**How-to: linking the physical and biogeochemical components of COBALT**

*This is a live document that will be updated as needed.*

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**### Setting up the physical (ROMS) model ###**

1. roms\_config.sh
   * Change ROMS\_SRC = [current directory]. All else stays the same.
2. hioekg.h
   * At this stage (getting only the physical model to run), no changes. Eventually, I can include COBALT specifics.
3. rmake -j2
   * This creates /build directory. If I want to change the source code, I can do that in /build, then go to the main directory and type rmake -j2 to recompile.
   * oceanM\* is the executable file that is created.
   * varinfo.dat is also created.
4. ocean.in
   * If changed, I don’t need to recompile using rmake -j2.
   * In this file, I tell the model where to find the starting NetCDF files:
     1. GRDNAME: Change pathway to hioekg-grid.nc
     2. ININAME: Change pathway to ini-his-##.nc. Note that the initialization file must contain the keyword “his”, or the script won’t be able to find it- this is an inherent ROMS oddity.
     3. BRYNAME: Change pathway to hioekg-bry.nc, the boundary conditions file.
     4. CLMNAME: Change pathway to hioekg-clim-##.nc, the climatology file.
     5. SSFNAME: Change pathway to river-hioekg.nc, the sources/sinks file.
     6. TIDENAME: Change pathway to hioekg-tide.nc, the tidal forcing file.
     7. FRCNAME: Change pathway to frc-wrfo.nc, the forcing file. Note that I can change NFFILES = #, located a few lines above, to point to multiple forcing files. This will happen later, when COBALT is run.
     8. DSTART: Change to match the ## on ini-his-##.nc.
        1. Presently, day2date.sh and date2day.sh are in /nest. These scripts translate dates and days. Example: date2day.sh 2011 1 1 → ## (translates to a day).
     9. TIDESTART: Change to match ## sourced from ncdump -h ./ncfiles/hioekg-tide.nc.
     10. NTIMES = # of timesteps = # of seconds in your timeframe (= 86,400 \* # days)/DT (seconds per step).
     11. NHIS: How often output is written in # seconds (ex: 360 = every hour).
     12. NtileI, NtileJ: Set at 8 and 8. Related to the number of cores used to run the model.
5. spinup.sh
   * More powerful than (can overwrite) ocean.in.
     1. ROMS\_START\_DAY: Change to match the ## on ini-his-##.nc.
     2. ROMS\_END\_DAY: Change to end day (n = number of run days; end day = start + n-1. Example: start day = 4018, end day = 4020, n = 3).
     3. ROMS\_RUN\_DAYS: Change to n.
     4. ROMS\_QUEUE\_NAME: Change to default.
     5. ROMS\_QUEUE: Change to match NtileI, NtileJ.
     6. ROMS\_RUN\_NAME: Ensure there are no spaces!
     7. ROMS\_FAIL\_INPUT: In case of failure, I can name a backup file. For now, left empty.

**### Running ROMS ###**

1. Copy the ini-his-##.nc file to /output. cycle\_roms will look for it there.
2. Dry run: cycle\_roms -d spinup.sh ...in /work, this command creates…
   * ini.nc: restart file, copied by the model from /output. The model will automatically change the dates, etc. according to specified cycle conditions.
   * irp.nc: ignore.
   * ocean.in: copied here, with automatically changed dates according to our pre-specified conditions.
   * varinfo.dat
3. If no dry run errors: cycle\_roms spinup.sh
4. qstat
   * Did it crash? Check run log in /work
   * If it crashed, rm -r work and rm -r HIOEKG\_TESTING\*

**### Setting up COBALT ###**

1. Navigate to /roms. Then: git clone ~powellb/roms/cobalt
2. cd /cobalt
3. git pull
4. Navigate to main dir. Then: rmake clean ….then: rmake -j2
5. As with ROMS, this creates: /build, oceanM\*, varinfo.dat
6. Copy and rename .in file from another iteration. Ex: cp /share/frinkraid3/tobiasf/hiig\_cobalt/hiig\_cobalt.in /share/frinkraid3/lindsayv/bp\_template/hioekg\_cobalt.in
7. hioekg\_cobalt.in:
   * ! Hout(idTvar) == 33\*T ….this tells the model to write all 33 variables. Comment out (!) for now.
   * Checked ocean.in and found that boundary conditions vary for the hioekg grid. They are all uniform for hiig. We changed col 1, 3, 4 to Cla and col 2 to Clo.
8. hioekg.h:
   * Copy the following segment from another .h file iteration and ensure DIAGNOSTICS\_BIO and DIAGNOSTICS are undefined:

#define BIOLOGY

#define BIO\_COBALT

#if defined BIO\_COBALT

# define OPTIC\_MANIZZA

# define COBALT\_MINERALS

# define COBALT\_PHOSPHORUS

# define COBALT\_IRON

# define COBALT\_CARBON

# undef DIAGNOSTICS /\* diagnostics files contain Chl-a and .. \*/

# undef DIAGNOSTICS\_BIO /\* derived biol. val. needed for restart and analysis$

# undef ANA\_BIOLOGY /\* analytical biology initial conditions \*/

# define ANA\_BPFLUX /\* analytical bottom passive tracers fluxes \*/

# define ANA\_SPFLUX /\* analytical surface passive tracers fluxes \*/

#endif

1. Navigate to main dir. Then: rmake -j2