Embarrassingly Parallel workflows and how to execute them



Embarrassingly parallel workflows

What?

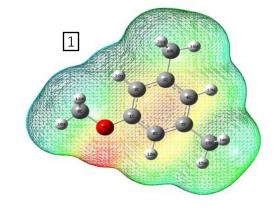
• Executing many independent small jobs simultaneously to use the hardware resource efficiently.

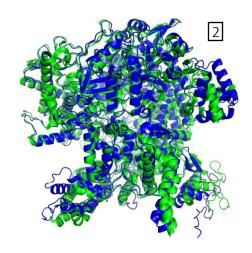
When?

- It is not possible to combine multiple runs/tasks into a single application.
- Large parameter sweep based on the same application or workflow with dependent pipeline steps.
- Workflow involves runs that are depending on several independent software which do not scale beyond a certain number of cores.

Why?

- Nodes are getting denser with respect to resources such as number of cores/threads, GPU cards, Memory.
- Applications do not necessarily scale even within a node: shared memory (OpenMP, MPI SHM, pthreads).







^{1.} Mathiyalagan, A., Manimaran, K., Muthu, K., Rajakantham, M., Density functional theory study on the electronic structures and spectral properties of 3,5-Dimethylanisole dye sensitizer for solar cell applications, Results in Chemistry, Volume 3, 2021

How?

Tools

- Linux background processes (within a node) along with numactl.
 - ► Supported on Snellius and requires prior knowledge of bash scripting and process placement using **numactl**.
 - ▶ Provides maximum manual control if one knows what to do.
- SLURM arrays (to perform similar jobs on multiple allocations).
 - Supported on Snellius and requires prior knowledge of SLURM array options.
 - ► Has some limitations.
- Services for execution of many jobs inside a single allocation, e.g. QCG-PilotJob (https://qcg-pilotjob.readthedocs.io/en/develop/).
 - Supported on Snellius and requires prior knowledge of Python scripting.







How?

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- Linux background processes (within a node) along with numactl.
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There are many more tools















SLURM arrays



Limitations

- SLURM job arrays offer a mechanism for submitting and managing collections of similar jobs.
- All jobs must have the **same initial options** (e.g. size, time limit, etc.).
- The max array size depends on the settings defined in the SLURM configuration file. On Snellius it's 30000.
- The allocation size per instance cannot be below the minimum allocation within SLURM. For instance, on Snellius it's 16 cores and 28 GiB of memory on the "rome" partition.
- One must wait for each task in the array to get allocated and finish.

```
#!/bin/bash
#SBATCH -N 1
#SBATCH -n 2
#SBATCH -p rome
#SBATCH -t 1
hostname

job.sh

$ sbatch --array=0-10 job.sh
```





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```



Will create 11 tasks!



Ways of control

- Jobs which are part of a job array will have the environment variable **SLURM_ARRAY_TASK_ID** set to its array index value.
- A maximum number of simultaneously running tasks from the job array may be specified using a
 "%" separator.

```
$ cat job.sh
#!/bin/bash
#SBATCH -N 1
#SBATCH -p rome
#SBATCH -t 1
echo "SLURM_ARRAY_TASK_ID: $SLURM_ARRAY_TASK_ID"
hostname

$ sbatch --array=0-10 job.sh
...
$ sbatch --array=0-10%2 job.sh
...
```





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...
```

Returns a task ID



Will tell SLURM to submit at most 2 tasks at the same time

Ways of control

Useful environment variables:

- **SLURM_ARRAY_JOB_ID** will be set to the first job ID of the array.
- **SLURM_ARRAY_TASK_ID** will be set to the job array index value.
- **SLURM_ARRAY_TASK_COUNT** will be set to the number of tasks in the job array.
- **SLURM_ARRAY_TASK_MAX** will be set to the highest job array index value.
- **SLURM_ARRAY_TASK_MIN** will be set to the lowest job array index value.



Hands-on



Hands-on

Clone the repository

• https://github.com/sara-nl/course-module-qcg-pilotjob

\$ cd ~

\$ git clone https://github.com/sara-nl/course-module-qcg-pilotjob

\$ cd course-module-qcg-pilotjob



Hands-on #1

Task

 Submit a job array and print hostname, TMPDIR, SLURM_ARRAY_JOB_ID

Steps

- Go to hands-on/example_01
- Take a look at the job script array_job.sh
- Submit the SLURM job script, check the SLURM log file

Questions

- Are host names the same?
- What are the names of **TMPDIR** that are reported?

```
#!/bin/bash
#SBATCH -N 1
#SBATCH -n 1
#SBATCH -t 10
#SBATCH -- array 0-11%3

echo "Running on "
hostname
echo "TMPDIR $TMPDIR"

echo "SLURM_ARRAY_JOB_ID $SLURM_ARRAY_JOB_ID"
echo "SLURM_ARRAY_TASK_ID $SLURM_ARRAY_TASK_ID"
echo "SLURM_ARRAY_TASK_COUNT $SLURM_ARRAY_TASK_COUNT"
echo "SLURM_ARRAY_TASK_MAX $SLURM_ARRAY_TASK_MAX"
echo "SLURM_ARRAY_TASK_MIN $SLURM_ARRAY_TASK_MIN"
```



Hands-on #2

Task

- Compute the average of one column in 1000 CSV files
- Aggregate the results in one CSV file.

Steps

- Go to hands-on/example_02
- Take a look at the job script array_job.sh
- Run prepare input.sh
- Submit the SLURM job script
- Run aggregate.sh when all jobs are finished

Questions

 What is the total execution time and SBUs spent on this task?

```
#SBATCH -p rome
module load 2023
module load Python/3.11.3-GCCcore-12.3.0
cp -r $SLURM_SUBMIT_DIR/input_mod $TMPDIR/
cp -r $SLURM_SUBMIT_DIR/average.py $TMPDIR/
cp -r $SLURM SUBMIT DIR/average.py $TMPDIR/
cd $TMPDIR
echo "TMPDIR = $TMPDIR"
input_file_path=input_mod/${SLURM_ARRAY_TASK_ID}_*
echo "Analyzing file: $input_file_path"
python3 average.py $input_file_path
```



QCG-PilotJob



QCGPilot-Job

Job manager inside SLURM

- Submits jobs within a single large allocation across multiple nodes.
- Does not have to wait for small individual allocations like in SLURM arrays.
- Tries to optimize resources for each job based on requirements such that the queue is always full.
- Possibility of restarting failed/timed out jobs.
- One can also specify complex result-based job dependencies.

Some caveats and drawbacks

- One needs to estimate, the total time of all the jobs combined.
- Job/system state files get produced in the submission directory.
- Might bring some complexity into execution of a Singularity containers with embedded MPI-based codes.
- In the case of problems, the log files may not be very expressive.



Workflow

SLURM job script

QCG-PilotJob python script

Executable

Output

Describes resources, loads the QCG-PilotJob module and runs the QCG-PilotJob python script Invokes the QCG-PilotJob
Manager that aggregates all
your jobs along with
resources and conditions
based on which jobs need
to be invoked

This is the main application that one wants to execute

Job output with QCG-PilotJob metrics



QCGPilot-Job: Set up the environment

- The QCG-PilotJob package is available as a module in the 2023 environment.
- Note that the environment from the login node is not transferred to the compute nodes, unless defined in, e.g., the .bashrc file. Thus, you have to re-load the QCG-PilotJob package in your job script.

```
$ module purge$ module load 2023$ module load QCG-PilotJob/0.14.1-foss-2023a
```



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QCGPilot-Job: SLURM job script

```
run.sh
#SBATCH -n 16
module load 2023
module load QCG-PilotJob/0.14.1-foss-2023a
python test.py
```



Workflow

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Job output with QCG-PilotJob metrics



- Work with the **QCG-PilotJob** manager consists of a few mandatory steps:
 - Creating an instance of the QCG-PilotJob Manager
 - creation of a class object
 - Waiting for all submitted jobs to finish
 - will wait until some or all submitted to the QCG-PilotJob Manager jobs finish
 - Calling for the **finish()** method at the end of the Python script
 - this method terminates the background thread in which the instance of a QCG-PilotJob Manager has been run



test.py

```
manager = LocalManager()
print('available resources: ', manager.resources())
manager.wait4all()
manager.finish()
```

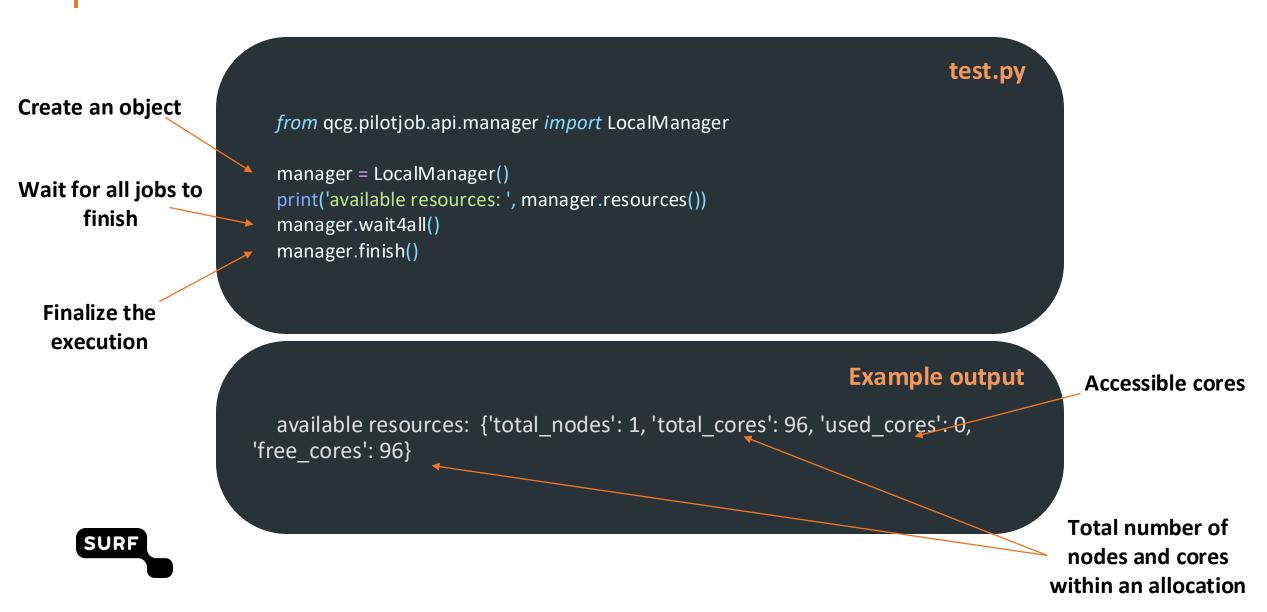
from qcg.pilotjob.api.manager import LocalManager

Example output

```
available resources: {'total_nodes': 1, 'total_cores': 96, 'used_cores': 0, 'free_cores': 96}
```



test.py **Create an object** from qcg.pilotjob.api.manager import LocalManager manager = LocalManager() Wait for all jobs to print('available resources: ', manager.resources()) finish manager.wait4all() manager.finish() Finalize the execution **Example output** available resources: {'total_nodes': 1, 'total_cores': 96, 'used_cores': 0, 'free_cores': 96} SURF



QCGPilot-Job: Create jobs

- To execute multiple jobs within a single SLURM allocation we need to:
 - Create an object of the **Jobs** class
 - Populate it with some parameters (describe jobs)
 - Submit the created object to the QCG-PilotJob Manager

```
...
from qcg.pilotjob.api.job import Jobs

jobs = Jobs()
jobs.add(...)
jobs_ids = manager.submit(jobs)
print('submited jobs: ', str(job_ids))
...
```



QCGPilot-Job: Job description (main parameters)

- **name** the job name
- **exec** path to the executable program
- args executable program arguments
- **script** bash script content
- stdin path to file which content should be passed to the standard input stream
- stdout path to the file where standard output stream should be saved
- stderr path to the file where standard error stream should be saved
- modules list of modules that should be loaded before job start
- **numCores** number of required cores specification
- **numNodes** number of required nodes specification
- **iteration** iterations definition
- model model of execution



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QCGPilot-Job: execution models

- **default** only a single process is launched within the allocation
- threads is designed for running OpenMP tasks on a single node
- openmpi the processes are started with the mpirun command
- **intelmpi** same but for Intel MPI
- **srunmpi** the processes are started with the srun command

Read more about execution models in the official docs:

https://qcg-pilotjob.readthedocs.io/en/develop/execution_models.html



QCGPilot-Job: Calling for an executable

```
test.py
from qcg.pilotjob.api.manager import LocalManager
from qcg.pilotjob.api.job import Jobs
manager = LocalManager()
jobs = Jobs()
jobs.add(script='echo "job ${it} executed at `date` @ `hostname`"',
     name='test_job',
    stdout='job.out.${it}',
    iteration=4)
job names = manager.submit(jobs)
print('submited job names: ', str(job_names))
job status = manager.status(job names)
print('job status: ', job_status)
manager.wait4all()
manager.finish()
```



Hands-on



Hands-on #3

Task

• Execute **512** independent short jobs on two nodes on the "rome" partition. Note that one node on the "rome" partition has 128 cores.

Steps

- Go to hands-on/example_03
- Take a look at qcg_job.py and qcg_job.sh
- Submit the SLURM job script, check the results

Questions

- What host names are reported?
- What additional files and directories are created?

```
from qcg.pilotjob.api.job import Jobs
from qcg.pilotjob.api.manager import LocalManager
manager = LocalManager()
jobs = Jobs()
for job in range(512):
  jobs.add(name="job {}".format(job),
       exec='hostname',
       stdout='output/job.{}.out'.format(job),
       stderr='output/job.{}.err'.format(job),
       model='default',
       numCores={ "exact" : 1},
       iteration=1)
print("-- submit jobs --")
manager.submit(jobs)
print("-- wait for all jobs --")
manager.wait4all()
manager.finish()
print("-- finished")
```



Hands-on #4

Task

- Compute the average of one column in 1000 CSV files.
- Aggregate the results in one CSV file.

Steps

- Go to hands-on/example_04
- Take a look at **README.md**, **qcg_job_v0.py** and **qcg_job.sh**
- Extract the input data (input.tar.gz)
- Submit the SLURM job script, check the results

Steps

- The *v0 script has a problem. Can you spot it?
- Execute qcg_job_v1.py, compare results with the results from qcg_job_v0.py

```
job names = []
for filename in glob(os.path.join("input/*.csv"), recursive = False):
  job names.append(os.path.basename(filename))
manager = LocalManager()
jobs = Jobs()
for jname in job names:
  print("submit {}".format(jname))
  jobs.add(name=jname,
       exec='python3',
       args=["average.py",
          os.path.join("input", jname)],
       stdout='average {}'.format(jname),
       stderr='job.{}.err'.format(jname),
       modules=[
      "2023", "Python/3.11.3-GCCcore-12.3.0"],
       iteration=1
jobs.add(name="aggregate",
     script='cat average *.csv | sort',
     stdout='result.csv',
     stderr='aggregate.err')
```

