



# CONFLEX 8

## What is CONFLEX?

CONFLEX Corporation provides conformation search and analysis software for examining the conformational space of small and large molecules. Identifying these conformers helps researchers in the selection of better quality leads during the discovery process. CONFLEX also includes algorithms for predicting IR, NMR, CD, and UV-Vis spectra.

CONFLEX also develops and licenses the CONFLEX Interface, a visualization and analysis platform especially designed for analysing CONFLEX outputs, e.g. conformational analyses, spectra output, and crystal packing, spectra, etc.

CONFLEX software products provide meaningful answers to both the expert computational chemist as well as the experimental and medicinal chemist investigating the role of molecular conformation. Designed for chemists by chemists, CONFLEX products exhibit high-accuracy, intuitive interfaces, and powerful command-line operation for interfacing with other modeling packages.

New features in CONFLEX 8 and later include Crystal Search and Optimization Powder Diffraction Prediction, and the ability to run CONFLEX from ChemOffice products.

## NEW IN CONFLEX 8.C

1. - Implement DRC (Dynamic Reaction Coordinate) Method
2. Conformation Search invoking external Gaussian program
3. Parallelization of Crystal Structure Optimization using OpenMP
4. Hybrid parallelization of Crystal Search using OpenMP/MPI
5. Speed up checking conformers by examining dihedral angle
6. Revised atomic weight for use in calculation

### CONFLEX 8 Interface Features -

1. Accelerated drawing of molecule by using OpenGL SL
2. Animation for vibrational mode
3. Displaying crystal surface by (h,k,l) indices
4. Line display of molecule
5. Geometry label between unconnected atoms
6. Watch List feature for multiple geometry labels display
7. Geometry label between molecules inside crystal
8. New toolbar
9. Support for new features of CONFLEX 8
10. Enhancement for reading of PDB file



### **Modifying Molecules**

- Gaussian checkpoint file
- GAMESS log file
- Firefly log file
- Sybyl mol2 file
- Copy & Paste from ChemDraw
- Modify bond multiplicity

### **Control Features**

- Prepare and Run CONFLEX Calculations
- Monitor and control local machine and server processes
- Prepare and Run calculations for Gaussian, GAMESS and Firefly

### **Visualize Calculation Results**

- Display spectra: IR, NMR, CD, UV-Visible, etc.
- Zoom-In and Out on spectra
- Save plots as textual data files
- Report absolute NMR chemical shifts and shifts relative to reference compounds
- Create surfaces for molecular orbitals and electron density

### **Display Formats**

- 3D solid and translucent
- Color surfaces by a property
- Control surface threshold values
- Control surface transparency
- Automatically load binary cubed created by CONFLEX
- Automatically save computed cubes for future use



## Conformation Search-

### Conformational Search Algorithm in CONFLEX

For convenience, the structures being processed are referred to differently depending on the particular stage of the search process:

- input structure is the input at the beginning of a search
- initial structure is called from the conformer storage database at the beginning of each perturbation cycle
- starting (trial) structure is the perturbed structure before geometry-optimization
- optimized structure is the structure after geometry-optimization
- stored structure is the optimized structure that survived the redundancy test, and it is saved in the conformer storage.

The algorithms for searching conformational space or a torsional hypersurface involve repeated sampling from the vast conformational space. The process, which is illustrated below (a curved arrow indicates a looping subprocess), has the following steps:

- (1) generation of an appropriate starting structure
- (2) geometry-optimization of the starting structure
- (3) comparison of the optimized structure with the stored conformers.

Finally, a structure passing all comparisons is added to the list of stored conformers.

### Local Perturbation

If the perturbation cannot move the starting structure from the territory to which it initially belonged, subsequent geometry-optimization will return it to the same structure. The territories of similar conformers may be located in close vicinity in the conformational space, constituting a local network of local territories, and less similar conformers may be considered to belong to different localities. Therefore, the method of perturbing an initial structure to produce a new candidate conformer is also responsible for the efficiency of search.

To ensure exhaustive generation of all possible starting structures, local perturbation is applied to every flexible part in the initial structure. The following three modes of perturbation are designed to mimic the elementary process in the thermal movements of a molecule undergoing conformational change: corner flap and edge flip for endocyclic parts, and stepwise rotation for acyclic parts.

### Optimization

#### Pre-check during optimization

The time required to perform systematic perturbations on the initial structure comprises only a few percent of the total computing time, while by far the most time-consuming step is the geometry-optimization. Therefore, the pre-check is an effective way to increase the efficiency of the conformational space search. In CONFLEX, a structure that is being geometry-optimized is frequently compared with all the stored conformers during the optimization, and that calculation is stopped as soon as the candidate structure is identified as superimposable with one of the stored structures. However, if comparison is made too often, the comparison time will take up a significant part of the total time when the number of stored structures



increases. Therefore, with this option, CONFLEX will perform the comparison at 0, 10, 20, and every 10 iterations until 200 iteration, and every 50 iterations thereafter. This strategy reduces the total computing time by 30 to 60%.

## Comparison

### Comparison using conformational distance

The similarity between two conformers can be quickly identified by comparing the root mean square of differences in the corresponding pair of dihedral angles,  $f^A$  and  $f^B$ . This method is fast and accurate. To save time, the dihedral angles of a stored conformer are retrieved for comparison rather than re-calculating those dihedral angles each time.

$$d_{conf} = \sqrt{\frac{\sum_{i=1}^{N_{dihedral}} (f_i^A - f_i^B)^2}{N}}$$

Part of PARALLEL CONFLEX was developed under a “Grant-in-Aid for Project Costs Associated with Innovation Creation with the Collaboration of Industry, Government, and Universities” of the Japan Ministry of Education, Culture, Sports, Science and Technology.

For Further Details & Queries, Contact:

### Scube Scientific Software Solutions (P) Ltd

An ISO 9001:2008 Certified Company

1217, 12<sup>th</sup> Floor, Hemkunt Chambers

89, Nehru Place, New Delhi 110019

Phone: 91-1141618828/29

Email: [info@scubeindia.com](mailto:info@scubeindia.com)