### **Creating a TensorFlow Environment in HPC**

Loading the conda module: module load miniconda3

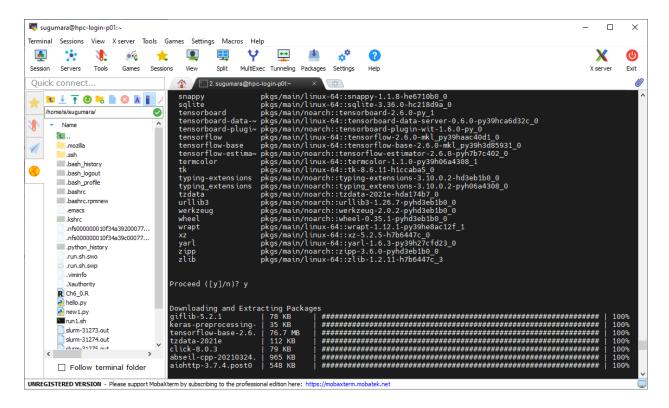
Initialize bash shell to run conda commands:

conda init bash
source ~/.bashrc

For creating the tensorflow environment, type the following command:

conda create -n tf tensorflow

Type "y" once the relevant packages have been identified to install. It takes a bit of time to install all the packages.



Once the installation is complete, for the changes to take effect, close and re-open your current shell.

After starting a new terminal, execute the following command to activate the tf environment:

conda activate tf

### **Installing keras**

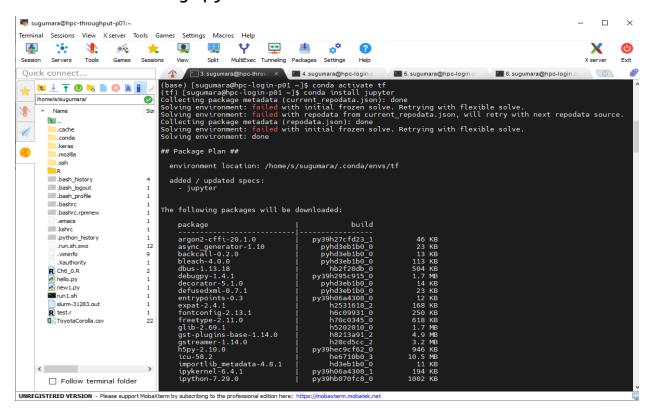
To install the keras package in the **tf** environment, type the following command: **conda install keras** 

# **Installing sklearn**

To install the sklearn package in the **tf** environment, type the following command: pip install sklearn

### **Installing Jupyter Notebook**

In the **tf** environment, to install Jupyter Notebook, type the following command: **conda install jupyter** 



After the relevant packages are gathered, type "y" to proceed with the installation. This will also take some time.

Once the jupyter notebook installation is complete in the **tf** environment, you will get the "done" messages.

Preparing transaction: done Verifying transaction: done Executing transaction: done

Now you are ready to run jupyter notebook.

### **Using Jupyter Notebook on Matilda**

There are two basic methods for running Jupyter Notebook on the Matilda HPC compute nodes: a) Interactive scheduled job, and b) SBATCH Job.

#### **Interactive Scheduled Job using SRUN**

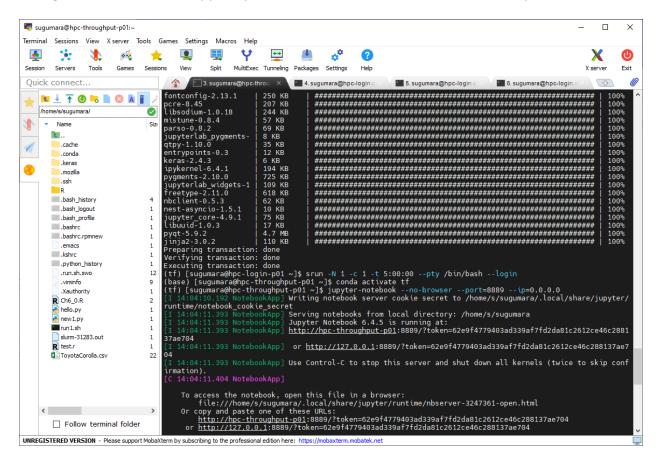
The first method involves invoking a schedule interactive job to begin the process. Run the following command:

Then, activate the tf environment.

conda activate tf

Start the Jupyter Notebook Server

Once the jupyter notebook server starts, you will get a URL that can be used to connect to the server through a browser. You can copy and paste this URL into a browser after the next step.



Workshop: New Computational Resource Training (Matilda HPC cluster)

Vijayan Sugumaran, School of Business Administration

Center for Data Science and Big Data Analytics

Before we can connect to the jupyter notebook server, we need to initiate a port forwarding session.

From another shell on your workstation, initiate a port forwarding session to the compute node as shown below:

ssh -N -L 8889:hpc-throughput-p01:8889 username@hpc-login.oakland.edu

Make sure to change "username" to your actual username. Also, make sure to substitute in the actual port used as well as the actual node you are logged into (in this example we are running on hpc-throughput-p01).

Now open a browser and enter the URL that was generated when the Jupyter Notebook Server started:

http://127.0.0.1:8889/?token=47ef2216d4ce8e14f30967def52d6e8dd6a0db0514692b00

You should now be connected to the Jupyter Notebook. Please again note to substitute the actual port used for "8889" above (also your token will be different than the one shown above). Just copy and paste the appropriate link.

#### PRECAUTIONS AND NOTES

There are several issues to keep in mind when running Jupyter Notebooks on Matilda. These are highlighted below.

#### **PORTS**

The default port for Jupyter notebooks is "8888". Since others may be running a notebook on the node on which your job is running, it is possible that port will be in-use and an error will occur. If this happens, increment the port number until you find one that is not being used. This can be controlled either in the interactive job session, or by making a change to the job script for port.

#### LOGIN NODE

Please exercise care if running Jupyter Notebooks on the login node. Login is not meant for intensive jobs and notebooks consuming inordinate resources may be killed without warning.

When ever practical, you should be running your notebook on a compute node as a schedule job (interactive or batch).

## **Executing a Python Script File**

#### **Example Python file: new.py**

import tensorflow as tf from tensorflow import keras as ke print('\n TensorFlow version:', tf.\_\_version\_\_) print(' Keras version:', ke.\_\_version\_\_) print ('\n Hello World \n')

#### SLURM File to run the new.py Python File: run.sh

#!/bin/bash
#SBATCH --job-name=mySerialjob
#SBATCH --nodes=1
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=1
#SBATCH --time=0-00:20:00
#SBATCH --mem=3102
source ~/.bashrc
conda activate tf
python new.py

# Submitting the batch file

sbatch run.sh

# Directing the output to a file (say python.out)

Modify the last line in the run.sh file as follows:

#### SLURM File: run1.sh

#!/bin/bash
#SBATCH --job-name=mySerialjob
#SBATCH --nodes=1
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=1
#SBATCH --time=0-00:20:00
#SBATCH --mem=3102
source ~/.bashrc
conda activate tf
python new.py > python.out

# Running a simple Linear Regression model in Python

SLURM File: run2.sh

#!/bin/bash
#SBATCH --job-name=mySerialjob
#SBATCH --nodes=1
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=1
#SBATCH --time=0-00:20:00
#SBATCH --mem=3102
source ~/.bashrc
conda activate tf
python LinearRegression.py > LinearRegression.out

# Running a Multiple Linear Regression model in Python

SLURM File: run3.sh

#!/bin/bash
#SBATCH --job-name=mySerialjob
#SBATCH --nodes=1
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=1
#SBATCH --time=0-00:20:00
#SBATCH --mem=3102
source ~/.bashrc
conda activate tf
python MLR.py > MLR.out

## Running an R script file

SLURM File: run4.sh

#!/bin/bash
#SBATCH --job-name=mySerialjob
#SBATCH --nodes=1
#SBATCH --ntasks-per-node=1
#SBATCH --cpus-per-task=1
#SBATCH --time=0-00:20:00
#SBATCH --mem=3102
module load R
Rscript test.r > test.out