NAME

PyMOLConvertPMLToPSE.py - Convert PML to PSE

SYNOPSIS

PyMOLConvertPMLToPSE.py [--feedback <yes or no>] [--overwrite] [-w <dir>] -i <infile> -o <outfile>

PyMOLConvertPMLToPSE.py -h | --help | -e | --examples

DESCRIPTION

Convert PyMOL script language (PML) file to PyMOL session (PSE) file.

The supported input and output file formats are PML (.pml) and PSE (.pse).

OPTIONS

-f, --feedback <yes or no> [default: yes]

PyMOL output feedback during loading of PML file. This option may not work in all versions of PyMOL across various platforms.

-e, --examples

Print examples.

-h, --help

Print this help message.

-i, --infile <infile>

Input file name.

-o, --outfile <outfile>

Output file name.

--overwrite

Overwrite existing files.

-w, --workingdir <dir>

Location of working directory which defaults to the current directory.

EXAMPLES

To convert a PML file to a PSE file, type:

```
% PyMOLConvertPMLToPSE.py -i Sample.pml -o Sample.pse
```

To convert a PML file to a PSE file along with turning off PyMOL feedback during loading of PML file, type:

```
% PyMOLConvertPMLToPSE.py -f no -i Sample.pml -o Sample.pse
```

AUTHOR

Manish Sud(msud@san.rr.com)

SEE ALSO

PyMOLConvertLigandFileFormat.py, PyMOLSplitChainsAndLigands.py, PyMOLVisualizeMacromolecules.py

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The functionality available in this script is implemented using PyMOL, a molecular visualization system on an open source foundation originally developed by Warren DeLano.

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