

User Guide

AutoDock Version 4.2

Updated for version 4.2.6

Automated Docking of Flexible Ligands to Flexible Receptors

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Automated Docking

Introduction

AutoDock is an automated procedure for predicting the interaction of ligands with biomacromolecular targets. The motivation for this work arises from problems in the design of bioactive compounds, and in particular the field of computer-aided drug design. Progress in biomolecular x-ray crystallography continues to provide important protein and nucleic acid structures. These structures could be targets for bioactive agents in the control of animal and plant diseases, or simply key to the understanding of fundamental aspects of biology. The precise interaction of such agents or candidate molecules with their targets is important in the development process. Our goal has been to provide a computational tool to assist researchers in the determination of biomolecular complexes.

In any docking scheme, two conflicting requirements must be balanced: the desire for a robust and accurate procedure, and the desire to keep the computational demands at a reasonable level. The ideal procedure would find the global minimum in the interaction energy between the substrate and the target protein, exploring all available degrees of freedom (DOF) for the system. However, it must also run on a laboratory workstation within an amount of time comparable to other computations that a structural researcher may undertake, such as a crystallographic refinement. In order to meet these demands a number of docking techniques simplify the docking procedure. AutoDock combines two methods to achieve these goals: rapid grid-based energy evaluation and efficient search of torsional freedom.

The current version of AutoDock, using the Lamarckian Genetic Algorithm and empirical free energy scoring function, typically will provide reproducible docking results for ligands with approximately 10 flexible bonds. Our related software, AutoDock Vina (<http://vina.scripps.edu>), uses a simpler scoring function that allows a faster search method, and provides reproducible results for larger systems with upwards of 20 flexible bonds. A more complete discussion of options is included below in the section "Choosing a Protocol for Your Application."

This guide includes information on the methods and files used by AutoDock and information on use of AutoDockTools to generate these files and to analyze results.

Getting Started with AutoDock

AutoDock and **AutoDockTools**, the graphical user interface for AutoDock are available on the WWW at:

<http://autodock.scripps.edu/>

The WWW site also includes many resources for use of AutoDock, including detailed **Tutorials** that guide users through basic AutoDock usage, docking with flexible rings, and virtual screening with AutoDock. Tutorials may be found at:

<http://autodock.scripps.edu/faqs-help/tutorial>

AutoDock calculations are performed in several steps: 1) preparation of coordinate files using **AutoDockTools**, 2) precalculation of atomic affinities using **AutoGrid**, 3) docking of ligands using **AutoDock**, and 4) analysis of results using **AutoDockTools**.

Step 1—Coordinate File Preparation. AutoDock4.2 is parameterized to use a model of the protein and ligand that includes polar hydrogen atoms, but not hydrogen atoms bonded to carbon atoms. An extended PDB format, termed **PDBQT**, is used for coordinate files, which includes atomic partial charges and atom types. The current AutoDock force field uses several atom types for the most common atoms, including separate types for aliphatic and aromatic carbon atoms, and separate types for polar atoms that form hydrogen bonds and those that do not. PDBQT files also include information on the torsional degrees of freedom. In cases where specific sidechains in the protein are treated as flexible, a separate PDBQT file is also created for the sidechain coordinates. AutoDockTools, the Graphical User Interface for AutoDock, may be used for creating PDBQT files from traditional PDB files.

Step2—AutoGrid Calculation. Rapid energy evaluation is achieved by precalculating atomic affinity potentials for each atom type in the ligand molecule being docked. In the AutoGrid procedure the protein is embedded in a three-dimensional grid and a probe atom is placed at each grid point. The energy of interaction of this single atom with the protein is assigned to the grid point. AutoGrid affinity grids are calculated for each type of atom in the ligand, typically carbon, oxygen, nitrogen and hydrogen, as well as grids of electrostatic and desolvation potentials. Then, during the AutoDock calculation, the energetics of a particular ligand configuration is evaluated using the values from the grids.

Step 3—Docking using AutoDock. Docking is carried out using one of several search methods. The most efficient method is a Lamarckian genetic algorithm (LGA), but traditional genetic algorithms and simulated annealing are also available. For typical systems, AutoDock is run several times to give several docked conformations, and analysis of the predicted energy and the consistency of results is combined to identify the best solution.

Step 4—Analysis using AutoDockTools. AutoDockTools includes a number of methods for analyzing the results of docking simulations, including tools for clustering results by conformational similarity, visualizing conformations, visualizing interactions between ligands and proteins, and visualizing the affinity potentials created by AutoGrid.

What's New?

AutoDock 4.2 includes several enhancements over the methods available in AutoDock 3.0.

Sidechain Flexibility. AutoDock 4.2 allows incorporation of limited sidechain flexibility into the receptor. This is achieved by separating the receptor into two files, and treating the rigid portion with the AutoGrid energy evaluation and treating the flexible portion with the same methods as the flexible ligand.

Force Field. The AutoDock 4.2 force field is designed to estimate the free energy of binding of ligands to receptors. It includes an updated charge-based desolvation term, improvements in the directionality of hydrogen bonds, and several improved models of the unbound state.

Expanded Atom Types. Parameters have been generated for an expanded set of atom types including halogens and common metal ions.

Desolvation Model. The desolvation model is now parameterized for all supported atom types instead of just carbon. Because of this, the `constant` function in AutoGrid is no longer used, since desolvation of polar atoms is treated explicitly. The new model requires calculation of a new map in AutoGrid that holds the charge-based desolvation information.

Unbound State. Several models are available for estimating the energetics of the unbound state, including an extended model and a model where the unbound state is assumed to be identical with the protein-bound state.

For users of AutoDock 4.0, there are several changes in AutoDock 4.2:

Default Unbound State. The default model for the unbound state has been changed from “extended” to “bound=unbound”. This is in response to persistent problems when docking sterically-crowded ligands. The “extended” unbound state model is available in AutoDock 4.2 through use of the “unbound extended” keyword.

Backwards Compatibility. We have made every attempt to ensure that docking parameter files generated for use in AutoDock 4.0 should be correctly run by AutoDock 4.2.

For users of AutoDock 4.2.3 or 4.2.4, there are several changes in AutoDock 4.2.5:

Finer Control of Output. In response to the widespread use of AutoDock in virtual screening, we have modified the “outlev” command to allow more control over the level of output. The default of “1” will now output primarily information on the docked conformations and analysis, and higher levels will provide diagnostic information.

Program will Halt with Critical Errors. Several error conditions that previously gave warnings will now cause AutoDock to halt. This is a response to use of AutoDock in virtual screening,

where the user may not examine each individual docking experiment, and critical errors may not be noticed.

Ligand Internal Electrostatics are now 'on' by Default. The electrostatic interactions between non-bonded atoms in flexible ligands are now considered 'on' by default. Previous releases of AutoDock required the "intelec" command to turn this on. If you wish to ignore these interactions and restore the previous default behavior, use "intelec off" in your DPF.

Force Field Consistency. Smoothing of potentials has been added to internal energy potentials, to make them consistent with intermolecular energy potentials. This will have a small effect on conformations when docking with rigid receptors, and possibly a significant effect on conformations and predicted free energies when docking with flexible receptors. In addition, an error in output of energies with flexible receptors has been corrected, and AutoDock's intra-ligand desolvation potential cutoff distance has been increased to match AutoGrid's.

For users of AutoDock 4.2.5, there are several changes in AutoDock 4.2.6:

Platforms. More computer platforms are supported:

- Linux2 on Intel i86 (32-bit) and on Intel x86_64 (64-bit)
- Linux3 on Intel x86_64 (64-bit)
- Macintosh OS X 10.5 (Leopard) on PowerPC (32- and 64-bit), OS X 10.5-10.9 (Leopard, Snow Leopard, Lion, Mountain Lion, and Mavericks) on Intel i86 (32-bit) and Intel x86_64 (64-bit)
- Solaris 8 (SunOS 5.8) on SPARC
- Windows 5 (XP), 6 (Vista), 7, 8.1 on Intel i86.

Now, both AutoDock and AutoGrid are compiled using double-precision arithmetic. There is also better cross-platform compatibility of the internal random number generator.

Improved Error Checking. There is improved error checking of command-line arguments. AutoDock now checks the atom numbers that define internal and "flexres" torsions.

Job and Run Provenance and Reproducibility. Each docking log file (dlg) always contains the host name, run date, working directory, and names of input PDBQT files. Each docking run always contains its initial random number seeds, its ending total energy, and its final state in a uniform format suitable for automated analysis. Invoking "autodock4 (or autogrid4) -version" reports compile-time configuration options.

Clustering of Multiple Search Algorithms. Now, multiple search methods can be used in a single AutoDock job: for example, 50 runs of Lamarckian Genetic Algorithm followed by 50 runs of Simulated Annealing. The runs are done serially: no results carry over from one algorithm to the next. All results are ranked and clustered together in the analysis step at the end of the entire job.

Visualization of Simulated Annealing and Local-Search-Only Runs. You can now use ADT (AutoDock Tools) to visualize results from AutoDock jobs that use simulated annealing or local-search-only. You must download the latest build of ADT from <http://mglttools.scripps.edu/downloads/latest>

4.2.6 Release Limitation. The “do_local_only” command runs the pseudo-solis-wets algorithm, even if the solis-wets has been specified using “set_local sw1”. This applies only to “do_local_only”: the “ga_run” command will use whichever local search has been specified. (We recommend the pseudo-solis-wets for all local searches: “set psw1”).

For more information about this release, see the Release 4.2.6 Notes on the AutoDock 4.2 *download* web page.

Support

AutoDock is distributed, with full source code, *free of charge*. There are some caveats, however. Firstly, since we receive limited funding to support the academic community of users, we cannot guarantee response to queries on installation and use. While there is documentation, it may require at least some basic Unix abilities to install. If you still need help:

- (1) Ask your local system administrator or programming guru for help about compiling, using Unix/Linux, *etc.*
- (2) Consult the AutoDock web site, where you will find a wealth of information and a FAQ (Frequently Asked Questions) page with answers on AutoDock:
<http://autodock.scripps.edu/faqs-help>
- (3) If you can't find the answer to your problem, send your question to the AutoDock List (ADL) or the AutoDock Forum. There are many seasoned users of computational chemistry software and some AutoDock users who may already know the answer to your question. You can find out more about the ADL on the WWW at:
<http://mgldev.scripps.edu/mailman/listinfo/autodock>
The Forum is available on the WWW at:
<http://mgl.scripps.edu/forum>
- (4) If you have tried (1), (2) and (3), and you still cannot find an answer, send email to goodsell@scripps.edu for questions about AutoGrid or AutoDock; or to rhuey@scripps.edu for questions about AutoDockTools.

Thanks for your understanding!

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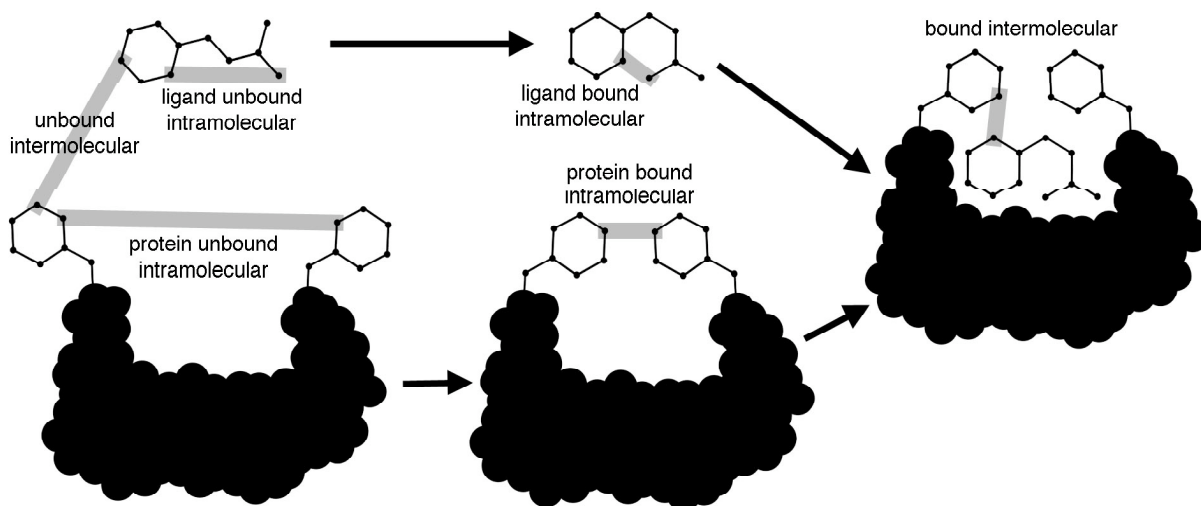
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Theory

Overview of the Free Energy Scoring Function

AutoDock 4.2 uses a semi-empirical free energy force field to evaluate conformations during docking simulations. The force field was parameterized using a large number of protein-inhibitor complexes for which both structure and inhibition constants, or K_i , are known.



The force field evaluates binding in two steps. The ligand and protein start in an unbound conformation. In the first step, the intramolecular energetics are estimated for the transition from these unbound states to the conformation of the ligand and protein in the bound state. The second step then evaluates the intermolecular energetics of combining the ligand and protein in their bound conformation.

The force field includes six pair-wise evaluations (V) and an estimate of the conformational entropy lost upon binding (ΔS_{conf}):

$$\Delta G = (V_{bound}^{L-L} - V_{unbound}^{L-L}) + (V_{bound}^{P-P} - V_{unbound}^{P-P}) + (V_{bound}^{P-L} - V_{unbound}^{P-L} + \Delta S_{conf})$$

where L refers to the “ligand” and P refers to the “protein” in a ligand-protein docking calculation.

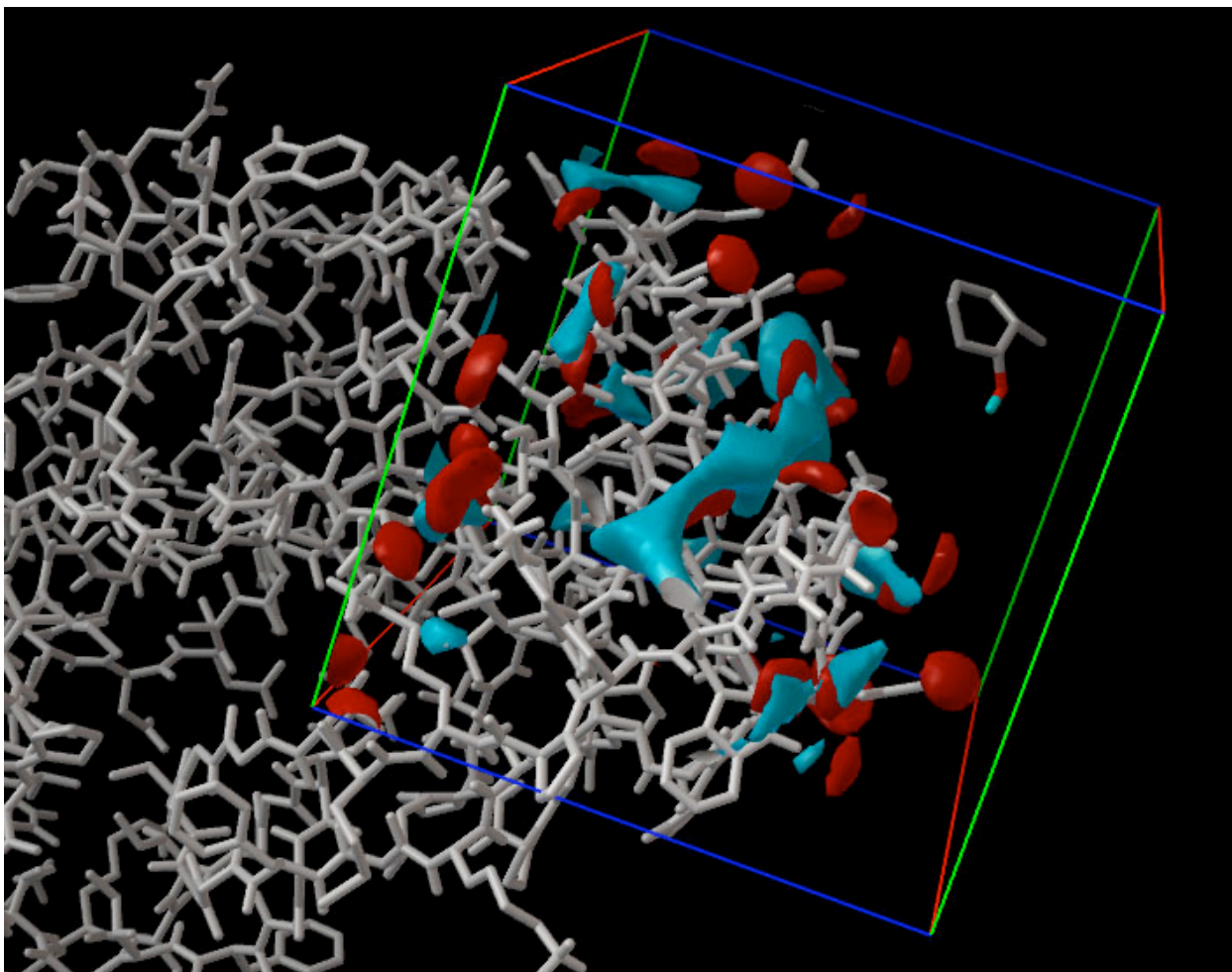
Each of the pair-wise energetic terms includes evaluations for dispersion/repulsion, hydrogen bonding, electrostatics, and desolvation:

$$V = W_{vdw} \sum_{i,j} \left(\frac{A_{ij}}{r_{ij}^{12}} - \frac{B_{ij}}{r_{ij}^6} \right) + W_{hbond} \sum_{i,j} E(t) \left(\frac{C_{ij}}{r_{ij}^{12}} - \frac{D_{ij}}{r_{ij}^{10}} \right) + W_{elec} \sum_{i,j} \frac{q_i q_j}{e(r_{ij}) r_{ij}} + W_{sol} \sum_{i,j} (S_i V_j + S_j V_i) e^{(-r_{ij}^2 / 2\sigma^2)}$$

The weighting constants W have been optimized to calibrate the empirical free energy based on a set of experimentally determined binding constants. The first term is a typical 6/12 potential for dispersion/repulsion interactions. The parameters are based on the Amber force field. The second term is a directional H-bond term based on a 10/12 potential. The parameters C and D are assigned to give a maximal well depth of 5 kcal/mol at 1.9Å for hydrogen bonds with oxygen and nitrogen, and a well depth of 1 kcal/mol at 2.5Å for hydrogen bonds with sulfur. The function E(t) provides directionality based on the angle t from ideal H-bonding geometry. The third term is a screened Coulomb potential for electrostatics. The final term is a desolvation potential based on the volume of atoms (V) that surround a given atom and shelter it from solvent, weighted by a solvation parameter (S) and an exponential term with distance-weighting factor $\sigma=3.5\text{\AA}$. For a detailed presentation of these functions, please see our published reports, included in Appendix IV.

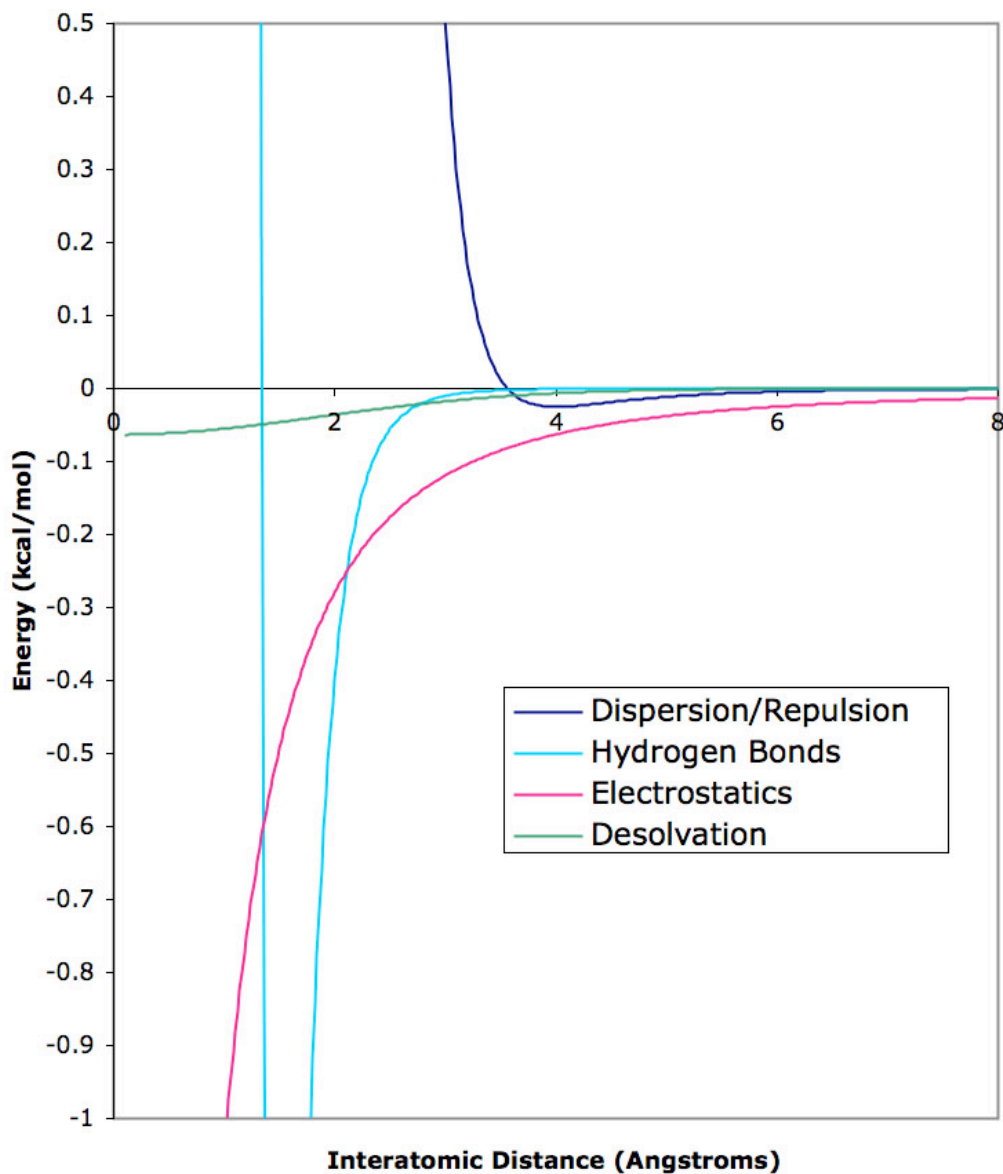
By default, AutoGrid and AutoDock use a standard set of parameters and weights for the force field. The `parameter_file` keyword may be used, however, to use custom parameter files. The format of the parameter file is described in Appendix I.

Several methods for estimating the contribution of the unbound state are implemented in AutoDock. In AutoDock 3.0 and earlier versions, an assumption is made that the unbound form of the ligand (V_{bound}^{L-L} in the equation above) is the same as the final docked conformation of the ligand (V_{unbound}^{L-L}), yielding a final contribution $V_{\text{bound}}^{L-L} - V_{\text{unbound}}^{L-L} = 0$. AutoDock 4.1 introduced a method of generating an extended form of the ligand to model the unbound state. Reports from users, however, revealed that the method caused significant problems with sterically-crowded molecules, and the default method was changed to the bound=unbound assumption in AutoDock 4.2 and later. In addition, there is an option for a user-defined unbound state.



Viewing Grids in AutoDockTools. The protein is shown on the left in white bonds, and the grid box is shown on the right side. The blue contours surround areas in the box that are most favorable for binding of carbon atoms, and the red contours show areas that favor oxygen atoms. A ligand is shown inside the box at upper right.

AutoDock 4.1 Force Field



AutoDock Potentials. Examples of the four contributions to the AutoDock force field are shown in this graph. The dispersion/repulsion potential is for interaction between two carbon atoms. The hydrogen bond potential, which extends down to a minimum of about -2 kcal/mol, is shown for an oxygen-hydrogen interaction. The electrostatic potential is shown for interaction of two oppositely-charged atoms with a full atomic charge. The desolvation potential is shown for a carbon atom, with approximately 10 atoms displacing water at each distance.

Using AutoDock

STEP 1: Preparing Coordinates

The first step is to prepare the ligand and receptor coordinate files to include the information needed by AutoGrid and AutoDock. These coordinate files are created in an AutoDock-specific coordinate file format, termed PDBQT, which includes:

- 1) Polar hydrogen atoms;
- 2) Partial charges;
- 3) Atom types;
- 4) Information on the articulation of flexible molecules.

For a typical docking calculation, you will create a file of coordinates for the receptor, and a separate file of coordinates for the ligand. In dockings where selected amino acids in the receptor are treated as flexible, you will create a third file that includes the coordinates of the atoms in the flexible portions of the receptor.

In a typical study, the user prepares coordinate files in several steps using AutoDockTools. A detailed tutorial is available on the AutoDock WWW site to guide you through this process. The first two steps may be performed using the tools in the `Edit` menu of AutoDockTools, or with other molecular modeling programs:

- 1) Add hydrogen atoms to the molecule.
- 2) Add partial charges.

Then, read the molecule into AutoDockTools using the `Ligand` (for the ligand) or `Grid` (for the receptor) menus, and create the PDBQT file:

- 3) Delete non-polar hydrogens and merge their charges with the carbon atoms.
- 4) Assign atom types, defining hydrogen bond acceptors and donors and aromatic and aliphatic carbon atoms.
- 5) Choose a root atom that will act as the root for the torsion tree description of flexibility.
- 6) Define rotatable bonds and build the torsion tree.

There are a few things to keep in mind during this process:

Be Critical. AutoDockTools and PMV currently use a modified version of Babel to add hydrogen atoms and assign charges. Unfortunately the method has trouble with some molecules. In those cases, hydrogen positions and charges may be assigned by the user's preferred method, *e.g.* using Reduce, InsightII, Quanta, Sybyl, AMBER or CHARMM.

Check Your Hydrogen Positions. In addition, most modeling systems add polar hydrogens in a default orientation, typically assuming each new torsion angle is 0° or 180° . Without some form

of refinement, this can lead to spurious locations for hydrogen bonds. One option is to relax the hydrogens and perform a molecular mechanics minimization on the structure. Another is to use a program like “pol_h” which takes as input the default-added polar hydrogen structure, samples favorable locations for each movable proton, and selects the best position for each. This “intelligent” placement of movable polar hydrogens can be particularly important for tyrosines, serines and threonines.

Watch for Disordered Residues. Care should be taken when the PDB file contains disordered residues, where alternate location indicators (column 17) have been assigned. For each such atom, the user must select only one of the possible alternate locations, making sure that a locally consistent set is chosen.

Randomize Starting Coordinates When Redocking. In redocking experiments, where coordinates from a known protein-ligand complex are separated and docked, it is important to randomize the conformation of the ligand before it is docked. The techniques used to implement rotation of the ligand may be biased to prefer values of zero rotation, so to obtain an unbiased result, create a pdbqt file with the randomized ligand coordinates using the "Randomize" command in the ADT Ligand menu, then use this randomized coordinate file for docking experiments.

Please note: coordinate preparation is the most important step in the docking simulation. The quality and accuracy of the docked results will only be as good as the quality of the starting coordinates. Be critical and carefully examine hydrogen positions, atom type assignments, partial charges, and articulation of the molecules to ensure that they make sense chemically. If you are using the Babel method within AutoDockTools to add charges and hydrogens, carefully check the results and make corrections if necessary—it often has trouble with molecules such as nucleotides.

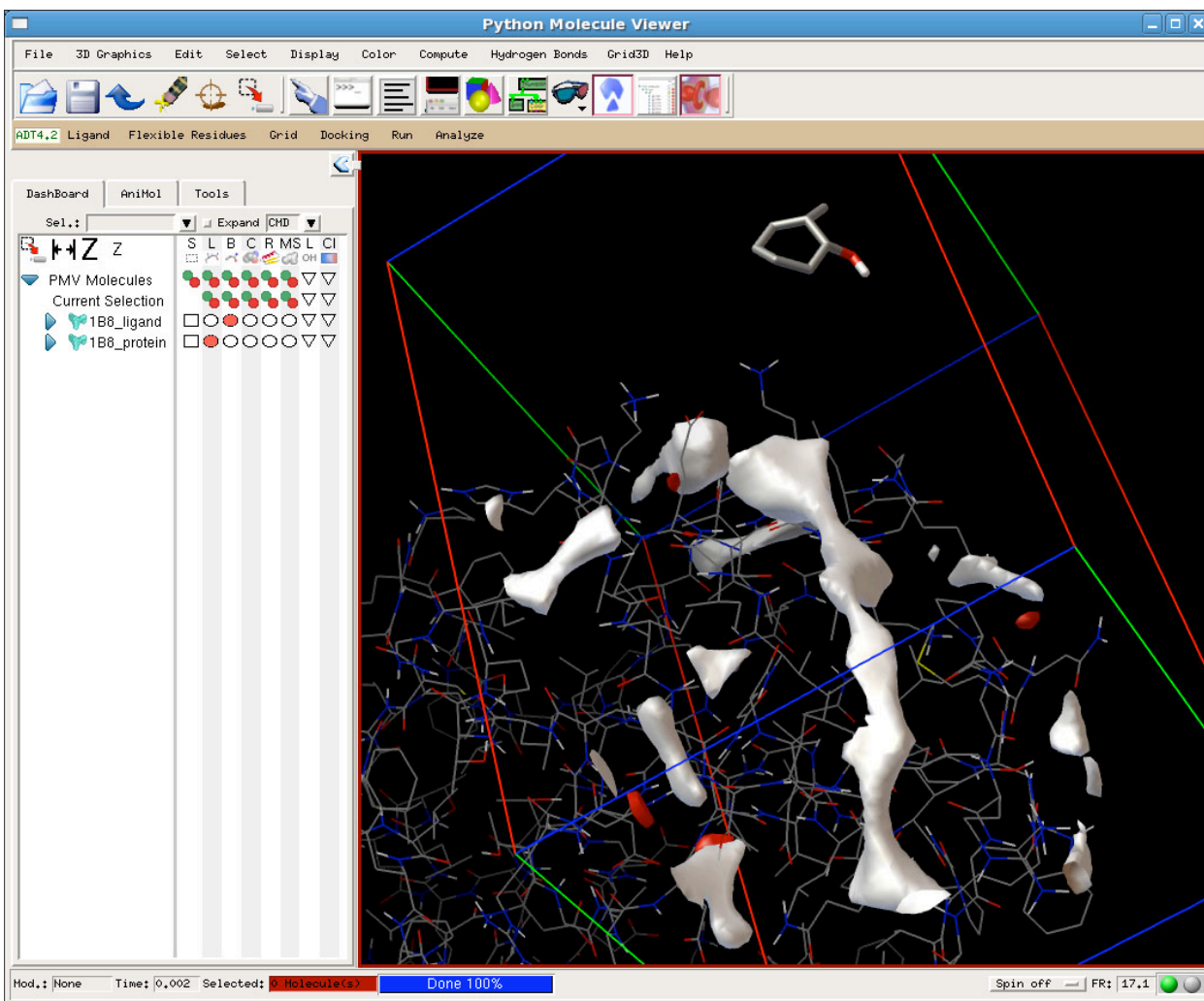
Creating PDBQT files in AutoDockTools

Overview of AutoDockTools

AutoDockTools is a set of commands implemented within the Python Molecular Viewer (PMV), providing a Graphical User Interface for AutoGrid and AutoDock. It is available at: <http://autodock.scripps.edu/resources/adt>.

The AutoDockTools window has several parts:

- 1) at the top are menus that access the general methods available in PMV. These include tools for reading and writing coordinates and images, for modifying coordinates, for selection, and for visualization.
- 2) a row of buttons at the top allows quick access to the most popular tools of PMV
- 3) below the buttons, there are a series of menus that access the AutoDock-specific tools of AutoDockTools.
- 4) the 3-D molecular viewer is at center right.
- 5) the Dashboard, located to the left of the viewer, allows quick selection, visualization, and coloring of molecules currently displayed in the viewer.



Hydrogen Atoms and Charges

The tools available in PMV are used to read coordinates in PDB and other formats, to add hydrogens, to select portions of the molecule, and to add partial charges. These functions are all accessed through menus at the top of the PMV window. A few useful commands will be described here—for more information on the many other functions of PMV, please see the PMV documentation.

File>ReadMolecule: opens a browser that allows reading of PDB coordinate files.

Edit>Delete: several options for deleting entire molecules, selected sets of atoms, or hydrogen atoms.

Edit>Hydrogens>Add: options for adding all hydrogens or polar hydrogens using Babel.

Edit>Charges: options for computing Gasteiger charges for arbitrary molecules using Babel.

Ligand PDBQT Files – the “Ligand” Menu

Once ligand coordinates are created with hydrogen atoms and charges, they can be processed in the “Ligand” menu to create the ligand PDBQT file.

Ligand>Input>QuickSetup: uses defaults to create the PDBQT file. PDB files can be read from the PMV viewer or from a file, and written directly to a new PDBQT file. Please note that hydrogen atoms will not be added.

Ligand>Input>Open: reads coordinates from a file.

Ligand>Input>Choose: chooses a molecule already read into PMV.

Ligand>Input>OpenAsRigid: reads an existing PDBQT file and writes a new file with NO active torsions.

Ligand>TorsionTree>ChooseRoot: manual selection of the root atom.

Ligand>TorsionTree>DetectRoot: automatic detection of the root that provides the smallest largest subtree.

Ligand>TorsionTree>ShowRootExpansion: for molecules with several atoms in the root, displays small spheres to show all atoms in the root, including atoms connected to each root atom by rigid bonds.

Ligand>TorsionTree>ShowRootMarker: displays a sphere on the root atom.

Ligand>TorsionTree>ChooseTorsions: launches an interactive browser for choosing rotatable bonds. Rotatable bonds are shown in green, and non-rotatable bonds are shown in red. Bonds that are potentially rotatable but treated as rigid, such as amide bonds and bonds that are made rigid by the user, are shown in magenta. Rotation of rotatable bonds may be switched on and off by clicking on the bonds.

Ligand>TorsionTree>SetNumberOfTorsions: sets the number of rotatable bonds in the ligand by leaving the specified number of bonds as rotatable. The two options will choose the torsions that rotate either the fewest atoms in the ligand or the most atoms in the ligand.

Ligand>AromaticCarbon>SetNames: clicking on atom positions will switch carbon atoms between aromatic and aliphatic. Aromatic carbons are shown in green. Click on the “Stop” button when finished.

Ligand>AromaticCarbon>AromaticityCriterion: Sets the angular deviation from planarity that AutoDockTools uses to identify aromatic rings.

Ligand>Output>RandomizethenSaveasPDBQT: randomizes the conformation of the ligand and writes the formatted PDBQT file.

Ligand>Output: opens a browser to write the formatted PDBQT file.

Rigid Receptor PDBQT Files – the “Grid” Menu

For docking calculations using rigid receptor coordinates, add the hydrogen atoms and charges in PMV, then read the coordinates into AutoDockTools using the “Grid” menu.

Grid>Macromolecule>Open: launches a browser to open an existing PDBQT file.

Grid>Macromolecule>Choose: chooses a molecule that has been previously read into PMV. It will merge non-polar hydrogen atoms and charges, assign aromatic carbons, and prompt the user to write a PDBQT file.

Flexible Receptor PDBQT Files – the “FlexibleResidues” Menu

For docking calculations with selected flexibility in the receptor, add the hydrogen atoms and charges in PMV, then create two PDBQT files in AutoDockTools, one for the rigid portion of the receptor and one for the flexible atoms.

FlexibleResidues>Input>OpenMacromolecule: launches a browser to open an existing PDBQT file.

FlexibleResidues>Input>ChooseMacromolecule: chooses a molecule that has been previously read into PMV. It will merge non-polar hydrogen atoms and charges, assign aromatic carbons, and prompt the user to write a PDBQT file.

FlexibleResidues>ChooseTorsionsInCurrentlySelectedResidues: flexible residues are chosen using the tools in the PMV “Select” menu, then this option is used to assign these residues as flexible. As with the ligand, you can choose which bonds to keep rotatable by clicking on the bonds.

FlexibleResidues>RedisplayMacromolecule: cleans up the display.

FlexibleResidues>Output>SaveRigidPDBQT:

FlexibleResidues>Output>SaveFlexiblePDBQT: these two commands launch a browser to write PDBQT files for the rigid portion of the receptor and the flexible portion of the receptor.

STEP 2: Running AutoGrid

AutoDock requires pre-calculated *grid maps*, one for each atom type present in the ligand being docked. This helps to make the docking calculations fast. These maps are calculated by **AutoGrid**. A grid map consists of a three-dimensional lattice of regularly spaced points, surrounding (either entirely or partly) and centered on some region of interest of the macromolecule under study. This could be a protein, enzyme, antibody, DNA, RNA or even a polymer or ionic crystal. Typical grid point spacing varies from 0.2Å to 1.0Å, and the default is 0.375Å (roughly a quarter of the length of a carbon-carbon single bond). Each point within the grid map stores the potential energy of a ‘*probe*’ atom or functional group that is due to all the atoms in the macromolecule.

AutoGrid requires a grid parameter file to specify the files and parameters used in the calculation. The grid parameter file usually has the extension “.gpf”. As described below, AutoDockTools may be used to create the grid parameter file. A full description of the grid parameter file is included in Appendix I.

To run AutoGrid, the command is issued as follows:

```
% autogrid4 -p macro.gpf [-l macro.glg]
```

where ‘-p macro.gpf’ specifies the grid parameter file, and ‘-l macro.glg’ specifies the log file written during the grid calculation. If no log file is specified, the output is written to the terminal.

AutoGrid writes out the grid maps in ASCII form, for readability and portability; AutoDock expects ASCII format grid maps. For a description of the format of the grid map files, see Appendix I. Check the minimum and maximum energies in each grid map: these are reported at the end of the AutoGrid log file (here, it is “macro.glg”). Minimum van der Waals’ energies and hydrogen bonding energies are typically -10 to -1 kcal/mol, while maximum van der Waals’ energies are clamped at +10⁵ kcal/mol. Electrostatic potentials tend to range from around -10³ to +10³ kcal/mol/e: if these are both 0, check to make sure that partial charges have been assigned on the macromolecule.

As well as the grid maps, AutoGrid creates two files, with the extensions ‘.fld’, and ‘.xyz’. The former is a *field file* summarizing the grid maps, and the latter describes the spatial extent of the grids in Cartesian space.

Creating grid parameter files in AutoDockTools

The tools available in “grid” menu of AutoDockTools may be used to create grid parameter files.

Grid>OpenGPF: gets parameters from an existing grid parameter file.

Grid>Macromolecule: has options for opening an existing PDBQT file or choosing a molecule that has been read using PMV.

Grid>SetMapTypes: tools to define the atom types for the grids that will be calculated. Grids must be calculated for each type of atom in the ligand, and if flexible sidechains are used in the receptor, their atom types must also be included. The option “Directly” allows the user to input the list of atom types directly. Other options allow the user to define the atom types based on a ligand or flexible residue that has been read by PMV, or to open ligand or flexible residue PDBQT and use the atom types in these files.

Grid>SetMapTypes>SetUpCovalentMap: specifies parameters for creation of a covalent map, which may be used in specialized applications to favor binding of a given ligand atom in a single position. This is particularly useful for docking of covalent complexes between ligands and proteins. This will calculate a separate grid with atom type “Z” with a favorable Gaussian well at the coordinates given. The potential will have zero energy at the site, rising to the energy barrier height in surrounding areas.

Grid>GridBox: launches interactive commands for setting the grid dimensions and center. To enter numbers on the thumbwheel, place the cursor over the thumbwheel and type in the new value. Right clicking on the thumbwheel gives more options. IMPORTANT: when finished, use the “close saving current” option in the “File” menu on the Grid Options Panel. Options in the “Center” menu on the browser provide different methods to choose the center of the grid box.

Grid>OtherOptions: allows specification and editing of an existing parameter file.

Grid>Output: writes a new grid parameter file.

Grid>EditGPF: interactive editor for grid parameter files, which allows viewing of the latest grid parameter file written by AutoDockTools.

STEP 3: Docking with AutoDock

AutoDock uses one of several conformational search algorithms to explore the conformational states of a flexible ligand, using the maps generated by AutoGrid to evaluate the ligand-protein interaction at each point in the docking simulation. In a typical docking, the user will dock a ligand several times, to obtain multiple docked conformations. The results may be clustered to identify similar conformations—this is described in more detail in the section on Analysis (Step 4, below).

AutoDock requires: 1) grid maps for each atom type in the ligand, calculated by AutoGrid, 2) a PDBQT file for the ligand, and 3) a docking parameter file that specifies the files and parameters for the docking calculation. AutoDockTools may be used to generate the docking parameter file, as described below, which typically has the extension “.dpf”. A full description of the docking parameter file is included in Appendix I. AutoDock writes the final docked coordinates into the docking log file. As described in Step 4 below, these docked conformations may be viewed using AutoDockTools, they may be written as PDBQT files using AutoDockTools, or they may be taken directly from the docking log file using a text editor.

An AutoDock calculation is started from the command line using the following command:

```
% autodock4 [-i][-u][-t] -p lig.dpf [-l lig.dlg]
```

Input parameters are specified by “-p lig.dpf”, and the log file containing the output and results from the docking is defined by “-l lig.dlg”. This is the normal usage of AutoDock, and performs a standard docking calculation.

-p dpf_filename

Specifies the docking parameter file.

-l dlg_filename

Specifies the docking log file. If this is omitted, output will be written to a file with the same root name as the dpf.

-i

This is used to *ignore* any grid map header errors that may arise due to conflicting filenames. This overrides the header checking that is normally performed to ensure compatible grid maps are being used.

-u, -h

This returns a helpful message describing the command line *usage* of AutoDock.

-t

This instructs AutoDock to parse the PDBQT file to check the *torsion* definitions, and then stop.

-version

This returns a message describing the version of AutoDock being used, and then stops.

Choosing a protocol for your application

AutoDock provides a number of different methods for doing the docking simulation, and different methods might be useful for different applications. This section includes some guidelines for choosing the best approach.

1) Conformation Search. AutoDock provides several methods for doing the conformation search. Currently, the Lamarckian Genetic Algorithm provides the most efficient search for general applications, and in most cases will be the technique used. It is typically effective for systems with about 10 rotatable bonds in the ligand. The Genetic Algorithm may also be run without the local search, but this is typically less efficient than the Lamarckian GA-LS combination. Simulated Annealing is also less efficient than the Lamarckian Genetic Algorithm, but it can be useful in applications where search starting from a given point is desired. Local Search may be used to optimize a molecule in its local environment.

2) Number of Evaluations. Each of the search methods includes parameters for determining the amount of computational effort that will be used in the search. In the GA methods, this parameter is `ga_num_evals`, and in simulated annealing, this is `nacc` and `nrej`. The defaults given for these parameters are typically sufficient for docking systems with 10 or fewer rotatable bonds, and shorter simulations may often be used for systems with very few rotatable bonds. For complex systems with many more rotatable bonds than this, it is not generally effective simply to increase the number of evaluations. Rather, it is best to look for simpler formulations of the system, such as breaking a large ligand into two pieces and docking them separately, or freezing some rotatable bonds in likely conformations.

3) Model for the Unbound Ligand. In order to estimate a free energy of binding, AutoDock needs to estimate an energy for the unbound state of the ligand and protein. Several options are available for this. By default, AutoDock4.2 uses the assumption that the conformation of the unbound ligand and protein are the same as the conformation of the ligand and protein in the complex. Because these two conformations are the same, the total contribution of the internal energy (the interaction of atoms within the ligand or the interaction of atoms within the protein) will be zero, and reported in line 4 of the energy breakdown in the docking log file.

AutoDock4.0 used a different model, where the ligand was assumed to be in an extended state in solution, and an energy was calculated for this extended state before the docking simulation was performed. This model may be used in AutoDock4.2 by using the key word “unbound_model_extended.” This keyword will launch the calculation of the extended model and then will report the difference between the internal energy of the unbound model and the internal energy of the ligand when it is bound to the protein. In studies where many separate dockings are performed with the same ligand, this energy for the extended ligand may be precalculated and then used in the free energy calculation by using the key word “unbound_model_extended_energy VALUE.”

The user may also use other methods to calculate the energy of the unbound ligand outside of AutoDock. In this case, the keyword “unbound_energy VALUE” may be used to set the internal energy of the unbound state to a desired value. This value will then be used in the difference between the bound and unbound states to estimate the free energy.

4) Redocking Studies for Validation. Redocking studies may be used to validate the docking methods being used for a particular system. A known system is chosen with a similar conformational complexity--with a similar number of atoms and similar number of rotatable bonds. The known complex is then separated and docked, to evaluate the success of the docking method in reproducing the experimentally-known complex. These types of studies are also often used when comparing different docking methods. It is essential to randomize the ligand coordinates before the redocking simulation, to remove any bias that is caused by having the desired docked complex exactly equivalent to the starting coordinates.

5) Special Cases. AutoDock4.2 includes a number of optional methods for use in specialized applications. For instance, the keyword `intnbp_r_eps` may be used to override the standard parameters for the internal energy calculation. This has been used to model flexible cyclic molecules, but creating a special set of atom types to close rings during a docking simulation (this method is described in more detail in a tutorial on the AutoDock WWW site). Other optional features include methods for adding torsional constraints, and options for modifying the force field and analysis.

Creating docking parameter files in AutoDockTools

The tools available in the “Docking” menu of AutoDockTools may be used to create docking parameter files.

Docking>OpenDPF: gets parameters from an existing docking parameter file.

Docking>Macromolecule>SetRigidFilename:

Docking>Macromolecule>SetFlexibleResiduesFilename: these two commands specify the PDBQT file name that will be used for the rigid receptor, and if flexible receptor residues are used, specifies the PDBQT file name for the flexible portion of the receptor.

Docking>Ligand>Choose

Docking>Ligand>Open: These two commands allow the user to choose a ligand that is already read into ADT, or open an existing ligand PDBQT file.

Docking>Ligand>Ligand_Parameters: opens a panel for setting various ligand parameters, including the starting values for the translation, rotation, and torsion angles. For details, see the full description of the docking parameter file in the Appendix I.

Docking>SearchParameters>GeneticAlgorithmParameters:

Docking>SearchParameters>SimulatedAnnealingParameters:

Docking>SearchParameters>LocalSearchParameters: these three commands open a panel for setting the parameters used by each of the search algorithms, such as temperature schedules in simulated annealing and mutation/crossover rates in genetic algorithms. For details of each parameter, see the full description in the Appendix.

Docking>DockingParameters: opens a panel for setting the parameters used during the docking calculation, including options for the random number generator, options for the force field, step sizes taken when generating new conformations, and output options. For details of each parameter, see the full description in the Appendix I.

Docking>OtherOptions: specifies the name of an external atomic parameter file, if used.

Docking>Output>LamarckianGA:

Docking>Output>GeneticAlgorithm:

Docking>Output>SimulatedAnnealing:

Docking>Output>LocalSearch: These four commands write the docking parameter file using one of the four available search methods.

Docking>Edit: interactive editor for docking parameter files, which allows viewing of the latest docking parameter file written by AutoDockTools.

STEP 4: Evaluating the Results of a Docking

At the end of a docking simulation, AutoDock writes the coordinates for each docked conformation to the docking log file, along with information on clustering and interaction energies. AutoDockTools provides options for analyzing the information stored in the docking log file.

Information in the Docking Log

The **analysis** command in the docking parameter file causes AutoDock to perform a cluster analysis of the different docked conformations – the minimum energy found in each run. The results of this analysis are reported as a histogram, which may be found by searching for the word “HISTOGRAM” (all in capital letters) in the docking log file. This is followed by a table of RMSD values within each cluster.

AutoDock then writes coordinates for the conformation of best predicted energy in each cluster (to write coordinates for the best conformation from each run, include the keyword **write_all** in the docking parameter file). A header for each conformation includes information on the predicted energy of binding, broken down into several components, along with information on the state variables of the conformation. The coordinates are written in a modified PDB format, with four real values appended after the x,y,z coordinates: the vdW+hbond+desolvation energy of interaction of the atom, the electrostatic interaction of the atom, the partial charge, and the RMSD from the reference conformation.

The amount of information included in the docking log may be controlled using the “outlev” parameter, ranging from very minimal output for large virtual screens, to the default that is read by ADT (with information on docked conformations and clustering), to more verbose files that are useful for methods development.

Analyzing Docking Results with AutoDockTools

Options in the “Analyze” menu of AutoDockTools may be used to process and analyze the results from a docking simulation.

Analyze>Dockings>Open: opens a docking log file.

Analyze>Dockings>OpenAutoDockVinaResult: opens a docking log file from AutoDock Vina.

Analyze>Dockings>OpenAutoDockVirtualScreeningResult: opens an expanded result file that includes information on the conformation, clustering, and interactions with the receptor.

Analyze>Dockings>OpenAll: opens a set of docking log files in a directory.

Analyze>Dockings>Select: selects from a set of log files previously read into AutoDockTools.

Analyze>Dockings>Clear: clears log files that have been read into AutoDockTools.

Analyze>Dockings>ShowAsSpheres: creates a sphere at the center of mass of each docked conformation, which may be colored according to the predicted energy of interaction.

Analyze>Dockings>ShowInteractions: creates a specialized visualization to highlight interactions between the docked conformation of the ligand and the receptor. By default, the ligand is shown as ball-and-stick, surrounded by a molecular surface. The surface is colored with atomic colors in regions that contact the receptor, and gray in regions that are not in contact. Portions of the receptor that are in contact with the ligand are shown with ball-and-stick and spacefilling spheres. Hydrogen bonds are shown as a string of small spheres. A dialogue box is also launched that provides many other options for visualization.

Analyze>Dockings>WriteAutoDockVirtualScreeningResult: writes an expanded result file that includes information on the conformation, clustering, and interactions with the receptor.

Analyze>Macromolecule: options to open a macromolecule PDBQT file or choose a macromolecule that is already read into PMV.

Analyze>Grids>Open

Analyze>Grids>OpenOther: Opens a grid map file and launches the AutoDockTools grid visualizer. A dialogue box allows specification of the contour level and several rendering options. The contour level slider and input box limits the range to favorable energies. The “sampling” value is used to create coarse representations of complex maps—set to 1, it uses the actual grid spacing, set to higher values, it decimates the map to coarser grid spacing. The “Grid3D” tool is also available in the PMV menu for more advanced representation methods for grid visualization. The “OpenOther” command allows opening of grid map files that are not specified in the current docking log that is being displayed.

Analyze>Conformations>Play

Analyze>Conformations>PlayRankedByEnergy: Opens a window with controls for stepping through conformations as a movie. “Play” will use the order of conformations as they were found in the docking calculations, and “PlayRankedByEnergy” will order the conformations from lowest energy to highest energy. The “&” button opens a window with additional options:

ShowInfo opens a panel that displays information on the predicted energy of interaction, RMSD, etc.

BuildHbonds and ColorbyATOM/vdW/elect/total allow visualization of hbonds and interaction energies.

PlayMode and PlayParameters modify the parameters of the player.

BuildCurrent will build a new set of coordinates in the viewer for the conformation currently specified in the player. This is useful for displaying multiple conformations in the same view. BuildAll will build coordinates for all conformations in the player.

WriteCurrent will write a PDBQT file for the current conformation in the player. WriteAll will write separate PDBQT files for all conformations in the player. WriteComplex will write a PDBQT file for the current conformation of the ligand and the receptor.

Analyze>Conformations>Load: Launches an interactive browser that allows selection of clustered docked conformations. Information on the predicted interaction energy is shown at the top, and individual conformations may be chosen in the bottom panel. The “rank” value gives the cluster_rank—for instance, “1_3” is the third most favorable conformation in the best cluster. Buttons at the bottom, which may be revealed by enlarging the window, will write the current coordinates and dismiss the window.

Analyze>Conformations>ViewInitialPopulation: Tools to display all members of the population in a genetic algorithm search. Requires a DLG from a run with a specialized output level: “outlev runvvv”.

Analyze>Clusterings>Show: Tools to show an interactive histogram of clustered conformations.

Analyze>Clusterings>Recluster: Reclusters docked conformations based on new tolerances. Several values may be input in the dialogue window for use in reclustering. The results may be analyzed using **Clusterings>Show**.

Analyze>Clusterings>ReclusterOnSubset: Reclusters docked conformations using only a selected set of atoms. The selection is performed using the tools in the “select” menu of PMV, and then using the “save current selection as a set” option.

Appendix I: AutoDock File Formats

PDBQT Format for Coordinate Files

Extension: .pdbqt

```
"ATOM %5d %-4s %1s %-3s %1s %4d %1s %8.3f %8.3f %8.3f %6.2f %6.2f %4s %6.3f %2s \n",  
atom_serial_num, atom_name, alt_loc, res_name, chain_id, res_num, ins_code, x, y, z,  
occupancy, temp_factor, footnote, partial_charge, atom_type  
(The " " symbol is used to indicate one space.)
```

The PDBQT format adds four things to standard formatted PDB files:

- 1) partial charges are included in each ATOM or HETATM record, substituting for the fields in columns 67-76.
- 2) AutoDock atom types (which may be one or two letters) are included in each ATOM or HETATM record in columns 78-79.
- 3) To allow flexibility in the ligand, it is necessary to assign the rotatable bonds. AutoDock can handle up to MAX_TORS rotatable bonds: this parameter is defined in "autodock.h", and is ordinarily set to 32. If this value is changed, AutoDock must be recompiled. *Please note that AutoDock4.2 is currently effective for systems with roughly 10 torsional degrees of freedom, and systems with more torsional flexibility may not give consistent results.* Torsions are defined in the PDBQT file using the following keywords:

ROOT / ENDROOT
BRANCH / ENDBRANCH

These keywords use the metaphor of a tree. See the diagram below for an example. The "root" is defined as the central portion of the ligand, from which rotatable 'branches' sprout. Branches within branches are possible. Nested rotatable bonds are rotated in order from the "leaves" to the "root". The PDBQT keywords must be carefully placed, and the order of the ATOM or HETATM records often need to be changed in order to fit into the correct branches. AutoDockTools is designed to assist the user in placing these keywords correctly, and in re-ordering the ATOM or HETATM records in the ligand PDBQT file.

- 4) The number of torsional degrees of freedom, which will be used to evaluate the conformational entropy, is specified using the TORSDOF keyword followed by the integer number of rotatable bonds. In the current AutoDock 4.2 force field, this is the total number of rotatable bonds in the ligand, including rotatable bonds in hydroxyls and other groups where

only hydrogen atoms are moved, but excluding bonds that are within cycles. The value in the PDBQT file can be overridden in the AutoDock DPF using the “torsdof” statement.

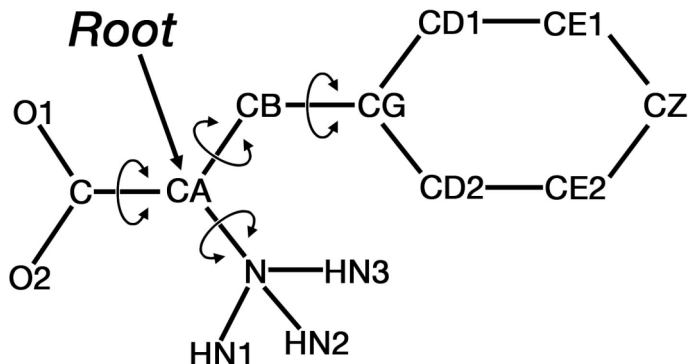
Note: AutoDockTools, AutoGrid and AutoDock do not recognize or write out PDB “CONNECT” records.

Sample PDBQT file

```

REMARK 4 active torsions:
REMARK status: ('A' for Active; 'I' for Inactive)
REMARK 1 A between atoms: N_1 and CA_5
REMARK 2 A between atoms: CA_5 and CB_6
REMARK 3 A between atoms: CA_5 and C_13
REMARK 4 A between atoms: CB_6 and CG_7
ROOT
ATOM 1 CA PHE A 1 25.412 19.595 12.578 1.00 12.96 0.287 C
ENDROOT
BRANCH 1 2
ATOM 2 N PHE A 1 25.225 18.394 13.381 1.00 13.04 -0.065 N
ATOM 3 HN3 PHE A 1 25.856 17.643 13.100 1.00 0.00 0.275 HD
ATOM 4 HN2 PHE A 1 25.558 18.517 14.337 1.00 0.00 0.275 HD
ATOM 5 HN1 PHE A 1 24.247 18.105 13.350 1.00 0.00 0.275 HD
ENDBRANCH 1 2
BRANCH 1 6
ATOM 6 CB PHE A 1 26.873 20.027 12.625 1.00 12.45 0.082 C
BRANCH 6 7
ATOM 7 CG PHE A 1 27.286 20.629 13.923 1.00 12.96 -0.056 A
ATOM 8 CD2 PHE A 1 27.470 22.001 14.050 1.00 12.47 0.007 A
ATOM 9 CE2 PHE A 1 27.877 22.571 15.265 1.00 13.98 0.001 A
ATOM 10 CZ PHE A 1 28.108 21.754 16.360 1.00 13.84 0.000 A
ATOM 11 CE1 PHE A 1 27.919 20.380 16.242 1.00 13.77 0.001 A
ATOM 12 CD1 PHE A 1 27.525 19.821 15.027 1.00 11.32 0.007 A
ENDBRANCH 6 7
ENDBRANCH 1 6
BRANCH 1 13
ATOM 13 C PHE A 1 25.015 19.417 11.141 1.00 13.31 0.204 C
ATOM 14 O2 PHE A 1 24.659 20.534 10.507 1.00 12.12 -0.646 OA
ATOM 15 O1 PHE A 1 25.024 18.283 10.608 1.00 13.49 -0.646 OA
ENDBRANCH 1 13
TORSDOF 4

```



PDBQT Format for Flexible Receptor Sidechains

Flexible sidechains in the receptor are treated explicitly during AutoDock simulation. AutoDock requires a separate PDBQT file with atomic coordinates of the sidechains that will be treated as flexible. Atomic coordinates and branching keywords for each amino acid is placed between BEGIN_RES and END_RES records. The atom linking the amino acid to the protein, which will remain in fixed position during the simulation, is included as the root. The atoms included in the flexible residue PDBQT must be omitted from the PDBQT for the rigid portions of the receptor. For instance, in the example below, the CA atom of the PHE residue is used as the root of the flexible residue. It is included in the flexible sidechain PDBQT file, and it will be omitted from the rigid protein PDBQT file.

Sample flexible residue file, with two flexible amino acids

```
BEGIN_RES PHE A 53
REMARK 2 active torsions:
REMARK status: ('A' for Active; 'I' for Inactive)
REMARK 1 A between atoms: CA and CB
REMARK 2 A between atoms: CB and CG
ROOT
ATOM 1 CA PHE A 53 25.412 19.595 12.578 1.00 12.96 0.180 C
ENDROOT
BRANCH 1 2
ATOM 2 CB PHE A 53 26.873 20.027 12.625 1.00 12.45 0.073 C
BRANCH 2 3
ATOM 3 CG PHE A 53 27.286 20.629 13.923 1.00 12.96 -0.056 A
ATOM 4 CD1 PHE A 53 27.525 19.821 15.027 1.00 11.32 0.007 A
ATOM 5 CE1 PHE A 53 27.919 20.380 16.242 1.00 13.77 0.001 A
ATOM 6 CZ PHE A 53 28.108 21.754 16.360 1.00 13.84 0.000 A
ATOM 7 CE2 PHE A 53 27.877 22.571 15.265 1.00 13.98 0.001 A
ATOM 8 CD2 PHE A 53 27.470 22.001 14.050 1.00 12.47 0.007 A
ENDBRANCH 2 3
ENDBRANCH 1 2
END_RES PHE A 53
BEGIN_RES ILE A 54
REMARK 2 active torsions:
REMARK status: ('A' for Active; 'I' for Inactive)
REMARK 3 A between atoms: CA and CB
REMARK 4 A between atoms: CB and CG1
ROOT
ATOM 9 CA ILE A 54 24.457 20.591 9.052 1.00 12.30 0.180 C
ENDROOT
BRANCH 9 10
ATOM 10 CB ILE A 54 22.958 20.662 8.641 1.00 11.82 0.013 C
ATOM 11 CG2 ILE A 54 22.250 19.367 9.046 1.00 12.63 0.012 C
BRANCH 10 12
ATOM 12 CG1 ILE A 54 22.266 21.867 9.298 1.00 13.03 0.002 C
ATOM 13 CD1 ILE A 54 20.931 22.246 8.670 1.00 14.42 0.005 C
ENDBRANCH 10 12
ENDBRANCH 9 10
END_RES ILE A 54
```

AutoGrid Grid Parameter File: GPF

Extension: `.gpf`

The grid parameter file specifies an AutoGrid calculation, including the size and location of the grid, the atom types that will be used, the coordinate file for the rigid receptor, and other parameters for calculation of the grids. Unlike previous versions of AutoGrid, the pairwise atomic parameters are now read from a separate file (described below) or taken from defaults in AutoGrid.

All delimiters where needed are white spaces. Default values, where applicable, are given here in square brackets [thus]. A comment must be prefixed by the “#” symbol, and can be placed after a space at the end of a parameter line, or on a line of its own. Upper/lower case is ignored in keywords but is significant in atom names and file names. File names cannot contain white space or non-ASCII characters. Although ideally it should be possible to give AutoGrid keywords in any order, not every possible combination has been tested, so it would be wise to stick to the following order.

AutoGrid Keywords and Commands

parameter_file <existing atomic parameter file name>

(Optional) User-defined atomic parameter file (format described in the next section). By default, AutoGrid uses internal parameters.

npts <integer> <integer> <integer>

[40, 40, 40]

Number of *x*-, *y*- and *z*-grid points. Each *must* be an even integer number. When added to the central grid point, there will be an odd number of points in each dimension. The number of *x*-, *y*- and *z*-grid points need not be equal.

gridfld <new grid file name>

The grid field filename, which will be written in a format readable by AutoDock. The filename extension is ‘.fld’.

spacing <float>

[0.375 Å]

(Optional) The grid point spacing, in Å. Grid points are orthogonal and uniformly spaced in AutoDock: this value is used in each dimension.

receptor_types <string>

[A C HD N O A S A]

Atom types present in the receptor, separated by spaces; *e.g.* for a typical protein, this will be, “A C HD N OA SA”. Atom types are one or two letters, and several specialized types are used in the AutoDock4.2 forcefield, including: C (aliphatic carbon), A (aromatic carbon), HD (hydrogen that donates hydrogen bond), OA (oxygen that accepts hydrogen bond), N (nitrogen that doesn’t accept hydrogen bonds), SA (sulfur that accepts hydrogen bonds).

ligand_types <string>

[A C HD N NA OA SA]

Atom types present in the ligand, separated by spaces, such as, “A C HD N NA OA SA”.

receptor <existing receptor file name>

Macromolecule filename, in PDBQT format.

gridcenter <float> <float> <float>

gridcenter auto

[auto]

The user can explicitly define the center of the grid maps, respectively the x , y and z coordinates of the center of the grid maps (units: Å, Å, Å.) Or the keyword “auto” can be given, in which case AutoGrid will center the grid maps on the center of the macromolecule.

smooth <float>

[0.5 Å]

(Optional) Smoothing parameter for the pairwise atomic affinity potentials (both van der Waals and hydrogen bonds). For AutoDock4, the force field has been optimized for a value of 0.5 Å.

map <new map file name>

Filename of the grid map for each ligand atom type; the extension is usually “.X.map”, where “X” is the atom type. One line must be included for each atom type in the **ligand_types** command, in the order given in that command.

elecmap <new map file name>

Filename for the electrostatic potential energy grid map to be created; filename extension ‘.e.map’.

dsolvmap <new map file name>

Filename for the desolvation potential energy grid map to be created; filename extension ‘.d.map’.

dielectric <float>

[-0.1465]

(Optional) Dielectric function flag: if negative, AutoGrid will use *distance-dependent* dielectric of Mehler and Solmajer; if the float is positive, AutoGrid will use this value as the dielectric constant. AutoDock4 has been calibrated to use a value of -0.1465.

Sample Grid Parameter File (from tutorial)

```
npts 60 60 60 # num.grid points in xyz
gridfld lhsg.maps.fld # grid_data_file
spacing 0.375 # spacing(A)
receptor_types A C HD N OA SA # receptor atom types
ligand_types A C NA OA N HD # ligand atom types
receptor lhsg.pdbqt # macromolecule
gridcenter 2.5 6.5 -7.5 # xyz-coordinates or auto
smooth 0.5 # store minimum energy w/in rad(A)
map lhsg.A.map # atom-specific affinity map
map lhsg.C.map # atom-specific affinity map
map lhsg.NA.map # atom-specific affinity map
map lhsg.OA.map # atom-specific affinity map
map lhsg.N.map # atom-specific affinity map
map lhsg.HD.map # atom-specific affinity map
elecmap lhsg.e.map # electrostatic potential map
dsolvmap lhsg.d.map # desolvation potential map
dielectric -0.1465 # <0, AD4 distance-dep.diel;>0,
constant
```

Atomic Parameter File

Filename: **AD4.1_bound.dat**

Atomic parameters are assigned by default from values internal to AutoGrid and AutoDock, but custom parameters may be read from a file. The file includes weighting parameters for each term in the free energy function, and parameters for each atom type:

```
FE_coeff-vdW <float>  
FE_coeff-hbond <float>  
FE_coeff-estat <float>  
FE_coeff-desolv <float>  
FE_coeff-tors <float>
```

These are followed by pairwise atomic parameters for each type of atom:

```
atom_par <string> 6*<float> 4*<integer>
```

Each atom_par record includes:

1. Atom type.
2. Rii = sum of the vdW radii of two like atoms (Å).
3. epsii = vdW well depth (kcal/mol)
4. vol = atomic solvation volume (Å³)
5. Rij_hb = H-bond distance between heteroatom and hydrogen (Å)
value is included in the heteroatom record and set to zero for hydrogens
6. epsij_hb = well depth for hydrogen bonds (kcal/mol)
7. hbond = integer indicating the type of hbond
 - 0, no hbond
 - 1, spherical H donor
 - 2, directional H donor
 - 3, spherical acceptor
 - 4, directional N acceptor
 - 5, directional O/S acceptor
8. rec_index = initialized to -1, used to hold number of atom types
9. map_index = initialized to -1, used to hold the index of the AutoGrid map
10. bond_index = used to detect bonds of different lengths, see “mdist.h” for information

Default Atomic Parameter File AD4.1_bound.dat

```

#
#           Free Energy Coefficient
#           -----
FE_coeff_vdW    0.1662
FE_coeff_hbond  0.1209
FE_coeff_estat  0.1406
FE_coeff_desolv 0.1322
FE_coeff_tors   0.2983

#
#           Atom      Rii           Rij_hb      rec_index
#           Type      epsii        solpar      epsij_hb    map_index
#           --         -----        -----        ---      -
#           --         -----        -----        ---      -
#           --         -----        -----        ---      -
atom_par H      2.00  0.020   0.0000   0.00051  0.0  0.0  0  -1  -1  3  # Non H-bonding Hydrogen
atom_par HD     2.00  0.020   0.0000   0.00051  0.0  0.0  2  -1  -1  3  # Donor 1 H-bond Hydrogen
atom_par HS     2.00  0.020   0.0000   0.00051  0.0  0.0  1  -1  -1  3  # Donor S Spherical Hydrogen
atom_par C      4.00  0.150  33.5103  -0.00143  0.0  0.0  0  -1  -1  0  # Aliphatic Carbon
atom_par A      4.00  0.150  33.5103  -0.00052  0.0  0.0  0  -1  -1  0  # Aromatic Carbon
atom_par N      3.50  0.160  22.4493  -0.00162  0.0  0.0  0  -1  -1  1  # Non H-bonding Nitrogen
atom_par NA     3.50  0.160  22.4493  -0.00162  1.9  5.0  4  -1  -1  1  # Acceptor 1 H-bond Nitrogen
atom_par NS     3.50  0.160  22.4493  -0.00162  1.9  5.0  3  -1  -1  1  # Acceptor Spherical Nitrogen
atom_par OA     3.20  0.200  17.1573  -0.00251  1.9  5.0  5  -1  -1  2  # Acceptor 2 H-bonds Oxygen
atom_par OS     3.20  0.200  17.1573  -0.00251  1.9  5.0  3  -1  -1  2  # Acceptor Spherical Oxygen
atom_par F      3.09  0.080  15.4480  -0.00110  0.0  0.0  0  -1  -1  4  # Non H-bonding Fluorine
atom_par Mg     1.30  0.875   1.5600  -0.00110  0.0  0.0  0  -1  -1  4  # Non H-bonding Magnesium
atom_par MG     1.30  0.875   1.5600  -0.00110  0.0  0.0  0  -1  -1  4  # Non H-bonding Magnesium
atom_par P      4.20  0.200  38.7924  -0.00110  0.0  0.0  0  -1  -1  5  # Non H-bonding Phosphorus
atom_par SA     4.00  0.200  33.5103  -0.00214  2.5  1.0  5  -1  -1  6  # Acceptor 2 H-bonds Sulphur
atom_par S      4.00  0.200  33.5103  -0.00214  0.0  0.0  0  -1  -1  6  # Non H-bonding Sulphur
atom_par Cl     4.09  0.276  35.8235  -0.00110  0.0  0.0  0  -1  -1  4  # Non H-bonding Chlorine
atom_par CL     4.09  0.276  35.8235  -0.00110  0.0  0.0  0  -1  -1  4  # Non H-bonding Chlorine
atom_par Ca     1.98  0.550   2.7700  -0.00110  0.0  0.0  0  -1  -1  4  # Non H-bonding Calcium
atom_par CA     1.98  0.550   2.7700  -0.00110  0.0  0.0  0  -1  -1  4  # Non H-bonding Calcium
atom_par Mn     1.30  0.875   2.1400  -0.00110  0.0  0.0  0  -1  -1  4  # Non H-bonding Manganese
atom_par MN     1.30  0.875   2.1400  -0.00110  0.0  0.0  0  -1  -1  4  # Non H-bonding Manganese
atom_par Fe     1.30  0.010   1.8400  -0.00110  0.0  0.0  0  -1  -1  4  # Non H-bonding Iron
atom_par FE     1.30  0.010   1.8400  -0.00110  0.0  0.0  0  -1  -1  4  # Non H-bonding Iron
atom_par Zn     1.48  0.550   1.7000  -0.00110  0.0  0.0  0  -1  -1  4  # Non H-bonding Zinc
atom_par ZN     1.48  0.550   1.7000  -0.00110  0.0  0.0  0  -1  -1  4  # Non H-bonding Zinc
atom_par Br     4.33  0.389  42.5661  -0.00110  0.0  0.0  0  -1  -1  4  # Non H-bonding Bromine
atom_par BR     4.33  0.389  42.5661  -0.00110  0.0  0.0  0  -1  -1  4  # Non H-bonding Bromine
atom_par I      4.72  0.550  55.0585  -0.00110  0.0  0.0  0  -1  -1  4  # Non H-bonding Iodine
atom_par Z      4.00  0.150  33.5103  -0.00143  0.0  0.0  0  -1  -1  0  # Non H-bonding covalent map
atom_par G      4.00  0.150  33.5103  -0.00143  0.0  0.0  0  -1  -1  0  # Ring closure Aliphatic C
atom_par GA     4.00  0.150  33.5103  -0.00052  0.0  0.0  0  -1  -1  0  # Ring closure Aromatic C
atom_par J      4.00  0.150  33.5103  -0.00143  0.0  0.0  0  -1  -1  0  # Ring closure Aliphatic C
atom_par Q      4.00  0.150  33.5103  -0.00143  0.0  0.0  0  -1  -1  0  # Ring closure Aliphatic C

```

Grid Map File

Extension: **.map**

The first six lines of each grid map describe the spatial features of the maps and the files used or created. These headers are checked by AutoDock to ensure that they are appropriate for the requested docking. The remainder of the file contains grid point energies, written as floating point numbers, one per line. They are ordered according to the nested loops: $z(y(x))$, so x is changing fastest. The coordinate system is right-handed, and the actual file contains one more element than the NELEMENTS specified because the maps always have an odd number of elements in each direction. The “CENTER” is the position of the middle coordinate point, in the receptor (macromolecule) reference frame.

Sample Grid Map File

```
GRID_PARAMETER_FILE vac1.nbc.gpf
GRID_DATA_FILE 4phv.nbc_maps.fld
MACROMOLECULE 4phv.new.pdbq
SPACING 0.375
NELEMENTS 50 50 80
CENTER -0.026 4.353 -0.038
125.095596
123.634560
116.724602
108.233879
:
```

Grid Map Field File

Extension: .maps.fld

This is essentially two files in one. It is both an AVS field file, which may be read by a number of scientific visualization programs, and an AutoDock input file with AutoDock-specific information in the comments at the head of the file. AutoDock uses this file to check that all the maps it reads in are compatible. For example, in this file, the grid spacing is 0.375 Angstroms, there are 60 intervals in each dimension (and 61 actual grid points), the grid is centered near (16., 39., 1.), it was calculated around the macromolecule 'protein.pdbqt', and the AutoGrid parameter file used to create this (and the maps) was 'protein.gpf'. This file also points to a second file, 'protein.maps.xyz', which contains the minimum and maximum extents of the grid box in each dimension, *x*, *y*, and *z*. Finally, it lists the grid map files that were calculated by AutoGrid, here 'protein.A.map', 'protein.C.map', etc.

Sample Grid Map Field File

```
# AVS field file
#
# AutoDock Atomic Affinity and Electrostatic Grids
#
# Created by autogrid4.
#
#SPACING 0.375
#NELEMENTS 60 60 60
#CENTER 16.000 39.000 1.000
#MACROMOLECULE protein.pdbqt
#GRID_PARAMETER_FILE protein.gpf
#
ndim=3                # number of dimensions in the field
dim1=61               # number of x-elements
dim2=61               # number of y-elements
dim3=61               # number of z-elements
nspace=3              # number of physical coordinates per point
veclen=8              # number of affinity values at each point
data=float            # data type (byte, integer, float, double)
field=uniform         # field type (uniform, rectilinear, irregular)
coord 1 file=protein.maps.xyz filetype=ascii offset=0
coord 2 file=protein.maps.xyz filetype=ascii offset=2
coord 3 file=protein.maps.xyz filetype=ascii offset=4
label=A-affinity     # component label for variable 1
label=C-affinity     # component label for variable 2
label=HD-affinity    # component label for variable 3
label=N-affinity     # component label for variable 4
label=OA-affinity    # component label for variable 5
label=SA-affinity    # component label for variable 6
label=Electrostatics # component label for variable 7
label=Desolvation    # component label for variable 8
#
# location of affinity grid files and how to read them
#
variable 1 file=protein.A.map filetype=ascii skip=6
variable 2 file=protein.C.map filetype=ascii skip=6
variable 3 file=protein.HD.map filetype=ascii skip=6
variable 4 file=protein.N.map filetype=ascii skip=6
variable 5 file=protein.OA.map filetype=ascii skip=6
variable 6 file=protein.SA.map filetype=ascii skip=6
variable 7 file=protein.e.map filetype=ascii skip=6
variable 8 file=protein.d.map filetype=ascii skip=6
```

AutoDock Docking Parameter File: DPF

Extension: **.dpf**

The docking parameter file specifies the files and parameters for an AutoDock calculation, including the map files that will be used for the docking, the ligand coordinate files, and parameters for the search. Unlike previous versions of AutoDock, the pairwise atomic parameters used for the internal energy calculation may now read from a separate file (described above), or taken from defaults in AutoDock.

All delimiters where needed are white spaces. Default values, where applicable, are given here in square brackets [thus]. A comment must be prefixed by the “#” symbol, and can be placed after a space at the end of a parameter line, or on a line of its own. Upper/lower case is ignored in keywords but is significant in atom names and file names. File names cannot contain white space or non-ASCII characters. Although ideally it should be possible to give AutoDock keywords in any order, not every possible combination has been tested, so it would be wise to stick to the following order.

Parameter to define the version

autodock_parameter_version <version>

[4.2]

Defines the version of the parameters that are going to follow in the rest of the DPF. By default, this keyword is set to the value of '4.2' but it can be changed in the future to support several compatibility modes among different versions of AutoDock.

Parameter to set the amount of output

outlev { <symbolic name> | <integer> }

[adt] or [1]

(Optional) Set the output level of data written into the docking log file. Either the symbolic names or the numeric values can be used in the DPF. Values of "adt", "runv" and higher are compatible with the result analysis tools in AutoDockTools. The highly verbose levels are provided for development and debugging work, and the minimal levels are provided for data-intensive applications such as virtual screening.

Symbolic	Numeric	Result
min	-2	minimal - energy breakdown and state of one result
minclust	-1	energy breakdown, states, coords of clustering results

basic	0	echoes input, parms used, final coords and state from each run
adt	1	ADT-compatible output during docking
default	1	default value is same as "adt"
runv	2	more verbose run - expanded output during docking
ligread	3	expanded output during ligand setup (e.g., the nonbond matrix)
recread	4	expanded output during receptor map setup
runvv	5	still more verbose run (e.g., min/max/median per "N" evals)
runvvv	6	most verbose supported run (e.g., state vars per "N" evals)
etables	7	energy table / scoring function atom-by-atom details
nbinte	8	report of nonbond internal energy table (see analysis.cc)
nbintev	9	detailed report of nonbond internal energy table (see analysis.cc)

Atomic parameters for pairwise energy evaluation

parameter_file <existing atomic parameter file name>

(Optional) Atomic parameter file used for pairwise energy evaluation in internal energies and interactions between ligand and flexible sidechains. If this is not given, AutoDock uses default parameters identical to values in the file AD4.1_bound.dat.

intelec [off]

(Optional) By default in AutoDock 4.2.5 and later, internal ligand electrostatic energies will be calculated. To ignore those terms, include "intelec off" in the DPF. Note that this is only relevant for flexible ligands.

intnbp_r_eps <float><float><integer><integer><string><string>

(Optional) This optional keyword allows the user to override manually the internal energy potential for a given class of interactions. The parameters are: r_{eq} , ϵ , n , m , and the two atom types, where r_{eq} is the equilibrium distance for the bottom of the energetic well, ϵ is the depth of the well, n and m are the coefficients. For instance, the command "intnbp_r_eps 1.5 10. 12 6 OA FE" will set up a potential with well depth of 10 kcal/mol at a distance of 1.5 Å for interaction between oxygen and iron atoms. The potential $V(r)$ is calculated with the expression:

$$V(r) = C_n/r^n - C_m/r^m$$

$$C_n = m/(n-m) * \epsilon * r_{eq}^n$$

$$C_m = n/(n-m) * \epsilon * r_{eq}^m$$

A special atom type “G” has been created for using this feature for ring closure simulations. Please see the tutorial for more information.

torsdof <integer>

(Optional) Overrides the number of torsional degrees of freedom appearing in the ligand PDBQT file. This term affects the reported binding energy but not the conformational search because it is constant for any particular run.

Command to set the seeds for the random number generator

**seed { pid | time | <integer> } { pid | time | <integer> }
[pid time]**

(Optional) AutoDock search operations use a pseudo-random number generator which, for each docking job, must be ‘seeded’ with two integers, in any combination of explicit integers, the keyword “time” or the keyword “pid”. The keyword “time” sets a seed based on the current time, and “pid” sets a seed to the operating system’s process ID of the currently executing AutoDock process. The default seed set (pid time) will yield different docking results for each AutoDock run; to have instead completely repeatable results, use two explicit integers.

Parameters defining the grid maps to be used

ligand_types <string>

Atom names for all atom types present in ligand, using the same blank-separated, one or two letter atom types used in AutoGrid.

fld <existing .fld file name>

Grid data field file created by AutoGrid (must have the extension “.fld”).

map <existing map file name>

Filename for the **AutoGrid** affinity grid maps. This keyword plus filename must be repeated for all atom types in the order specified by the “ligand_types” command. In all map files a 6-line header is required, and energies must be ordered according to the nested loops z(y(x)).

elecmap <existing map file name>

Filename for the electrostatics grid map. 6-line header required, and energies must be ordered according to the nested loops z(y(x)).

desolvmap <existing map file name>

Filename for the desolvation grid map. 6-line header required, and energies must be ordered according to the nested loops z(y(x)).

Parameters defining the state of the unbound ligand

(Optional) **unbound_energy** <float>

Sets the internal energy of the unbound state to the value.

(Optional) **unbound_model_extended**

Launches a calculation to find an extended conformation of the ligand, then uses this conformation to calculate the internal energy of the unbound state. The AutoDock4.0 keyword “compute_unbound_extended” will perform the same process.

(Optional) **unbound_model_extended_energy** <float>

Sets the internal energy of the unbound state to the value. This also sets the default atomic parameters used for pairwise energy evaluate to be appropriate for the extended unbound model.

Parameters defining the ligand and its initial state

move <existing PDBQT file name>

Filename for the PDBQT coordinate file of the ligand to be docked.

about <float> <float> <float>

[automatically calculated]

(Optional) Use this keyword to specify the center of the ligand, *about* which rotations will be made. (The coordinate frame of reference is that of the ligand PDBQT file.) The default rotation center is the mean x,y,z -coordinates of the ligand root atoms. Units: Å, Å, Å.

tran0 <float> <float> <float>

tran0 random

[automatically calculated]

(Optional) Initial coordinates for the center of the ligand, in the same frame of reference as the receptor grid maps. Every docking simulation specified in the docking parameter file starts the ligand from this location.

Alternatively, the user can just give the keyword “random” and AutoDock will pick random initial coordinates instead. Units: Å, Å, Å.

quaternion0 <float> <float> <float> <float>

axisangle0 <float> <float> <float> <float>

quat0 <float> <float> <float> <float> (synonym for “axisangle0”)

quaternion0 random

[random]

(Optional) Initial ligand rigid-body orientation

quaternion0: Q_x, Q_y, Q_z, Q_w . Specified as quaternion. (Units: none,none,none, none.) AutoDock will automatically normalize. A ‘no rotation’ (identity) quaternion would be ‘0 0 0 1’.

axisangle0: $Axis_x$, $Axis_y$, $Axis_z$, $Angle_\theta$. Specified as axis-angle: $Axis_x$, $Axis_y$, $Axis_z$ define the unit vector of rotation, and $Angle_\theta$ defines the angle of rotation about this vector. (Units: none,none,none, degrees.) AutoDock will automatically normalize the vector. A ‘no rotation’ (identity) axis-angle would be ‘1 0 0 0’.

Alternatively, the user can just give the keyword “random” and AutoDock will pick a random 3-D orientation. Each docking simulation specified in the docking parameter file will begin at this same random rigid body rotation.

dihe0 <float> ...
dihe0 random

[random]

Initial **relative** dihedral angles; there must be a floating point number specified on this line for each rotatable bond in the PDBQT file. Each value specified here will be added to the corresponding torsion angle in the input PDBQT file, at the start of each run. Torsion angles are specified by only two atoms, so the definition of rotations is relative to the input conformation of the ligand, not an absolute conformation. Units: °.

Parameters defining ligand step sizes for simulated annealing [SA] calculations

tstep <float>
tstep <float> <float>

[2.0 Å]

(Optional, SA only) The first form, with one argument, defines the maximum translation jump for the first cycle that the ligand may make in one simulated annealing step. When “trnrf” is less than 1, the reduction factor is multiplied with the tstep at the end of each cycle, to give the new value for the next cycle. The second form allows the user to specify the value for the first cycle and the last cycle: AutoDock then calculates the reduction factor that satisfies these constraints. Units: Å.

qstep <float>

[50.0°]

(Optional, SA only) Maximum angular step size for the orientational component. Units: °.

dstep <float>

[50.0°]

(Optional, SA only) Maximum dihedral (torsion) step size. Units: °.

Parameters defining optional ligand torsion constraints for simulated annealing

barrier <float>

[10000.0]

(Optional, SA only) This defines the energy-barrier height applied to constrained torsions. When the torsion is at a preferred angle, there is no torsion penalty: this torsion’s energy is zero. If the

torsion angle falls within a disallowed zone, however, it can contribute up to the full barrier energy. Since the torsion-energy profiles are stored internally as arrays of type ‘unsigned short’, only positive integers between 0 and 65535 are allowed.

gausstorcon <integer> <float> <float>

(Optional, SA only) Adds a constraint to a torsion. The torsion number is identified by an integer. This identifier comes from the list at the top of the AutoDockTools-generated input ligand PDBQT file (on the REMARK lines). An energy profile will be calculated for this torsion. An inverted Gaussian is added for each new constraint. To completely specify each Gaussian, two floating point numbers are needed: the *preferred angle* and the *half-width* respectively (both in degrees). Note that the preferred angle should be specified in the range -180° to $+180^\circ$; numbers outside this range will be wrapped back into this range. This angle, χ , is *relative* to the original torsion angle in the input structure. The *half-width* is the difference between the two angles at which the energy is half the barrier. The smaller the half-width, the tighter the constraint.

If you wish to constrain to absolute-valued torsion angles, it will be necessary to zero the initial torsion angles in the ligand. The problem arises from the ambiguous 2-atom definition of the rotatable bond *B-C*. To identify a torsion angle unambiguously, 4 atoms must be specified: *A-B-C-D*. The sign convention for torsion angles is anti-clockwise (counter-clockwise) with positive angles, clockwise negative.

There is no limit to the number of constraints that can be added to a given torsion. Each new torsion-constraint energy profile is combined with the pre-existing one by selecting the minimum energy of either the new or the existing profiles.

Please note that in our tests, torsion constrains are highly inefficient, and are only effective when used in systems with few degrees of freedom in the ligand, and only a few torsion constraints.

showtorpen

(Optional, SA only) (Use only with “gausstorcon”) This switches on the storage and subsequent output of torsion energies. During each energy evaluation, the penalty energy for each constrained torsion, as specified by the “gausstorcon” command, will be stored in an array. At the end of each run, the final docked conformation’s state variables are output, but with this command, the penalty energy for each torsion will be printed alongside its torsion angle.

Parameters for cluster analysis of docked conformations

rmstol <float>

[2.0Å]

(Optional) When more than one run is carried out in a given job, cluster analysis or ‘structure binning’ will be performed, based on all-atom root mean square deviation (RMSD), ranking the resulting families of docked conformations in order of increasing energy. The lowest energy representative from each cluster is written in PDBQT format to the log file. Normally, AutoDock uses the ligand residue number from the input PDBQT file; to number the clustered conformations incrementally from 1, use “output_resnum_as runnum”, see below. (Units: Å).

rmsref <existing PDB/PDBQT file name>

(Optional) If included, the RMSD of the docked conformations will be calculated with respect to the coordinates in the PDB or PDBQT file specified here. This is useful when the experimentally determined complex conformation of the ligand is known. The order of the atoms in this file must match that in the input PDBQT file given by the **move** command. These values of RMSD will be output in the last column of the final PDBQT records, after the clustering has been performed. If this keyword is not included, the RMSD is calculated based on the starting position of the ligand.

rmsnosym

(Optional) The default method for structure binning allows for atom similarity, as in a tertiary-butyl which can be rotated by $\pm 120^\circ$, but in other cases it may be desirable to bypass this similar atom type checking and calculate the RMSD on a one-for-one basis. The symmetry checking algorithm scans all atoms in the reference structure, and selects the nearest atom of identical atom type to be added to the sum of squares of distances. This works well when the two conformations are very similar, but this assumption breaks down when the two conformations are translated significantly. Symmetry checking can be turned off using the **rmsnosym** command; omit this command if you still want symmetry checking.

rmsatoms all

(Optional) If this keyword is included, RMSD calculation will be performed using both ligand and flexible receptor sidechain atoms. If an “rmsref” file is specified, it must include both ligand and flexible receptor atom coordinates.

rmsmode { atype | unique_pair }
rmsmode heavy_atoms_only

(Optional; default “atype” with all atoms) If included, this keyword will modify the symmetry checking used in the RMSD calculation. With “atype” (default), the algorithm will evaluate RMSD based on the nearest atom between the two structures with the same atom type. With “unique_pair”, each individual atom will be paired at most one time. If the “heavy_atoms_only” keyword is included, in a separate DPF line, hydrogen atoms will be omitted from the calculation, otherwise all atoms are included.

output_resnum_as { resnum | runnum }

(Optional; default “resnum”) Normally, AutoDock keeps the original residue number of the input ligand PDBQT file. With “runnum”, AutoDock re-numbers the starting position to residue-number 0, and any cluster-representatives are numbered incrementally from 1, according to their rank (rank 1 is the lowest energy cluster). [This keyword replaces the obsolete “-k” flag.]

Parameter for AutoDock ‘Cluster mode’ run

cluster <existing PDBQT file name>

(Clustering multi-job output only.) AutoDock will go into ‘cluster mode’. Only use this command to perform cluster analysis on the combined output, <PDBQTfilename>, of several jobs. This command can be very useful when many jobs have been distributed to several

machines and run in 'parallel'. The docking parameter file will need the following keywords: `rmstol` and `types`; and optionally `write_all_cluster_members` and/or `rmsnosym`. You must first extract the USER lines along with the ATOM records, since AutoDock parses these lines to determine what the energy of that particular conformation was. For more information, see the example DPF files given later.

Parameter for calculating energy of a ligand

epdb

This keyword will report the energy of the ligand included in the "move" command. This command may be used to calculate the energy of a particular ligand conformation without (or before) performing a docking. Note that all "about", "tran0", "quaternion0", "dihe0" settings are ignored in the epdb calculation.

Parameters for simulated annealing [SA] searches

e0max <float> <positive_integer>

[0., 10000]

(Optional, SA only) This keyword stipulates that the ligand's initial state cannot have an energy greater than the first value, nor can there be more than the second value's number of retries. Typical energy values range from 0 to 1000 kcal/mol. If the initial energy exceeds this value, a new random state is generated and tested. This process is iterated until the condition is satisfied. This can be particularly useful in preventing runs starting in exceptionally high energy regions. In such cases, the ligand can get trapped because it is unable to take a long enough translational jump. In those grids where the ligand is small enough to fit into the low energy regions with ease, there will not be many iterations before a favorable location is found. But in highly constrained grids, with large ligands, this initialization loop may run almost indefinitely.

rt0 <float>

[500. cal/mol].

(Optional, SA only) Initial "annealing temperature"; this is actually the absolute temperature multiplied by the gas constant R . $R = 8.314 \text{ J mol}^{-1} \text{ K}^{-1} = 1.987 \text{ cal mol}^{-1} \text{ K}^{-1}$. (Units: cal mol^{-1} .)

linear_schedule (synonyms: **schedule_linear** **linsched** **schedlin**)
geometric_schedule
[**linear_schedule**]

(Optional, SA only) The default "linear_schedule" uses a linear or *arithmetic* temperature reduction schedule during *Monte Carlo* simulated annealing. The "geometric_schedule" keyword uses instead a *geometric* reduction schedule, according to the **rtrf** parameter described next. If the linear schedule is used, any **rtrf** parameters will be ignored. The first simulated annealing cycle is carried out at the annealing temperature **rt0**. At the end of each cycle, the temperature is reduced by (**rt0/cycles**). The advantage of the linear schedule is that the system samples evenly across the temperature axis, which is vital in entropic calculations. Geometric temperature reduction schedules, on the other hand, under-sample high temperatures and over-sample low temperatures.

rtrf <float>

(Optional, SA geometric schedule only) Annealing temperature reduction factor, g [0.90 cycle^{-1}]. At the end of each cycle, the annealing temperature is multiplied by this factor, to give that of the next cycle. This must be positive but < 1 in order to cool the system. Gradual cooling is recommended, so as to avoid “*simulated quenching*”, which tends to trap systems into local minima.

runs <integer>

[50]

Number of automated docking runs. Can instead be specified in the “simanneal” statement following.

cycles <integer>

[50]

(Optional, SA only) Number of temperature reduction cycles.

accs <integer>

[30000]

(Optional, SA only) Maximum number of accepted steps per cycle.

rejs <integer>

[30000]

(Optional, SA only) Maximum number of rejected steps per cycle.

select <character>

[m]

(Optional, SA only) State selection flag. This character can be either **m** for the *minimum* state, or **l** for the *last* state found during each cycle, to begin the following cycle.

trnrf <float>

[1.0]

(Optional, SA only) Per-cycle reduction factor for translation steps.

quarf <float>

[1.0]

(Optional, SA only) Per-cycle reduction factor for orientation steps.

dihrf <float>

(Optional, SA only) Per-cycle reduction factor for torsional dihedral steps [1.].

Parameters for genetic algorithm, Lamarckian GA and evolutionary programming searches

ga_pop_size <positive_integer>

[150]

(Optional, GA/LGA/LS only) This is the number of individuals in the population. Each individual is a coupling of a genotype and its associated phenotype. Typical values range from 50 to 200.

ga_num_evals <positive_integer>

[2500000]

(Optional, GA/LGA/LS only) Set the maximum number of energy evaluations performed during each GA, LGA, or LS run.

ga_num_generations <positive_integer>

[27000]

(Optional, GA/LGA only) This is the maximum number of generations simulated during each GA or LGA run.

ga_elitism <integer>

[1]

(Optional, GA/LGA only) This is used in the selection mechanism of the GA. This is the number of top individuals that are guaranteed to survive into the next generation.

ga_mutation_rate <float>

[0.02]

(Optional, GA/LGA only) This is a floating point number from 0 to 1, representing the probability that a particular gene is mutated. This parameter is typically small.

ga_crossover_rate <float>

[0.80]

(Optional, GA/LGA only) This is a floating point number from 0 to 1 denoting the crossover rate. Crossover rate is the expected number of pairs in the population that will exchange genetic material. Setting this value to 0 turns the GA into the evolutionary programming (EP) method, but EP would probably require a concomitant increase in the `ga_mutation_rate` in order to be effective.

ga_window_size <positive_integer>

[10]

(Optional, GA/LGA only) This is the number of preceding generations to take into consideration when deciding the threshold for the worst individual in the current population.

Genetic algorithm parameters

set_ga

This command sets the global optimizer to be a genetic algorithm [GA]. This is required to perform a GA search. This passes any 'ga_' parameters specified **before** this line to the global optimizer object. If this command is omitted, or it is given before the 'ga_' parameters, your choices will not take effect, and the default values for the optimizer will be used.

To use the traditional (non-Lamarckian) genetic algorithm, do not specify the local search parameters, and do not use the "set_sw1" or "set_psw1" commands.

To use the **Lamarckian genetic algorithm**, you must also specify the parameters for local search, and then issue either the 'set_sw1' or 'set_psw1' command. The 'set_sw1' command uses the strict Solis and Wets local search algorithm, whereas 'set_psw1' uses the pseudo-Solis and Wets algorithm (see below).

Parameters for local search

sw_max_its <positive_integer>

[300]

(Optional, LGA/LS only) This is the maximum number of iterations that the local search procedure applies to the phenotype of any given individual, per generation.

sw_max_succ <positive_integer>

[4]

(Optional, LGA/LS only) This is the number of successes in a row before a change is made to the "rho" parameter in Solis & Wets algorithms. This is an unsigned integer and is typically around four.

sw_max_fail <positive_integer>

[4]

(Optional, LGA/LS only) This is the number of failures in a row before Solis & Wets algorithms adjust "rho." This is an unsigned integer and is usually four to eight.

sw_rho <float>

[1.0]

(Optional, LGA/LS only) This is a parameter of the Solis & Wets algorithms. It defines the initial variance, and specifies the size of the local space to sample.

sw_lb_rho <float>

[0.01]

(Optional, LGA/LS only) This is the lower bound on rho, the variance for making changes to genes (*i.e.* translations, orientation and torsions). rho can never be modified to a value smaller than "sw_lb_rho".

ls_search_freq <float>

[0.06 for LGA, 1.0 for LS]

(Optional, LGA only) This is the probability of any particular phenotype being subjected to local search.

Commands to choose and set the local search method (LGA or LS)

Both of these commands, 'set_sw1' and 'set_psw1', pass any 'sw_' parameters set before this line to the local searcher. If you forget to use this command, or give it before the 'sw_' keywords, your choices will not take effect, and the default values for the optimizer will be used. Currently, the psw1 method has shown the best performance and is used as the default.

set_sw1

Instructs AutoDock to use the classical Solis and Wets local searcher, using the method of uniform variances for changes in translations, orientations, and torsions.

set_psw1

Instructs AutoDock to use the pseudo-Solis and Wets local searcher. This method maintains the relative proportions of variances for the translations in Å and the rotations in radians. These are typically 0.2 Å and 0.087 radians to start with, so the variance for translations will always be about 2.3 times larger than that for the rotations (*i.e.* orientation and torsions).

Commands to specify the search method

simanneal <integer>

[50]

This command instructs AutoDock to do the specified number of docking runs using the simulated annealing (SA) search engine. All relevant parameters for the simulated annealing job must be set first. These are indicated above by [SA] in each keyword description.

do_local_only <integer>

[50]

This keyword instructs AutoDock to carry out only the local search of a global-local search; the genetic algorithm parameters are ignored, with the exception of the population size. This is an ideal way of carrying out a minimization using the same force field as is used during a docking calculation. The "ga_run" keyword should not be given. The number after the keyword determines how many local search simulations will be performed.

do_global_only <integer>

[50]

This keyword instructs AutoDock to carry out dockings using only a global search, *i.e.* the traditional genetic algorithm. The local search parameters are ignored. The "ga_run" keyword should not be given. The number after the keyword determines how many dockings will be performed.

ga_run <integer>

[50]

This command invokes the Lamarckian genetic algorithm search engine, and performs the requested number of dockings. All appropriate parameters must be set first: these are listed above by “ga_”.

Command to perform clustering of docked conformations

analysis

This performs a cluster analysis on results of a docking, and writes the results to the log file. The docked conformations are sorted in order of increasing energy and then compared by root mean square deviation. A histogram is printed showing the number in each cluster, and if more than one member, the cluster’s mean energy. Furthermore, a table is printed to the docking log file of cluster rmsd and reference rmsd values.

Sample Docking Parameter File (LGA method, from tutorial)

```
autodock_parameter_version 4.2      # used by autodock to validate parameter set
outlev ADT                          # diagnostic output level
seed pid time                       # seeds for random generator
unbound_model bound                 # state of unbound ligand

ligand_types A C NA OA N HD       # atoms types in ligand
fld lhsg.maps.fld                # grid_data_file
map lhsg.A.map                   # atom-specific affinity map
map lhsg.C.map                   # atom-specific affinity map
map lhsg.NA.map                  # atom-specific affinity map
map lhsg.OA.map                  # atom-specific affinity map
map lhsg.N.map                   # atom-specific affinity map
map lhsg.HD.map                  # atom-specific affinity map
elecmap lhsg.e.map              # electrostatics map
desolvmap lhsg.d.map            # desolvation map
move ind.pdbqt                  # small molecule
about 0.3689 -0.2148 -4.9865    # small molecule root center

tran0 random                        # initial coordinates/A or random
quaternion0 random                  # initial orientation
dihe0 random                        # initial dihedrals (relative) or random

ga_pop_size 150                     # number of individuals in population
ga_num_evals 2500000                # maximum number of energy evaluations
ga_num_generations 27000            # maximum number of generations
ga_elitism 1                        # top individuals to survive to next generation
ga_mutation_rate 0.02               # rate of gene mutation
ga_crossover_rate 0.8               # rate of crossover
set_ga                           # set the above parameters for GA or LGA

sw_max_its 300                      # iterations of Solis & Wets local search
sw_max_succ 4                       # consecutive successes before changing rho
sw_max_fail 4                       # consecutive failures before changing rho
sw_rho 1.0                          # size of local search space to sample
sw_lb_rho 0.01                      # lower bound on rho
ls_search_freq 0.06                 # probability of performing local search
set_psw1                          # set the above pseudo-Solis & Wets parameters

ga_run 10                           # do this many hybrid GA-LS runs

rmstol 2.0                          # cluster_tolerance/A
analysis                          # perform a ranked cluster analysis
```

Lines in **bold** are required for this job.

Lines in *italics* are optional and show default values.

Appendix II: Customizing the Docking Protocol

A variety of options are available within AutoDock for customizing the docking protocol for a given application, by customizing the docking parameters in the DPF. A DPF can be subdivided into sections, each specifying a different aspect of the calculation. Some of these sections are common to every calculation and some are more specific. Usually, a DPF contains a **generic section**, a **ligand-specific section**, a **search-specific section**, and finally an **analysis section**. Hence a DPF can then be built in a modular fashion by combining different sections.

For example, the typical simulated annealing DPF is composed of the following sections:

- generic section
- ligand-specific section
- simulated annealing section
- cluster analysis [optional]

whereas a Lamarckian Genetic Algorithm DPF will contain both genetic algorithm and local search sections:

- generic section
- ligand-specific section
- genetic algorithm section
- local search section
- cluster analysis [optional]

The typical parameters used for the common AutoDock calculations will be described. For each calculation type, refer to the *DPF Examples* section. For a detailed description of each keyword, refer to the *AutoDock Docking Parameter File* section.

Generic section

In the first section are usually specified parameters controlling generic aspects of the calculation that are independent from the type of calculation itself. All are optional.

```
autodock_parameter_version 4.2
outlev ADT
intelec
seed pid time
unbound_model bound
```

The first keyword **autodock_parameter_version** defines the version of the parameters that are going to follow in the rest of the DPF. By default, this keyword is set to the value of "4.2" but it can be changed to support several compatibility modes among different versions of AutoDock.

If a customized forcefield (see *Atomic Parameter File* section) is going to be used, it can be specified by adding a line similar to the following, after the AutoDock version keyword :

```
parameter_file autodock_custom_forcefield.dat
```

Other options are also available. The **outlev** sets the amount of detail that is going to be printed in the output DLG for every step of the calculation. **intelec** enable the inclusion of the electrostatic term in the calculation of the internal energy; this is the default in AutoDock4.2.5 and later. The search methods available in AutoDock are all stochastic and are performed with a random initial state at every run. The random number generator is by default seeded with the process identification number (PID) assigned by the operating system to the AutoDock calculation (**pid** value) and the current time (**time** value). The **unbound_model** keyword defines the energy model used to calculate the energy of the unbound ligand before the docking. By default, this energy is set to be equal to the bound state.

Ligand-specific section

This section contains the keywords that are specific to the ligand to be docked and its properties:

```
receptor
fld receptor.maps.fld
map receptor.A.map
map receptor.C.map
map receptor.HD.map
map receptor.N.map
map receptor.OA.map
map receptor.S.map
elecmap receptor.e.map
desolvmap receptor.d.map
move ligand.pdbqt
```

Ligand atom types (**ligand_types** keyword) are declared first, then associated to the map files (**map** keyword) for each type. The order of the **map** entries must match the one specified in the **ligand_types** keyword. As explained in Appendix III, this section can be used to set up special calculations. The atom types must include *at least* all those present in the ligand to be docked (see below), but more can be specified allowing use of the same DPF for different ligands. The limitations are the maximum number of atom types of AutoDock and the amount of memory available on the computer where the calculation is performed. Independently from the ligand atom types, an electrostatic interaction map (**elecmap** keyword) and a desolvation map (**desolvmap** keyword) must be always specified.

Finally, the **move** keyword defines the ligand PDBQT filename to be read for the calculation. If the calculation includes flexible receptor residues, the **flexres** keyword must be used to specify the filename containing the flexible residues coordinates, adding the following line after the ligand **move** keyword:

Note that if flexible residues are going to be used, affinity maps must be calculated only on the rigid part of the receptor; ADT has tools to help do this.

Search-specific section

In this section, the type of search method is going to be specified. Currently, AutoDock supports the following search methods (see *Choosing a protocol for your application* section): Simulated Annealing (SA), Local Search (LS), Genetic Algorithm (GA) and Lamarckian Genetic Algorithm (LGA). Depending on the chosen search method, different group of keywords will be used in the DPF.

Multiple search methods are allowed in a single AutoDock job: such as 20 runs using Simulated Annealing, 20 runs using the Lamarckian Genetic Algorithm, and 20 runs using local-search-only. The runs are done serially and no results carry over from one method to another. However, all results are ranked and clustered together in the analysis step at the end of the entire job.

Simulated annealing

(sample file: simulated_annealing/1dwd_simulated_annealing_long.dpf)

If the simulated annealing search method is going to be performed, keywords are used to specify the initial states for the sampling (global search), and how the temperature reduction and the ligand movement are simulated (local search). All are optional.

```
tstep 2.0
qstep 5.0
dstep 5.0
rt0 616.0
```

First, the size with which the search space is sampled is specified for ligand translation (**tstep** keyword), orientation (**qstep** keyword) and torsions (**dstep** keyword). Optimal values for these keywords are 0.2 Angstrom/step and 5 degrees/step. The initial annealing temperature is also set (**rt0** keyword) to 100 cal/mol.

```
linear_schedule
trnrf 1.0
quarf 1.0
dihrf 1.0
cycles 50
accs 25000
rejs 25000
select m
```

During the annealing, the step sizes are scaled. The initial state is then modified during the annealing phase. At each step, the simulated temperature is reduced linearly, while translation (**trnrf** keyword), orientation (**quarf** keyword), and dihedral (**dihrf** keyword) steps are not changed. The number of temperature reductions is set with the **cycles**

keyword. The number of accepted (**accs** keyword) and rejected (**rejs** keyword) steps at each cycle are specified. The state selected (**select** keyword) to begin the following temperature reduction cycle is the minimum result found so far ('m'). Finally, the simulated annealing simulation may be started by the trigger keyword **simanneal**, with a total of 10 simulated annealing runs to be performed:

```
Simanneal 10
```

Local search

(sample file: local_search_lig/1dwd_local_only_long.dpf)

With the local search, only the local space is sampled, performing a sort of “minimization” of the ligand in the current position.

```
sw_max_its 300
sw_max_succ 4
sw_max_fail 4
sw_rho 1.0
sw_lb_rho 0.01
set_psw1
```

A local search consists of a number of iterations (**sw_max_its** keyword) during which rotational, translational, and torsional degrees of freedom of the ligand are randomly sampled by a given step. After a given number of successful (**sw_max_succ** keyword) or unsuccessful (**sw_max_fail** keyword) attempts, the sampling step is enlarged or reduced, respectively, within a rho factor range (**sw_rho**, **sw_lb_rho** keywords) and the local search continued. The most efficient local search method in AutoDock, the pseudo-Solis-Wet algorithm is selected with the **set_psw1** keyword.

The local search method may be executed with 10 independent runs with the **do_local_only** keyword:

```
do_local_only 10
```

Lamarckian Genetic Algorithm

(sample file: dock_flexlig/1dwd_1dwd.dpf)

With the genetic algorithm, a population of ligand poses is generated and optimized iteratively, and the global search space is mainly sampled.

```
ga_pop_size 150
ga_num_evals 2500000
ga_num_generations 27000
ga_elitism 1
ga_mutation_rate 0.02
ga_crossover_rate 0.8
ga_window_size 10
ga_cauchy_alpha 0.0
ga_cauchy_beta 1.0
set_ga
```

The size of the initial population is defined by the **ga_pop_size** keyword. The GA search is performed until either the maximum number of evaluations (**ga_num_evals** keyword) or the maximum number of generations (**ga_num_generations** keyword) limits are reached.

At each generation step, one individual each generation will survive unmodified (**ga_elitism** keyword), while chances of mutation (**ga_mutation_rate** keyword) and crossover between individual chromosomes (**ga_crossover_rate** keyword) are allowed. The last 10 generations are going to be considered when deciding how to rank the individuals in the current population (**ga_window_size** keyword). The genetic algorithm search is enabled (**set_ga** keyword) and 10 independent runs are performed with the **ga_run** keyword:

```
ga_run 10
```

The LGA combines local search and genetic algorithm to provide both efficient global space coverage and local search optimization. Consequently, there will be both GA and LS keywords.

With the genetic algorithm, a population of ligand poses is generated and optimized iteratively, and the global search space is mainly sampled.

Analysis section

In this section, all operations not necessarily related to docking can be specified (i.e. results clustering, single-point energy estimation).

Energy estimation

(sample file: eval_lig/1dwd_epdb.dpf)

The energy estimation (**epdb** keyword) is used to calculate the energy of a ligand pose as found in a complex, such as in an X-ray crystallographic structure, without performing any searches. The coordinates of the ligand will not be changed, and grid maps will be used only to estimate the different energy contributions. The **epdb** keyword is specified without any options.

Clustering options

(sample file: recluster/recluster.dpf)

AutoDock provides tools for clustering the results either at the end of each docking or by joining together multiple docking results and re-clustering them. First, the clustering RMSD tolerance (**rmstol** keyword) is specified. By default, AutoDock takes into account symmetry, which improves significantly the clustering results, but this can be turned off (see **rmsnosym** keyword description). By default, only the single best score resulting from each cluster is written in the output file, but it is possible to save all poses in all clusters, the **write_all** keyword must be used. If the calculation will re-cluster poses previously generated, the file containing them will be specified with the **cluster** keyword, followed by the PDBQT filename containing all the poses (i.e. USER, ATOM and/or HETATM entries extracted from the multiple DLG's). Finally, the actual clustering is performed by specifying the **analysis** keyword.

Docking Parameter Files (DPF) Examples

Simulated Annealing Docking (sample file:

simulated_annealing/1dwd_simulated_annealing_long.dpf, default values in italics)

```
## GENERIC SECTION
autodock_parameter_version 4.2      # used by autodock to validate parameter set
outlev adt
intelec                             # calculate internal electrostatics
seed 28641 1106107140              # seeds for random generator

## LIGAND-SPECIFIC SECTION
ligand_types A C HD N OA S        # atoms types in ligand
fld 1dwd_rec.maps.fld # grid_data_file
map 1dwd_rec.A.map # atom-specific affinity map
map 1dwd_rec.C.map # atom-specific affinity map
map 1dwd_rec.HD.map # atom-specific affinity map
map 1dwd_rec.N.map # atom-specific affinity map
map 1dwd_rec.OA.map # atom-specific affinity map
map 1dwd_rec.S.map # atom-specific affinity map
elecmap 1dwd_rec.e.map # electrostatics map
desolvmap 1dwd_rec.d.map # desolvation map
move 1dwd_lig.pdbqt # small molecule

## SIMULATED ANNEALING SEARCH PARAMETERS SECTION
tstep 0.2 # translation step/A
qstep 5.0 # quaternion step/deg
dstep 5.0 # torsion step/deg
rt0 100.0 # initial annealing temperature (times gas constant)
linear_schedule # use linear, arithmetic temperature reduction
cycles 50 # number of temperature reduction cycles
accs 30000 # maximum number of accepted steps per cycle
rejs 30000 # maximum number of rejected steps per cycle
select m # state selection flag: (m)inimum or (l)ast state

## PERFORM SEARCH SECTION
simanneal 10

## ANALYSIS SECTION
rmstol 0.5 # cluster_tolerance/A
analysis # perform a ranked cluster analysis
```

Local Search (sample file: local_search_lig/1dwd_local_only_long.dpf, default values in italics)

```

## GENERIC SECTION
autodock_parameter_version 4.2      # used by autodock to validate parameter set
outlev basic                        # less verbose output than with "ADT"
intelec                              # calculate internal electrostatics

## LIGAND-SPECIFIC SECTION
ligand_types A C HD N OA S         # atoms types in ligand
fld ldwd_rec.maps.fld # grid_data_file
map ldwd_rec.A.map # atom-specific affinity map
map ldwd_rec.C.map # atom-specific affinity map
map ldwd_rec.HD.map # atom-specific affinity map
map ldwd_rec.N.map # atom-specific affinity map
map ldwd_rec.OA.map # atom-specific affinity map
map ldwd_rec.S.map # atom-specific affinity map
elecmap ldwd_rec.e.map # electrostatics map
desolvmap ldwd_rec.d.map # desolvation map
move ldwd_lig.pdbqt # small molecule
about 32.34 14.05 24.92 # small molecule center

## FREE ENERGY ENTROPY ADJUSTMENT SECTION
torsdof 10 # torsional degrees of freedom

## LOCAL SEARCH PARAMETERS SECTION
sw_max_its 300 # iterations of Solis & Wets local search
sw_max_succ 4 # consecutive successes before changing rho
sw_max_fail 4 # consecutive failures before changing rho
sw_rho 1.0 # size of local search space to sample
sw_lb_rho 0.01 # lower bound on rho
ls_search_freq 1.00 # probability of performing local search on individual
set_pswl # set the above psw Solis & Wets parameters

## PERFORM SEARCH SECTION
do_local_only 50 # do this many hybrid GA-LS runs

## ANALYSIS SECTION
rmstol 0.5 # cluster_tolerance/A
analysis # perform a ranked cluster analysis

```

Lamarckian Genetic Algorithm Docking (sample file: dock_flexlig/ldwd_ldwd.dpf, default values in italics)

```
## GENERIC SECTION
autodock_parameter_version 4.2      # used by autodock to validate parameter set
outlev adt                          # diagnostic output level
seed pid time                        # seeds for random generator

## LIGAND-SPECIFIC SECTION
ligand_types A C HD N OA S          # atoms types in ligand
fld ldwd_rec.maps.fld              # grid_data_file
map ldwd_rec.A.map                  # atom-specific affinity map
map ldwd_rec.C.map                  # atom-specific affinity map
map ldwd_rec.HD.map                 # atom-specific affinity map
map ldwd_rec.N.map                  # atom-specific affinity map
map ldwd_rec.OA.map                 # atom-specific affinity map
map ldwd_rec.S.map                  # atom-specific affinity map
elecmap ldwd_rec.e.map              # electrostatics map
desolvmap ldwd_rec.d.map            # desolvation map
move ldwd_lig.pdbqt                 # small molecule
about 32.34 14.05 24.92             # small molecule center

## INITIAL SEARCH STATE SECTION
tran0 random                        # initial coordinates/A or random
quaternion random                   # initial quaternion
dihe0 random                         # initial dihedrals (relative) or random

## FREE ENERGY ENTROPY ADJUSTMENT SECTION
torsdof 10                          # torsional degrees of freedom

## SEARCH-SPECIFIC SECTION
ga_pop_size 150                     # number of individuals in population
ga_num_evals 2500000                 # maximum number of energy evaluations
ga_num_generations 27000             # maximum number of generations
ga_elitism 1                         # number of top individuals to survive to next
generation
ga_mutation_rate 0.02                # rate of gene mutation
ga_crossover_rate 0.8                # rate of crossover
set_ga                               # set the above parameters for GA or LGA

## LOCAL SEARCH PARAMETERS SECTION
sw_max_its 300                       # iterations of Solis & Wets local search
sw_max_succ 4                        # consecutive successes before changing rho
sw_max_fail 4                        # consecutive failures before changing rho
sw_rho 1.0                           # size of local search space to sample
sw_lb_rho 0.01                       # lower bound on rho
ls_search_freq 0.06                   # probability of performing local search on individual
set_pswl                             # set the above pseudo Solis & Wets parameters

## PERFORM SEARCH SECTION
ga_run 10                            # do this many hybrid GA-LS runs

## ANALYSIS SECTION
rmstol 0.5                           # cluster_tolerance/A
analysis                             # perform a ranked cluster analysis
```

Single-point Energy Estimation (sample file: eval_lig/1dwd_epdb.dpf)

```
## GENERIC SECTION
autodock_parameter_version 4.2      # used by autodock to validate parameter
set
outlev ADT                          # diagnostic output level

## LIGAND-SPECIFIC SECTION
ligand_types A C HD N OA S          # atoms types in ligand
fld 1dwd_rec.maps.fld               # grid_data_file
map 1dwd_rec.A.map                   # atom-specific affinity map
map 1dwd_rec.C.map                   # atom-specific affinity map
map 1dwd_rec.HD.map                  # atom-specific affinity map
map 1dwd_rec.N.map                   # atom-specific affinity map
map 1dwd_rec.OA.map                  # atom-specific affinity map
map 1dwd_rec.S.map                   # atom-specific affinity map
elecmap 1dwd_rec.e.map               # electrostatics map
desolvmap 1dwd_rec.d.map             # desolvation map
move 1dwd_lig.pdbqt                 # small molecule

## EVALUATE LIGAND ENERGY in RECEPTOR SECTION
epdb                                 # small molecule to be evaluated
```

Re-clustering of PDBQT Poses (sample file: recluster/recluster.dpf)

```
# GENERIC PARAMETERS
autodock_parameter_version 4.2      # used to validate parameter set
outlev ADT                          # diagnostic output level
ligand_types A C HD N OA S         # atoms types in ligand

# OPTIONAL
rmsref ldwd_lig_xray.pdbqt         # reference for RMSD calculation

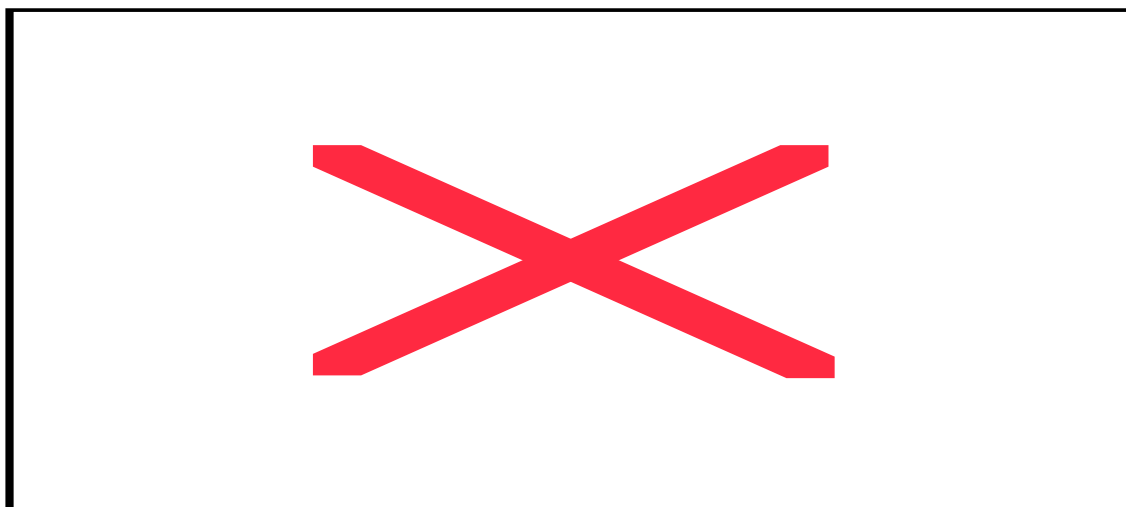
# RMS MODE
rmsmode unique_pair                # set symmetry handling option
rmstol 2.0                          # cluster rms tolerance
write_all                           # write all poses in each cluster
cluster poses.pdbqt                 # input PDBQT file containing all poses

# PERFORM ANALYSIS
analysis                            # perform a ranked cluster analysis
```

Appendix III: Docking Flexible Rings with AutoDock

1. Introduction

AutoDock is not able to manage directly the flexibility associated with bonds in cyclic molecules, which leads to cyclic portions of the ligands to be considered as rigid. Different approaches can be used to dock macrocyclic molecules, like identifying one or more low energy conformations and docking them as different ligands, but generating them and docking them separately can be a time-consuming task. As an alternative, an indirect method may be used to manage the ring as a fully flexible entity and use the AutoDock conformation search to explore its flexibility. The method was initially developed for version 3.05, and now is implemented in version 4.2. The protocol converts the cyclic ligand into its corresponding acyclic form by removing a bond, and then docks the fully flexible molecule in the open form. A special atom type definition allows AutoDock to restore the original cycle structure during the calculation while exploring the cycle conformations during the search. The protocol can be subdivided in



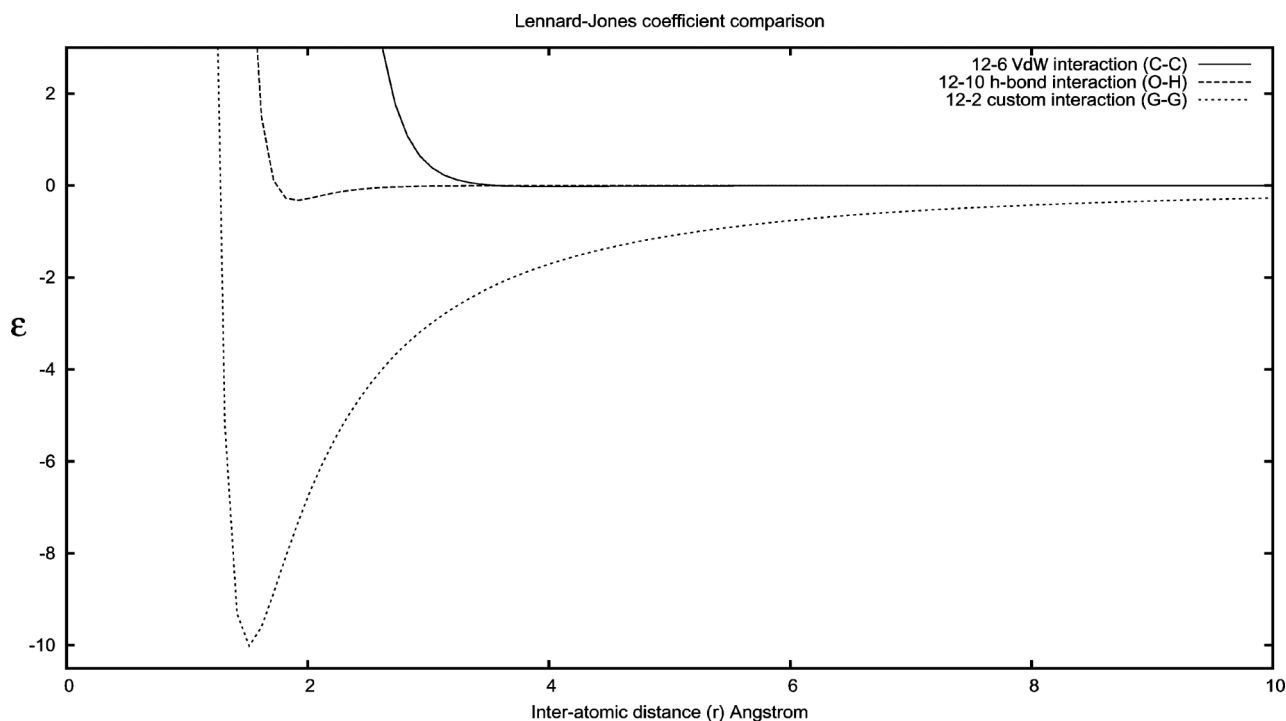
three main steps:

RING OPENING (a): by removing a bond, the ring is opened and the ligand is transformed to an acyclic form.

LIGAND PRE-PROCESSING (b): the ligand is processed following the standard AutoDockTools protocol, but the edge atoms are replaced with G atoms.

DOCKING AND RING CLOSURE (c): the ligand is docked applying a 12-2 pseudo-Lennard-Jones potential to the G-atoms that restore the cyclic structure.

To restore the closed ring geometry a custom long range pseudo-Lennard-Jones 12-2 potential is applied to these atoms during the docking calculation. This potential is effective at long range distances and guarantees the ring closure even with large cycles.



Ring closure parameters. Comparison between standard 12-6 van der Waals, 12-10 hydrogen bond and 12-2 pseudo-Lennard-Jones potentials, before the AutoDock smoothing function is applied.

No extra maps are calculated for the G atoms because, for sake of evaluation of ligand-protein interaction, they are considered as normal carbon atoms. Therefore, C maps are used in their place. During the docking process, the potential guides the edge atoms next to each other resulting in an effective ring closure, while allowing the GA algorithm to explore the ring conformations.

2. Flexible rings

Opening the ring

To convert the molecule into the acyclic form, the bond to be disrupted must be identified. The way the acyclic form is obtained influences the subsequent the ring closure. The following guidelines may help to choose which bond to remove while keeping the calculation simple and improving the quality of the final results:

Keep number rotatable bonds low

The ring opening can dramatically increase the total number of rotatable bonds, requiring longer calculation times. Therefore, when less flexible or partially rigid regions are present they should not be broken. Bonds resulting in shorter chains should be preferred.

Break carbon-carbon bonds

For sake of calculation consistency, the bond to be broken should be between two identical atom types. AutoDock supports aliphatic and aromatic carbon atoms. Atoms different than carbon can be used but they will require a special

parameterization (see 4.Extension and Limits).

Avoid chiral atoms (...whenever possible)

Due to the lack of directionality and the united atom description of hydrogens, original chirality is *not guaranteed* if a bond between one or more chiral carbon atoms is broken. When all ring carbons are chiral (e.g. natural compounds, antibiotics) any bond can be suitable, while chirality in docking results should be inspected and manually corrected if necessary.

Once the ring is disrupted, the previously connected atoms must be renamed as "G" in the atom type column of the PDBQT file:

```
[...]  
HETATM  21  CD4 UIN B 100      -2.919  22.061  19.604  1.00 19.90    0.005  
G  
[...]  
HETATM  24  CD3 UIN B 100      -3.821  22.402  20.791  1.00 19.60    0.005  
G  
[...]
```

The 12-2 potential is defined in the DPF using the `intnb_r_eps` keyword to override the AutoDock internal interaction parameter table, using the following syntax :

```
intnbp_r_eps  1.51 10.000000 12 2  G G
```

AutoDock, when a diagnostic outlev of "etables" is used, will acknowledge the new parameterization in the DLG:

```
Ring closure distance potential found for atom type G :  
Equilibrium distance   = 1.51 Angstroms  
Equilibrium potential  = 10.000042 Kcal/mol  
Pseudo-LJ coefficients = 12 - 2
```

```
Calculating internal non-bonded interaction energies for docking calculation;
```

```
Non-bonded parameters for G-G interactions, used in internal energy  
calculations:
```

$$E_{G,G} = \frac{281.0}{r^{12}} - \frac{27.4}{r^2}$$

More than one ring

Multiple flexible rings can be docked by disrupting a bond for each ring and using a different atom type for each edge atom pair. AutoDock includes four ring closure carbon atom types: G, J, Q (aliphatic) and GA (aromatic), then up to four flexible rings can be docked simultaneously. For

example, if a second ring is opened then the next two edge atoms are renamed as J, and the DPF will include an extra `intnb_r_eps` keyword and another C map reference. While there is no actual limitation to the number of cycles that can be opened in the same molecule, there is the implicit limit of the docking complexity, as well as the maximum number of rotatable bonds allowed. If further atom types need to be defined (e.g., -S-S- disulfide bond), a customized atomic parameter file must be generated and included in the DPF with the `parameter_file` keyword.

Limitations

Using this approach for docking flexible rings can save a lot of time compared to rigid ring docking of different conformations, but there are some limitations associated with the protocol implementation:

Chirality. Hydrogen atoms bound to chiral edge atoms will be merged in the *united-atom* model used in AutoDock, then chirality information is lost. In the docking process G-atoms can eventually approach each other from directions different than the original geometry, leading to potentially wrong chirality.

Bond distance. The pseudo-Lennard-Jones potential describes the ideal equilibrium distance of the two G-atoms, corresponding to the equilibrium C-C bonding distance (~1.5 Å). The final distance although can be slightly bigger, because of the van der Waals repulsion between the two atoms preventing atomic volume overlaps.

Energy calculation. During the calculation the pseudo-Lennard-Jones potential provides an extra energy contribution to the total energy sum to induce the ring closure. This can result in an overall shift of the final energy to lower values. While not being an actual limitation, it should be considered to avoid comparisons between scores obtained with and without flexible rings.

For these reasons, the final docking result should be refined by inspecting the chirality and performing a geometry refinement to correct bonding angles and distances.

This is the DPF corresponding to the example structure in the introduction:

```
autodock_parameter_version 4.1      # used by autodock to validate parameter set
outlev ADT                          # diagnostic output level
seed pid time                        # seeds for random generator
unbound_model bound                 # state of unbound ligand
ligand_types A C G HD OA           # atoms types in ligand
fld protein.maps.fld               # grid data file
map protein.A.map                   # atom-specific affinity map
map protein.C.map                   # atom-specific affinity map
map protein.C.map                   # C map for G atoms
map protein.HD.map                  # atom-specific affinity map
map protein.OA.map                  # atom-specific affinity map
elecmap protein.e.map               # electrostatics map
desolvmap protein.d.map             # desolvation map
intnbp_r_eps 1.51 10.000000 12 2 G G # pseudo-LJ potential
move ligandG.pdbqt                 # small molecule
about -0.8665 18.5882 20.1623      # small molecule center
tran0 random                        # initial coordinates/A or random
quat0 random                        # initial quaternion
dihe0 random                        # initial dihedrals (relative) or random
torsdof 8                           # torsional degrees of freedom

ga_pop_size 350                     # number of individuals in population
ga_num_evals 2500000                # maximum number of energy evaluations
ga_num_generations 27000            # maximum number of generations
ga_elitism 1                         # number of top individuals to survive to next generation
ga_mutation_rate 0.02               # rate of gene mutation
ga_crossover_rate 0.8               # rate of crossover
set_ga                               # set the above parameters for GA or LGA

sw_max_its 300                       # iterations of Solis & Wets local search
sw_max_succ 4                       # consecutive successes before changing rho
sw_max_fail 4                       # consecutive failures before changing rho
sw_rho 1.0                           # size of local search space to sample
sw_lb_rho 0.01                      # lower bound on rho
ls_search_freq 0.26                 # probability of performing local search on individual
set_pswl                             # set the above Solis & Wets parameters

ga_run 100                           # do this many hybrid GA-LS runs
rmstol 2.0                           # cluster_tolerance/A
analysis                             # perform a ranked cluster analysis
```

3. Reference

Forli, S., et al. *J. Chem. Inf. Model.*, 2007, 47, 1481–1492

4. Tutorial

<http://autodock.scripps.edu/faqs-help/tutorial/flexible-rings-docking>

Appendix IV: AutoDock References

AutoDock 4.2

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