# Discussion 3: SCC

SCC dashboard: https://scc-ondemand1.bu.edu/pun/sys/dashboard/

**0. Download the `discussion_3.ipynb` from the link below**

Link: https://github.com/DL4DS/fa2025_discussions/blob/main/discussion_3.ipynb

**1. Create a session on SCC**

- Access /projectnb/ds542/student/
    - Click "Files" and select /projectnb/ds542/student/your_name
    - Upload `discussion_3.ipynb` from GitHub to the SCC folder
- Create a session
    - Click "Interactive apps" - "Jupyter Notebook"
      (I know you all might have different preferences for executing Python job, you can directly click the Login Nodes above to run via command line, also you can request VS code server and TensorBoard server, or even a Remote Desktop. But for this time please request the Jupyter Notebook server first.)
    - List of modules to load (space separated):
      select `miniconda` and `academic-ml/fall-2025` modules
    - Pre-Launch Command (optional):
      fill `conda activate fall-2025-pyt`
      if you are requesting a TensorFlow environment, fill `conda activate fall-2025-tf`
    - Interface:
      choose `lab`
    - Working Directory:
      select `/projectnb/ds542/students/your_name`
    - Number of hours: `2`
    - Number of cores: `1`
    - Number of gpus: `1`
    - GPU compute capability: `3.5` (you can choose 6.0 or higher for your other tasks)
    - Projects: `ds542`

**2. Implement a 10k * 10k Matrix Multiplication on GPU**

**3. Import the dataset from shared folder and run a shallow network for training**

```
df = pd.read_csv('/projectnb/ds542/materials/diabetes.csv')
```

The dataset is the same one from your `hw3` question 2-3, this step is to tell how you can read files from shared folders. For example, for your group projects, you can upload datasets under `/projectnb/ds542/projects/` directory.