

Huygens Professional and Core on HPC Bunya Guide

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Abstract

A brief guide on how to use Huygens Professional and Core on HPC Bunya, including running Huygens Core by submitting a job to the Simple Linux Utility for Resource Management (SLURM) scheduler.

Preamble

This is HPC Bunya:

<https://rcc.uq.edu.au/systems/high-performance-computing/bunya>.

If you haven't done so already, apply for a Bunya account here:

<https://services.qriscloud.org.au/services/request/new/ee6def64259741a095c1fed20743e3fb>.

Copy questions 2) - 8) into the "Request details" box on the form and provide details for each item. Incomplete applications will be rejected and applicants will be required to fill in a new form.

Bunya training is available here:

<https://rcc.uq.edu.au/training-support/training-courses>.

Register via email to rcc-support@uq.edu.au to attend UQ-only training sessions.

Read the Bunya user guide here:

<https://github.com/UQ-RCC/hpc-docs/blob/main/guides/Bunya-User-Guide.md>

and the Bunya OnDemand guide here:

<https://github.com/UQ-RCC/hpc-docs/blob/main/guides/OnDemand-Guide.md>.

You can then request access to Huygens Professional and Core on HPC Bunya using this link:

<https://services.qriscloud.org.au/access/6211d1e3482544b2b73fc85156446e2c/member>.

Running Huygens Professional and Core via OnDemand

1. Go to the OnDemand site:
<https://bunya-ondemand.rcc.uq.edu.au/>
2. Navigate to Interactive Apps > GPU-Accelerated Desktop. Give the job a name, choose your Bunya account group, and specify the number of GPUs, CPU cores per task, number of tasks, and maximum running time. Click "Launch."
3. OnDemand will prompt: "Please be patient as your job currently sits in queue. The wait time depends on the number of cores as well as time requested."
Click "Launch GPU-Accelerated Desktop" when the desktop is running (Fig. 1).

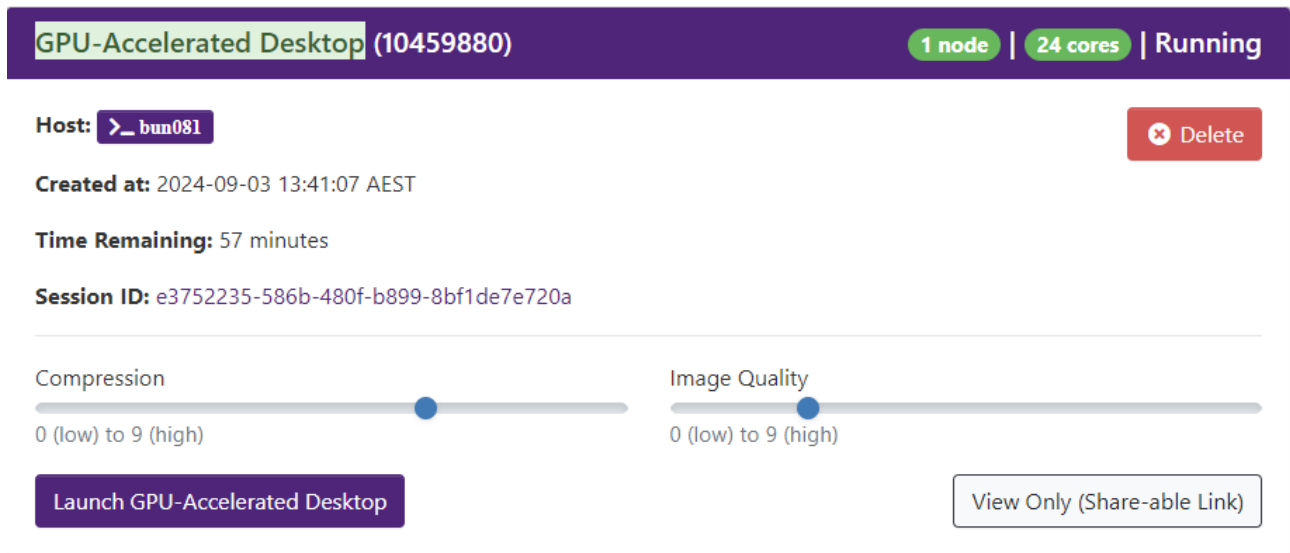


Figure 1: HPC Bunya OnDemand GPU-accelerated desktop running.

- On the visualisation desktop, open a MATE terminal by navigating to Applications > System Tools > MATE Terminal and type: `module load huygens/25.04.0-p4`
`huygenspro`
 (Fig. 2).

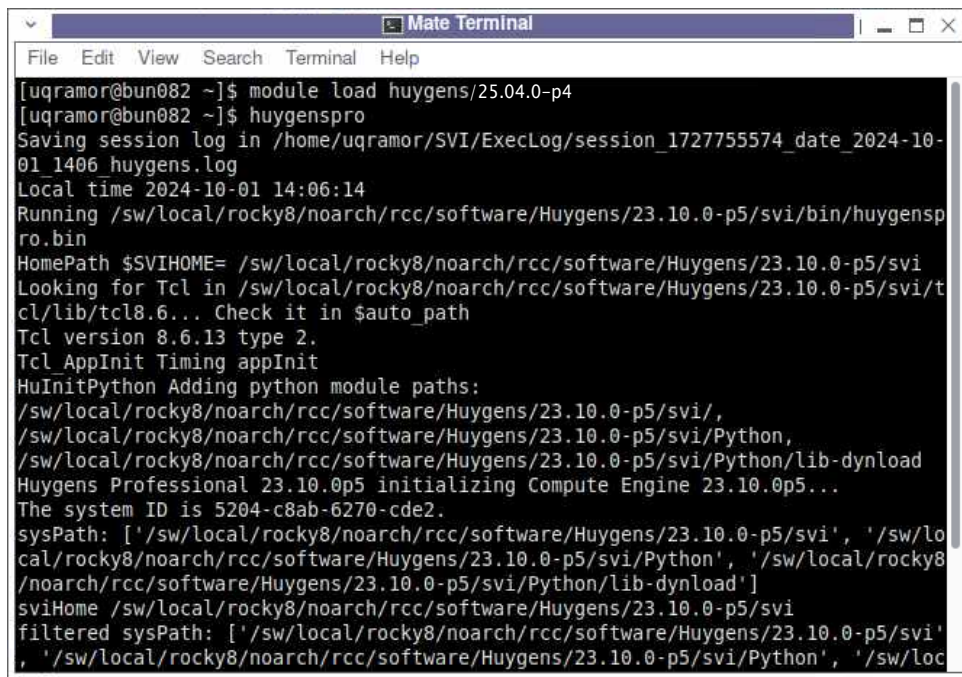


Figure 2: Running Huygens Professional via the MATE terminal.

5. This launches the Huygens Professional graphical user interface (GUI, Fig. 3).

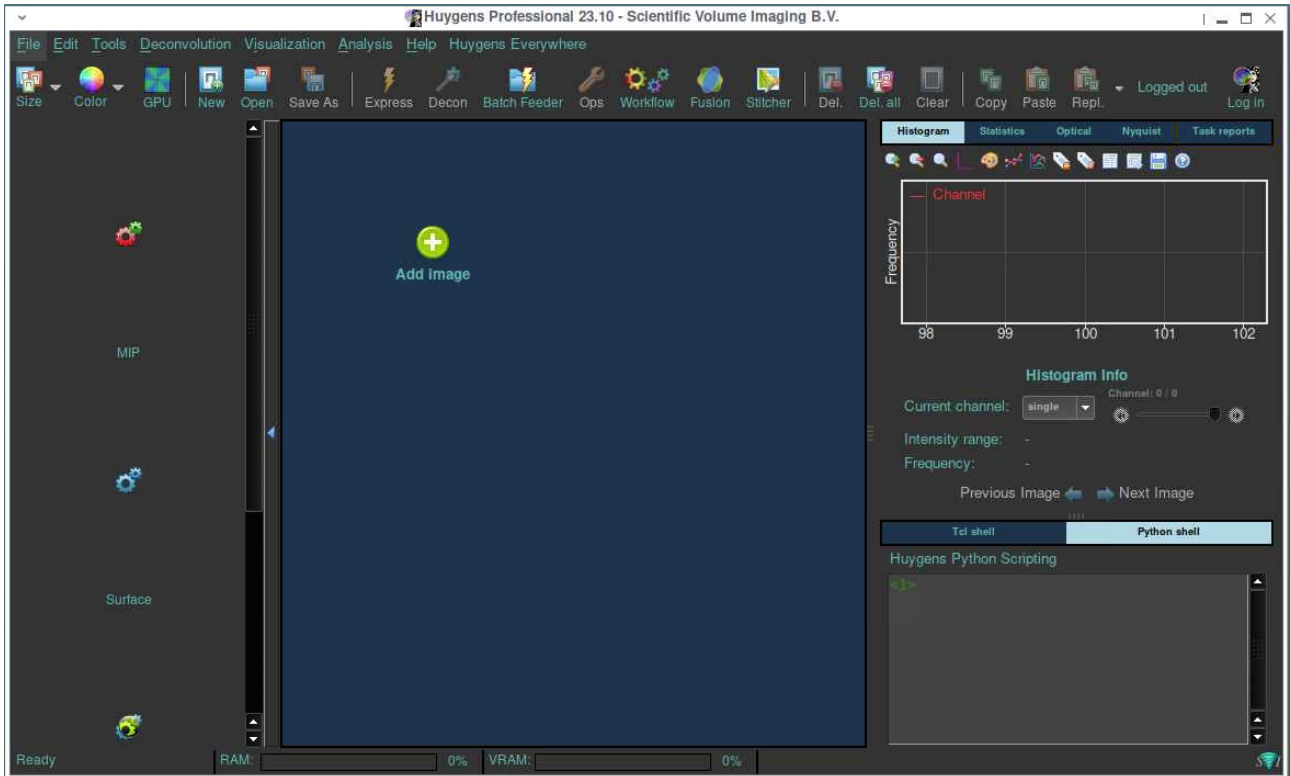


Figure 3: The Huygens Professional GUI.

6. Open an image and create a microscope template as normal (Fig. 4).

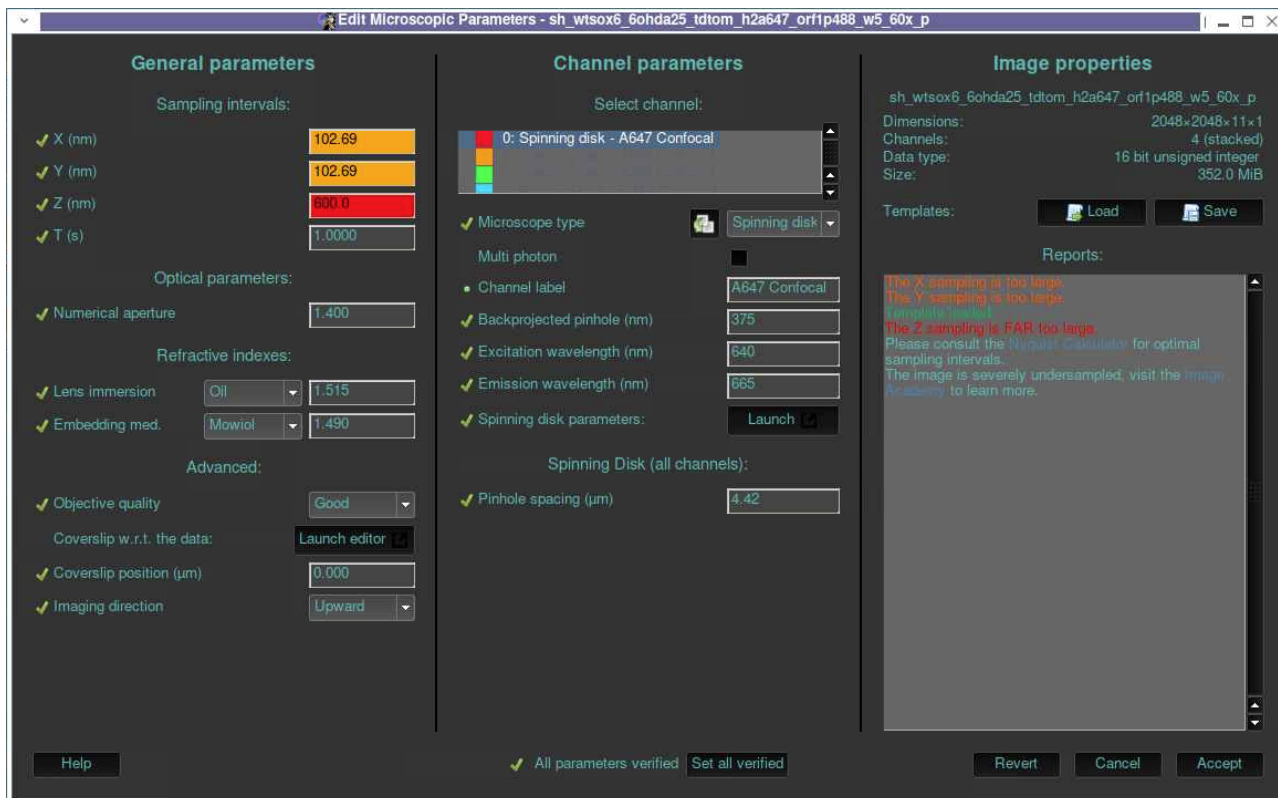


Figure 4: Creating a microscope template.

7. Do a deconvolution run using the wizard and save the deconvolution template as normal (Fig. 5).

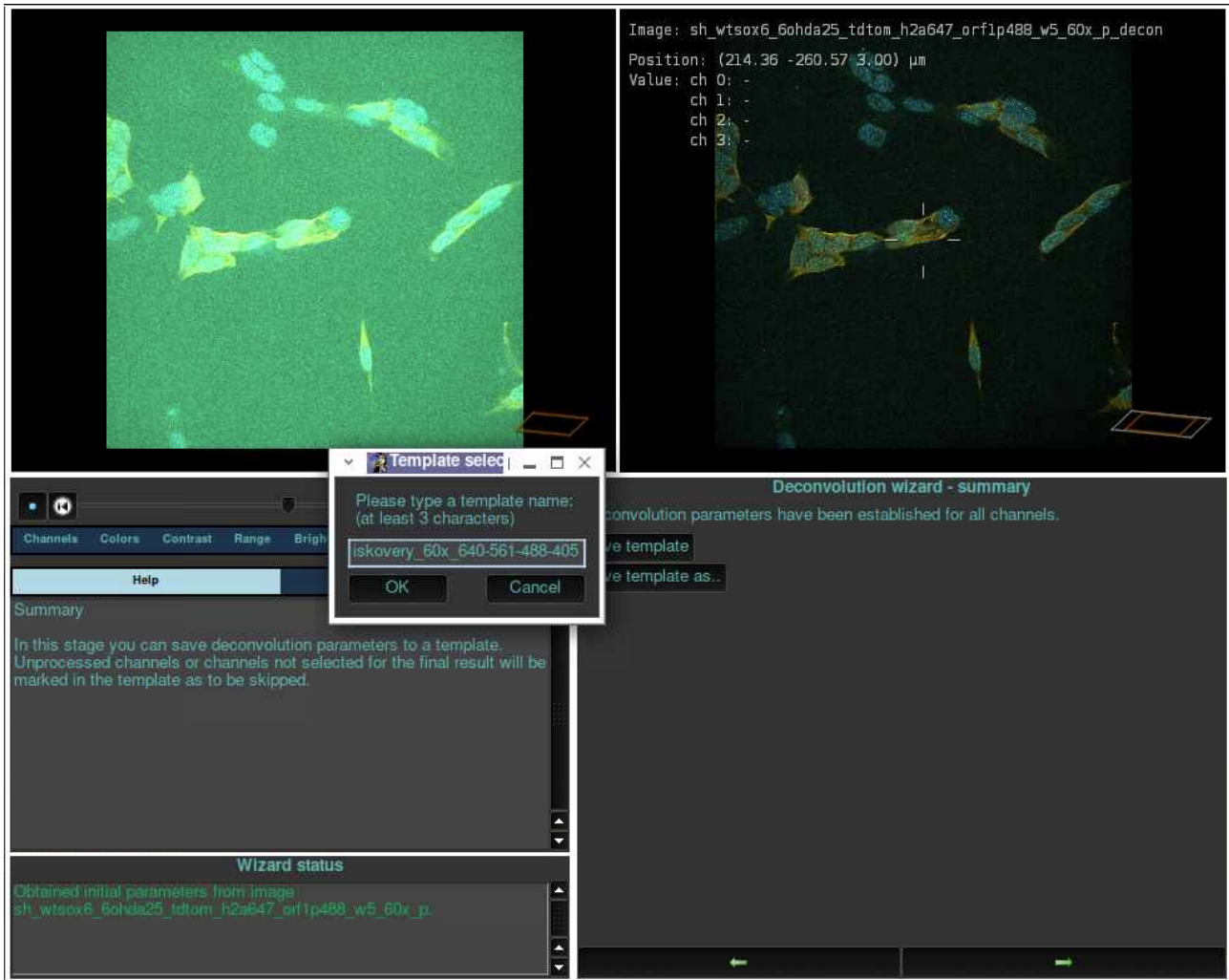


Figure 5: Saving a deconvolution template.

8. Open the Workflow Processor and create a batch job, specifying the input images or folder, the microscope template, deconvolution template, and output file format and directory (Fig. 6).

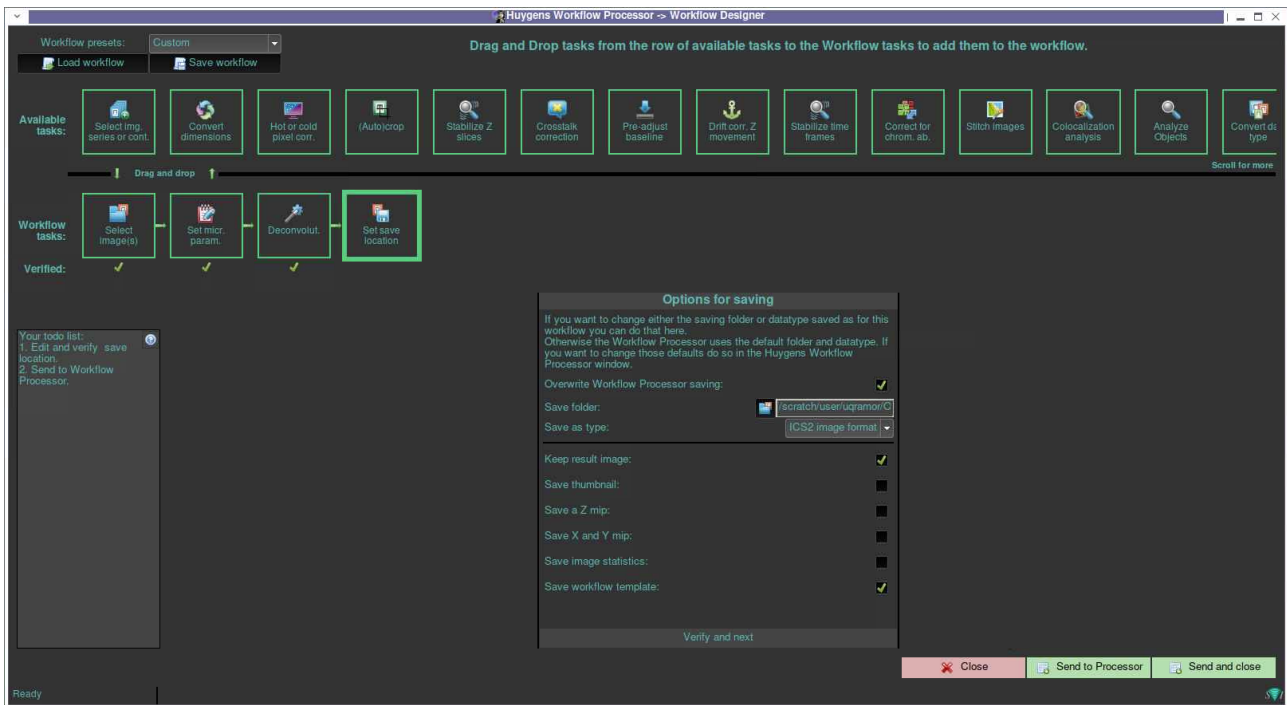


Figure 6: Creating a batch job on the Workflow Processor.

- Save the batch template (.hgsb file, Fig. 7). You will use this template file to run batch jobs with Huygens Core, on the visualisation desktop and on SLURM.

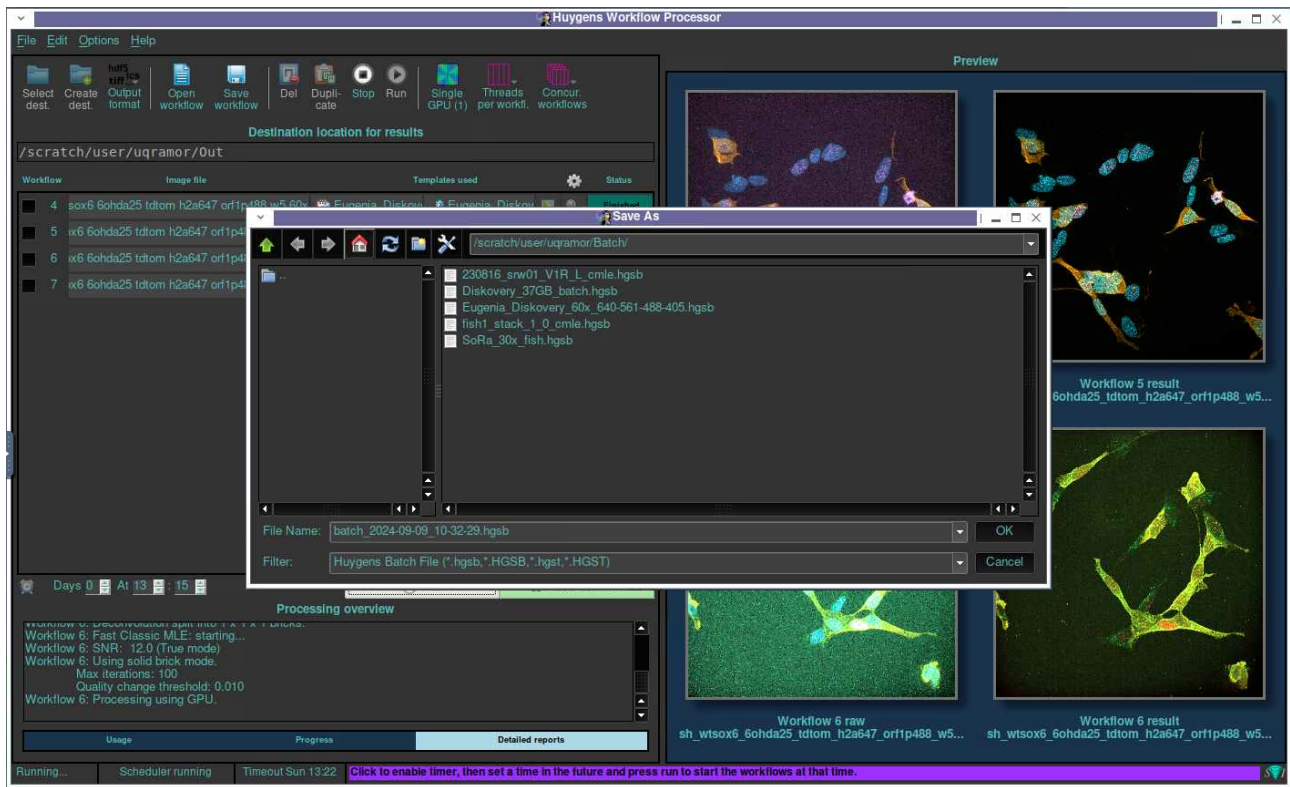


Figure 7: Saving a batch template.

10. Run Huygens Core by opening a new terminal and typing:

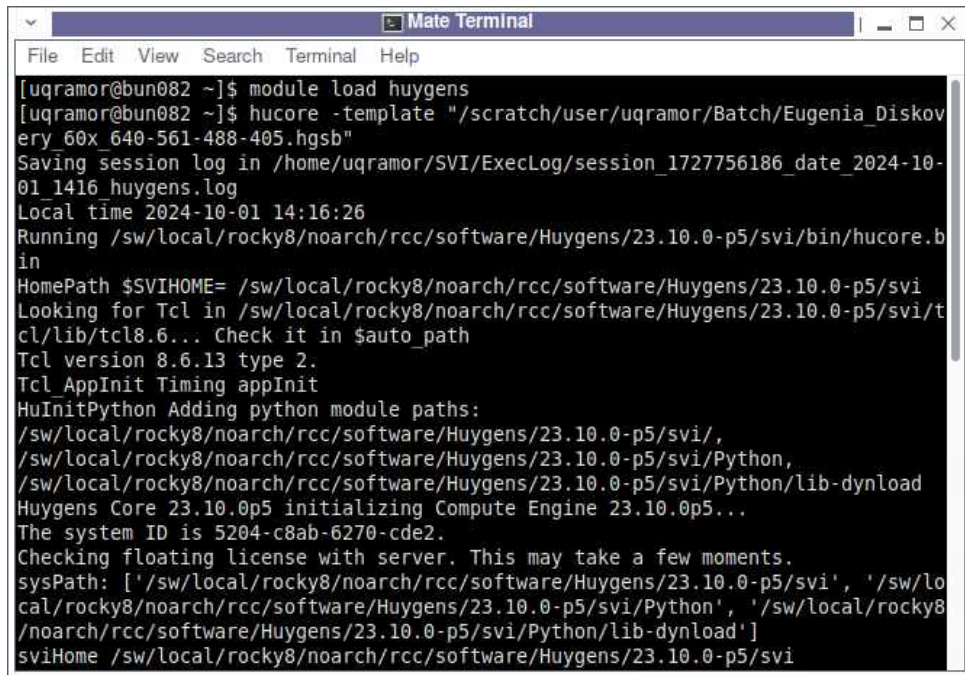
```
module load huygens
hucore -template 'batch.template.location'
```

for example,

```
hucore -template '/scratch/user/uqramor/Batch/Eugenia_Diskcovery_60x_640-561-488-405.hgsb'
```

(Fig. 8).

Huygens Core will then run the batch job and save the outputs in the directory specified on the batch template.



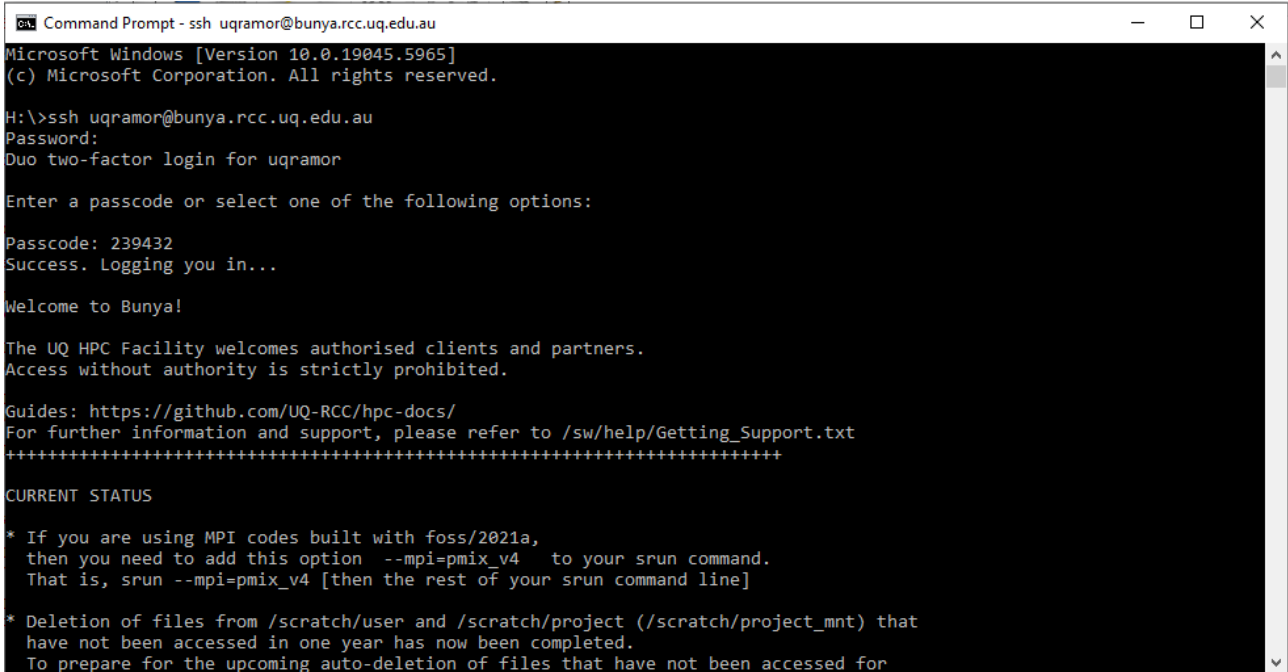
```
Mate Terminal
File Edit View Search Terminal Help
[uqramor@bun082 ~]$ module load huygens
[uqramor@bun082 ~]$ hucore -template "/scratch/user/uqramor/Batch/Eugenia_Diskcovery_60x_640-561-488-405.hgsb"
Saving session log in /home/uqramor/SVI/ExecLog/session_1727756186_date_2024-10-01_1416_huygens.log
Local time 2024-10-01 14:16:26
Running /sw/local/rocky8/noarch/rcc/software/Huygens/23.10.0-p5/svi/bin/hucore.b
in
HomePath $SVIHOME= /sw/local/rocky8/noarch/rcc/software/Huygens/23.10.0-p5/svi
Looking for Tcl in /sw/local/rocky8/noarch/rcc/software/Huygens/23.10.0-p5/svi/t
cl/lib/tcl8.6... Check it in $auto_path
Tcl version 8.6.13 type 2.
Tcl_AppInit Timing appInit
HuInitPython Adding python module paths:
/sw/local/rocky8/noarch/rcc/software/Huygens/23.10.0-p5/svi/,
/sw/local/rocky8/noarch/rcc/software/Huygens/23.10.0-p5/svi/Python,
/sw/local/rocky8/noarch/rcc/software/Huygens/23.10.0-p5/svi/Python/lib-dynload
Huygens Core 23.10.0p5 initializing Compute Engine 23.10.0p5...
The system ID is 5204-c8ab-6270-cde2.
Checking floating license with server. This may take a few moments.
sysPath: ['/sw/local/rocky8/noarch/rcc/software/Huygens/23.10.0-p5/svi', '/sw/lo
cal/rocky8/noarch/rcc/software/Huygens/23.10.0-p5/svi/Python', '/sw/local/rocky8
/noarch/rcc/software/Huygens/23.10.0-p5/svi/Python/lib-dynload']
sviHome /sw/local/rocky8/noarch/rcc/software/Huygens/23.10.0-p5/svi
```

Figure 8: Running Huygens Core via OnDemand.

Huygens SLURM on Bunya

1. On your machine, open a terminal window. Log on to Bunya by typing:
`ssh USERID@bunya.rcc.uq.edu.au`

Enter your UQ password. Go through the Duo authentication prompts. You will then be logged on to Bunya (Fig. 9).



```
Command Prompt - ssh uqramor@bunya.rcc.uq.edu.au
Microsoft Windows [Version 10.0.19045.5965]
(c) Microsoft Corporation. All rights reserved.

H:\>ssh uqramor@bunya.rcc.uq.edu.au
Password:
Duo two-factor login for uqramor

Enter a passcode or select one of the following options:

Passcode: 239432
Success. Logging you in...

Welcome to Bunya!

The UQ HPC Facility welcomes authorised clients and partners.
Access without authority is strictly prohibited.

Guides: https://github.com/UQ-RCC/hpc-docs/
For further information and support, please refer to /sw/help/Getting_Support.txt
*****

CURRENT STATUS

* If you are using MPI codes built with foss/2021a,
then you need to add this option --mpi=pmix_v4 to your srun command.
That is, srun --mpi=pmix_v4 [then the rest of your srun command line]

* Deletion of files from /scratch/user and /scratch/project (/scratch/project_mnt) that
have not been accessed in one year has now been completed.
To prepare for the upcoming auto-deletion of files that have not been accessed for
```

Figure 9: Connecting to Bunya via ssh on a terminal window.

- By default, you will be on the /home directory. Print the current working directory:

```
$ pwd
```

(Note: “\$” indicates a command line and is not part of the command.)

UQ RCC requires that all jobs are called from the /scratch directory. Change to your /scratch directory:

```
$ cd /scratch/user/USERID
```

(Fig. 10).

```

Command Prompt - ssh uqramor@bunya.rcc.uq.edu.au
* Deletion of files from /scratch/user and /scratch/project (/scratch/project_mnt) that
  have not been accessed in one year has now been completed.
  To prepare for the upcoming auto-deletion of files that have not been accessed for
  more than 90 days, please ensure inactive files and data are backed up and archived
  to a safe space (like RDM) if required.

+++++
Last login: Mon Jun 30 12:24:12 2025 from 10.49.123.43
[uqramor@bunya1 ~]$ pwd
/home/uqramor
[uqramor@bunya1 ~]$ ls
Desktop  Downloads  HuygensGpu.txt  ondemand  Public  Templates
Documents  HuygensError.txt  Music  Pictures  SVI  Videos
[uqramor@bunya1 ~]$ cd /scratch/user/uqramor
[uqramor@bunya1 uqramor]$ ls
980                               hucore140.sh  slurm-14650771.out
Batch                             hucore.sh     slurm-14773396.out
Batch2                            Installer     slurm-9772222.out
Blue                              Out           slurm-9807939.out
Collaborate                       slurm-1000130.out  slurm-9843496.out
Convallaria_63x_1Pt4NA_561-488_SR_AirySheppardRings_decon_Meas.ics  slurm-10002720.out  slurm-9843961.out
Convallaria_63x_1Pt4NA_561-488_SR_AirySheppardRings_decon_Theo.ics  slurm-10349960.out  slurm-9844437.out
Demo Images                       slurm-10350521.out  slurm-9844830.out
Discovery                         slurm-11014598.out  slurm-9978485.out
hucore21.sh                       slurm-11971477.out  SoRa
hucore2.sh                         slurm-11974178.out  tmp
hucore3.sh                         slurm-11975827.out  Yokogawa
[uqramor@bunya1 uqramor]$
    
```

Figure 10: Printing the current working directory and changing to the scratch directory.

3. Create a script to submit your job to the SLURM scheduler. Use vi, or a similar editor. Give the script a name, and use .sh as the extension (Fig. 11).

Watch QCIF's quick overview of vi here:

https://www.youtube.com/watch?v=TuR9d9Z_Fis

```
[uqramor@bunya2 uqramor]$ cat hucore2.sh
#!/bin/bash -l

#SBATCH --nodes=1
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=24
#SBATCH --mem=16G
#SBATCH --job-name=HUCORE
#SBATCH --time=01:00:00
#SBATCH --qos=gpu
#SBATCH --partition=gpu_cuda
#SBATCH --gres=gpu:140:1
#SBATCH --account=a_qbi_microscopy

module load huygens
hucore -template "/scratch/user/uqramor/Batch/Eugenia_Discovery_60x_640-561-488-405.hgsb"
[uqramor@bunya2 uqramor]$
```

Figure 11: An example script to submit a Huygens Core job to SLURM.

A short description of the lines on the script follows. The Bunya User Guide has more information.

```
#!/bin/bash -l
```

→ We are using BASH (the Bourne Again SHell), a shell program and command language for Linux. The -l command makes the shell a login shell.

The SBATCH commands are for allocating resources:

```
#SBATCH --nodes=1 → number of nodes
```

```
#SBATCH --ntasks-per-node=1 → 1 for single- and multi-thread jobs
```

```
#SBATCH --cpus-per-task=24 → number of threads
```

```
#SBATCH --mem=16G → RAM per job in MB, GB, TB; see the Bunya guide
```

```
#SBATCH --job-name=HUCORE → the name you give your job
```

```
#SBATCH --time=01:00:00 → time the job needs to complete; max=168 hrs for gpu_cuda, =24hrs for gpu_viz
```

```
#SBATCH --qos=gpu → the Quality of Service name; see the QoS guide
```

```
#SBATCH --partition=gpu_cuda → you are using the GPU partition;
```

```
#SBATCH --gres=gpu:140:1 → GPU type and number; in this example, using one L40 GPU; can also use gres=gpu:nvidia_a100_80gb_pcie.1g.10gb:1 or the L40s
```

```
#SBATCH --account=a_qbi_microscopy → your accounting group
```

The next two lines launch Huygens Core for batch runs:

```
module load huygens → launches the Huygens module
```

```
hucore -template “.hgsb batch file” → launches Huygens Core and runs the batch job as specified in the template
```

4. Submit the job to SLURM:
`$ sbatch SCRIPT.FILENAME`

```
[uqramor@bunya2 uqramor]$ sbatch hucore2.sh
Submitted batch job 14773396
[uqramor@bunya2 uqramor]$
```

Figure 12: Submitting the job to SLURM.

5. Check the status in the job queue:
`$ squeue --me`

```
[uqramor@bunya2 uqramor]$ squeue --me
JOBID PARTITION NAME USER ST TIME NODES NODELIST(REASON)
14773396 gpu_cuda HUCORE uqramor R 0:36 1 bun080
[uqramor@bunya2 uqramor]$
```

Figure 13: Checking the status in the queue.

6. Monitor the job by using the `tail` command.
`$ tail -f slurm-JOBID.out`

To exit the `tail` command, press `Ctrl + C`.

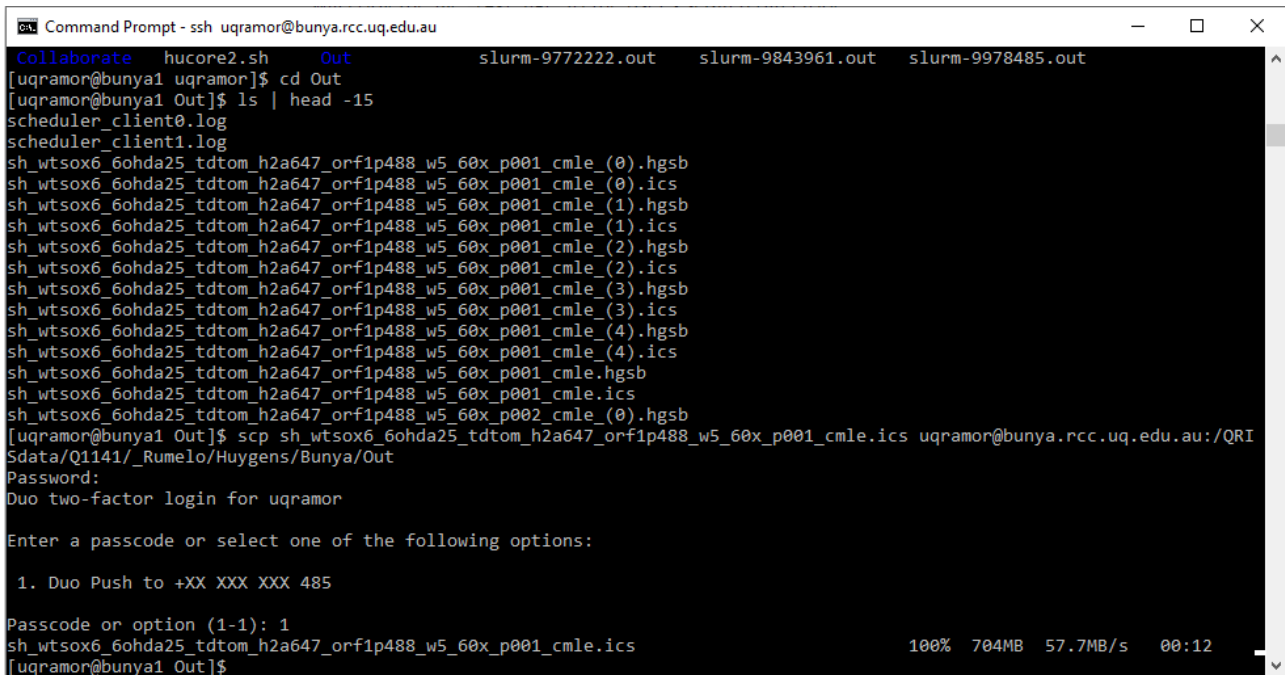
```
Command Prompt - ssh uqramor@bunya.rcc.uq.edu.au
[uqramor@bunya2 uqramor]$ tail -f slurm-14773396.out

Bleaching correction for task cmle:3:
z dim: 1.000
t dim: 1.000
Doing task imgSave...
Scaling mode while saving: -cmode scale
Scaling mode while saving: -cmode scale
Saving image using command: sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle_14_save {/scratch/user/uqramor/Out/sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle_(14).ics} -type ics2 -cmode scale
Successfully saved results to: {/scratch/user/uqramor/Out/sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle_(14).ics}
Launching workflow 6 for client 0, ID: 2 on cpu group 0
Setting export option type to hdf5
Setting export option multidir to 0
Setting export option cmode to scale
Setting export option compr to 0
Setting export option subResolutions to 0
Setting export option subSamplingFactor to 2
Complete envArr:
key gpuDevice ; val 0
key useMultiGpu ; val 0
key OMP_DYNAMIC ; val 0
key retainProcess ; val false
key inputConversion ; val int
key resultDir ; val /scratch/user/uqramor/Out
key attemptGpu ; val 1
key exportFormat ; val type hdf5 multidir 0 cmode scale
key timeOut ; val 172800
key concurrentJobCnt ; val 1
```

Figure 14: Monitoring the job.

7. When the job is done, use scp (secure copy) to transfer individual files to your RDM collection:

```
$ scp FILENAME USERID@bunya.rcc.uq.edu.au:/RDM_FILE_PATH
```



```
Command Prompt - ssh uqramor@bunya.rcc.uq.edu.au
Collaborate hucore2.sh Out slurm-9772222.out slurm-9843961.out slurm-9978485.out
[uqramor@bunya1 uqramor]$ cd Out
[uqramor@bunya1 Out]$ ls | head -15
scheduler_client0.log
scheduler_client1.log
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle_(0).hgsb
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle_(0).ics
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle_(1).hgsb
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle_(1).ics
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle_(2).hgsb
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle_(2).ics
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle_(3).hgsb
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle_(3).ics
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle_(4).hgsb
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle_(4).ics
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle.hgsb
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle.ics
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p002_cmle_(0).hgsb
[uqramor@bunya1 Out]$ scp sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle.ics uqramor@bunya.rcc.uq.edu.au:/QRI
Sdata/Q1141/_Rumelo/Huygens/Bunya/Out
Password:
Duo two-factor login for uqramor

Enter a passcode or select one of the following options:

1. Duo Push to +XX XXX XXX 485

Passcode or option (1-1): 1
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle.ics 100% 704MB 57.7MB/s 00:12
[uqramor@bunya1 Out]$
```

Figure 15: Transferring a file using scp.

or copy the whole output directory:

```
$ scp -r OUTPUT_DIRECTORY USERID@bunya.rcc.uq.edu.au:/RDM_FILE_PATH
```

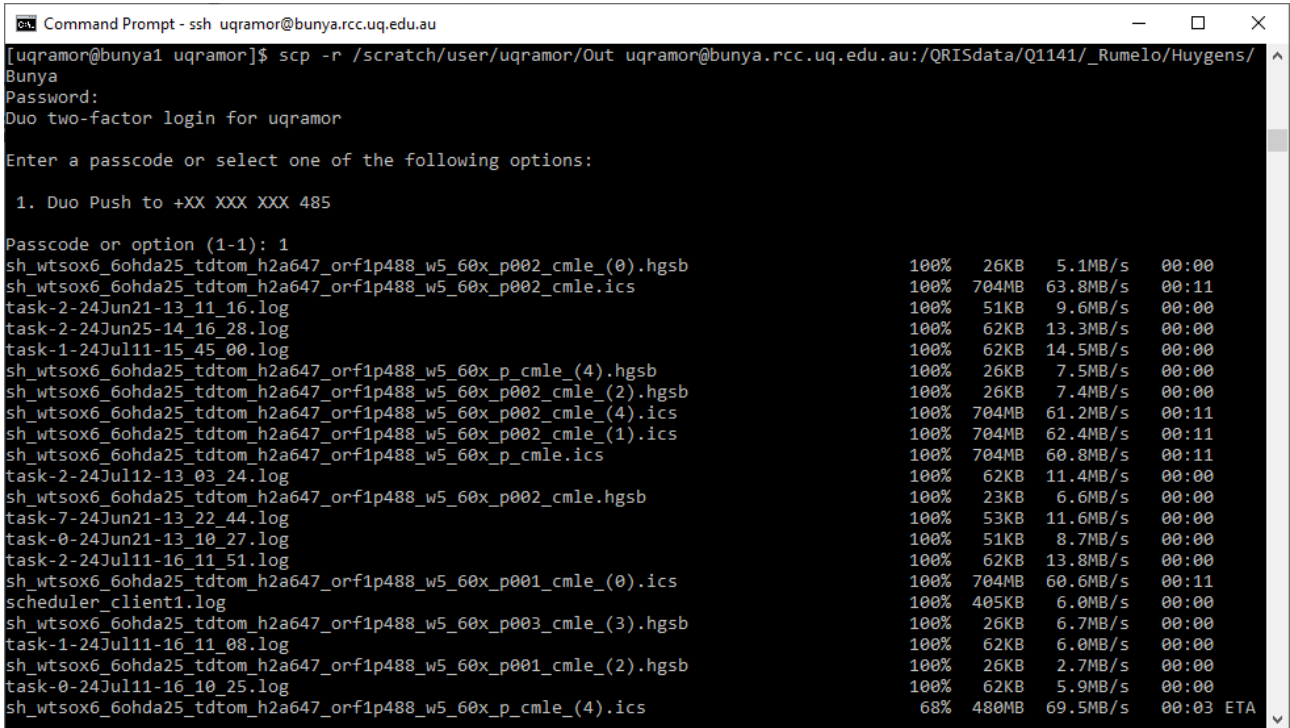


Figure 16: Transferring the output directory using scp.

Acknowledgments

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