

Porting CIME based models

Jim Edwards

CESM Software Engineering Group

Options for porting CIME

1. Using the predefined 'homebrew' or 'centos7-linux' definitions
 - A good option for personal use on a mac or centos based system with gnu compilers
 - May require root access to the system to install prerequisites
2. Defining a new machine locally in your `$HOME/.cime` directory
 - A good option for personal use when option 1 won't work.
3. Defining a new machine and submitting a CIME pull request
 - Use this when the system is to be shared among multiple users.

Using homebrew or centos7-linux

1. Homebrew (for macs)

- Install homebrew <https://brew.sh>
- Install gcc
- Install netcdf and mpich with the --build-from-source -cc=gcc-8 options
- Create directories \$HOME/projects/scratch \$HOME/projects/cesm-inputdata
- Use the --machine homebrew option to create_newcase

2. Centos7-linux

- Install modules (modules.sourceforge.net)
- Install gcc, mpich, netcdf as modules
- Create directories \$HOME/cesm/inputdata \$HOME/cesm/scratch
- Use the --machine centos7-linux option to create_newcase

The \$HOME/.cime directory

When you use a CIME model it will look for a directory \$HOME/.cime

You may put several files in that directory for CIME to use.

1. config: custom settings used by the python scripts
2. config_machines.xml: custom machine description
3. config_compilers.xml: custom compiler instructions
4. config_batch.xml: custom batch system instructions

Steps for Porting CIME using files in \$HOME/.cime

1. Copy `cime/config/xml_schemas/config_machines_template.xml` to `$HOME/.cime/config_machines.xml`
2. Edit that file and change values to fit your machine
3. Create, build and submit a case.
 - a. If build errors occur due to incompatible compiler flags edit the file `Macros.make` to resolve.
 - b. If submit errors occur due to incompatible batch system flags edit `env_batch.xml` to resolve.
4. Once you can successfully build and submit a case transfer the changes in `Macros.make` to `$HOME/.cime/config_compilers.xml` and those in `env_batch.xml` to `$HOME/.cime/config_batch.xml`
5. Run CIME system tests to verify port.

config

The config file may contain custom settings for several variables used by the case control (python) code, it may also be used to customize the case control code logging system.

Most ports will not require this file.

config_machines.xml

This file contains most of the details CIME needs to know about your machine.

If your machine is not defined by the default config_machines.xml file this is where you should begin.

You may start by copying the file
cime/config/xml_schemas/config_machines_template.xml

to \$HOME/.cime/config_machines.xml

You will then edit the file and fill in the required information.

Config_machines.xml

These file header lines should not require any changes:

```
<?xml version="1.0"?>
<!-- This is an ordered list, not all fields are required, optional fields are noted below. -->
<config_machines version="2.0">
<!-- MACH is the name that you will use in machine options -->
```

The machine definition starts with a name and a description, the name must be unique in config_machines.xml:

```
<machine MACH="mymachine">
  <!-- DESC: a text description of the machine, this field is current not used in code-->
  <DESC>SITE VENDOR platform, os is ---, xx pes/node, batch system is ---</DESC>
```

The next field is an optional identifier, NODENAME_REGEX which will make the --machine command line entry optional

```
<!-- NODENAME_REGEX: a regular expression used to identify this machine
it must work on compute nodes as well as login nodes, use machine option
to create_test or create_newcase if this flag is not available -->
<NODENAME_REGEX>.*.cheyenne.ucar.edu</NODENAME_REGEX>
```


Config_machines.xml

Next we need to indicate what Operating System is used here:

```
<!-- OS: the operating system of this machine. Passed to cppflags for  
      compiled programs as -DVALUE recognized are LINUX, AIX, Darwin, CNL -->
```

```
<OS>LINUX</OS>
```

```
<!-- PROXY: optional http proxy for access to the internet-->
```

```
<PROXY> https://howto.get.out </PROXY>
```

COMPILERS is a list of compiler names available on this system, these must each match a compiler name in config_compilers.xml

```
<!-- COMPILERS: compilers supported on this machine, comma separated list, first is default -->
```

```
<COMPILERS>intel,gnu</COMPILERS>
```

MPILIBS

```
<!-- MPILIBS: mpilibs supported on this machine, comma seperated list,  
      first is default, mpi-serial is assumed and not required in this list-->
```

```
<MPILIBS>mpt,openmpi,impi</MPILIBS>
```

PROJECT (optional)

```
<!-- PROJECT: A project or account number used for batch jobs  
      can be overridden in environment or $HOME/.cime/config -->
```

```
<PROJECT>couldbethis</PROJECT>
```

Config_machines.xml

```
<!-- CIME_OUTPUT_ROOT: Base directory for case output,  
      the case/bld and case/run directories are written below here -->  
<CIME_OUTPUT_ROOT>/glade/scratch/$USER</CIME_OUTPUT_ROOT>  
  
<!-- DIN_LOC_ROOT: location of the inputdata data directory  
      inputdata is downloaded automatically on a case by case basis as  
      long as the user has write access to this directory.  We recommend that  
      all cime model users on a system share an inputdata directory  
      as it can be quite large -->  
<DIN_LOC_ROOT>${ENV{CESMDATAROOT}}/inputdata</DIN_LOC_ROOT>  
  
<!-- DOUT_S_ROOT: root directory of short term archive files, short term  
      archiving moves model output data out of the run directory, but  
      keeps it on disk-->  
<DOUT_S_ROOT>${CIME_OUTPUT_ROOT}/archive/${CASE}</DOUT_S_ROOT>  
<!-- BASELINE_ROOT: Root directory for system test baseline files -->  
<BASELINE_ROOT>${ENV{CESMDATAROOT}}/cesm_baselines</BASELINE_ROOT>  
<!-- CCSM_CPRNC: location of the cprnc tool, compares model output in testing-->  
<CCSM_CPRNC>${ENV{CESMDATAROOT}}/tools/cime/tools/cprnc/cprnc.cheyenne</CCSM_CPRNC>
```

Config_machines.xml

```
<!-- GMAKE: gnu compatible make tool, default is 'gmake' -->  
<GMAKE></GMAKE>  
<!-- GMAKE_J: optional number of threads to pass to the gmake flag -->  
<GMAKE_J>8</GMAKE_J>
```

BATCH_SYSTEM should match a name in config_batch.xml

```
<!-- BATCH_SYSTEM: batch system used on this machine,  
supported values are: none, cobalt, lsf, pbs, slurm -->  
<BATCH_SYSTEM>pbs</BATCH_SYSTEM>  
  
<!-- SUPPORTED_BY: contact information for support for this system  
this field is not used in code -->  
<SUPPORTED_BY>cseg</SUPPORTED_BY>
```

Config_machines.xml

```
<!-- MAX_TASKS_PER_NODE: maximum number of threads*tasks per  
shared memory node on this machine,  
should always be >= PES_PER_NODE -->
```

```
<MAX_TASKS_PER_NODE>36</MAX_TASKS_PER_NODE>
```

```
<!-- PES_PER_NODE: number of physical PES per shared node on  
this machine, in practice the MPI tasks per node will not exceed this value -->
```

```
<MAX_MPITASKS_PER_NODE>36</MAX_MPITASKS_PER_NODE>
```

```
<!-- PROJECT_REQUIRED: Does this machine require a project to be specified to  
the batch system? See PROJECT above -->
```

```
<PROJECT_REQUIRED>TRUE</PROJECT_REQUIRED>
```

Config_machines.xml

```
<!-- mpirun: The mpi exec to start a job on this machine, supported values
      are values listed in MPILIBS above, default and mpi-serial -->
<mpirun mpilib="mpt">
  <!-- name of the executable used to launch mpi jobs -->
  <executable>mpiexec_mpt</executable>
  <!-- arguments to the mpiexec command, the name attribute here is ignored-->
  <arguments>
    <arg name="ntasks">-np {{ total_tasks }} </arg>
    <arg name="labelstdout">-p "%g:" </arg>
    <arg name="threadplacement"> omplace </arg>
  </arguments>
</mpirun>
```

Config_machines.xml

Software module systems

```
<!-- allowed types are none, module, soft -->
<module_system type="module">
  <modules>
    <command name="purge"/>
    <command name="load">ncarenv/1.0</command>
  </modules>
  <modules compiler="intel">
    <command name="load">intel/16.0.3</command>
    <command name="load">mkl</command>
  </modules>
</module system>
```

Config_machines.xml

Expected result:

`$HOME/.cime/config_machines.xml` validates

```
<!-- environment variables, a blank entry will unset a variable -->  
<environment_variables>  
  <env name="OMP_STACKSIZE">256M</env>  
  <env name="MPI_TYPE_DEPTH">16</env>  
</environment_variables>
```

Closure:

```
</machine>  
</config_machines>
```

Test and confirm xml correctness:

```
xmllint --noout --schema cime/config/xml_schemas/config_machines.xsd $HOME/.cime/config_machines.xml
```

config_compilers.xml

The config_compilers.xml file has a default definition for each supported compiler.

This definition can be amended with a machine specific section:

```
<compiler MACH="hobart" COMPILER="nag">
  <CPPDEFS>
    <!-- needed for nag pio build.. -->
    <append> -DNO_C_SIZEOF </append>
  </CPPDEFS>
  <LD_FLAGS>
    <append> -lpthread</append>
  </LD_FLAGS>
  <SLIBS>
    <append> -L/usr/local/nag/lib/NAG_Fortran </append>
  </SLIBS>
</compiler>
```


Test and confirm xml correctness:

```
xmllint --noout --schema cime/config/xml_schemas/config_compilers.xsd $HOME/.cime/config_compilers.xml
```

Expected result:

```
$HOME/.cime/config_compilers.xml validates
```

In addition make sure that the generated Macros.make is as expected.

config_batch.xml

Default definitions for each batch queueing system which can be amended.

```
<!-- bluewaters is PBS -->
<batch_system MACH="bluewaters" type="pbs" >
  <directives>
    <directive>-l nodes={{ num_nodes }}:ppn={{ tasks_per_node }}:xe</directive>
    <directive default="/bin/bash" > -S {{ shell }} </directive>
  </directives>
  <queues>
    <queue walltimemax="24:00:00" default="true">regular</queue>
    <queue walltimemax="00:30:00" jobmin="1" jobmax="512">debug</queue>
  </queues>
</batch_system>
```

Resources for help

CGD Forum: <http://forum.cgd.ucar.edu/>

ESMCI development (CIME): <https://github.com/ESMCI/cime>

The CESM UltraFast Ensemble Consistency Test

With this test you will conduct three model runs of 9 timesteps each.

Postprocess the output files to add metadata about the origin of the run.

Upload to <http://www.cesm.ucar.edu/models/cesm2/verification/>

Your runs are then compared to an ensemble of about 300 members.

Pass or Fail is determined by whether your runs fit within the bounds of the ensemble.

See <http://www.cesm.ucar.edu/models/cesm2/python-tools/> for details