



Running containers in Metacentrum Sitola – Laboratory seminar 6. 10. 2021



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Running containers in Metacentrum

- Containers with Singularity
- Machine/Deep Learning frameworks, Alphafold2 in Metacentrum
- Tips for running containers



- Singularity
 - Containers in HPC world
 - “Integration is more important than isolation”
 - Runs in user-space
 - Singularity Image Format
 - All frontend/compute nodes in Metacentrum
 - Default binded /storage/* + support GPU, Infiniband
 - builder.metacentrum.cz – create/modify SIF images
 - group **builders**, subuid/subgid feature
 - definition files
 - Performance note: loop **inside** 1 container vs. loop running containers

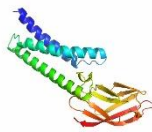
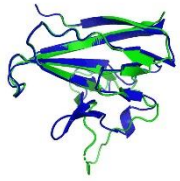


- Run docker image `$ singularity run docker://busybox`
 - In cache – download + build image + run ; 2nd run from cached image
- Build and run SIF image
 - `$ singularity build BB.SIF docker://busybox`
`$ singularity shell BB.SIF`
`Singularity>` shell inside container, Ctrl-d to exit
- Modify image in 3 steps – use argument `-f` *OR run as root*
 - `$ singularity build -f -s BB.sbox docker://busybox`
`$ singularity shell -f -w BB.sbox` in shell `touch /MY_FILE` and exit
`$ singularity build -f BBmod.SIF BB.sbox`
 + check if /MY_FILE file exists `$ singularity exec BBmod.SIF ls /`
- Definition files



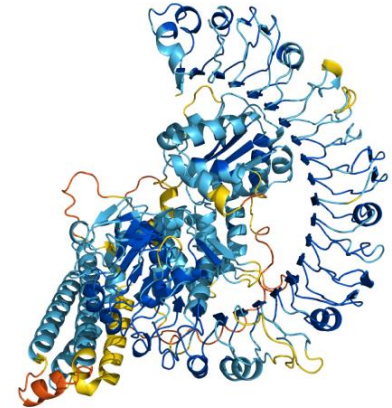
- PBS scheduling system
 - Queue – gpu – limits walltime to 24h, longer jobs possible in gpu_long
 - Resources gpu_cap – cuda35 to cuda80
- Hardware
 - more GPU clusters
 - 250 GPU cards – from Tesla K40 (2013) to A100 (2020)
 - 2021 – new cluster 90x GPU





AlphaFold2 in Metacentrum

- **Highly accurate protein structure prediction with AlphaFold, see [1]**
- Published in July 2021
 - Docker image and 2TB of data
 - “DNN inference on GPU”
- Wiki <https://wiki.metacentrum.cz/wiki/AlphaFold>
 - Prepared scripts to run in Metacentrum on GPU
 - Parameters – input fasta file(s) + output dir
- cca 1h+ jobs
 - CPU+GPU computation
 - Memory 200G+



[1] Jumper, J., Evans, R., Pritzel, A. *et al.* Highly accurate protein structure prediction with AlphaFold. *Nature* **596**, 583–589 (2021)



- NVIDIA GPU CLOUD – NGC <https://ngc.nvidia.com/>
- AI, Machine/Deep Learning containers with GPU support
 - CUDA, libs, ... inside images, needs only drivers in Metacentrum
 - TensorFlow, PyTorch + many other tools
 - “Tuned” docker images with documentation
 - **Singularity support**
- SIF images in Metacentrum
[/cvmfs/singularity.metacentrum.cz/NGC/](https://cvmfs/singularity.metacentrum.cz/NGC/)

**NVIDIA**®

https://wiki.metacentrum.cz/wiki/NVidia_deep_learning_frameworks

- Pytorch example - MNIST Word Language Model
 - `qsub MNIST-WLM.job`

```
#!/bin/bash
#PBS -q gpu
#PBS -l select=1:ncpus=2:ngpus=1:mem=64gb:scratch_local=8gb:gpu_cap=cuda61
#PBS -l walltime=1:00:00
cd $SCRATCHDIR && wget https://github.com/pytorch/examples/archive/refs/heads/master.zip
unzip -q master.zip && cd examples-master/word_language_model/
singularity exec --nv -B $SCRATCHDIR --pwd $PWD \
  /cvmfs/singularity.metacentrum.cz/NGC/PyTorch\21.09-py3.SIF python ./main.py --cuda --epochs 6
clean_scratch
```

- `--nv` for GPU, `-B` binds `$SCRATCHDIR`
- SIF image from Metacentrum storage

- TensorFlow example – modify NGC image

- `$ singularity run TensorFlow:21.09-tf2-py3.SIF pip list | grep addons`
`tensorflow-addons 0.13.1`

- Definition file for building singularity image, latest version of tf-addons

```
Bootstrap: localimage
From: /cvmfs/singularity.metacentrum.cz/NGC/TensorFlow:21.09-tf2-py3.SIF
%post
pip install tensorflow-addons==0.14.0
```

- `$ singularity build -f TF-addons0.14.SIF TFaddons.def`

- `$ singularity run TF-addons0.14.SIF pip list | grep addons`
`tensorflow-addons 0.14.0`

- Jupyter notebooks – interactive jobs
 - `jupyter.cloud.metacentrum.cz`
 - PBS job + singularity + image with Jupyter (e.g. NGC TF, PyTorch)
 - https://wiki.metacentrum.cz/wiki/NVidia_deep_learning_frameworks
 - web access to compute node
- Papermill
 - *tool for parameterizing, executing, and analyzing Jupyter Notebooks*
 - saved `input.ipynb` -> set parameters ->
-> run PBS job -> `output.ipynb`

```
import papermill as pm
pm.execute_notebook(
    'path/to/input.ipynb',
    'path/to/output.ipynb',
    parameters = dict(alpha=0.6, ratio=0.1)
)
```

- Singularity image – saved READ-ONLY workspace
 - File vs. directory with virtual environment
 - Easy to transfer, and share
 - stable environment

- Use PYTHONUSERBASE
 - add python modules for development, then modify image
 - best way: for each image different directory



- Depreacted or changed functions in frameworks
 - live development -> version skip -> lost of warning on deprecated/changed functions
- New colleagues onboarding
 - same environment
 - time saving
- ML Reproducibility challenge <https://paperswithcode.com/rc2021>
 - Task: „replicate the main claim described in papers“



PyTorch

```
pip install transformers py3nvml
```

```
from transformers import PyTorchBenchmark,  
PyTorchBenchmarkArguments
```

```
args = PyTorchBenchmarkArguments(  
    models=["bert-base-uncased"],  
    batch_sizes=[8, 16, 32],  
    sequence_lengths=[8, 32, 128, 512]  
    training=True,  
    verbose=True,  
    env_print=True,  
)
```

```
benchmark = PyTorchBenchmark(args)  
results = benchmark.run()
```

```
print(results)
```

TensorFlow

```
pip install transformers py3nvml
```

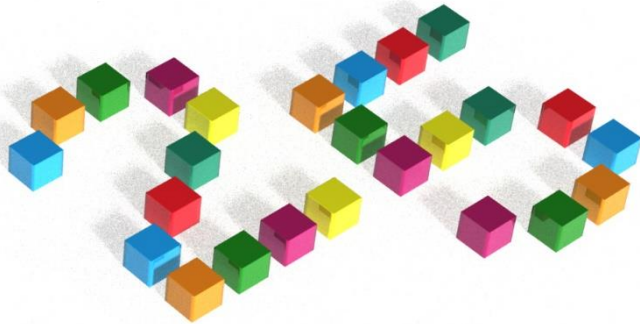
```
from transformers import TensorFlowBenchmark,  
TensorFlowBenchmarkArguments
```

```
args = TensorFlowBenchmarkArguments(  
    models=["bert-base-uncased"],  
    batch_sizes=[8, 16, 32],  
    sequence_lengths=[8, 32, 128, 512]  
    training=True,  
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)
```

```
benchmark = TensorFlowBenchmark(args)  
results = benchmark.run()
```

```
print(results)
```





Thanks for your attention!



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