

Running PERIGEE with the Greenshields-Weller Benchmark

0. When getting a brand new machine, please go through steps 0. ~ 0.7.

We assume your system is Linux, such as Ubuntu. If you are a OS X user, there are some different steps which will not be introduced here.

Learn about basic terminal commands and vi commands.

In this guide, **filename** will be noted in bold. Operations in Terminal will be shown as follows:

```
$ (command1)
```

```
$ (command2)
```

We also assume you have a handy editor such as VsCode.

0.1. Install external libraries following [this](#). And here are some tips :

MPICH:

If you have a hard life with error info about “Fortran compiler”, and gfortran installation doesn’t work, try to download another version of mpich:

```
$ wget https://www.mpich.org/static/downloads/3.4.2/mpich-3.4.2.tar.gz
```

then add a new configuration option:

```
$ ./configure --prefix=$HOME/lib/mpich-3.4.2 FFLAGS=-fallow-argument-mismatch 2>&1 |  
tee c.txt
```

VTk:

We’d better install the OpenGL(Glut) library before installing VTK.

If you install VTK on a cluster such as Taiyi, do:

```
$ cmake $HOME/lib/VTK-7.1.1-src -DCMAKE_BUILD_TYPE:String=Release  
-DCMAKE_INSTALL_PREFIX:PATH=$HOME/lib/VTK-7.1.1-OPT -DVTK_Group_StandAlone:BOOL=OFF  
-DVTK_Group_Rendering:BOOL=OFF -DModule_vtkCommonMath:BOOL=ON  
-DModule_vtkCommonMisc:BOOL=ON -DModule_vtkCommonCore:BOOL=ON  
-DModule_vtkCommonSystem:BOOL=ON -DModule_vtkIOCore:BOOL=ON -DModule_vtkIOLegacy:BOOL=ON  
-DModule_vtkIOXML:BOOL=ON
```

METIS:

Install metis before installing petsc, then you can use the option “--with-metis-dir=” rather than “--download-metis” later.

PETSc:

We prefer another version now:

```
$ wget http://ftp.mcs.anl.gov/pub/petsc/release-snapshots/petsc-3.16.6.tar.gz
```

And an advanced installation configuration:

```
$ ./configure --with-x=0 -with-pic --with-make-np=6 --with-mpi-compilers=0  
--with-mpi-dir=$HOME/lib/mpich-3.4.2/ --with-scalar-type=real --with-precision=double
```

```
--with-chaco=1 --download-chaco --with-hypre=1 --download-hypre --with-spai=1
--download-spai --with-sundials2=1 --download-sundials2 --with-mumps=1 --download-mumps
--with-scalapack=1 --download-scalapack --with-blacs=1 --download-blacs --with-spooles=1
--download-spooles --with-superlu_dist=1 --download-superlu_dist --with-superlu=1
--download-superlu --download-fblaslapack --with-metis-dir=$HOME/lib/metis-5.0.3
--with-ml=1 --download-ml --with-eigen=1 --download-eigen --with-debugging=no
COPTFLAGS="-O3 -march=native -mtune=native" CXXOPTFLAGS="-O3 -march=native -mtune=native"
FOPTFLAGS="-O3 -march=native -mtune=native" --prefix=$HOME/lib/petsc-3.16.6-opt
```

(It's a long command, please confirm your lib version, fit them where are **highlighted**.)

If you want to update your cmake to version 3.20, add an option:

```
..... --download-cmake .....
```

Similarly :

```
..... --download-make .....
```

If you have a hard life with error info about Fortran/mpich-dir/MPI etc. , change the **highlighted options** to:

```
..... --with-mpi-compilers=1 --with-cc=gcc --download-mpich .....
```

(Of course, you installed gcc in advance since you have been a C/C++ programmer.)

For the further learning of petsc, we suggest you doing:

```
$ ./configure --help
```

to have a look, then you can try your individual configuration, dealing with error info by yourself.

SLEPc:

The version of slepc should be suited to your petsc. If your petsc is version 3.16.6:

```
$ wget https://slepc.upv.es/download/distrib/slepc-3.16.3.tar.gz
```

Sometimes the environment variations created by temporary *export* commands cannot be detected, you should write them into **~/.bashrc** file:

```
$ sudo vi ~/.bashrc
```

(Move to the bottom, press 'a', write:

```
export PETSC_DIR=$HOME/lib/petsc-3.16.6-opt
```

```
export SLEPC_DIR=$HOME/lib/slepc-3.16.3-src
```

export **PETSC_ARCH= [your arch]** (If your PETSC_ARCH is required, view [thier website](#), download a users manual to know what is PETSC_ARCH. **Otherwise ignore this line.**)

then press 'esc', input ':wq!', press 'enter' .)

```
$ source ~/.bashrc
```

If the document's name is **slepc-3.16.3-src**, you must add **"-src"** to the end of SLEPC_DIR. If it doesn't work either, write the **variations** into **/etc/environment** without *export* (It's a system-wide profile, take it carefully), then restart the machine.

Gmsh and ParaView:

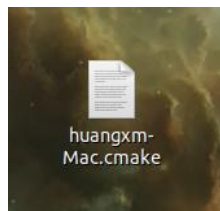
View [Gmsh's website](#) and download a package for installation is not bad. Same for [ParaView](#).

You can call them in Terminal to check your installation on linux(Mac users need alias):

```
$ gmsh
```

```
$ paraview
```

0.2. View [this page](#), download `machine_name.cmake`, rename it appropriately:



Open it with an editor, replace these arguments according to your libraries' path and configuration:

```
15 # In the guide, vtk directory is $HOME/lib/VTK-7.1.1-shared
16 set(VTK_DIR /home/jliu/lib/VTK-7.1.1-shared/lib/cmake/vtk-7.1)
17
18 # Modify the PETSC_DIR variable to point to the location of PETSc.
19 set(PETSC_DIR /home/jliu/lib/petsc-3.11.3)
20
21 # Modify the PETSC_ARCH variable. You can find it in your configuration
22 # output. If you forget it, go to your PETSc home director and open
23 # configure.log. Go the end of the file, and you shall find the value
24 # of PETSC_ARCH
25 set(PETSC_ARCH arch-linux2-c-debug)
26
27 # Modify the METIS_DIR.
28 # Note: If your PETSc has METIS installed, the conf
29 # file will directly load that METIS; otherwise this METIS will
30 # be used for PERIGEE. This means, if you are sure that you have
31 # METIS in PETSc, you do not have to specify the METIS_DIR variable.
32 set(METIS_DIR /home/jliu/lib/metis-5.0.3)
33
34 # Modify the HDF5_ROOT, pointing to your hdf5 library location
35 set(HDF5_ROOT /home/jliu/lib/hdf5-1.8.16)
36
```

```
71 # $PETSC_DIR/$PETSC_ARCH/bin, or the mpich you specified for
72 # PETSc install.
73 set(CMAKE_C_COMPILER /home/jliu/lib/petsc-3.11.3/bin/mpicc)
74 set(CMAKE_CXX_COMPILER /home/jliu/lib/petsc-3.11.3/bin/mpicxx)
75 set(CMAKE_CXX_STANDARD 11)
76 if( ${CMAKE_BUILD_TYPE} MATCHES "Release" )
```

then save it.

DO NOT use “\$HOME” to replace “/home/xxx/” as follows:

```
15 # In the guide, vtk directory is $HOME/lib/VTK-7.1.1-shared
16 set(VTK_DIR $HOME/lib/VTK-7.1.1-shared/lib/cmake/vtk-7.1)
17
18 # Modify the PETSC_DIR variable to point to the location of PETSc.
19 set(PETSC_DIR $HOME/lib/petsc-3.16.6-opt)
20
21 # Modify the PETSC_ARCH variable. You can find it in your configuration
22 # output. If you forget it, go to your PETSc home director and open
23 # configure.log. Go the end of the file, and you shall find the value
24 # of PETSC_ARCH
25 set(PETSC_ARCH .)
26
27 # Modify the METIS_DIR.
28 # Note: If your PETSc has METIS installed, the conf
29 # file will directly load that METIS; otherwise this METIS will
30 # be used for PERIGEE. This means, if you are sure that you have
31 # METIS in PETSc, you do not have to specify the METIS_DIR variable.
32 set(METIS_DIR $HOME/lib/metis-5.0.3)
33
34 # Modify the HDF5_ROOT, pointing to your hdf5 library location
35 set(HDF5_ROOT $HOME/lib/hdf5-1.8.16)
36
```

```
72 # PETSc install.
73 set(CMAKE_C_COMPILER $HOME/lib/petsc-3.16.6-opt/bin/mpicc)
74 set(CMAKE_CXX_COMPILER $HOME/lib/petsc-3.16.6-opt/bin/mpicxx)
75 set(CMAKE_CXX_STANDARD 11)
76 if( ${CMAKE_BUILD_TYPE} MATCHES "Release" )
```

0.3. Open your Terminal, do:

```
$ echo $MACHINE_NAME
```

to check whether there is an environment variation called MACHINE_NAME. If there isn't, think about a good name of your machine, and write it into ~/.bashrc :

```
$ sudo vi ~/.bashrc
```

(write)

```
export MACHINE_NAME=HXMmac
```

 (for me)

(save and exit) (Do you remember how to use vi to do that?)

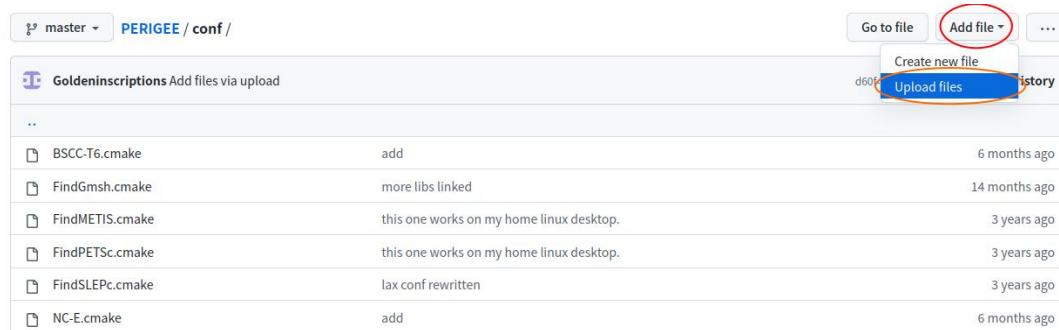
```
$ source ~/.bashrc
```

View [this page](#), download **system_lib_loading.cmake**, open it with an editor, move to the last “elseif” branch, add a similar branch under it:

```
51 elseif( $ENV{MACHINE_NAME} MATCHES "NC-E")
52 | message(STATUS "NC-E ningxia")
53 | include(${CMAKE_CURRENT_LIST_DIR}/NC-E.cmake)
54 elseif( $ENV{MACHINE_NAME} MATCHES "HXMLinux")
55 | message(STATUS "Huangxm's Linux")
56 | include(${CMAKE_CURRENT_LIST_DIR}/huangxm-Linux.cmake)
57 elseif( $ENV{MACHINE_NAME} MATCHES "HXMTaiyi")
58 | message(STATUS "Huangxm's Taiyi")
59 | include(${CMAKE_CURRENT_LIST_DIR}/huangxm-Taiyi.cmake)
60
61 elseif( $ENV{MACHINE_NAME} MATCHES "HXMmac") # Your MACHINE_NAME
62 | message(STATUS "Huangxm's Mac")
63 | include(${CMAKE_CURRENT_LIST_DIR}/huangxm-Mac.cmake) # Your CmakeFile's name
64
65 else($ENV{MACHINE_NAME} MATCHES "poincare")
66 | message(STATUS "The system cannot be identified.")
67 endif( $ENV{MACHINE_NAME} MATCHES "poincare")
68
69 # End of the file
```

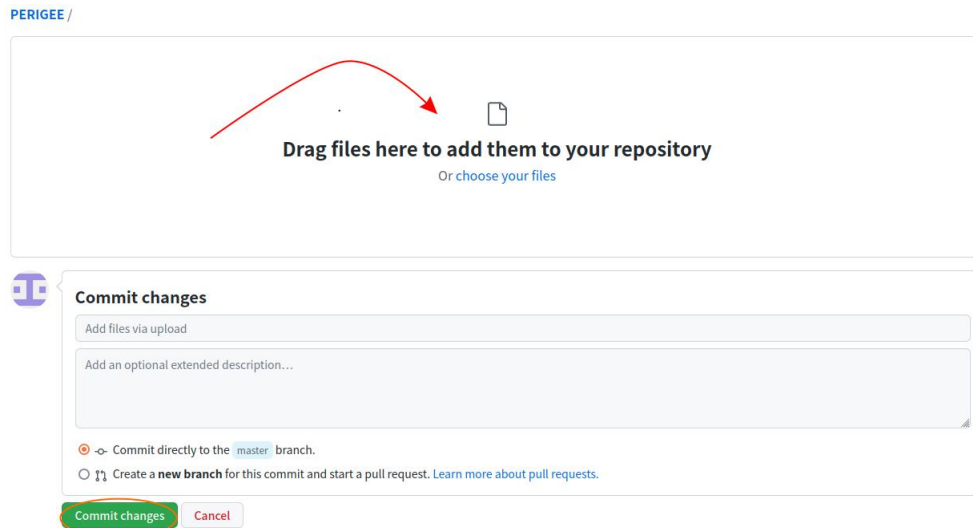
“STATUS” in the middle line will be shown while running PERIGEE, name it as you like, then save the file.

0.4. View [this page](#) again, upload your cmakefile and the edited system_lib_loading.cmake:

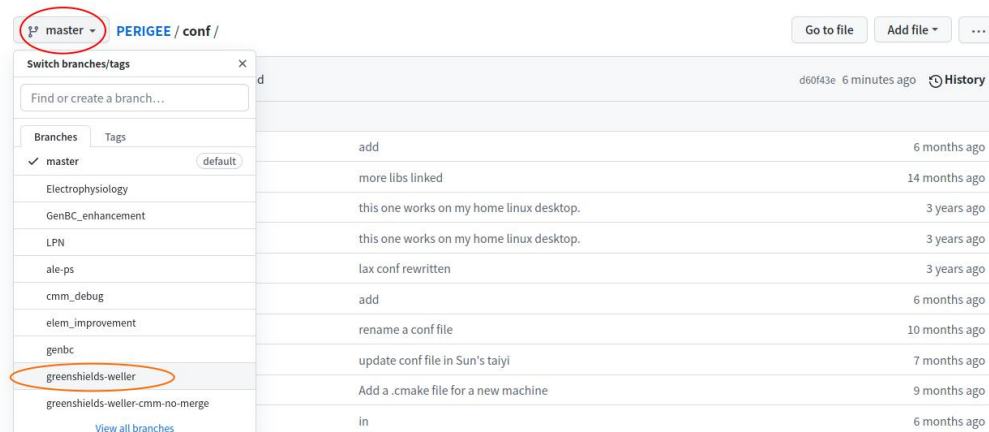


The screenshot shows a web-based file management interface. At the top, there's a header with 'master' and 'PERIGEE / conf /'. On the right, there are buttons for 'Go to file', 'Add file', and a three-dot menu. Below the header, there's a section titled 'Goldeninscriptions Add files via upload'. To the right of this section, there's a dropdown menu with 'Create new file' and 'Upload files' (which is highlighted with a red circle). Below this, there's a table listing files:

File Name	Action	Time
BSCC-T6.cmake	add	6 months ago
FindGmsh.cmake	more libs linked	14 months ago
FindMETIS.cmake	this one works on my home linux desktop.	3 years ago
FindPETSc.cmake	this one works on my home linux desktop.	3 years ago
FindSLEPc.cmake	lax conf rewritten	3 years ago
NC-E.cmake	add	6 months ago



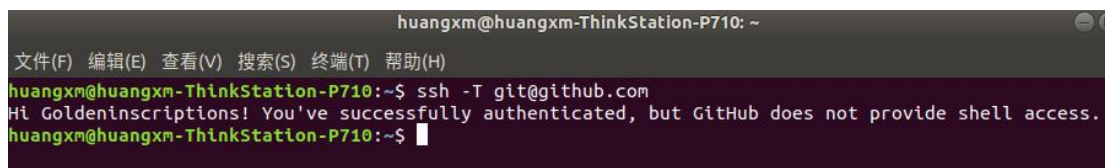
As we want to test the Greenshields-Weller benchmark this time, we shift to the branch “greenshields-weller”, and upload two files once again.



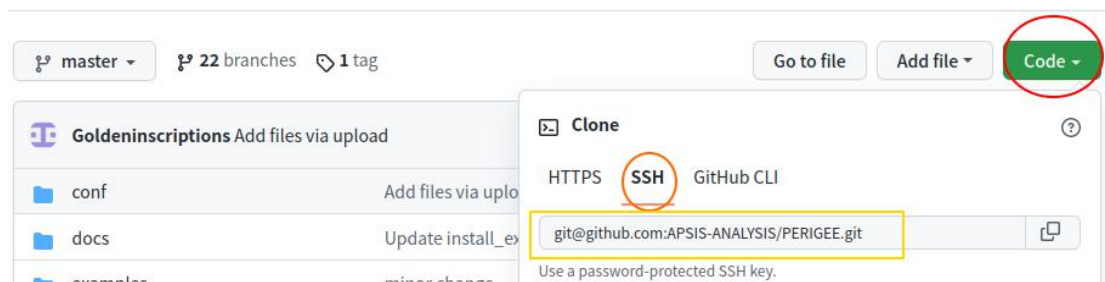
0.5. Let’s download PERIGEE source codes to you machine, we suggest using git:

```
$ sudo apt install git
```

After installation, [set a ssh-key](#) to your github account, and test it:



View the [page](#) of PERIGEE, copy this line:



Select a place to download our source codes, for me:

```
$ cd $HOME
$ mkdir codes
$ cd codes
$ git clone git@github.com:APSYS-ANALYSIS/PERIGEE.git
```

As we want to test the Greenshields-Weller benchmark, we **have to** shift to the branch “greenshields-weller”:

```
$ cd PERIGEE
$ git branch
$ git checkout greenshields-weller
$ git branch
```

0.6. There is one more environment variation which should be set in your machine:

```
$ sudo vi ~/.bashrc
(write)
export LD_LIBRARY_PATH=$HOME/VTK-7.1.1-shared/lib:$LD_LIBRARY_PATH
(save and exit)
$ source ~/.bashrc
```

0.7. Now check your preparation:

Compiler: cmake

Libs: mpich, VTK, hdf5, metis, PETSc, SLEPc, Gmsh, ParaView

Environment variations: PATH, LD_LIBRARY_PATH, MACHINE_NAME

Files uploaded: **your cmakefile, system_lib_loading.cmake**

Source codes downloaded: PERIGEE

Furthermore, some shell scripts are prepared to simplify following steps.

To run a shell script in Terminal:

```
$ sh [script_name.sh]
```

On a cluster such as Taiyi, some operations **must** be done with scripts.

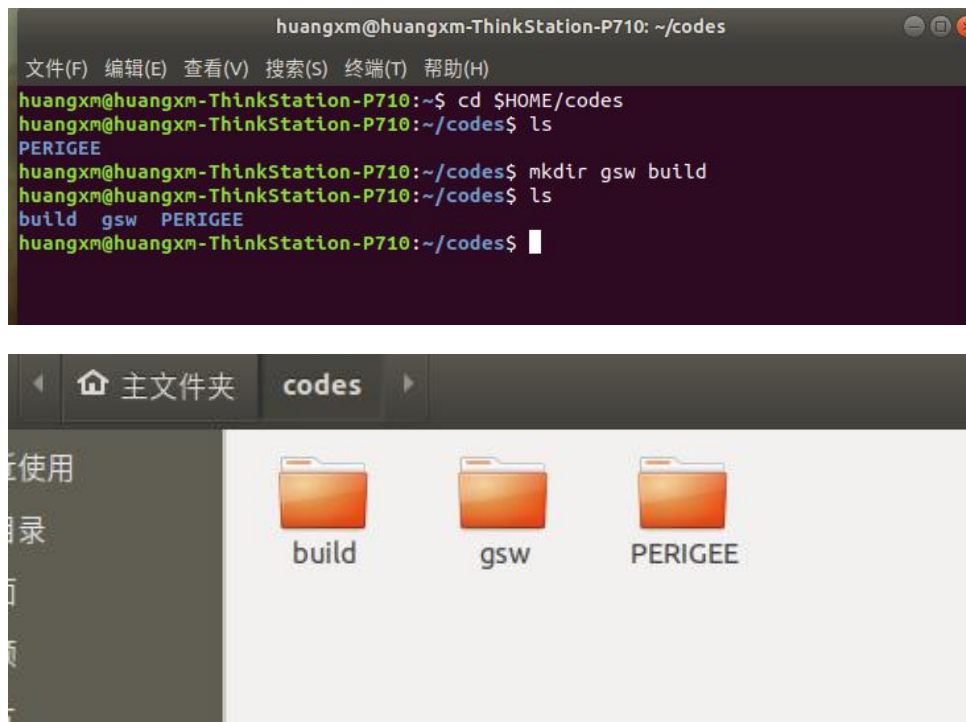
1. Our tutorial starts here formally:

Open a new Terminal, go to the directory you downloaded PERIGEE in:

```
$ cd $HOME/codes      (for me)
$ ls
$ mkdir gsw build
$ ls
```

We built a directory called “build” where we will compile PERIGEE to get an executable program, and another directory called “gsw” where we will put our project files and data.

You can also see them directly on the window:



Do:

```
$ cd PERIGEE/input/gmsh
$ ls
```

You can see many .geo files, they restore geometric information and mesh information of our models. What we need is **fsi_cylinder_wBL.geo**, let's copy it to “gsw”:

```
$ cd ../../../../gsw
$ cp ../PERIGEE/input/gmsh/fsi_cylinder_wBL.geo . (Here is a dot at the end)
$ ls
```

Open it with gmsh to have a look:

```
$ gmsh fsi_cylinder_wBL.geo
```

And open it with editor:

```
$ xdg-open fsi_cylinder_wBL.geo
```

Try to reset some digital arguments and save it, then observe the difference with gmsh.

Here are some **recommended** trying:

```
打开(O)  [Icon]
Point(1) = {0, 0, 0};
Point(2) = {1, 0, 0};
Point(3) = {0, 1, 0};
Point(4) = {-1, 0, 0};
Point(5) = {0, -1, 0};
Point(6) = {1.2, 0, 0};
Point(7) = {0, 1.2, 0};
Point(8) = {-1.2, 0, 0};
Point(9) = {0, -1.2, 0};

Circle(1) = {2, 1, 3};
Circle(2) = {3, 1, 4};
Circle(3) = {4, 1, 5};
Circle(4) = {5, 1, 2};
Circle(5) = {6, 1, 7};
Circle(6) = {7, 1, 8};
Circle(7) = {8, 1, 9};
Circle(8) = {9, 1, 6};

Line(9) = {7, 3};
Line(10) = {6, 2};
Line(11) = {9, 5};
Line(12) = {8, 4};

h_bl = 0.8;

Point(10) = {h_bl, 0, 0, 1.0};
Point(11) = {0, h_bl, 0, 1.0};
Point(12) = {-h_bl, 0, 0, 1.0};
Point(13) = {0, -h_bl, 0, 1.0};

Line Loop(9) = {16, 13, 14, 15};
Plane Surface(9) = {9};

Transfinite Surface {1,2,3,4,5,6,7,8};

Extrude {0, 0, 10} {
  Surface{1,2,3,4,5,6,7,8,9}; Layers 150;
}

Physical Surface("ftop") = {218, 152, 130, 196, 174};
Physical Surface("fbot") = {9, 5, 6, 7, 8};
```

More importantly, these **three parameters** determine the mesh size. You can try to set a larger ---but not too large---number, **otherwise the memory cost and the time cost would exponentially increase.**

For beginners, we recommend 4, 4, 20.

```
Transfinite Line {9,10,11,12} = 4 Using Progression 1;
Transfinite Line {-17,-18,-19,-20} = 4 Using Progression 1.05;
Transfinite Line {1,2,3,4,5,6,7,8,13,14,15,16} = 20 Using Progression 1;
```

Now (in the directory of "gsw") do:

```
$ gmsh fsi_cylinder_wBL.geo -3 -format msh2
$ ls
```

which means to convert the .geo file to a .msh file with 3-D modeling.

Our PERIGEE will use **fsi_cylinder_wBL.msh** later. You can have a look at the mesh by:

```
$ gmsh fsi_cylinder_wBL.msh
```


2. Let's compile the source codes of PERIGEE:

```
$ cd $HOME/codes/build
$ cmake ../PERIGEE/examples/tet4_fsi
```

You must see the identifications info as follows:

```
-- CMAKE_RANLIB: /usr/bin/ranlib
-- Huangxm's Linux
-- Found PETSc: /home/huangxm/lib/petsc-3.16.6-opt/.lib/libpetsc.so
-- Found HDF5: /home/huangxm/lib/hdf5-1.8.16/lib/libhdf5.so;/usr/lib64/libz.so
(found version "1.8.16")
-- Use METIS in PETSc: /home/huangxm/lib/petsc-3.16.6-opt/.lib/libmetis.so
-- External Libraries: vtkChartsCorevtkCommonColorvtkCommonCorevtkCommonDataModel
vtkFiltersGeneralvtkCommonComputationalGeometryvtkFiltersCompositingvtkRendering
Context2DvtkRenderingCorevtkFiltersGeometryvtkFiltersSourcesvtkIOXMLParsevtkExp
atvtkDomainsChemistryOpenGL2vtkRenderingOpenGL2vtkMathsvtkFiltersGenericvt
kFiltersHybridvtkImagingSourcesvtkFiltersHypersurfacevtkFiltersPointsvtkFilter
sProgrammablevtkFiltersSMPltkFiltersStatisticsvtkInteractionStylevtkInteraction
WidgetsvtkImagingColorvtkRenderingAnnotatevtkIOIcvtkNetCDFvtkNetCDF_cxxvtkIOEx
portvtkRenderingGL2PSOpenGL2vtkIONetCDFvtkIOPLVtkIOParallelvtkjsoncppvtkIOPar
allelXMLvtkIOSQLvtksysImageStenciltkInteractionImagevtkRenderingContextOpenGL
2vtkRenderingContextOpenGL2/home/huangxm/lib/petsc-3.16.6-opt/.lib/libpetsc.so
/home/huangxm/lib/petsc-3.16.6-opt/.lib/libmetis.so/home/huangxm/lib/petsc-3.16.6-opt/.lib/libhdf5.so
/usr/lib64/libz.so/usr/lib/x86_64-linux-gnu/libdl.so/usr/lib/x86_64-linux-gnu/libc.so
----- Compiler setup -----
-- CMAKE_CXX_COMPILER: /home/huangxm/lib/mpich-3.3/bin/mpicxx
-- CMAKE_C_COMPILER: /home/huangxm/lib/mpich-3.3/bin/mpicc
-- CMAKE_C_FLAGS:
```

Otherwise, your libs may not be identified successfully, you should select another name as your MACHINE_NAME, reset it in ~/.bashrc and **system_lib_loading.cmake**. Try “cmake” again until your libs are identified.

For the Greenshields-Weller benchmark, we compiled **tet4_fsi**, there are other examples in the directory: /PERIGEE/examples .

Then, do:

```
$ make -j 6
$ ls
```

to get executable programs.

3. Now we do the preprocessing, let's move to “gsw” then all data will be created there:

```
$ cd ../gsw
$ ../build/gmshIO -gmsh_file fsi_cylinder_wBL.msh
$ ls
```

gmshIO is the first executable program we run, which converts the .msh file to some .vtu/.vtp files. It will take a few minutes.

“nElem” means the number of elements. This case is with mesh arguments: 4, 4, 20.

```
names: fluid      solid
nElem: 753300     205200
etype: 4  4
nLocBas: 4  4
=== Total node number : 166704
=== Total element number : 1008360
=== Gmsh FileIO::write vtp for ftop.d
```

4. We will deal with these .vtu/.vtp files with `preprocess_fsi`:

```
huangxm@huangxm-ThinkStation-P710:~/codes/gsw$ ls
fbot_fluid.vtp  fsi_cylinder_wBL.geo  ftop_fluid.vtp  fwall_solid.vtp  solid.vtu  swall_solid.vtp
fluid.vtu      fsi_cylinder_wBL.msh  fwall_fluid.vtp  sbot_solid.vtp   stop_solid.vtp  whole_vol.vtu
```

Before that, do:

```
$ xdg-open ../PERIGEE/examples/tet4_fsi/preprocess_fsi.cpp
```

You can find that it requires we change the name of files we input:

```
40 // Input files
41 std::string geo_file("./whole_vol.vtu");
42
43 std::string geo_f_file("./lumen_vol.vtu");
44 std::string geo_s_file("./tissue_vol.vtu");
45
46 std::string sur_f_file_wall("./lumen_wall_vol.vtp");
47 std::string sur_f_file_in_base( "./lumen_inlet_vol_" );
48 std::string sur_f_file_out_base("./lumen_outlet_vol_");
49
50 std::string sur_s_file_interior_wall("./tissue_interior_wall_vol.vtp");
51
52 std::string sur_s_file_wall("./tissue_wall_vol.vtp");
53 std::string sur_s_file_in_base( "./tissue_inlet_vol_" );
54 std::string sur_s_file_out_base("./tissue_outlet_vol_");
```

Therefore, we have a shell script `change_names.sh` to do that, and here are the rules:

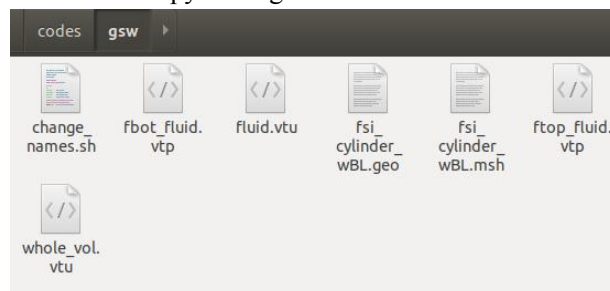
```
# After command 'gmshIO -gmsh_file ...', we got some vtu/vtp files.
# Change their names by referring to '../PERIGEE/examples/tet4_fsi/preprocess_fsi.cpp'.
# 'f' means 'fluid' -----> lumen
# 's' means 'solid' -----> tissue
# 'f_s' -----> interior
# KEEP 'whole_vol.vtu'.

mv fluid.vtu lumen_vol.vtu
mv fwall_fluid.vtp lumen_wall_vol.vtp
mv fbot_fluid.vtp lumen_inlet_vol_000.vtp
mv ftop_fluid.vtp lumen_outlet_vol_000.vtp

mv fwall_solid.vtp tissue_interior_wall_vol.vtp

mv solid.vtu tissue_vol.vtu
mv swall_solid.vtp tissue_wall_vol.vtp
mv sbot_solid.vtp tissue_inlet_vol_000.vtp
mv stop_solid.vtp tissue_outlet_vol_000.vtp
```

You should copy it to “gsw”:



Do:

```
$ sh. change_names.sh
```

```
$ ../build/preprocess_fsi -cpu_size 10
```

It will take a few minutes.

“-cpu_size” means the number of cpu cores you request, if you are not sure about how many cores your have, do:

```
$ cat /proc/cpuinfo
```

5. After preprocessing, we can run the solver **fsi_tet4_3d** directly:

```
$ ../build/fsi_tet4_3d -cpu_size 10
```

or use a run-script.sh:

```
$ sh run-script.sh (recommended)
```

you can check every argument of it by comparing with their comments in .cpp files:

```
$ xdg-open run-script.sh
```

```
$ xdg-open ../PERIGEE/examples/tet4_fsi/fsi_driver.cpp
```

It will print all arguments, and when you see this:

```
====> Start Finite Element Analysis:
Time = 0.000000e+00, dt = 1.000000e-06, index = 0, 12:53:07
--- M updated Init res 2-norm: 5.379476e+03
--- KSP: 3, 2.265395e+01 --- KSP: 4, 8.804061e-09 --- nl_res: 2.265416e+01
--- KSP: 3, 2.940734e-02 --- KSP: 6, 2.165685e-11 --- M updated --- nl_res: 2.940652e-02
--- KSP: 3, 4.324923e-05 --- KSP: 6, 7.299010e-14 --- nl_res: 4.324871e-05
=== NR ite: 3, r_error: 8.039576e-09, a_error: 4.324871e-05
```

The solver is working well, and we shall wait for a long time.

(Waiting...)

After the solving process, you will get some files with prefix “SOL”:

```
huangxm@huangxm-ThinkStation-P710:~/codes/gsw$ ls
apart dot_SOL_velo_900000500 node_mapping_v.h5 SOL_pres_900002000
change_names.sh dot_SOL_velo_900001000 npart.h5 SOL_velo_900000000
dot_SOL_disp_900000000 dot_SOL_velo_900001500 preprocessor_cmd.h5 SOL_velo_900000500
dot_SOL_disp_900000500 dot_SOL_velo_900002000 run-script.sh SOL_velo_900001000
dot_SOL_disp_900001000 epart.h5 SOL_disp_900000000 SOL_velo_900001500
dot_SOL_disp_900001500 fsi_cylinder_wBL.geo SOL_disp_900000500 SOL_velo_900002000
dot_SOL_disp_900002000 fsi_cylinder_wBL.msh SOL_disp_900001000 solver_cmd.h5
dot_SOL_pres_900000000 lumen_inlet_vol_000.vtp SOL_disp_900001500 tissue_inlet_vol_000.vtp
dot_SOL_pres_900000500 lumen_outlet_vol_000.vtp SOL_disp_900002000 tissue_interior_wall_vol.vtp
dot_SOL_pres_900001000 lumen_vol.vtu SOL_pres_900000000 tissue_outlet_vol_000.vtp
dot_SOL_pres_900001500 lumen_wall_vol.vtp SOL_pres_900000500 tissue_vol.vtu
dot_SOL_pres_900002000 material_model.h5 SOL_pres_900001000 tissue_wall_vol.vtp
dot_SOL_velo_900000000 node_mapping_p.h5 SOL_pres_900001500 whole_vol.vtu
```

Their quantity and the suffixes depend on your time/step and recording configurations:

```
打开(O)  run-script.sh
~/codes/gsw
mpirun -np 10 ../build/fsi_tet4_3d -nz_estimate 300 \
-nqp tet 5 -nqp tri 13 \
-init_step 1.0e-6 -fina_time 2.0e-3 \
-nl_refreq 2 -nl_rtol 1.0e-6 -nl_atol 1.0e-15 -nl_dtol 1.0e2 \
-nl_maxits 8 \
-log_view -ttan_freq 100 -sol_rec_freq 500 \
-is_restart NO -restart_index 79500 -restart_time 7.95e-3 \
-restart_step 1.0e-7 \
```

Of course you can scroll up to read the summary to get more informations:

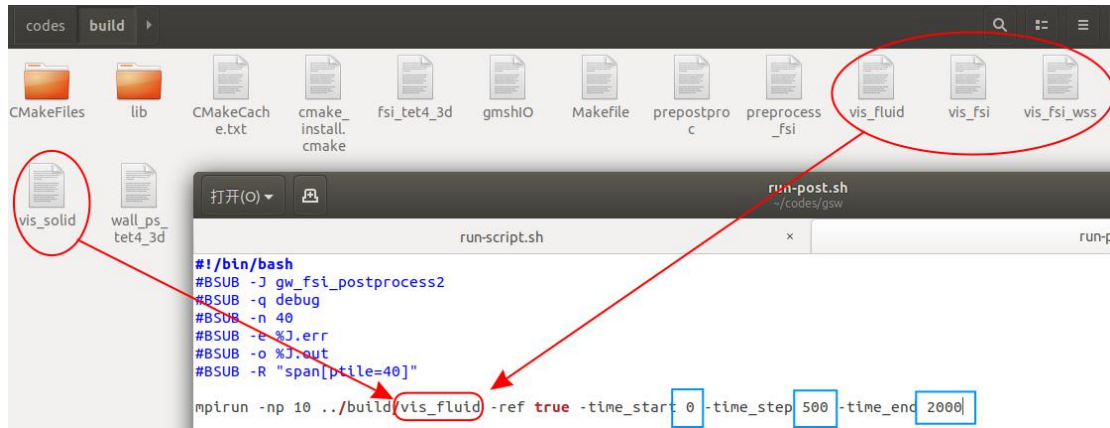
```
=== NR ite: 3, r_error: 9.378994e-07, a_error: 1.892985e-03
Time = 2.001000e-03, dt = 1.000000e-06, index = 2001, 22:21:27
*****
*** WIDEN YOUR WINDOW TO 120 CHARACTERS. Use 'enscript -r -fCourier9' to print this document ***
*****
----- PETSc Performance Summary: -----
../build/fsi_tet4_3d on a named huangxm-ThinkStation-P710 with 10 processors, by huangxm Mon Oct 24 22:21:27 2022
Using Petsc Release Version 3.16.6, Mar 30, 2022

Time (sec):      2.699e+04      1.000      2.699e+04      Total
Objects:         1.331e+05      1.000      1.331e+05
Flop:            1.599e+12      1.038      1.574e+12      1.574e+13
```


6. Now, we do the postprocessing:

```
$ ../build/prepostproc -cpu_size 10
```

prepostproc does the “preprocessing” for our postprocess. When it is done, copy the script **run-post.sh** to “gsw”, open it with your editor and open “build” on the window:



These **four files** with prefix “vis_” are all the postprocessor, you should select one of them according to your requirement. The **time parameter** should strictly match with your “SOL_file” sequence:

```
huangxm@huangxm-ThinkStation-P710:~/codes/gsw$ ls
apart                  dot_SOL_velo_900000500  node_mapping_v.h5      SOL_pres_900002000
change_names.sh        dot_SOL_velo_900001000  npart.h5              SOL_velo_900000000
dot_SOL_disp_900000000 dot_SOL_velo_900001500  preprocessor_cmd.h5    SOL_velo_900000500
dot_SOL_disp_900000500 dot_SOL_velo_900002000  run-script.sh          SOL_velo_900001000
dot_SOL_disp_900001000 epart.h5               SOL_disp_900000000     SOL_velo_900001500
dot_SOL_disp_900001500 fsi_cylinder_wBL.geo    SOL_disp_900000500     SOL_velo_900002000
dot_SOL_disp_900002000 fsi_cylinder_wBL.msh    SOL_disp_900001000     solver_cmd.h5
dot_SOL_pres_900000000 lumen_inlet_vol_000.vtp SOL_disp_900001500     tissue_inlet_vol_000.vtp
dot_SOL_pres_900000500 lumen_outlet_vol_000.vtp SOL_disp_900002000     tissue_interior_wall_vol.vtp
dot_SOL_pres_900001000 lumen_vol.vtu           SOL_pres_900000000     tissue_outlet_vol_000.vtp
dot_SOL_pres_900001500 lumen_wall_vol.vtp      SOL_pres_900000500     tissue_vol.vtu
dot_SOL_pres_900002000 material_model.h5       SOL_pres_900001000     tissue_wall_vol.vtp
dot_SOL_velo_900000000 node_mapping_p.h5       SOL_pres_900001500     whole_vol.vtu
```

Save the script and run it:

```
$ sh run-post.sh
```

```
$ ls
```

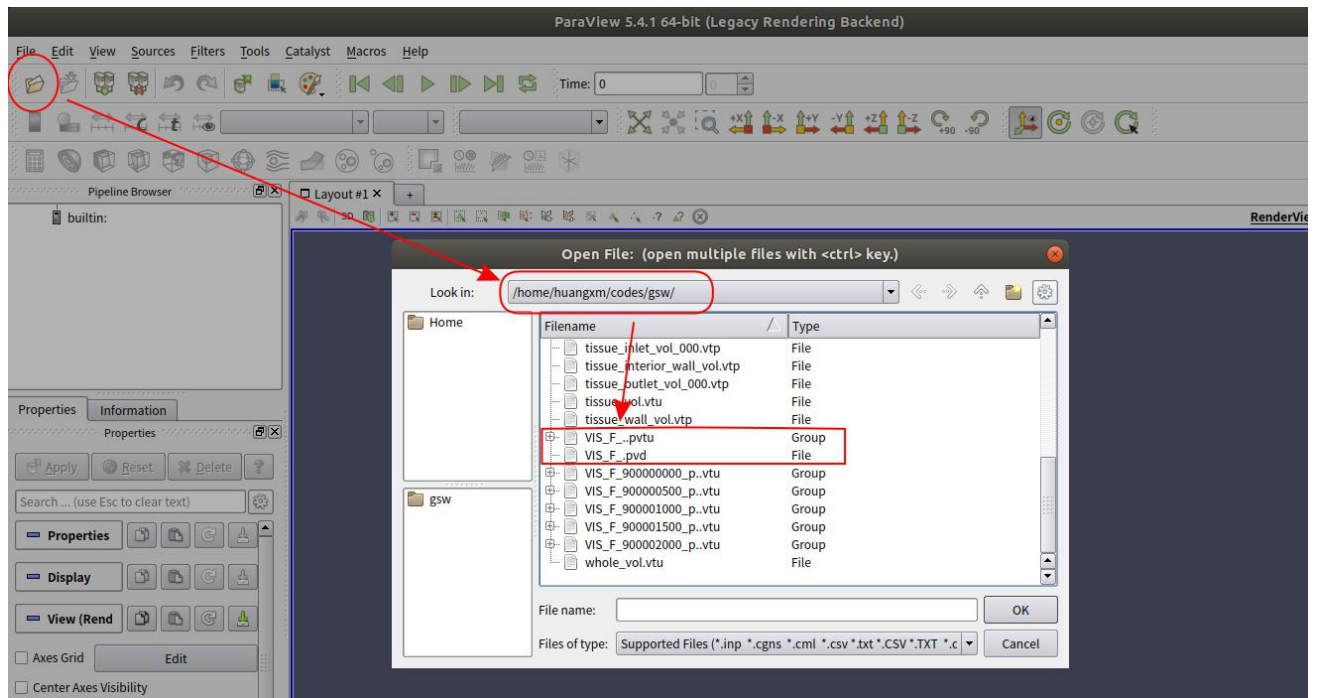
More .vtu/.vtp files are created with prefix “VIS_”, which restore our solutions and can be viewed with ParaView:

```
~/codes/gsw$ ls
er_wBL.msh      SOL_disp_900001000  VIS_F_900000000_p0000.vtu  VIS_F_900000500_p0008.vtu  VIS_F_900001500_p0005.vtu
et_vol_000.vtp  SOL_disp_900001500  VIS_F_900000000_p0001.vtu  VIS_F_900000500_p0009.vtu  VIS_F_900001500_p0006.vtu
et_vol_000.vtp  SOL_disp_900002000  VIS_F_900000000_p0002.vtu  VIS_F_900000500_pvtu      VIS_F_900001500_p0007.vtu
vtu             SOL_pres_900000000  VIS_F_900000000_p0003.vtu  VIS_F_900001000_p0000.vtu  VIS_F_900001500_p0008.vtu
_vol.vtp        SOL_pres_900000500  VIS_F_900000000_p0004.vtu  VIS_F_900001000_p0001.vtu  VIS_F_900001500_p0009.vtu
odel.h5         SOL_pres_900001000  VIS_F_900000000_p0005.vtu  VIS_F_900001000_p0002.vtu  VIS_F_900001500_pvtu
ng_p.h5         SOL_pres_900001500  VIS_F_900000000_p0006.vtu  VIS_F_900001000_p0003.vtu  VIS_F_900002000_p0000.vtu
ng_v.h5         SOL_pres_900002000  VIS_F_900000000_p0007.vtu  VIS_F_900001000_p0004.vtu  VIS_F_900002000_p0001.vtu
                SOL_velo_900000000  VIS_F_900000000_p0008.vtu  VIS_F_900001000_p0005.vtu  VIS_F_900002000_p0002.vtu
.h5             SOL_velo_900000500  VIS_F_900000000_p0009.vtu  VIS_F_900001000_p0006.vtu  VIS_F_900002000_p0003.vtu
mapping_p.h5     SOL_velo_900001000  VIS_F_900000000_pvtu       VIS_F_900001000_p0007.vtu  VIS_F_900002000_p0004.vtu
mapping_v.h5     SOL_velo_900001500  VIS_F_900000500_p0000.vtu  VIS_F_900001000_p0008.vtu  VIS_F_900002000_p0005.vtu
.h5             SOL_velo_900002000  VIS_F_900000500_p0001.vtu  VIS_F_900001000_p0009.vtu  VIS_F_900002000_p0006.vtu
                solver_cmd.h5       VIS_F_900000500_p0002.vtu  VIS_F_900001000_pvtu       VIS_F_900002000_p0007.vtu
or_cmd.h5       tissue_inlet_vol_000.vtp  VIS_F_900000500_p0003.vtu  VIS_F_900001500_p0000.vtu  VIS_F_900002000_p0008.vtu
n               tissue_interior_wall_vol.vtp  VIS_F_900000500_p0004.vtu  VIS_F_900001500_p0001.vtu  VIS_F_900002000_p0009.vtu
.sh             tissue_outlet_vol_000.vtp  VIS_F_900000500_p0005.vtu  VIS_F_900001500_p0002.vtu  VIS_F_900002000_pvtu
00000000        tissue_vol.vtu          VIS_F_900000500_p0006.vtu  VIS_F_900001500_p0003.vtu  VIS_F_900002000_pvtu
00000500        tissue_wall_vol.vtp     VIS_F_900000500_p0007.vtu  VIS_F_900001500_p0004.vtu  whole_vol.vtu
```

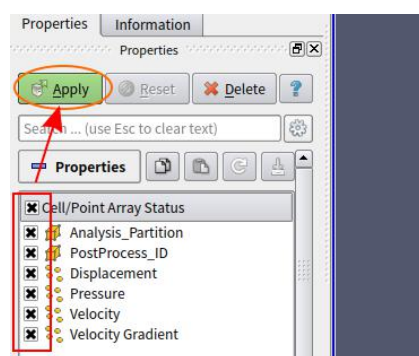
7. Finally, we visualize our solutions:

```
$ paraview
```

Then open the file **VIS_F_.pvd** or **VIS_F_.pvtu**, both of them consist of all solutions. If you just want a part of your solutions, open the VIS_files with number suffixes such as **VIS_F_900000500_p.vtu**.



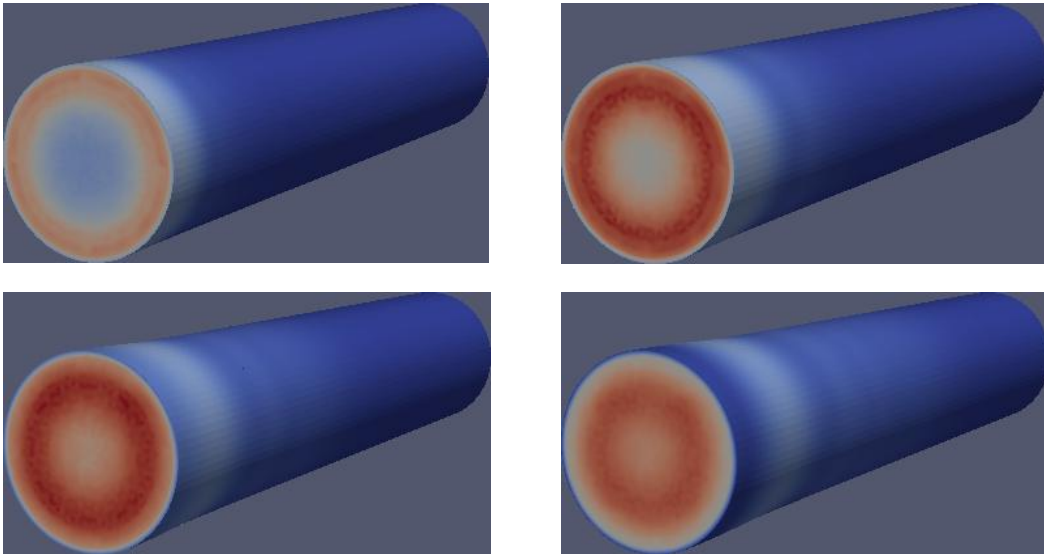
For example, we choose **VIS_F_.pvu**, select the information you want, then click “Apply” :



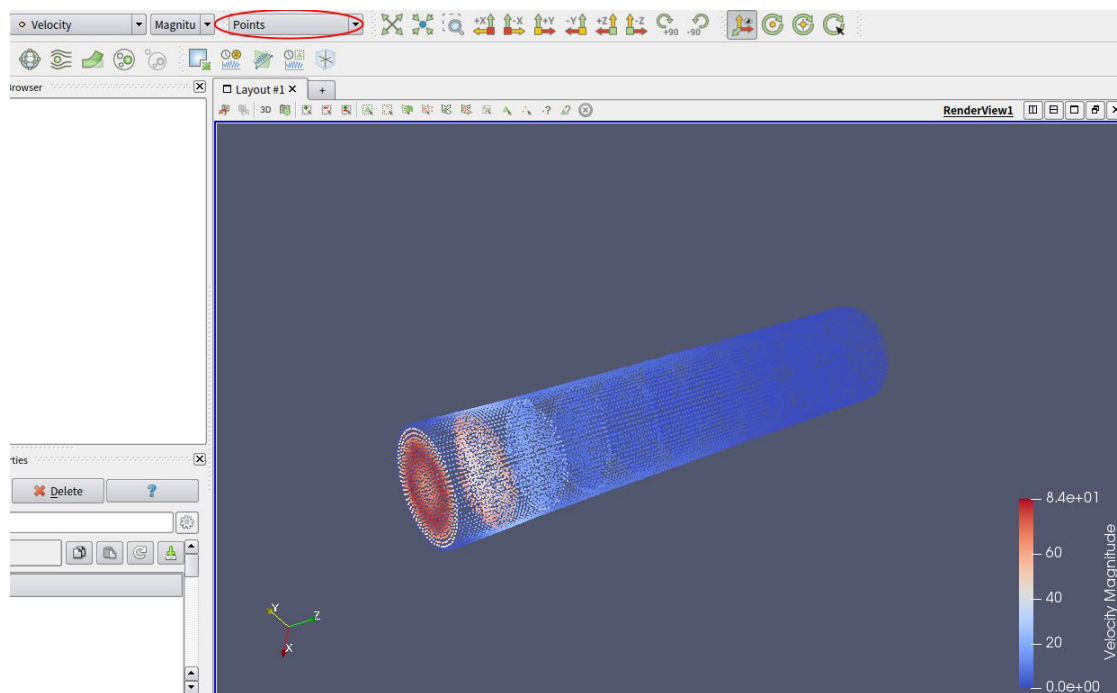
When a grey and ugly cylinder appears on your window, select a physical quantity on the head, click “PLAY” :

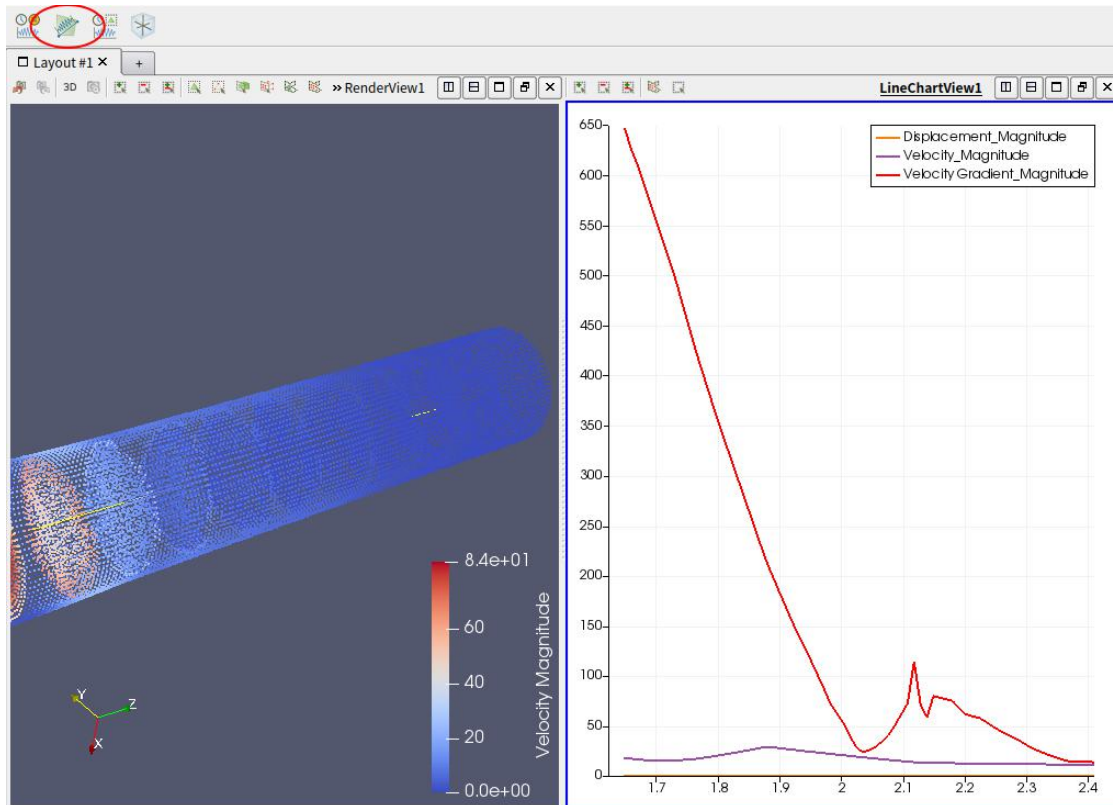


Then you will see a “pulse” flow into our model like this:



Explore ParaView by yourself, for example:





8. If you followed this guide much too strictly and got the same result as we showed, maybe you found that the “pulse” came to a halt as soon as it just started.

That’s because we set a short time for analysis with purpose of teaching:

```

打开(O)  run-script.sh ~/codes/gsw
mpirun -np 10 ../build/fsi_tet4_3d -nz_estimate 300 \
  -nqp_tet 5 -nqp_tri 13 \
  -init_step 1.0e-6 -fina_time 2.0e-3 \
  -nl_refreq 2 -nl_rtol 1.0e-6 -nl_atol 1.0e-15 -nl_dtol 1.0e2 \
  -nl_maxits 8 \
  -log_view -ttan_freq 100 -sol_rec_freq 500 \
  -is_restart NO -restart_index 79500 -restart_time 7.95e-3 \
  -restart_step 1.0e-7 \
  -restart_u_name SOL_U_re \

```

With 10 cores, 1×10^6 elements and 2000 steps, this progress would be finished in one day if everything goes well.

Now, set a larger “-fina_time”, try to get a complete “pulse”. (we’d better not change “-init_step”, unfit steps would make iterations divergent.)

By the way, try to get rid of this guide.

End