Gmail **Max Curie <maxcurie19960630@gmail.com>**

GENE Input files

2 messages

Halfmoon, Michael R <mhalfmoon@austin.utexas.edu> Tue, Jan 22, 2019 at 5:23 PM
To: Max Curie <maxcurie19960630@gmail.com>, Benjamin Verma <benjamin.verma@gmail.com>
Cc: "Kotschenreuther, M T" <mtk@austin.utexas.edu>, "ehab@utexas.edu" <ehab@utexas.edu>, "Hatch, David R" <drhatch@austin.utexas.edu>, "Michoski, Craig" <michoski@ices.utexas.edu>

All,

Before running these cases make sure to recompile GENE with the necessary tools for post-processing with a set of Python scripts, to do this:

1. Go to the /bin directory in the GENE home directory and open the .mk file.
2. Find the variable FUTILS and on the line where it is set to no, change that to a yes.
3. Go back to the home directory and type gmake -j, and you're done.

Attached are the parameters files for two different scans in GENE. The parameters-ky file will run linear calculations for a scan of ky for fixed temperature and pressure gradients. The parameters-omega file indicates that the temperature and pressure gradients will be scanned, the value of omt depends on omn- as seen in the scanlist and scan arguments. Note, omn(1) refers to the value of the density gradient of the first species- in this case ions.

The easiest way to set up these runs will be to use the ./newprob command in your GENE directory twice- once for the ky scan and again for the omega scan, and replace the respective parameters files with those attached. Place the attached parameters files in the separate prob directories, and rename them to 'parameters'. In the parameters files, the value of the variable diagdir is the desired location for your output directory (once your run has been submitted it will have the format scan000x where x is the run number, GENE ensures that your previous runs don't get overwritten when running from the same working directory), make sure that this points to your Scratch directory, and that the final subdirectory you have chosen currently exists, i.e. I would use the command mkdir ky-scan in my $SCRATCH directory *before* submitting my run.

The following is the input of my submit.cmd file:

```
#!/bin/bash -l

#SBATCH -p debug

#SBATCH -n 32

#SBATCH -t 00:10:00

#SBATCH -J GENE

#SBATCH -C haswell

#SBATCH -o ./%x.%j.out
```

```
#SBATCH -e ./%x.%j.err

##uncomment for particular account usage

##SBATCH -A <ACCOUNT>


## fix formatted output in cray env

if [ "$PE_ENV" == "CRAY" ]; then

  export FILENV=my_filenenv

  assign -U on g:sf

fi


## set openmp threads

export OMP_NUM_THREADS=1


# run GENE

#srun -n $SLURM_NTASKS ./gene_cori


# run scanscript

./scanscript --np 32 --ppn 32 --mps 4 --syscall='srun -n 32 ./gene_cori'
```

Note, I have changed the queue from regular to debug, I have commented the srun ./gene_cori command and uncommented the ./scanscript line, and replaced the $SLURM_NTASKS variable on the ./scanscript line with the known value of 32.

To the submit batch script on Cori, use the following command:

sbatch submit.cmd

A good indicator that your simulation is complete would be the eigenvalues found in the scan.log file, however this can appear empty if your simulation ran out of time- if that happens, use the command grep gamma * to print the eigenvalues for each run that were completed.

If you run into any issues regarding compiling, running, or analyzing your runs, just shoot me an email or come by my office.

-Michael Halfmoon

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2 attachments

parameters-omega
5K

parameters-ky
5K

Ehab Hassan <ehab@utexas.edu> Wed, Jan 23, 2019 at 10:57 AM
To: "Halfmoon, Michael R" <mhalfmoon@austin.utexas.edu>, Max Curie <maxcurie19960630@gmail.com>, Benjamin Verma <benjamin.verma@gmail.com>
Cc: "Kotschenreuther, M T" <mtk@austin.utexas.edu>, "Hatch, David R" <drhatch@austin.utexas.edu>, "Michoski, Craig" <michoski@ices.utexas.edu>, Gabriele Merlo <merlo.gabriele@gmail.com>

Hi Guys, I think to compile GENE code in Cori you need to download the unstable version (not to worry - it is stable but still under development) of GENE using this command:
git clone https://username@gitta.rzg.mpg.de/~GENE/guest/git.py/gene.git -b unstable genecode

you have to have an account name and password to be able to do that. So you need to register in their GENE code website, here:
http://genecode.org/

Before compiling GENE, you need to load the following packages in Cori:
module load cray-petsc-complex
module load cray-petsc-complex
module load cray-fftw
module load cray-hdf5-parallel
module load craype
module load python

Hence, you can compile the code by simply write:
gmake

Once the code finishes it compilation procedure, you need to follow what Michael Halfmoon said about editing the /bin/Cori.mk file and switch FUTILS = no to yes.

Finally, you will need to recompile the code by simply typing what Michael Halfmoon mentioned earlier in his email:
gmake -j

Wish you all the best!
[Quoted text hidden]
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Ehab A. Hassan
Research Scholar
IFS@UT:Austin