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# PyVOL Documentation

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# CONTENTS

<b>1</b>	<b>Introduction</b>	<b>1</b>
1.1	Overview . . . . .	1
1.2	Quick Installation into PyMOL . . . . .	1
1.3	Example Basic Run . . . . .	1
<b>2</b>	<b>Installation</b>	<b>2</b>
2.1	Installation into PyMOL from PyPI . . . . .	2
2.2	Installation into PyMOL Using a Packaged Installer . . . . .	2
2.3	Manual Installation . . . . .	2
2.4	MSMS Installation . . . . .	3
2.5	Updating . . . . .	3
2.6	Uninstalling . . . . .	3
<b>3</b>	<b>General Usage</b>	<b>4</b>
3.1	Pocket Specification . . . . .	4
3.2	Extra Ligand Options . . . . .	5
3.3	Sub-pocket Partitioning . . . . .	5
3.4	Display and Output Options . . . . .	6
<b>4</b>	<b>Shell Interface</b>	<b>7</b>
4.1	Running from the Shell . . . . .	7
4.2	Template Configuration File Generation . . . . .	7
4.3	Notes on Output . . . . .	7
<b>5</b>	<b>Development</b>	<b>8</b>
5.1	Package Design . . . . .	8
5.2	Algorithm Design . . . . .	8
5.3	GUI Design . . . . .	8
5.4	Version Incrementation . . . . .	8
5.5	Distribution . . . . .	8
5.6	Documentation . . . . .	9
<b>6</b>	<b>PyVOL Package</b>	<b>10</b>
6.1	Submodules . . . . .	10
6.2	PyVOL Cluster Module . . . . .	10
6.3	PyVOL Identify Module . . . . .	11
6.4	PyVOL Pymol Interface Module . . . . .	12
6.5	PyVOL Pymol Utilities Module . . . . .	13
6.6	PyVOL Spheres Module . . . . .	14
6.7	PyVOL Utilities Module . . . . .	15
6.8	PyVOL Main Entry Point . . . . .	16

6.9 PyVOL GUI . . . . .	16
<b>Python Module Index</b>	<b>17</b>
<b>Index</b>	<b>18</b>

## INTRODUCTION

### 1.1 Overview

PyVOL is a python library packaged into a [PyMOL](#) GUI for identifying protein binding pockets, partitioning them into sub-pockets, and calculating their volumes. PyVOL can be run as a PyMOL plugin through its GUI or the PyMOL prompt, as an imported python library, or as a command-line program. Visualization of results is exclusively supported through PyMOL though exported surfaces are compatible with standard 3D geometry visualization programs.

### 1.2 Quick Installation into PyMOL

PyVOL can be installed into any python environment, but installing directly into PyMOL 2.0+ is easiest. Download the [installer zip file](#) and then use the plugin manager to install that file.

```
https://github.com/schlessingerlab/pyvol/blob/master/installers/pyvol-installer.zip
```

This installs the PyVOL GUI. Select *PyVOL* under the plugins menu, and then select *Install from PyPI* under the settings tab to fetch PyVOL and any missing dependencies. For academic users and non-academic users with the Schrodinger incentive PyMOL distribution, installation is now complete. For all others, see [manual installation of msms](#).

### 1.3 Example Basic Run

The simplest calculation just using the PyMOL prompt is to load a protein of interest and then run the *pocket* command. This is an example for the Sorafenib-bound structure of BRAF:

```
fetch 1UWH
pocket "1UWH and chain B"
```

## INSTALLATION

PyVOL has been packaged into installers that contain all dependencies, but normal distribution is through PyPI and accessed through *pip*. PyVOL can consequently be installed into any python environment. For convenience, the PyMOL GUI contains an installer for easy installation into PyMOL 2.0+.

### 2.1 Installation into PyMOL from PyPI

Download the [basic installer zip file](https://github.com/schlessingerlab/pyvol/blob/master/installers/pyvol-installer.zip) and then use the PyMOL plugin manager to install that file.

```
https://github.com/schlessingerlab/pyvol/blob/master/installers/pyvol-installer.zip
```

This installs the PyVOL GUI. Select *PyVOL* under the plugins menu, and then select *Install from PyPI* under the settings tab to fetch PyVOL and any missing dependencies. For academic users and non-academic users with the Schrodinger incentive PyMOL distribution, installation is now complete. For all others, see manual installation of *msms* [below](#).

### 2.2 Installation into PyMOL Using a Packaged Installer

This option is useful if deploying PyVOL onto computers without internet access. Download the [full installer zip file](https://github.com/schlessingerlab/pyvol/blob/master/installers/pyvol-full-installer.zip) and then use the PyMOL plugin manager to install that file.

```
https://github.com/schlessingerlab/pyvol/blob/master/installers/pyvol-full-installer.  
↪ zip
```

This installs the PyVOL GUI. Select *PyVOL* under the plugins menu, and then select *Install from Local Cache* under the settings tab to install PyVOL and any missing dependencies from a cache contained within the installer itself. For academic users and non-academic users with the Schrodinger incentive PyMOL distribution, installation is now complete. For all others, see manual installation of *MSMS* [below](#).

### 2.3 Manual Installation

PyVOL minimally requires biopython, MSMS, numpy, pandas, scipy, scikit-learn, trimesh, and msms in order to run. PyVOL is available for manual installation from [github](#) or through *PyPI*. Most conveniently:

```
pip install bio-pyvol
```

Again, for academic users and non-academic users with the Schrodinger incentive PyMOL distribution, installation is now complete. For all others, see manual installation of *MSMS* [below](#).

## 2.4 MSMS Installation

MSMS is provided with PyVOL for ease of use for academic users. It alternatively can be installed on MacOS and Linux using the bioconda channel:

```
conda install -c bioconda msms
```

Otherwise MSMS must be installed manually by downloading it from [MGLTools](#) and adding it to the path.

## 2.5 Updating

PyVOL can be updated through the PyMOL GUI simply by clicking *Check for Updates* under the settings tab and subsequently clicking *Update PyVOL* if an update has been identified. The new version of the PyVOL back-end will notify you if it expects an updated GUI. If the GUI also needs to be updated, uninstall the *pyvol\_gui* using the first tab of the plugin manager and then install the updated GUI using the second tab to install the [basic installer zip file](#)

Alternatively, PyVOL can be manually updated via the command line:

```
pip update bio-pyvol
```

## 2.6 Uninstalling

PyVOL can be uninstalled through its GUI. Simply click *Uninstall PyVOL* to remove the back-end. Then use the plugin manager to uninstall the *pyvol\_plugin*.

Again, PyVOL can also be uninstalled via the command line:

```
pip uninstall bio-pyvol
```

## GENERAL USAGE

The GUI and shell command line prompts recapitulate the PyMOL prompt interface with few exceptions. General usage of PyVOL is shown here with specific examples and modifications for the other interfaces in the following pages. Programmatic invocation of internal functions is supported and covered through the module documentation.

### 3.1 Pocket Specification

PyVOL by default recognizes the largest pocket and returns the volume and geometry for it. However, manual identification of the pocket of interest is generally preferable. This can be done through specification of a ligand, a residue, or a coordinate. If a specification is given, the mode is changed to specific by default.

#### 3.1.1 Default Behavior:

```
pocket protein_selection, mode=largest
```

#### 3.1.2 Ligand Specification:

```
pocket protein_selection, mode=specific, ligand=ligand_selection  
pocket protein_selection, ligand=ligand_selection
```

#### 3.1.3 Residue Specification:

```
pocket protein_selection, mode=specific, resid=A15  
pocket protein_selection, resid=A15  
pocket protein_selection, mode=specific, residue=residue_selection  
pocket protein_selection, residue=residue_selection
```

where the `resid` is written as `<Chain><Residue number>` (e.g. B432). If there is only one chain in the selection, the chain ID can be excluded.

#### 3.1.4 Coordinate Specification:

```
pocket protein_selection, mode=specific, pocket_coordinate="5.0 10.0 15.0"  
pocket protein_selection, pocket_coordinate="5.0 10.0 15.0"
```

where the coordinate is provided as three floats separated by spaces and bounded by quotation marks.

### 3.1.5 Calculation of All Pockets

Alternatively, PyVOL can return the surfaces and volumes for all pockets above a minimum volume that are identified. By default, this volume cutoff is set at 200 Å<sup>3</sup>.

```
pocket protein_selection, mode=all, minimum_volume=200
```

## 3.2 Extra Ligand Options

When a ligand is provided, the atoms of the ligand can be used to identify both minimum and maximum extents of the calculated binding pocket.

### 3.2.1 Ligand Volume Inclusion

To include the volume of the ligand in the pocket volume (useful for when the ligand extends into bulk solvent), use the `lig_incl_rad` parameter:

```
pocket protein_selection, ligand=ligand_selection, lig_incl_rad=0.0
```

where the value of `lig_incl_rad` is added to the Van der Waals radii of each atom in the ligand selection when calculating the exterior surface of the protein.

### 3.2.2 Ligand-defined Maximum Volume

The atoms of the ligand can also be used to define a maximum boundary to the calculated pocket by specifying the `lig_excl_rad` parameter:

```
pocket protein_selection, ligand=ligand_selection, lig_excl_rad=2.0
```

where the value of `lig_excl_rad` is added to the Van der Waals radii of each atom in the ligand selection when calculating the exterior surface of the protein.

## 3.3 Sub-pocket Partitioning

Sub-partitioning is enabled by setting the `subdivide` parameter to `True`:

```
pocket protein_selection, subdivide=True
```

Parameters controlling the number of sub-pockets identified generally perform well using defaults; however, they can be easily adjusted as needed. The two most important parameters are the minimum radius of the largest sphere in each sub-pocket (this excludes small sub-pockets) and the maximum number of clusters:

```
pocket protein_selection, subdivide=True, min_subpocket_rad=1.7, max_clusters=10
```

If the number of clusters must be reduced, sub-pockets are merged on the basis of connectivity between the defining sets of tangent spheres. Practically, sub-pockets with a greater surface area boundary are merged first.



## 3.4 Display and Output Options

By default, PyVOL simply outputs a log containing volumes and, when invoked through PyMOL, displays pocket boundaries as semi-translucent surfaces. This behavior can be extensively customized.

The output name for all computed PyMOL objects and the base filename for any output files can be specified using the prefix option:

```
pocket protein_selection, prefix=favprot
```

PyVOL can also write the input and output files to a directory if given an output directory. In this case it writes out the input protein and ligand structures, a csv report of all calculated volumes, and paired csv/obj files containing tangent sphere collections and 3D triangulated mesh files respectively.

```
pocket protein_selection, output_dir=chosen_out_dir
```

Calculated surfaces can be visualized in three different ways by setting the `display_mode` parameter. The following three commands set the output as a solid surface with transparency, a wireframe mesh, and a collection of spheres. Color is set with the `color` parameter and transparency (when applicable) with the `alpha` parameter:

```
pocket protein_selection, display_mode=solid, alpha=0.85, color=skyblue
pocket protein_selection, display_mode=mesh, color=red
pocket protein_selection, display_mode=spheres, color=firebrick
```

where `alpha` is `[0, 1.0]` and the `color` is any color defined within PyMOL. The presets should generally be sufficient, but custom colors can be chosen using the commands given on the PyMOL wiki.

## SHELL INTERFACE

PyVOL can also be run from the system command line using bash or any standard shell. If installed using `pip`, a `pyvol` entry point should be automatically installed and made available on the path. Otherwise, manual invocation of `pyvol/___main__.py` should work.

### 4.1 Running from the Shell

From the command-line, PyVOL is run exclusively using a configuration file.

```
python -m pyvol <input_parameters.cfg>
```

### 4.2 Template Configuration File Generation

A template configuration file with default values supplied can be generated using:

```
python -m pyvol -t <output_template.cfg>
```

### 4.3 Notes on Output

Currently, PyVOL only reports standard log output to stdout when run this way. So if an output directory is not provided, there is no easy way to retrieve the results.

## DEVELOPMENT

### 5.1 Package Design

The main PyVOL algorithm is run from `identify.py`. There are two interfaces to this module which prepare user supplied inputs: `pyvol/pymol_interface.py` and the commandline entry point in `pyvol/__main__.py`. The PyMOL interface can be accessed directly through the PyMOL prompt or run using the included GUI. The command line entry point is evoked using a configuration file.

### 5.2 Algorithm Design

The primary algorithmic logic is supplied in `identify.py` which acts as the only interface between the user-facing modules and the computational back-end.

The Spheres class holds all of the geometric information about proteins and pockets. It represents any object as a collection of spheres by holding their coordinates, radii, and cluster identifications in a 5D numpy array. Surface triangulation using MSMS and many other convenience functions are included in the class itself. The methods contained in the separate `cluster.py` would largely work as methods in the Spheres class but have been separated due to that class becoming too large and the specificity of those methods to subpocket partitioning.

### 5.3 GUI Design

The GUI was developed using Qt Designer and run using PyQt5.

### 5.4 Version Incrementation

PyVOL uses a standard incrementation scheme. The version of the back-end must be updated in `setup.py`, `pyvol/__init__.py`, and `docs/source/conf.py`. The GUI version is set in `pyvolgui/__init__.py`, and the the version of the GUI that the back-end expects is set again in `pyvol/__init__.py`.

### 5.5 Distribution

The code is hosted on github by the Schlessinger Lab. The PyVOL backend is distributed through PyPI. This process of uploading to PyPI is automated in the `dev/build.sh` script. Installers are packaged using the `dev/package_plugins.sh` script. Documentation is generated and pushed to the github-hosted documentation website with the `dev/document.sh`

script. All three are combined in the *dev/rebuild.sh* script. The plugin will be available both from the github page and through the official PyMOL wiki.

## 5.6 Documentation

Documentation is largely in the google style. Module documentation is collated using *sphinx-apidoc*. The documentation website is built using the *sphinx-rtd-theme* and maintained on the gh-pages branch of PyVOL. The *pyvol\_manual.pdf* is generated using sphinx's evocation of pdfTeX. PyPI can apparently not parse rst files, so the README.rst is converted to a md file using pandoc just prior to deployment.

## PYVOL PACKAGE

## 6.1 Submodules

## 6.2 PyVOL Cluster Module

`pyvol.cluster.cluster_within_r(spheres, radius, allow_new=True)`

Cluster spheres with the same radius using DBSCAN, modifying input data in situ

**Args:** spheres (Spheres): complete set of input spheres radius (float): radius at which clustering is to occur  
allow\_new (bool): permit new clusters? (Default value = True)

`pyvol.cluster.cluster_between_r(spheres, ref_radius, target_radius)`

Cluster spheres from a target radius to a reference radius, modifying input data in situ

**Args:** spheres (Spheres): complete set of input spheres ref\_radius (float): radius from which cluster identities will be drawn target\_radius (float): radius to which cluster identities will be propagated

`pyvol.cluster.cluster_improperly_grouped(spheres, radius, min_cluster_size=1, max_clusters=None)`

Reassigns improperly clustered spheres to ‘proper’ clusters, modifying input data in situ

**Args:** spheres (Spheres): complete set of input spheres radius (float): radius at which closest groups are identified min\_cluster\_size (int): minimum number of spheres in a ‘proper’ cluster (Default value = 1)  
max\_clusters (int): maximum number of ‘proper’ clusters (Default value = None)

`pyvol.cluster.extract_groups(spheres, surf_radius=None, prefix=None)`

Extracts spheres belonging to each cluster from the complete input set and optionally calculates bounded surfaces

**Args:** spheres (Spheres): complete set of input spheres surf\_radius: radius used to calculate bounding spheres for individual groups (Default value = None) prefix: prefix to identify new surfaces (Default value = None)

**Returns:** group\_list ([Spheres]): a list of Spheres objects each corresponding to a different cluster

`pyvol.cluster.hierarchically_cluster_spheres(spheres, ordered_radii, min_new_radius=None, min_cluster_size=10, max_clusters=None)`

Cluster spheres by grouping spheres at large radius and propagating those assignments down to smaller radii

**Args:** spheres (Spheres): complete set of input spheres ordered\_radii ([float]): list of radii ordered from largest to smallest min\_new\_radius (float): smallest spheres to keep (Default value = None) min\_cluster\_size (int): minimum number of spheres in a cluster (Default value = 10) max\_clusters (int): maximum number of clusters (Default value = None)

`pyvol.cluster.identify_closest_grouped(spheres, group, radius)`

Identifies the closest ‘properly’ grouped cluster to a specified group

**Args:** spheres (Spheres): complete set of input spheres group (float): group for which to identify the closest clusters radius (float): radius at which to perform the search

**Returns:** group (float): passthrough of input group closest (float): id of the closest cluster magnitude (int): number of pairwise closest connections between the queried group and the closest identified cluster

`pyvol.cluster.merge_sphere_list(s_list, r=None, g=None)`

**Args:** s\_list ([Spheres]): list of input spheres r (float): radius value to assign to output Spheres (Default value = None) g (float): group value to assign to output Spheres (Default value = None)

**Returns:** merged\_spheres (Spheres): a single Spheres object containing the merged input lists

`pyvol.cluster.reassign_group(spheres, source_group, target_group)`

Reassign a group in place

**Args:** spheres (Spheres): complete set of input spheres source\_group (float): group to change target\_group (float): new group id

`pyvol.cluster.reassign_groups_to_closest(spheres, group_list, radius, iterations=None, preserve_largest=False)`

Reassign a group to the closest group as identified by maximum linkage; operates in place

**Args:** spheres (Spheres): complete set of input spheres group\_list ([float]): list of group ids which are to be iteratively reassigned radius (float): radius at which searches are to take place iterations (int): number of times to attempt to reassign groups (Default value = None) preserve\_largest: keep the group id of the group with more members? (Default value = False)

`pyvol.cluster.remove_interior(spheres)`

Remove all spheres which are completely enclosed in larger spheres; operates in place

**Args:** spheres (Spheres): complete set of input spheres

`pyvol.cluster.remove_overlap(spheres, radii=None, spacing=0.1, iterations=20, tolerance=0.02)`

Remove overlap between groups; operates in place

**Args:** spheres (Spheres): complete set of input spheres radii ([float]): radii at which to perform searches for overlap (Default value = None) spacing (float): binning radius (Default value = 0.1) iterations (int): number of times to attempt overlap removal (Default value = 20) tolerance (float): overlap tolerance (Default value = 0.02)

## 6.3 PyVOL Identify Module

`pyvol.identify.pocket(prot_file, mode='largest', lig_file=None, coordinate=None, resid=None, residue_coordinates=None, min_rad=1.4, max_rad=3.4, lig_excl_rad=None, lig_incl_rad=None, subdivide=False, minimum_volume=200, min_subpocket_rad=1.7, min_subpocket_surf_rad=1.0, max_clusters=None, prefix=None, output_dir=None, constrain_inputs=False)`

Calculates the SES for a binding pocket

**Args:** prot\_file (str): filename for the input pdb file containing the peptidee mode (str): pocket identification mode (can be largest, all, or specific) (Default value = “largest”) lig\_file (str): filename for the input pdb file containing a ligand (Default value = None) coordinate ([float]): 3D coordinate used for pocket specification (Default value = None) resid (str): residue identifier for pocket specification (Default value = None) residue\_coordinates ([float]): 3D coordinate of an atom in a surrounding residue used for pocket specification (Default value = None) min\_rad (float): radius for SAS calculations (Default value = 1.4) max\_rad (float): radius used to identify the outer, bulk solvent exposed surface (Default value = 3.4) lig\_excl\_rad

(float): maximum distance from a provided ligand that can be included in calculated pockets (Default value = None) `lig_incl_rad` (float): minimum distance from a provided ligand that should be included in calculated pockets when solvent border is ambiguous (Default value = None) `subdivide` (bool): calculate subpockets? (Default value = False) `minimum_volume` (float): minimum volume of pockets returned when running in 'all' mode (Default value = 200) `min_subpocket_rad` (float): minimum radius that identifies distinct subpockets (Default value = 1.7) `min_subpocket_surf_rad` (float): radius used to calculate subpocket surfaces (Default value = 1.0) `max_clusters` (int): maximum number of clusters (Default value = None) `prefix` (str): identifying string for output (Default value = None) `output_dir` (str): filename of the directory in which to place all output; can be absolute or relative (Default value = None) `constrain_inputs` (bool): restrict quantitative input parameters to tested values? (Default value = False)

**Returns:** `pockets` ([Spheres]): a list of Spheres objects each of which contains the geometric information describing a distinct pocket or subpocket

```
pyvol.identify.subpockets(bounding_spheres, ref_spheres, min_rad, max_rad,
                           min_subpocket_rad=1.7, min_subpocket_surf_rad=1.0,
                           max_subpocket_rad=None, sampling=0.1, inclusion_radius_buffer=1.0,
                           min_cluster_size=50, max_clusters=None, prefix=None)
```

**Args:** `bounding_spheres` (Spheres): a Spheres object containing both the peptide and solvent exposed face external spheres `ref_spheres` (Spheres): a Spheres object holding the interior spheres that define the pocket to be subdivided `min_rad` (float): radius for original SES calculations (Default value = 1.4) `max_rad` (float): radius originally used to identify the outer, bulk solvent exposed surface (Default value = 3.4) `min_subpocket_rad` (float): minimum radius that identifies distinct subpockets (Default value = 1.7) `min_subpocket_surf_rad` (float): radius used to calculate subpocket surfaces (Default value = 1.0) `max_subpocket_rad` (float): maximum spheres radius used for subpocket clustering (Default value = None) `sampling` (float): radial sampling frequency for clustering (Default value = 0.1) `inclusion_radius_buffer` (float): defines the inclusion distance for nonextraneous spheres in combination with `min_rad` and `max_rad` (Default value = 1.0) `min_cluster_size` (int): minimum number of spheres that can constitute a proper cluster (Default value = 50) `max_clusters` (int): maximum number of clusters (Default value = None) `prefix` (str): identifying string for output (Default value = None)

**Returns:** `pockets` ([Spheres]): a list of Spheres objects each of which contains the geometric information describing a distinct subpocket

```
pyvol.identify.write_report(all_pockets, output_dir, prefix)
Write a brief report of calculated volumes to file
```

**Args:** `all_pockets` ([Sphere]): a list of Spheres objects each of which contains the complete information about a distinct pocket or subpocket `output_dir` (str): output directory, relative or absolute `prefix` (str): identifying prefix for output files

## 6.4 PyVOL Pymol Interface Module

```
pyvol.pymol_interface.load_pocket(spheres_file, name=None, display_mode='solid',
                                   color='marine', alpha=0.85)
```

**Args:** `spheres_file` (str): filename `name` (str): internal display name (Default value = None) `display_mode` (str): display mode (Default value = "solid") `color` (str): PyMOL color string (Default value = 'marine') `alpha` (float): transparency value (Default value = 0.85)

```
pyvol.pymol_interface.pocket (protein, mode=None, ligand=None, pocket_coordinate=None,
                               residue=None, resid=None, prefix=None, min_rad=1.4,
                               max_rad=3.4, lig_excl_rad=None, lig_incl_rad=None,
                               display_mode='solid', color='marine', alpha=0.85, out-
                               put_dir=None, subdivide=None, minimum_volume=200,
                               min_subpocket_rad=1.7, min_subpocket_surf_rad=1.0,
                               max_clusters=None, excl_org=False, constrain_inputs=True)
```

Calculates the SAS for a binding pocket and displays it

**Args:** protein (str): PyMOL selection string for the protein mode (str): pocket identification mode (can be largest, all, or specific) (Default value = None) ligand (str): PyMOL selection string for the ligand (Default value = None) pocket\_coordinate ([float]): 3D coordinate used for pocket specification (Default value = None) residue (str): PyMOL residue selection string for pocket specification (Default value = None) resid (str): residue identifier for pocket specification (Default value = None) prefix (str): identifying string for output (Default value = None) min\_rad (float): radius for SAS calculations (Default value = 1.4) max\_rad (float): radius used to identify the outer, bulk solvent exposed surface (Default value = 3.4) lig\_excl\_rad (float): maximum distance from a provided ligand that can be included in calculated pockets (Default value = None) lig\_incl\_rad (float): minimum distance from a provided ligand that should be included in calculated pockets when solvent border is ambiguous (Default value = None) display\_mode (str): display mode for calculated pockets (Default value = "solid") color (str): PyMOL color string (Default value = 'marine') alpha (float): transparency value (Default value = 0.85) output\_dir (str): filename of the directory in which to place all output; can be absolute or relative (Default value = None) subdivide (bool): calculate subpockets? (Default value = None) minimum\_volume (float): minimum volume of pockets returned when running in 'all' mode (Default value = 200) min\_subpocket\_rad (float): minimum radius that identifies distinct subpockets (Default value = 1.7) min\_subpocket\_surf\_rad (float): radius used to calculate subpocket surfaces (Default value = 1.0) max\_clusters (int): maximum number of clusters (Default value = None) excl\_org (bool): exclude non-peptide atoms from the protein selection? (Default value = False) constrain\_inputs (bool): constrain input quantitative values to tested ranges? (Default value = True)

## 6.5 PyVOL Pymol Utilities Module

```
pyvol.pymol_utilities.construct_palette (color_list=None, max_value=7, min_value=1)
```

Construct a palette

**Args:** color\_list ([str]): list of PyMOL color strings (Default value = None) max\_value (int): max palette index (Default value = 7) min\_value (int): min palette index (Default value = 1)

**Returns:** palette ([str]): list of color definitions

```
pyvol.pymol_utilities.display_pseudoatom_group (spheres, name, color='gray60',
                                                  palette=None)
```

Displays a collection of pseudoatoms

**Args:** spheres (Spheres): Spheres object holding pocket geometry name (str): display name color (str): PyMOL color string (Default value = 'gray60') palette ([str]): palette (Default value = None)

```
pyvol.pymol_utilities.display_spheres_object (spheres, name, state=1, color='marine', al-
                                              pha=0.7, mode='solid', palette=None)
```

Loads a mesh object into a cgo list for display in PyMOL

**Args:** spheres (Spheres): Spheres object containing all geometry name (str): display name state (int): model state (Default value = 1) color (str): PyMOL color string (Default value = 'marine') alpha (float): transparency value (Default value = 0.7) mode (str): display mode (Default value = "solid") palette ([str]): palette (Default value = None)

```
pyvol.pymol_utilities.mesh_to_solid_CGO (mesh, color='gray60', alpha=1.0)
```

Creates a solid CGO object for a mesh for display in PyMOL



**Args:** mesh (Trimesh): Trimesh mesh object color (str): PyMOL color string (Default value = 'gray60') alpha (float): transparency value (Default value = 1.0)

**Returns:** cgobuffer (str): CGO buffer that contains the instruction to load a solid object

`pyvol.pymol_utilities.mesh_to_wireframe_CGO (mesh, color='gray60', alpha=1.0)`

Creates a wireframe CGO object for a mesh for display in PyMOL

**Args:** mesh (Trimesh): Trimesh mesh object color (str): PyMOL color string (Default value = 'gray60') alpha (float): transparency value (Default value = 1.0)

**Returns:** cgobuffer (str): CGO buffer that contains the instruction to load a wireframe object

## 6.6 PyVOL Spheres Module

**class** `pyvol.spheres.Spheres` (*xyz=None, r=None, xyzr=None, xyzrg=None, g=None, pdb=None, bv=None, mesh=None, name=None, spheres\_file=None*)

Bases: object

**copy** ()

**calculate\_surface** (*probe\_radius=1.4, cavity\_atom=None, coordinate=None, all\_components=False, exclusionary\_radius=2.5, largest\_only=False, noh=True, minimum\_volume=200*)

Calculate the SAS for a given probe radius

**Args:** probe\_radius (float): radius for surface calculations (Default value = 1.4) cavity\_atom (int): id of a single atom which lies on the surface of the interior cavity of interest (Default value = None) coordinate ([float]): 3D coordinate to identify a cavity atom (Default value = None) all\_components (bool): return all pockets? (Default value = False) exclusionary\_radius (float): maximum permissible distance to the closest identified surface element from the supplied coordinate (Default value = 2.5) largest\_only (bool): return only the largest pocket? (Default value = False) noh (bool): remove waters before surface calculation? (Default value = True) minimum\_volume (int): minimum volume of pockets returned when using 'all\_components' (Default value = 200)

**identify\_nonextraneous** (*ref\_spheres, radius*)

Returns all spheres less than radius away from any center in ref\_spheres using cKDTree search built on the non-reference set

**Args:** ref\_spheres (Spheres): object that defines the pocket of interest radius (float): maximum distance to sphere centers to be considered nonextraneous

**Returns:** nonextraneous (Spheres): a filtered Spheres object

**nearest** (*coordinate, max\_radius=None*)

Returns the index of the sphere closest to a coordinate; if max\_radius is specified, the sphere returned must have a radius <= max\_radius

**Args:** coordinate (float nx3): 3D input coordinate max\_radius (float): maximum permissible distance to the nearest sphere (Default value = None)

**Returns:** nearest\_index: index of the closest sphere

**nearest\_coord\_to\_external** (*coordinates*)

Returns the coordinate of the sphere closest to the supplied coordinates

**Args:** coordinates (float nx3): set of coordinates

**Returns:** coordinate (float 1x3): coordinate of internal sphere closest to the supplied coordinates

**remove\_duplicates** (*eps=0.01*)

Remove duplicate spheres by identifying centers closer together than *eps* using DBSCAN

**Args:** *eps* (float): DBSCAN input parameter (Default value = 0.01)

**remove\_ungrouped** ()

Remove all spheres that did not adequately cluster with the remainder of the set

**remove\_groups** (*groups*)

Remove all spheres with specified group affiliations

**Args:** *groups* ([float]): list of groups to remove

**write** (*filename, contents='xyzrg', output\_mesh=True*)

Writes the contents of *\_xyzrg* to a space delimited file

**Args:** *filename* (str): filename to write the report and mesh if indicated *contents* (str): string describing which columns to write to file (Default value = "xyzrg") *output\_mesh* (bool): write mesh to file? (Default value = True)

**xyzrg**

Retrieve the coordinates, radii, and group ids

**xyzr**

Retrieve coordinates and radii

**xyz**

Retrieve the coordinates

**r**

Retrieve the radii

**g**

Retrieve the group indices

## 6.7 PyVOL Utilities Module

`pyvol.utilities.check_dir` (*location*)

Ensure that a specified directory exists

**Args:** *location* (str): target directory

`pyvol.utilities.coordinates_for_resid` (*pdb\_file, resid, chain=None, model=0*)

Extract the 3D coordinates for all atoms in a specified residue from a pdb file

**Args:** *pdb\_file* (str): filename of the specified pdb file *resid* (int): residue number *chain* (str): chain identifier (Default value = None) *model* (int): model identifier (Default value = 0)

**Returns:** *coordinates* ([[float]]): 3xN array containing all atomic positions

`pyvol.utilities.run_cmd` (*options, in\_directory=None*)

Run a program using the command line

**Args:** *options* ([str]): list of command line options *in\_directory* (str): directory in which to run the command (Default value = None)

`pyvol.utilities.surface_multiprocessing` (*args*)

A single surface calculation designed to be run in parallel

**Args:**

**args: a tuple containing:** spheres (Spheres): a Spheres object containing all surface producing objects  
probe\_radius (float): radius to use for probe calculations  
kwargs (dict): all remaining arguments accepted by the surface calculation algorithm

**Returns:** surface (Spheres): the input Spheres object but with calculated surface parameters

`pyvol.utilities.sphere_multiprocessing(spheres, radii, workers=None, **kwargs)`

A wrapper function to calculate multiple surfaces using multiprocessing

**Args:** spheres (Spheres): input Spheres object  
radii ([float]): list of radii at which surfaces will be calculated  
workers (int): number of workers (Default value = None)  
kwargs (dict): all remaining arguments accepted by surface calculation that are constant across parallel calculations

**Returns:** surfaces ([Spheres]): a list of Spheres object each with its surface calculated

## 6.8 PyVOL Main Entry Point

`pyvol.__main__.create_default_cfg(cfg_file='defaults.cfg')`

Writes a template cfg file to disk

**Args:** cfg\_file (str): target configuration file (Default value = “defaults.cfg”)

`pyvol.__main__.run_from_cfg(cfg_file)`

**Args:** cfg\_file (str): input cfg that specifies a PyVOL job

## 6.9 PyVOL GUI

`pyvol.pyvol_gui.__init__.pyvol_window()`

Launches a window to select a file

`pyvol.pyvol_gui.__init__.browse_pocket_file(form)`

Launches a window to select a file

`pyvol.pyvol_gui.__init__.install_remote_pyvol(form)`

Attempts a de novo PyVOL installation using pip

`pyvol.pyvol_gui.__init__.install_local_pyvol(form)`

`pyvol.pyvol_gui.__init__.uninstall_pyvol(form)`

Attempts to uninstall PyVOL using pip

`pyvol.pyvol_gui.__init__.update_pyvol(form)`

Attempts to update PyVOL using pip

`pyvol.pyvol_gui.__init__.refresh_installation_status(form, check_for_updates=False)`

Check for updates and adjust the GUI to reflect the current installation status and availability of updates

**Args:** check\_for\_updates (bool): query servers to see if an update is available? (Default value = False)

`pyvol.pyvol_gui.__init__.run_gui_load(form)`

Loads a precalculated pocket into PyMOL

`pyvol.pyvol_gui.__init__.run_gui_pyvol(form)`

Runs a PyVOL calculation

## PYTHON MODULE INDEX

### p

- `pyvol.__main__`, [16](#)
- `pyvol.cluster`, [10](#)
- `pyvol.identify`, [11](#)
- `pyvol.pymol_interface`, [12](#)
- `pyvol.pymol_utilities`, [13](#)
- `pyvol.pyvol_gui.__init__`, [16](#)
- `pyvol.spheres`, [14](#)
- `pyvol.utilities`, [15](#)

## B

`browse_pocket_file()` (in module `pyvol.pyvol_gui.__init__`), 16

## C

`calculate_surface()` (`pyvol.spheres.Spheres` method), 14

`check_dir()` (in module `pyvol.utilities`), 15

`cluster_between_r()` (in module `pyvol.cluster`), 10

`cluster_improperly_grouped()` (in module `pyvol.cluster`), 10

`cluster_within_r()` (in module `pyvol.cluster`), 10

`construct_palette()` (in module `pyvol.pymol_utilities`), 13

`coordinates_for_resid()` (in module `pyvol.utilities`), 15

`copy()` (`pyvol.spheres.Spheres` method), 14

`create_default_cfg()` (in module `pyvol.__main__`), 16

## D

`display_pseudoatom_group()` (in module `pyvol.pymol_utilities`), 13

`display_spheres_object()` (in module `pyvol.pymol_utilities`), 13

## E

`extract_groups()` (in module `pyvol.cluster`), 10

## G

`g` (`pyvol.spheres.Spheres` attribute), 15

## H

`hierarchically_cluster_spheres()` (in module `pyvol.cluster`), 10

## I

`identify_closest_grouped()` (in module `pyvol.cluster`), 10

`identify_nonextraneous()` (`pyvol.spheres.Spheres` method), 14

`install_local_pyvol()` (in module `pyvol.pyvol_gui.__init__`), 16

`install_remote_pyvol()` (in module `pyvol.pyvol_gui.__init__`), 16

## L

`load_pocket()` (in module `pyvol.pymol_interface`), 12

## M

`merge_sphere_list()` (in module `pyvol.cluster`), 11

`mesh_to_solid_CGO()` (in module `pyvol.pymol_utilities`), 13

`mesh_to_wireframe_CGO()` (in module `pyvol.pymol_utilities`), 14

## N

`nearest()` (`pyvol.spheres.Spheres` method), 14

`nearest_coord_to_external()` (`pyvol.spheres.Spheres` method), 14

## P

`pocket()` (in module `pyvol.identify`), 11

`pocket()` (in module `pyvol.pymol_interface`), 12

`pyvol.__main__` (module), 16

`pyvol.cluster` (module), 10

`pyvol.identify` (module), 11

`pyvol.pymol_interface` (module), 12

`pyvol.pymol_utilities` (module), 13

`pyvol.pyvol_gui.__init__` (module), 16

`pyvol.spheres` (module), 14

`pyvol.utilities` (module), 15

`pyvol_window()` (in module `pyvol.pyvol_gui.__init__`), 16

## R

`r` (`pyvol.spheres.Spheres` attribute), 15

`reassign_group()` (in module `pyvol.cluster`), 11

`reassign_groups_to_closest()` (in module `pyvol.cluster`), 11

`refresh_installation_status()` (in module `pyvol.pyvol_gui.__init__`), 16

`remove_duplicates()` (*pyvol.spheres.Spheres*  
    *method*), 14  
`remove_groups()` (*pyvol.spheres.Spheres* *method*),  
    15  
`remove_interior()` (*in module pyvol.cluster*), 11  
`remove_overlap()` (*in module pyvol.cluster*), 11  
`remove_ungrouped()` (*pyvol.spheres.Spheres*  
    *method*), 15  
`run_cmd()` (*in module pyvol.utilities*), 15  
`run_from_cfg()` (*in module pyvol.\_\_main\_\_*), 16  
`run_gui_load()` (*in* *module*  
    *pyvol.pyvol\_gui.\_\_init\_\_*), 16  
`run_gui_pyvol()` (*in* *module*  
    *pyvol.pyvol\_gui.\_\_init\_\_*), 16

## S

`sphere_multiprocessing()` (*in* *module*  
    *pyvol.utilities*), 16  
`Spheres` (*class in pyvol.spheres*), 14  
`subpockets()` (*in module pyvol.identify*), 12  
`surface_multiprocessing()` (*in* *module*  
    *pyvol.utilities*), 15

## U

`uninstall_pyvol()` (*in* *module*  
    *pyvol.pyvol\_gui.\_\_init\_\_*), 16  
`update_pyvol()` (*in* *module*  
    *pyvol.pyvol\_gui.\_\_init\_\_*), 16

## W

`write()` (*pyvol.spheres.Spheres* *method*), 15  
`write_report()` (*in module pyvol.identify*), 12

## X

`xyz` (*pyvol.spheres.Spheres* *attribute*), 15  
`xyzr` (*pyvol.spheres.Spheres* *attribute*), 15  
`xyzrg` (*pyvol.spheres.Spheres* *attribute*), 15