

# The Land (CLM5) and BGC (Coupled and Ocean) Tutorial Session

Keith Oleson, Erik Kluzek, Matt Long  
CGD/NCAR



U.S. DEPARTMENT OF  
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# CLM5.0 Offline – “I” compsets

Compsets are shortcuts designed for specific cases... treat them as starting points for all cases

"I" compsets run the clm/datm/rof/cism and no seaice/ocean/atm/wave models

SP = Satellite Phenology; BGC = Biogeochemistry

<u>Short Name</u>	<u>Description</u>
I2000Clm50Sp	CLM50SP, yr. 2000 pfts, CO <sub>2</sub> , aerosol <sub>dep</sub> Long Name: 2000_DATM%GSWP3v1_CLM50%SP_SICE_SOCN_MOSART_CISM2%NOEVOLVE_SWAV
I1850Clm50BgcCrop	CLM50BGC+Crop, yr 1850 pfts, CO <sub>2</sub> , aerosol <sub>dep</sub> Long Name: 1850_DATM%GSWP3v1_CLM50%BGC-CROP_SICE_SOCN_MOSART_CISM2%NOEVOLVE_SWAV
IHistClm50BgcCrop	CLM50BGC+Crop, 1850-2010 pfts, CO <sub>2</sub> , aerosol <sub>dep</sub> + N <sub>dep</sub> Long Name: HIST_DATM%GSWP3v1_CLM50%BGC-CROP_SICE_SOCN_MOSART_CISM2%NOEVOLVE_SWAV

[/glade/p/cesm/tutorial/cesm2.0.0\\_tutorial/cime/scripts/query\\_config –compsets clm](#)

Atmospheric forcing for these compsets are from Global Soil Wetness Project (GSWP3) for 1901-2014.

In exercise A, you will try the I2000Clm50Sp compset

In exercise B, you will try the IHistClm50BgcCrop compset

In exercise C, you will again use the I2000Clm50Sp compset and modify input data

# Exercise A. Basic CLM5 usage

Goal: Run the CLM50SP at  $\sim 1^\circ$  lat/lon  
horizontal resolution for five days

In this exercise you will try the I2000Clm50Sp  
compset.

# Exercise B. Differences between compsets

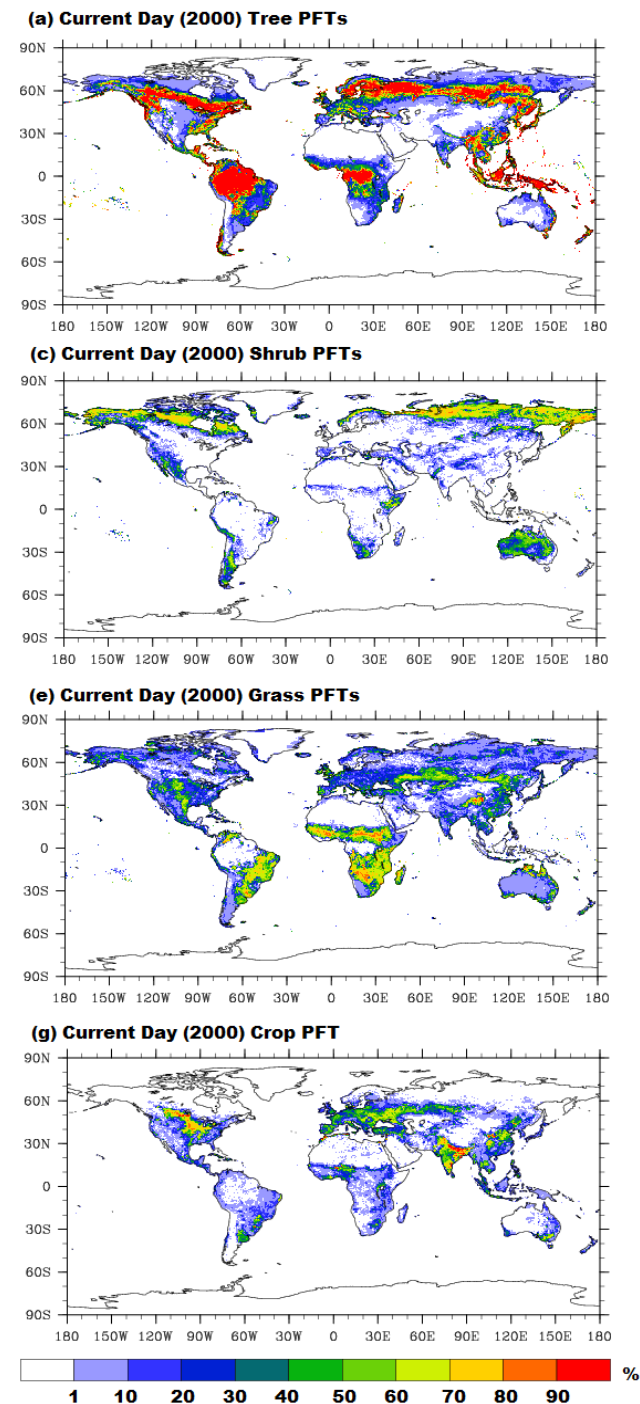
Goal: Create a case with a different compset and see how settings change automatically for you. Contrast the history files from exercise (A) and (B).

In this exercise you will try the IHistClim50BgcCrop compset which is a 20<sup>th</sup> century transient run using GSWP3v1 atmospheric forcing and the biogeochemistry model including crops.

# Exercise C. Understanding and modifying input data

Goal: Learn what inputs CLM needs and what they look like

Here we will again use the I2000CIm50Sp compset, modify one of the plant functional type properties, and compare results to exercise A.



# Exercise A. detailed steps

## 1) Create the case...

```
cd /glade/p/cesm/tutorial/cesm2.0.0_tutorial/cime/scripts
```

```
./create_newcase --case ~/cases/i.day5.a --compset I2000CIm50Sp --res f09_g17_gl4 --project UESM0006 --run-unsupported
```

```
#!/create_newcase --help
```

...for documentation

## 2) Setup the case...

```
cd ~/cases/i.day5.a
```

```
# You need not change env_build.xml for this case to work, but now would be the time to make such changes
```

```
# Execute setup
```

```
./case.setup
```

# Exercise A. detailed steps

## 3) Change the clm namelist...

#Since we are running just five days and history output default is monthly averages, we will change the clm namelist to get daily average output

#Add hist\_nhtfrq and set to -24 (i.e., 24 hrs, daily average) in the clm namelist

```
$EDITOR user_nl_clm
```

#Add this line:

```
hist_nhtfrq = -24
```

#Generate the namelists (look at Ind\_in in CaseDocs directory once the following is done)

```
./preview_namelists
```

## 4) Use dedicated batch queues and shorten the requested run time

```
./xmlchange --subgroup case.run JOB_QUEUE=R1410520
```

```
./xmlchange --subgroup case.run JOB_WALLCLOCK_TIME=1:00:00
```

```
./xmlchange --subgroup case.st_archive JOB_QUEUE=R1410520
```

# Exercise A. detailed steps

5) Build the case and compile the code...

```
qcmd -- ./case.build
```

6) Submit the run...

```
./case.submit
```

```
# to see the $jobID and whether the job is pending or running
```

```
qstat
```

```
# to kill the job if necessary
```

```
qdel $jobID
```

```
# run executes in /glade/scratch/$USER/i.day5.a/run
```

```
# land history output at the end of the run will be moved to
```

```
# /glade/scratch/$USER/archive/i.day5.a/lnd/hist
```

```
# look at the history file in this directory, e.g., using ncview (module load ncview)
```

```
# ncview i.day5.a.clm2.h0.0001-01-01-00000.nc &
```

```
# note that there will be six time samples in this file, ignore the first one, it is an initialization step  
and is not a daily average
```



# Exercise B. detailed steps

1) Create the case...

```
cd /glade/p/cesm/tutorial/cesm2.0.0_tutorial/cime/scripts
```

```
./create_newcase --case ~/cases/i.day5.b --compset IHistCIm50BgcCrop --res f09_g17_gl4 --project UESM0006 --run-unsupported
```

2) Note differences between this case and the case created in exercise A

```
cd ~/cases
```

```
#For example,
```

```
diff i.day5.a/env_run.xml i.day5.b/env_run.xml
```

3) Setup the case...

```
cd ~/cases/i.day5.b
```

```
#Execute setup
```

```
./case.setup
```

# Exercise B. detailed steps

## 4) Change the clm namelist...

#Since we are running just five days and history output default is monthly averages, we will change the clm namelist to get daily average output

#Add hist\_nhtfrq and set to -24 (i.e., 24 hrs) in the clm namelist

`$EDITOR user_nl_clm`

#Add this line:

`hist_nhtfrq = -24`

#Generate the namelists (look at Ind\_in in CaseDocs directory once the following is done)

`./preview_namelists`

## 5) Use dedicated batch queues and shorten the requested run time

`./xmlchange --subgroup case.run JOB_QUEUE=R1410520`

`./xmlchange --subgroup case.run JOB_WALLCLOCK_TIME=1:00:00`

`./xmlchange --subgroup case.st_archive JOBS_QUEUE=R1410520`

## 6) Build the case and compile the code...

`qcmd -- ./case.build`

# Exercise B. detailed steps

7) Now compare the CaseDocs directories in i.day5.b and i.day5.a (in particular you could compare Ind\_in) and note the differences, e.g.,

```
diff CaseDocs/Ind_in ../i.day5.a/CaseDocs/Ind_in
```

8) Submit the run...

```
./case.submit
```

9) Compare the history files from these two runs (e.g., side by side using “ncview”). Note the extra variables in the file produced from exercise B (biogeochemistry variables). Specific fields to compare (leaf and stem area index [TLAI, TSAI], transpiration and canopy and ground evaporation [FCTR, FCEV, FGEV]). What do you think negative values of FCEV and FGEV mean?

# Exercise C. detailed steps

1) Look at `Ind_in` in the exercise A case

Find the parameter file specified by the “paramfile” namelist item. Look at variable “`rholvis`” using `ncview` or `ncdump -v rholvis`. This is the visible leaf reflectance for every pft.

2) Create a case like the one in exercise A but with a different case name (i.e., `i.day5.a_pft`), e.g.,

```
cd /glade/p/cesm/tutorial/cesm2.0.0_tutorial/cime/scripts  
./create_clone --case ~/cases/i.day5.a_pft --clone ~/cases/i.day5.a
```

3) Modify the `rholvis` parameter in the pft-physiology file.

Use `nco` or `ncl` to modify the pft-physiology file. Change the visible leaf reflectance (variable `rholvis`) for pft #4 (tropical broadleaf evergreen tree).

First, make a copy of the file, e.g., in your scratch directory

```
cd /glade/scratch/$USER  
cp /glade/p/cesmdata/cseg/inputdata/Ind/clm2/paramdata/clm5_params.c171117.nc ./  
chmod u+w clm5_params.c171117.nc
```

# Exercise C. detailed steps

You can use either of a couple of ways to change the file:

E.g., could use ncap2 (module load nco):

```
mv clm5_params.c171117.nc clm5_params.c171117.new.nc
ncap2 -v -s 'rholvis(4)=0.4' clm5_params.c171117.new.nc clm5_params.c171117.nc
ncks -A clm5_params.c171117.nc clm5_params.c171117.new.nc
```

Or, e.g., could use NCL (module load ncl):

Save the following ncl script to filename.ncl:

```
begin
  a = addfile("clm5_params.c171117.nc","w")
  rholvis = a->rholvis
  rholvis(4) = 0.4d
  a->rholvis = rholvis
end
```

and then type:

```
ncl filename.ncl
```

and rename file:

```
mv clm5_params.c171117.nc clm5_params.c171117.new.nc
```

Look at the new file to make sure your changes worked, e.g.,

```
ncdump -v rholvis clm5_params.c171117.new.nc
```

# Exercise C. detailed steps

4) Follow the steps in exercise A to setup model (./case.setup) for i.day5.a\_pft, change the clm namelist to point to new pft-physiology file (using user\_nl\_clm; paramfile = '/glade/scratch/\$USER/clm5\_params.c171117.new.nc'), then build (qcmd -- ./case.build) and run (./case.submit).

Compare history output against that generated in exercise A, e.g., use ncdiff. What differences do you see? Specific fields to compare (FSRVD, FSRVI, FSR, FSA, FSH, FCTR, TV, TSA).

NOTE: For any tasks other than setting up, building, submitting cases (e.g., using ncl or nco) you should probably do these tasks on geyser/caldera.. (execdav --account=UESM0006).