Deep Learning in Medicine

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Lab 4: HPC

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Today, we will go through the useful resources and requirements to set up your HPC account and environment which you'll need for your assignments as well as your course project.

Basic documentation:

- Greene introduction Read about the greene cluster and the nodes available
- Getting access, connecting etc You need to install the NYU VPN and activate it to access Greene. Use ssh in linux/MAC or Putty in windows.
- <u>Slurm Best-practices</u> Resource on wait times for different requirements

Other resources

<u>Prof. K Cho's tutorial</u> Detailed instructions

Available GPUS:

- V100s (32 GB RAM) 10 Nodes
- RTX8000 (48 GB RAM) 65 Nodes

Singularity: <u>Documentation</u>, <u>Paper</u>

Takeaway is that this leads to improved performance through some optimized node management for your experiments.

High-level idea: make a read-only filesystem which will be used exclusively to **host your conda environment** and other static files which you constantly re-use for each job.