Conformator – Conformer Generation

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Conformator is a robust, knowledge-based tool for the accurate generation of 3D conformer ensembles. It rapidly explores the conformational space of small molecules to provide representative ensembles essential for docking,

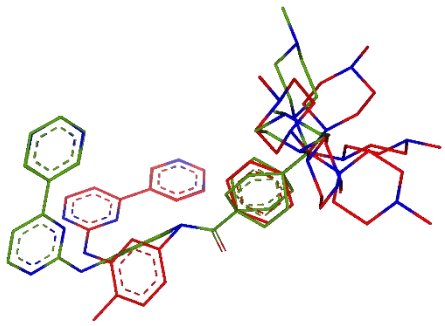
How Does Conformator Work?

Conformator employs a incremental construction algorithm to generate conformer ensembles. Rather than relying solely on force fields, it utilizes an expert-derived torsion angle library to assign chemically relevant geometries.

The process begins by removing existing 3D coordinates and canonicalizing the input structure to define a unique reference state. The molecule is subsequently assembled in a fragment-based manner. Preferred torsion angles are assigned to acyclic bonds using statistical distributions derived from the Cambridge Structural Database (CSD), while bond lengths and valence angles are determined according to VSEPR-based geometries. To limit the combinatorial growth of conformational space, sampling is biased toward bonds located near the molecular core, whereas terminal regions are explored with reduced sampling density, thereby emphasizing global molecular topology. The generated conformations are then subjected to a clustering step and redundant structures are removed, yielding a compact and diverse conformer ensemble that efficiently represents the accessible conformational space.

Advantages

- High accuracy (median RMSD 0.47 Å) with chemically correct geometries.
- Robustly processes >99.9% of molecules from any 2D or 3D input.



Features of Conformator

- **Knowledge-Driven Torsion Sampling:** Conformator moves beyond simple force-field enumerations by utilizing a proprietary torsion angle library derived from the Cambridge Structural Database (CSD). By assigning experimentally preferred torsion angles to rotatable bonds, the algorithm ensures generated ensembles reflect chemically realistic conformations found in nature.
- **Adaptive Sphere Exclusion Clustering:** To prevent redundancy, a deterministic, RMSD-based adaptive sphere exclusion clustering algorithm is employed. As conformers are generated, geometrically similar structures are filtered out on the fly, ensuring the final ensemble is maximally diverse for a given size.
- **Input Independence:** The algorithm is designed to be completely independent of input coordinates. It accepts 2D formats (SMILES) or 3D formats (SDF, MOL2) and canonicalizes the input to generate fresh, unbiased 3D coordinates from scratch.

Application Scenarios

High-quality conformer ensembles are essential for both ligand- and structure-based computational workflows. Conformator generates representative, low-energy conformations that capture bioactive molecular shapes, supporting pharmacophore modeling, shape-based virtual screening, 3D-QSAR analyses, and docking preparation by providing reliable starting geometries and conformational coverage suitable for large-scale screening applications.

Literature

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