

IMPLEMENTATION OF GLOMERULAR SEGMENTATION MODEL - HISTOCLOUD ON HIPERGATOR

Connect to HiperGator by any of the two methods.

- Use the below command in cmd to connect to HiperGator

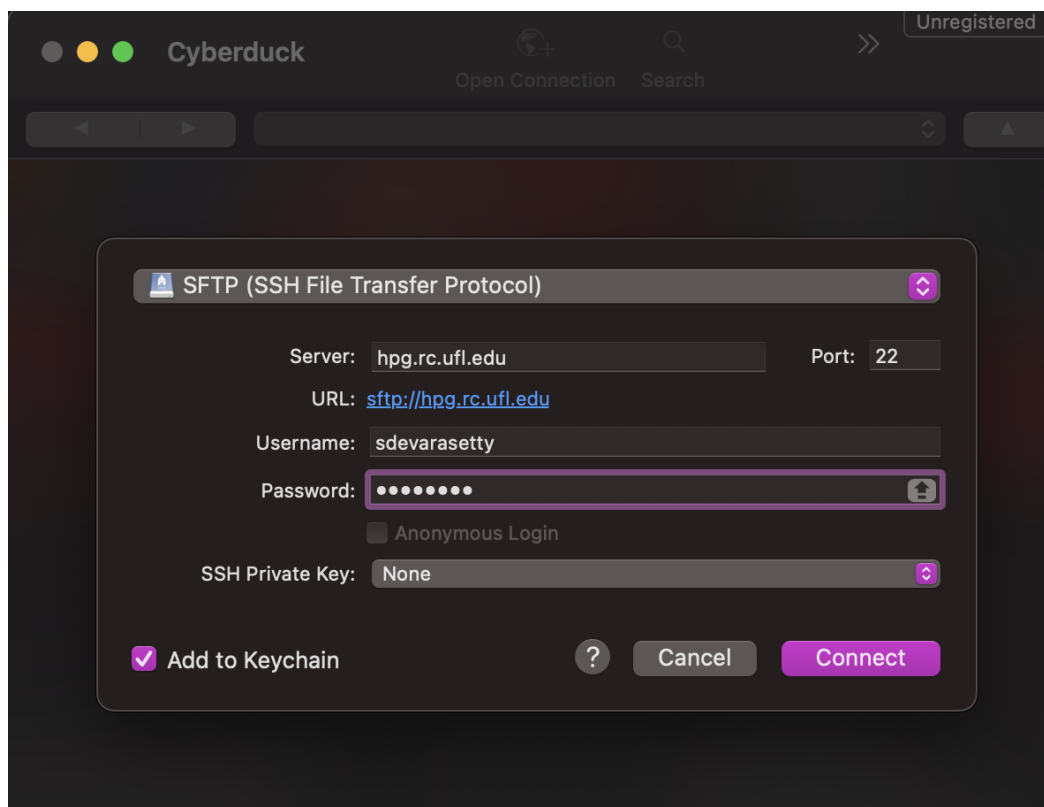
```
ssh <username>@hpg.rc.ufl.edu
```

```
sd@sumanths-macbook-air ~ % ssh sdevarasetty@hpg.rc.ufl.edu
[sdevarasetty@hpg.rc.ufl.edu] Password:
[sdevarasetty@hpg.rc.ufl.edu] Duo two-factor login for sdevarasetty@ufl.edu

Enter a passcode or select one of the following options:

1. Duo Push to +XX XXXXX X2266
2. Duo Push to XXX-XXX-1332
3. Phone call to +XX XXXXX X2266
4. Phone call to XXX-XXX-1332
```

- Use an SFTP Client like Winscp / Cyberduck to connect to HiperGator (Host Name: hpg.rc.ufl.edu; Port Number: 22)



Implementation

- The working directory after login will be /home/

- In HiperGator, use blue folder to store files
- Go to root/blue/pinaki.sarder/

```
cd /
cd /blue/pinaki.sarder/<username>
```

- In root/blue/pinaki.sarder/ store the following:
 - All the input whole slide image data in 'svs' format for segmentation
 - Singularity container
 - Glomerular Segmentation model
 - The Codes Folder with Slurm and Python files

Fields and parameters in the Slurm file

- In the Slurm file and specify the following:
 - The number of nodes to allocate for this job

```
#SBATCH --nodes=1
```

- The number of Tasks to launch

```
#SBATCH --ntasks=1
```

- The number of CPU's per task to allocate

```
#SBATCH --cpus-per-task=6
```

- The amount of memory per CPU to allocate in megabytes

```
#SBATCH --mem-per-cpu=16000mb
```

- The partition to which this job should be submitted. In this case, it is the partition that has GPUs available.

```
#SBATCH --partition=gpu
```

- The number of GPU's to allocate

```
#SBATCH --gpus=geforce:1
```

- The wall-clock time limit for the job, in hours:minutes:seconds.

```
#SBATCH --time=2:00:00
```

- The name of the job

```
#SBATCH --job-name="GlomSegmentation"
```

- The file to which the standard output and error streams will be written.

```
#SBATCH --output=GlomSeg_SD.out
```

- The email address of the user

```
#SBATCH --mail-user= <username>@uf1.edu
```

- Define the path to the singularity container that will be used to run the job

```
CONTAINER=/blue/pinaki.sarder/nlucarelli/BL_segmentation/njlucare_deeplab_
```

- This is the actual command to run the job. Specify the paths to data (The folder with all the whole slide image data in svf format), Segmentation model directory, Python script to run the image segmentation on the input data and all the parameters.

```
singularity exec --nv -B  
$(pwd):/exec/,/blue/pinaki.sarder/sdevarasetty/GlomSegData/:/data/,/blue/p  
segmentation-model-8-14-20/:/model/ $CONTAINER python3  
/exec/deeplab/vis.py --model_variant xception_65 --atrous_rates 6 --  
atrous_rates 12 --atrous_rates 18 --output_stride 16 --  
decoder_output_stride 4 --checkpoint_dir /model/model.ckpt-400000 --  
dataset_dir /data/
```

Instructions to run the Slurm file

- Move to the directory with the Slurm file and use the following command to run the job on HiperGator

```
sbatch s_run.sh
```

```
[sdevarasetty@login2 sdevarasetty]$ cd BL_segmentation/  
[sdevarasetty@login2 BL_segmentation]$ ls  
deeplab GlomSeg.out GlomSeg_SD.out Inference_All_Membranous_Data.out Membran  
ous_utils models_log_2309 output files s_run.sh training.out transfer_files  
.sh Transfer.out t_run.sh  
[sdevarasetty@login2 BL_segmentation]$ sbatch s_run.sh  
Submitted batch job 59039558  
[sdevarasetty@login2 BL_segmentation]$
```

- To get information about the jobs that are currently in the Slurm queue, use this command shows the job ID, partition, name, user, state, Time, nodes, Nodelist(Reason). This command can be useful for monitoring the progress of the submitted job.

```
squeue -A pinaki.sarder
```

```
[sdevarasetty@login2 BL_segmentation]$ squeue -A pinaki.sarder  
JOBID PARTITION NAME USER ST TIME NODES NODELIST(REASON)  
59038940 gpu sys/dash tan.m R 14:11 1 c0309a-s33  
59039558 gpu GlomSegm sdevaras R 3:41 1 c38a-s33  
59025269 gpu sys/dash j.fermin R 1:47:24 1 c0309a-s13  
59010996 hpg-defau sys/dash nlucarel R 3:49:59 1 c0706a-s1
```