```
#=========================================================================
# ------------------------
# | CVS File Information |
# ------------------------
#
# $RCSfile: nem_join.inp,v $
#
# $Author: rwstotz $
#
# $Date: 1998/05/19 14:09:28 $
#
# $Revision: 1.4 $
#
# $Name:  $
#=========================================================================

###########################################################################
###
# GENERAL NOTES
#
# 1) Any line beginning with a "#" is considered a comment and will be
# ignored by the file parser.
#
# 2) The order of the lines IS NOT significant.
#
# 3) Any lines that are optional are marked as such in this file. Unless
# otherwise noted a line is required to exist in any input file.
#
# 4) The default file name expected by nem_join is "nem_join.inp". This
# can be overridden on the command line (see the nem_join.man file for
# more on this).
#
# 5) The case of words IS NOT significant, e.g., "file" IS equivalent to
# "FILE" or "File", etc.
#
# 6) Blank lines are ignored.
#
###########################################################################
###

#+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++
+++
# Input FEM file = <filename>
#
# This line contains the name of the original input ExodusII file which was
# spread over the parallel disks.
#---------------------------------------------------------------------------
---
Input FEM file= ps.gen

#+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++
```

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+++
# Scaler Results FEM file = <filename>
#
# This line is OPTIONAL.
#
# This line contains the name of the ExodusII file to which is the results
# will be written. This file is created by nem_join. If no name is given,
# then a name will be generated from the Input FEM File name by adding
# a “-out.e” to the Input FEM file base name.
#-------------------------------------------------------------------------
---
Scalar Results FEM file= ps-out.e

#+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++
+++
# Use Scalar Mesh File = <yes/no>
#
# This line is OPTIONAL.
#
# If a scalar mesh file (presumably “Input FEM file”) for this problem is
# available, then a great deal of time can be saved by using ex_copy
# to generate the basis for the results file. If a file is not available,
# then nem_join will create one from the information in the spread files.
# The default for this option is “no”.
#-------------------------------------------------------------------------
---
Use Scalar Mesh File= yes

#+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++
+++
# Parallel Results file base name = <base filename>
#
# This line contains the base name of the parallel ExodusII files that
# contain the results. The base name is the parallel filename without
# the trailing .<# proc>.<file #> on it. This file must contain the
# Nemesis global information.
#-------------------------------------------------------------------------
---
Parallel Results file base name= ps.e

#+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++
+++
# Number of Processors = <integer>
#
# This is the number of Processors that the parallel files were written
# for. It should be the same as the number of parallel files.
#-------------------------------------------------------------------------
---
Number of Processors= 4

#+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++
```

```
+++
# Debug = <integer>
#
# This is an OPTIONAL line and if omitted defaults to the value of 0. Valid
# values are 0 <= value <= 10.
#
# A value of 1 or 2 essentially causes nem_spread to output more information
# about where it is and what it's doing. As the value is increased more
# and more information about the operations nem_spread is performing and
# the results of those operations is output to the screen. Values above 2
# are probably only useful for small example problems and those users
# familiar with the specifics of how nem_spread works.
#-----------------------------------------------------------------------
---
Debug= 4

#+++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++
+++
# Parallel Disk Info = <options>
#
# This line gives all of the information about the parallel file system
# being used. There are a number of options that can be used with it,
# although for most cases only a couple will be needed. The options are:
#
#number=<integer> - this is the number of parallel disks that the
#                        results files are spread over. This number must
#                        be specified, and must be first in the options
#                        list.
#list={list}      - OPTIONAL, If the disks are not sequential, then a
#                      list of disk numbers can be given. This list should
#                       be enclosed in brackets "{}", and the disk numbers
#                        can be seperated by any of the following comma,
#                        blank space, tab, or semicolon.
#offset=<integer> - OPTIONAL, This is the offset from zero that the
#                     disk numbers begin with. If no number is specified,
#                        this defaults to 1. This option is ignored if
#                        "list" is specified.
#zeros            - OPTIONAL, This specifies that leading zeros are
#                        used in the parallel file naming convention. For
#                        example, on the Paragon, the file name for the
#                        first pfs disk is "/pfs/tmp/io_01/". If this is
#                       specified, then the default is not to have leading
#                        zeros in the path name, such as on the teraflop
#                        machine "/pfs/tmp_1/".
#stage_on         - OPTIONAL, This turns on staged reads. The default
#                        is not to stage the reads.
#
#-----------------------------------------------------------------------
---
Parallel Disk Info= number=4, list={1,2,10,12}, offset=1, zeros, stage_on
```

```
#++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++
+++
# Parallel file location = <options>
#
# This line gives all of the information about where the parallel files are
# located. There are only two options for this line, and both must be
# specified. The options are:
#root=<root directory name>
#  This line is used to specify what the name of the root directory is
#  on the target machine. This can be any valid root directory
#  name. For example, if one is running on an SGI workstation and
#  using the “tflop” numbering scheme then you could use something
#  similar to “/usr/tmp/pio_” in this field so that files would be
#  written to root directories named:
#/usr/tmp/pio_1
#/usr/tmp/pio_2
#.
#.
#.
#/usr/tmp/pio_<Parallel Disk Info, number>
#
#subdir=<subdirectory name>
#  This line specifies the name of the subdirectory, under the root
#  directory, where files are to be written. This is tacked onto
#  the end of the “root” after an appropriate integer is added to
#  “root”. Continuing with the example given for “root”, if “subdir”
#  had a value of “run1/input” files would be written to directories
#  named:
#/usr/tmp/pio_1/run1/input/
#/usr/tmp/pio_1/run1/input/
#.
#.
#.
#/usr/tmp/pio_<Parallel Disk Info, number>/run1/input/
#
#-----------------------------------------------------------------------
---
Parallel file location= root=/pfs/tmp_, subdir=glh/run1
```