



#### **Outline**

Part II - Practical Guidelines for Running a Project:

Choosing Hyperparameters – a bit of exploration and exploitation

Job workflow - make it efficient and easy to organize

**CPUs vs GPUs** 

Parallelizing Models and Multinode Execution, with an exercise

## **Choosing Hyperparameters**

- Hyperparameters are found by searching, not by the network algorithm
- Generally, hyperparameters related to:

   architecture (layers, units, activation, filters, ...)
   algorithm (learning rate, optimizer, epochs, ...)
   efficient learning (batch size, normalization, initialization, ...)
- Some options are determined by task:
   e.g. the loss function, using CNN vs MLP, ...
- Use what works, from related work or the latest recommendations,

## Hyperparameters Search

- Can take a long time, hard to find global optimal
- Start with small data, short runs to get sense of range of good parameter values
- Easy but possibly time-consuming method:
   grid search over uniformly spaced values
- Do "exploration" then "exploitation", ie search wide then search deep Keras Tuner functions can help with the wide search (Raytune is similar tool for Pytorch)



## **Keras Hyperparameter Search Tool**

Keras Hypertuner class implements several search strategies:

Hyperband is like a tournament of hyperparameter configurations

RandomSearch will search randomly through the space of configurations

Bayesian optimization is like a function approximation to pick out next configuration



#### Keras Tuner code snippet

Set up function to make the model

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Set up hyperparameter choices

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Define 'tuner' object: use the wrapper and model fit to search

configurations

strides=1

## **Workflow and Organizing Jobs**

Job Level: What makes sense to include in each job?

Model Level: run & test model for each parameter configuration

Data Level: loop through cross validation datasets (if applicable)

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Model Level: run & test model for each parameter configuration

Data Level: loop through cross validation datasets (if applicable)

- Consider how long a model runs for 1 configuration of hyperparameters
- Organize jobs into reasonable chunks of work
- For large models consider model-checkpoints
- Tensorboard is available on Expanse (ask for details to run securely)

## note on using GPU

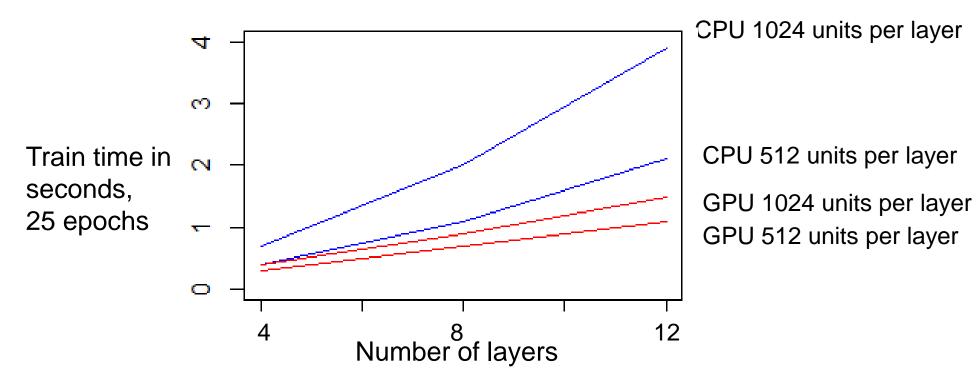
- GPU node has multiple GPU devices
- By default tensforflow will run on 0<sup>th</sup> gpu device if GPU is available, otherwise it will use all CPU cores available

Code snippet to check for GPU devices

import tensorflow as tf

gpu\_devices = tf.config.list\_physical\_devices("GPU")

## GPU shared (V100) vs CPU (128 cores) For MLP with Dense Layers, 80000x200 data matrix



GPUs faster, but you might have to wait more in job queue; also some memory limits compared to CPU, may need to use smaller batch size



## Parallelism in Deep Learning

Two Goals

1 Speed Up Learning - as data scales up training takes longer

2 Optimize Memory - as models scale up they take up too much memory e.g. V100s have 32Gb limit and 8B float32 parameters would fill that



## **Parallelism strategies**

- Data Parallelism: partition data and copy the model across devices, (this is probably easiest thing to do, least programming)
- Pipeline Parallelism: split up the model across devices, i.e. inter-layer (you organize layers)
- Tensor Parallelism: split up weight matrix across devices, i.e. intra-layer (model has to support it)

## Reducing memory footprint

 Using mixed precision (e.g. bfloat16 for weights) lowers memory at a cost of accuracy

 'DEEPSPEED' package partitions the optimization calculations at a cost of communication

## Parallel DL models with multiple nodes/devices

Data Parallel:

Each device trains a copy of the model with a part of the data Weight updates have to be aggregated across devices

Main tools on Expanse:

Keras/Tensorflow 'strategy' (simple for multidevice on 1 node) or

**Horovod MPI wrappers (for multinode)** 

## Keras/Tensorflow strategy single GPU node

1. Get a list of gpu devices available

```
gpus_list = tf.config.experimental.list_physical_devices('GPU')
```

2. Set up a 'mirror' strategy

```
mirrored_strategy = tf.distribute.MirroredStrategy(["GPU:0", "GPU:1", "GPU:2", "GPU:3"])
```

3. Use strategy scope around the model definition (so model gets copied)

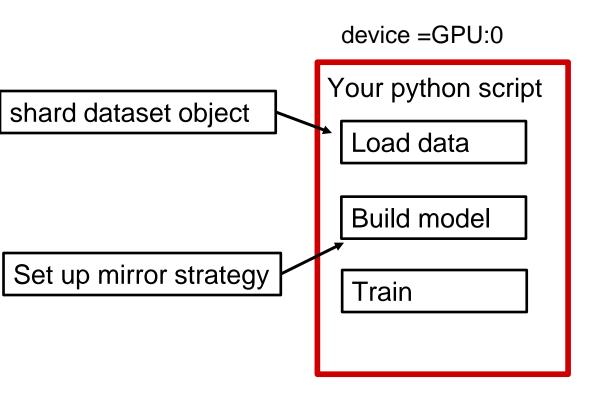
```
with mirrored_strategy.scope():
    multi_dev_model=build_model()
```

4. A tensorflow dataset object will 'shard' (ie split up) data among GPU devices

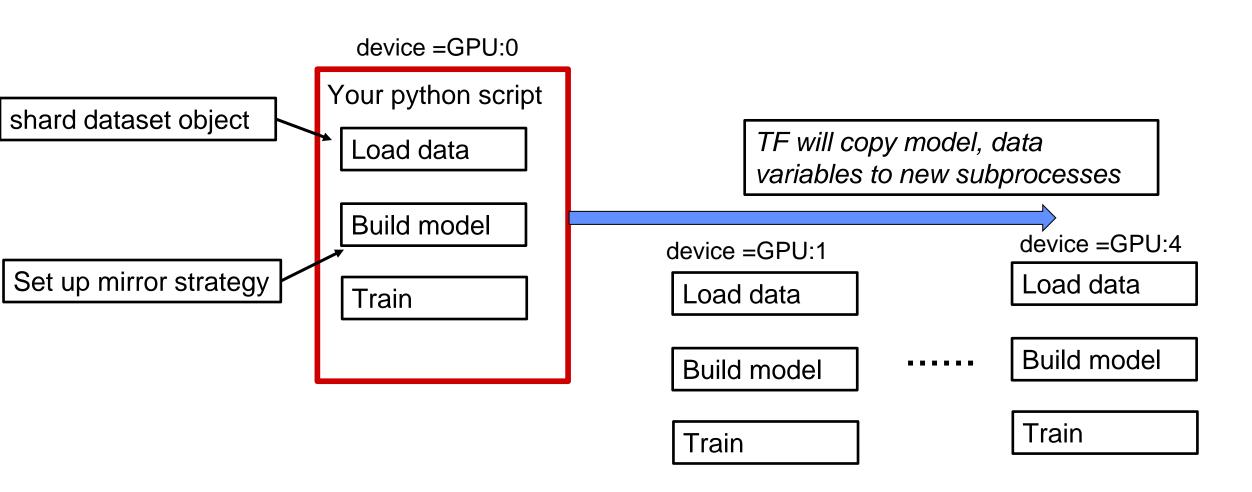
```
train_dataset = tf.data.Dataset.from_tensor_slices((X_train, Y_train)) ...
```



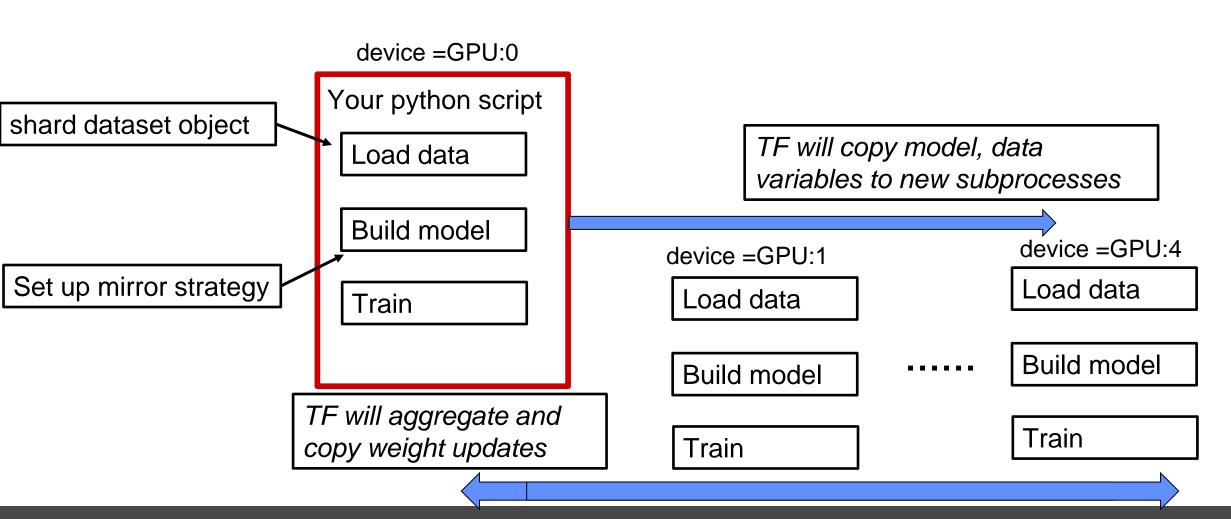
## Mirror Strategy single GPU node



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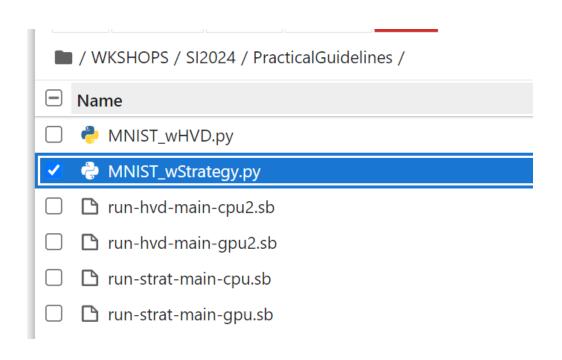
## Mirror Strategy single GPU node



## Keras/Tensorflow strategy single GPU node

#### **Example, in github repo find:**

MNIST\_wStrategy.py run-strat-main-gpu.sb run-strat-main-cpu.sb



#### From terminal window submit a batch job:

```
4rodrig@login01 PracticalGuidelines]$
4rodrig@login01 PracticalGuidelines]$ sbatch run-strat-main-gpu.sb
```



## Keras/Tensorflow strategy single GPU node

#### View your job queue and 'ssh' into the GPU node

```
[p4rodrig@login01 PracticalGuidelines]$ squeue -u $USER

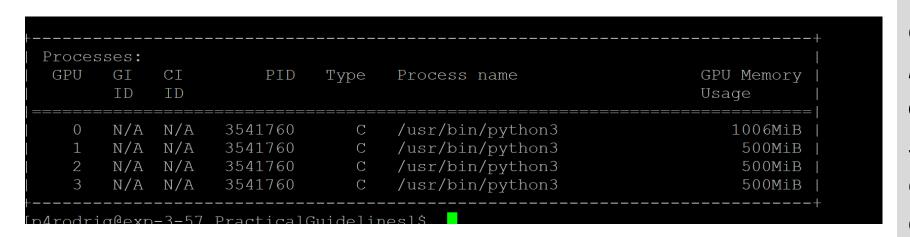
JOBID PARTITION NAME USER ST TIME NODES NODELIST(REASON)

32768950 gpu tfstrat- p4rodrig R 4:07 1 exp-3-57

32768191 shared galyleo- p4rodrig R 1:53:30 1 exp-1-48

[p4rodrig@login01 PracticalGuidelines]$ ssh exp-3-57
```

#### In the GPU node run 'nvidia-smi' to view GPU usage



TF has
copied the
model into
each GPU,
sharded the
data, and
coordinated
learning

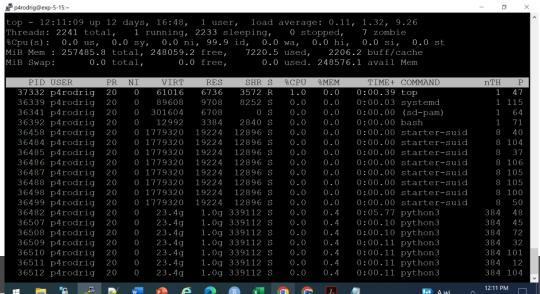


## Keras/Tensorflow strategy single CPU node

#### View your job queue and 'ssh' into the CPU node

```
[p4rodrig@login02 PracticalGuidelines]$ sbatch run-strat-main-cpu.sb
Submitted batch job 32783480
[p4rodrig@login02 PracticalGuidelines]$ squeue -u $USER
             JOBID PARTITION
                                           USER ST
                                  NAME
                                                          TIME
                                                                NODES NODELIST (REA
SON)
                     compute galyleo- p4rodrig PD
          32783384
                                                         0:00
                                                                    1 (Priority)
          32783480
                     compute tfstrat- p4rodrig R
                                                         0:42
                                                                    1 \exp -5 - 15
```

## In the CPU node run top –u \$USER Then 'H', 'f', down arrow to 'n-th', space bar to toggle, (repeat for P), esc



TF uses threads and available CPU cores for parallelization

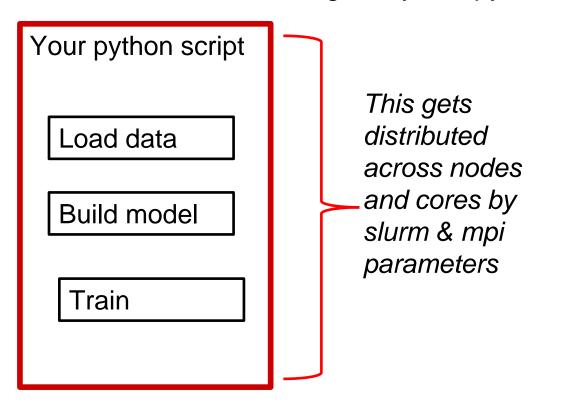


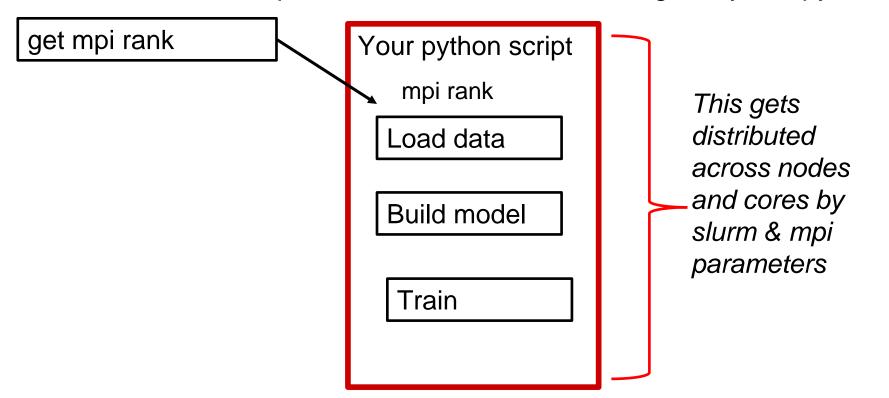
## Keras/Tensorflow strategy multiple GPU/CPU node

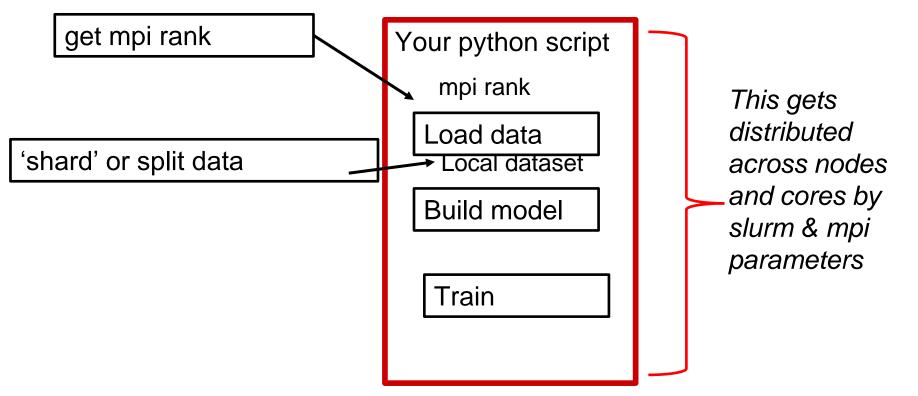
Keras also has a 'multiworker' strategy but it requires setting up config files with IP addresses

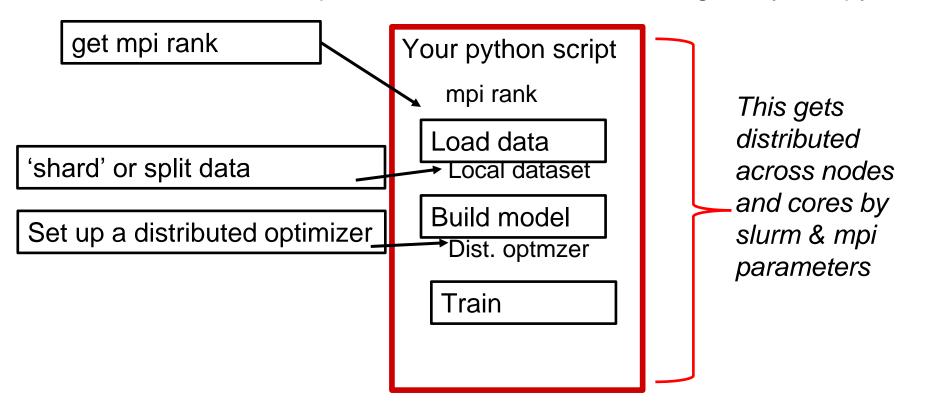
But, on HPC systems resources are shared so IP addresses are dynamic

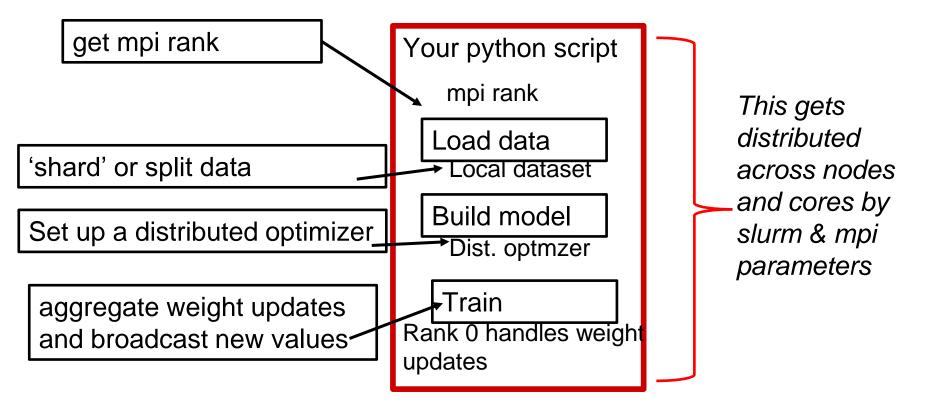
Thus, it is better to use Horovod with MPI and slurm batch job











## mpi launches one instance per processor

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In slurm batch script:

mpirun –n **number of tasks** singularity  $\rightarrow$  python

device =GPU:0

device =GPU:0

device =GPU:0

Your python script

mpi rank

Load data

Local dataset

Build model

Dist. optmzer

Train

Rank 0 handles updates

Your python script

mpi rank

Load data

Local dataset

Build model

Dist. optmzer

Train

Your python script

mpi rank

Load data

Local dataset

Build model

Dist. optmzer

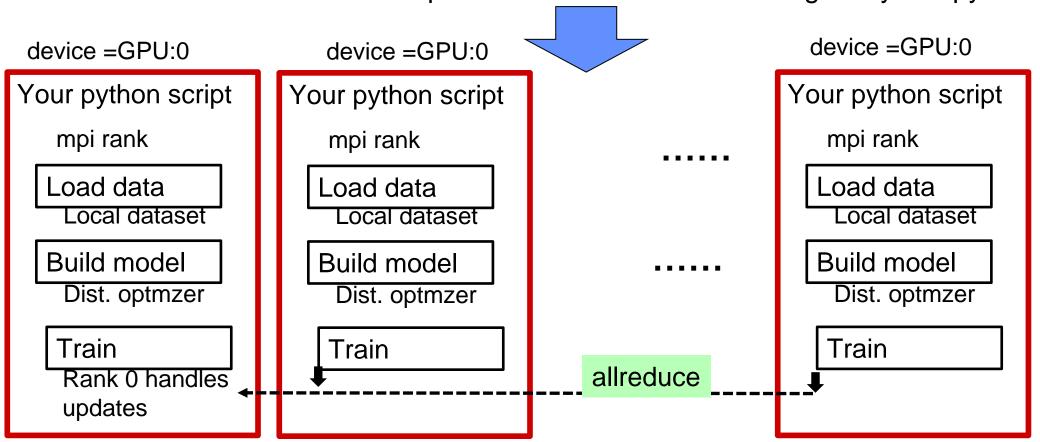
Train



# For each batch: Horovod will aggregate & share weights updates

In slurm batch script:

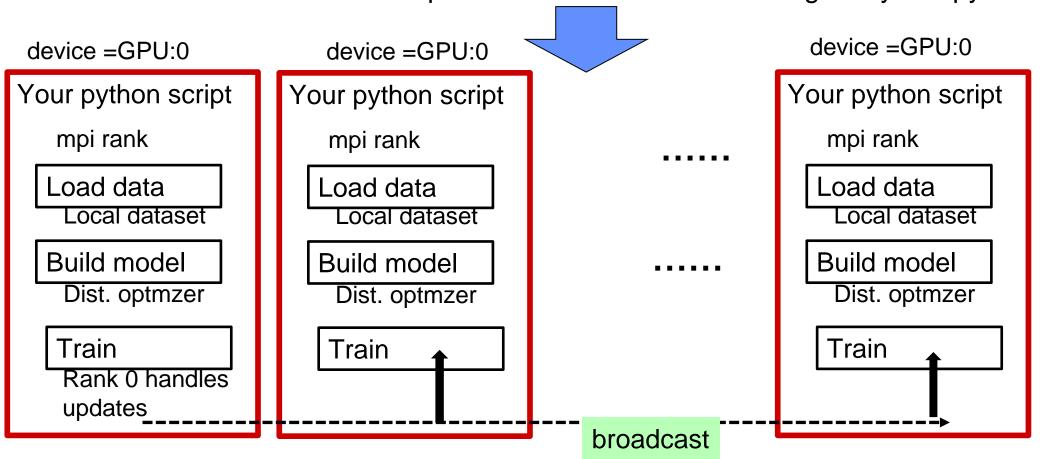
mpirun –n **number of tasks** singularity → python



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In slurm batch script:

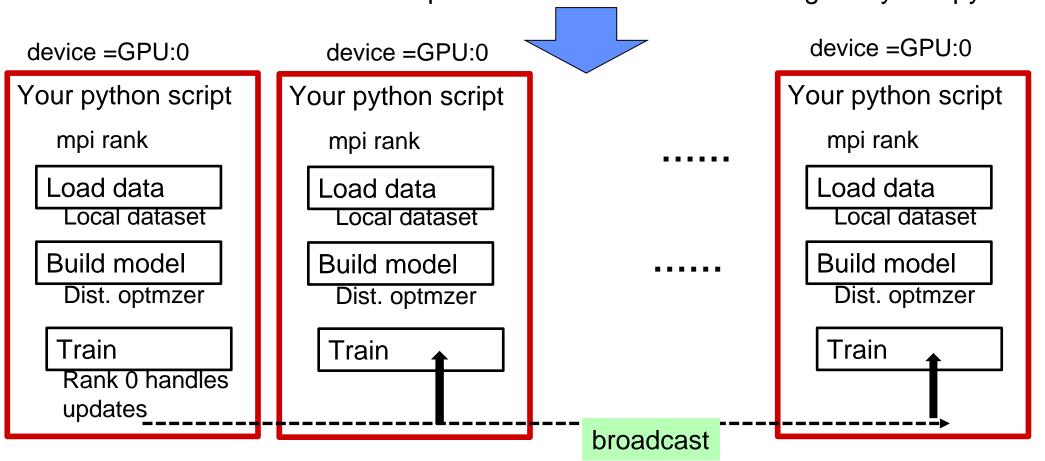
mpirun –n **number of tasks** singularity → python



# For each batch: Horovod will aggregate & share weights updates

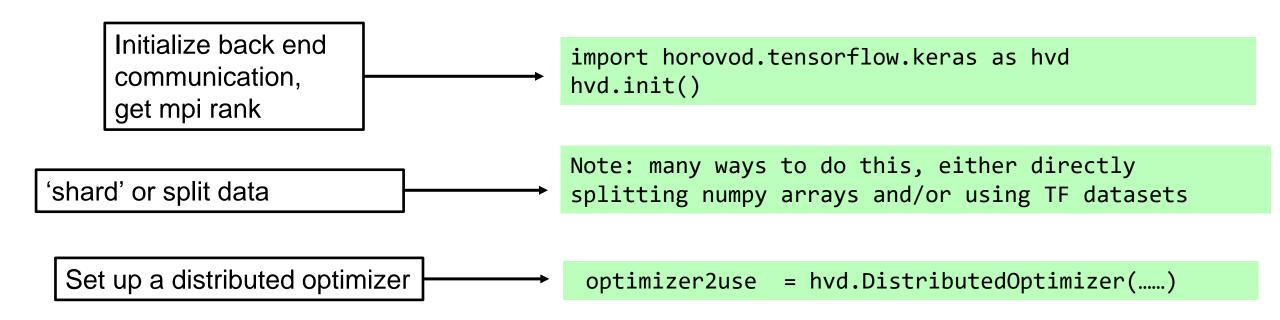
In slurm batch script:

mpirun –n **number of tasks** singularity  $\rightarrow$  python



Bigger batch size helps, but it uses more memory

### **Code snippets – Horovod functions**

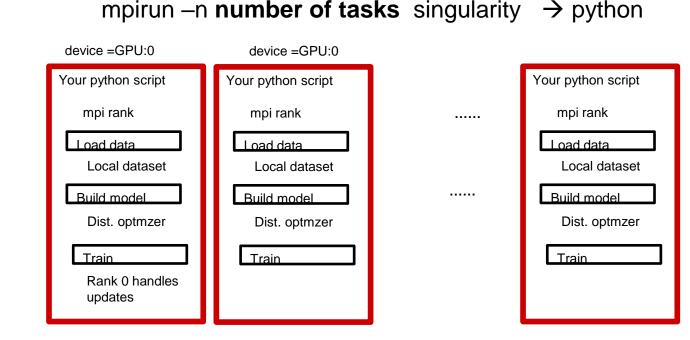


Horovod takes care of the communication for training and updating weights



## Exercise, multinode MNIST programming and execution

- Goal: Get familiar with Keras and Horovod coding for multinode execution
- Goal: Get familiar with slurm batch script multinode parameters
- Let's login and start a notebook (see next pages for quick overview)



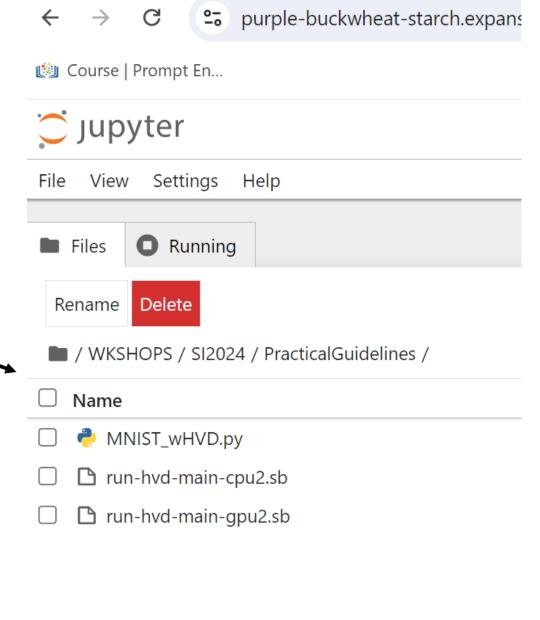
#### In terminal

#### \$ jupyter-compute-tensorflow

In jupyter notebook session open the *MNIST\_wHVD* notebook

Open the *run-hvd-main-cpu2.sb* slurm batch script

Follow instructions in the notebook and batch script



Initialize back end communication, get mpi rank

```
import horovod.keras as hvd
hvd.init()
print('INFO, global rank:',hvd.rank(), ' localrank ',hvd.local_rank())
#------
```

split data using numpy arrays

```
# ------
per_worker_batch_size = 32  #Pick factors of 32 (especially for GPU)
num_workers = hvd.size()
```

Set up a distributed optimizer to manage weight updates

#### Your Task:

- run sbatch command for the slurm script (for cpu)
- change number of cpus to use, rerun, and review stdout output file

```
Launcher
                        10 # 2
11 # Do a File->open of the run-hvd-main-cpu2.sb slurm batch script
12 #
           optionally edit the number of cpus to use, try for example 4,8,16, and/or 32
13 # 3
14 # In a terminal window, submit the script and review the job status
              1$ sbatch run-hvd-main-cpu2.sb
16 #
              1$ squeue -u your-userid
17 #
18 # Optionally, ssh into the running nodes and run top command (top -u userid)
19 #
20 # 4
21 # After the ich finishes look at the atdout tyt file
                        jupyter run-hvd-main-cpu2.sb✓ 15 minutes ago
                                                                                                                                Logout
                                   View Language
                                                                                                                              Plain Text
                           #SBATCH --job-name=tfhvd-cpu
                           #SBATCH --account=use300
                           #SBATCH --partition=compute
                           #SBATCH --nodes=2
                           #SBATCH --ntasks-per-node=16 #<<<<<---- change this to 16 and observe changes in training time
                           #SBATCH --cpus-per-task=1
                           #SBATCH --mem=243G
                           #SBATCH --time=00:15:00
                        11 #SBATCH --output=slurm.cpu2.%x.o%j.out
```

```
[p4rodrig@login01 MNODE_wHVD]$
[p4rodrig@login01 MNODE_wHVD]$ grep 'done, rk: 15' stdout_*
stdout_cpu2_mnist_32.txt:INFO,done, rk: 15 train time: 2.48225 secs
stdout_mainhvd_cpu2.txt:INFO,done, rk: 15 train time: 2.31222 secs
[p4rodrig@login01 MNODE_wHVD]$
[p4rodrig@login01 MNODE_wHVD]$
```

Pause ... you might find trade offs in communication vs cpus

```
in113@login01 3.3.Practical-Training]$ grep 'done, rank: 0 train' stdout_cpu2_mnist_*
ut_cpu2_mnist_16.txt:INFO,done, rank: 0 train time: 19.10057 secs
ut_cpu2_mnist_32.txt:INFO,done, rank: 0 train time: 15.46317 secs
ut_cpu2_mnist_8.txt:INFO,done, rank: 0 train time: 33.32454 secs
in113@login01 3.3.Practical-Training]$
```



End

