



Concatenation of chemical files

User Manual

Version 1.0

for program version 1.0 (or higher)

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1. General Information about MN.JOIN

MN.JOIN concatenates structure files to one single file.

The program MN.JOIN

- reads structure files saved in MDL MOL or SD file format
- processes datasets with 99.9% conversion rate
- handles datasets of hundreds of thousands of chemical structures
- supports the SD file format for saving the output files

2. Installation

2.1. Requirements

MN.JOIN is available for common UNIX platforms (x86 Linux, Sun Solaris, SGI IRIX, DEC AlphaStation). It is also available for Microsoft Windows NT4/2000/XP.

The program runs in a batch mode.

2.2. Installation Steps for UNIX Operating Systems (IRIX, Solaris, Linux)

- 1.) Create a subdirectory, e.g., mn_join
(for system administrators when installing software locally, e.g. /usr/local/bin/mn_join).
- 2.) Copy the file mn_join_<version>.<os>.gz to the subdirectory mn_join
- 3.) Unpack the distribution by executing the gunzip command:
gunzip mn_join_<version>.<os>.gz
- 4.) Rename the file mn_join_<version>.<os> to mn_join.
Please note: mn_join_<version>.<os> is a binary file.
- 5.) Add the mn_join subdirectory name to the environment variable PATH in your .login or .cshrc files (.profile or .bashrc).

Launch MN.JOIN with the command

```
mn_join -version or /usr/local/bin/mn_join/mn_join -version
```

2.3. Installation Steps for Microsoft Windows Operating Systems (NT4/2000/XP)

Although administrator privileges are not necessary, we recommend logging in as administrator. Double-click on the executable setup program and follow the instructions on the screen.

After successful installation there is no need to reboot your PC.

3. Uninstallation

3.1. Uninstallation Steps for UNIX Operating Systems (IRIX, Solaris, Linux)

Log in as root and delete the file mn_join in your installation directory carefully (default path during installation was /usr/local/bin/mn_join/).

3.2. Uninstallation Steps for Microsoft Windows Operating Systems (NT4/2000/XP)

Log in as administrator, launch the uninstaller and follow the on-screen instructions.

4. Problems and Help!

If you have any difficulties with the installation of MN.JOIN or if any problems occur while running MN.JOIN, please send all your inquiries to the following address:

Molecular Networks GmbH Computerchemie
Nägelsbachstr. 25
91052 Erlangen
Germany,

or contact us by email support@mol-net.de,
or by fax +49-(0)9131 - 81 56 69.

Please mention the program version of MN.JOIN (`mn_join -version`), include your input file and the output file on an MS/DOS diskette (3½”) or send it to us by email. These files will help us to analyze the problem; if your system displays any error messages, please add them to your report.

You can also use the report form at the end of this manual.

5. Release Notes

5.1. Version 1.0

First release of MN.JOIN

6. Getting Started

6.1. UNIX operating systems

Twelve example files `c_<01-12>.sdf` submitted with the distribution contain the structure information of twelve molecules in SD format. Copy these files into the subdirectory "alkanes" of your working directory and type the following command:

```
mn_join -outfile alkanes.sdf alkanes/*
```

MN.JOIN now creates the output files named `alkanes.sdf`.

6.2. Microsoft Windows operating systems

Twelve example files `c_<01-12>.sdf` submitted with the distribution contain the structure information of twelve molecules in SD format. Copy these files into the subdirectory "alkanes" of your working directory and open a DOS shell. Change the working directory to the directory where you installed `mn_join` by using the `cd` command then type the following command:

```
mn_join -outfile alkanes.sdf alkanes/*
```

MN.JOIN now creates the output file named `alkanes.sdf`.

If you have no permission writing to the directory in which the program was installed, set the **-directory** option for specifying another directory:

```
UNIX: mn_join -directory /tmp -outfile alkanes.sdf alkanes/*
```

```
Windows: mn_join -directory C:/temp -outfile alkanes.sdf  
alkanes/*
```

7. Program Use

7.1. Synopsis

The general synopsis for using MN.JOIN is:

```
mn_join [ -option(s) ] [ infile ]
```

An overview of the various options is given in Table 1 and in a more detailed one in the following chapter. `Infile` is the input file name. If no file name is given, the program reads from standard input.

<code>[-directory dirname]</code>	specifies the output directory
<code>[-feedback 0/n]</code>	prints a control message after processing a block of n items
<code>[-format fmt]</code>	specifies the output format name
<code>[-h]</code> or <code>[-help]</code>	shows a brief help message about the usage of the program
<code>[-stat]</code>	writes statistical information about the number of successfully processed records and processing failures
<code>[-outfile filename]</code>	defines the name of the output file
<code>[-version]</code>	prints version and licensing information

Table 1: Overview of all options

7.2. General Program Features

The file type of the input file is automatically recognized. If no input file is specified, or the file name „-“ is used, the program reads from standard input.

If you are running MN.JOIN under a UNIX operating system, there are some more features reading input files (see chapter 8 “Extended Features Only Available for the UNIX Operating Systems” for more details).

The file name of the output file is either explicitly set with the **-outfile** option or automatically derived from the input file and the given output file format (**-format**). The special filename `stdout` can be used to direct output to the standard output channel.

7.3. Supported file formats for input files

The program will automatically detect the supported file format of the input files. Thus, there is no need for a parameter specifying the input format.

The supported file format is listed in the table below.

Full Format Name	Default Input-Extension	Read	Comment
MDL Molfile	mol	Yes	
MDL SDF	sdf	Yes	
SMILES	smi	Yes	

Table 2: Overview of the supported input file formats

7.4. Program Features in More Detail

-format <abbreviation of the output format>

The parameter **format** is specified for selecting the output format.

The supported file formats are listed in the table below.

Full Format Name	Default Output-Extension	Write	Comment
MDL SDF	mdl	Yes	
SMILES	smi	Yes	

Table 3: Overview of the supported output file formats

Please use the abbreviation of the format names for specifying your desired file format using the **-format** option. If no output file is specified, the output has the same name (but with an updated suffix) and is written in the same directory as the input file. The extension of the resulting output file is sometimes different to the given abbreviation (see the previous table). If the output file is specified explicitly with the **-outfile** parameter, this file name including the chosen suffix, will be used.

Default value:

Parameter without a default value

Example:

Generating a MDL SD-file:

```
mn_join -format sdf -outfile alkanes.sdf /examples/c_*.sdf
```

Remarks:

If this option is not used, an attempt is made to guess the output file format from its suffix by the given **-outfile** parameter.

-outfile <filename.extension>

The parameter **outfile** defines the name of the output file. MN.JOIN automatically recognizes the desired output format, thus in most cases it is not necessary to specify the output format. If you are using MN.JOIN on a UNIX operating system the output file name can also be an anonymous ftp URL.

Default value:

Parameter without a default value

Example:

Generating a MDL SD-file:

```
mn_join -outfile alkanes.sdf ./examples/c_*.sdf
```

-directory <dirname>

This parameter sets the target directory. If the directory does not yet exist, it will be created.

Default value:

The directory of the output files is the same as of the corresponding input files, or the current directory, if the input file names do not contain directory information.

Example:

Generating a MDL SD-file saved in a given directory:

```
UNIX: mn_join -outfile alkanes.sdf -directory /tmp/alkanes  
./examples/c_*.sdf
```

```
Windows: mn_join -outfile alkanes.sdf -directory C:/Temp/alkanes  
./examples/c_*.sdf
```

-feedback 0/n

If the parameter **feedback** is set to a value larger than zero, a control message is printed after processing a block of n structures. The current record number and the object name are printed on the standard error channel. Only structures which are actually written out are counted.

Default value:

It is not active by default.

Example:

Generating a MDL SD-file printing dots for every fifth records:

```
mn_join -outfile alkanes.sdf -feedback 5 ./examples/c_*.sdf
```

-stat

If this flag is set, statistical information about the number of successfully processed records and conversion failures is written to the standard error channel.

Default value:

This flag is deactivated by default.

Example:

Generating a MDL SD-file showing the statistical information of the conversion:

```
mn_join -outfile alkanes.sdf -stat ./examples/c_*.sdf
```

Output:

```
Convert file alkanes1_12.sdf
Successfully read 12 records, failed 0
Successfully wrote 12 records, failed 0.
```

-version

If this flag is set, the version and licensing information is printed.

Default value:

This flag is deactivated by default.

Example:

Showing the program version:

```
mn_join -version
```

-h or -help

If this flag is set, a brief help message about the usage of the program is shown.

Default value:

This flag is deactivated by default.

Example:

Show the help message:

```
mn_join -h or mn_join -help
```

8. Extended Features Only Available for the UNIX Operating Systems

Input files can be processed in compressed or gzip-ed form without prior unpacking. The input file name arguments may each be a local file, an URL (http, ftp, gopher, file) or an email message file containing the structure data in the main body or as one or more attachments. URL retrieval and compression can be combined.

9. Frequently Asked Questions (FAQ)

10. Error Messages

MN.JOIN does not process the single input structure although a valid SMILES string is given

Running MN.JOIN under Windows the very last line of the input structure must be empty.

11. Known Problems and Limitations

12. Technical Support

The MN.JOIN Web Site

If you have problems while running MN.JOIN please have a look at the Support- and FAQ web site of MN.JOIN. The pages are available at <http://www.mol-net.de>

Reporting Problems

If your problem is not listed in these web pages please report it to the MN.JOIN team at Molecular Networks. Please make sure to provide us with all important data for replicating your problem on our machines. Therefore please use the report form on the next page.

Updates

If you have licensed the program MN.JOIN with maintenance you will automatically receive updates every time a new release is launched.

Contact Information

Distribution and Maintenance for MN.JOIN is handled by Molecular Networks Computerchemie, Erlangen, Germany.

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Nägelsbachstraße 25
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Tel. +49 9131/815668

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13.Report Form

In case of problems occurring during installation or running MN.JOIN, please complete the following form and send it or fax it to

Molecular Networks GmbH Computerchemie

Nägelsbachstraße 25

91052 Erlangen

Germany

FAX: +49-(0)9131-815669

User:

MN.JOIN program and version number (`mn_join -version`):

Command line to run MN.JOIN:

Error and warning messages by MN.JOIN:

System messages:

Short description:

Please include the input file and output file generated by MN.JOIN on a 3½" diskette written in MS/DOS format or send an e-mail to support@mol-net.de attaching these files. These files will help us to analyze your problems. All data will be treated confidentially.

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