# TRAINING 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
```

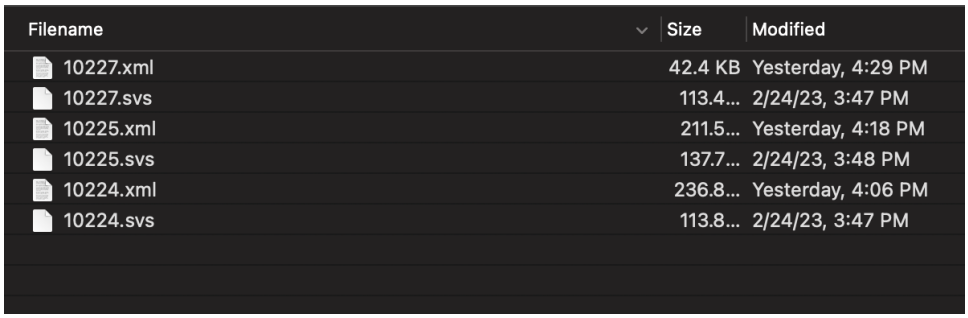
- Use an SFTP Client like Winscp / Cyberduck to connect to HiperGator (Host Name: hpg.rc.ufl.edu; Port Number: 22)

**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 follwing:
  - All the input whole slide image data in 'svs' format and the corresponding 'xml' files for training.




  - 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=8
```

- The amount of memory per CPU to allocate in megabytes

```
#SBATCH --mem-per-cpu=7000mb
```

- 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
```

- For training using multiple GPU's

```
#SBATCH --gpus=geforce:2
```

- To allocate multiple GPUs

```
#SBATCH --gpus=geforce:2
```

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

```
#SBATCH --time=5:00:00
```

- The name of the job

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

- The path to which the trained model will be written

```
#SBATCH --output_model= <give path here>
```

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

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

- The email address of the user

```
#SBATCH --mail-user= <username>@ufl.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 both svs and xml formats), Training Python script and all the parameters.

```
   singularity exec --nv -B
$(pwd):/exec/,/blue/pinaki.sarder/sdevarasetty/GlomSegData/:/data/
$CONTAINER python3 /exec/deeplab/train.py --model_variant xception_65 --
atrous_rates 6 --atrous_rates 12 --atrous_rates 18 --output_stride 16 --
decoder_output_stride 4 --dataset_dir /data/ --train_crop_size 512 --
train_logdir /exec/models_log_2309/ --fine_tune_batch_norm True --
train_batch_size 4 --num_clones 2 --tf_initial_checkpoint
/blue/pinaki.sarder/sdevarasetty/glom-segmentation-model-8-14-
20/model.ckpt-400000
```

**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 t_run.sh
```

```
[sdevarasetty@login6 sdevarasetty]$ cd BL_segmentation/
[sdevarasetty@login6 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@login6 BL_segmentation]$ sbatch t_run.sh
Submitted batch job 59133345
[sdevarasetty@login6 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@login6 BL_segmentation]$ sbatch t_run.sh
Submitted batch job 59133345
[sdevarasetty@login6 BL_segmentation]$ squeue -A pinaki.sarder
             JOBID PARTITION     NAME     USER ST       TIME  NODES NODELIST(REA
SON)
          59133345       gpu Model_Tr sdevaras  R       1:14      1 c0309a-s13
          59109133       gpu sys/dash    tan.m  R    5:51:41      1 c0309a-s5
          59133387       gpu     FCNN nlucarel  R       0:11      1 c0309a-s13
[sdevarasetty@login6 BL_segmentation]$
```