Phase Command-Line Pharmacophore Modeling

This document summarizes the complete command-line pharmacophore model development workflow. The starting point is one or more Maestro files containing multiconformer models for the ligands of interest. A Phase project is created from these ligands, after which a series of steps is followed, directly analogous to the Develop Pharmacophore Model workflow in Maestro. The full description of the commands is given in Chapter 12 of the *Phase User Manual*. On Windows, you can run these commands in a Schrodinger Command Prompt window, which you open from the Start menu; you do not need to include `$SCHRODINGER` or `$SCHRODINGER/utilities` in the command when running in this window.

Create/Add to a Project:

```
$SCHRODINGER/utilities/pharm_project {-new|-add} -mae maefile [-ignoreTitles] [-stereo]
    [-act actProp] [-conf confProp]
```

Modify Master Data:

```
$SCHRODINGER/utilities/pharm_data [-log|-exp] [-multiply scale] [-commit] [-restore]
    [-active aboveVal] [-inactive belowVal] [-train numTrain [-rand seed [-pharm_set] [-sort]]]
    [-conf confProp] [-group [titles]|-ungroup]
```

Create Pharmacophore Sites:

```
$SCHRODINGER/utilities/pharm_create_sites -setup [-fd fdFile]
$SCHRODINGER/phase_feature create_sites [job-options]
$SCHRODINGER/utilities/pharm_create_sites -cleanup
```

Find Common Pharmacophores:

```
$SCHRODINGER/utilities/pharm_find_common -setup -sites numSites [-match minMatch] [-freq]
$SCHRODINGER/phase_partition find_common [job-options]
$SCHRODINGER/phase_multiPartition find_common [-minSites n] [job-options]
$SCHRODINGER/utilities/pharm_find_common -cleanup
```

Score Hypotheses with Respect to Actives:

```
$SCHRODINGER/utilities/pharm_score_actives -setup [-tol] [-act|-prop weight] [-conf weight]
$SCHRODINGER/phase_scoring score_actives [job-options]
$SCHRODINGER/utilities/pharm_score_actives -cleanup
```

Score Hypotheses with Respect to Inactives:

```
$SCHRODINGER/utilities/pharm_score_inactives -setup -w weight
$SCHRODINGER/phase_inactive score_inactives [job-options]
$SCHRODINGER/utilities/pharm_score_inactives -cleanup
```

Cluster Hypotheses by Geometric Similarity:

```
$SCHRODINGER/utilities/pharm_cluster_hypotheses -setup [-link method]
$SCHRODINGER/phase_hypoCluster cluster_hypotheses [job-options]
$SCHRODINGER/utilities/pharm_cluster_hypotheses -cleanup [-report level]
```

Build QSAR Models:

```
$SCHRODINGER/utilities/pharm_build_qsar -setup [-model type] [-grid spacing] [-factors n]
     [-tvalue tmin [-exclude n] [-rand seed]] [-atomTypeVol]
$SCHRODINGER/phase_multiQsar build_qsar [job-options]
$SCHRODINGER/utilities/pharm_build_qsar -cleanup
```

Preserve Project Data in a Tar Archive:

```
$SCHRODINGER/utilities/pharm_archive -step stepName -tar tarFile [-gzip]
```

Once pharmacophore hypotheses and QSAR models have been developed, a number of other command-line utilities may be run:

Align Project Ligands or New Molecules to a Pharmacophore Hypothesis:

```
$SCHRODINGER/phase_find_matches [options]
```

Align/Merge a Pair of Hypotheses:

```
$SCHRODINGER/utilities/align_hypoPair -fixed fixedHypoID -free freeHypoID -new newHypoID
    [-dtol deltaDist] [-match minSites] [-mix] [-equiv equivFile] [-merge method] [-keep maxAlign]
    [-rmsd rmsdFile] [-sim [simFile] [-rmsdMax rmsdMax]]
```

Create Excluded Volumes Automatically:

```
$SCHRODINGER/utilities/create_xvolShell -hypo hypoID [-ref maeFile] [-buff dist] [-grid spacing]
    [-partial atoms [-mask dist]] [-hydrogens] [-append] [-cut]
$SCHRODINGER/utilities/create_xvolClash -hypo hypoID -pos maeFilePos -neg maeFileNeg
    [-freq minClash] [-buff dist] [-grid spacing] [-hydrogens] [-append]
$SCHRODINGER/utilities/create_xvolReceptor -hypo hypoID -receptor maeFileRec
    [-ligand maeFileLig] [-radius r|-rprop rpropName] [-scale s|-sprop spropName]
    [-buff dmin] [-limit dmax] [-hydrogens] [-append]
```

Analyze QSAR Predictions within Hit Files:

```
$SCHRODINGER/utilities/phase_qsar_stats -hypo hypoID [-hits hitFile [-act actProp] [-plot csvFile]]
    [-out outFile]
```

Visualize QSAR Models:

```
$SCHRODINGER/utilities/qsarVis -hyp hypoID -mol molname [-volume_qsar] [-class name]
    [-pc posThresh] [-nc negThresh] [-trans value] [-npls plsFactors]
```

In the above commands, *job-options* represents the standard Job Control options:

`-HOST` *host*	Run the job on the specified host.
`-LOCAL`	Run the job in the current directory, rather than in a temporary scratch directory.
`-TMPDIR` *tmpdir*	Use *tmpdir* for temporary files.
`-WAIT`	Do not return control to the shell until the job finishes.
`-INTERVAL` *N*	Interval in seconds between output updates.
`-NICE`	Run the job at reduced priority.