

## NAME

ModifySDFFilesDataFields.pl - Modify data fields in SDFFile(s)

## SYNOPSIS

ModifySDFFilesDataFields.pl SDFFile(s)...

ModifySDFFilesDataFields.pl [-d, --detail *infolevel*] [--datafieldscommon *newfieldlabel*, *newfieldvalue*, [*newfieldlabel*, *newfieldvalue*,...]] [--datafieldsmap *newfieldlabel*, *oldfieldlabel*, [*oldfieldlabel*,...]; [*newfieldlabel*, *oldfieldlabel*, [*oldfieldlabel*,...]]] [--datafieldsmapfile *filename*] [--datafieldURL *URLDataFieldLabel*, *CGIScriptPath*, *CGIParameName*, *CmpdIDFieldLabel*] [-h, --help] [-k, --keepolddatafields *all* | *unmappedonly* | *none*] [-m, --mode *molname* | *datafields* | *both*] [--molnamemode *datafield* | *labelprefix*] [--molname *datafieldname* or *prefixstring*] [--molnamereplace *always* | *empty*] [-o, --overwrite] [-r, --root *rootname*] [-w, --workingdir *dirname*] SDFFile(s)...

## DESCRIPTION

Modify *molname* line and data fields in *SDFFile(s)*. *Molname* line can be replaced by a data field value or assigned a sequential ID prefixed with a specific string. For data fields and modification of their values, these types of options are supported: replace data field labels by another set of labels; combine values of multiple data fields and assign a new label; add specific set of data field labels and values to all compound records; and others.

The file names are separated by space. The valid file extensions are *.sdf* and *.sd*. All other file names are ignored. All the SD files in a current directory can be specified either by *\*.sdf* or the current directory name.

## OPTIONS

-d, --detail *infolevel*

Level of information to print about compound records being ignored. Default: *1*. Possible values: *1, 2 or 3*.

--datafieldscommon *newfieldlabel*, *newfieldvalue*, [*newfieldlabel*, *newfieldvalue*,...]

Specify data field labels and values for addition to each compound record. It's a comma delimited list of data field label and values pair. Default: *none*.

Examples:

```
DepositionDate, YYYY-MM-DD
Source, www.domainname.org, ReleaseData, YYYY-MM-DD
```

--datafieldsmap *newfieldlabel*, *oldfieldlabel*, [*oldfieldlabel*,...]; [*newfieldlabel*, *oldfieldlabel*, [*oldfieldlabel*,...]]

Specify how various data field labels and values are combined to generate a new data field labels and their values. All the comma delimited data fields, with in a semicolon delimited set, are mapped to the first new data field label along with the data field values joined via new line character. Default: *none*.

Examples:

```
Synonym, Name, SystematicName, Synonym; CmpdID, Extreg
HBondDonors, SumNHOH
```

--datafieldsmapfile *filename*

Filename containing mapping of data fields. Format of data fields line in this file corresponds to --datafieldsmap option.

Example:

```
Line 1: Synonym, Name, SystematicName, Synonym; CmpdID, Extreg
Line 2: HBondDonors, SumNHOH
```

--datafieldURL *URLDataFieldLabel*, *CGIScriptPath*, *CGIParameName*, *CmpdIDFieldLabel*

Specify how to generate a URL for retrieving compound data from a web server and add it to each compound record.

*URLDataFieldLabel* is used as the data field label for URL value which is created by combining

*CGIScriptPath*, *CGIParameName*, *CmpdIDFieldLabel* values: *CGIScriptPath?CGIParameName=CmpdIDFieldLabelValue*. Default: *none*

.

Example:

```
Source, http://www.yourdomain.org/GetCmpd.pl, Reg_ID, Mol_ID
```

-h, --help

Print this help message.

-k, --keepolddatafields *all* | *unmappedonly* | *none*

Specify how to transfer old data fields from input SDFFile(s) to new SDFFile(s) during *datafields* | *both* value of -m, --mode option: keep all old data fields; write out the ones not mapped to new fields as specified by --datafieldsmap or --datafieldsmapfile options; or ignore all old data field labels. For *molname* -m --mode, old datafields are always kept. Possible values: *all* | *unmappedonly* | *none*. Default: *none*.

-m, --mode *molname* | *datafields* | *both*

Specify how to modify SDF file(s): *molname* - change molname line by another datafield or value; *datafield* - modify data field labels and values by replacing one label by another, combining multiple data field labels and values, adding specific set of data field labels and values to all compound, or inserting an URL for compound retrieval to each record; *both* - change molname line and datafields simultaneously. Possible values: *molname* | *datafields* | *both*. Default: *molname*

--molnamemode *datafield* | *labelprefix*

Specify how to change molname line for -m --mode option values of *molname* | *both*: use a datafield label value or assign a sequential ID prefixed with *labelprefix*. Possible values: *datafield* | *labelprefix*. Default: *labelprefix*.

--molname *datafieldname* or *prefixstring*

Molname generation method. For *datafield* value of --molnamemode option, it corresponds to datafield label name whose value is used for molname; otherwise, it's a prefix string used for generating compound IDs like *labelprefixstring*<Number>. Default value, *Cmpd*, generates compound IDs like *Cmpd*<Number> for molname.

--molnamereplace *always* | *empty*

Specify when to replace molname line for -m --mode option values of *molname* | *both*: always replace the molname line using --molname option or only when it's empty. Possible values: *always* | *empty*. Default: *empty*.

-o, --overwrite

Overwrite existing files.

-r, --root *rootname*

New SD file name is generated using the root: <Root>.<Ext>. Default new file name: <InitialSDFileName>ModifiedDataFields.<Ext>. This option is ignored for multiple input files.

-w, --workingdir *dirname*

Location of working directory. Default: current directory.

## EXAMPLES

To replace empty molname lines by *Cmpd*<*CmpdNumber*> and generate a new SD file *NewSample1.sdf*, type:

```
% ModifySDFilesDataFields.pl -o -r NewSample1 Sample1.sdf
```

To replace all molname lines by *Mol\_ID* data field generate a new SD file *NewSample1.sdf*, type:

```
% ModifySDFilesDataFields.pl --molnamemode datafield
--molnamereplace always -r NewSample1 -o Sample1.sdf
```

To replace all molname lines by *Mol\_ID* data field, map *Name* and *CompoundName* to a new datafield *Synonym*, and generate a new SD file *NewSample1.sdf*, type:

```
% ModifySDFilesDataFields.pl --molnamemode datafield
--molnamereplace always --molname Mol_ID --mode both
--datafieldsmap "Synonym,Name,CompoundName" -r
NewSample1 -o Sample1.sdf
```

To replace all molname lines by *Mol\_ID* data field, map *Name* and *CompoundName* to a new datafield *Synonym*, add common fields *ReleaseDate* and *Source*, and generate a new SD file *NewSample1.sdf* without keeping any old SD data fields, type:

```
% ModifySDFilesDataFields.pl --molnamemode datafield
--molnamereplace always --molname Mol_ID --mode both
--datafieldsmap "Synonym,Name,CompoundName"
--datafieldscommon "ReleaseDate,yyyy-mm-dd,Source,
www.mayachemtools.org" --keepolddatafields none -r
NewSample1 -o Sample1.sdf
```

Preparing SD files PubChem deposition:

Consider a SD file with these fields: *Mol\_ID*, *Name*, *Synonyms* and *Systematic\_Name*. And *Mol\_ID* data field uniquely identifies your compound.

To prepare a new SD file *CmpdDataForPubChem.sdf* containing only required *PUBCHEM\_EXT\_DATASOURCE\_REGID* field, type:

```
% ModifySDFilesDataFields.pl --m datafields
--datafieldsmap
"PUBCHEM_EXT_DATASOURCE_REGID,Mol_ID"
-r CmpdDataForPubChem -o Sample1.sdf
```

To prepare a new SD file *CmpdDataForPubChem.sdf* containing only required *PUBCHEM\_EXT\_DATASOURCE\_REGID* field and replace molname line with *Mol\_ID*, type:

```
% ModifySDFfilesDataFields.pl --molnamemode datafield
--molnamereplace always --molname Mol_ID --mode both
--datafieldsmap
"PUBCHEM_EXT_DATASOURCE_REGID,Mol_ID"
-r CmpdDataForPubChem -o Sample1.sdf
```

In addition to required PubChem data field, you can also add optional PubChem data fields.

To map your Name, Synonyms and Systematic\_Name data fields to optional PUBCHEM\_SUBSTANCE\_SYNONYM data field along with required ID field, type:

```
% ModifySDFfilesDataFields.pl --molnamemode datafield
--molnamereplace always --molname Mol_ID --mode both
--datafieldsmap
"PUBCHEM_EXT_DATASOURCE_REGID,Mol_ID;
PUBCHEM_SUBSTANCE_SYNONYM,Name,CompoundName"
-r CmpdDataForPubChem -o Sample1.sdf
```

To add your <domain.org> as PUBCHEM\_EXT\_SUBSTANCE\_URL and link substance retrieval to your CGI script <[http://www.yourdomain.org/GetCmpd.pl,Reg\\_ID,Mol\\_ID](http://www.yourdomain.org/GetCmpd.pl,Reg_ID,Mol_ID)> via PUBCHEM\_EXT\_DATASOURCE\_REGID field along with optional and required data fields, type:

```
% ModifySDFfilesDataFields.pl --molnamemode datafield
--molnamereplace always --molname Mol_ID --mode both
--datafieldsmap
"PUBCHEM_EXT_DATASOURCE_REGID,Mol_ID;
PUBCHEM_SUBSTANCE_SYNONYM,Name,CompoundName"
--datafieldscommon
"PUBCHEM_EXT_SUBSTANCE_URL,domain.org"
--datafieldURL "PUBCHEM_EXT_DATASOURCE_URL,
http://www.yourdomain.org/GetCmpd.pl,Reg\_ID,Mol\_ID"
-r CmpdDataForPubChem -o Sample1.sdf
```

And to add a publication date and request a release data using PUBCHEM\_PUBLICATION\_DATE and PUBCHEM\_DEPOSITOR\_RECORD\_DATE data fields along with all the data fields in earlier examples, type: optional fields, type:

```
% ModifySDFfilesDataFields.pl --molnamemode datafield
--molnamereplace always --molname Mol_ID --mode both
--datafieldsmap
"PUBCHEM_EXT_DATASOURCE_REGID,Mol_ID;
PUBCHEM_SUBSTANCE_SYNONYM,Name,CompoundName"
--datafieldURL "PUBCHEM_EXT_DATASOURCE_URL,
http://www.yourdomain.org/GetCmpd.pl,Reg\_ID,Mol\_ID"
--datafieldscommon
"PUBCHEM_EXT_SUBSTANCE_URL,domain.org,
PUBCHEM_PUBLICATION_DATE,YYY-MM-DD,
PUBCHEM_DEPOSITOR_RECORD_DATE,YYYY-MM-DD"
-r CmpdDataForPubChem -o Sample1.sdf
```

## AUTHOR

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## SEE ALSO

[InfoSDFfiles.pl](#), [JoinSDFfiles.pl](#), [MergeTextFilesWithSD.pl](#), [SplitSDFfiles.pl](#), [SDFfilesToHTML.pl](#)

## COPYRIGHT

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