## Introduction to Using Expanse for AI Jobs

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## Outline

- Parallelization in Tensorflow
- Expanse Notebooks and Open On Demand
- Starting Jupyter notebook and simple MNIST
   example
- An example running multinode on Expanse An example running Keras NLP tool in conda environment, w/Juptyer Lab





## Things to think about for running a project

- Choosing Hyperparameters a bit of exploration and exploitation
- Need to figure out efficient Job workflow
- On HPC, CPU work fine for many cases, you will want to use GPUs for 'large' models and/or large datasets.
- Model saves and/or checkpoints are available in tensorflow; tensorboard available but needs to be secure (ask for details)





## **Python Notebook vs Scripts**

• On HPC you may want to run batch jobs on a script not a notebook.

**1** Papermill is one tool

**2 Or, you can use** "*jupyter nbconvert --to script your-python.ipynb*" in the batch job.

Also, turnoff plot display, save plots in files, and use a configuration file to pass in parameters





## Parallel DL models with multiple nodes/devices

• The main approach to parallelize training: Data Parallel:

Main tools: Keras/Tensorflow 'strategy' or use Horovod MPI wrappers





## Keras/Tensorflow strategy single GPU node

Set up a 'mirror' strategy

mirrored\_strategy = tf.distribute.MirroredStrategy(["GPU:0", "GPU:1", "GPU:2", "GPU:3"])

You also need the strategy scope around the model definition so that it can make copies

if (n\_gpus>0):
 with mirrored\_strategy.scope():
 multi\_dev\_model=build\_model()

Then train as normal (use batch size multiple of 32)





## Keras/Tensorflow strategy multiple GPU node

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

On HPC systems resources are shared so IP addresses are dynamic

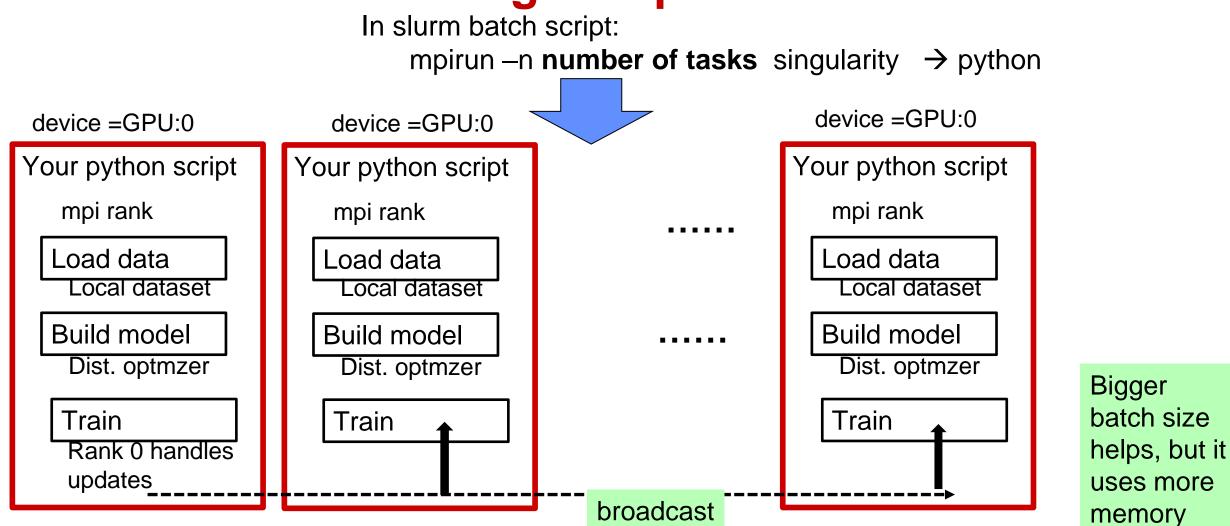
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Better to use Horovod with MPI and slurm batch job





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

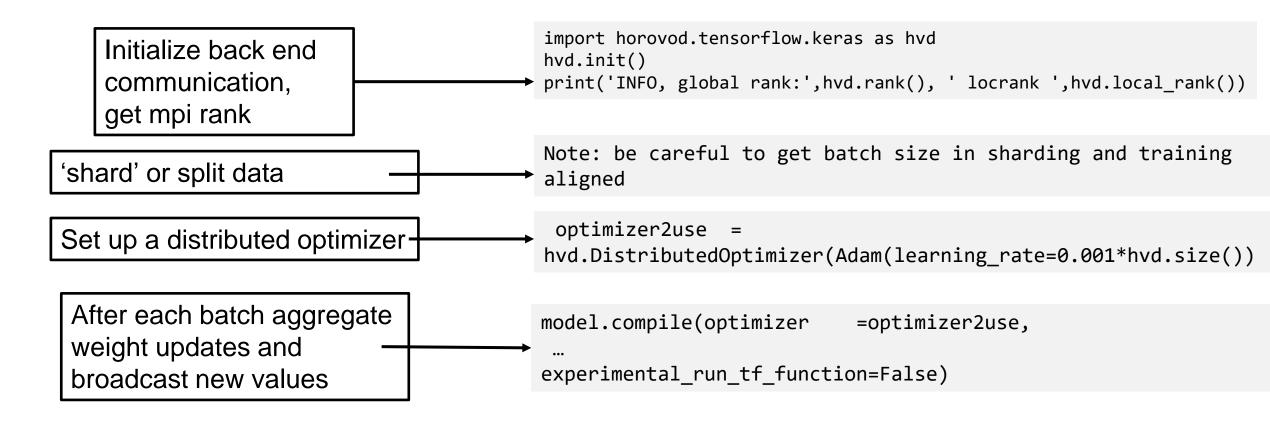


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## **Code snippets – Horovod functions**

Not many lines of code, but becareful with sharding, batch size, See https://horovod.readthedocs.io/en/latest/keras.html

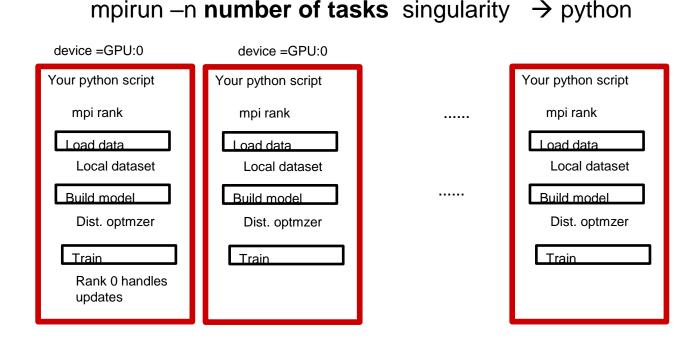




# Exercise, multinode MNIST programming and execution

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- 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)



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## **Accessing Expanse**

- Command line interface to run Slurm jobs
- Expanse user portal has web interface to start Jupyter lab/notebooks

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Slurm jobs can also start a notebook



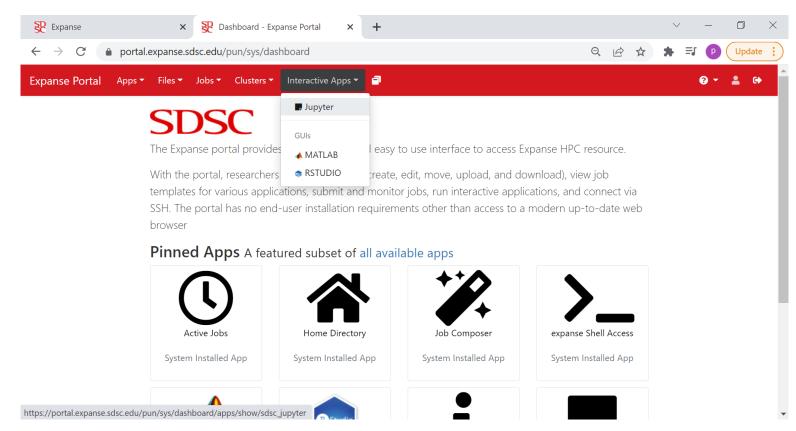


C  pelvis-daisy-faceplate.expanse-user-content.sdsc.edu/edit/WKSHOPS/CIML23/MNODE_wHVD/run-hvd-main-c	Logout	
File Edit View Language	Plain Text	
<pre>2 3 #SBATCHjob-name=tfhvd-cpu 4 #SBATCHaccount=use300 5 #SBATCHnation=compute 6 #SBATCHnodes=2 7 #SBATCHntasks-per-node=16 #&lt;&lt;&lt;&lt;&lt; change this to 16 and observe changes in training time 8 #SBATCHmem=2436 10 #SBATCHtime=00:15:00 11 #SBATCHoutput=slurm.cpu2.%x.o%j.out 12 13 # set up modules 14 module reset 15 module load slurm 16 module load slurm 17 module load openmpi/4.1.3 #open mpi 18 module load singularitypro/3.9 #container 19 module list 10 14 # set up some environmental settings 22 export OMPI_MCA_btl='self,vader' 23 export UCX_TLS='shm_rc,ud,dc' 24 export UCX_NET_DEVICES='mlx5_0:1' </pre>		stdout_* time: 2.48225 secs
[p4rodrig@login01 MNODE_wHVD]\$ [p4rodrig@login01 MNODE_wHVD]\$ [p4rodrig@login01 MNODE_wHVD]\$ [p4rodrig@login01 MNODE_wHVD]\$ [p4rodrig@login01 MNODE_wHVD]\$ [p4rodrig@login01 MNODE_wHVD]\$	• 1J LIAIN	time: 2.31222 secs

 $\checkmark$ 

## The expanse user portal (open on demand) https://portal.expanse.sdsc.edu

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Login in with ACCESS credentials (NSF CI coordination at <u>https://access-ci.org/</u>)

For local workshops use the assigned "train## ' account and go to:

https://portal.expanse.sdsc.edu/training





## **Galyleo Utility for Jupyter Notebooks**

- A tool that launches a Jupyter Lab/Notebook server on a compute node
- Establishes a secured HTTPS connection between that compute node and your web browser (reverse proxy)

For details:

https:/github.com/mkandes/galyleo

https://education.sdsc.edu/training/interactive202112\_running\_jupyter\_notebooks\_on\_expanse/ index.html



## **Sample Galyleo scripts**

• A script that loads a conda environment to compute node (cpu)

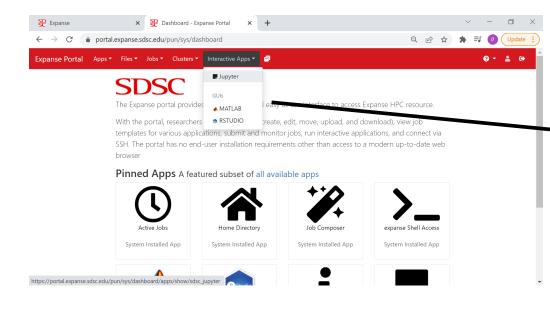
/cm/shared/apps/sdsc/galyleo/galyleo.sh launch --account gue998 --partition compute --nodes 1 --memory 242 --cpus 128 --time-limit 01:00:00 --conda-env keras-nlp24 --conda-yml keras-nlp24-cpu.yaml --mamba

• A script that loads a singularity image to gpu node

/cm/shared/apps/sdsc/galyleo/galyleo.sh launch -A gue998 -p gpu -n 10 -M 93 -G 4 -t 00:30:00 -e singularitypro/3.9 --bind /expanse,/scratch -s /cm/shared/apps/containers/singularity/pytorch/pytorch-latest.sif

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Expanse user portal: launch a jupyter notebook session

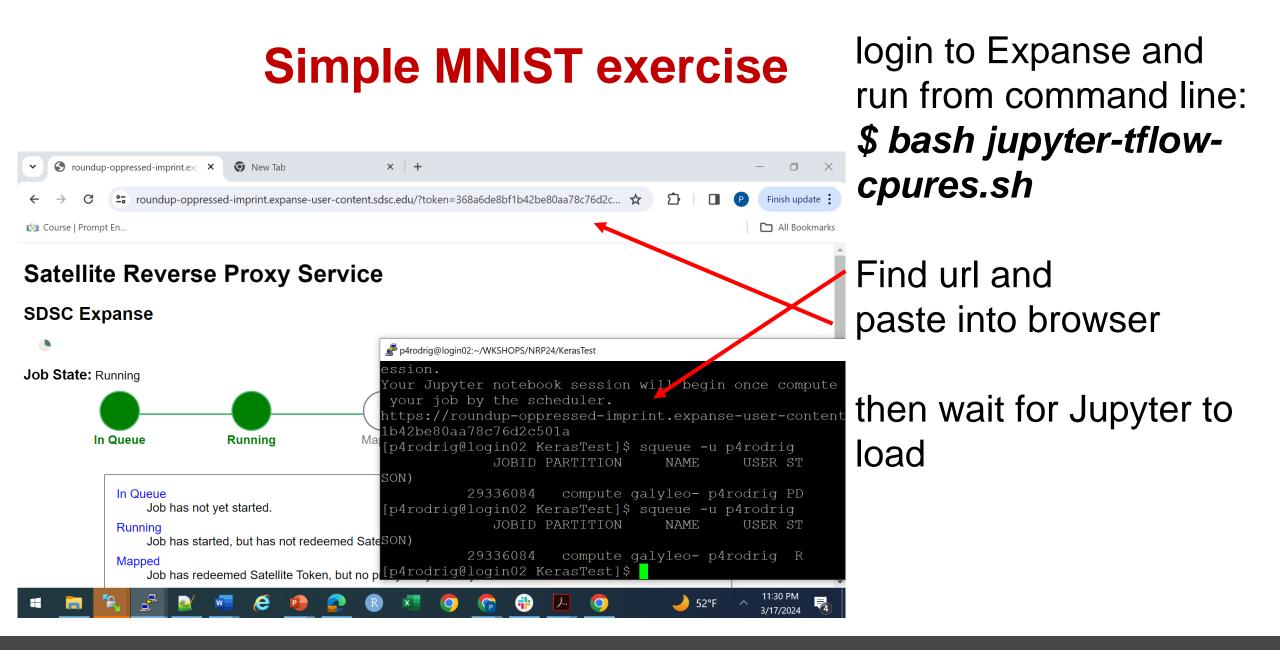
Or

login to Expanse and run: \$ bash jupyter- ... -cpures.sh

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	Partition (Please choose the gpu, gpu-shared, or gpu-preempt as the partition if using gpus):						
(1 ) (i	compute						
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	GPUs (optional):						
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Memory required pe	Singularity Image File Location: (Use your own or to include from existing container library at /cm/shared/apps/container e.g.,						
16	/cm/shared/apps/containers/singularity/pytorch/pytorch-latest.sif)						
	/cm/shared/apps/containers/singularity/tensorflow/tensorflow-latest.sif						
GPUs (optional):	Environment modules to be loaded (E.g., to use latest version of system Anaconda3 include cpu,gcc,anaconda3):						
	singularitypro/3.9						
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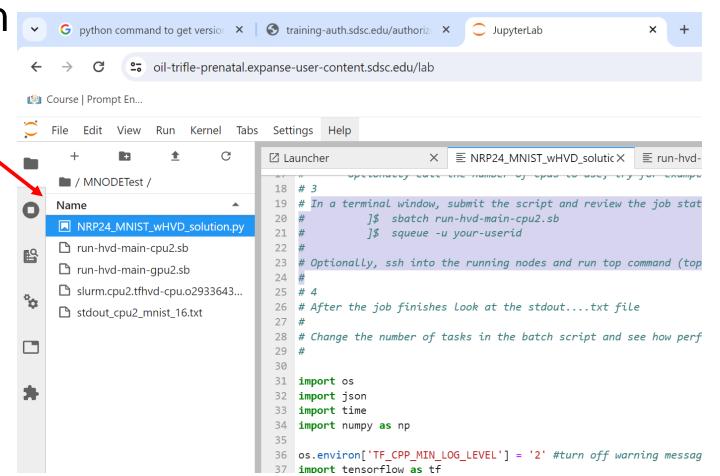
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In jupyter notebook session open the MNIST\_Intro notebook

Review notebook or just select Edit-> clear all cels Run-> Run all cells







## **Simple MNIST multinode exercise**

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#SBATCH --job-name=tfhvd-cpu #SBATCH --account=use300 #SBATCH --partition=compute 6 #SBATCH --nodes=2 #SBATCH --ntasks-per-node=16 #<<<<<---- change this to 16 and observe changes in training time #SBATCH --cpus-per-task=1 9 #SBATCH --mem=243G 10 #SBATCH --time=00:15:00 11 #SBATCH --output=slurm.cpu2.%x.o%j.out 12 × 🖾 Launcher 13 #----- set up modules ------14 module reset 15 module load slurm 16 module load gcc/10.2.0 #compiler, unix 17 module load openmpi/4.1.3 #open mpi 18 module load singularitypro/3.9 #container 19 module list 20 21 #----- set up some environmental settings -----export OMPI MCA btl='self,vader' 22 23 export UCX\_TLS='shm,rc,ud,dc' 24 export UCX NET DEVICES='mlx5 0:1' 25 export UCX MAX RNDV RAILS=1 26 27 #cd into the working directory, slurm puts you there 28 29 #----- execute the mpirun command to launch container instances 30 mpirun -n \${SLURM NTASKS} singularity exec --bind /expanse,/scratch /cm/shared/apps/containers/singularity/tensorflow/tensorflow-latest.sif python3 ./NRP24 MNIST wHVD solution.py > stdout cpu2 mnist \${SLURM NTASKS}.txt 31

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In MNODE\_Test directory, see the slurm script: run-hvd-main-cpu2res.sb

Many lines for slurm commands and environment set up

**Note:** mpirun launches instances of 'singularity exec ...'

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#### In MNODE\_Test directory

Python script: MNIST\_wHVD\_exercise notebook

Slurm script: *run-hvd-main-cpu2.sb* 

In a terminal window, submit the script and review the job status

- ]\$ sbatch run-hvd-main-cpu2.sb
- ]\$ squeue -u your-userid

Optional run top c Look for

## Simple MNIST multinode exercise

etrain94@login02:~/MNODETest	—	
[etrain94@login02 ~/MNODETest]\$ ls		
NRP24_MNIST_wHVD_solution.py		
run-hvd-main-cpu2.sb		
run-hvd-main-gpu2.sb		
slurm.cpu2.tfhvd-cpu.o29336438.out		
stdout_cpu2_mnist_16.txt		
[etrain94@login02 ~/MNODETest]\$		
[etrain94@login02 ~/MNODETest]\$		
[etrain940]ogin02 ~/MNODETest1\$		

	[p4rodrig@login01 MNODE_wHVD]\$
	<pre>[p4rodrig@login01 MNODE_wHVD]\$ grep 'done, rk: 15' s</pre>
lly, ssh into the running hodes and	Stdout_cpu2_mnist_32.txt:INFO,done, rk: 15 train ti
command (ton uncorid)	<pre>stdout_mainhvd_cpu2.txt:INFO,done, rk: 15 train tim</pre>
command (top -u userid)	[p4rodrig@login01 MNODE_wHVD]\$
' 'done' in the stdout file	[p4rodrig@login01 MNODE_wHVD]\$
	[n/rodrig@login01_MNODE_TUND]\$



Note: on Expanse we have gpu-debug queue (30 min limit, 1 device), and gpushared queue (1 device) and gpu queue (4 devices per GPU node)

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You can run:

\$ squeue –u userid to see nodes running your job

\$ ssh exp-XX-YY to login to node

\$ top –u userid to see processing on a CPU job

									100 zombie , 0.0 si, 0.0 st	
									9.1 buff/cache	
iB Swar					.0 free				0.2 avail Mem	
			our		0 1100					
PID	USER	PR	NI	VIRT	RES	SHR :	5 %CPU	%MEM	TIME+ COMMAND	
460166	p4rodrig	20	0	2967760	362936	181296	R 99.4	0.1	0:11.58 python3	4
460163	p4rodrig			2967760	363028	181380	R 99.2		0:11.15 python3	
460161	p4rodrig			2967764	363072	181420 1	R 99.0		0:11.24 python3	3
460153	p4rodrig			2967760	363688	181204	R 98.5		0:12.33 python3	3
460167	p4rodrig			2967760	362904	181260 1	3 98.3		0:11.55 python3	4
460155	p4rodrig			2967744	362908	181280 1	R 98.1		0:11.92 python3	
460158	p4rodrig			2967760	362880	181240 1	R 97.9		0:10.39 python3	
460164	p4rodrig			2967764	363004	181360 1	R 97.9		0:10.01 python3	4
460162	p4rodrig	20		2541772	363332	181692 1	3 97.9		0:11.78 python3	3
460154	p4rodrig			2967760	362992	181352 1	R 97.3		0:11.32 python3	4
460156	p4rodrig			2967756	362972	181332 1	R 92.8		0:08.37 python3	4
460160	p4rodrig	20		2902224	363032	181388 1	R 89.1		0:11.38 python3	
460169	p4rodrig								0:10.25 python3	
	p4rodrig			2967760					0:10.16 python3	4
	p4rodrig			2967760	362932	181292			0:08.42 python3	
									0:10.22 python3	
460428	p4rodrig	20		67360	7088	3484 1		0.0	0:00.26 top	12
458820				89628	9512				0:00.06 systemd	
458836	p4rodrig				12812				0:00.00 (sd-pam)	12

#### Or run: \$ nvidia-smi to see usage on GPU devices

P4rodrig@login02:/expanse/lustre/projects/sds164/p4rodrig/TFwh	lVDtests		- 🗆 ×
[p4rodrig@login02 TFwHVDtests]\$ s JOBID PARTITION		TIME NODE	S NODELIST (REA
SON) 21782434 gpu tfhv [p4rodrig@login02 TFwHVDtests]\$ s [p4rodrig@exp-10-57 ~]\$ nvidia-sm Wed Apr 19 17:50:57 2023	vd-gp p4rodrig R ssh exp-10-57		
+   NVIDIA-SMI 510.39.01 Driver			
GPU Name Persistence-M   Fan Temp Perf Pwr:Usage/Cap 	Bus-Id Disp.A	Volatile   GPU-Util 	Uncorr. ECC   Compute M.   MIG M.
	00000000:18:00.0 Off		0
1 Tesla V100-SXM2 On   N/A 37C P0 55W / 300W 			0   Default   N/A

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## **KerasNLP**

- KerasNLP is an extension to Keras
- KerasNLP has several pre-trained LLMs (large language models). Each model comes with related modules, for example:
  - GPT2Backbone the model without task specific output layers
  - GPT2CausalLM the model with output predictions
  - GPT2CausalLMPreprocessor the preprocessor that feeds model.fit





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Exercise, use pre-trained BERT and compare different BERT versions

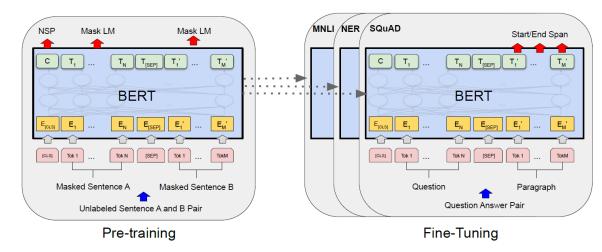




### BERT

## (Bidirectional Encoder Representations from Transformers)

- 1 Pretrain on:
- fill-in-the-blank
- binary classification if 2 sentences go together



Devlin, etal, 2019

### 2 Fine tune on variety of tasks





Keras NLP package has several BERT versions

So let's start with 'bert-small' (28M parameters)

For reference: BERT<sub>BASE</sub> (L=12, H=768, Attn=12, Total Parameters=110M) BERT<sub>LARGE</sub> (L=24, H=1024, Attn=16, Total Parameters=340M).

GA models/ 2-layer BERT model where all input is bert\_tiny\_en\_uncased lowercased. Trained on English Wikipedia + BERT 4M BooksCorpus. 4-layer BERT model where all input is bert small en uncased BERT lowercased. Trained on English Wikipedia + 28M BooksCorpus. 8-layer BERT model where all input is bert medium en uncased lowercased. Trained on English Wikipedia + BERT 41M BooksCorpus. 12-layer BERT model where all input is bert\_base\_en\_uncased BERT 109M lowercased. Trained on English Wikipedia + BooksCorpus. 12-layer BERT model where case is maintained. bert base en BERT 108M Trained on English Wikipedia + BooksCorpus. 12-layer BERT model. Trained on Chinese bert base zh BERT 102M Wikipedia. 12-layer BERT model where case is maintained. Trained on trained on Wikipedias of 104 bert base multi BERT 177M languages

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## **Notebook exercise using KerasNLP**

- In a terminal window start the notebook session for keras-nlp
  - ...]\$ cd KerasTest

...]\$ bash jupyter-keras-nlp-cpu2res.sh

(need to set up conda environment)

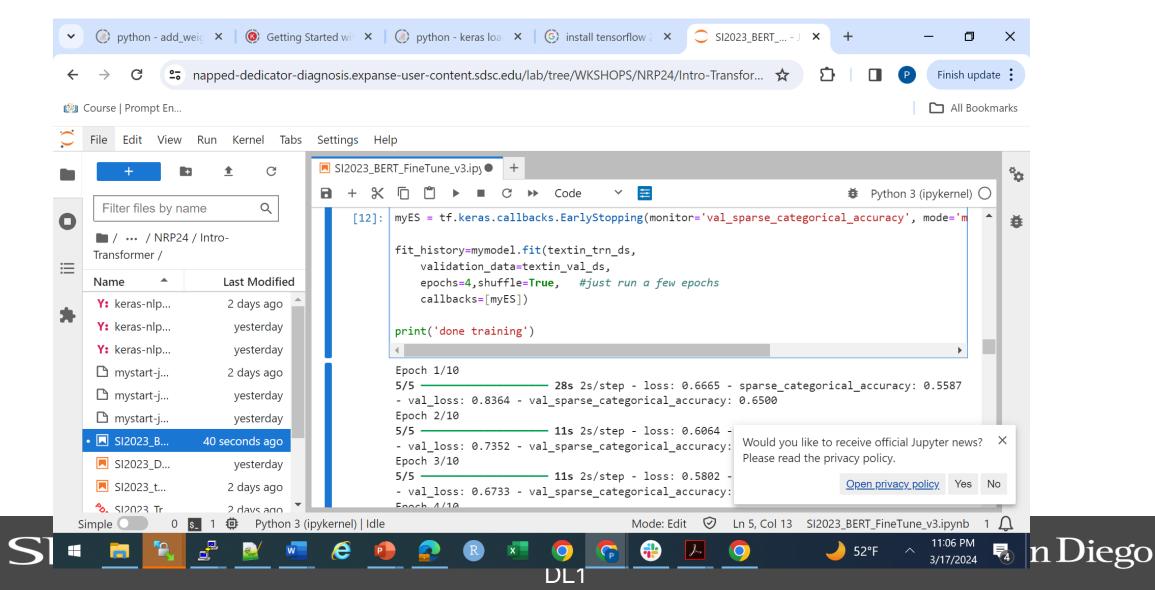
• Open the URL and look for:

BERT\_FineTune\_v3.ipynb notebook

Select Edit->clear all cells; Run -> Run all cells
 (or select Kernel -> restart Kernal and run all cells)

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#### END



