CC-IN2P3 GPU usage in CPPM

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CAF meeting

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GPU usage at CPPM

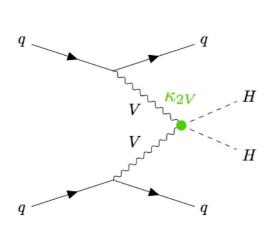
- Using GPUs for machine learning model training for the flavour tagging in ATLAS;
 - Running training for developments for the b-tagging for Run4 with HL-LHC samples
 - Running training for developing the tagger for the Boosted Higgs -> $\tau\tau$
- Multi-GPUs are indispensable for the development of the b-jet tagger for Run4, which uses ~115M jets.

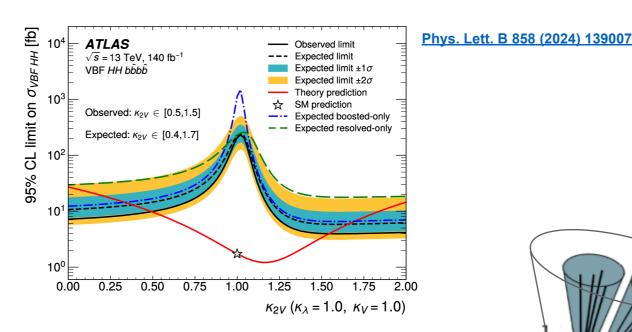
Today going to report about the jobs on Boosted Higgs -> $\tau\tau$ tagger, which uses ~ 20M jets, multi-GPUs are favorable but can also be tested with single-GPU.

Boosted Higgs -> $\tau\tau$ tagger

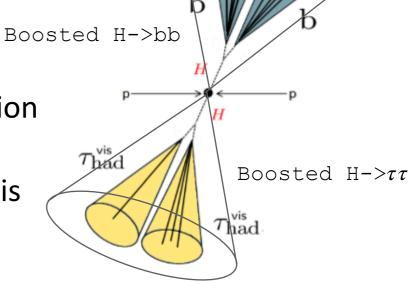
- \circ Boosted Higgs-> $\tau\tau$ tagging can play an important role in
 - High mass resonant searches
 - Exclusion of the BSM coupling for non-resonant analysis

(ex. κ_{2V} in VBF **HH** analysis)





- \circ Aiming the use in the boosted HH->bbau au analysis
- Higgs-> $\tau\tau$ tagger is being developed as a natural extension of the existing GNN-based Boosted Higgs->bb tagger (GN2X tagger), expecting easier integration into analysis frameworks



Salt framework

- Using <u>salt</u> framework for the trainings
 - Model-training framework, developed for the flavour tagging algorithm
 - Salt framework is easy to use with prebuilt docker images, via Singularity It can be used with a connection to CVMFS
 - Alternative way to use salt framework is use it in a conda environment

How using GPU at CCIN2P3

o GPU batch jobs can be submitted via Singularity container, with sbatch command

```
$sbatch -t 0-10:00 -n 1 --gres=gpu:v100:1 --mem 8G launchSingularity.sh
```

lauchSingularity.sh

```
#!/bin/bash
# Job name
#SBATCH --job-name=salt
# Job log
#SBATCH --output=serial_test_%j.log
# choose the GPU queue
#SBATCH -p GPU
# requesting one node
#SBATCH --nodes=1
# Only if you really need it!
# #SBATCH --exclusive
# keep environment variables
#SBATCH --export=ALL
# requesting 4 V100 GPU
# (remove the "v100:" if you don't care what GPU)
#SBATCH --gres=gpu:v100:1
# note! this needs to match --trainer.devices!
#SBATCH --ntasks-per-node=1
# number of cpus per task
# don't use this if you have exclusive access to the node
# #SBATCH --cpus-per-task=10
# request enough memory
#SBATCH --mem=8G
# Timelimit
#SBATCH -t 0-10:00
# Change log names; %j gives job id, %x gives job name
#SBATCH --output=/pbs/home/m/mfujimot/HHbbtautau/salt/salt/submit/logs/slurm-%j.%x.out
# optional separate error output file
#SBATCH --error=/pbs/home/m/mfujimot/HHbbtautau/salt/salt/submit/logs/slurm-%j.%x.err
# launch singularity
```

singularity exec --nv --bind \$PWD,/pbs,/cvmfs,/sps \

launch job.sh

```
#!/bin/bash
                                                          #echo ${CUDA_VISIBLE_DEVICES}
                                                          # print host info
                                                          echo "Hostname: $(hostname)"
                                                          #echo "CPU count: $(cat /proc/cpuinfo | awk '/^processor/{print $3}' | tail -1)"
                                                          # print gpu info
                                                          nvidia-smi
                                                          # run the training
                                                          cd /pbs/home/m/mfujimot/HHbbtautau/salt/salt
                                                          echo "Moved dir, now in: ${PWD}"
                                                          echo "Running training script..."
                                                          salt fit --help
                                                          salt fit --config configs/GN2X.yaml --trainer.devices=1 --trainer.accelerator gpu --force
/cvmfs/unpacked.cern.ch/gitlab-registry.cern.ch/atlas-flavor-tagging-tools/algorithms/salt:0-4 ${PWD}/launch_job.sh
```

GPU running status at CCIN2P3

- Works perfectly when requesting single GPU
- In many cases, need to wait ~1 day before the job starts running due to the batch queue.
- When requesting multi-GPUs (gres=gpu:v100:2), it does not run with the error:

raise RuntimeError(

RuntimeError: Timed out initializing process group in store based barrier on rank: 0, for key: store_based_barrier_key:1 (world_size=2, worker_count=1, timeout=0:30:00)

Lots of helps from the CCIN2P3 HelpDesk: tickets

This error is still there even after the updates of the Slurm cluster in 06.26.24

(versions of drivers/CUDA at CCIN2P3, Tesla V100-PCIE-32GB)

Nvidia drivers version: 550.54.15

Cuda version: 12.4.1

GPUs at CPPM server

Same salt setup (with the same version of the salt) ran successfully in the
 CPPM local server with multi-GPUs, with Singularity but without slurm batch

```
$singularity run --nv --bind $PWD,/share/users/fujimoto/
/cvmfs/unpacked.cern.ch/gitlab-registry.cern.ch/atlas-flavor-tagging-tools/
algorithms/salt:0-4 salt fit
--config /atlas/fujimoto/BoostedDiTau/salt_latest/salt/salt/configs/GN2X.yaml
--trainer.devices=3
--force
```

(versions of drivers/CUDA at CPPM, 3 GPUs: NVIDIA GeForce RTX 2080)

Nvidia drivers version: 545.23.08 Cuda version: 12.3

Now later version is used in CCIN2P3.

-> It seems the problem is not because of the versions of the drivers/CUDA.

Additional option in launchSingularity.sh might be needed

GPUs at Paris-Saclay

- Salt framework with multi-GPUs also worked at Paris-Saclay <u>mesocenter</u> by Inès Combes (IJCLab)
- Used it in a conda environment (anaconda 3: anaconda3/2022.10/gcc-11.2.0)
 via slurm batch

```
#!/bin/bash
#SBATCH -- job-name=training GN2X tau
#SBATCH --output=training_%j.log
#SBATCH --partition=gpua100
#SBATCH --time=24:00:00
#SBATCH --mem=50G
#SBATCH -n 1
#SBATCH --gres=gpu:4
#SBATCH --gpus-per-task=4
#SBATCH --error=errorJob_%j.txt
#SBATCH --export=ALL
# Module load
module purge
module load anaconda3/2022.10/gcc-11.2.0
module load cuda/10.2.89/intel-19.0.3.199
echo "Hostname: $(hostname)"
echo "CPU count: $(cat /proc/cpuinfo | awk '/^processor/{print $3}' | tail -1)"
# Activate anaconda environment code
source activate /qpfs/users/combesi/salt/conda/envs/salt
echo ${CUDA_VISIBLE_DEVICES}
cd /qpfs/users/combesi/salt/salt/
salt fit --config configs/GN2X_tau.yaml --force
```

(versions of drivers/CUDA at Paris-Saclay mesocenter, 4 GPUs: Nvidia A100 GPUs)

```
Nvidia drivers version: 535.104.05
Cuda version: 10.2.89
```

The conda environment needs to be installed to try this approach on CCIN2P3

Summary

- Doing the flavour tagger training with GPUs with salt framework.
 Multi-GPU usage is necessary.
- At CCIN2P3, it works perfectly when requesting single GPU.
 Many thanks to the CCIN2P3 Helpdesk for lots of helps!
 Multi-GPU functionality appears to have unresolved challenges.
- Multi-GPU usage is supported on some French institute resources, and the salt framework operates seamlessly, suggesting the framework itself is not the source of any issues.

Backup

Using multi-GPU with batch

GPU batch jobs can be submitted via Singularity container, with sbatch command

\$sbatch -t 0-10:00 -n 1 --gres=gpu:v100:2 --mem 8G launchSingularity.sh

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# (remove the "v100:" if vou don't care what GPU)
#SBATCH --gres=gpu:v100:2
# note! this needs to match --trainer.devices!
#SBATCH --ntasks-per-node= 2
# number of cpus per task
# don't use this if you have exclusive access to the node
# #SBATCH --cpus-per-task=10
# request enough memory
#SBATCH --mem=8G
# Timelimit
#SBATCH -t 0-10:00
```

Change log names; %j gives job id, %x gives job name

singularity exec --nv --bind \$PWD,/pbs,/cvmfs,/sps \

optional separate error output file

launch singularity

launch job.sh

```
#!/bin/bash
                                                              #echo ${CUDA_VISIBLE_DEVICES}
                                                             # print host info
                                                              echo "Hostname: $(hostname)"
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                                                              # print gpu info
                                                              nvidia-smi
                                                             # run the training
                                                              cd /pbs/home/m/mfujimot/HHbbtautau/salt/salt
                                                              echo "Moved dir, now in: ${PWD}"
                                                              echo "Running training script..."
                                                              salt fit --help
                                                              salt fit --config configs/GN2X.yaml --trainer.devices=2 }-trainer.accelerator gpu --force
#SBATCH --output=/pbs/home/m/mfujimot/HHbbtautau/salt/salt/submit/logs/slurm-%j.%x.out
#SBATCH --error=/pbs/home/m/mfujimot/HHbbtautau/salt/salt/submit/logs/slurm-%j.%x.err
   /cvmfs/unpacked.cern.ch/gitlab-registry.cern.ch/atlas-flavor-tagging-tools/algorithms/salt:0-4 ${PWD}/launch_job.sh
```