

# 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](mailto: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).

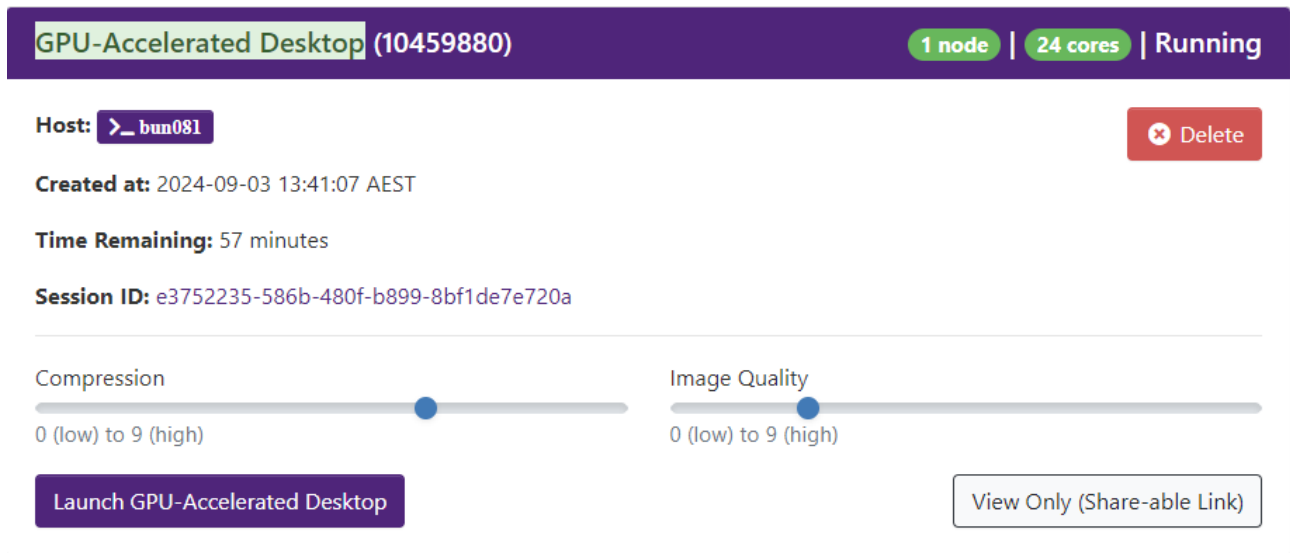


Figure 1: HPC Bunya OnDemand GPU-accelerated desktop running.

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

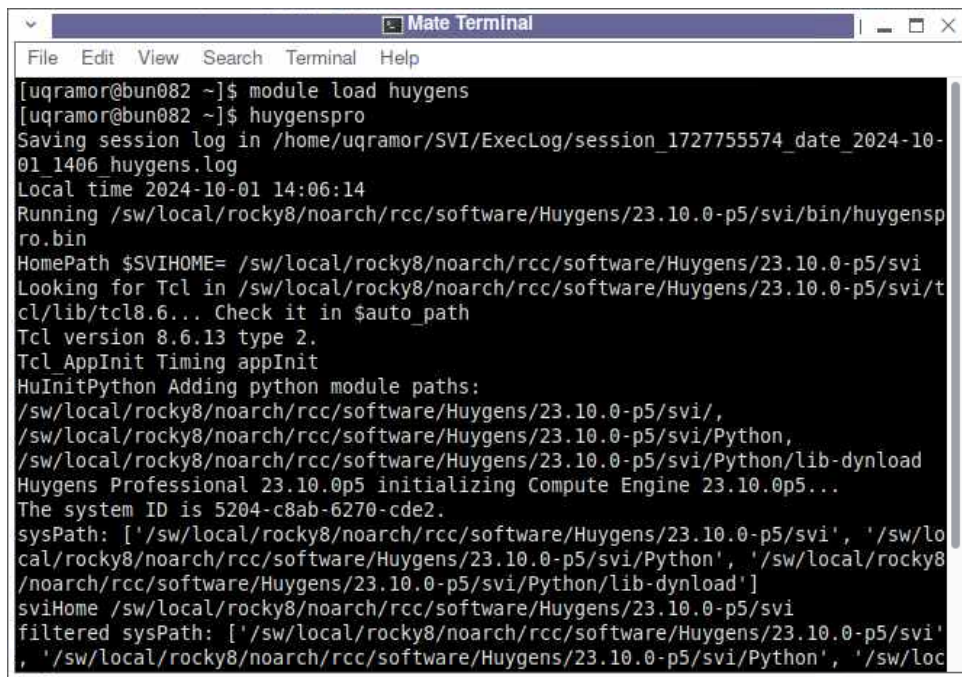


Figure 2: Running Huygens Professional via the MATE terminal.

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

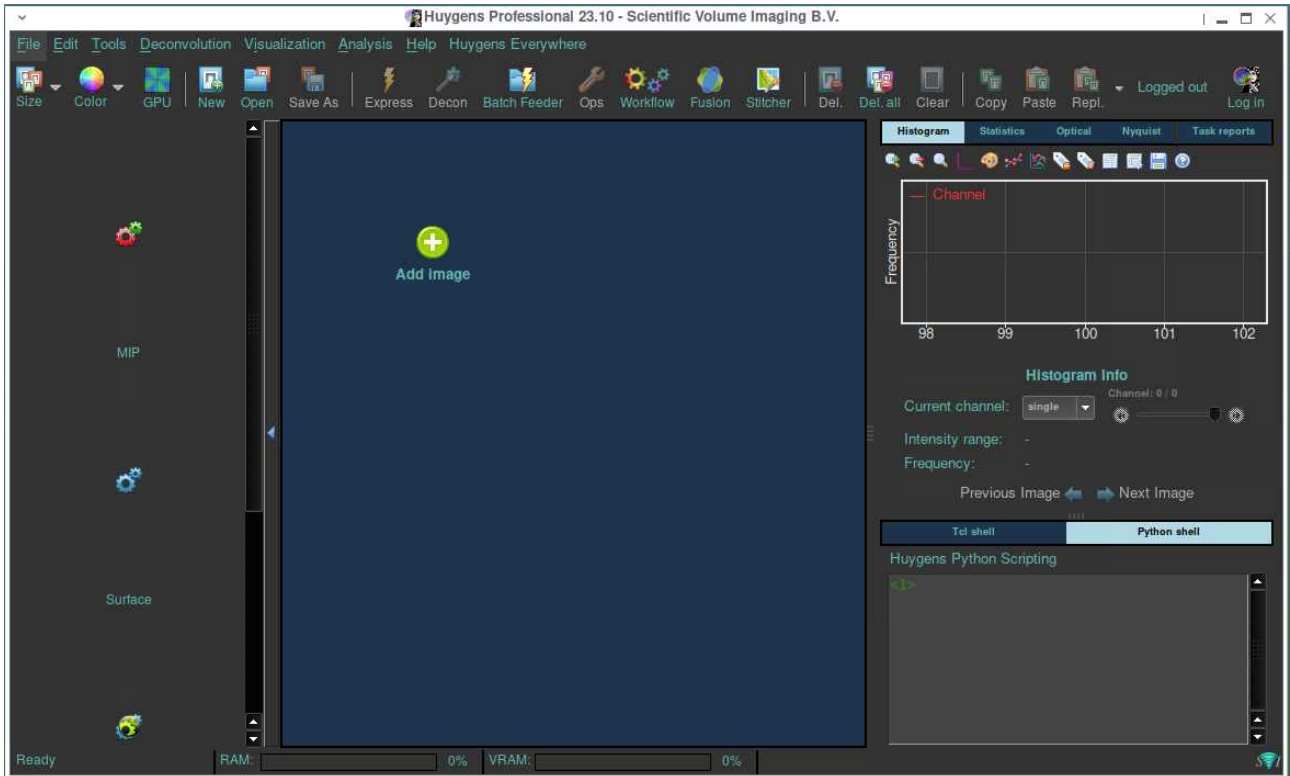


Figure 3: The Huygens Professional GUI.

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

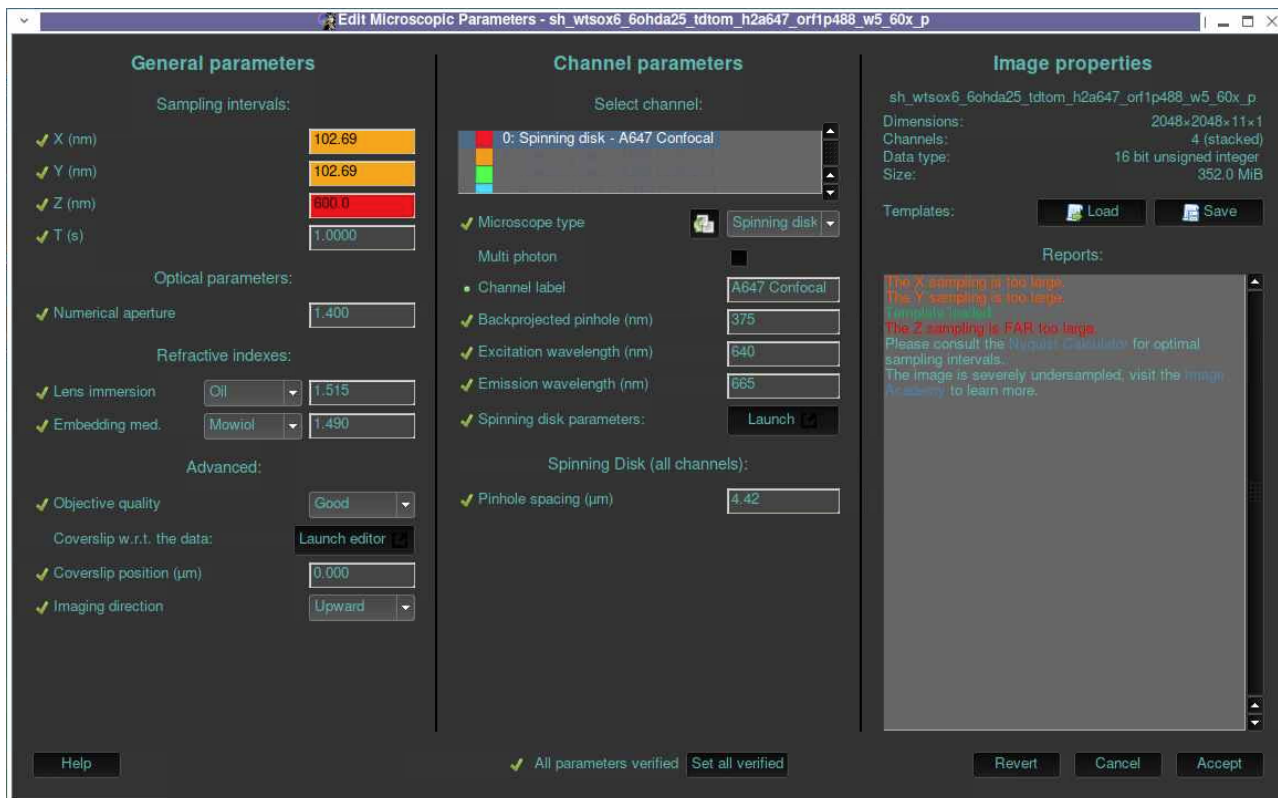


Figure 4: Creating a microscope template.

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

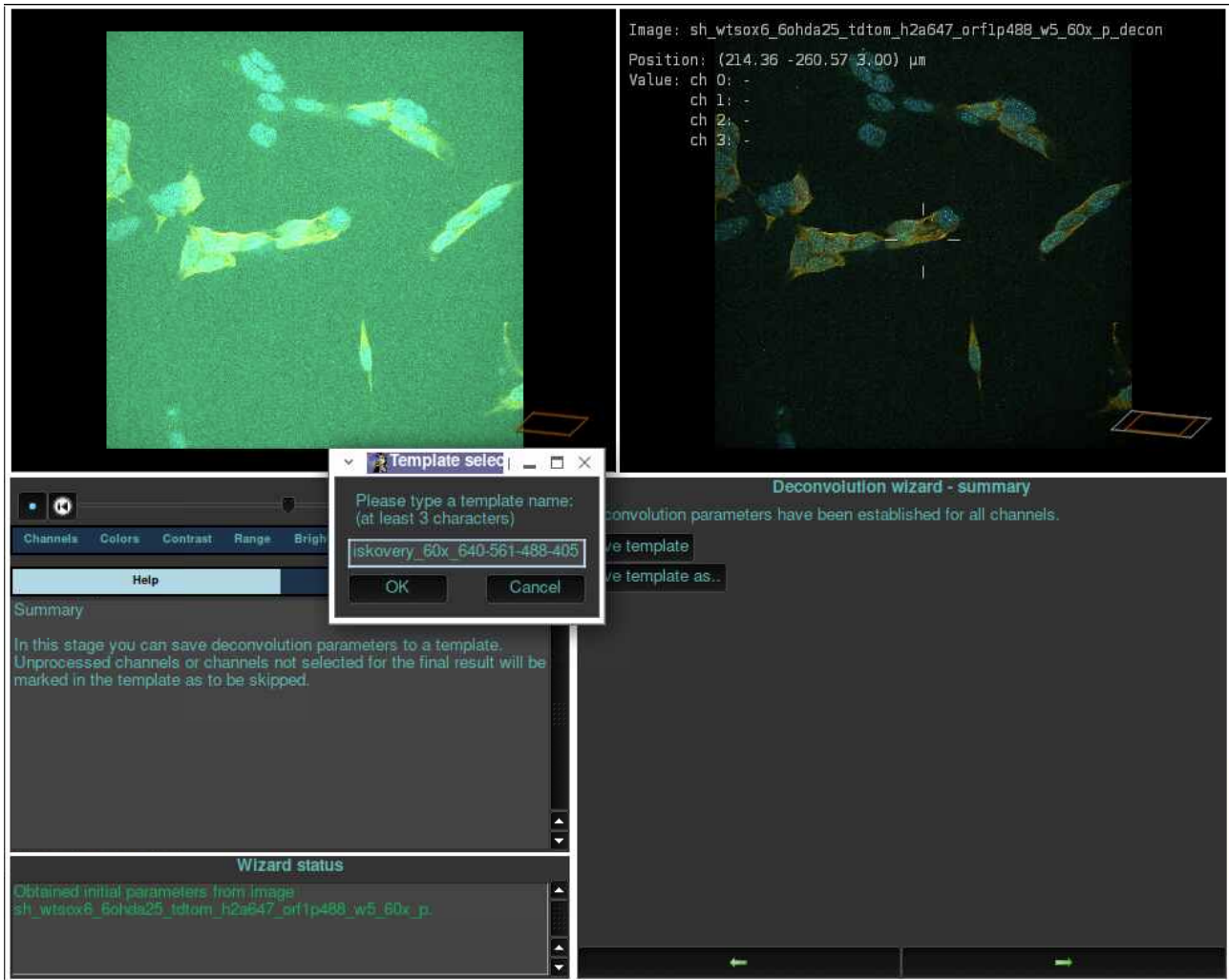


Figure 5: Saving a deconvolution template.

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).

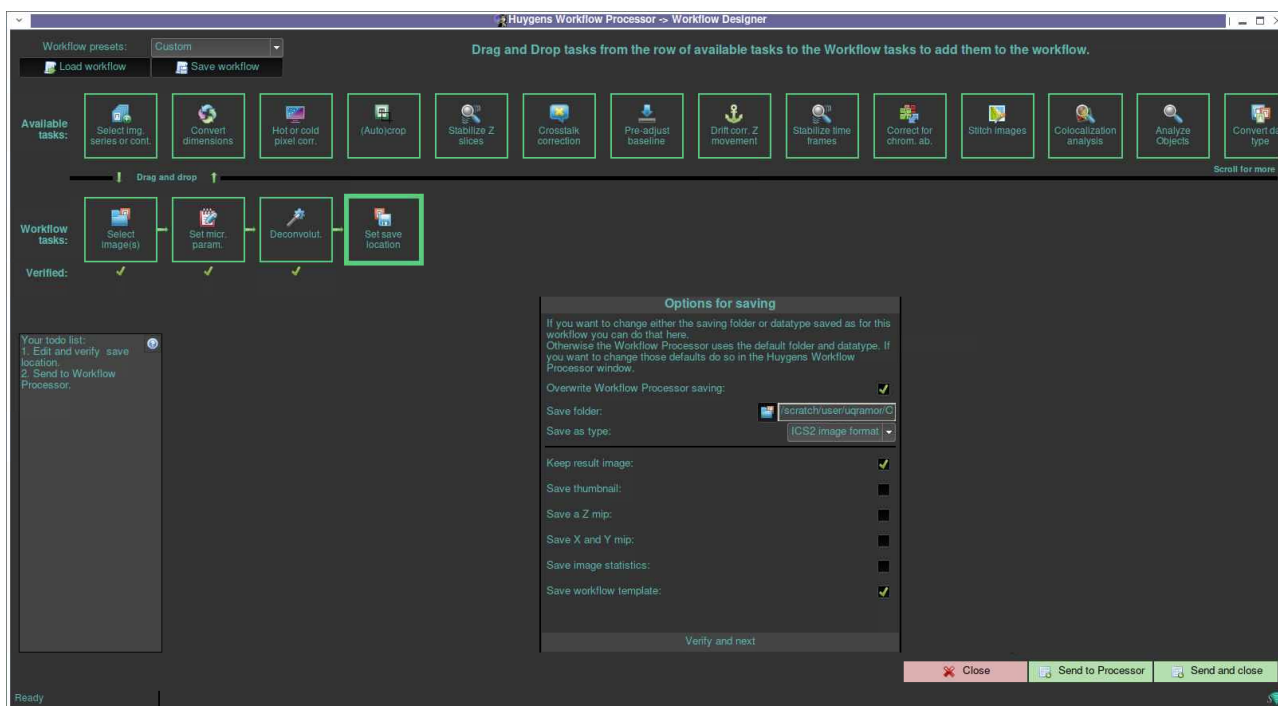


Figure 6: Creating a batch job on the Workflow Processor.

- 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.

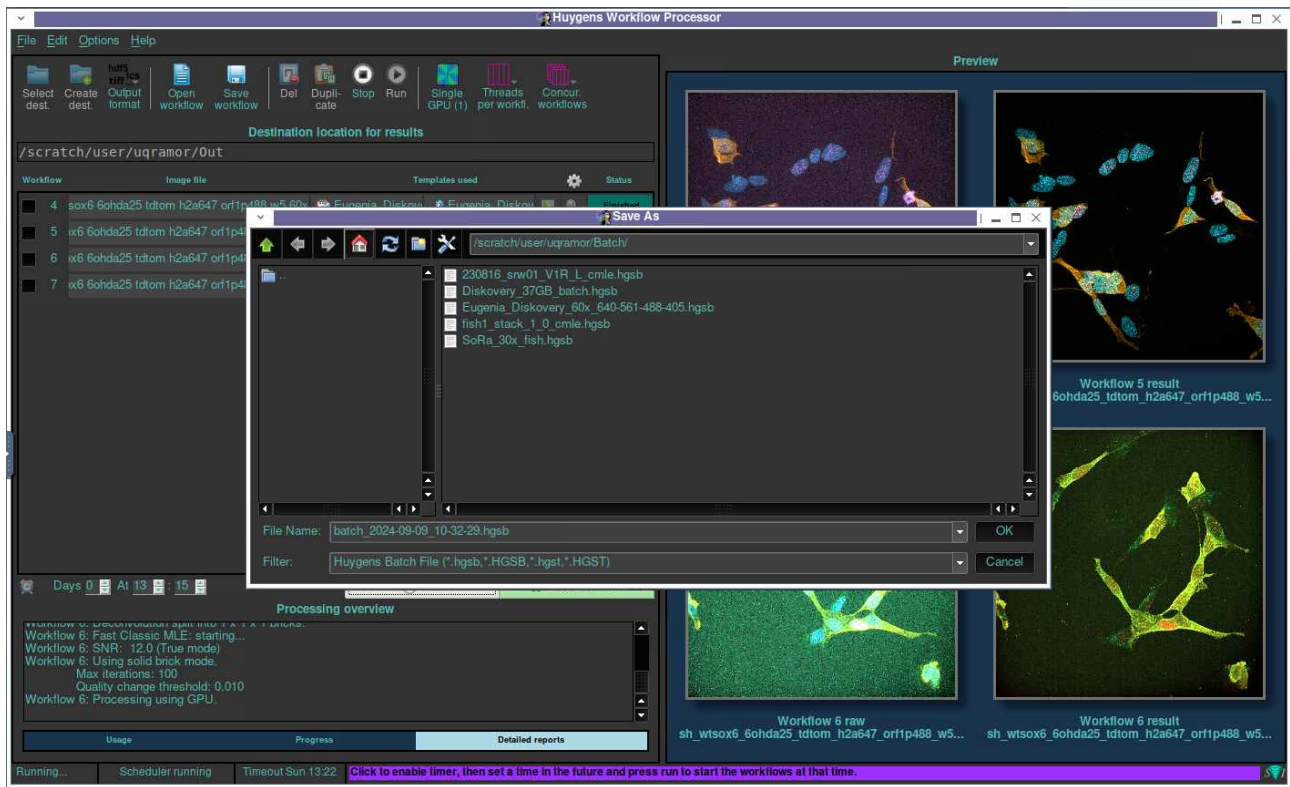


Figure 7: Saving a batch template.

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

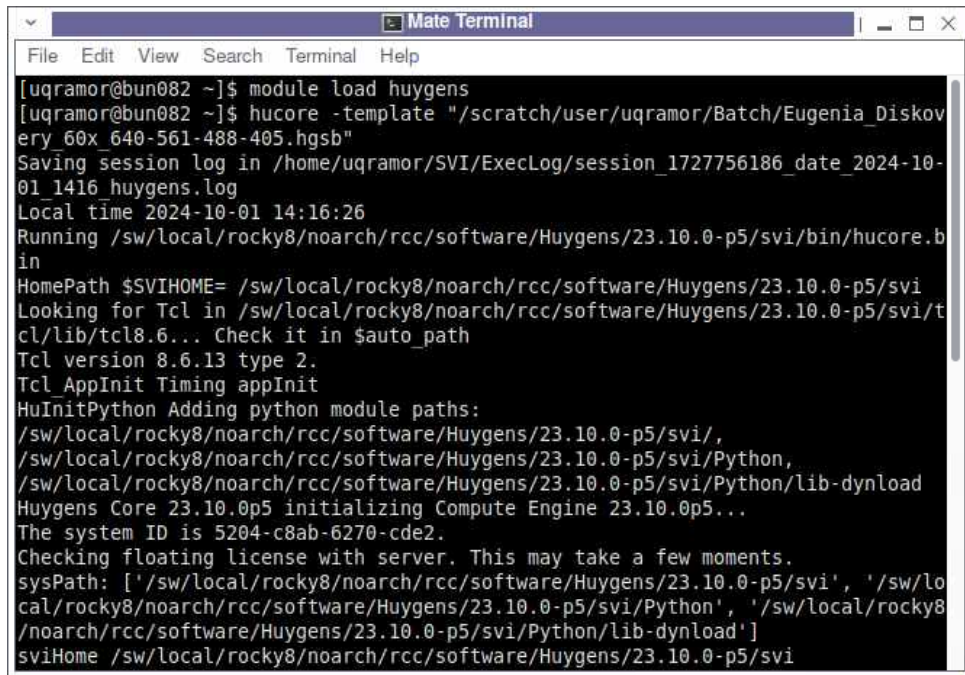
```
module load huygens
hucore -template 'batch.template.location'
```

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
```

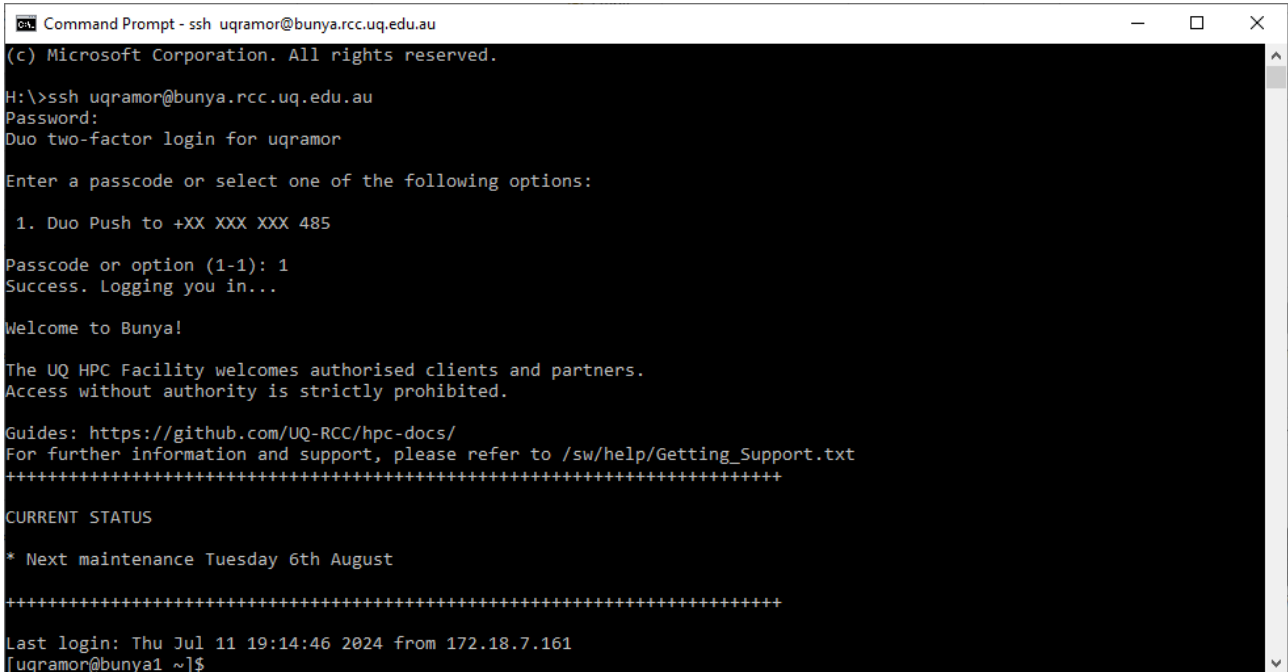
Figure 8: Running Huygens Core via OnDemand.



## 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).



```

ca Command Prompt - ssh uqramor@bunya.rcc.uq.edu.au
(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:

 1. Duo Push to +XX XXX XXX 485

Passcode or option (1-1): 1
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

* Next maintenance Tuesday 6th August

+++++

Last login: Thu Jul 11 19:14:46 2024 from 172.18.7.161
[uqramor@bunya1 ~]$

```

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

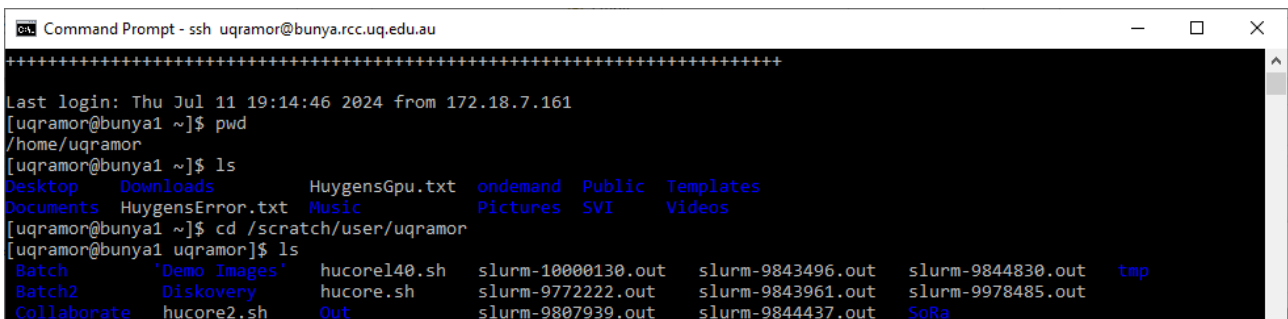
2. By default, you will be on the /home directory. Print the current working directory:  
\$ pwd

(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).



```

ca Command Prompt - ssh uqramor@bunya.rcc.uq.edu.au
+++++

Last login: Thu Jul 11 19:14:46 2024 from 172.18.7.161
[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
Batch      'Demo Images'  hucore140.sh  slurm-10000130.out  slurm-9843496.out  slurm-9844830.out  tmp
Batch2     Diskovery      hucore.sh     slurm-9772222.out  slurm-9843961.out  slurm-9978485.out
Collaborate hucore2.sh     Out           slurm-9807939.out  slurm-9844437.out  SoRa

```

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

```
[uqramor@bunya1 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 --constraint=cuda48gb
#SBATCH --gres=gpu:1
#SBATCH --account=a_qbi_microscopy

module load huygens
hucore -template "/scratch/user/uqramor/Batch/Eugenia_Discovery_60x_640-561-488-405.hgsb"
[uqramor@bunya1 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`

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

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

`#SBATCH --constraint=cuda48gb` → the GPU RAM specified, in aiming to use a particular GPU; for an A100 MIG slice, use “`--constraint=cuda10gb`”, for H100 and A100, use “`--constraint=cuda80gb`”, or “`--constraint=cuda48gb`”

`#SBATCH --gres=gpu:1` → GPU number

`#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@bunya1 uqramor]$ sbatch hucore2.sh
Submitted batch job 10002720
```

Figure 12: Submitting the job to SLURM.

5. Check the status in the job queue:

```
$ squeue --me
```

```
[uqramor@bunya1 uqramor]$ squeue --me
JOBID PARTITION NAME USER ST TIME NODES NODELIST(REASON)
11014598 gpu_cuda HUCORE uqramor PD 0:00 1 (Priority)
11013736 gpu_viz Viz_Desk uqramor R 45:39 1 bun082
11013730 gpu_viz Viz_Desk uqramor R 45:56 1 bun122
[uqramor@bunya1 uqramor]$
```

Figure 13: Checking the status in the queue.

6. Monitor the job by using the `tail` command.

```
$ tail -f slurm-JOBID.out
```

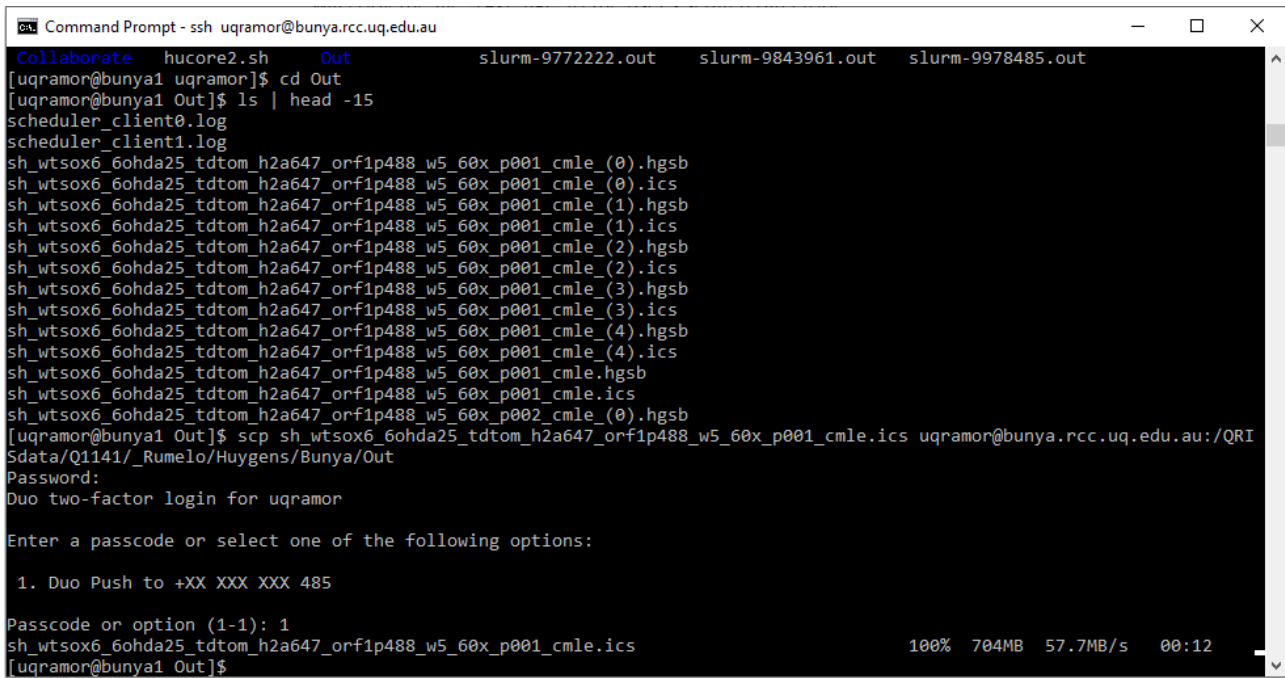
To exit the `tail` command, press `Ctrl + C`.

```
[uqramor@bunya1 uqramor]$ tail -f slurm-11014598.out
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_p003_cmle_9_save {/scratch/user/uqramor/Out/sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p003_cmle_9}.ics} -type ics2 -cmode scale
Successfully saved results to: {/scratch/user/uqramor/Out/sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p003_cmle_9}.ics}
Template /scratch/user/uqramor/Batch/Eugenia_Discovery_60x_640-561-488-405.hgsb successfully processed
Tcl_AppInit App init time 209.50
Local time 2024-10-01 15:12:27
```

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 huco2.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
```

```

Command Prompt - ssh uqramor@bunya.rcc.uq.edu.au
[uqramor@bunya1 uqramor]$ scp -r /scratch/user/uqramor/Out uqramor@bunya.rcc.uq.edu.au:/QRISdata/Q1141/_Rumelo/Huygens/
Bunya
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_p002_cmle_(0).hgsb      100% 26KB 5.1MB/s 00:00
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p002_cmle_(2).hgsb    100% 704MB 63.8MB/s 00:11
task-2-24Jun21-13_11_16.log                                             100% 51KB 9.6MB/s 00:00
task-2-24Jun25-14_16_28.log                                             100% 62KB 13.3MB/s 00:00
task-1-24Jul11-15_45_00.log                                             100% 62KB 14.5MB/s 00:00
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p_cmle_(4).hgsb     100% 26KB 7.5MB/s 00:00
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p002_cmle_(2).hgsb    100% 26KB 7.4MB/s 00:00
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p002_cmle_(4).ics    100% 704MB 61.2MB/s 00:11
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p002_cmle_(1).ics    100% 704MB 62.4MB/s 00:11
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p_cmle_(1).ics      100% 704MB 60.8MB/s 00:11
task-2-24Jul12-13_03_24.log                                             100% 62KB 11.4MB/s 00:00
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p002_cmle.hgsb       100% 23KB 6.6MB/s 00:00
task-7-24Jun21-13_22_44.log                                             100% 53KB 11.6MB/s 00:00
task-0-24Jun21-13_10_27.log                                             100% 51KB 8.7MB/s 00:00
task-2-24Jul11-16_11_51.log                                             100% 62KB 13.8MB/s 00:00
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle_(0).ics    100% 704MB 60.6MB/s 00:11
scheduler_client1.log                                                 100% 405KB 6.0MB/s 00:00
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p003_cmle_(3).hgsb    100% 26KB 6.7MB/s 00:00
task-1-24Jul11-16_11_08.log                                             100% 62KB 6.0MB/s 00:00
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p001_cmle_(2).hgsb    100% 26KB 2.7MB/s 00:00
task-0-24Jul11-16_10_25.log                                             100% 62KB 5.9MB/s 00:00
sh_wtsox6_6ohda25_tdtom_h2a647_orf1p488_w5_60x_p_cmle_(4).ics      68% 480MB 69.5MB/s 00:03 ETA

```

Figure 16: Transferring the output directory using scp.

## Acknowledgments

We thank Jake Carroll, Sarah Walters, Marlies Hankel, Edan Scriven, and Owen Powell of UQ RCC and Vincent Schoonderwoert of SVI for making Huygens Professional and Core happen on Bunya OnDemand and SLURM, Eugenia Ferreiro of the QBI Faulkner Lab for the use of her image data for testing, and Andrew Thompson of QBI Microscopy for help with testing.

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