

Pencil Code: Quick Start guide

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May 19, 2021

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1 Required software

1.1 LINUX

A FORTRAN and a C compiler are needed to compile the code. Both compilers should belong to the same distribution package and version (e.g. GNU GCC or Intel). For HDF5 and MPI support, you need to install the package ‘libhdf5-openmpi-dev’ that automatically pulls in the GNU compilers and OpenMPI. On a recent ubuntu system this is done with:

```
sudo apt install libhdf5-openmpi-dev
```

1.2 MACOS X

For MAC, you first need to install XCODE from the website <http://developer.apple.com/>, where you have to register as a member. Alternatively, an easy to install gfortran binary package can be found at the website <http://gcc.gnu.org/wiki/GFortranBinaries>. Just download the archive and use the installer contained therein. It installs into ‘/usr/local/gfortran’ with a symbolic link in ‘/usr/local/bin/gfortran’. It might be necessary to add the following line to the “.cshrc”-file in your ‘/home’ folder:

```
setenv PATH /usr/local/bin:\$PATH
```

2 Download the Pencil Code

The Pencil Code is an open source code written mainly in FORTRAN and available under GPL. General information can be found at our official homepage:

<http://pencil-code.nordita.org/>.

The latest version of the code can be downloaded with `svn`. In the directory where you want to put the code, type:

```
svn checkout https://github.com/pencil-code/pencil-code/trunk/ pencil-code
```

Alternatively, you may also use `git`:

```
git clone https://github.com/pencil-code/pencil-code.git
```

More details on download options can be found here: <http://pencil-code.nordita.org/download.php>

The downloaded ‘pencil-code’ directory contains several sub-directories:

1. ‘doc’: you may build the latest manual as PDF by issuing the command `make` inside this directory
2. ‘samples’: contains many sample problems
3. ‘config’: has all the configuration files
4. ‘src’: the actual source code
5. ‘bin’ and ‘lib’: supplemental scripts
6. ‘idl’, ‘python’, ‘julia’, etc.: data processing for diverse languages

3 Configure the shell environment

You need to load some environment variables into your shell. Please change to the freshly downloaded directory:

```
cd pencil-code
```

Probably you use a sh-compatible shell (like the LINUX default shell `bash`), there you just type:

```
. sourceme.sh
```

(In a csh-compatible shell, like `tcsh`, use this alternative: `source sourceme.csh`)

4 Your first simulation run

4.1 Create a new run-directory

Now create a run-directory and clone the input and configuration files from one of the samples that fits you best to get started quickly (here from ‘`pencil-code/samples/1d-tests/jeans-x`’):

```
mkdir -p /data/myuser/myrun/src
cd /data/myuser/myrun
cp $PENCIL_HOME/samples/1d-tests/jeans-x/*.in ./
cp $PENCIL_HOME/samples/1d-tests/jeans-x/src/*.local src/
```

Your run should be put outside of your ‘`/home`’ directory, if you expect to generate a lot of data and you have a tight storage quota in your ‘`/home`’.

4.2 Linking to the sources

One command sets up all needed symbolic links to the original Pencil Code directory:

```
pc_setupsrc
```

4.3 Makefile and parameters

Two basic configuration files define a simulation setup: “`src/Makefile.local`” contains a list of modules that are being used, and “`src/cparam.local`” defines the grid size and the number of processors to be used. Take a quick look at these files...

4.3.1 Single-processor

An example “`src/Makefile.local`” using the module for only one processor would look like:

```
MPICOMM=nompicomm
```

For most modules there is also a “no”-variant which switches that functionality off.

In “`src/cparam.local`” the number of processors needs to be set to 1 accordingly:

```
integer, parameter :: ncpus=1,nprocx=1,nprocy=1,nprocz=ncpus/(nprocx*nprocy)
integer, parameter :: nxgrid=128,nygrid=1,nzgrid=128
```

4.3.2 Multi-processor

If you like to use MPI for multi-processor simulations, be sure that you have a MPI library installed and change “src/Makefile.local” to use MPI:

```
MPICOMM=mpicomm
```

Change the `nopus` setting in “src/cparam.local”. Think about how you want to distribute the volume on the processors — usually, you should have 128 grid points in the x-direction to take advantage of the SIMD processor unit. For compilation, you have to use a configuration file that includes the “_MPI” suffix, see below.

4.4 Compiling...

In order to compile the code, you can use a pre-defined configuration file corresponding to your compiler package. E.g. the default compilers are `gfortran` together with `gcc` and the code is being built with default options (not using MPI) by issuing the command:

```
pc_build
```

Alternatively, for multi-processor runs (still using the default GNU-GCC compilers):

```
pc_build -f GNU-GCC_MPI
```

4.4.1 Using a different compiler (optional)

If you prefer to use a different compiler package (e.g. with MPI support or using `ifort`), you may try:

```
pc_build -f Intel
pc_build -f Intel_MPI
pc_build -f Cray
pc_build -f Cray_MPI
```

More pre-defined configurations are found in the directory “pencil-code/config/compilers/*.conf”.

4.4.2 Changing compiler options (optional)

Of course you can also create a configuration file in any subdirectory of ‘pencil-code/config/hosts/'. By default, `pc_build` looks for a config file that is based on your `host-ID`, which you may see with the command:

```
pc_build -i
```

You may add your modified configuration with the filename “host-ID.conf”, where you can change compiler options according to the Pencil Code manual. A good host configuration example, that you may clone and adapt according to your needs, is “pencil-code/config/hosts/IWF/host-andromeda-GNU_Linux-Linux.conf”.

4.5 Running...

The initial conditions are set in “start.in” and the parameters for the main simulation run can be found in “run.in”. In “print.in” you can choose which quantities are written to the file “data/time_series.dat”.

Be sure you have created an empty ‘data’ directory.

```
mkdir data
```

It is now time to run the code:

```
pc_run
```

If everything worked well, your output should contain the line

```
start.x has completed successfully
```

after initializing everything successfully. It would then start running, printing in the console the quantities specified in “print.in”, for instance,

```
---it-----t-----dt-----rhom-----urms-----uxpt-----uypt-----uzpt-----
      0      0.00 4.9E-03 1.000E+00  1.414E+00  2.00E+00  0.00E+00  0.00E+00
     10      0.05 4.9E-03 1.000E+00  1.401E+00  1.98E+00  0.00E+00  0.00E+00
     20      0.10 4.9E-03 1.000E+00  1.361E+00  1.88E+00  0.00E+00  0.00E+00
    .....

```

ending with

```
Simulation finished after      xxxx  time-steps
.....
Wall clock time/timestep/meshpoint [microsec] = ...
```

An empty file called “COMPLETED” will appear in your run directory once the run is finished.

If you work with one of the samples or an identical setup in a new working directory, you can verify the correctness of the results by checking against reference data, delivered with each sample:

```
diff reference.out data/time_series.dat
```

Welcome to the world of Pencil Code!

4.6 Troubleshooting...

If compiling fails, please try the following — with or without the optional `_MPI` for MPI runs:

```
pc_build --cleanall
pc_build -f GNU-GCC_MPI
```

If some step still fails, you may report to our mailing list: <http://pencil-code.nordita.org/contact.php>. In your report, please state the exact point in this quick start guide that fails for you (including the full error message) — and be sure you precisely followed all non-optional instructions from the beginning.

In addition to that, please report your operating system (if not LINUX-based) and the shell you use (if not bash). Also please give the full output of these commands:

```
bash
cd path/to/your/pencil-code/
source sourceme.sh
echo $PENCIL_HOME
ls -la $PENCIL_HOME/bin
cd samples/1d-tests/jeans-x/
gcc --version
gfortran --version
pc_build --cleanall
```

```
pc_build -d
```

If you plan to use MPI, please also provide the full output of:

```
mpicc --version
mpif90 --version
mpiexec --version
```

5 Data post-processing

5.1 IDL visualization (optional, recommended)

5.1.1 GUI-based visualization (recommended for quick inspection)

The most simple approach to visualize a Cartesian grid setup is to run the Pencil Code GUI and to select the files and physical quantities you want to see:

```
IDL> .r pc_gui
```

If you miss some physical quantities, you might want to extend the two IDL routines `pc_get_quantity` and `pc_check_quantities`. Anything implemented there will be available in the GUI, too.

5.1.2 Command-line based processing of “big data”

Please check the documentation inside these files:

“pencil-code/idl/read/pc_read_var_raw.pro”	efficient reading of raw data
“pencil-code/idl/read/pc_read_subvol_raw.pro”	reading of sub-volumes
“pencil-code/idl/read/pc_read_slice_raw.pro”	reading of any 2D slice from 3D snapshots
“pencil-code/idl/pc_get_quantity.pro”	compute physical quantities out of raw data
“pencil-code/idl/pc_check_quantities.pro”	dependency checking of physical quantities

in order to read data efficiently and compute quantities in physical units.

5.1.3 Command-line based data analysis (may be inefficient)

Several IDL-procedures have been written (see in ‘pencil-code/idl’) to facilitate inspecting the data that can be found in raw format in ‘jeans-x/data’. For example, let us inspect the time series data

```
IDL> pc_read_ts, obj=ts
```

The structure `ts` contains several variables that can be inspected by

```
IDL> help, ts, /structure
```

```
** Structure <911fa8>, 4 tags, length=320, data length=320, refs=1:
  IT          LONG      Array[20]
  T           FLOAT     Array[20]
  UMAX        FLOAT     Array[20]
  RHOMAX      FLOAT     Array[20]
```

The diagnostic `UMAX`, the maximal velocity, is available since it was set in “jeans-x/print.in”. Please check the manual for more information about the input files.

We plot now the evolution of UMAX after the initial perturbation that is defined in “start.in”:

```
IDL> plot, ts.t, alog(ts.umax)
```

The complete state of the simulation is saved as snapshot files in “jeans-x/data/proc0/VAR*” every dsnap time units, as defined in “jeans-x/run.in”. These snapshots, for example “VAR5”, can be loaded with:

```
IDL> pc_read_var, obj=ff, varfile="VAR5", /trimall
```

Similarly tag_names will provide us with the available variables:

```
IDL> print, tag_names(ff)
T X Y Z DX DY DZ UU LNRHO POTSELF
```

The logarithm of the density can be inspected by using a GUI:

```
IDL> cslice, ff.lnrho
```

Of course, for scripting one might use any quantity from the ff structure, like calculating the average density:

```
IDL> print, mean(exp(ff.lnrho))
```

5.2 Python visualization (optional)

Be advised that the PYTHON support is still not complete or as feature-rich as for IDL. Furthermore, we move to PYTHON3 in 2020, and not all the routines have been updated yet.

5.2.1 Python module requirements

In this example we use the modules: numpy and matplotlib. A complete list of required module is included in “pencil-code/python/pencil/README”.

5.2.2 Using the ‘pencil’ module

After sourcing the “sourceme.sh” script (see above), you should be able to import the pencil module:

```
import pencil as pc
```

Some useful functions:

“pc.read.ts”	read “time_series.dat” file. Parameters are added as members of the class
“pc.read.slices”	read 2D slice files and return two arrays: (nslices,vsize,hsize) and (time)
“pc.visu.animate_interactive”	assemble a 2D animation from a 3D array

Some examples of postprocessing with PYTHON can be found in the PENCIL wiki:

<https://github.com/pencil-code/pencil-code/wiki/PythonForPencil>.