

# CONVERTING JUPYTER NOTEBOOKS TO PYTHON

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# Motivation for Today

- Jupyter Notebooks are great for exploring data and testing codes.
- When you are ready to perform a “production run”, you may not need to have the interaction of a Notebook.
- It would be nice if you could submit a job, log out, and come back later to see the results.

# Today's Notes

- Notes for today are on the git repository:

[https://github.com/jhuband/Converting Notebooks to Script.git](https://github.com/jhuband/Converting_Notebooks_to_Script.git)

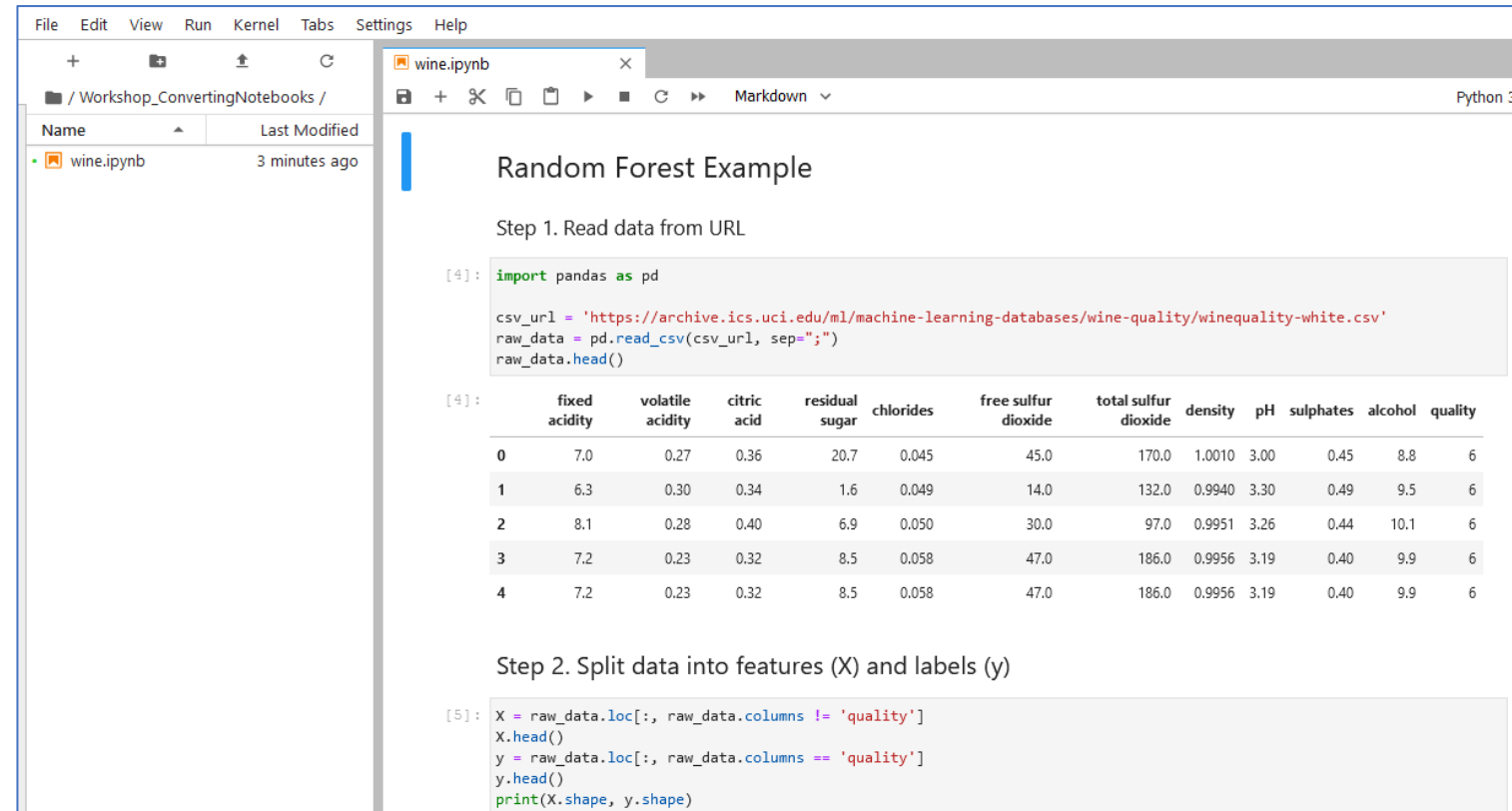
# METHOD #1

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Notebook is not on Rivanna

# First Sample Notebook

The first sample notebook, wine.ipynb, is a Random Forest algorithm that tries to determine the quality of wine based on several features.



```
File Edit View Run Kernel Tabs Settings Help
+ / Workshop_ConvertingNotebooks /
Name Last Modified
• wine.ipynb 3 minutes ago
```

### Random Forest Example

Step 1. Read data from URL

```
[4]: import pandas as pd

csv_url = 'https://archive.ics.uci.edu/ml/machine-learning-databases/wine-quality/winequality-white.csv'
raw_data = pd.read_csv(csv_url, sep=";")
raw_data.head()
```

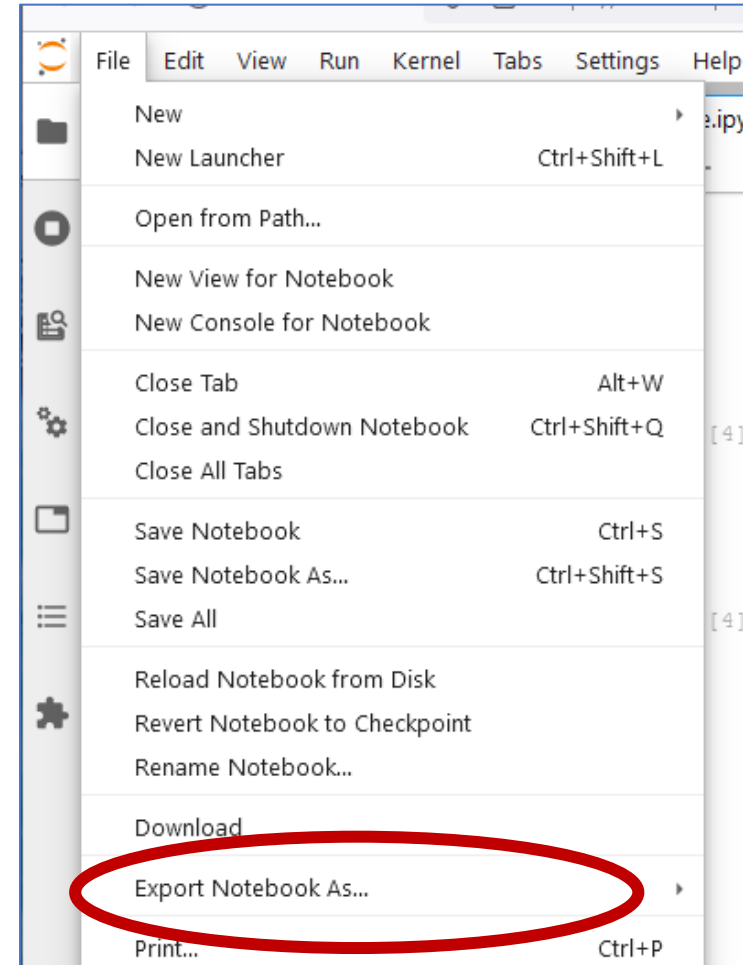
	fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	pH	sulphates	alcohol	quality
0	7.0	0.27	0.36	20.7	0.045	45.0	170.0	1.0010	3.00	0.45	8.8	6
1	6.3	0.30	0.34	1.6	0.049	14.0	132.0	0.9940	3.30	0.49	9.5	6
2	8.1	0.28	0.40	6.9	0.050	30.0	97.0	0.9951	3.26	0.44	10.1	6
3	7.2	0.23	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.9	6
4	7.2	0.23	0.32	8.5	0.058	47.0	186.0	0.9956	3.19	0.40	9.9	6

Step 2. Split data into features (X) and labels (y)

```
[5]: X = raw_data.loc[:, raw_data.columns != 'quality']
X.head()
y = raw_data.loc[:, raw_data.columns == 'quality']
y.head()
print(X.shape, y.shape)
```

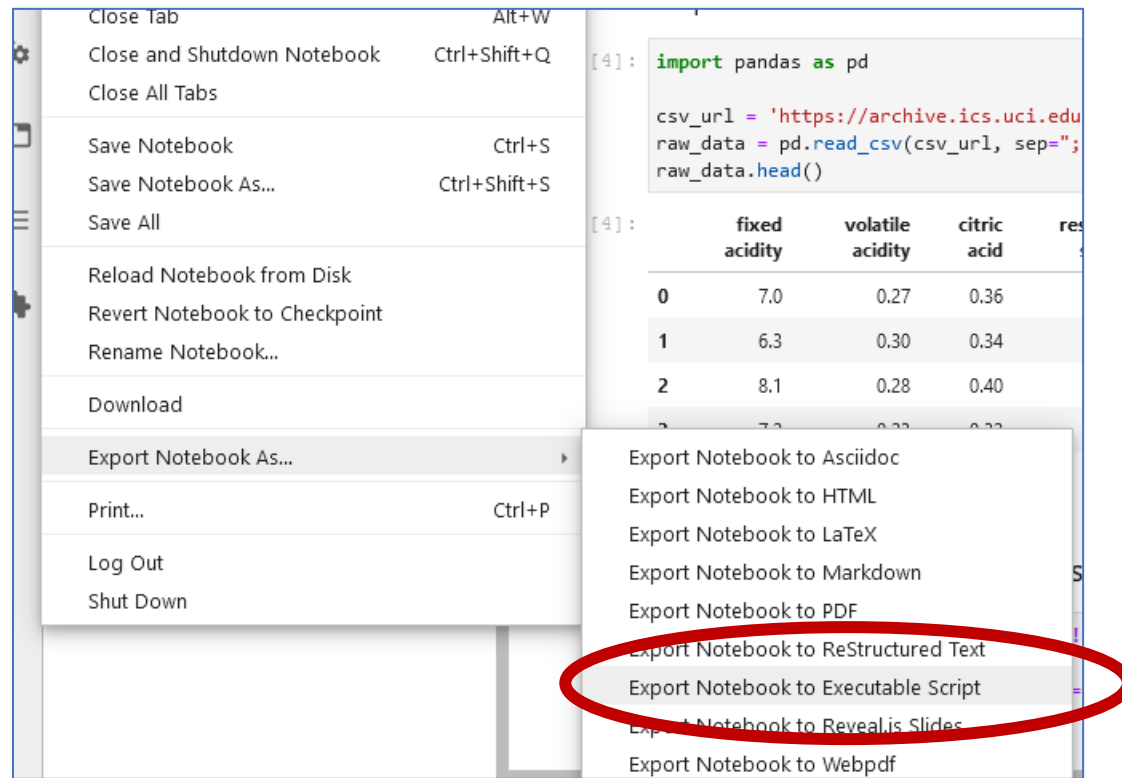
# Converting the Notebook to Python

- Click on  
**File > Export Notebook As >**



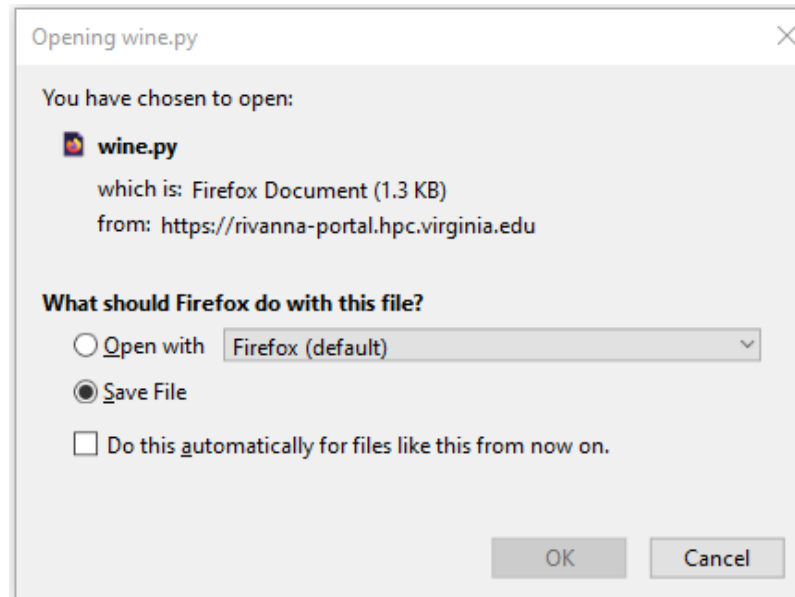
# Converting the Notebook to Python

- In the drop-down box, select **Export Notebook to Executable Script**



# Converting the Notebook to Python

- You may be asked about opening/saving the files





# METHOD #2

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Notebook is on Rivanna

# Creating Python Script on Rivanna

- Open a terminal window and move to the directory where the notebook is located.
- Type the following:

```
module load anaconda  
jupyter nbconvert --execute --to python wine.ipynb
```

- The *jupyter nbconvert* command will create a file with the same base name but with the `.py` extension.

# RUNNING A PYTHON SCRIPT ON RIVANNA

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Modules  
Slurm scripts

# Using Modules on Rivanna

- Modules are our organizational tool for making software applications available on Rivanna.
- To have access to Python (at least a more current version of Python), you will need to type:

```
module load anaconda
```

- To see what you have loaded, you can type:

```
module list
```

# Hands-on Activity

- Open a terminal window on Rivanna and try the following activities:

```
module purge  
python --version
```

```
module load anaconda  
python --version
```

# Writing a Slurm script for the Code

- Slurm is the resources manager on Rivanna.
- We have to go through Slurm to run the code on a compute node
- Sample Slurm script, called submit\_wine.slurm:

```
#!/bin/bash
#SBATCH --nodes=1                #total number of nodes for the job
#SBATCH --ntasks=1              #how many copies of code to run
#SBATCH --time=00:10:00         #amount of time for the whole job
#SBATCH --partition=standard     #the queue/partition to run on
#SBATCH --account=Rivanna-training #the account/allocation to use

module purge
module load anaconda/2020.11-py3.8 #load modules my job needs
python wine.py                    #command-line execution of my job
```

# Hands-on Activity

- In your terminal window type:

```
sbatch submit_wine.slurm
```

- To check on its progress, type

```
sacct
```

- When it is done, you can look at the output. For example:

```
cat slurm-32631211.out
```

# Tweaking the Results

- Notice that the plot which was in the Notebook, does not appear in the Slurm output file.
- The plots appear when the code runs in an interactive mode, like with Jupyter Notebooks.
- When running in a batch mode, you will need to instruct the code to write the plot to a separate file:

```
fig, ax = plt.subplots()
ax.barh(range(len(importances)), importances[indices])
ax.set_yticks(range(len(importances)))
_ = ax.set_yticklabels(np.array(X.columns)[indices])
## Save plot to a file
plt.savefig('Wine_Features.png')
```



# Viewing the Image File

- To view the image file, you can
  - Go to the Open OnDemand Dashboard;
  - Click on Files > Home Directory;
  - Move into the appropriate folder;
  - Highlight the image file; and
  - Click “view”.
- Go back to your Jupyter Notebook. In the File Explorer column, double-click on the image file.

# RUNNING A MORE COMPLICATED SCRIPT ON RIVANNA

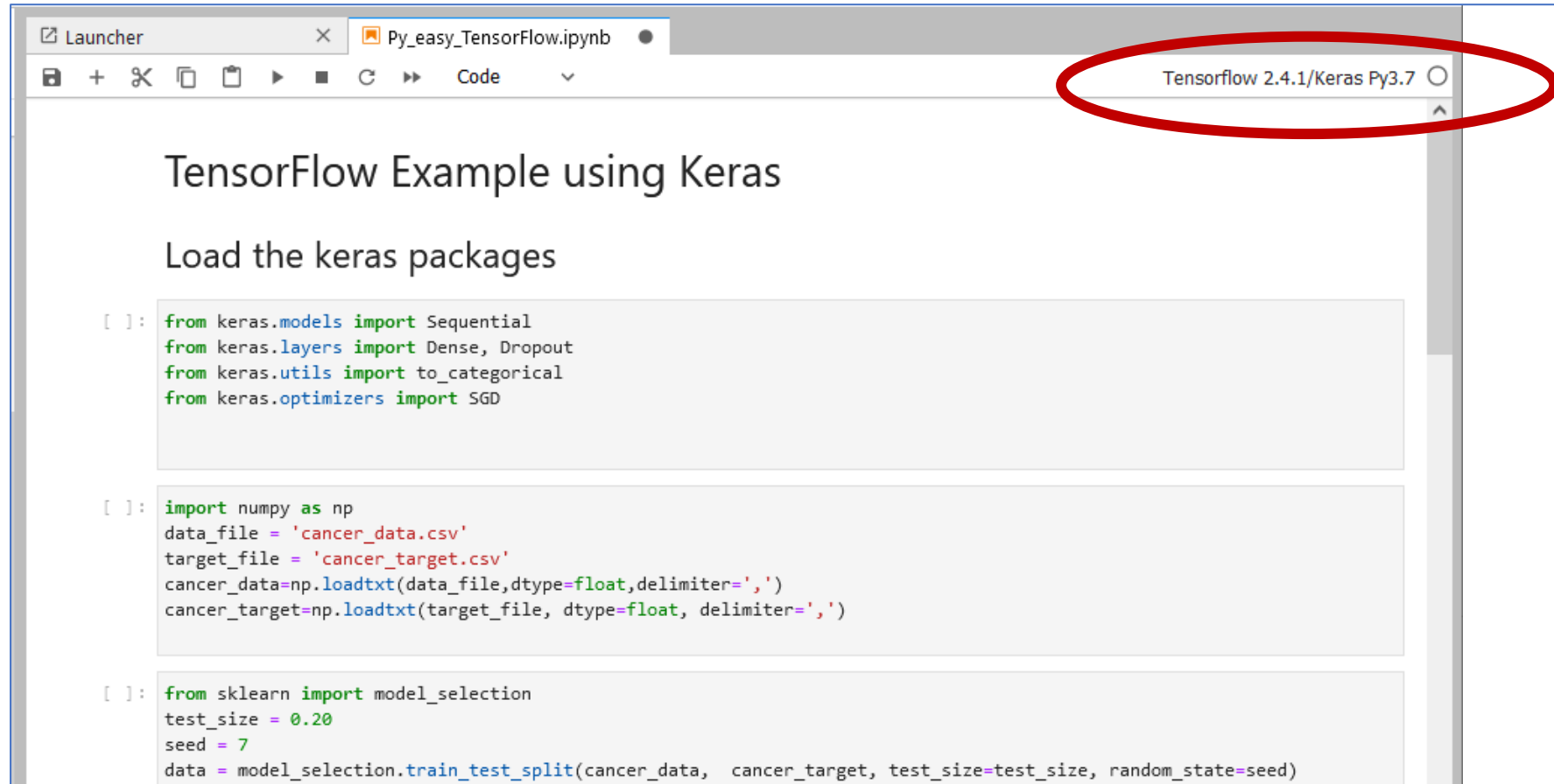
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Kernels  
Containers

# Second Sample Notebook

The next sample notebook, Py\_easy\_TensorFlow.ipynb, is a TensorFlow algorithm that tries to predict if a tumor is malignant or benign.

A major difference here is the **kernel** that the notebook uses.



The screenshot shows a Jupyter Notebook titled "Py\_easy\_TensorFlow.ipynb" in a "Launcher" window. The top right corner of the notebook interface displays "Tensorflow 2.4.1/Keras Py3.7", which is circled in red. The notebook content includes a title "TensorFlow Example using Keras" and a section "Load the keras packages". Below this, there are three code cells. The first cell imports Keras components: Sequential, Dense, Dropout, to\_categorical, and SGD. The second cell imports numpy and loads data from 'cancer\_data.csv' and 'cancer\_target.csv'. The third cell imports sklearn's model\_selection module and performs a train-test split.

```
[ ]: from keras.models import Sequential
from keras.layers import Dense, Dropout
from keras.utils import to_categorical
from keras.optimizers import SGD

[ ]: import numpy as np
data_file = 'cancer_data.csv'
target_file = 'cancer_target.csv'
cancer_data=np.loadtxt(data_file,dtype=float,delimiter=',')
cancer_target=np.loadtxt(target_file, dtype=float, delimiter=',')

[ ]: from sklearn import model_selection
test_size = 0.20
seed = 7
data = model_selection.train_test_split(cancer_data, cancer_target, test_size=test_size, random_state=seed)
```

# Jupyter Kernels Overview

- The kernel defines the underlying environment in which the Notebook will run.
- In our first example, the kernel was Python 3.
- But, other kernels exist that run as containers or conda environments. These kernels provide customized environments or even languages such as R or Julia.
- When working with kernels other than Python 3, we will need to identify the environment needed to run the code.

# Kernels & Containers

- We have several kernels, such as Tensorflow 2.4.1/Keras Py3.7, that run as containers.
- To recreate this environment in a Slurm script, we will need to
  - Find the appropriate modules for the container, and
  - Invoke the container with Singularity to recreate the kernel environment.

# Searching for Kernel Modules

- Pick a key word in the kernel name and search on it with the `module spider` command:

```
module spider tensorflow
```

# Searching for Kernel Modules

- The module spider command will give you a list of possible modules

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tensorflow:

---

Description:

TensorFlow is an open-source software library for Machine Intelligence.

Versions:


tensorflow/1.12.0-py36

tensorflow/2.1.0-py37

tensorflow/2.4.1

tensorflow/2.7.0

tensorflow/2.8.0



Closest to version of  
our kernel

# Searching Kernel Modules Versions

- For more details, we can include the version number in the module spider command:

```
module spider tensorflow/2.4.1
```

- Resulting Output:

-----  
tensorflow: tensorflow/2.4.1  
-----

...

You will need to load all module(s) on any one of the lines below before the "tensorflow/2.4.1" module is available to load.

singularity/3.7.1

← Important Information



# Running Singularity Modules

- If the version information shows “singularity” as a requirement for the module, then the module sets up a container.
- Loading the modules will tell us the name of the container.
- To run a container, we have to run singularity with the name of the container and the name of our script:

```
singularity run --nv <container_name> <script_name>
```

- Plus, if we are running on GPUs, we need to use the --nv option to make singularity aware of the available hardware.

# Hands-on Activity

- In your terminal window type:

```
module load singularity/3.7.1
```

```
module load tensorflow/2.4.1
```

- Notice what is written to the screen. This is the command to run the container.
- Go ahead and convert the Notebook Py\_easy\_TensorFlow.ipynb to a Python script.

# Slurm script for a Container on a GPU

- In addition to requesting the GPU partition, we need to ensure that a GPU device is requested.
- Sample Slurm script:

```
#!/bin/bash
#SBATCH --nodes=1                #total number of nodes for the job
#SBATCH --ntasks=1              #how many copies of code to run
#SBATCH --time=00:10:00         #amount of time for the whole job
#SBATCH --partition=gpu         #the queue/partition to run on
#SBATCH --gres=gpu:1
#SBATCH -account=rivanna-training #the account/allocation to use

module purge
module load singularity/3.7.1 tensorflow/2.4.1
singularity run --nv $CONTAINERDIR/tensorflow-2.4.1.sif Py_easy_TensorFlow.py
```

# Hands-on Activity

- Submit the Slurm script to run the `Py_easy_TensorFlow.py` code

# NEED HELP?

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Thursdays: 10 am – noon

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