB files due to large number of the molecules. This is so done because the maximum residue number permitted is 9999. Turning this feature on will enable DL\_FIELD to lump all these water molecules and define under a single Molecular Group in the *dl\_poly.FIELD* file.

- 12.** ATOM\_KEY display format. This settings allow user to select the display convention of the ATOM\_KEYS in *dl\_poly.CONFIG* and *dl\_poly.FIELD* files. This setting can take two options: Internally defined DL\_FIELD format or the standard format according to the type of potential scheme selected. In the case of OPLS2005, CVFF and PCFF, the DL\_FIELD format is expressed in the DL\_F Notation, which is obtained *in-situ* from the corresponding ATOM\_TYPES.
- 13.** Vdw display format. Except for PCFF and COMPASS, all potential schemes use 12-6 Lennard-Jones for the vdw interactions.

$$V(r_{ij}) = \epsilon \left[ \left( \frac{R}{r_{ij}} \right)^{12} - 2 \left( \frac{R}{r_{ij}} \right)^6 \right]$$

Where  $R$  is the distance at which  $V$  is minimum and is related to the steric parameter,  $\sigma$ , as

$$R = \sqrt[6]{2}\sigma$$

In DL\_POLY, the Lennard-Jones parameters can be displayed in two alternative formats: the 12-6 form and the 'LJ' form with the corresponding equation as shown below:

$$V(r_{ij}) = \frac{A}{r_{ij}^{12}} - \frac{B}{r_{ij}^6} \qquad V(r_{ij}) = \epsilon \left[ \left( \frac{\sigma}{r_{ij}} \right)^{12} - \left( \frac{\sigma}{r_{ij}} \right)^6 \right]$$

The 12-6 form The LJ form

Therefore, the display format can be changed from one to the other using the following relationships:

$$A = 4\epsilon\sigma^{12} \qquad B = 4\epsilon\sigma^6$$

The A and B parameters will be shown if the vdw display option is set to 1. Otherwise,  $\epsilon$  and  $\sigma$  are shown when the vdw display option is set to 2. This option does not apply to the PCFF scheme.

Note that in certain older versions of DL\_POLY, such as version 2.20 or before, will give an error message of 'unrecognised directives'. This may be due to older DL\_POLY 2 versions not able to recognise the expression of 'LJ' form. If that is the case, use 12-6 form instead. Better still, please use DL\_POLY\_4 or later!

- 14.** Apply to ORGANIC force fields only. Specify mixing rule for the parameter epsilon ( $\epsilon$ , potential well-depth) for LJ12-6 between two atoms. This can be either geometric or arithmetic. The recommended setting is 'default' which means DL\_FIELD will automatically set the correct rule depending on the force field scheme.
- 15.** For ORGANIC force fields only. Specify mixing rule for the parameter sigma ( $\sigma$ , steric parameter) for LJ12-6 between two atoms. This can be either geometric or arithmetic. The recommended setting is 'default' which means DL\_FIELD will automatically set the correct rule depending on the force field scheme.
- 16.** For INORGANIC force fields only. Specify mixing rule for the parameter epsilon ( $\epsilon$ , potential well-depth) for LJ12-6 between two atoms. This can be either geometric or arithmetic.
- 17.** For INORGANIC force fields only. Specify mixing rule for the parameter sigma ( $\sigma$ , steric parameter) for LJ12-6 between two atoms. This can be either geometric or arithmetic.
- 18.** Applicable to multiple potential systems only. Specify the [mixing rule](#) for the parameter epsilon ( $\epsilon$ , potential well-depth) for LJ12-6 between two atoms from two different potential schemes. Usually, DL\_FIELD will not determine the mixed parameters and leave blanks if the vdw atom pair involves one atom from an ORGANIC force field and the other from an INORGANIC force field. The vdw parameters for INORGANIC force fields are defined explicitly for a pair of atoms, A-B. However, if one of the atoms is a generic, A-X, (see *DLPOLY\_INORGANIC\_clay.par* file) then DL\_FIELD will carry out the calculation to derive the mixed parameter for the atom pair. Alternatively, [VDW FIX directive](#) can be used to explicitly define both the functional forms and the vdw parameters for any pairs of atoms.
- 19.** For multiple potential systems only. Specify the [mixing rule](#) for the parameter sigma ( $\sigma$ , steric parameter) for LJ12-6 between two atoms from two different potential schemes. Usually, DL\_FIELD will not determine the mixed parameters and leave blanks if the vdw atom pair involves one atom from an ORGANIC force field and the other from an INORGANIC force field. The vdw parameters for INORGANIC force fields are defined explicitly for a pair of atoms, A-B. However, if one of the atoms is a generic, A-X, (see *DLPOLY\_INORGANIC\_clay.par* file) then DL\_FIELD will carry out the calculation to derive the mixed parameter for the atom pair. Alternatively, [VDW FIX directive](#) can be used to explicitly define both the functional forms and the vdw parameters for a pair of atoms.
- 20.** Display additional information. This setting allows the option to display additional information in a PDB file in *dl\_poly.CONFIG* and *dl\_poly.FIELD* files. Information that can display are the amino acid residue sequence obtained from the user's protein PDB file.
- 21.** Freeze atoms switch. This option, when switched on (1), will read the [**FREEZE**] directives to decide which atoms to be frozen. This directive can appear anywhere in the *dl\_field.control* file after the option settings.

The [**FREEZE**] directive takes the following data in the following order:

```
FREEZE           Molecular_Group           atom_filter
```

The *Molecular\_Group* takes the label of the protein chain ID or protein molecular label. Only one [**FREEZE**] directive is allowed for each Molecular Group.

The *atom\_filter* key determines which atoms to be frozen within a Molecular Group. The available keys are shown in the table below.

<b>Atom_filter key</b>	<b>Selection effects</b>
-----	
<b>All_backbone</b>	All backbone atoms of amino acids ( $\alpha$ -carbon, amide carbon and nitrogen)
<b>c-alpha</b>	( $\alpha$ -carbon on in amino acids)
<b>all</b>	All atoms in a Molecular Group
<b>User-specified atom key</b>	only affect a particular type of atoms

- 22.** Tether atoms switch. This option, when switched on (1), will read [**TETHER**] directives to decide which atoms to be tethered. The current version of DL\_FIELD only allows harmonic as the constraint potential form for a tethered atom. This directive can appear anywhere in the *dl\_field.control* file after the option settings.

The [**TETHER**] directive takes the following data in the following order:

*TETHER*                      *Molecular\_Group*                      *atom\_filter*    *spring\_constant*

The *Molecular\_Group* takes the label of the protein chain ID or protein molecular label. Only one [**TETHER**] directive is allowed for each Molecular Group.

The *atom\_filter* key determines which atoms to be tethered within a Molecular Group. The available keys are shown in the table above. The *spring\_constant* takes a value with the same unit as defined in the potential energy scheme.

Note that the *atom\_filter* keys **all\_backbone** and **c\_alpha** are only applicable to molecules containing amino acids such as protein molecules. Molecules that do not contain amino acid will not be affected even if it contains similar types of atoms.

While DL\_FIELD allows both [**FREEZE**] and [**TETHER**] directives to be defined at the same time for a given molecular group, it is up to the user to ensure both directives do not apply to same type of atoms. The example *control* file switched on the setting for frozen atom (Option **21**) and off for tethered atom. Consequently, the [**FREEZE**] directive will be read by DL\_FIELD, while ignoring the [**TETHER**] directive.

- 23.** Constrained bonds switch. This option, when it is switched on (1), will read [**CONSTRAIN**] directives to decide which atoms to be constrained. This option is different from the [**FREEZE**] directive. In the former case, the atom's position is fixed in space, whereas [**CONSTRAIN**] restricts the position of an atom relative to another atom. This directive is used to constrain bond distances, for instance, to reduce the degrees of freedom and increase the simulation time step. When



running simulations, the **shake** directive in the DL\_POLY's *CONTROL* file must be used.

The [**CONSTRAIN**] directive reads the parameters in the following order:

*CONSTRAIN*            *Molecular\_Group*            *atom\_filter*

The *molecular\_group* takes the label of the protein chain ID or protein molecular label. Only one [**CONSTRAIN**] directive is allowed for each molecular group. The *atom\_filter* key determines which bonds were to be constrained. The available options are shown in the table below.

<b>Atom_filter key</b>	<b>Selection effects</b>
<b>h-bond</b>	only affect bonds that contained H atoms
<b>rigid_water</b>	(For water molecules only). Constrain structure become a rigid-like body as a whole
<b>all</b>	All atoms in a Molecular Group

Note that when applying [**CONSTRAIN**] directives with *atom\_filter* keys as **h-bond** or **all** to water models, the two O-H bonds of a water molecule will be constrained BUT not the angle (H-O-H). The water molecules are still somewhat flexible.

To make a rigid water molecule, use **rigid\_water** *atom\_filter* key. This is a special command applicable to water models only. Using this command, the H-H, in addition to O-H bonds, will be constrained. The **rigid\_water** *atom\_filter* key must always apply to some water models such as the original TIP3P model because there is no LJ parameter on the hydrogen atom and no force constant on the H-O-H angle. Failure to do so will result in wrong water structure and the simulation may crash.

[Chapter 8](#) lists all the available water models.

Note: Do not confuse **rigid\_water** *atom\_filter* key with rigid body definition for water (using the [**RIGID**] directive. See Option **19** below). In the former case, constrain methods such as SHAKE algorithm are used to maintain the bond lengths in an iterative manner. For this reason, bond constrain methods are usually computationally slower than rigid body calculations. If your water model is not equilibrated, apply **rigid\_water** to the water model in the first instance, setting SHAKE tolerance limit to  $10^{-5}$  or below. Once the model is equilibrated, change the water model to rigid body.

- 24.** Rigid body switch. This option when it is switched on will read [**RIGID**] directives in the *control* file to decide which Molecular Groups where rigid bodies should be applied and defined in the *dl\_poly.FIELD* file. For example, the following [**RIGID**] directives state that rigid bodies will be applied to molecules belong to Molecular Groups Grp\_A and Grp\_C only.

```

...
...
#####
FREEZE Grp_D all_backbone

CONSTRAIN Grp_B h_bond

RIGID Grp_A
RIGID Grp_C

#####

```

Do not confuse with the [**RIGID**] directives defined within a MOLECULE. In this case, the [**RIGID**] directives specify how a [rigid body](#) should be defined *within* a MOLECULE. Note that, in the above example, rigid bodies only assign to MOLECULEs belong to either Grp\_A or Grp\_C but not to any other MOLECULEs belong to other molecular groups, even though [**RIGID**] directives are defined in those MOLECULEs. Similarly, no rigid body will be applied if DL\_FIELD cannot locate any [**RIGID**] directive in MOLECULEs belong to Grp\_A or Grp\_C.

- 25.** Periodic boundary condition. Defines the type of periodic boundary conditions for the user model. This is essential for models that contain molecules that wrap around the periodic box. DL\_FIELD will use this information to use the appropriate minimum image convention to determine bond connections and energy calculations.

This option takes the following values: 0 (no periodic boundary), 1 (cubic box), 2 (orthorhombic), 3 (parallelepiped) and 6 (slab). These values are the same as that of *imcon* value as described in the DL\_POLY manual.

If the value is set to 0, then DL\_FIELD will ignore the cell vectors define below or cell parameters define in the user's configuration file. Otherwise, DL\_FIELD will read the cell vectors below to determine the boundary conditions.

If the value is set to 'auto', DL\_FIELD will automatically determine the simulation box dimensions and assign the appropriate *imcon* value for the DL\_POLY's CONFIG file. In this case, DL\_FIELD will ignore the cell vectors define below. Instead, it will look for the unit cell parameters (from the CRYST statement) in the configuration file and convert them to the corresponding cell vectors. If this information is not available, then DL\_FIELD will return an error.

- 26.** Cell vectors. Determine simulation box size and shape, centred at (0,0,0). If a periodic boundary condition is defined in Option **25**, then these cell vectors will be used to determine how the boundary condition is applied. DL\_FIELD will insert these values into *dl\_poly.CONFIG* file.

The cell vectors consist of three sets of numbers, referring to vectors **a**, **b** and **c**:

$$\mathbf{a} = ix + jy + kz, \mathbf{b} = px + qy + rz, \mathbf{c} = ux + vy + wz$$

where *i*, *j*, *k*, etc, define the simulation box dimension and size. DL\_FIELD can inter-convert between cell parameters and cell vectors. For instance, if Option **25** is switched to 'auto', DL\_FIELD will look cell parameters in the user configuration

file such as the PDB file and convert this to the corresponding cell vectors for *dl\_field.CONFIG* file.

- 27.** 1-4 scaling factor for coulombic interaction. User can redefine the scaling factor and override the default value for all potential schemes. To retain the recommended values for a potential scheme, just put 'default'. Any other number will be used as the scaling factor instead. For example, if the value is *b*, then this would be the new scaling factor and DL\_POLY will scale the 1-4 intra-interactions as:  $V(1-4) \times b$ .

[Section 3.11](#) describes the default scaling factors for ORGANIC force fields.

- 28.** 1-4 scaling factor for vdw interaction. User can redefine the scaling factor and override the default value for all potential schemes. To retain the recommended values for a particular potential scheme, just put 'default'. Any other number will be used as the scaling factor instead. For example, if the value is *b*, then this would be the new scaling factor and DL\_POLY will scale the 1-4 intra-interactions as:  $V(1-4) \times b$ .

[Section 3.5](#) describes the default 1-4 scaling factors for ORGANIC force fields.

- 29.** Assign initial Gaussian random velocities, scaled to a temperature, to every ATOM in *dl\_poly.CONFIG* file. The random number generator is seeded with system time. Therefore, different velocities are generated each time when DL\_FIELD is run.
- 30.** Option to translate user's configuration such that the centre of gravity of the whole system is centred at the origin (0, 0, 0).
- 31.** Solvate model. This option instructs DL\_FIELD to add solvent molecules to the user's configuration (solute). The number of solvent molecules added will depend on the dimension of the simulation box size specified in Options **25** and **26**, which must be either a cubic (1) or an orthorhombic (2).

Addition of solvent molecules involves the use of appropriate pre-equilibrated solvent template box located in the */solvent* directory. The minimum cell size must not be less than 20 Å and there is no maximum size limit. Ideally, the simulation box size should be in the multiple of 20 Å. Otherwise, the solvent template box will be truncated at the edge of the simulation box.

If Option **30** is switched on, then the whole user's configuration is re-positioned before the solvation is taken place. Distance criteria sets the limit within which no solvent molecule from the solute will be located.

DL\_FIELD will skip the solvation step if the keyword 'none' is specified. Otherwise, DL\_FIELD will solvate the user's configuration based on the type of solvent specified. The range of solvents available are listed in the file *solvent\_list* located in the */solvent* directory.

In addition to the type of solvents, users can also specify the FF scheme for the solvent. For instance, the example control file shows the following command:

```
tip3p_e 1.7 default
```

This means TIP3P water model for Ewald sum is used as the solvent and the water molecules must be at least 1.7 Å away from the solute and the FF model for the solvent is located in the default FF setting, which is OPLS2005, as specified in Option **1**.

If the FF scheme specified is different from Option **1**, then DL\_FIELD will automatically change to a multiple potential scenario and setup the FF model accordingly. For example, the command

```
etoh 1.7 amber16_gaff
```

instructs DL\_FIELD to solvate the system with ethanol (EtOH), using Amber GAFF as the FF model for the solvent. The vdw parameters for atoms between the solute and solvent components will be derived according to the mixing rules defined in Options **18** and **19** (for multiple potential).

- 32.** Add counter ions. If the total charge in the system is not balanced then set this option to 'on' will cause DL\_FIELD to add either chloride (charge value -1.0) or sodium ions (charge value +1.0), depending on the net charge of the system. Charge neutrality cannot be achieved if there is a partial net charge in the system.
- 33.** Carry out MM calculations within DL\_FIELD according to the chosen potential scheme. While two-, three- and four-bodies energy components can be accurate, the non-bonded vdw and Coulombic electrostatic components are not. The values can vary according to the cut off values chosen and there is no energy calculation or any correction beyond the cut off values. These energy components, and hence the total energy, are therefore recommended to be used as a reference only.

A word of warning, time taken to do calculations for large systems can be long. The calculations only involve one CPU and memory usage is kept to minimum so that it is possible to calculate energies even for very large systems on a typical PC.

- 34.** Cut off distance values, in unit Angstrom, for the electrostatic energy calculations. These options are relevant only if the MM option is switched on. For more accurate result, set these to some large values. If there is a periodic boundary condition, Option **25**, then the cut off distances must not be larger than half of the cell length.
- 35.** Cut off distance values, in unit Angstrom, for the vdw energy calculations. These options are relevant only if the MM option is switched on. For more accurate result, set these to large values. If there is a periodic boundary condition, Option **25**, then the cut off distances must not be larger than half of the cell length.

## 4.1 Running DL\_POLY Program

DL\_FIELD *control* file also contains a *DL\_POLY control* section. It instructs DL\_FIELD how to run DL\_POLY via a fork process. Note that the *DL\_POLY control* feature is only

applicable to Unix/Linux (including the Window Subsystem for Linux, WSL), or within the Cygwin environment for Window machines. In addition, a pre-compiled DL\_POLY program must also reside in the same machine.

The *DL\_POLY control* feature can carry out two independent tasks: single-point calculation and multi-tier equilibrations. The feature forms part of the integrated workflow environment within DL\_FIELD. Once DL\_FIELD has setup the force field model, it will then automatically create the necessary sets of DL\_POLY files: CONFIG (copied from *dl\_poly.CONFIG*), FIELD (copied from *dl\_poly.FIELD*) and CONTROL files (created according to the user-selected task). These DL\_POLY files will be automatically copied into the directory where DL\_POLY program is located.

Below shows a *DL\_POLY control* section.

```
***** DL_POLY control *****
1      * Run DL_POLY program
DLPOLY.Z * DL_POLY executable filename
/home/user/dl_field_4.5/output * absolute path to DL_POLY program
0      * MM calculation 1=on 0=off
0 3    * Equilibration on(1)/off(0) level (1,2 or 3)
1000   * Timestep for DL_POLY runs.
9.0    * cutoff (vdw and electrostatic)
1000   * Time limit for DL_POLY run (in seconds)
```

The correct DL\_POLY path must be specified (highlighted in **bold**). By default, the executable filename for DL\_POLY is *DLPOLY.Z*. Simulation time can be controlled by adjusting the MD time step and the non-bonded cut off value. This may be crucial, especially if the user system model is large, as the simulation is done on a local machine (rather than a HPC!).

### Single point calculation

DL\_FIELD will create a simple CONTROL file with zero time step. This means no dynamics will be carried out. Instead, DL\_POLY exits once the configuration energy of the initial system is calculated.

### Equilibration

Strictly speaking, DL\_FIELD does not carry out the normal equilibration process, per se. Rather, the CONTROL files contain sets of DL\_POLY *directives* to suppress run-away system energies and to disentangle any locked, high-energy conformations, perhaps due to poor initial configuration setup. Therefore, the equilibration feature as mentioned here is by no means a substitution to the proper equilibration processes. The final CONFIG file, which contained the relaxed structure, can then be transferred to an HPC system to carry out further equilibration processes.

Up to three levels of equilibrations can be specified. The number refer to the successive DL\_POLY runs, each with a different CONTROL file that contain directives to eventually relax the system model. Level 1 is the least restrictive process and run DL\_POLY once. Level 2 will run DL\_POLY twice with two different CONTROL files, and so on.

## 5 User-defined Force Field (*udff*)

While new force field information can be added to the standard library files, *\*.sf* and *\*.par*, such practices can become inconvenient and error-prone when user-defined models were to migrate to latest standard library files whenever a new DL\_FIELD version is released.

However, new parameters and molecular templates can be defined in the user-defined force field (*udff*) file, without having to tamper with the standard library files. Users can simply migrate *udff* files to future DL\_FIELD releases that contain the latest update of the standard library files.

There are two *udff* files included as examples, the *alcohol.udff* and the *vdw\_fix.udff*. To use these files, just insert the appropriate path and the filename in Option **6** in the *dl\_field.control* file. Only one *udff* file can be used at any one time. Users can create as many *udff* files as they like but the files created must always end with the extension *.udff*.

### 5.1 File Format

The *udff* file can be treated as a combination of both *.sf* and *.par* files. In other words, all **DIRECTIVES** from the *.sf* and *.par* files can be included in the *udff* file.

The order of a **DIRECTIVE** is not important, so long it is enclosed with the appropriate **END DIRECTIVE** statement. For instance, the potential parameters definition can be sandwiched somewhere between two **MOLECULE** definitions. Such flexibility allows user to arrange information in the file according to personal tastes.

Similar to the standard library files, a *udff* file must include the directives **POTENTIAL** *potential\_scheme* and **UNIT** *energy\_unit*. DL\_FIELD allows multiple **POTENTIAL** definitions in the *udff* file. All information belongs to the relevant force field scheme must be enclosed within the appropriate **POTENTIAL** and **END POTENTIAL** directives. If no *udff* information can be located for the force field scheme specified in the *control* file (Option **1**), DL\_FIELD will notify this to the user but **will not** treat this as an error.

### 5.2 Functionality

When an *udff* file is specified in Option **6** of the *control* file, DL\_FIELD will set up a molecular model database in the computer memory by first reading information from the *udff* file before it proceeds to read the standard library file of the selected potential scheme (Option **1**) in the *control* file.

MOLECULEs that already exist in the standard library files can be overridden by redefining them in the *udff* file. To override an existing MOLECULE, redefine it in the *udff* file with the same MOLECULE\_TYPE. For instance, consider the *alcohol.udff* file in the *Examples/* directory, the MOLECULE methanol is redefined in the *udff* file. The only changes made are the charges on some of the ATOMs (compare this with methanol defined in *DLPOLY\_CHARM22\_prot.sf*).

By switching the Verbosity mode Option **7** to 'on', DL\_FIELD will display which MOLECULEs have been overridden.

Potential parameters can also be overridden if ATOM\_KEYS are matched. This can be either matched with ATOM\_KEYS appear in the same sequence or with the alternative

but equivalent sequence. For instance, an angle interaction is defined for ATOM\_KEYS A-B-C in a *.par* file. DL\_FIELD will subsequently override the corresponding potential parameters even if it is defined as C-B-A in the *udff* file.

The *udff* file cannot override an existing ATOM\_TYPE defined in the standard *.sf* file. This is because any change to the ATOM\_KEY will lead to invalid potential sets defined in the standard *.par* file. However, a new ATOM\_TYPE can still be defined, either with a completely new ATOM\_KEY or with an existing ATOM\_KEY from the library file. In other words, the ATOM\_TYPE is unique while the ATOM\_KEYS are not.

Note that all ATOM interactions must be explicitly defined in *udff* files. DL\_FIELD does not recognise the symbol 'X' (refer to as 'any atom') as one of the ATOM\_KEY. Generic interactions involving ATOM X must still be defined in the *.par* file.

Each **POTENTIAL** block in *udff* file must contain its own **UNIT**. If potential parameters are also specified, DL\_FIELD will assume the values are described in the same energy unit. DL\_FIELD will do automatic conversion if the unit is different from what is specified in the control file (Option **2**), which is the final unit in the *dl\_poly.FIELD* file.

## 6 User's Atomic Configuration File Format

DL\_FIELD recognises user's configuration file in the following formats: PDB, *mol2* and simple *xyz*. Note that not all DL\_FIELD features are made available to all file formats. This is especially true for the *mol2* format, since it is the newest format being introduced into DL\_FIELD framework.

PDB file format is applicable to all force field schemes implemented in DL\_FIELD.

### 6.1 The PDB Format

Although PDB format is a popular format for proteins and other bio molecules, other molecular models such as metals and inorganic molecules can also be described in the PDB format.

DL\_FIELD adheres to strict PDB standard format and different information must contain within the appropriate columns in a PDB file. However, not all information will be required by DL\_FIELD and only those relevant to the conversion process will be discussed here.

Each ATOM definition that precedes with the PDB statement 'ATOM' and/or 'HETATM' will be read by DL\_FIELD. Table below lists data that will be read by DL\_FIELD for each ATOM.

DL\_FIELD also recognises the CRYST1 statement which contains the unit cell parameters of the system. By setting the periodic boundary condition to *auto* (Option **25**) in the [control](#) file, the program will look for the cell parameter information and convert it to the corresponding cell vectors.

Note that DL\_FIELD will process a PDB file until the END statement is encountered. **Any atoms after these statements will be ignored.** In addition, DL\_FIELD will also ignore the 'TER' statement.

<b>Column range (inclusive)</b>	<b>Data</b>	<b>Remark</b>
<b>13-16</b>	<i>Atom label</i>	If <i>element symbol</i> is not defined, then this data will be treated as the element symbol for the atom. Any numerical characters will be ignored.
<b>18-20</b>	<i>Residue names</i>	Residue names such as those of amino acids. Equivalent to the MOLECULE_KEYS.
<b>21</b>	<i>Reserves for residue names</i>	Some residue names such as those of carbohydrates may contain more than three characters. The fourth one will be located here.
<b>22</b>	<i>Chain ID</i>	If <i>Molecular Group name</i> is not defined, this information will be used as the Molecular Group for the atom.
<b>23-26</b>	<i>Residue sequence</i>	Numerical sequence for molecules such as amino acids or carbohydrates.
<b>29-56</b>	<i>X,y,z coordinates</i>	Location of the atom in x,y,z coordinates.
<b>70-76</b>	<i>Molecular group name</i>	Molecular group name definition. This will override <i>Chain ID</i> if it is defined.
<b>77-79</b>	<i>Element symbol</i>	The element symbol of the atom. If this is not defined, then <i>Atom label</i> will be used to determine the element symbol of the atom.



### 6.1.1 Pre-processing

Most of the PDB files for bio molecules were constructed from X-ray crystallography data. These 'raw PDB' files must be pre-processed by the user using some other third party software to produce a 'readable format' for DL\_FIELD. The following steps are needed to be taken by the users.

(1) Decide which molecular residues to delete that involve multiple occupancies in crystalline structures.

(2) Usually, hydrogen atoms are not visible to X-rays and they are not assigned in the PDB file. The molecules must therefore be pre-filled with hydrogen atoms by using other third-party packages. The terminal residues must also be appropriately terminated.

(3) In most cases, DL\_FIELD defines a bond between two atoms according to distance criteria. The connectivity of atoms within a molecule must be within a reasonable range and not deviate significantly from the equilibrium length. The distance criteria can be relaxed or tightened somewhat using Option **3**, the Conversion Criteria in the *control* file.

(4) For protein systems, decide the charge states of some amino acids, such as histidine (HIS), lysine (LYS), glutamic acid (GLU), etc., by adding or deleting the appropriate hydrogen atoms. Force field schemes such as CHARMM, AMBER, etc will have different three-letter notations for amino acids of different charge states. However, standard notation such as HIS (for histidine for instance) can be left unchanged and DL\_FIELD will automatically determine the charge state based on the positions of the hydrogen atoms and assign the appropriate potential parameters accordingly.

(5) For cysteine (CYS) molecules with disulphide bonds, thiolate hydrogen atoms must be removed. DL\_FIELD will automatically define a disulphide bonds between the molecules, provided the S-S distance is within a 'sensible' value.

### 6.1.2 Conversion Processes

The conversion of a PDB file into *dl\_poly.CONFIG* and *dl\_poly.FIELD* files involve several stages. First, the PDB file is scanned once in order to determine the number of Molecular Group available. Then, ATOMs and their interactions will be grouped according to different molecular groups in the *dl\_poly.FIELD* file.

A large multi-component molecular system can be grouped into several Molecular Groups so that each Molecular Group contain a component of the molecular system. For instance, group a protein molecule into a Molecular Group and define all water molecules with another Molecular Group. This not only saves computational resources on memory usage but also produces a more compact FIELD file layout.

Note that DL\_FIELD assumes no covalent bond between ATOMs from any two different Molecular Groups.

After that, DL\_FIELD will read the PDB file in more details, one residue at a time. The residue (equivalent to the MOLECULE\_KEY) can either be a single distinct molecule or a linked molecule (like an amino acid residue in a protein). Firstly, DL\_FIELD will look for any MOLECULE templates in the *udff* file. After that, it will search the *.sf* library file, looking for a match with the residue structure.

It is considered match if the residue label is matched with a MOLECULE\_KEY in the library file. However, DL\_FIELD will still flag up an error if the matched MOLECULE

template is topologically not the same as that of residue structure (by matching with the connectivity matrix).

The next step is to rearrange the atoms within the residue according to the sequence defined in the MOLECULE template. All ATOMs will be written out in the same sequence to the *dl\_poly.CONFIG* and *dl\_poly.FIELD* files. The molecular interactions are then defined base on the connectivity information of the MOLECULE template.

### 6.1.3 Linked Residues in Proteins

For protein molecules, the residues are automatically converted from a three-letter notation, ABC, to -ABC- to indicate linkages exist between molecules and DL\_FIELD will define potential parameters involving these linkages. However, the three-letter notation is retained (without the hyphens) if it is an isolated molecule.

User can use standard three-letter notations for amino acids with various charge states. For instance, use HIS rather than explicitly define HSD or HSE for histidine residues in CHARMM. DL\_FIELD will automatically determine the nature of charge state and assign the potential parameters accordingly.

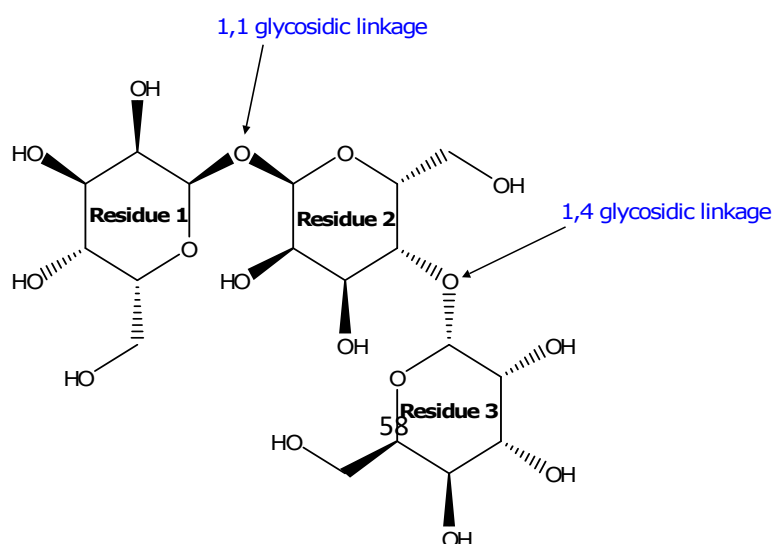
The standard three-letter notations for terminal amino acids can also be used. DL\_FIELD will automatically determine the type of terminal states, such as normal ammonium or carboxylate terminals or even acetylated N-terminus or methylated C-terminus etc.

### 6.1.4 Linked Residues in Carbohydrates

For carbohydrates molecules in CHARMM (note: This section does not apply to CHARMM36\_carb): The simplest carbohydrate molecules exist as monomers called monosaccharides. It can form polymeric structures via glycosidic oxygen linkages to give disaccharides, oligosaccharides and polysaccharides. The basic monosaccharides are usually consisted of six-membered pyranose sugars such as glucose and their anomeric counterparts (the  $\alpha$ - and  $\beta$ - anomers). Other members of pyranose monosaccharides also exist, with the -OH groups adopting various orientations. Examples of these are altrose, allose, galactose, etc.

In CHARMM force field, all pyranose molecules are based on  $\alpha$ -glucose (AGLC). The program will identify various keywords in CHARMM, referring to different pyranose members as AGLC. If the user is unsure of the identity of a pyranose member, just define the keyword 'AGLC' in the *Residue names* column (18-21) in the PDB file.

For example, consider a carbohydrate molecule consists of three pyranose units connected via 1,1 and 1,4 glycosidic linkages as shown in the diagram below. The corresponding PDB file (*glucose3\_1.pdb*) is available in the *Examples/* directory in the DL\_FIELD package.



Another carbohydrate structure, *glucose3\_2.pdb*, is also contained in the *Examples/* directory. Both structures are identical with identical geometrical structure. The only difference is the assignment of oxygen linkage. For instance, the 1,1 glycosidic oxygen is assigned to residue id = 2 in *glucose3\_1.pdb* whereas, the same oxygen is assigned to residue id = 1 in *glucose3\_2.pdb*. DL\_FIELD will be able to convert both structures to give similar potential interactions.

The exact way of grouping of the glycosidic oxygen into a residue is not important. However, inner pyranose units must always contain one glycosidic oxygen (Residue 2 in this example).

The Glycam potential is a stand-alone potential force field that is compatible with AMBER force field. It has a complete set of all anomeric and enantiomeric structures of sugars, and some of the derivatives such as amino sugars. The corresponding potential parameters use case-sensitive atom types to distinguish them from other standard AMBER potentials. For instance, the aliphatic carbon is defined as 'Cg' in Glycam. In the case of DL\_FIELD, a prefix 'G\_' is added to indicate such distinction. Therefore, Cg in the standard Glycam potential is equivalent to G\_Cg in DL\_FIELD.

The complexity and variety of glyco-molecules can be systematically classified based on notations suggested by Woods group (M. L. DeMarco and R. J. Woods, 'Structural glycobiology: A game of snakes and ladders' *Glycobiology*, **18**, 426-440 (2008)). DL\_FIELD fully adopts this notation. In the case of L-sugars, the notation is expressed as XxX, where the middle character is a small letter x. DL\_FIELD will automatically reassign it as a corresponding D-sugar with capital 'X'. This should not change the potential assignment since chemically both D- and L-sugars are identical with the same set of atomic partial charges.

All Glycam structures are defined as individual unit links. For this reason, DL\_FIELD will automatically reassign a notation XXX as -XXX- internally during the FF setup processes.

#### 6.1.5 Nuclei Acids

Nuclei acids consist of three components: a 5-carbon sugar unit, a phosphate group and a nucleobase. For the sugar unit, it can be either ribose or the deoxyribose derivative, of which the hydroxyl group at C2 is replaced with a hydrogen for the derivative form. For this reason, nucleic acids can be classified as either RNA (R) or DNA (D), which correspond to nucleic acids with ribose or deoxyribose units, respectively.

There are altogether five different nucleobases: adenine (A), cytosine (C), guanine (G), thymine (T) and uracil (U). However, uracil can only be found in RNA, while thymine can only be found in DNA. Nuclei acids are therefore named after the nucleobases.

Nuclei acids formed phosphate links at the 3-and 5-position of the sugar units to form a nucleic acid sequence of polymeric chain, adopting a helical strand. RNA consists of one such strand, whereas, DNA consists of two helical strands that bind to each other via hydrogen bonds between two nucleobases – one from each stand. The specific order of these nucleobase-pairs enables storing and transmitting coded instruction as genes.

In DL\_FIELD, the following standard notation for nucleic acids are used: the first character is always either 'R' or 'D', referring to RNA or DNA, respectively. The second character represent the nucleobases, as shown above. For example, for adenine in RNA, the residue notation is -RA-. However, only the residue label RA, without hyphen, is needed in PDB. DL\_FIELD will automatically add the hyphens if it is a nucleic acid residue

that forms phosphate links. Otherwise, it would be treated as a stand-alone nucleotide with no link and the original label, RA, is retained.

The chain termination occurs at the 3- and 5- positions of the sugar units, which can be hydroxyl phosphate (P), or hydroxyl (O). DL\_FIELD will automatically detect the terminal type and assign suitable parameters accordingly. For example, for RNA adenine with hydroxyl phosphate terminal at the 5-position, the residue label will be changed from RA to -RA5P-. For DNA guanine with hydroxyl termination at the 3-position, the residue label will be changed from DG to -DG3O-.

## 6.2 The XYZ Format (.xyz)

Unlike the PDB file format, the xyz format contains much fewer information and is free-formatted. DL\_FIELD only reads the element symbols and the corresponding coordinates of the structure. Below shows the general form of a xyz file.

```
[Number of atoms]
[SPACE, or CRYST1 statement or some remark or title]
Element_symbol    x1  y1  z1
Element_symbol    x2  y2  z2
Element_symbol    x3  y3  z3
.....
```

Remark statements can be placed anywhere in the file, with a symbol '#' at the beginning of each line.

The xyz file format is applicable to all [FF schemes](#), including those of inorganic. For ORGANIC FF, template-based FF schemes such as CHARMM and AMBER, DL\_FIELD will attempt to identify the types and number of molecules in a Molecular Group. After that, DL\_FIELD will search through the library and look for correct templates based on number of atoms in a molecule and its corresponding molecular weight as matching criteria. For ORGANIC FF schemes that allow topological analysis approach, DL\_FIELD will bypass any attempt to look for MOLECULE templates. Instead, DL\_FIELD will carry out fully automatic assignment of ATOM\_TYPES and determine the corresponding potential parameters accordingly, including any improper and inversion potentials. For example: OPLS, CVFF and PCFF all allow topological-based molecular analysis.

For INORGANIC force fields, the **MOLECULE\_KEY** directive must be used (see below).

### 6.2.1 The xyz features

The various directives that can be used in xyz files are described in more details as follows:

#### (a) CRYST1 statement

This is similar to the CRYST1 statement in a PDB file, to specify the crystal structure and cell parameters of a structure. DL\_FIELD recognises such statement if it appears at the 'title' section of the file, which may look something like this:

```
451
CRYST1  83.908  20.7302253  17.9859383759  90.00  90.00  90.00 (P 1)
C  10.000000  1.390000  0.000000
C  10.000000  0.695000  1.204000
C  10.000000 -0.695000  1.204000
...
...
```

DL\_FIELD will read the CRYST1 statement and convert the cell parameters to the corresponding cell vectors for the *dl\_poly.CONFIG* file. To use this feature, Option **25** in the control file must set to *auto*.

(b) The **MOLECULAR\_GROUP** directive

Atoms can be grouped by using the **MOLECULAR\_GROUP** directive, which will also appear in the *dl\_poly.FIELD* file. For example, consider a xyz molecular system consists of a cyclodextrin molecule and a phenylalanine molecule:

```

170
Cyclodextrin with PHE.
# MOLECULAR_GROUP CYC
C -6.049000 0.945000 0.569000
C -6.341000 2.134000 -0.313000
C -5.113000 3.000000 -0.453000
C -4.574000 3.388000 0.915000
...
...
# MOLECULAR_GROUP PHE
C -0.830000 0.683000 2.322000
C -0.114000 -0.185000 3.052000
C 0.873000 -0.882000 2.472000
C 1.110000 -0.714000 1.164000
C 0.405000 0.151000 0.413000
...
...

```

The 170-atom system is divided into two Molecular Groups: CYC and PHE. The TETHER and FREEZE features (Options **21** and **22** in the *control* file) can also be applied on these Molecular Groups. Note that to apply bond constrains (Option **23**) in xyz systems, only the atom filter **h-bond** can be used, which applies constrains to all hydrogen-containing bonds within a Molecular Group.

For ORGANIC force fields, if no **MOLECULAR\_GROUP** is specified, a default Molecular Group will be assigned, called 'xyz', to the whole system.

For INORGANIC force fields, the directive **MOLECULAR\_GROUP** must always be specified.

(c) The **MOLECULE\_KEY** directive

This directive is always needed for INORGANIC xyz systems. It must be specified along with a **MOLECULAR\_GROUP** and only one **MOLECULE\_KEY** can be specified for each **MOLECULAR\_GROUP**. Consider a xyz configuration file as follows:

In this example, the Molecular Group A1 is defined, along with the

```

1056
CRYST1 19.952 24.790 79.262 90.00 90.00 78.39 P1 0
# MOLECULE_GROUP A1 MOLECULE_KEY CC1
O 4.337000 8.034000 23.538000
O 4.337000 16.128000 23.538000
O 5.639000 3.987000 23.538000
O 19.301000 8.034000 23.538000
O 19.301000 16.128000 23.538000
C 20.603000 3.987000 23.538000
O 14.313000 8.034000 23.538000
...
...

```

MOLECULE\_KEY CC1, which refers to a calcium carbonate model (see `lib/inorganic_ternary_oxide.sf` file). The force field `inorganic_ternary_oxide` must also be specified in the *control* file (Option **1**).

(d) The **POTENTIAL** directive

This directive specifies the type of force field scheme and it is only used in [multiple potential](#) models. The position of the directive indicates the range of application of the force field to atoms. Any atoms immediately after the directive would apply to the same force field type until another **POTENTIAL** directive is encountered. The **POTENTIAL** directives are automatically activated if the keyword 'multiple' is used in the *control* file (Option **1**). Otherwise, these directives will be ignored if a force field scheme is specified in the *control* file.

### 6.2.2 Special Note on xyz format

(a) For protein models, users are advised to use the *PDB* format. There is no guarantee DL\_FIELD can convert these structures correctly in the xyz format. This is because protein molecules are usually fitted to a specific set of parameters. For this reason, amino acid residues are still defined as MOLECULE templates.

(b) When noble gases are included in the xyz molecular systems, DL\_FIELD assumes there is no bonding with rest of the atomic systems. The non-bonded interactions (vdw and Coulombic) are assumed to be the only interactions for noble gases.

(c) To model solvated (non-bonded) charged ions, user must specify the charge state in the xyz file. For instance, a chloride anion will be expressed as 'Cl-', rather than just 'Cl' in the xyz file. In this case, DL\_FIELD will automatically assign it as a chloride anion, rather than a normal chlorine atom. DL\_FIELD will only consider the non-bonded interactions for charged ions, just like point (b).

Do not specify the charge state if a charged atom is expected to form bonds with other atoms. For example, specify an ammonium nitrogen simply as N, rather than N+ in the xyz file.

(d) DL\_FIELD can detect water molecules and will assign them as the TIP3P model by default. To solvate the system with other water models, use Option **31** in the *control* file.

### 6.2.3 Auto-identification of template-based FF systems

This is a powerful and flexible feature first introduced in DL\_FIELD version 4.6. DL\_FIELD now allows user to express molecular system using the simple xyz format for template-based FF models. Traditionally, a PDB format would be needed, to specify explicitly the residue labels, to indicate which MOLECULE templates to use.

For instance, consider the following xyz structure:

```

21
H 0.721000 5.934000 0.953000
C 0.185000 5.739000 0.000000
O -0.158000 4.366000 0.000000
H 0.666000 3.872000 0.000000
H 0.721000 5.934000 -0.953000
H -0.770000 10.307000 0.000000
H -0.770000 6.307000 0.000000
H 0.721000 9.934000 0.953000
C 0.185000 9.739000 0.000000
O -0.158000 8.366000 0.000000
H 0.666000 7.872000 0.000000
H 0.721 9.934 -0.953
C 0.995 0.329 -0.000
H 1.844 -0.392 0.000
H 1.096 0.975 -0.902
H 1.096 0.976 0.901
C -0.340 -0.404 0.000
H -0.456 -1.038 0.907
H -0.457 -1.039 -0.907
H -2.235 0.073 0.000
O -1.394 0.538 -0.000

```

By using, say, CHARMM36\_CGENFF (CHARMM General Force Field), which is a template-based FF scheme, DL\_FIELD will automatically group and identify the molecules in the file. After that, DL\_FIELD will search the library (and *udff*) files to identify the suitable MOLECULE template. In this example, two types of molecules were detected: methanol and ethanol, and there are two methanol molecules and one ethanol molecule. This information is shown in the *dl\_field.output* file as follows:

```

...
...
>>>>Reading coordinates in Molecular Group XYZ

The molecule has no cyclic structure.
ATOM_TYPES mapping (DL_F notation): See output/dlf_notation.output
file.

Total different type of molecules: 2

Molecule type 1
Total number: 2
Num of atoms in the molecule: 6
Molecular mass: 32.042780
Composition: C1 H4 O1

Molecule type 2
Total number: 1
Num of atoms in the molecule: 9
Molecular mass: 46.070220
Composition: C2 H6 O1

The following type of molecules have been identified:
Molecule type 1: methanol (MEOH)
Molecule type 2: ethanol (ETOH)
...
...

```

After that, the usual FF conversion will be carried out, based on the template matching procedure as would be the case for a PDB file. If a suitable MOLECULE template cannot be located, then an error will be generated.

### 6.3 The Tripos *mol2* Format

Tripos Mol2 file is a complete, portable representation of a SYBYL (SLN) molecule. Unlike the *PDB* format, *mol2* files are free format and can contain detailed information of molecular structures.

The *mol2* format is only applicable to the following ORGANIC force fields: OPLS2005, CVFF, PCFF and AMBER16\_GAFF.

A typical *mol2* file consists of a series of *data records* classified according to the *Record Type Indicator (RTI)*. Essentially, the *RTIs* divide a *mol2* file into several sections. A section begins with a *RTI* and ends at the next *RTI* or the end of the file. All *RTIs* must always begin with the '@' at column 1. There are many *RTIs* but DL\_FIELD only recognises a small set of 'essential' *RTIs* for the purposes of force field conversions. These *RTIs* are shown below:

@<TRIPOS>MOLECULE - information about a molecule.

@<TRIPOS>ATOM - information about an atom within a molecule.

@<TRIPOS>BOND - bond connectivity information of a molecule.

@<TRIPOS>CRYSIN - crystal cell parameters



```

@<TRIPOS>MOLECULE
aniline      (molecule name)
14 14 1 0 0  (number of atom, number of bonds, number of residues, 0, 0)
SMALL       (molecule type: SMALL, BIOPOLYMER, PROTEIN, etc)
USER_CHARGES (charge type, or NO_CHARGES)
              (leave blank!)
This is an example (Comment, can leave blank)
@<TRIPOS>ATOM
 1 C   -1.1604  0.7227 -0.0729 C.ar  1  ****  0.0000 (atom index, atom label, x,y,z coordinates, atom_key,
 2 C   -1.1598 -0.6198 -0.0771 C.ar  1  ****  0.0000 residue id, residue key, charge values)
 3 C   -0.0005 -1.2919 -0.0018 C.ar  1  ****  0.0000
 4 C    1.1589 -0.6205  0.0779 C.ar  1  ****  0.0000
 5 C    1.1597  0.7220  0.0823 C.ar  1  ****  0.0000
 6 C   -0.0003  1.3949  0.0069 C.ar  1  ****  0.0000
 7 H   -2.1205  1.2629 -0.1353 H    1  ****  0.0000
 8 H   -2.1126 -1.1716 -0.1426 H    1  ****  0.0000
 9 H   -0.0007 -2.3948 -0.0053 H    1  ****  0.0000
10 H    2.1116 -1.1729  0.1399 H    1  ****  0.0000
11 H    2.1199  1.2616  0.1482 H    1  ****  0.0000
12 N   -0.0001  2.6626  0.0110 N.3   1  ****  0.0000
13 H    0.9052  3.1895  0.0732 H    1  ****  0.0000
14 H   -0.9054  3.1901 -0.0479 H    1  ****  0.0000
@<TRIPOS>BOND
 1  1  2  2  (bond index, atom pair that formed a bond, bond type: 1=single, 2=double, 3=triple, am=amide, ar=aromatic)
 2  1  6  1
 3  1  7  1
 4  2  3  1
 5  2  8  1
 6  3  4  2
 7  3  9  1
 8  4  5  1
 9  4 10  1
10  5  6  2
11  5 11  1
12  6 12  1
13 12 13  1
14 12 14  1
@<TRIPOS>CRYSTAL
12.0 33.0 44.0 90.0 90.0 90.0 space_group setting (cell parameters: a, b, c, alpha, beta, gamma)

```

Example above shows a simple *.mol2* file for aniline molecule, indicating the meaning of each section (in red).

### Special Note on mol2 format

- Unlike the xyz format, DL\_FIELD does not recognise the directives such as **MOLECULAR\_GROUP**, **MOLECULE\_KEY** and **POTENTIAL**.
- If the atom keys in the *mol2* file match (by making references to the appropriate *.par* file) with that of the potential scheme specified in the DL\_FIELD *control* file, then these will be treated as the ATOM\_KEYS straight away without carrying out any procedure to determine the ATOM\_TYPES. The corresponding charge values will also be taken from the *mol2* file, if these were specified.
- If DL\_FIELD fails to match the atom keys, then it will read the atom label in the *mol2* file and setup the force field model and carry out the auto-assignment of ATOM\_TYPES similar to that of the xyz format. In this case, the charge values will

be determined in the usual way and will NOT extract from the *mol2* file. Note that DL\_FIELD will make best guess to convert 'Atom label' to element symbols.

Beware: The matching of atom keys as mentioned in (c) and (d) is not fool-proof. For instance, PCFF and Amber16\_GAFF share similar ATOM\_KEYS for some of the ATOM\_TYPES. DL\_FIELD may be fooled into thinking the atom keys in a *mol2* file is of PCFF which in fact is of Amber GAFF or *vice versa*.

### ***Production of the mol2 file using AMBER's Antechamber***

The *mol2* is a popular file format which can be produced in many modelling packages. This section explains how one can use the powerful AMBER's Antechamber software to produce a *mol2* files, which can be read by DL\_FIELD to produce Amber GAFF model in DL\_POLY's FIELD in a single step.

Consider a molecule, say ascorbic acid (Vitamin C). To produce a *mol2* file, assume the initial input file that contains a single ascorbic acid molecule called *ascorbic.pdb*, the following command can be issued in Amber:

```
antechamber -if pdb -i ascorbic.pdb -fo mol2 -o ascorbic_acid.mol2 -c bcc
```

This instructs *antechamber* to produce a *mol2* output file. Use this file as the user's input configuration in DL\_FIELD and use *amber16\_gaff* scheme (Option **1** in the *control* file). The same input file can also be used for other force field schemes, such as OPL2005. In this case, the element symbols will be extracted from 'atom labels' and DL\_FIELD will treat the configuration as if it is a *xyz* file and the usual conversion procedure will be used to setup the force field model. For more information about *antechamber*, please refer to Amber Manual.

Similar to the *xyz* format, a *dif\_notation.output* file will be produced after each successful conversion.

The example below shows a *mol2* file of an ascorbic acid (vitamin C) molecule, produced by using the Antechamber software, with AM1-BCC charge method.

```
@<TRIPOS>MOLECULE
```

```
****
```

```
20 20 1 0 0
```

```
SMALL
```

```
bcc
```

```
@<TRIPOS>ATOM
```

1 C	0.5320	0.6960	0.5130 c3	1 ***	0.140400
2 C1	1.1130	-0.7070	0.4630 c3	1 ***	0.102100
3 H	1.1810	1.3910	1.0910 h1	1 ***	0.065200
4 O	-0.7190	0.6670	1.1730 oh	1 ***	-0.591800
5 H1	0.3760	1.1160	-0.5050 h1	1 ***	0.065200
6 H2	0.9650	-1.2210	1.4420 h1	1 ***	0.064700
7 O1	0.4260	-1.4590	-0.5120 oh	1 ***	-0.599800
8 C2	2.5880	-0.7270	0.0980 c3	1 ***	0.148300
9 O2	3.3640	-0.0400	1.0670 os	1 ***	-0.398900
10 H3	2.7690	-0.2680	-0.9010 h1	1 ***	0.112700
11 C3	3.1190	-2.1380	0.1410 c2	1 ***	0.041900
12 C4	4.2130	-0.9780	1.5850 c	1 ***	0.713800
13 O3	5.0310	-0.7710	2.4570 o	1 ***	-0.549500
14 H4	-1.1250	1.5360	1.1300 ho	1 ***	0.414000
15 H5	0.8040	-2.3420	-0.5630 ho	1 ***	0.423000
16 O4	4.8120	-3.2890	1.4290 oh	1 ***	-0.472100
17 C5	4.0860	-2.2150	1.0540 ce	1 ***	-0.111100
18 O5	2.6680	-3.1720	-0.6010 oh	1 ***	-0.467100
19 H6	3.1950	-3.9540	-0.3620 ho	1 ***	0.452000
20 H7	5.3850	-3.0020	2.1610 ho	1 ***	0.447000

```
@<TRIPOS>BOND
```

```
1 1 2 1
2 1 3 1
3 1 4 1
4 1 5 1
5 2 6 1
6 2 7 1
7 2 8 1
8 4 14 1
9 7 15 1
10 8 9 1
11 8 10 1
12 8 11 1
13 9 12 1
14 11 17 2
15 11 18 1
16 12 13 2
17 12 17 1
18 16 17 1
19 16 20 1
20 18 19 1
```

```
@<TRIPOS>SUBSTRUCTURE
```

```
1 *** 1 TEMP 0 **** ** 0 ROOT
```

## 7 The Output File (*dl\_field.output*)

This is the output file where the conversion process of a user's atomic configuration is recorded. The output file is separated into several sections and the level of reporting details can be selected by switching the verbosity Option **7** in the *control* file to 1 (on) or 0 (off):

### (1) CONTROL STATUS REPORT

Display options that have been selected in the *control* file.

### (2) FORCE FIELD INITIALISATION

In this section, DL\_FIELD reports the reading status of the *udff* (if requires), *.sf* and *.par* files. After that, computer memory is allocated to set up model structure databases.

### (3) CONVERSION STATUS REPORT

This is the main section of *dl\_field.output* which reports the conversion process of user configuration model into *dl\_poly.CONFIG* and *dl\_poly.FIELD* files.

Below show a section of the conversion process of a protein (with Verbosity mode switch on):

```

*** Mapping 1. HIS ***
...
***** Need patching *****
Residue -HSE- of id = 1
*****Patch normal N-termination****

User config neighbour list:
1 --2 3 4 5
2 --1
3 --1
4 --1
5 --1 6 7 18
6 --5
...
17 --16
18 --5 19
19 --18
All atoms matched: User atom index > matched atom labels
1 > n
2 > hn1
3 > hn2
4 > hn3
5 > ca
6 > ha
...
17 > h4
18 > c
19 > o
Total charge for residue 1 (-HSE-) is 1.000000.

```

In this example, the first residue is a histidine molecule. DL\_FIELD will determine this charged species to be a HSE (CHARMM notation for a histidine protonated at the N3 position) with N-termination (-NH<sub>3</sub>).

The 'User config neighbour list' shows the connectivity of all atoms where the numbers refer to the atom index number. For example, atom 1 is connected to atoms 2, 3, 4 and 5

The 'All atoms matched:' list identifies the user atoms with atom labels defined for the histidine molecule in the *.sf* file. In this example, it turns out that atom 1 is 'n'; atoms 2, 3 and 4 are 'hn' and atom 5 is 'ca'. The atom list will be reordered and assigned with the corresponding *atom keys* for the *dl\_poly.CONFIG* and *dl\_poly.FIELD* files.

The neighbour list and information on matching atoms will not be displayed when the Verbosity mode is switched off.

Another example is given below. Here, PCFF potential scheme is used to convert a chlorobenzene (CBEN) structure.

```

*** Mapping 1. CBEN ***
User config neighbour list:
1 --7
2 --6
3 --4
4 --3 5 7
5 --4 6 12
6 --2 5 8
7 --1 4 9
8 --6 9 10
9 --7 8 11
10 --8
11 --9
12 --5

*** For Residue 1. CBEN
Following atoms are mismatched:
c2  h2  c6  h6

Might be due to symmetrical close-loop structure.
Attempt to break symmetry with nn=1
Reassign: 1 > h3
Reassign: 2 > h6
Reassign: 3 > h2
Reassign: 10 > h5
Reassign: 11 > h4

Okay, everything is fine now.

All atoms matched: User atom index > matched atom labels
1 > h3
2 > h6
3 > h2
4 > c2
5 > c1
6 > c6
7 > c3
8 > c5
9 > c4
10 > h5
11 > h4
12 > cl

```

In this example, DL\_FIELD detects mismatch of atoms due to symmetrical nature of the molecule (the benzene group). Depending on the initial arrangement of atoms in user's configuration file, this may sometimes occur where atoms are assigned to correct ATOM\_TYPES but in the wrong positions. A second conversion attempt is made by

introducing dummy atoms to break the symmetry, ensuring all atoms are correctly matched and in the right positions.

#### (4) LINKAGE INFORMATION BETWEEN RESIDUES

At this stage, all atoms within every residue have been matched and the force field parameters have been assigned. In this section, the DL\_FIELD determines the linkage information between two neighbouring residues and this information is useful to check for any undiscovered/undesirable bonds between two atoms from different residues.

Once this information is obtained, DL\_FIELD will determine force field parameters that describe the interactions between two connecting residues. Below shows a section of the output data (for a protein molecule):

```
...
Link pair: -thr- (3844) and -glu- (3846) of c-n distance=1.331446
Link pair: -glu- (3859) and -cys- (3861) of c-n distance=1.330719
Link pair: -glu- (3857) and -asp- (4011) of od1-oc2 distance=0.730184
Warning: od1-oc2 pair may not be a valid link for protein amino acid. It is not considered as a bond.
Link pair: -cys- (3869) and -cys- (3871) of c-n distance=1.328854
Link pair: -cys- (3868) and -cys- (3977) of s-s distance=2.025060
Link pair: -cys- (3879) and -hse- (3881) of c-n distance=1.326833
...
```

In most cases, DL\_FIELD will pick up the usual C-N amide linkages but occasionally the disulphide S-S linkages as well. The latter information is useful to indicate the **possible** S-S bond and, consequently, may have to delete the thiolate hydrogens in the user's PDB file and rerun DL\_FIELD.

Occasionally, unintended atom distances may also be flagged up as a warning to indicate the potential source of problem during equilibration. For instance, the example above shows two oxygen atoms are too close to each other in -glu- (3857) and -asp- (4011). This warning only applies to protein molecules.

#### NOTE:

(1) Even if a S-S linkage is listed, DL\_FIELD does not guarantee a bond is established. Though it is rare, this **will** happen if the macro definition S\_S in the *dl\_field.h* include file is smaller than the actual distance measured between the S-S linkage. If this happens, locate the program statement

```
#define S_S 2.135
```

in the *dl\_field.h* file and increase the maximum bond length for S\_S (2.135). Recompile DL\_FIELD and rerun the conversion. Alternatively, select the [Conversion criteria](#) (Option **3**) in the *control* file to 'loose' and run DL\_FIELD again.

(2) DL\_FIELD allows more than one linkage between a same pair of residues. However, conversion will fail if an atom from a residue has more than one link to other atoms from the other residues. This can be avoided by defining the two residues as a single MOLECULE.

## 8 Solution Maker

The Solution Maker is a flexible feature that allows users to setup a disordered system, be it a liquid or a solution (two-component system consists of solute and solvent molecules) model, based on a single molecule template input file. DL\_FIELD will then setup the force field model in a single step.

The Solution Maker is located at [Option 10](#) in the *control* file. The required parameters are shown below as an example:

```
0 0.94 g/cm^3 1.9 * Solution Maker: on/off, density, unit, cut off)
```

The first value is the switch which takes two values: off (0) and on (1). The second parameter dictates the number of molecules in the system, depending on the unit use in the third parameter and the simulation box size specified (it has to be an orthogonal system). The fourth parameter, in unit Ångström, indicates the minimum distance between the molecules.

The third parameter allows the following units - density:  $g/cm^3$  or  $kg/m^3$ , concentration:  $mol/dm^3$ , or *molecule*, which simply indicates the number of molecules require in the system.

For example, to setup an ethanoic acid liquid force field model, an input molecular structure (either in the PDB or xyz format) contained only a single ethanoic acid molecule is needed which acts as a template. Then, the following options may be used for the Solution Maker. For instance, the following parameters were used:

```
1 1.05 g/cm^3 1.8
```

DL\_FIELD will then automatically duplicate a number of ethanoic acid molecules require base on the input unit ( $g/cm^3$ ) and cell vectors ([Option 26](#)). The molecules are systematically added by, first of all, randomly orientate the molecular template before it is placed in the system. The centre of gravity of each molecule is located approximately around some imaginary grid points in succession. These grid points were pre-determined base on the simulation box size and the size of the molecular template. After that, DL\_FIELD will set up the force field model and generate the require output files, *dl\_poly.FIELD* and *dl\_poly.CONFIG*.

If DL\_FIELD fails to insert all the molecules, reduce the fourth parameter (1.8) to some lower value and try again. This enable DL\_FIELD to pack more molecules in the system, as the critical distance between molecules is reduced. Obviously, doing so would create a high-energy system which would need careful equilibration. Alternatively, if the input molecular structure is flexible, perhaps try to use different conformations.

The Solution Maker can be used to create a two-component system, such as a solution model. For example, to setup an ethanoic acid solution of concentration 0.1 M with water as solvent, the following command can be used:

```
1 0.1 mol/dm^3 1.9
```

A suitable solvent type, such as a water model, must be selected, in [Option 31](#) in the *control* file.

User can also specify a fixed number of molecules to be inserted. For example:

```
1 15 molecules 6.4
```

This instructs DL\_FIELD to duplicate and insert 15 molecules, each is at least 6.4 Å apart from one another in the system. The extent of molecular separation can be increased by increasing the cut off value. Obviously, this is only feasible for dilute systems. Highly concentrated systems or pure liquid systems would naturally need a smaller cut off value to pack more molecules in the simulation box.

In order to create a truly disordered system, further equilibration is needed and can be achieved in the DL\_POLY program.

## 8.1 Water Models

The following water models are available in most *.sf* files and the structure templates are located in the *solvent/* directory.

(1) Original TIP3P. Key: *TP3O* (*water\_tip3p*)

W. L. Jorgensen, J. Chandrasekhar and J. D. Madura, 'Comparison of simple potential functions for simulating liquid water', *J. Chem. Phys.* **79**, 926-935 (1983)

(2) Modified TIP3P for CHARMM. Key: *TIP3* (*water\_tip3p\_c*)

This is fitted using CHARMM-type atom-based, force-shifted for long-range electrostatic calculations. Can be implemented as both constrained (use **rigid\_water** *filter\_atom* key) or flexible models.

Note: The CHARMM molecular models were fitted to the rigid version of the modified TIP3P model.

(3) Modified TIP3P with particle mesh ewald (PME) summation. Key: *TP3E* (*water\_tip3p\_pme*)

This is fitted using PME long-range electrostatic calculations that does not include Lennard-Jones parameters on the hydrogen atoms. The version DL\_FIELD uses is derived from Model B of D.J. Price and C. L. Brooks III, *J. Chem. Phys.* **121**, 10096 (2004).

Can only be implemented as a constrained (use **rigid\_water** *filter\_atom* key) model or as a rigid model using the [**RIGID**] directive.

(4) Original SPC water (*SPC*) and SPC/E water (*SPCE*)

Three-site water model and SPC/E includes corrections for self-polarization and improved structural and diffusion properties.

W. L. Jorgensen, J. Chandrasekhar and J. D. Madura, 'Comparison of simple potential functions for simulating liquid water', *J. Chem. Phys.* **79**, 926-935 (1983)

H.J.C. Berendsen, J. R. Grigera and T.P. Straatsma, *J. Phys. Chem.* **91**, 6269 (1987)

(5) TIP4P water (*TIP4*)

A four-site water model with an off-center point charge for oxygen. Can only be implemented as rigid model using the [**RIGID**] directive.

W. L. Jorgensen, J. Chandrasekhar and J. D. Madura, 'Comparison of simple potential functions for simulating liquid water', *J. Chem. Phys.* **79**, 926-935 (1983)

(6) TIP5P water (*TIP5*)

A five-site water model with two pseudo points representing the lone pairs on the oxygen atom. Can only be implemented as a rigid model using the [**RIGID**] directive.

M.W. Mahoney and W.L. Jorgensen, *J. Chem. Phys.* **112**, 8910 (2000).

(7) TIP5P water for PME calculations (*TP5E*)



Slight modification to the original TIP5P for PME calculations.  
S. W. Rick, *J. Chem. Phys.* **120**, 6085 (2004)

Note that use of modified TIP3P (*TIP3*) for CHARMM is usually recommended. However, inclusion of other water models in the *.sf* file does not mean the endorsement of DL\_FIELD's author to use other water models. They are included as alternative choices at the user's discretion.

However, there are some works being carried out to investigate the structural and dynamical effects on molecules using different water models. User is recommended to consult these papers:

P. Mark and L. Nilsson, 'Molecular dynamics simulations of the Ala-Pro dipeptide in water: Conformational dynamics of trans and cis isomers using different water models', *J. Phys. Chem. B* **105**, 8028-8035 (2001)

P. Mark and L. Nilsson, 'A molecular dynamics study of tryptophan in water', *J. Phys. Chem. B* **106**, 9440-9445 (2002)

D. C. Glass, M. Krishnan, D. R. Nutt and J. C. Smith, 'Temperature dependence of protein dynamics simulated with three different water models', *J. Chem. Theory Comput.* **6**, 1390-1400 (2010)

## 9 Inorganic Force Fields

Despite the inherent differences between organic and inorganic materials in terms of their chemical nature, the force field libraries for inorganic systems have the same format as those of organic systems. In other words, all standard libraries share the same **DIRECTIVES**.

The [connectivity](#) for all ATOMS in inorganic MOLECULEs must be defined as either the self-CONNECT type or the auto-CONNECT type. The normal CONNECT type is not available in the INORGANIC force field. Example below shows the definition of the core-shell model of a magnesium oxide MOLECULE.

```

ATOM_TYPE   key   element mass   remark
...
Mg2+#6c_binary_oxide1 Mg1c   Mg    24.3050 Ref. 1 Mg core
Mg2+#6s_binary_oxide1 Mg1s   Mg     0.0000 Ref. 1 Mg shell
O2-#8c_binary_oxide1 O1c    O    15.9994 Ref. 1 O core, on Li2O, Na2O etc
O2-#8s_binary_oxide1 O1s    O     0.0000 Ref. 1 O shell on Li2O, Na2O etc
...
END ATOM_TYPE

MOLECULE_TYPE
...
magnesium_oxide1      MO1    40.3044 Ref. 1, MgO cubic
...
END MOLECULE_TYPE

MOLECULE magnesium_oxide1 4 0.0      Ref. 1
Mg1c Mg2+#6c_binary_oxide1  1.580
Mg1s Mg2+#6s_binary_oxide1  0.420
O2c  O2-#6c_binary_oxide1   0.513
O2s  O2-#6s_binary_oxide1  -2.513
CONNECT Mg1c > Mg1c
CONNECT Mg1s > Mg1s
CONNECT O2c > O2c
CONNECT O2s > O2s
SHELL Mg1c Mg1s
SHELL O2c O2s
END MOLECULE

```

The self-CONNECT type means that the atom labels in the PDB file must also be the same as those of ATOM\_KEYS defined in the MOLECULE. Note that, unlike the MOLECULEs defined for the ORGANIC force fields, the number of ATOMS in the PDB file does not have to correspond to that defined in the **MOLECULE** directive. An example PDB file for the MgO MOLECULE is shown below.

```

HETATM   1 Mg1c MO1    1      0.000  0.000  0.000      Mg
HETATM   1 Mg1s MO1    1      0.000  0.000  0.000      Mg
HETATM   2 O2c MO1    1      0.000  2.104  0.000      O
HETATM   3 Mg1c MO1    1      0.000  4.208  0.000      Mg
HETATM   3 Mg1s MO1    1      0.000  4.208  0.000      Mg
HETATM   4 O2c MO1    1      0.000  6.312  0.000      O
HETATM   4 O2s MO1    1      0.000  6.312  0.000      O
HETATM   5 O2c MO1    1      2.104  0.000  0.0      O
HETATM   5 O2s MO1    1      2.104  0.000  0.0      O
HETATM   6 Mg1c MO1    1      2.104  2.104  0.0      Mg
HETATM   6 Mg1s MO1    1      2.104  2.104  0.0      Mg
HETATM   7 O2c MO1    1      2.104  4.208  0.0      O
...
...

```

The core and shell components of a polarisable atom is usually located very close to each other and both can be exactly at the same location in the initial model set up. DL\_FIELD will automatically match up these components, provided the core-shell distances are less than 0.5 Å. The MgO shell model example is in the *Examples/* directory with the filename *mgo\_shell.pdb*.

If no shell or core components are given, DL\_FIELD will automatically add and define the missing components in DL\_POLY files (see [Section 9.2](#)).

Unlike ORGANIC force fields, which uses LJ functions by default, the INORGANIC force fields can use different functional forms for the vdw interactions. The vdw parameters in the INORGANIC force fields are defined in pairs of ATOM\_KEYS as follows:

KEY1 KEY2 *functional\_form* *parameter\_1* *parameter\_2* *parameter\_3* *Remark*

The available *functional forms* are as follows:

Lennard-Jones 12-6: 
$$V(r_{ij}) = \frac{A}{r_{ij}^{12}} - \frac{B}{r_{ij}^6}$$

Morse: 
$$V(r_{ij}) = D_e[1 - e^{-\alpha(r_{ij}-R)}]^2$$

Buckingham: 
$$E(r_{ij}) = A_{ij} \exp\left(-\frac{r_{ij}}{\rho}\right) - \frac{C_{ij}}{r_{ij}^6}$$

General LJ n-m: 
$$V(r_{ij}) = \frac{\epsilon}{n-m} \left[ m \left( \frac{R}{r_{ij}} \right)^n - n \left( \frac{R}{r_{ij}} \right)^m \right]$$

The vdw *parameters* must be defined in the same order as that of DL\_POLY. For *functional forms* with only two parameters such as the Lennard-Jones 12-6, *parameter\_3* must be set to zero (0.0). Below shows an example list vdw parameters, extracted from the *DLPOLY\_INORGANIC.par* file.

<b>VDW</b>	type	parameters
Li1 O1s	buckingham	426.480 0.300 0.0 ! Ref. 1 Li2O
Na1 O1s	buckingham	1271.504 0.300 0.0 ! Ref. 1 Na2O
K1 O1s	buckingham	3587.570 0.300 0.0 ! Ref. 1 K2O
Mg1s O2s	buckingham	2457.243 0.261 0.0 ! Ref. 1 Mg shell - O shell
Mg2s O5s	buckingham	821.600 0.3242 0.0 ! Ref. 2 set 2, Table 3
Mg3 O10	buckingham	1152.000 0.3065 0.0 ! Ref. 7 Mg-O rigid ion
...		
<b>END VDW</b>		

All inorganic force field models are classified according to the type of materials in different library files. This allows user to more efficiently locate and identify the appropriate models to use. The available material classifications are shown below. They are by no means complete as more new classes will be added in future software releases.

(a) Binary oxides (*INORGANIC\_binary\_oxides*)

This class of materials consist exclusively two types of elements, one of which must be the oxygen. The class has a general formula of  $M_xO_y$ . Examples of binary

oxides including mineral oxides, metal oxides and gas oxides such as carbon dioxide, sulphur dioxide, etc.

(b) Binary halides (*INORGANIC\_binary\_halides*)

This class of materials consist exclusively two types of elements, one of which must be a halide (F, Cl, Br or I). The class has a general formula of  $M_xX_y$ , where X is a halide.

(c) Ternary oxides (*INORGANIC\_ternary\_oxides*)

This class of materials consist exclusively three types of elements, one of which must be the oxygen. The class has a general formula of  $M_xX_yO_z$ . Example of such including carbonate minerals such as aragonite ( $CaCO_3$ ).

(d) Clay minerals (***INORGANIC\_clay***)

The inorganic force field including CLAYFF for modelling clay minerals. This is defined in **MOLECULE** general\_CLAYFF with the corresponding MOLECULE\_KEY of CLYF. All ATOMs are defined as auto-CONNECT that allows variable number of neighbours for most ATOM\_KEYS.

**ANGLE ONLY** and **BOND ONLY** directives are used to selectively define the necessary bonds and angles depending on the neighbouring atoms in the system.

To use this force field, the CLYF residue label must be inserted in the PDB file or using the directive **MOLECULE\_KEY** CLYF in the xyz file, and all atoms must be labelled with the correct ATOM\_KEYS.

The force field scheme also contains a set of generic Lennard-Jones vdw force field, which can be mixed with the vdw parameters from other force field schemes including those of ORGANIC types.

(e) Glassy materials (***INORGANIC\_glass***)

These materials consist of a random mixture of ionic species such as metal ions, silicates and phosphates, etc. Some of these models also use three-body interactions.

(f) Zeolites (***INORGANIC\_zeolite***)

These are highly ordered rigid materials, consist of pores and channels of various sizes. Some of these models also use three-body interactions.

Inorganic systems can also be expressed in the xyz format. Similar to the PDB format, the Molecular Group and the MOLECULE\_KEYS can be defined by inserting the following directives in the configuration file:

**MOLECULAR\_GROUP** something **MOLECULE\_KEY** MO3

For more details about inorganic systems in xyz format, please see [Section 6.2](#).

## 9.2 Auto setup of core-shell systems.

DL\_FIELD can automatically detect the type of MOLECULE template and insert core (or shell) component if needed. To use this feature, a 'clean' configuration file would be needed, which only contains the usual atomic species with no or incomplete core or shell element.

When the program is run, DL\_FIELD will look for the **MOLECULE\_KEY** and decide if it is a rigid ion or a core-shell model. If the latter is used, DL\_FIELD will automatically

identify the missing components and automatically add these into *dl\_poly.CONFIG* and *dl\_poly.FIELD* files.

## 10 Multiple Potential Systems

DL\_FIELD allows different potential schemes apply on different parts of a system model. This type of model is called the multiple potential system. The multiple potential feature can be implemented in both PDB and xyz files.

The word 'multiple' must be used in Option **1** of the *control* file, to instruct DL\_FIELD to look for the potential scheme definitions, which is indicated by the **POTENTIAL** directive in the configuration file.

### 10.1 Implementation for PDB files

The example below illustrates the use of three different potential schemes on a system model consists purely of methanol molecules (extracted from the *multiple\_potential\_pdb\_1.pdb* file from the *Examples/* directory).

```
REMARK POTENTIAL AMBER
HETATM 1 C MEOH 1 0.185 0.739 -0.000 GRP1 C
HETATM 2 H MEOH 1 -0.770 1.307 0.000 GRP1 H
HETATM 3 H MEOH 1 0.721 0.934 -0.953 GRP1 H
HETATM 4 H MEOH 1 0.721 0.934 0.953 GRP1 H
HETATM 5 O MEOH 1 -0.158 -0.634 -0.000 GRP1 O
HETATM 6 H MEOH 1 0.666 -1.128 -0.000 GRP1 H
REMARK POTENTIAL OPLS2005
HETATM 8 H MEOH 1 -0.770 6.307 0.000 GRP2 H
HETATM 10 H MEOH 1 0.721 5.934 0.953 GRP2 H
HETATM 7 C MEOH 1 0.185 5.739 -0.000 GRP2 C
HETATM 11 O MEOH 1 -0.158 4.366 -0.000 GRP2 O
HETATM 12 H MEOH 1 0.666 3.872 -0.000 GRP2 H
HETATM 9 H MEOH 1 0.721 5.934 -0.953 GRP2 H
HETATM 8 H MEOH 2 -0.770 10.307 0.000 GRP2 H
HETATM 10 H MEOH 2 0.721 9.934 0.953 GRP2 H
HETATM 7 C MEOH 2 0.185 9.739 -0.000 GRP2 C
HETATM 11 O MEOH 2 -0.158 8.366 -0.000 GRP2 O
HETATM 12 H MEOH 2 0.666 7.872 -0.000 GRP2 H
HETATM 9 H MEOH 2 0.721 9.934 -0.953 GRP2 H
HETATM 1 C MEOH 3 0.185 -3.261 -0.000 GRP3 C
HETATM 2 H MEOH 3 -0.770 -2.693 0.000 GRP3 H
HETATM 3 H MEOH 3 0.721 -3.066 -0.953 GRP3 H
HETATM 4 H MEOH 3 0.721 -3.066 0.953 GRP3 H
HETATM 5 O MEOH 3 -0.158 -4.634 -0.000 GRP3 O
HETATM 6 H MEOH 3 0.666 -5.128 -0.000 GRP3 H
REMARK POTENTIAL CHARMM22_prot
HETATM 8 H MEOH 1 3.230 6.307 0.000 GRP4 H
HETATM 10 H MEOH 1 4.721 5.934 0.953 GRP4 H
HETATM 7 C MEOH 1 4.185 5.739 -0.000 GRP4 C
HETATM 11 O MEOH 1 3.842 4.366 -0.000 GRP4 O
HETATM 12 H MEOH 1 4.666 3.872 -0.000 GRP4 H
HETATM 9 H MEOH 1 4.721 5.934 -0.953 GRP4 H
END
```

The example model basically consists of five methanol molecules. The first methanol is assigned to the AMBER FF; the following three to the OPLS2005 FF and the last molecule is assigned to the CHARMM22\_prot FF.

Note that the example given above is just an illustration. Notice the ease and flexibility of applying multiple-potential schemes in a molecular model. Such a model is obviously nonsensical!

The location of the **POTENTIAL** directive determines the extent of the FF application. For instance, if the statement **POTENTIAL** OPLS2005 is removed, then the first four molecules will be assigned to the AMBER FF and the last molecule to the CHARMM22\_prot.

It is advisable to place the **POTENTIAL** directive statements within the PDB's REMARK statement. This is to ensure the directive statements do not interfere with the PDB file structure and can still be viewed using some standard molecular viewer programs.

Note that a **POTENTIAL** directive statement can only be placed **at the beginning** of a Molecular Group. For instance, the Molecular Group GRP2 as shown above contains two methanol molecules. Placing the **POTENTIAL** OPLS2005 statement somewhere in the middle of GRP2 scope will generate an error.

In the multiple potential scheme, all structures will be converted and assigned with the appropriate parameters according to the rules specific to the force field scheme. In order to distinguish atoms that belong to different force field schemes, a unique suffix will be appended to the ATOM\_KEYS as shown below:

X\_\$

The X is the ATOM\_KEY and '\$' is the unique label assign to a given FF scheme according to the order of appearance of each scheme in a user model. This label basically consists of alphabets 'A', 'B', 'C', etc.

For instance, from the given previous example, atoms that belong to **POTENTIAL** AMBER, OPLS2005 and CHARMM22\_prot will be assigned with the \_A, \_B and \_C suffixes respectively. In this case, the primary alkane carbon in AMBER is described as CT\_A, where CT is the standard AMBER key. For CHARMM22\_prot, the same carbon atom is described as CT3\_C, where CT3 is the standard CHARMM key.

## 10.2 Implementation for xyz Files

Molecular Groups can naturally be defined within a PDB file within the appropriate columns (See [Section 6.1](#)). For xyz file, the **MOLECULAR\_GROUP** directive would be needed. For example, consider the *multiple\_potential\_3.xyz* file in the *Examples/* directory, of which the relevant parts are shown below:

The example shows several methanol molecules classified into four groups, GRP1, GRP2, GRP3 and GRP4. If the multiple keyword is used in the control files, DL\_FIELD will setup a multiple potential model that contains CVFF and OPLS2005 force fields. Within the CVFF force field, atoms will be classified into GRP1, GRP2 and GRP3, while the ATOM\_KEYS will be assigned with a suffix \_A. The OPLS2005 force field will be applied to the last molecule with a suffix \_B and is associated with the Molecular Group GRP4.

```

30
Multiple potential schemes for methanol molecules
# MOLECULAR_GROUP GRP1 POTENTIAL cvff
C 0.185000 0.739000 0.000000
H -0.770000 1.307000 0.000000
H 0.721000 0.934000 -0.953000
H 0.721000 0.934000 0.953000
O -0.158000 -0.634000 0.000000
H 0.666000 -1.128000 0.000000
# MOLECULAR_GROUP GRP2
H -0.770000 6.307000 0.000000
H 0.721000 5.934000 0.953000
...
...
O -0.158000 8.366000 0.000000
H 0.666000 7.872000 0.000000
H 0.721000 9.934000 -0.953000
# MOLECULAR_GROUP GRP3
C 0.185000 -3.261000 0.000000
H -0.770000 -2.693000 0.000000
H 0.721000 -3.066000 -0.953000
H 0.721000 -3.066000 0.953000
O -0.158000 -4.634000 0.000000
H 0.666000 -5.128000 0.000000
# POTENTIAL opls2005 MOLECULAR_GROUP GRP4
H 3.230000 6.307000 0.000000
H 4.721000 5.934000 0.953000
C 4.185000 5.739000 0.000000
O 3.842000 4.366000 0.000000
H 4.666000 3.872000 0.000000
H 4.721000 5.934000 -0.953000

```

For INORGANIC force fields, both **MOLECULAR\_GROUP** and **MOLECULE\_KEY** directives (see [Section 6.2](#)) must be defined on the same statement line in the xyz file. For example, consider a mixed organic-inorganic system such as the *multiple\_potential\_4.xyz* file in the *Examples/* directory:

```

33
# POTENTIAL OPLS2005 MOLECULAR_GROUP A1
C 0.995000 0.329000 5.000000
H 1.844000 -0.392000 5.000000
H 1.096000 0.975000 4.098000
H 1.096000 0.976000 5.901000
C -0.340000 -0.404000 5.000000
H -0.456000 -1.038000 5.907000
H -0.457000 -1.039000 4.093000
H -2.235000 0.073000 5.000000
O -1.394000 0.538000 5.000000
# POTENTIAL inorganic_binary_oxide MOLECULE_KEY MO3 MOLECULAR_GROUP A2
O 0.000000 6.312000 0.000000
Mg 0.000000 0.000000 0.000000
O 0.000000 2.104000 0.000000
Mg 0.000000 4.208000 0.000000
O 2.104000 0.000000 0.000000
Mg 2.104000 2.104000 0.000000
O 2.104000 4.208000 0.000000
...
...

```



The example above shows a simple system consists of an ethanol molecule (organic) and magnesium oxide (inorganic). For the organic part, the **MOLECULE\_KEY** directive is not required. DL\_FIELD will automatically determine the chemical structure base on the element symbols and assign the force field parameters automatically for the OPLS2005 force field.

For the inorganic part, the **MOLECULE\_KEY** directive must be defined, along with the **MOLECULAR\_GROUP**. The **MOLECULE\_KEY** directive indicates which MOLECULE template to look for by the DL\_FIELD program. Unlike the organic systems, only one **MOLECULE\_KEY** would be allowed for a Molecular Group. In contrast to the PDB format, normal element symbols are allowed and DL\_FIELD will attempt to determine the corresponding ATOM\_KEYS. However, the success of such attempts is not guaranteed, especially for more complex inorganic systems. For this reason, DL\_FIELD can also recognise the actual ATOM\_KEYS, instead of just element symbols. For instance, consider a clay mineral with an organic molecule (benzene) as shown below:

```

451
CRYST1 83.908 20.7302253 17.9859383759 90.00 90.00 90.00 (P 1)
# POTENTIAL CVFF MOLECULAR_GROUP ORG1
C 10.000000 1.390000 0.000000
C 10.000000 0.695000 1.204000
C 10.000000 -0.695000 1.204000
C 10.000000 -1.391000 0.000000
C 10.000000 -0.695000 -1.204000
C 10.000000 0.695000 -1.204000
H 10.000000 2.450000 0.000000
H 10.000000 1.225000 2.123000
H 10.000000 -1.226000 2.122000
H 10.000000 -2.451000 0.000000
H 10.010000 -1.226000 -2.122000
H 10.000000 1.225000 -2.122000
# POTENTIAL inorganic_clay MOLECULAR_GROUP CLY MOLECULE_KEY CLYF
st -2.675000 -6.024000 4.703000
st -2.700000 -6.039000 -4.313000
st -2.776000 -3.444000 -8.761000
ob -3.282000 -7.370000 -7.946000
ob -3.236000 -7.348000 0.934000
ob -3.229000 -2.154000 0.953000
...
...

```

In this example, the organic part would still be determined by DL\_FIELD and assign CVFF parameters. For the inorganic part, the actual ATOM\_KEYS are used for CLAYFF (st, ob, etc). DL\_FIELD recognises this automatically and assign the parameters accordingly. Otherwise, certain ambiguous situation may arise, as for instance, same element symbols but with different coordination and therefore different sets of parameters may be needed. However, such ambiguity will eventually be reduced in subsequent DL\_FIELD releases.

### 10.3 Mixing Lennard-Jones 12-6 Potentials

DL\_FIELD can mix 12-6 Lennard-Jones potentials for a given non-bonded atom pair belong to different FF schemes. The mixing rule for epsilon and sigma can be independently specified in Option **18** and Option **19** respectively. See [Section 3.10.1](#) for the available mixing schemes.

The mixing of LJ parameters can be applied for FF schemes that use the 12-6 functional forms. This means most of the ORGANIC FF schemes and a few INORGANIC ones such as the CLAYFF (clay force field).

#### 10.4 Mixing Lennard-Jones 9-6 Potentials

PCFF and COMPASS use the LJ 9-3 form. In this case, if PCFF and COMPASS are present in the system, the vdw parameters will be mixed according to the 6<sup>th</sup> order mixing rules\*:

$$\varepsilon = 2\sqrt{\varepsilon_i\varepsilon_j}\left(\frac{R_i^3R_j^3}{R_i^6+R_j^6}\right) \quad R = \left[\frac{(R_i^6+R_j^6)}{2}\right]^{\frac{1}{6}}$$

Where  $R_i$  and  $R_j$  are the minimum equilibrium distances for atom  $i$  and atom  $j$ , respectively with one from PCFF and the other from COMPASS. Note: The vdw mixing rules in Option **18** and Option **19** only applies to 12-6 functional forms.

\* M. Waldman and A.T. Hagler, *J. Comput. Chem.* **14**, 1077 (1993)

#### 10.5 Mixing Lennard-Jones 9-6 and 12-6 Potentials

In order to blend between LJ 9-6 and LJ 12-6 in a multiple potential setting, DL\_FIELD can transform LJ 9-6 to LJ 12-6 form. From such, the vdw parameters for mixed potential schemes can be derived based on the mixing rules specify in Option **18** and Option **19**. Obviously, this sort of transformation is only an approximation.

Similar to the 12-6 form, the 9-6 form can be expressed in terms of equilibrium distance,  $R$  or the steric parameter,  $\sigma$ .

$$V(r_{ij}) = \varepsilon \left[ 2 \left( \frac{R}{r_{ij}} \right)^9 - 3 \left( \frac{R}{r_{ij}} \right)^6 \right]$$

$$V(r_{ij}) = 6.75\varepsilon \left[ \left( \frac{\sigma}{r_{ij}} \right)^9 - \left( \frac{\sigma}{r_{ij}} \right)^6 \right]$$

with the following relationship:

$$R = 1.5^{\frac{1}{3}}\sigma \approx 1.144714\sigma$$

The corresponding LJ 12-6 forms would be expressed as follows:

$$V(r_{ij}) = \varepsilon \left[ \left( \frac{R}{r_{ij}} \right)^{12} - 2 \left( \frac{R}{r_{ij}} \right)^6 \right]$$

$$V(r_{ij}) = 4\varepsilon \left[ \left( \frac{\sigma}{r_{ij}} \right)^{12} - \left( \frac{\sigma}{r_{ij}} \right)^6 \right]$$

With the following relationship:

$$R = 2^{\frac{1}{6}}\sigma \approx 1.122462\sigma$$

If the values of  $R$  and  $\epsilon$  are transferred, as is, from LJ 9-6 to LJ 12-6, this will underestimate the density and surface energy would decrease. This is because the 9-6 form is softer on the repulsive part and more attractive at the dispersive part when compare with the 12-6 form.

By starting from a given set of 9-6 parameters, DL\_FIELD will fit numerically to derive the equivalent 12-6 parameters base on same area between the functions, over the interatomic distance from  $\sigma$  to 15 Å. The justification to do so is described below.

For example, consider the aromatic carbon in COMPASS FF of atom type c3a with  $R = 3.915$  Å and  $\epsilon = 0.068$  kcal/mol for LJ 9-6 functions. Graph below shows the corresponding LJ functions for the 9-6, fitted 12-6 and unfitted 12-6 (using the 9-6 parameters, as is).

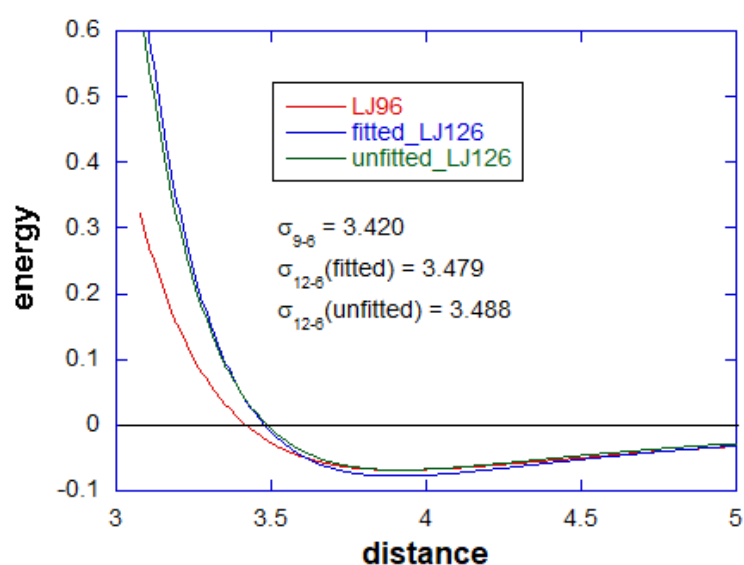


Table below shows the coefficient of determinations (goodness of fits) of LJ functions. The unfitted LJ 12-6\* (shown in graph above) used similar  $R$  and  $\epsilon$  of the LJ 9-6, while the unfitted LJ 12-6\*\* used the identical  $\sigma$  and  $\epsilon$  values of LJ 9-6.

	Fitted LJ 12-6	Unfitted LJ 12-6*	Unfitted LJ 12-6**
Short range ( $0.9\sigma$ to $\sigma$ )	-3.134618	-2.030590	0.639511
Near equilibrium ( $\sigma$ to $2\sigma$ )	0.923565	0.915493	0.941755
Long range ( $2\sigma$ to 15 Å)	0.948703	0.884641	0.805844
Overall ( $\sigma$ to 15 Å)	0.969042	0.965565	0.976322

As expected, the LJ 12-6 functions do not fit well relative to LJ 9-6 at the repulsive range, due to softness of the latter function. The fitting at the short range is vastly improved if the LJ 12-6 is forced to adopt the identical  $\sigma$  value (LJ 12-6\*\*). However, this results in the change of value of  $R$  due to differing relationships for LJ 9-6 and LJ 12-6 as shown above. For this reason, this would sacrifice the accuracy over longer range, with the fitting coefficient reduces to about 0.8058.

For the fitted LJ 12-6 parameters,  $\epsilon$  is 0.076 kcal/mol, which is slightly stronger to compensate for the more repulsive part of the 12-6 potential. At the same time, the

fitted R value is 3.905 Å which is quite similar to that of LJ 9-6 (3.915 Å). For this reason, it gives better fit to the dispersive part over longer range ( $2\sigma$  to 15 Å).

The fitting outcomes will be shown in *dl\_field.output* if the multiple potential systems involve the mixing of the LJ 9-6 and 12-6 functions and Option **7** (verbosity mode) is switched on.

Note that DL\_FIELD only provides a mean to automatically refit the parameters. It is still up to the user to test the validity of such mixing, as would be the case for all vdw mixing in a mixed potential system.

## 10.6 Using VDW\_MIX

DL\_FIELD permits the setting up of bio-inorganic models but make no attempt to mix the vdw parameters between organic and inorganic atoms. Such parameters can be inserted manually in the *dl\_poly.FIELD* file, or by making use of the **VDW\_FIX** directive.

Example below shows the latter part of the DL\_POLY's FIELD file, produced from the *multiple\_potential\_2.pdb* file from the *Examples/* directory.

```

...
Molecule name not_define
nummols 1
atoms 24
Mg3_B      0.00000  2.00000 12  0
O10_B     0.00000 -2.00000 12  0
finish
vdw 28
CT3_A CT3_A lj      0.0800  3.6705
HA_A  CT3_A lj      0.0420  3.0112
CT2_A CT3_A lj      0.0663  3.7730
OH1_A CT3_A lj      0.1103  3.4121
H_A   CT3_A lj      0.0607  2.0353
HA_A  HA_A  lj      0.0220  2.3520
CT2_A HA_A  lj      0.0348  3.1137
OH1_A HA_A  lj      0.0578  2.7529
H_A   HA_A  lj      0.0318  1.3760
CT2_A CT2_A lj      0.0550  3.8754
OH1_A CT2_A lj      0.0915  3.5146
H_A   CT2_A lj      0.0503  2.1377
OH1_A OH1_A lj      0.1521  3.1538
H_A   OH1_A lj      0.0836  1.7769
H_A   H_A   lj      0.0460  0.4000
Mg3_B Mg3_B buck    0.0000  0.0000  0.0000
O10_B Mg3_B buck   26566.2720  0.3065  0.0000
O10_B O10_B buck   524868.3600  0.1490  667.8466
CT3_A Mg3_B ????.xxx xxx
CT3_A O10_B ????.xxx xxx
HA_A  Mg3_B ????.xxx xxx
HA_A  O10_B ????.xxx xxx
CT2_A Mg3_B ????.xxx xxx
CT2_A O10_B ????.xxx xxx
OH1_A Mg3_B ????.xxx xxx
OH1_A O10_B ????.xxx xxx
H_A   Mg3_B ????.xxx xxx
H_A   O10_B ????.xxx xxx
close

```

The example model consists of ethanol molecules and magnesium oxide. The organic molecule is associated with the Molecular Group 'ETOH'. For magnesium oxide, Molecular Group is not defined in the PDB file (see *multiple\_potential\_2.pdb*) and DL\_FIELD assigns the Molecular Group to the inorganic materials as 'not\_define'.

The ethanol molecule is assigned to the CHARMM22\_prot FF, while a rigid-ion INORGANIC\_binary\_oxide FF model is assigned to magnesium oxide. The ATOM\_KEYS were appended with the suffixes '\_A' and '\_B', respectively to distinguish the atoms to which FF schemes they belong.

The vdw LJ mixing rules are applied to organic atom pairs according to the CHARMM's mixing rules, while the vdw interactions for magnesium oxide are described by a set of Buckingham (buck) potentials. However, DL\_FIELD does not do cross mixing between atom pairs of different FF schemes. All such possible cross combinations are listed as question marks and crosses. It is up to the user to manually insert the suitable parameters for these atom pairs.

As mentioned earlier, the **VDW\_FIX** directive can be used in DL\_FIELD to insert these mixed vdw parameter sets automatically, for instance, in an *udff* file as shown below:

```
POTENTIAL inorganic_binary_oxide

UNIT kcal/mol

VDW_FIX charmm22_prot
CT3 Mg3 mors 2.40 3.50 0.52
Mg3 H lj 0.06 2.88 0.0
END VDW_FIX

END POTENTIAL
```

By requesting DL\_FIELD to read the *udff* file, the following FIELD file will be produced.

```
...
H_A CT3_A lj 0.0607 2.0353
HA_A HA_A lj 0.0220 2.3520
CT2_A HA_A lj 0.0348 3.1137
OH1_A HA_A lj 0.0578 2.7529
H_A HA_A lj 0.0318 1.3760
CT2_A CT2_A lj 0.0550 3.8754
OH1_A CT2_A lj 0.0915 3.5146
H_A CT2_A lj 0.0503 2.1377
OH1_A OH1_A lj 0.1521 3.1538
H_A OH1_A lj 0.0836 1.7769
H_A H_A lj 0.0460 0.4000
Mg3_B Mg3_B buck 0.0000 0.0000 0.0000
O10_B Mg3_B buck 26566.2720 0.3065 0.0000
O10_B O10_B buck 524868.3600 0.1490 667.8466
CT3_A Mg3_B mors 2.4000 3.5000 0.5200
CT3_A O10_B ???? xxx xxx
HA_A Mg3_B ???? xxx xxx
HA_A O10_B ???? xxx xxx
CT2_A Mg3_B ???? xxx xxx
CT2_A O10_B ???? xxx xxx
OH1_A Mg3_B ???? xxx xxx
OH1_A O10_B ???? xxx xxx
H_A Mg3_B lj 0.0600 2.8800
H_A O10_B ???? xxx xxx
close
```

New parameters are now inserted in the vdw section, highlighted in bold, in different functional forms such as the Lennard-Jones 12-6 (lj) function and the Morse (mors) potential function. Please note that these are arbitrary values and do not copy them for your own model setup and calculations!

## 11 Beyond the Standard (Potential) Models

This chapter describes some of the features available in DL\_FIELD that can be used to modify the standard potential schemes according to user's needs. Note that features in this Chapter do not apply to xyz files since they are only used within a MOLECULE definition.

### 11.1 Pseudo Atoms

In DL\_FIELD, a pseudo atom is an imaginary particle that can take any atomic mass and charge and can optionally include inter-molecular interactions (vdw and coulombic). Its position is fixed relative to other atom or group of atoms within a MOLECULE. In other words, [**RIGID**] directives that involve all pseudo atoms must be issued within the **MOLECULE** definition. Otherwise, DL\_FIELD will flag up an error.

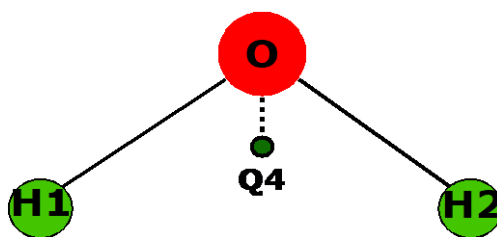
However, pseudo element symbols only take a certain subset of two-character format in the form of QX, where X = 0 to 9 and A to V (case insensitive). This is how DL\_FIELD identify an *atom\_type* as a pseudo atom. For instance, Q3, QD are arbitrary pseudo atom symbols. QW, QX, QY and QZ are pre-defined for DL\_FIELD internal use only.

Pseudo atom is a useful feature to modify the existing standard potential model for a particular user's model. For instance, inclusion of a pseudo atom into -N=N- to model the polarisability of the bond. There are some restrictions when using a pseudo atom within a MOLECULE:

- (a) The pseudo element symbol and its corresponding ATOM\_KEY and ATOM\_LABEL must be exactly matched with identical characters of the form QX.
- (b) The pseudo ATOM\_TYPE is unique within a MOLECULE. In other words, if there are more than one pseudo atoms in a MOLECULE, each individual pseudo ATOM must be assigned with different pseudo element symbols. However, similar pseudo ATOMS can be re-used for different MOLECULEs.
- (c) A [**RIGID**] directive that contains a pseudo ATOM must always be issued within the MOLECULE. The directive must also contain at least one normal ATOM.
- (d) Pseudo ATOMS must not be connected to any other atoms within the MOLECULE. In other words, pseudo ATOMS are not physically or covalently connected with any other atoms. Its positions relative to the others are held fixed by issuing a [**RIGID**] directive as mentioned above.
- (e) For the reason given in (d), a self-CONNECT directive must be issued for a pseudo ATOM:

**CONNECT** QX > QX

An example usage of pseudo ATOM is shown in MOLECULE water\_tip4p, which is the standard TIP4P water model available in the *DLPOLY\_CHARMM22\_prot.sf* file. A pseudo ATOM is defined with ATOM\_KEY Q4. The pseudo ATOM is used in the TIP4P model as a pseudo point charge with no vdw interaction:



The definition of TIP4P MOLECULE in DL\_FIELD are as follows:

```

...
ATOM_TYPE   key   element  mass  remark
...
pseudo_tip4p  Q4    Q4         0.000  TIP4P pseudo point
...
END ATOM_TYPE

MOLECULE_TYPE key    mw      remark
...
water_tip4p     TIP4   18.015  Standard TIP4P
...
END MOLECULE_TYPE

MOLECULE water_tip4p 4 0.0
O   O_tip4p      0.00
H1  H_tip4p     0.52
H2  H_tip4p     0.52
Q4  pseudo_tip4p -1.04
CONNECT O   > H1 H2
CONNECT H1  > O
CONNECT H2  > O
CONNECT Q4  > Q4
RIGID O H1 H2 Q4
END MOLECULE TIP4P
...
...

```

Note that Q4 does not have to confine for use in TIP4P water only. The same pseudo point can be reused for other purposes in the other MOLECULE definitions.

## 11.2 Core-shell Models

The [core-shell](#) models that are commonly encountered in inorganic systems can also be applied for ORGANIC force fields in DL\_FIELD. An example is given in the */Examples* directory for the core-shell version of ethanol molecules for CHARMM force field (*ethanol\_shell.pdb*). The corresponding *udff* file (*alcohol.udff*) contains the definition for the core-shell version of the ethanol MOLECULE, *ethanol\_sh*:

```

MOLECULE ethanol_sh 10 0.0   Ethanol (ethyl alcohol) - shell model
C1 Cp_alkane      -0.27
H11 HC_alkane    0.09   H11 H21
H12 HC_alkane    0.09   | |
H13 HC_alkane    0.09   H12--C1--C2--O--H
C2 Cs_alkane     0.05   | | \
H21 HC_alkane    0.09   H13 H22 OZ
H22 HC_alkane    0.09
O O_hydroxyl_core 0.10
OZ O_hydroxyl_shl -0.76
H HO_alcohol     0.43
CONNECT C1 > H11 H12 H13 C2
CONNECT H11 > C1
CONNECT H12 > C1
CONNECT H13 > C1
CONNECT C2 > C1 H21 H22 O
CONNECT H21 > C2
CONNECT H22 > C2
CONNECT O > C2 H
CONNECT OZ > OZ
CONNECT H > O
SHELL O OZ
END MOLECULE

```

Note that the ATOM\_LABEL O is used for the core-component. Whereas, the OZ is in fact the ATOM\_KEY for the shell component of the oxygen atom, which must be defined as a [self-CONNECT](#) ATOM.

For the ORGANIC force fields, instead of the core, the shell part of an atom will be defined in the FIELD file for the 1-4 vdw interactions. The 1-4 vdw interactions for the core part will always be zero. For this reason, DL\_FIELD will look for the 1-4 vdw parameters for the shell-part of an atom. For the 1-4 Coulombic interactions, the DL\_POLY directive **exclude** should be used in the CONTROL file to consider all possible combinations of 1-4 core-shell interactions. This directive is automatically included in DL\_FIELD's *dl\_poly.CONTROL* file.

Example below shows the vdw definition for the MOLECULE *ethanol\_sh* (extracted from *alcohol.udff*).

```

VDW   Eps  Rmin/2  Eps_1-4  Rmin/2,1-4  Remark
O_cr   0.00  0.00    0.0    0.0    !
OZ    -0.1521 1.7700 0.0    0.0    !
END VDW

```

Note that the vdw parameters are defined for the shell since the 'chemistry' is occurred at the shell part of the atoms and the core must be set to zero. This will ensure that there is no vdw interaction between the core part of the atom with all other ATOMS.

For CHARMM and CHARMM19 potential schemes, if *Eps\_1-4* and *Rmin/2,1-4* are set to some finite values, then these values will be used for the 1-4 vdw interactions instead.



## 12 The DL\_F Notation

The DL\_F Notation is a universal atom typing notation that is uniquely implemented in DL\_FIELD. It is a consistent atom typing scheme that is contiguous across different force field schemes. Assignment of types of atoms, and therefore the appropriate potential parameters, in a molecular system is usually a non-trivial task. This is because different potential schemes usually have different sets of complicated rules how types of atoms are being assigned. The task is further complicated by the fact that the descriptions of these atom types are frequently cryptic in nature. Take an example, a methyl carbon atom is represented as 'CT3' and c3 in CHARMM and PCFF, respectively. Whereas, OPLSAA just expresses it as 'CT'.

The introduction of the DL\_F Notation allows DL\_FIELD to assign ATOM\_TYPES based on a single conversion scheme that works across different FF schemes. This smoothens data transitions and minimises learning curves on user's side when converting molecular models among different FF schemes.

The DL\_F notation applies to most FF schemes including OPLS2005, PCFF, CVFF, AMBER GAFF, OPLS CL&P and all CHARMM components. By using these FFs, DL\_FIELD can convert structures in all formats (PDB, xyz, and mol2 with some exceptions). Upon successful conversion, DL\_FIELD will also generate an output file called *dff\_notation.output* in the *output/* directory. The file essentially contains atomic structures listed in DL\_F Notation.

The Notation avoids the use of cryptic symbols and all ATOM\_TYPES are described in self-explanatory, easy to understand form, while at the same time can precisely indicate the chemical nature of each atom in a molecule.

Originally, DL\_F Notation was only applicable to covalent molecules, such as general organic molecules and even specific classes of biomolecules such as sugars and proteins. This has now been extended to include inorganic molecules (See [Section 12.8](#))

For more information about the DL\_F Notation and how the conversion works please refer to the following references:

C. W. Yong, *J. Chem. Inf. Model.* **56**, 1405-1409 (2016)

C. W. Yong, SSRN (2022), <http://dx.doi.org/10.2139/ssrn.4254942>

The use of the DL\_F Notation to annotate molecular interactions at atomistic scales was demonstrated in the following reference:

C. W. Yong and I. T. Todorov, *Molecules* **23**, 36 (2018)

### 12.1 The DL\_F Atoms

The DL\_F notation only recognises a number of atoms in the Periodic Table of the Elements. They include elements that are commonly encountered in organic molecules: hydrogen (H), carbon (C), oxygen (O), nitrogen (N), sulphur (S), phosphorus, boron (B), silicon (Si), alkaline metals, alkaline earth metals and all halides and noble gases.

### 12.2 The Chemical Group (CG) and Chemical Group Index (CGI)

The term Chemical Group (*CG*) refers broadly to the functional group in chemistry. The *CGs* are similar to functional groups in organic chemistry but within the context of chemical elements for molecular simulations. A *CG* consists of a specific group of *DL\_F Atoms* and bonds within a molecular structure that exhibits a characteristic chemical behaviour of the molecule. Every *CG* is also represented by a unique *CG* index number, *CGI*, ranged between 1-9999.

Some examples of *CG* are *alkane*, *aldehyde*, *alcohol*, *acylhalide*, etc, with the corresponding unique *CGI* of 1, 17, 15, 18, respectively. For a complete list please refer to *DLF\_notation* file in the *lib/* directory.

In some cases, a *CG* refers to a special group of molecule. For instance, *cyclopropyl* and *cyclobutyl* are *CGs* that contained saturated carbon atom in a 3-member and 4-member ring, respectively. These molecules usually have different structural behaviour and therefore assigned with different sets of potential parameters. On the other hand, the atoms from other cycloalkanes such as cyclopentane and cyclohexane are generally assigned to the *cycloalkane CG*. DL\_FIELD also recognises certain complex *CGs*. For instance, *pyrene* (581), *hydantoin* (600) and *xanthine* (706).

### 12.3 Primary DL\_F Tokens

These are supporting tokens that can be expressed optionally along with a *DL\_F Atom*. They are used to locate or to distinguish one *DL\_F Atoms* from another within a *CG*. The available primary tokens are shown below:

*p*, *s*, *t*, *q* – refer to the degrees of substitution on either carbon (*C*) and nitrogen (*N*) atoms, depending on the number of connected hydrogen (*H*) atoms. The *C* and *N* atoms can be classified into primary (*p*), secondary (*s*), tertiary (*t*) and quaternary (*q*) atoms.

For carbon atoms, this can be *Cp*, *Cs*, *Ct* and *Cq*, which refer to carbon atoms with three, two, one and zero hydrogen (*H*) atoms attach to a carbon atom.

For *N* atoms, *Np*, *Ns* and *Nt* refer to two, one and zero *H* atoms attach to an *N* atom. In some special cases such as the *ammonium CG*, which contain four bonds, *Np*, *Ns*, *Nt* and *Nq* refer to nitrogen atoms with three, two, one and zero hydrogen (*H*) atoms attach to a nitrogen atom.

'*n* – refer to the degree of general substitution, where *n* refers to the degree of substitution with a range of 1 to 3. It is similar to the above with the exception that the degree of substitutions depends on the number of substituted atoms connected to the atom. These substituted atoms are often belonged to other *CGs*. For instance, *C'2* in the *alkane CG* means secondary (second degree) substitution where two of the hydrogen atoms were substituted with some other atoms such as nitrogen, oxygen, etc, **but not** with another *C* atom belong to the *alkane*.

*E* – refers to a terminal position within a *CG* (the 'end' atom).

*L* – refers to a link, or non-terminal (inner) *PA* within a *CG*.

The positive (+) and negative (-) signs refer to the charge state of a *DL\_F Atom*.

1, 2, 3, etc – numerical values. These tokens usually apply to aromatic or pyranose cyclic compounds.

## 12.4 Secondary DL\_F Tokens

This is a group of optional supporting tokens that can be expressed along with a *DL\_F Atom*, to indicate the way or the type of atom to which it is connected to. The available tokens are shown below:

*R* - next to an aryl carbon atom.

*U* - next to an unsaturated carbon atom (such as alkene, alkyne type).

*A* - alpha, refers to the first atoms that connect directly to an atom within a *CG*.

*B* - beta, refers to the second atoms that connect directly to an atom within a *CG*.

*G* - gamma, refers to the third atoms that connect directly to an atom within a *CG*.

Element symbols of the neighbouring *DL\_F Atom* itself.

## 12.5 The Notation Rules

The following lists the rules in using the DL\_F Notation.

- (a) Every *DL\_F Atom* in a system model will have an *ATOM\_TYPE* that associates with a *CG* tag to which it belongs. This means that the corresponding *DL\_F ATOM\_KEY* will associate with the corresponding *CGI*.
- (b) Every *DL\_F Atom* can only associate with not more than one token from **each group** of the *DL\_F token*. This means that there can be only one token, either from the *Primary DL\_F Token* or the *Secondary DL\_F Token* that associates with a *DL\_F Atom*. However, two tokens are permissible only if each is originated from both *Primary* and *Secondary Token* groups.
- (c) Single-valence *DL\_F Atoms* such as hydrogen and halogens must always express along with a *Secondary DL\_F Token*. This is usually the element symbol of a neighbouring *DL\_F Atom*.

## 12.6 The Notation Expressions

In a DL\_F expression, each *ATOM\_TYPE* is referenced to an *ATOM\_KEY*. The DL\_F *ATOM\_TYPES* are expressed as follows:



Where *A* is the element symbol of a *DL\_F Atom*, *[t]* is the optional *DL\_F token* and *CGname* is the name of the Chemical Group to which the atom *A* belongs.

The corresponding DL\_F *ATOM\_KEYS* are expressed as follows:



Where *A* is the element symbol of a DL\_F Atom, *CGI* is the Chemical Group index number and *[t]* is the optional *DL\_F token*.

The optional expression, *#n*, is called the version number. If there are more than one version of identical *ATOM\_TYPES*, but may share different parameters, then *#n* would be

needed, where  $n$  is an arbitrary integer. Different values of  $n$  differentiate one version of ATOM\_TYPE from the others. The version labelling would be needed, especially for [MISC\\_FF](#) scheme, which include a range of FF models from different sources.

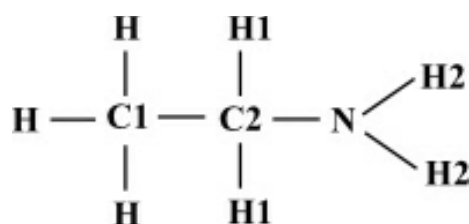
For example, a primary alkyl carbon atom has the DL\_F ATOM\_TYPE of *Cp\_alkane* with the corresponding ATOM\_KEY of *C1p*. In this example, C is the carbon atom, *p* is a primary token refers to *primary* and *alkane* is the CG, which has the unique CGI of 1.

The alkyl hydrogen atoms are expressed as *HC\_alkane* with the ATOM\_KEY *H1C*. In this case, C is a *Secondary DL\_F Token* which is the neighbouring DL\_F Atom to which the hydrogen atom is connected to.

If there are, say, two versions of identical ATOM\_TYPES, then this can be distinguished from each other's as *Cp\_alkane#1*, *Cp\_alkane#2* with the corresponding ATOM\_KEYS of *C1p#1* and *C1p#2*, respectively.

## 12.7 Organic Molecules Examples

The following lists several example structures together with the assignment of ATOM\_TYPES in the DL\_F Notation.



(a) Ethylamine

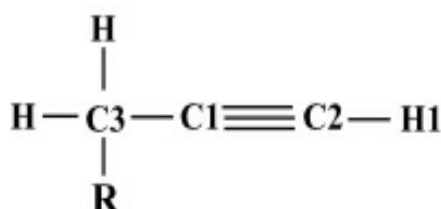
This is a primary amine and DL\_FIELD will assign the ATOM\_TYPES (ATOM\_KEYS in bracket) for each atom as follows:

C1 = *Cp\_alkane* (*C1p*)  
 C2 = *Cs\_alkane* (*C1s*)  
 H = *HC\_alkane* (*H1C*)  
 H1 = *HC\_alkane* (*H1C*)  
 N = *Np\_amine* (*N45p*)  
 H2 = *HN\_amine* (*H45N*)

Note that DL\_FIELD will automatically search for any conditional modification based on the chosen FF scheme and reassign an ATOM\_TYPE accordingly. For example, the C2 atom can be reassigned as *CA\_amine* with the ATOM\_KEY *C45A*, implicating the fact that the C2 will be assigned to a different sets of potential parameters due to the presence of the neighbouring nitrogen atom. Since H1 atoms are connected to C2, which is now an alpha atom amine, they will also reassign to become *HA\_amine* (*H45A*).

Note that such conditional modifications will only apply if needed depending on the nature and the type of FF chosen. Even then, users can still make out cognitively the identity of the atom despite the change of the ATOM\_TYPE expression.

(b) Propyne



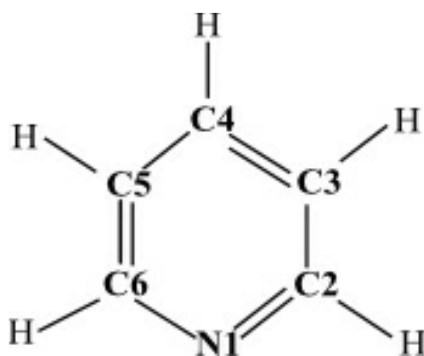
This is an alkyne and DL\_FIELD will assign the ATOM\_TYPES (ATOM\_KEYS in bracket) for each atom as follows:

C1 = CL\_alkyne (C3L)  
 C2 = CE\_alkyne (C3E) - terminal alkyne carbon  
 H1 = HC\_alkyne (H3C)  
 C3 = Cs\_alkane (C1s)  
 H = HC\_alkane (H1C)

Once again, DL\_FIELD will automatically search for any necessary reassignment. For instance, in OPLS2005, the C1 atom can be assigned with different parameter sets depending on the neighbouring atom, which is the C3, a secondary alkane carbon atom. DL\_FIELD can reassign C1 as CCs\_alkyne (C3Cs). If R = H, then the C3 would be Cp\_alkane (C1s) and the C1 will be reassigned as CCp\_alkyne (C3Cp).

Note that Rule (2) as described in [Section 12.5](#) still holds where the 'C' in C3Cs is the Secondary DL\_F Token and the 's' in C3Cs is the Primary DL\_F Token.

(c) Pyridine



The DL\_F notation apply specific rules for most aromatic cyclic compounds. The aromatic carbon atoms are distinguished from one another by a numerical token assigned serially around the ring. In the case of hydrogen atoms, they are assigned with the generic ATOM\_TYPE HC\_aromatic. Take example for a pyridine molecule, DL\_FIELD will assign the atoms as follows:

N1 = N1\_pyridine (N501-1)  
 C2 = C2\_pyridine (C501-2)  
 C2 = C3\_pyridine (C501-3)  
 C2 = C4\_pyridine (C501-4)  
 C2 = C5\_pyridine (C501-5)  
 C2 = C6\_pyridine (C501-6)  
 H = HC\_aromatic (H11C)

Where CGI of 501 and 11 refer to pyridine and the generic aromatic CGs respectively. Note that the numerical tokens are expressed as -1, -2, etc, in order to distinguish them from the CGI.

The *Examples/* directory contains a few xyz structures to illustrate the use of the DL\_F Notation. To do this, the value 1 must be selected for [Option 12](#) in the *control* file, to instruct DL\_FIELD to write out atoms in DL\_F Notation.

If the user configuration file is in the *xyz* or *mol2* formats, DL\_FIELD will produce a user-structure file, called the *dif\_notation.output* in the *output/* directory. The file contains a list of ATOM\_TYPES expressed in DL\_F Notation that match with the atoms in the user configuration.

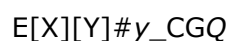
## 12.8 DL\_F Notation for Inorganic Systems

The standardised annotation for inorganic species had already made available in earlier versions of DL\_FIELD but was only made official from version 4.8 onwards.

An atom in organic molecules is usually identifiable based on its chemical characteristics that is almost always depending on the connectivity to its surroundings. For inorganic system, similar chemical characteristics can have different parameters depending on the types of inorganic materials and their coordination numbers. For this reason, while topologically speaking, the chemical structures of inorganic materials are generally less complex than those of organic molecules, annotating inorganic species are much less straight forward.

### 12.8.1 ATOM\_TYPE format

Similar to the DL\_F expression for organic atoms, each ATOM\_TYPE is referenced to an ATOM\_KEY. The DL\_F ATOM\_TYPES for inorganic species are expressed as follows:



E is the element symbol.

[X] is the formal charge value, including the charge sign. For instance, 2+, 2- or simply + or - for unit charge. It can be omitted if it is a neutral species (leave blank).

[Y] is the optional element symbol to which it is connected (or neighbouring) to E.

# is the (usual) coordination geometry or state of an atom and takes the following values for y:

- 2 = (coordinated to two atoms) linear
- 3 = (coordinated to three atoms), trigonal
- 4 = (coordinated to four atoms), tetrahedral, square planar
- 5 = (coordinated to five atoms), trigonal bipyramid, square pyramid.
- 6 = (coordinated to six atoms), octahedral, trigonal prismatic.
- 7 = (coordinated to seven atoms), octahedral, trigonal prismatic
- a = amorphous
- l = liquid state, for example, ions in solution
- g = gas phase
- c = core part of an atom.
- s = shell part of an atom.

Of note is that, in DL\_FIELD, the values of y are only indications how many neighbouring atoms are to be expected. The program does not necessarily flag up an error should the

neighbour criteria is not met. For instance, surface atoms have less coordination than those in the bulk. Even then, the Notation allows one to create ATOM\_TYPES, and hence, distinguish these atoms.

CG is the same as the organic counterparts, which is the Chemical Group for the inorganic systems. Examples are *binary\_oxide*, *binary\_halide*, *glass*, etc.

Q is the numerical suffix to distinguish different versions of force field models to which E belongs. For instance, the value Q is used to indicate a particular type of Fe<sup>3+</sup> from many different versions of potential models for iron(III) oxide, developed by different workers. In the standard library files, Q is usually referred to the reference source to which the parameters were derived from.

For example, the ATOM\_TYPE for Fe<sup>3+</sup> ion core in iron(III) oxide is described as

$$Fe3+\#6c\_binary\_oxide1$$

In this case, the suffix '1' refers to the particular set of potential models to which the Fe<sup>3+</sup> cation belongs. Note that since it is the core part of the cation, it means there must also be a shell part of the cation:

$$Fe3+\#6s\_binary\_oxide1$$

If the cation is a rigid ion model, then it can be expressed as

$$Fe3+\#6\_binary\_oxide2$$

Here, the suffix '2' distinguishes the cation from all other Fe<sup>3+</sup> ions that belong to different force field models.

### 12.8.2 ATOM\_KEY Format

The corresponding ATOM\_KEYS can be generated *in-situ* from the DL\_F ATOM\_TYPES. This means that there is no need to keep a separate reference list in the library files. The corresponding DL\_F keys for inorganic systems are expressed as follows:

$$E[Y]\#[y]I$$

Notice that the ATOM\_KEY does not convey all the information from the ATOM\_TYPE. This is because the ATOM\_KEY must be shortened to accommodate the restriction of up to the maximum permissible of 8 characters for atom labels in DL\_POLY files. For this reason, the abbreviated version of ATOM\_KEYS will be adopted with the following information being omitted (or abbreviated):

- (1) Use of *reduced* Chemical Group Index, I. This indicates the class of material to which atom E belongs. The quantity I is expressed in the reduced CGI form, where

$$I = CGI - 5000$$

For instance, the CGI for CG *glass* is 5050, I is therefore 5050-5000 = 50. The CGI values for different inorganic materials can be found in *DLF\_notation* file located in the *lib/* directory.

- (2) Charge value [X] and model version, Q, are omitted.
- (3) Atom state indication value, y, will be shown, only if y = c (core), or y = s (shell). The coordination number will be omitted.

Example 1: sodium oxide crystal adopts an antifluorite structure. The oxygen core anion is described as

*O2-#8c\_binary\_oxide1*

The corresponding ATOM\_KEY would be

*O#1*

Example 2: the oxygen atom that links with neighbouring silicon atoms in a clay framework is

*O2-Si#2\_clay1*

The corresponding ATOM\_KEY would be

*OSi#10*

Example 3: the shell part of the oxygen atom in a silicalite framework can be shown as:

*O2-#2s\_zeolite\_silicalite4*

The corresponding ATOM\_KEY would be

*O#s101*



## 13 Example Structures

The *Examples/* directory contains several sample structures. Look at the content of each file and convert these structures. Inspect the output files and see how DL\_FIELD works.

Not all force fields can work with every structure. An error will occur if certain information about a structure is not available for a chosen force field scheme.

The *control\_files/* directory contains a collection of *control* files named according to the example numbers. To convert these example structure, edit the *dl\_f\_path* and make sure the control file is pointed to the right location. For example, to convert the Example 5 structure, edit *dl\_f\_path* and define the control file component as:

```
control = control_files/example5.control
```

Now run DL\_FIELD. It will produce the corresponding *dl\_poly.CONFIG* and *dl\_poly.FIELD* (and possibly the *dlf\_notation.output*) files in the *output/* directory.

### 13.1 Example Files: PDB Format

#### (1a) *ethanol.pdb*

Contains a single ethanol molecule.

#### (2a) *sod1.pdb*

A superoxide dismutase protein structure. The protein consists of dimer orientated approximately 180 degree rotation relative to each other. Each monomer is given a Molecular Group names of SOD1 and SOD2 respectively. Notice that the protein contains histidine residues in various charge states.

After setting up force field for the protein, the *control* file then solvates the system with TIP3P CHARMM water model and automatically add counter ions.

#### (3a) *6pti.pdb*

This is bovine pancreatic trypsin, an example protein structure illustrated in the Amber 9 manual.

#### (4a) *b-All-a-Glc-OMe.pdb* (AMBER only)

A disaccharide methoxy-terminated structure. This is  $\beta$ -D-allopyranose-[1,3]- $\alpha$ -D-glucopyranose-1-OMe. DL\_FIELD recognises the standard Glycam naming convention for the carbohydrate structure. The *control* file also instructs DL\_FIELD to solvate the system with TIP4P water model.

#### (5a) *dodecylsulphate.pdb*

A single simple membrane molecule, constructed using some other molecular packages such as Chem3D. Note that the residue name has to change to SDS, which is the residue key for the molecule. The MOLECULE template can be found in the *.sf* file.

#### (6a) *ethanol\_auto1.pdb*, *ethanol\_auto2.pdb* and *alcohols.pdb* (CHARMM22\_prot only)

These are examples of alcohol structures that make use of the [auto-CONNECT](#) feature. The [udff](#) file called *alcohol.udff* must be used alongside with these structures. Please read the remarks included in each file.

When the *udff* file is read, DL\_FIELD converts the structures by using the **MOLECULE** ethanol template defined in the *udff* file, instead of using the standard **MOLECULE** ethanol template that is pre-defined in the library's *.sf* file.

The difference between *ethanol\_auto1.pdb* and *ethanol\_auto2.pdb* files is that the ethanol molecules in the former file are grouped with different residue id, whereas, the latter file lumped both molecules as a single residue with deliberate mixing of the atoms between them. This is to demonstrate DL\_FIELD can convert both configurations, unpicking the mixed atoms in the latter file into separate molecules.

The file *alcohols.pdb* contains two different types of alcohols but uses the same MOLECULE\_KEY (residue key), ROH as defined in the *alcohol.udff* file. This example file illustrates the use of the auto-CONNECT feature to construct a general MOLECULE template that applies to a class of molecules.

The example control files (*control\_files/example\_6a.control*), can be reused for all three PDB structures. Just change the input filenames in Option **8** of the *control* file.

(7a) *ethanol\_shell.pdb* (CHARMM22\_prot only)

An example use of the [core-shell](#) model in the organic force field. Here, the hydroxyl oxygen is assigned to core and shell components to mimic the polarizability effect of the atom. The *alcohol.udff* file must be used to convert this structure, which contains the **MOLECULE** ethanol\_sh template that is needed for the conversion.

(8a) *methanol.pdb* (CHARMM22\_prot only)

A single methanol molecule. The corresponding *udff* file (*alcohol.udff*) illustrates the overriding of the original **MOLECULE** methanol template in the *.sf* library file. Repeat DL\_FIELD run without the *udff* file and see what happens. You need to edit the *example8.control* file to do this (put *none* in Option **6**).

(9a) *mgo.pdb* and *mgo\_shell.pdb* (INORGANIC\_binary\_oxide force field)

Example use of the [INORGANIC](#) force field using the self-CONNECT feature. The *mgo.pdb* is a rigid ion model, whereas, *mgo\_shell.pdb* is the core-shell model of magnesium oxide. You need to edit *example9.control* to change the input filename.

(10a) *caco3.pdb* (INORGANIC\_ternary\_oxide force field)

An example use of a more complicated force field for inorganic systems. This is aragonite (calcium carbonate mineral) in water (SPC). The structure is converted by using the **MOLECULE** calcium\_carbonate1 template, which contain the auto-CONNECT and **ANGLE ONLY** features for DL\_FIELD to automatically set up bonds on the carbonate ions only. To convert this structure, the periodic boundary condition (Option **25**), has to set to *auto*. This will instruct DL\_FIELD to read the cell parameter information (CRYST1) in the PDB file.

(11a) *alkane.pdb* (CHARMM19 united atom model)

A C18 alkane chain, making use of the MOLECULE alkane defined in the *DLPOLY\_CHARMM19.sf* file. The MOLECULE alkane has the auto-CONNECT feature, which can be used to convert any united-atom alkanes.

The following examples illustrate the use of [multiple potential](#) schemes in a molecular system. These files are just some examples to show the capability of DL\_FIELD. The FF implementations are correct but that does not mean the subsequent model set up is valid!

To convert the following structures, set the force field scheme require, Option **1**, to *multiple* in the *control* file. This will instruct DL\_FIELD to read the input files and look for the **POTENTIAL** directives. In addition, Option **18** and **19** must be defined, to indicate the mixing rules between the different potential schemes in the model.

(12a) *multiple\_potential\_1.pdb* (AMBER, OPLS2005 and CHARMM22\_prot - multiple)

Apply three different potential schemes on five methanol molecules: The first molecule is assigned to the AMBER, the following three molecules to the OPLS2005 and the last one to the CHARMM22\_prot. The vdw parameters (sigma and epsilon) between two different force fields are derived using the Fenders-Halsey [mixing scheme](#).

(13a) *multiple\_potential\_2.pdb* (CHARMM22\_prot and INORGANIC\_binary\_oxide FF - multiple)

A simple example of mixed organic-inorganic system. The single ethanol molecule is assigned to CHARMM22\_prot and the magnesium oxide cluster is assigned to rigid ion FF model from INORGANIC\_binary\_oxide. The PDB file shows that the ethanol molecule is assigned to a Molecular Group called 'ORG', whereas, Molecular Group is undefined for the magnesium oxide. For this reason, DL\_FIELD assigns the inorganic model to a default Molecular Group called 'not\_define' in the *dl\_poly.FIELD* file.

Note that the vdw parameters for organic-inorganic atoms pairs were not defined. However, these parameters can be defined by making use of the [VDW\\_FIX](#) directive.

An *udff* file (*vdw\_fix.udff*) is included in the *Examples/* directory to illustrate the use of the **VDW\_FIX** directive, for Examples (12a) and (13a). Repeat the conversions but this time include the *udff* file and see what happens. To do this, insert the path *Examples/vdw\_fix.udff* in Option **6** of the control file (*example13.control*).

When the **VDW\_FIX** is applied to the Example 13 structure, the vdw parameters for the atom pair HA CT3 are reassigned to that of the Morse potential in the CHARMM22\_prot FF. When the fix is applied to Example 13, the vdw atom pair OH1 Mg3 (mixed organic-inorganic) is assigned with a set of the Lennard-Jones parameters.

The use of different CHARMM FF components in a model can be demonstrated by revisiting the *sod1.pdb* file (Example (2a)). Inspection of the file shows that two **POTENTIAL** schemes have been assigned: The SOD1 Molecular Group has been assigned to CHARMM22\_prot, while SOD2 Molecular Group has been assigned to the CHARMM36\_prot force field. When a force field scheme is specified in Option 1, these directives will be ignored. When setting the Option **1** to *multiple*, then DL\_FIELD will assign the CHARMM22 force field to the first protein monomer (SOD1) and CHARMM36 to the second protein monomer (SOD2), according to the **POTENTIAL** directive in the PDB file.

(14a) *ionic\_liquid\_species.pdb* (OPLS\_CL\_P)

Contain two ionic liquid components, fluoroalkylimidazolium cation with tetrafluoroborate anion. Atom labels are expressed in DL\_F Notation in the *CONFIG* and *FIELD* files.

(15a) *nucleic.pdb* (CHARMM36\_nucl)

Example structure of DNA, which consists of adenine and thymine base pairs and -OH terminations at the end of strands at the 3- and 5- positions of the ribose units.

## 13.2 Example Files: xyz Format

The following examples illustrate the use of the xyz file format. For OPLS2005, PCFF, CVFF and inorganic FF only. All ATOM\_TYPES are expressed in the standard [DL F Notation](#). This is shown in *dl\_field.output* file under the heading:

ATOM\_TYPES mapping (DL\_F notation):

A separate file, *dlf\_notation.output* in the *output/* directory, is also created and contains user atomic structure expressed in DL\_F Notation. Try Option **12** to interchange atom labels into either force field-specific format and DL\_F Notation. Notice the difference in atom labels in *dl\_poly.FIELD* and *dl\_poly.CONFIG* files.

(1b) *amides.xyz*

An example system contains primary, secondary and tertiary amides, expressed in DL\_F Notation.

(2b) *alkyl\_ammonium.xyz*

An ammonium compound, together with a chloride anion. Note: the cation, N<sup>+</sup>, located within the molecule does not need the positive sign. Whereas, the *free* chloride ion, Cl, does. The structure is solvated with water (SPC/E model), from the *control* file.

(3b) *favipiravir.xyz*

This is an antiviral drug against influenza and the drug molecule is solvated with dimethyl sulphoxide from the *control* file.

(4b) *dynemicin\_a.xyz*

This is an anti-cancer drug, dynemicin A.

(5b) *mgo.xyz* (inorganic\_binary\_oxide)

This is the same structure as that of *mgo.pdb* (Example 9) but is expressed in the *xyz* format. For inorganic systems, both the **MOLECULE\_KEY**, which indicates the type of the inorganic material, and the **MOLECULAR\_GROUP**, to which the material belongs, must be explicitly defined in the file. Note that, element symbols can be used, instead of the ELEMENT\_KEYS as in the *mgo.pdb* file.

Initially, **MOLECULE\_KEY** MO3 is used, which is a rigid-ion model. One can use the same configuration file to setup a core-shell model by simply changing the **MOLECULE\_KEY** to MO1. DL\_FIELD will automatically add the necessary core (or shell) components into the system and set up the force field.

(6b) *caco3.xyz* (inorganic\_ternary\_oxide)

This is the same structure as that of *caco3.pdb* (Example 10a) but is expressed in the *xyz* format. The system is divided into two Molecular Groups: *A1*, which is assigned to calcium carbonate, and *WAT*, which is assigned to water molecules. The **MOLECULE\_KEYS** *CC1* and *SPC* are assigned to each group, of molecules, respectively. Same potential scheme is used for both groups of molecules (**POTENTIAL** *inorganic\_ternary\_oxide*). The keyword 'multiple' must be used for the FF scheme in the *example\_6b.control* file. Note that element symbols can be used, instead of the ELEMENT\_KEYS as would be the case in the *caco3.pdb* file.

(7b) *multiple\_potential\_3.xyz* (OPLS2005 and CVFF - multiple)

Illustrate multiple potential capability in *xyz* format. The example configurations consist of several methanol molecules. The positions of the **POTENTIAL** directives in the file indicate the extent of the force field schemes CVFF and OPLS2005. The CVFF methanol molecules are divided into three Molecular Groups: GRP1, GRP2 and GRP3, whereas the OPLS2005 methanol molecule belongs to Molecular Group GRP4. Inspect the *dl\_poly.FIELD* and *dl\_poly.CONFIG* files and see how they correspond to the input *xyz* file.

(8b) *multiple\_potential\_4.xyz* (OPLS2005 and inorganic\_binary\_oxide)

Illustrate multiple potential capability in *xyz* format with mixed inorganic-organic potential schemes. The structure is similar to the *multiple\_potential\_2.pdb* file in the Example 13. For the organic part, the ethanol molecule is assigned to the OPLS2005 force field, whereas, the inorganic part is assigned to *inorganic\_binary\_oxide* force field. The **MOLECULE\_KEY** directive must also be defined for the inorganic force field, to indicate the type of material. For organic force field, the directive **MOLECULE\_KEY** has no effect, and the molecule will be automatically determined by DL\_FIELD.

(9b) *multiple\_potential\_5.xyz* (*inorganic\_binary\_oxide* and *amber16\_gaff*)

This example illustrates the use of a template-base force field in *xyz* format. DL\_FIELD will automatically identify the molecules, rearrange and match with the MOLECULE template in the library files. Moreover, DL\_FIELD will detect the use of core-shell model on the inorganic material and append the model automatically.

(10b) *ionic\_liquid\_species.xyz* (OPLS\_CL\_P)

Another example to show the use of a template-base force field in *xyz* format. The file contains a guanidinium cation with dicyanamide anion. The atom labels are expressed in the standard CL&P force field in the *CONFIG* and *FIELD* files.

### 13.3 Example File: *mol2* Format

The *mol2* is the latest file format first made available in version 4.5. Only a subset of features is made available for the *mol2* configuration files. For instance, *mol2* files do not allow the setting up of a multiple potential models. However, the use of *.mol2* is one of the convenient ways to set up Amber GAFF force field models, a popular general force field for general organic molecules such as those of small drug molecules. The *.mol2* file can be readily [produced](#) using the Amber's *antechamber* program suite.

(1c) *ascorbic\_acid.mol2* (AMBER\_GAFF and OPLS2005)

This example file was produced from a starting PDB structure using the Amber's *antechamber* program and charges were assigned using the BCC-AM1 method. DL\_FIELD will detect if the atom keys contained in the file belong to Amber GAFF. It will not carry out the conversion process. Instead, the atom keys and charges will be used, *per se*, and setup the force field models for DL\_POLY.

If the force field scheme is changed to OPLS2005 (Option **1**) and run DL\_FIELD again, then DL\_FIELD will realise the atom keys in the *mol2* file do not belong to that of OPLS2005. In this case, normal conversion process according to the *xyz* procedures will be carried out, including the charges. DL\_FIELD **will not** take the charge values from the *mol2* file.

In both instances, a *dif\_notation.output* file will be produced, showing the actual chemical types for each atom in the system.

## 14 FAQ

**1.** DL\_FIELD has reported a successful conversion of my configuration file, but I notice that not all molecules in my file have been converted.

Answer: DL\_FIELD will terminate when the END keyword is encountered in your PDB file. These keywords may sometime appear in the middle of your file. Remove them and rerun DL\_FIELD.

**2.** DL\_FIELD fails to convert my protein file and report the following error:

'Error: c2 s1 s1 angle parameter not found'

What happens?

Answer: Identify the atom index numbers that give rise to this error and refer them to your file. This error could possibly arise because DL\_FIELD detect a possible disulphide linkage between cysteine residues and yet they are in reduced form (-SH). Remove the thiolate hydrogen from both residues and rerun DL\_FIELD.

**3.** DL\_FIELD reports the following type of error:

Matching of target atom *a = element* failed. Program exits. config\_pos=*some number*

\*\*\*\*\*

Fail to match atoms for *molecule* of id=*X*. Program exit.

Answers: This only occurs in matching of MOLECULE templates in [PDB files](#). There are few possibilities to these types of error:

- (a) The connectivity information (**CONNECT** directive) mismatches with the bond connectivities of the user's configuration. A particular pair of atoms within a user's molecule may be too far apart.

Turn on verbosity mode from *dl\_field.control* file and rerun DL\_FIELD. Look into *dl\_field.output* file. The offending molecule gives rise to this error is usually located at the end of the file. Check for the user config. neighbour list information and compare with the CONNECT statements of the molecule.

If there is a mismatch of neighbour list information, identify the particular missing pair and increase the bond length correspondingly. For instance, if DL\_FIELD failed to identify C-O bond (neighbour pair) in the molecule, increase the C\_O threshold value (`#define C_O ....`) in *dl\_field.h* program.

Alternatively, a poorly or non-equilibrated structure may also give rise to this error due to having two non-bonded atoms being too close to each other and DL\_FIELD misidentified them as a bonded entity.

- (b) Wrong element symbols. If elements are not explicitly defined in *element symbol* columns 77-79 of the user's PDB file then DL\_FIELD will attempt to extract the element symbols from the *atom\_label* (columns 13-16). Quite often these

columns contain other atom labels. While some measures have been programmed to resolve these, it is not failed safe.

**4.** DL\_FIELD fails to recognise some of the amino acid residues such as those with various charge states such as histidine. Why?

Answer: One possible common mistake is the use of potential-specific notation that works in one potential scheme but the notation is not recognised in the other potential scheme. For instance, a delta-protonated histidine is denoted as 'HSD' in CHARMM, while this is denoted as 'HID' in AMBER. It is advisable to use the standard 'HIS' notation and let to determine the charge state and assign the parameters according to the potential scheme chosen.

**5.** When comparing with other programs, I can't get the coulombic or vdw energy in agreement. Why?

Answers: The coulombic energy component in DL\_FIELD includes both the long-range interatomic charge-charge interactions as well as the 1-4 intra-interactions. DL\_FIELD does not calculate the pair energy beyond the cut off specified. For this reason, the coulombic energy component should be used as a reference only. To improve the accuracy of the energy, try to use large cut off values.

However, discrepancies can still arise due to slight variations of fundamental constants. Subsequently, slightly different coulombic constants being defined for scaling the coulombic energy in different programs. In DL\_FIELD, this constant is displayed in the energy component of *dl\_field.output* file, which can be different from those of DL\_POLY programs, or indeed, any other MD programs.

The coulombic constant can be adjusted by redefining the fundamental constants (electric permittivity, elementary charge value etc) located in the *dl\_field.h* header file. Nevertheless, such adjustments are a matter of artistic refinement that should not significantly influence the outcome of a simulation.

In the case of vdw, the energy variation is largely due to two factors: (a) rounding errors of the vdw parameters used and (b) the way cut off distance being treated. DL\_FIELD does not calculate pair-energy beyond the cut off specified. For this reason, the vdw energy component should be used as a reference only.

In DL\_POLY MD package, the vdw cut off correction may be treated differently compare with other programs. However, the 1-4 vdw interactions are usually in good agreement due to the fact that the 1-4 distances are usually within a typical cut-off range specified.

To improve the accuracy of the energy, try to use large cut off values so that all possible atom pairs are included.

**6.** I have set up the necessary molecular models and potential parameters but I still can't get DL\_FIELD to convert the structure.

Answer: There can be many reasons for this but one common mistake is that the information in the user PDB file is not in the proper location columns. Consult [Chapter 6](#) to make sure the information in the PDB file is in the correct columns and order.



**7.** I have defined new parameters in the *udff* file, but DL\_FIELD seems to read this information incorrectly.

Answer: Before you insert your own parameters, make sure you have consulted the standard *.par* file for the potential scheme of interest. The sequence and the number of parameters can be very different among the different schemes.

The sequence and the number of parameters appear in *udff* file must follow strictly that of the corresponding *.par* of a given potential scheme. For instance, AMBER requires six parameters to define a set of dihedral bond. All six parameters must be listed in the *udff* file and in the same order. Two of the parameters, namely the 1-4 vdw and coulombic scaling factors are listed in AMBER, whereas, they are not listed for the other potential schemes.

**8.** DL\_FIELD fails to convert my *xyz* structure and gives an error something like 'unknown CG'. What happen?

Answer: It means DL\_FIELD cannot recognise certain arrangement of the atoms in your molecule. Email me and I may be able to include the missing CG into DL\_FIELD. Another possibility is that DL\_FIELD failed to make correct determination the bond connectivity. Try to use a loose conversion in Option **3** and run DL\_FIELD again.



## **End of DL\_FIELD version 4.9 user manual**

C W Yong, November 2022

Please quote the following reference in your publication:

C W Yong, 'Descriptions and Implementations of DL\_F Notation: A Natural Chemical Expression System of Atom Types for Molecular Simulations', *J. Chem. Inf. Model.* **56**, 1405–1409 (2016)