Compiling the WRF-Hydro Code in Docker

1) Start up Docker. From within the docker environment, navigate over to the code directory.

```
cd ~/wrf_hydro_source/trunk/NDHMS
ls
```

2) Check environment settings in setEnvar.sh. These get sourced by the compile script, and we refer to them as "compile-time options."

```
vi setEnvar.sh
```

```
#!/bin/bash

### This will be called by either compile_offline_NoahMP.csh
### or compile_offline_Noah.csh

### turn on WRF_HYDRO for NoahMP
export WRF_HYDRO=1   <<-- You always want this set to 1 if running WRF-Hydro
components.

### turn on output information during running time.
export HYDRO_D=1   <<-- This turns debug messages on/off. You generally want
this on if just starting and running experiments, but it can also slow down the run so
we turn off for operational/fast cycles.

### turn on distributed parameters for NoahMP
export SPATIAL_SOIL=1   <<-- This turns on/off the 2d & 3d soil and vegetation
parameter options in NoahMP. If you turn this option on, you need to provide a
corresponding SPATIAL_FILENAME in the namelist.hrldas. Otherwise NoahMP will
use parameters from the lookup tables (SOILPARM.TBL, MPTABLE.TBL,
GENPARM.TBL).

### turn on RAPID model
export WRF_HYDRO_RAPID=0   <<-- This option activates the coupled RAPID
routing model. This is an experimental option so requires additional files and is not
actively supported.
```

```
### using large netcdf file definition.
export WRFIO_NCD_LARGE_FILE_SUPPORT=1
```
<<-- Activate support for large netcdf files. Make sure this is on for large domains (e.g., CONUS) and hyper-resolution domains.

```
### turn on wcoss flag
export NCEP_WCOSS=0
```
<<-- Only activated when compiling on WCOSS operational machines. Leave off for all other systems.

```
### turn nudging off
export WRF_HYDRO_NUDGING=0
```
<<-- This option turns on/off the nudging DA capabilities.

3) Compile the WRF-Hydro offline (i.e., not coupled to WRF) code.
`./configure`   <<-- Choose 2 (Linux gfort compiler dmpar) for the docker container. This configures the makefile and macros. You can change the selection depending on your local system. Sequential options are not currently supported for all configurations, but you can easily run the parallel executable on a single core. You generally only need to set this option once.

`./compile_offline_NoahMP.sh`   <<-- This calls the compile script for NoahMP-coupled version of WRF-Hydro and creates an executable binary.

`ls -lrt Run/`   <<-- Executable binaries are stored in the Run folder.

4) Explore other (non-code) files included in the repo.

```
cd template
ls
```
<<-- This directory includes templates for namelists and parameter tables that you need to run the model.
```
ls NoahMP
vi NoahMP/namelist.hrldas
```
<<- See the NoahMP namelist.hrldas File with Description of Options document for details
```
vi NoahMP/MPTABLE.TBL
vi NoahMP/SOILPARM.TBL
vi NoahMP/GENPARM.TBL
ls HYDRO
```

```
vi HYDRO/hydro.namelist
```
<<- See the [WRF-Hydro hydro.namelist File with Description of Options document](#) for details

```
vi HYDRO/HYDRO.TBL
```