

Segmenting Large Electron Microscopic Image Volumes

An Introduction to NBCR image analysis and segmentation tools



National Biomedical Computation Resource Summer Training Program @ UC San Diego

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Hands-On Session 2

Running CHM Train via chmutil on Rocce Cluster

Goals

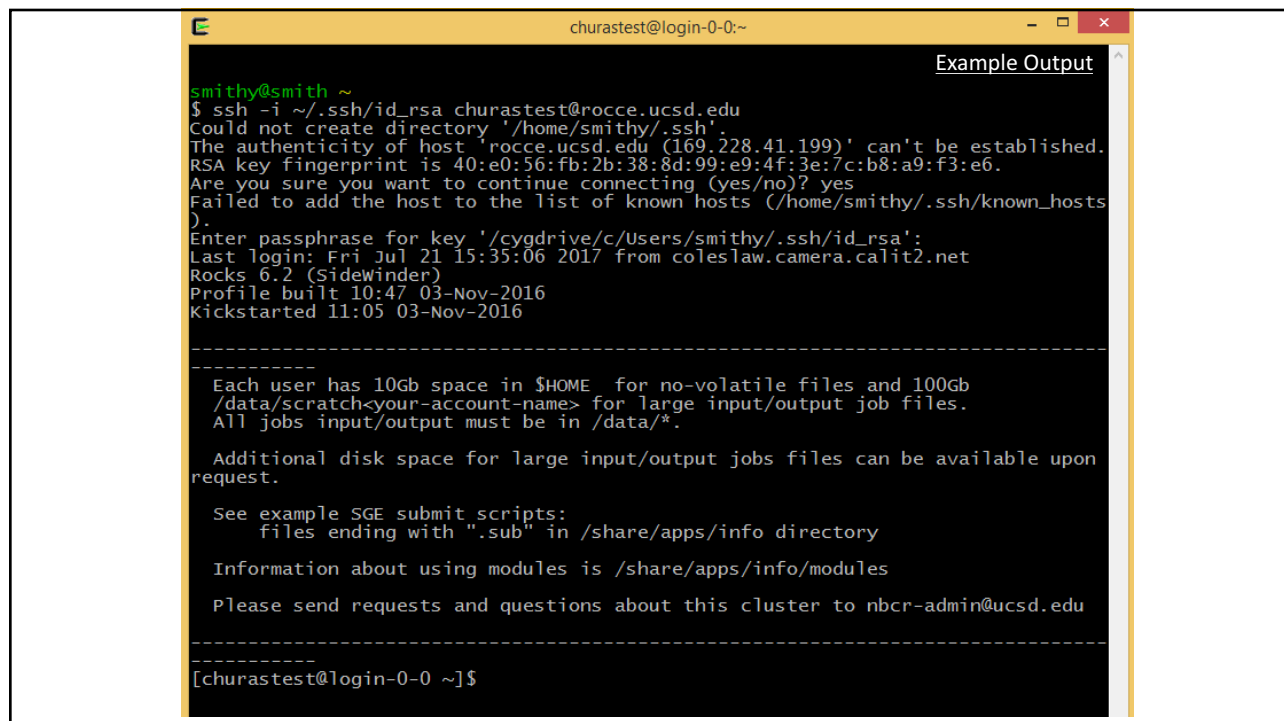
By the end of this session, you will be able to:

1. Install chmutil on Rocce Cluster
2. Upload training data to Rocce Cluster
3. Autocontrast training images
4. Create CHM Train job
5. Submit CHM Train job
6. Check on CHM Train job status

1. Install chmutil on Rocce Cluster

- A. Connect to Rocce Cluster via *ssh* by opening a terminal and invoking this command:

```
ssh -i ~/.ssh/id_rsa <USER>@rocce.ucsd.edu
```



```
churastest@login-0-0:~  
Example Output  
smithy@smith ~  
$ ssh -i ~/.ssh/id_rsa churastest@rocce.ucsd.edu  
Could not create directory '/home/smithy/.ssh'.  
The authenticity of host 'rocce.ucsd.edu (169.228.41.199)' can't be established.  
RSA key fingerprint is 40:e0:56:fb:2b:38:8d:99:e9:4f:3e:7c:b8:a9:f3:e6.  
Are you sure you want to continue connecting (yes/no)? yes  
Failed to add the host to the list of known hosts (/home/smithy/.ssh/known_hosts  
).  
Enter passphrase for key '/cygdrive/c/Users/smithy/.ssh/id_rsa':  
Last login: Fri Jul 21 15:35:06 2017 from coleslaw.camera.calit2.net  
Rocks 6.2 (Sidewinder)  
Profile built 10:47 03-Nov-2016  
Kickstarted 11:05 03-Nov-2016  
-----  
Each user has 10Gb space in $HOME for no-volatile files and 100Gb  
/data/scratch<your-account-name> for large input/output job files.  
All jobs input/output must be in /data/*.  
  
Additional disk space for large input/output jobs files can be available upon  
request.  
  
See example SGE submit scripts:  
files ending with ".sub" in /share/apps/info directory  
  
Information about using modules is /share/apps/info/modules  
  
Please send requests and questions about this cluster to nbc-admin@ucsd.edu  
-----  
[churastest@login-0-0 ~]$
```

1. Install chmutil on Rocce Cluster

These instructions are taken from <https://github.com/CRBS/chmutil/wiki/chmutil-on-rocce-cluster>

- A. Run these two commands to download and install Miniconda

```
qssh  
wget https://repo.continuum.io/miniconda/Miniconda2-latest-Linux-x86_64.sh  
bash Miniconda2-latest-Linux-x86_64.sh -b
```

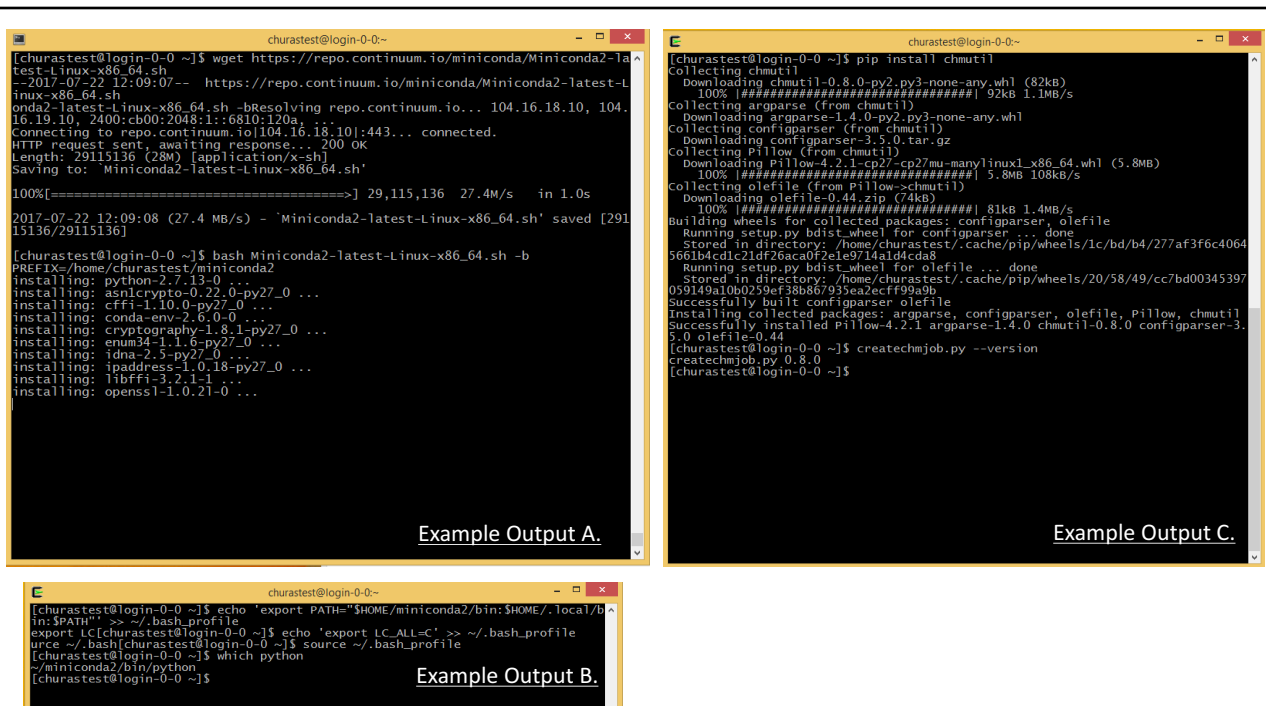
- B. Run these three commands to update startup scripts with the path to Miniconda

```
echo 'export PATH="$HOME/miniconda2/bin:$HOME/.local/bin:$PATH"' >> ~/.bash_profile  
echo 'export LC_ALL=C' >> ~/.bash_profile  
source ~/.bash_profile
```

- C. Run these two commands to install chmutil and verify installation by calling `createchmjob.py`

```
pip install chmutil  
createchmjob.py --version  
exit
```

Note: The above commands only have to be run once



2. Upload training data to Rocce

- A. If still connected, disconnect from Rocce by typing *exit*

exit

- B. **Either** download the *download_dataset_2.zip* file from https://github.com/CRBS/nbcctrainingvm/blob/master/download_dataset_2.zip and unzip and enter it as before **OR** if you want, enter *download_dataset_1* directory where training data created from previous exercise.
- C. The directory will contain one item (more if you entered *download_dataset_1* folder):
- A directory, *train*, which contains two directories *images* and *labels* that contain training data created in previous exercise.
- D. The training data is already in correct format, so we just need to upload it to Rocce:

scp -i ~/.ssh/id_rsa -r train <USER>@rocce.ucsd.edu:/data/scratch/<USER>/.

This will recursively upload the *train* directory to */data/scratch/<USER>* directory on Rocce.

Note: Be sure to replace *<USER>* above with your Rocce username.

Directory Structure:

```

graph TD
    A[download_dataset_2] --> B[train]
    B --> C[images]
    B --> D[labels]
    C --> E[x.001.png]
    C --> F[x.002.png]
    D --> G[x.001.png]
    D --> H[x.002.png]
  
```

Example Output

```

[churastest@login-0-0 churastest]$ exit
logout
Connection to rocce.ucsd.edu closed.

smithy@smith ~
$ ls Downloads/download_dataset_2.zip
Downloads/download_dataset_2.zip

smithy@smith ~
$ unzip Downloads/download_dataset_2.zip
Archive:  Downloads/download_dataset_2.zip
  creating: download_dataset_2/
  creating: download_dataset_2/train/
  creating: download_dataset_2/train/images/
  inflating: download_dataset_2/train/images/x.000.png
  inflating: download_dataset_2/train/images/x.001.png
  creating: download_dataset_2/train/labels/
  inflating: download_dataset_2/train/labels/x.000.png
  inflating: download_dataset_2/train/labels/x.001.png

smithy@smith ~
$ cd download_dataset_2

smithy@smith ~/download_dataset_2
$ ls
train

smithy@smith ~/download_dataset_2
$ scp -i ~/.ssh/id_rsa -r train churastest@rocce.ucsd.edu:/data/scratch/churaste
st
Could not create directory '/home/smithy/.ssh'.
The authenticity of host 'rocce.ucsd.edu (169.228.41.199)' can't be established.
RSA key fingerprint is 40:e0:56:fb:2b:38:8d:99:e9:4f:3e:7c:b8:a9:f3:e6.
Are you sure you want to continue connecting (yes/no)? yes
Failed to add the host to the list of known hosts (/home/smithy/.ssh/known_hosts
).
Enter passphrase for key '/cygdrive/c/Users/smithy/.ssh/id_rsa':
x.000.png      100% 131KB 131.2KB/s  00:00
x.001.png      100% 133KB 133.4KB/s  00:00
x.000.png      100% 1242  1.2KB/s    00:00
x.001.png      100% 3638   3.6KB/s    00:00

smithy@smith ~/download_dataset_2
$
  
```

4. Create CHM Train job

We will be running the `chmutil` command `createchmtrainjob.py` to create [CHM](#) train job on the Rocce cluster. Here is a description of the arguments used in the command invocation below

- `--chmbin` Path to [CHM Singularity](#) binary (use path as shown below)
- `--cluster` Tells tool what cluster to generate job for. (currently Rocce & Comet are supported)
- `--stage` CHM parameter, sets number of stages (default 2)
- `--level` CHM parameter, sets number of levels (default 4)
- `--maxmem` Lets caller define amount of ram in gigabytes needed by job (default 90)

- A. Change to `/data/scratch/<USER>` and run `createchmtrainjob.py` with arguments as shown below

```
cd /data/scratch/<USER>
```

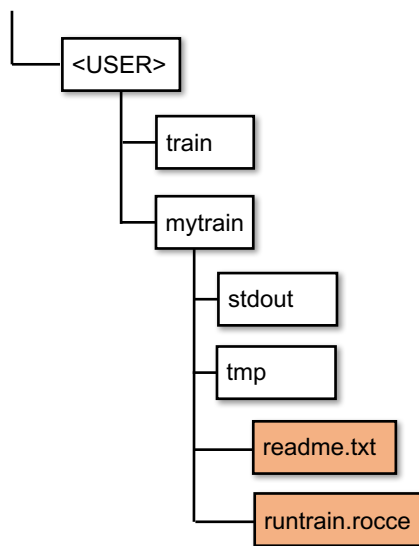
```
createchmtrainjob.py train/images train/labels mytrain --chmbin /data/churas/chm_s22.img --cluster rocce --stage 2 --level 1 --maxmem 12
```

The above command will create a new directory named `mytrain`.

For more information on how to use `createchmtrainjob.py` just run the command with no arguments or with `-h` flag (Example: `createchmtrainjob.py --help`)

<https://github.com/CRBS/chmutil/wiki/createchmtrainjob.py>

Directory Structure:



```
churastest@login-0-0:/data/scratch/churastest
[churastest@login-0-0 ~]$ cd /data/scratch/churastest
[churastest@login-0-0 churastest]$ createchmtrainjob.py ./train/images ./train/labels ./mytrain --chmbin /data/churas/chm_s22.img --cluster rocce --stage 2 --level 1 --maxmem 12

To submit run: cd /data/scratch/churastest/mytrain; qsub /data/scratch/churastest/mytrain/runtrain.rocce
[churastest@login-0-0 churastest]$
```

Example Output

5. Submit CHM Train job

Running *createchmtrainjob.py* from previous step creates a *mytrain* folder with a couple files and directories described here:

<i>stdout/</i>	Directory that will contain standard error and output file for training job. The file will be named <JOBID>.out
<i>tmp/</i>	Directory that will temporarily hold output from CHM Train. As the job finishes this directory will be renamed to <i>model/</i>
<i>readme.txt</i>	Text file with information about job (parameters passed to <i>createchmtrainjob.py</i>) as well as information on how to check on job status and get more help
<i>runtrain.rocce</i>	Generated script to run CHM Train job on Rocce cluster. This file is passed to SGE <i>qsub</i> command

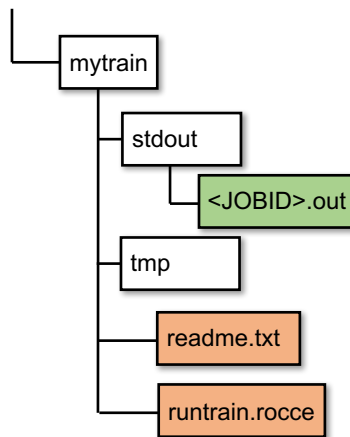
- A. When run successfully *createchmtrainjob.py* outputs a command to run to actually submit the job.

In the terminal copy the text to the right of “To submit run:” and paste it in the terminal to submit the job.

The text to copy will look similar to the text below:

```
cd /data/scratch/<USER>/mytrain; qsub /data/scratch/<USER>/runtrain.rocce
```

Directory Structure:



```
churastest@login-0-0/data/scratch/churastest/mytrain
[churastest@login-0-0 churastest]$ cd /data/scratch/churastest
[churastest@login-0-0 churastest]$ createchmtrainjob.py ./train/images/ ./train/
labels/ ./mytrain --chmbin /data/churas/chm_s22.img --cluster rocce --stage 2 --
level 1 --maxmem 12
To submit run: cd /data/scratch/churastest/mytrain; qsub /data/scratch/churastes
t/mytrain/runtrain.rocce
[churastest@login-0-0 churastest]$ cd /data/scratch/churastest/mytrain; qsub /d
ata/scratch/churastest/mytrain/runtrain.rocce
Your job 14706 ("chmtrainjob") has been submitted
[churastest@login-0-0 mytrain]$
```

Two red arrows point from the text below to the terminal output. One arrow points to the job ID '14706' and the other points to the job name 'chmtrainjob'.

<JOBID> Job name, can be set with
 --jobname flag passed
 to createchmtrainjob.py

Example Output

6. Check on CHM Train job status

When you run the *qsub* command as done in previous step, OGE/SGE will output a line of this format:

Your job <JOBID> ("<JOBNAME>") has been submitted

The <JOBID> is the identifier for the job and is used as the file name for the file containing standard error/output of job which is stored in *stdout/<JOBID>.out*. Contents of this text file can be examined for debugging purposes.

- A. To check on job status run *qstat* command that is a OGE/SGE command that outputs all jobs your account is running

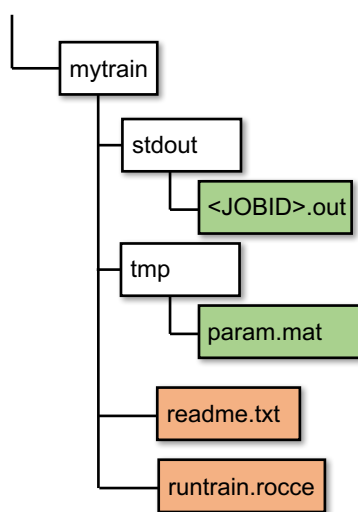
qstat

qstat will output jobs, one per row with current status.

If the job has finished or failed it will **NOT** be displayed in output.

Run *man qstat* for more information (type 'q' to quit)

Directory Structure:



```

churastest@login-0-0:/data/scratch/churastest/mytrain
[churastest@login-0-0 churastest]$ cd /data/scratch/churastest
[churastest@login-0-0 churastest]$ createchmtrainjob.py ./train/images/ ./train/
labels/ ./mytrain --chmbin /data/churas/chm_s22.img --cluster rocce --stage 2 --
level 1 --maxmem 12

To submit run: cd /data/scratch/churastest/mytrain; qsub /data/scratch/churastes
t/mytrain/runtrain.rocce

[churastest@login-0-0 churastest]$ cd /data/scratch/churastest/mytrain; qsub /d
ata/scratch/churastest/mytrain/runtrain.rocce
Your job 14706 ("chmtrainjob") has been submitted
[churastest@login-0-0 mytrain]$ qstat
job-ID   prior    name             user             state submit/start at     queue
-----
14706    0.505000  chmtrainjob     churastest       r      07/22/2017 09:59:30 all.q@gpu-1-7.
local
1
[churastest@login-0-0 mytrain]$
  
```

<JOBID> State of job
 r = running
 qw = waiting to run
 e = error
 h = held

Queue and machine running job

Example Output

6. Check on CHM Train job status

When *qstat* no longer displays the job, it is best to check the *stdout*<JOBID>.out file to verify correct operation.

This can be done with *tail* command which lets one view text files.

Is stdout
tail stdout/<JOBID>.out

A successful job will have the following on the last line:

chm_s22.img exited with code: 0

CHM Train writes output to tmp directory and when job completes the script renames the directory to *model*. It is a good idea to check for valid output in this *model* directory using the *ls* command

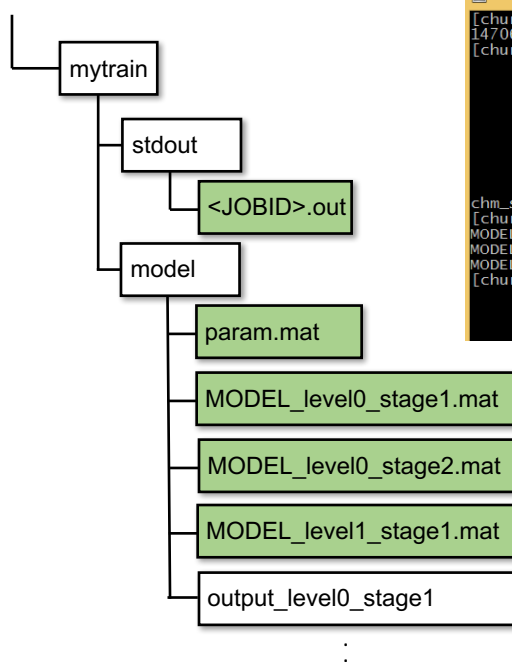
Is model

A successful run will have these files plus three *output_level..* directories:

param.mat, MODEL_level0_stage1.mat, MODEL_level0_stage2.mat, MODEL_level1_stage1.mat

For more information go to: <https://github.com/CRBS/chmutil/wiki/createchmtrainjob.py>

Directory Structure:



```
churastest@login-0-0:/data/scratch/churastest/mytrain
[churastest@login-0-0 mytrain]$ ls stdout/
14706.out
[churastest@login-0-0 mytrain]$ tail stdout/14706.out
Involuntary context switches: 7200
Swaps: 0
File system inputs: 262730
File system outputs: 129952
Socket messages sent: 0
Socket messages received: 0
Signals delivered: 0
Page size (bytes): 4096
Exit status: 0
chm_s22.img exited with code: 0
[churastest@login-0-0 mytrain]$ ls model/
MODEL_level0_stage1.mat  output_level0_stage1  param.mat
MODEL_level0_stage2.mat  output_level0_stage2
MODEL_level1_stage1.mat  output_level1_stage1
[churastest@login-0-0 mytrain]$
```

Example Output

More information on checking job completion can be found here:
<https://github.com/CRBS/chmutil/wiki/createchmtrainjob.py>