Habanero - Job Examples

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In order for the scripts in these examples to work, you will need to replace <ACCOUNT> with your group's account name.

Hello World

This script will print "Hello World", sleep for 10 seconds, and then print the time and date. The output will be written to a file in your current directory.

```bash
#!/bin/sh
#
# Simple "Hello World" submit script for Slurm.
#
# Replace <ACCOUNT> with your account name before submitting.
#
#SBATCH --account=<ACCOUNT>      # The account name for the job.
#SBATCH --job-name=HelloWorld    # The job name.
#SBATCH -c 1                     # The number of cpu cores to use.
#SBATCH --time=1:00              # The time the job will take to run.
#SBATCH --mem-per-cpu=1gb        # The memory the job will use per cpu core.

echo "Hello World"
sleep 10
date

# End of script
```

C/C++/Fortran

To submit a precompiled binary to run on Habanero, the script will look just as it does in the Hello World example. The difference is that you will call your executable file instead of the shell commands "echo", "sleep", and "date".

C/C++/Fortran MPI

Intel Parallel Studio

Habanero supports Intel Parallel Studio which provides a version of MPI derived from MPICH2. We encourage users to avail themselves of Intel MPI because it is faster and more modern than other versions. Also, all nodes on the cluster have Infiniband transport and that is the fabric that MPI jobs avail themselves of - which is another reason for a substantial boost of efficiency on the cluster.

To use Intel MPI, you must load the Intel module first:
In order to take advantage of Habanero architecture, your program should be (re)compiled on the cluster even if you used Intel for compiling it on another cluster (like Yeti). It is important to compile with the compiler provided by the module mentioned above. Note that you may have to set additional environment variables in order to successfully compile your program.

These are the locations of the C and Fortran compilers for Intel Studio:

```bash
$ module load intel-parallel-studio/2017
(...)
$ which mpiicc
/rigel/opt/parallel_studio_xe_2017/compilers_and_libraries_2017.0.098/linux/mpi/intel64/bin/mpiicc
$ which ifort
/rigel/opt/parallel_studio_xe_2017/compilers_and_libraries_2017.0.098/linux/bin/intel64/ifort
```

For programs written in C, use mpiicc in order to compile them:

```bash
$ mpiicc -o <MPI_OUTFILE> <MPI_INFILE.c>
```

The submit script below, named pi_mpi.sh, assumes that you have compiled a simple MPI program used to compute pi, (see mpi_test.c), and created a binary called pi_mpi:

```bash
#!/bin/sh
#SBATCH -A <ACCOUNT>
#SBATCH --time=30
#SBATCH -N 2
#SBATCH --exclusive
module load intel-parallel-studio/2017
mpiexec -bootstrap slurm ./pi_mpi
# End of script
```

The --exclusive flag will ensure that full nodes are being used in the runs (that's the reason why no memory specification is given). Each available core will give rise to another MPI thread. Without the flag, you can specify the number of tasks, or tasks per node, in order to limit the number of threads that will be created. For example, you can replace the directive containing the flag by:
#SBATCH --N 2
#SBATCH --ntasks-per-node=4

and your MPI code will run on 8 threads, with 4 on each of the 2 nodes requested.

**Job Submission**

$ sbatch pi_mpi.sh

**OpenMPI**

Habanero supports also OpenMPI from the GNU family.

To use OpenMPI, you must load the following module instead:

```bash
module load openmpi/gcc/64
mpiexec myprogram
```

Your program must be compiled on the cluster. You can use the the `module` command as explained above to set your path so that the corresponding `mpicc` will be found. Note that you may have to set additional environment variables in order to successfully compile your program.

```bash
$ module load openmpi/gcc/64
$ which mpicc
/rigel/opt/openmpi-2.0.1/bin/mpicc
```

Compile your program using `mpicc`. For programs written in C:

```bash
$ mpicc -o <MPI_OUTFILE> <MPI_INFILE.c>
```

**GPU (CUDA C/C++)**

The cluster includes two types of GPU servers: Nvidia K80s and Nvidia P100s.

- There are 14 K80 GPU servers, each with two dual K80 Tesla GPU accelerators, for a total of 4 GPU modules per server.
- There are 13 P100 servers, each with two P100 accelerators, for a total of 2 GPU modules per P100 server.

To use a GPU server you must specify the `--gres=gpu` option in your submit request, followed by a colon and the number of GPU modules you require (with a maximum of 4 per server for K80s and 2 per server for P100s).

Use the `--constraint=k80` or `--constraint=p100` directive if you’d like to request a specific type of GPU (k80 or P100).

Request a **K80** gpu, specify this in your submit script.
To request a **P100** gpu, specify this in your submit script:

```
#SBATCH --constraint=p100
```

Not all applications have GPU support, but some, such as MATLAB, have built-in GPU support and can be configured to use GPUs.

To build your CUDA code and run it on the GPU modules you must first set your paths so that the Nvidia compiler can be found. Please note you must be logged into a GPU node to access these commands. To login interactively to a GPU node, run the following command, replacing `<ACCOUNT>` with your account:

```
$ srun --pty -t 0-01:00 --gres=gpu:1 -A <ACCOUNT> /bin/bash
```

Load the cuda environment module which will add cuda to your PATH and set related environment variables. Note cuda 8.0 does not support gcc 6, so gcc 5 or earlier must be accessible in your environment when running nvcc.

```
$ module load gcc/4.8.5
```

Load the cuda module.

```
$ module load cuda80/toolkit
```

You then have to compile your program using **nvcc**:

```
$ nvcc -o <EXECUTABLE_NAME> <FILE_NAME.cu>
```

You can compile `hello_world.cu` sample code which can be built with the following command:

```
$ nvcc -o hello_world hello_world.cu
```

For non-trivial code samples, refer to Nvidia’s [CUDA Toolkit Documentation](https://docs.nvidia.com/cuda/index.html).

A Slurm script template, `gpu.sh`, that can be used to submit this job is shown below:
#!/bin/sh
#
#SBATCH --account=<ACCOUNT>      # The account name for the job.
#SBATCH --job-name=HelloWorld    # The job name.
#SBATCH --gres=gpu:1             # Request 1 gpu (Up to 4 on K80s, or up to 2 on P100s are valid).
#SBATCH -c 1                     # The number of cpu cores to use.
#SBATCH --time=1:00              # The time the job will take to run.
#SBATCH --mem-per-cpu=1gb        # The memory the job will use per cpu core.

module load cuda80/toolkit
./hello_world

# End of script

Job submission

$ sbatch gpu.sh

This program will print out "Hello World!" when run on a gpu server or print "Hello Hello" when no gpu module is found.

Example of R run

For this example, the R code below is used to generate a graph "Rplot.pdf" of a discrete Delta-hedging of a call. It hedges along a path and repeats over many paths. There are two R files required:

hedge.R

BlackScholesFormula.R

A Slurm script, hedge.sh, that can be used to submit this job is presented below:
#!/bin/sh

#hedge.sh

# Slurm script to run R program that generates graph of discrete Delta-hedging call

# Slurm directives
#
#SBATCH -A astro                 # The account name for the job.
#SBATCH -J DeltaHedge            # The job name.
#SBATCH -c 6                     # The number of cpu cores to use.
#SBATCH -t 1:00                  # The time the job will take to run.
#SBATCH --mem-per-cpu 1gb        # The memory the job will use per cpu core.

module load R

# Command to execute R code
R CMD BATCH --no-save --vanilla hedge.R routput

# End of script

---

**Batch queue submission**

```
$ sbatch hedge.sh
```

This program will leave several files in the output directory: slurm-<jobid>.out, Rplots.pdf, and routput (the first one will be empty).

**Installing R Packages on Habanero**

HPC users have two options for R packages:

1. Install packages locally in your user space that can be called by your programs (faster, see below).
2. E-mail [hpc-support@columbia.edu](mailto:hpc-support@columbia.edu) and request a package to be installed on all HPC nodes (slower).

**Local Installation**

After logging in to Habanero, start R:

```
$ module load R
$ R
```

You can see the default library paths (where R looks for packages) by calling `.libPaths()`:
> .libPaths()
[1] "/usr/lib64/R/library"  "/usr/share/R/library"
[3] "/usr/lib64/R/site-library"

These paths are all read-only, and so you cannot install packages to them. To fix this, we will tell R to look in additional places for packages.

Exit R and create a directory rpackages in /rigel/<GROUP>/users/<UNI>/.

$ mkdir /rigel/<GROUP>/users/<UNI>/rpackages

Go back into R and add this path to .libPaths()

$ R
> .libPaths("/rigel/<GROUP>/users/<UNI>/rpackages/")

Call .libPaths() to make sure the path has been added

> .libPaths()
[1] "/rigel/<GROUP>/users/<UNI>/rpackages/"
[2] "/usr/lib64/R/site-library"
[3] "/usr/lib64/R/library"

To install a package, such as the "sm" package, tell R to put the package in your newly created local library:

> install.packages("sm", lib="/rigel/<GROUP>/users/<UNI>/rpackages")

Select appropriate mirror and follow install instructions.

Test to see if package can be called:

> library(sm)
Package 'sm', version 2.2-3; Copyright (C) 1997, 2000, 2005, 2007
A.W.Bowman & A.Azzalini
type
help(sm) for summary information

In order to access this library from your programs, make sure you add the following line to the top of every program:

.libPaths("/rigel/<GROUP>/users/<UNI>/rpackages/")

Since R will know where to look for libraries, a call to library(sm) will be successful (however, this line is not necessary per se for the install.packages(...) call, as the directory is already specified in it).

Matlab

Matlab (single thread)
The file linked below is a Matlab M-file containing a single function, simPoissGLM, that takes one argument (lambda).

```
#!/bin/sh
#
# Simple Matlab submit script for Slurm.
#
#SBATCH --A astro                 # The account name for the job.
#SBATCH --J SimpleMLJob           # The job name.
#SBATCH --t 1:00                  # The time the job will take to run.
#SBATCH --mem-per-cpu=1gb        # The memory the job will use per cpu core.
module load matlab

echo "Launching an Matlab run"
date

#define parameter lambda
LAMBDA=10

#Command to execute Matlab code
matlab -nosplash -nodisplay -nodesktop -r "simPoissGLM($LAMBDA)" # > matoutfile

# End of script
```

**Batch queue submission**

```
$ sbatch simpoiss.sh
```

This program will leave several files in the output directory: slurm-<jobid>.out, out.mat, and matoutfile.

**Matlab (multi-threading)**

Matlab has built-in implicit multi-threading (even without applying its Parallel Computing Toolbox, PCT), which causes it to use several cores on the node it is running on. It consumes the number of cores assigned by Slurm. The user can activate explicit (PCT) multi-threading by specifying the number of cores desired also in the Matlab program.

The Torque submit script (simpoiss.sh) should contain the following line:

```
#SBATCH --c 6
```

The -c flag determines the number of cores (up to 24 are allowed).

For explicit multi-threading, the users must include the following corresponding statement within their Matlab program:
parpool('local', 6)

The second argument passed to parpool must equal the number specified with the ppn directive. Users who are acquainted with the use of commands like parfor need to specify explicit multi-threading with the help of parpool command above.

Note: maxNumCompThreads() is being deprecated by Mathworks. It is being replaced by parpool:

The command to execute Matlab code remains unchanged from the single thread example above.

Important note: On Yeti, where Matlab was single thread by default, it appeared that the more recent versions of Matlab took liberties to grab all the cores within a node even when fewer (or even only one) cores were specified as above. On Habanero, we believe this has been addressed by implementing a system mechanism which enforces the proper usage of the number of specified cores.

Python and JULIA

To use python you need to use:

```bash
$ module load anaconda
```

Here's a simple python program called "example.py" – it has just one line:
```
print ("Hello, World!")
```

To submit it on the Habanero Cluster, use the submit script "example.sh"

```bash
#!/bin/sh
#
# Simple "Hello World" submit script for Slurm.
#
#SBATCH --account=astro # The account name for the job.
#SBATCH --job-name=HelloWorld # The job name.
#SBATCH -c 1 # The number of cpu cores to use.
#SBATCH --time=1:00 # The time the job will take to run.
#SBATCH --mem-per-cpu=1gb # The memory the job will use per cpu core.

module load anaconda

#Command to execute Python program
python example.py

#End of script
```

If you use "ls" command you should see 2 programs:

```
example.sh
example.py
```
To submit it - please use:

```
$ sbatch example.sh
```

To check the output use:

```
$ cat slurm-463023.out
Hello, World!
```

Similarly, here is the "julia_example.jl" with just one line

```
$ cat julia_example.jl
println("hello world")
```

and

```
$ cat julia_example.sh
```

```
#!/bin/sh
#
# Simple "Hello World" submit script for Slurm.
#
#SBATCH --account=hblab # The account name for the job.
#SBATCH --job-name=HelloWorld # The job name.
#SBATCH -c 1 # The number of cpu cores to use.
#SBATCH --time=1:00 # The time the job will take to run.
#SBATCH --mem-per-cpu=1gb # The memory the job will use per cpu core.

module load julia

#Command to execute Python program
julia julia_example.jl

#End of script
```

After you finish creating those two files, if you use "ls" command you should see:

```
julia_example.jl
julia_example.sh
```
To submit it use:

```bash
$ sbatch julia_example.sh
Submitted batch job 463030
```

To check the output

```bash
$ cat slurm-463030.out
hello world
```

Julia Interactive Session Usage:

Step 1 >> start an interactive session (**use "astro" if you are a member of "astro" group, otherwise use your group name):

```bash
$ srun --pty -t 0-04:00 -A astro /bin/bash
$ module load julia/0.5.1
$ julia julia_example.jl
hello world

$ julia
_  
_ _ (_) | A fresh approach to technical computing
() | () (_| Documentation: http://docs.julialang.org
| | | | | Type "?help" for help.
| | | | | |__| 
| | | | | Version 0.5.1 (2017-03-05 13:25 UTC)
|_/_/ | '|||' Official http://julialang.org/ release
|__|__| x86_64-pc-linux-gnu

julia>

To quit Julia use "CTRL +D"
```

Tensorflow

The following describes how you can import tensorflow on GPU node.

First, run an interactive job requesting a GPU node

```bash
$ srun --pty -t 0-02:00:00 --gres=gpu:1 -A <group_name> /bin/bash
```

Load modules:
Start python and test tensorflow:

```$ python
Python 2.7.13 |Anaconda custom (64-bit)| (default, Dec 20 2016, 23:09:15)
[GCC 4.4.7 20120313 (Red Hat 4.4.7-1)] on linux2
Type "help", "copyright", "credits" or "license" for more information.
Anaconda is brought to you by Continuum Analytics.
Please check out: http://continuum.io/thanks and https://anaconda.org
>>> import tensorflow as tf
>>> hello = tf.constant('Hello, TensorFlow!')
>>> sess = tf.Session()
2018-02-18 07:46:45.428489: W
tensorflow/core/platform/cpu_feature_guard.cc:45] The TensorFlow library
wasn't compiled to use SSE4.1 instructions, but these are available on your
machine and could speed up CPU computations.
2018-02-18 07:46:45.428620: W
tensorflow/core/platform/cpu_feature_guard.cc:45] The TensorFlow library
wasn't compiled to use SSE4.2 instructions, but these are available on your
machine and could speed up CPU computations.
2018-02-18 07:46:45.428670: W
tensorflow/core/platform/cpu_feature_guard.cc:45] The TensorFlow library
wasn't compiled to use AVX instructions, but these are available on your
machine and could speed up CPU computations.
2018-02-18 07:46:45.428718: W
tensorflow/core/platform/cpu_feature_guard.cc:45] The TensorFlow library
wasn't compiled to use AVX2 instructions, but these are available on your
machine and could speed up CPU computations.
2018-02-18 07:46:45.428760: W
tensorflow/core/platform/cpu_feature_guard.cc:45] The TensorFlow library
wasn't compiled to use FMA instructions, but these are available on your
machine and could speed up CPU computations.
>>> print(sess.run(hello))
Hello, TensorFlow!
```
$ module load anaconda

2. If you haven’t already done so, initialize your jupyter environment.

$ jupyter notebook --generate-config

3. Start a python or ipython session.

$ ipython

4. Run the password hash generator. You will be prompted for a password, prompted again to verify, and then a hash of that password will be displayed.

```python
In [1]: from notebook.auth import passwd; passwd()
Enter password:
Verify password:
Out[1]: 'sha1:60bdb1:306fe0101ca73be2429edbab0935c545'
```

5. Cut and paste the hash into ~/.jupyter/jupyter_notebook_config.py

(Important: the following line in the file is commented out by default so please uncomment it first)

```
c.NotebookApp.password = 'sha1:60bdb1:306fe0101ca73be2429edbab0935c545'
```

Setting the password will prevent other users from having access to your notebook and potentially causing confusion.

**Running a Jupyter Notebook**

1. Log in to the submit node. Start an interactive job.

$ srun --pty -t 0-01:00 -A <ACCOUNT> /bin/bash

2. Get rid of XDG_RUNTIME_DIR environment variable

$ unset XDG_RUNTIME_DIR

3. Load the anaconda environment module.
$ module load anaconda

4. Look up the IP of the node your interactive job is running on.

    $ hostname -i
    10.43.4.206

5. Start the jupyter notebook, specifying the node IP.

    $ jupyter notebook --no-browser --ip=10.43.4.206

6. Look for the following line in the startup output to get the port number.

    The Jupyter Notebook is running at: http://10.43.4.206:8888/

7. From your local system, open a second connection to Habanero that forwards a local port to the remote node and port. Replace UNI below with your uni.

    $ ssh -L 8080:10.43.4.206:8888 UNI@habanero.rcs.columbia.edu

8. Open a browser session on your desktop and enter the URL 'localhost:8080' (i.e. the string within the single quotes) into its search field. You should now see the notebook.