

2022 APAC HPC-AI

Team NTHU-1 Presentation

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1 High Performance Computing with QUANTUM ESPRESSO

- Parameters
- Single Node
- Multiple Nodes
- Additional Supplement

2 Communications Performance with UCX

- Introduction
- Optimized Configurations
- Conclusion
- Running on DGX-A100

3 Deep-Learning-based DNA Sequence fast decoding

- Why do we choose this model?
- Model structure
- Tuning
 - Batch size
- Result

Section 1

High Performance Computing with QUANTUM ESPRESSO

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3 Deep-Learning-based DNA Sequence fast decoding

2022-10-24

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└ High Performance Computing with QUANTUM ESPRESSO

Section 1

High Performance Computing with QUANTUM ESPRESSO

- High Performance Computing with QUANTUM ESPRESSO
 - Parameters
 - Single Node
 - Multiple Nodes
 - Additional Supplement

• Communications Performance with UCX

• Deep-Learning-based DNA Sequence fast decoding

Parameters

-np, -diag, OMP_NUM_THREADS

Number of Processes (-np)

- Each node has 48 processes
- Cannot greater than 1536, must be an integer in $[1, 48]$ or $48x|1 \leq x \leq 32$
- Has effects on -npool & diagonalization

Diagonalization (-ndiag)

- Organized in a square 2D grid
- -ndiag needs to be n^2 , where n is an integer $\leq \frac{-np}{-npool}$

Number of OpenMP Threads (OMP_NUM_THREADS)

- OMP_NUM_THREADS \uparrow , CPU Time \uparrow (fixed -npool & NCPUS)
- Set OMP_NUM_THREADS to 1 and start to tune the other parameters

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High Performance Computing with QUANTUM
ESPRESSO
Parameters
Parameters

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-np, -diag, OMP_NUM_THREADS

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Number of OpenMP Threads (OMP_NUM_THREADS)

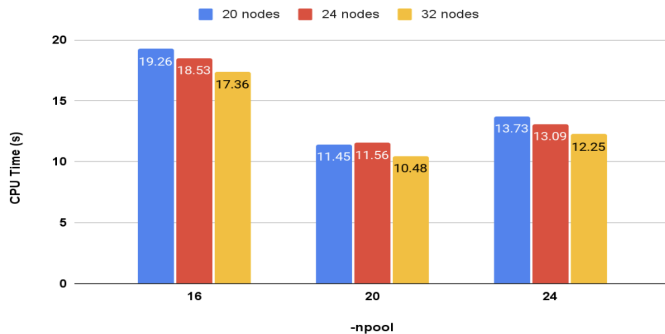
- OMP_NUM_THREADS \uparrow , CPU Time \uparrow (fixed -npool & NCPUS)
- Set OMP_NUM_THREADS to 1 and start to tune the other parameters

Parameters

-npool

Number of Pools (-npool)

- Must be a divisor of the total number of processes (-np)
- K-points will be subpartitioned into several pools
- The More -npool \Rightarrow The Better CPU Time



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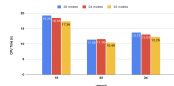
High Performance Computing with QUANTUM ESPRESSO
Parameters
Parameters

Parameters

-npool

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Single Node Performance of Gadi module

Average of 5 Times

# CPUs (np)	# pools (npool)	# linear algebra groups (ndiag)	CPU time [s]
48	24	4	1m53.138s
48	24	1	1m53.540s
40	20	4	1m52.794s
40	20	1	1m52.941s

2022-10-24

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High Performance Computing with QUANTUM ESPRESSO

Single Node

Single Node Performance of Gadi module

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40	20	4	1m52.794s
40	20	1	1m52.941s

Single Node Performance of Intel Compiler + Intel MPI

Average of 5 Times

# CPUs (np)	# pools (npool)	# linear algebra groups (ndiag)	CPU time [s]
48	24	4	1min58.916s
48	24	1	1min59.004s
40	20	4	1min56.944s
40	20	1	1min57.084s

2022-10-24

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High Performance Computing with QUANTUM ESPRESSO

Single Node

Single Node Performance of Intel Compiler + Intel MPI

Average of 5 Times

# CPUs (np)	# pools (npool)	# linear algebra groups (ndiag)	CPU time [s]
48	24	4	1min58.916s
48	24	1	1min59.004s
40	20	4	1min56.944s
40	20	1	1min57.084s

Summary

Script

```
#!/bin/bash
#PBS -l walltime=00:10:00
#PBS -l ncpus=40
#PBS -l mem=190GB
#PBS -l software=qe
#PBS -l wd
#PBS -P jx00
#PBS -N QE-single

module load qe
export OMP_NUM_THREADS=1
mpirun -np 40 pw.x -npool 20 -ndiag 4 -inp CeO2.in
```

2022-10-24

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└─ High Performance Computing with QUANTUM
ESPRESSO
└─ Single Node
└─ Summary

Summary

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```
#!/bin/bash
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module load qe
export OMP_NUM_THREADS=1
mpirun -np 40 pw.x -npool 20 -ndiag 4 -inp CeO2.in
```


Summary (cont.)

Result

```

g_psi      :      0.14s CPU      0.15s WALL (      175 calls)

Called by h_psi:
h_psi:calbec :      3.77s CPU      3.78s WALL (      202 calls)
vloc_psi    :     38.07s CPU     38.32s WALL (      202 calls)
add_vuspsi  :      4.26s CPU      4.27s WALL (      202 calls)

General routines
calbec      :      4.97s CPU      4.98s WALL (      228 calls)
fft         :      5.15s CPU      5.25s WALL (      349 calls)
ffts        :      0.26s CPU      0.28s WALL (       53 calls)
fftw        :     32.90s CPU     33.13s WALL (    19368 calls)
interpolate :      0.70s CPU      0.73s WALL (       27 calls)

Parallel routines

PWSCF       :    1m52.55s CPU    1m58.50s WALL

This run was terminated on:  0:21:13  130ct2022

=====
JOB DONE.
=====

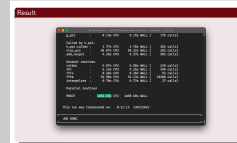
```

2022-10-24

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└ High Performance Computing with QUANTUM
ESPRESSO
└ Single Node
└ Summary (cont.)

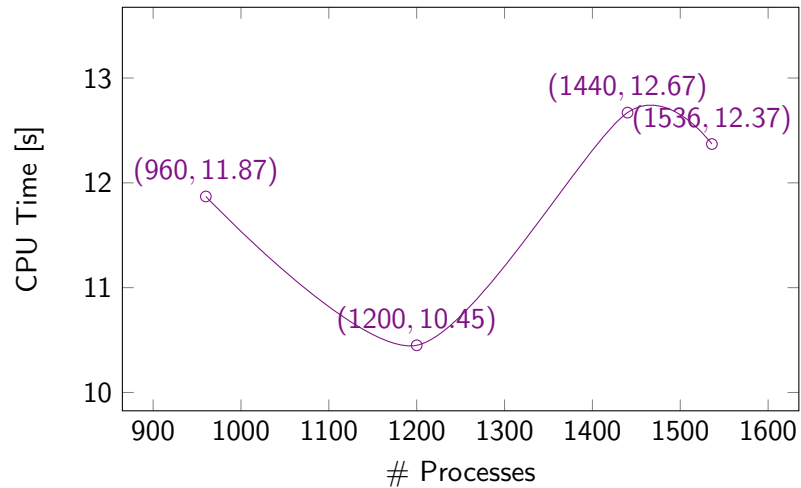
Summary (cont.)



CPU Time vs. # Processes

npools were 20, 20, 20, 24 resp.; ndiags were left as default

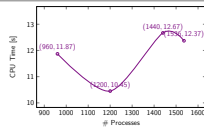
The More -np \Rightarrow The Better!!



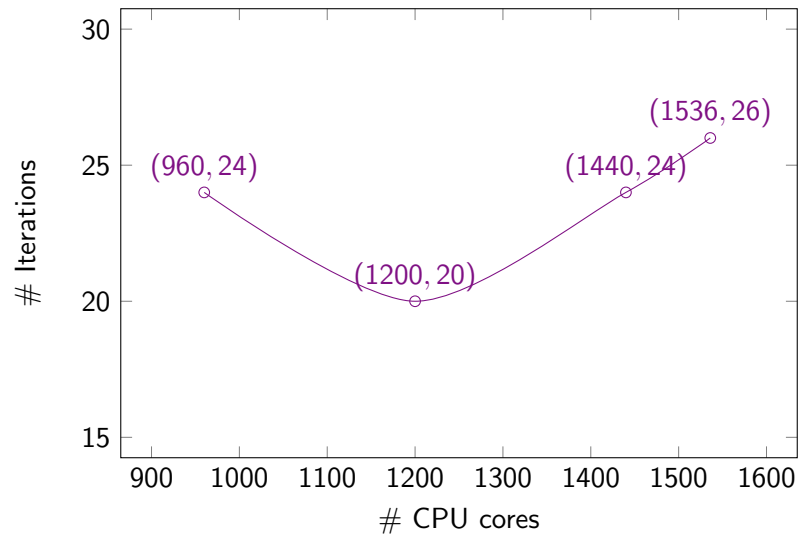
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2022-10-24

- High Performance Computing with QUANTUM ESPRESSO
- Multiple Nodes
- CPU Time vs. # Processes



Iterations vs. # CPU cores



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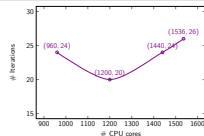
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└ High Performance Computing with QUANTUM ESPRESSO

└ Multiple Nodes

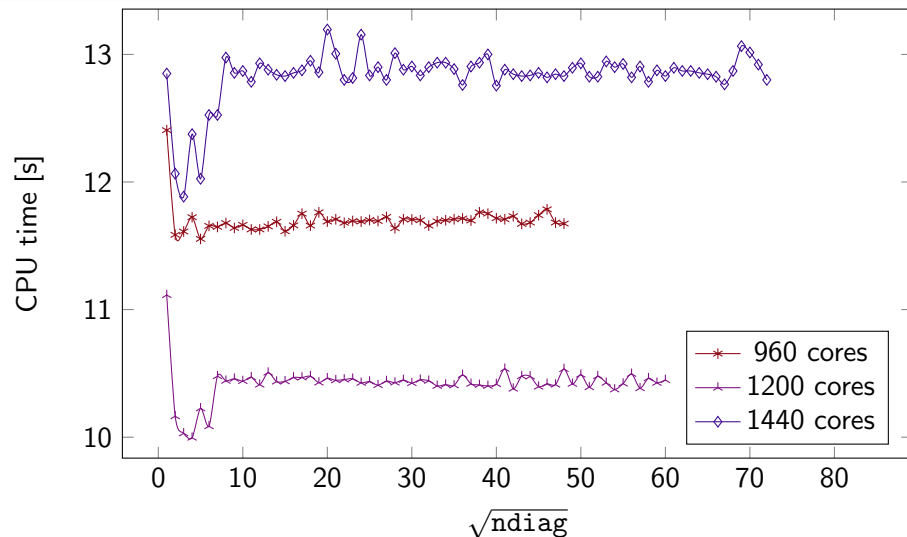
└ # Iterations vs. # CPU cores

Iterations vs. # CPU cores



CPU time vs. ndiag of different CPU cores

Average of 5 Times



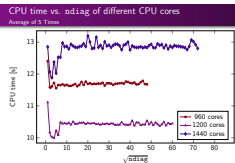
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High Performance Computing with QUANTUM ESPRESSO

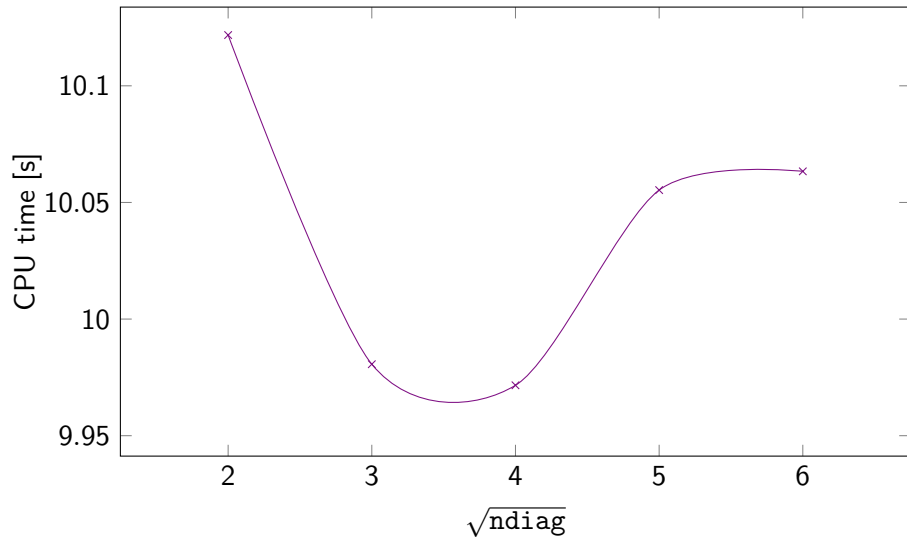
Multiple Nodes

CPU time vs. ndiag of different CPU cores



CPU time vs. ndiag of 1200 CPU cores

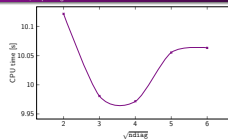
A closer, deeper insight



2022-10-24

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- High Performance Computing with QUANTUM ESPRESSO
- Multiple Nodes
- CPU time vs. ndiag of 1200 CPU cores



Conclusion

Script

```
#!/bin/bash
#PBS -l walltime=00:10:00
#PBS -l ncpus=1200
#PBS -l mem=760GB
#PBS -l software=qe
#PBS -l wd
#PBS -P jx00
#PBS -N QE-multi

module load qe
export OMP_NUM_THREADS=1
mpirun -np 1200 pw.x -npool 20 -ndiag 16 -inp CeO2.in
```

2022-10-24

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└─ High Performance Computing with QUANTUM
ESPRESSO
└─ Multiple Nodes
└─ Conclusion

Conclusion

Script

```
#!/bin/bash
#PBS -l walltime=00:10:00
#PBS -l ncpus=1200
#PBS -l mem=760GB
#PBS -l software=qe
#PBS -l wd
#PBS -P jx00
#PBS -N QE-multi

module load qe
export OMP_NUM_THREADS=1
mpirun -np 1200 pw.x -npool 20 -ndiag 16 -inp CeO2.in
```

Conclusion (cont.)

Result

```

g_psi      :      0.00s CPU      0.00s WALL (    147 calls)

Called by h_psi:
h_psi:calbec :      0.24s CPU      0.26s WALL (    168 calls)
vloc_psi    :      1.11s CPU      1.21s WALL (    168 calls)
add_vuspsi  :      0.16s CPU      0.18s WALL (    168 calls)

General routines
calbec      :      0.30s CPU      0.32s WALL (    188 calls)
fft         :      0.13s CPU      0.14s WALL (    271 calls)
ffts        :      0.11s CPU      0.15s WALL (     41 calls)
fftw        :      1.17s CPU      1.28s WALL (   15614 calls)
interpolate :      0.07s CPU      0.09s WALL (     21 calls)

Parallel routines

PWSCF       :      9.74s CPU     12.14s WALL

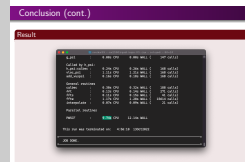
This run was terminated on:  4:56:10  130oct2022

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JOB DONE.
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```

2022-10-24

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 └ High Performance Computing with QUANTUM
 ESPRESSO
 └ Multiple Nodes
 └ Conclusion (cont.)

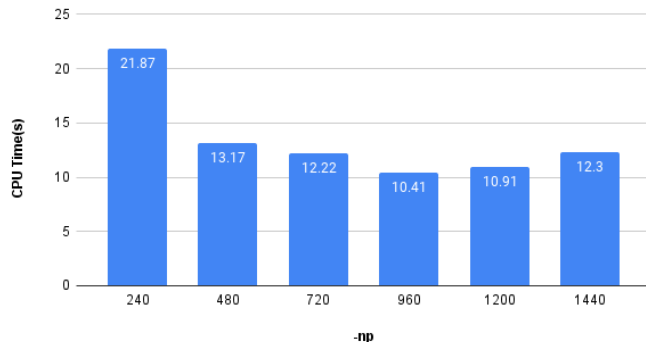


Additional Supplement

Compare to QE compiled by ourselves

- QE compiled by Intel Compiler with IntelMPI will have the better performance when -np equals to 960 instead of 1200 like the QE module on Gadi

CPU Time of the QE Compiled by Ourselves



2022-10-24

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High Performance Computing with QUANTUM
ESPRESSO
Additional Supplement
Additional Supplement

Additional Supplement

Compare to QE compiled by ourselves

• QE compiled by Intel Compiler with IntelMPI will have the better performance when -np equals to 960 instead of 1200 like the QE module on Gadi

CPU Time of the QE Compiled by Ourselves



Section 2

Communications Performance with UCX

1 High Performance Computing with QUANTUM ESPRESSO

2 Communications Performance with UCX

- Introduction
- Optimized Configurations
- Conclusion
- Running on DGX-A100

3 Deep-Learning-based DNA Sequence fast decoding

2022-10-24

2022 APAC HPC-AI

└ Communications Performance with UCX

Section 2

Communications Performance with UCX

1 High Performance Computing with Quantum ESPRESSO

2 Communications Performance with UCX

- Introduction
- Optimized Configurations
- Conclusion
- Running on DGX-A100

3 Deep-Learning-based DNA Sequence fast decoding

Problem

The benchmark is running on 16 GPUs, on each of which is a worker there with left and right dataframe distributed throughout all GPUs. It is our task that each worker merges its left and right dataframe, which means that a worker need communicate with others at scale.

2022-10-24

2022 APAC HPC-AI

└ Communications Performance with UCX

└ Introduction

└ Problem

Problem

The benchmark is running on 16 GPUs, on each of which is a worker there with left and right dataframe distributed throughout all GPUs. It is our task that each worker merges its left and right dataframe, which means that a worker need communicate with others at scale.

aftermath

Our task is Communications Performance with UCX. The task is about running some python code, these codes creates a central server to synchronize workers, and each worker merges its left and right dataframe. That means the workers need communicate with each others. And our job is to improving performance for this heavy-communication work.

The given benchmark ran on 16 GPUs, on each of which is a worker there with left and right dataframe distributed throughout all GPUs.

Objectives

Bandwidth of a worker

W.L.O.G., let's consider the worker with rank 0.

Define that $bw = \frac{\sum_{i=1}^{15} \text{size of Dataframe transferred}_i}{\sum_{i=1}^{15} \text{Wall time}_i}$.

$$\text{Bandwidth} = \frac{bw_{\text{left}} + bw_{\text{right}}}{2}$$

Throughput

$$\text{Throughput} = \frac{\# \text{ chunks} \times \text{Data processed}}{\text{Wall time}}$$

2022-10-24

2022 APAC HPC-AI

└ Communications Performance with UCX

└ Introduction

└ Objectives

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Bandwidth of a worker

W.L.O.G., let's consider the worker with rank 0.

Define that $bw = \frac{\sum_{i=1}^{15} \text{size of Dataframe transferred}_i}{\sum_{i=1}^{15} \text{Wall time}_i}$.

$$\text{Bandwidth} = \frac{bw_{\text{left}} + bw_{\text{right}}}{2}$$

Throughput

$$\text{Throughput} = \frac{\# \text{ chunks} \times \text{Data processed}}{\text{Wall time}}$$

nevikw39

There are two major metrics to measure the performance of the benchmark we run. We tried to discover the instinct meaning of the two by means of investigating and interpreting the codes provided.

The first one is the average bandwidth of all workers. For a particular worker, its bandwidth is the average of its left and right dataframe. For each side, it is the summation of size of dataframe transferred from and to all other workers divided by wall time.

Another one is throughput, which is the number of chunks time the total data processed by all workers divided by wall time.

We believe that there must be some relation between the two yet that throughput is more comprehensive, so we put more emphasis on it.

Baseline

Average of 10 iterations, small data set (i.e., each chunk with 10^6 rows), running on 16 GPUs over 4 Gadi Volta nodes.

Bandwidth

- 507.21 MiB/s

Throughput

- 4.27 GiB/s

2022-10-24

2022 APAC HPC-AI

- Communications Performance with UCX

- Optimized Configurations

- Baseline

aftermath

First, we run the job without modifying any code and configuration options, as our baseline. Here, the baseline ran on 16 GPUs over 4 Gadi Volta nodes, for 10 iterations, and for small data set, which means each chunk contains 10 to the power of 6 rows.

For the baseline, we got the bandwidth 507.21 megabytes per second, and the throughput 4.27 gigabyte per second.

Baseline

Average of 10 iterations, small data set (i.e., each chunk with 10^6 rows), running on 16 GPUs over 4 Gadi Volta nodes.

Bandwidth

• 507.21 MiB/s

Throughput

▼ 4.27 GiB/s

Enable Hardware Tag Matching

Avg. of 10 iterations, small data set, Gadi Volta nodes

Config

```
export UCX_RC_MLX5_TM_ENABLE=y
export UCX_DC_MLX5_TM_ENABLE=y
```

Bandwidth

- 521.87 MiB/s
- 102.8% speedup

Throughput

- 4.36 GiB/s
- 102.1% speedup

2022-10-24

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- └ Communications Performance with UCX
 - └ Optimized Configurations
 - └ Enable Hardware Tag Matching

nevikw39

We managed to find several UCX options that might help. The first option is to enable the hardware tag matching for both *Reliable Connected (RC)* and *Dynamically Connected (DC)* so that these works are offload to NICs. We can see that bandwidth somewhat dropped a bit while the throughput increased by a bit. The effect of this option is not so obvious.

Config

```
export UCX_RC_MLX5_TM_ENABLE=y
export UCX_DC_MLX5_TM_ENABLE=y
```

Bandwidth

- 521.87 MiB/s
- 102.8% speedup

Throughput

- 4.36 GiB/s
- 102.1% speedup

Enable various optimizations intended for homogeneous environment

Avg. of 10 iterations, small data set, Gadi Volta nodes

Config

```
export UCX_UNIFIED_MODE=y
```

Bandwidth

- 511.68 MiB/s
- 100.8% speedup

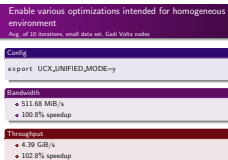
Throughput

- 4.39 GiB/s
- 102.8% speedup

2022-10-24

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- └ Communications Performance with UCX
 - └ Optimized Configurations
 - └ Enable various optimizations intended for homogeneous environment



nevikw39

Another option we tried is enabling the unified mode, implying that the local transport resources/devices of all entities which connect to each other are the same.

Nevertheless, this option would be conflict to the *rendezvous* scheme we would choose.

Similarly, the effect is also not so apparent.

Increase the amount of buffers added every time the receive / send memory pool grows

Avg. of 10 iterations, small data set, Gadi Volta nodes

Config

```
export UCX_TCP_RX_BUFS_GROW=16
export UCX_TCP_TX_BUFS_GROW=16
```

Bandwidth

- 513.73 MiB/s
- 101.2% speedup

Throughput

- 4.68 GiB/s
- 109.6% speedup

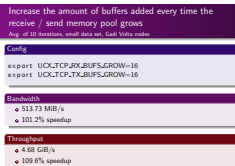
2022-10-24

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Communications Performance with UCX

Optimized Configurations

Increase the amount of buffers added every time the receive / send memory pool grows



aftermath

The two options here determine how much buffers are added every time the memory pool grows. The above one determines for the receive memory pool, while the below one determines for the send memory pool.

We have thought about that increasing the buffer grow rate may bring better performance for us. Therefore, we've tried to double the buffer grow rate. The default value of these two options are both 8, and we've modified both of them to 16. After the modification, the bandwidth increases to 513.73 MiB/s, and the throughput increases to 4.68 GiB/s, which really improves the performance.

Nonetheless, we found that this option would hardly give rise to ideal promotion in combination with others later.

Use **mutex** instead of **spinlock** for multithreading support in UCP

Avg. of 10 iterations, small data set, Gadi Volta nodes

Config

```
export UCX_USE_MT_MUTEX=y
```

Bandwidth

- 509.99 MiB/s
- 100.5% speedup

Throughput

- 4.71 GiB/s
- 110.3% speedup

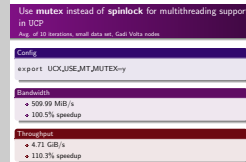
2022-10-24

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└ Communications Performance with UCX

└ Optimized Configurations

└ Use **mutex** instead of **spinlock** for multithreading support in UCP



aftermath

For this option, it determines which mechanism to use for Multithreading Support. It is set to n by default, which means not using mutex for multithreading support and using spinlock instead.

Both spinlock and mutex are common synchronization mechanism. The major difference between them is that the mechanism that mutex uses is sleep-waiting, while spinlock uses busy-waiting.

There are some pros and cons for both of them, and we have no idea which one is more efficient for the task. Hence we've tried both of them and discover that setting this option to y, which means using mutex do improve the performance. The bandwidth comes to 509.99 MiB/s, while the throughput comes to 4.71 GiB/s.

Enable UCX-Py non-blocking mode

Avg. of 10 iterations, small data set, Gadi Volta nodes

Config

```
export UCXPY_NON_BLOCKING_MODE=1
```

Bandwidth

- 590.62 MiB/s
- 116.4% speedup

Throughput

- 4.96 GiB/s
- 116.1% speedup

2022-10-24

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└ Communications Performance with UCX

└└ Optimized Configurations

└└└ Enable UCX-Py non-blocking mode

nevikw39

In addition, we enabled non-blocking progress mode of UCX-Py. This time, both bandwidth and throughput are about 1.16 times the baseline.

Config

```
export UCXPY_NON_BLOCKING_MODE=1
```

Bandwidth

- 590.62 MiB/s
- 116.4% speedup

Throughput

- 4.96 GiB/s
- 116.1% speedup

Set *Rendezvous* protocol to use *Active Messages* scheme

Avg. of 10 iterations, small data set, Gadi Volta nodes

Config

```
export UCX_RNDV_SCHEME=am
```

Bandwidth

- 546.51 MiB/s
- 107.7% speedup

Throughput

- 5.54 GiB/s
- 129.7% speedup

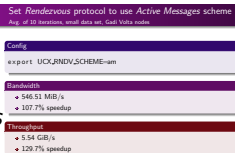
2022-10-24

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└ Communications Performance with UCX

└ Optimized Configurations

└ Set *Rendezvous* protocol to use *Active Messages* scheme



nevikw39

Even though this option is not documented in detail, we tried all available scheme, such as get/put zero copy, pipelined get/put zero copy, ..., finding that only active message brought a significant 30%-improvement in throughput.

Miscellanies

- UCX_IB_GPU_DIRECT_RDMA
- UCX_RNDV_THRESH
- UCX_TCP_TX_SEG_SIZE, UCX_TCP_RX_SEG_SIZE

2022-10-24

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└ Communications Performance with UCX

└└ Optimized Configurations

└└└ Miscellanies

Miscellanies

- UCX_IB_GPU_DIRECT_RDMA
- UCX_RNDV_THRESH
- UCX_TCP_TX_SEG_SIZE, UCX_TCP_RX_SEG_SIZE

nevikw39

Here are some options we used to try but find no concrete conclusion, such as explicitly use GPU Direct RDMA for HCA to access GPU pages directly, reduce the threshold to switch to RNDV protocol, enlarge copy-out buffer for TCP sending and receiving.

Optimal Combination of Configurations

Config

```
export UCX_RC_TM_ENABLE=y
export UCX_DC_TM_ENABLE=y

export UCX_USE_MT_MUTEX=y

export UCXPY_NON_BLOCKING_MODE=1

export UCX_RNDV_SCHEME=am

export UCX_IB_GPU_DIRECT_RDMA=y
export UCX_RNDV_THRESH=1024
export UCX_TCP_TX_SEG_SIZE=64k
export UCX_TCP_RX_SEG_SIZE=512k
```

2022-10-24

2022 APAC HPC-AI

└ Communications Performance with UCX

└ Conclusion

└ Optimal Combination of Configurations

Config

```
export UCX_RC_TM_ENABLE=y
export UCX_DC_TM_ENABLE=y

export UCX_USE_MT_MUTEX=y

export UCXPY_NON_BLOCKING_MODE=1

export UCX_RNDV_SCHEME=am

export UCX_IB_GPU_DIRECT_RDMA=y
export UCX_RNDV_THRESH=1024
export UCX_TCP_TX_SEG_SIZE=64k
export UCX_TCP_RX_SEG_SIZE=512k
```

aftermath

With the above attempts, we combine all configurations that would provide improvement to overall performance. The options we choose are listed here.

Overall Bandwidth Result

Avg. of 100 iterations on 16 GPUs over 4 Gadi Volta nodes

Small Data Set 1.06 GiB/s,
214.0% speedup in comparison to baseline (507.21 MiB/s)

Large Data Set 1.15 GiB/s,
290.1% speedup in comparison to baseline (405.89 MiB/s)

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└ Communications Performance with UCX

└ Conclusion

└ Overall Bandwidth Result

Small Data Set: 1.06 GiB/s,
214.0% speedup in comparison to baseline (507.21 MiB/s)
Large Data Set: 1.15 GiB/s,
290.1% speedup in comparison to baseline (405.89 MiB/s)

aftermath

This is our overall bandwidth result. For the small data set, the bandwidth of optimized our config is 1.06 GiB/s, which is more than twice of the baseline. And for the large data set, the bandwidth comes to 1.15 GiB/s, which is almost three times of the baseline.

Avg. of 100 iterations on 16 GPUs over 4 Gadi Volta nodes

Small Data Set 9.28 GiB/s,
217.3% speedup in comparison to baseline (4.27 GiB/s)

Large Data Set 12.37 GiB/s,
281.1% speedup in comparison to baseline (4.40 GiB/s)

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Communications Performance with UCX

Conclusion

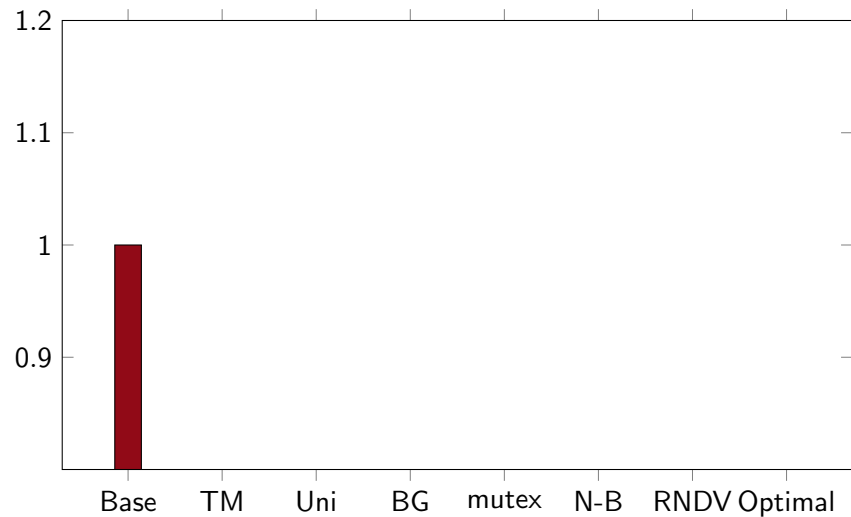
└ Overall Throughput Result

nevikw39

For the small data set, the throughput of optimized our config is more than twice the one of baseline. And for the large one, it's almost three times. Note that the speedup of throughput for both data set is not far from the speedup of bandwidth.

Bar graph of throughput speedup

Avg. of 10 iterations, small data set, Gadi Volta nodes



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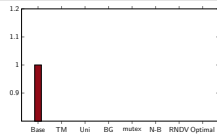
Communications Performance with UCX

Conclusion

Bar graph of throughput speedup

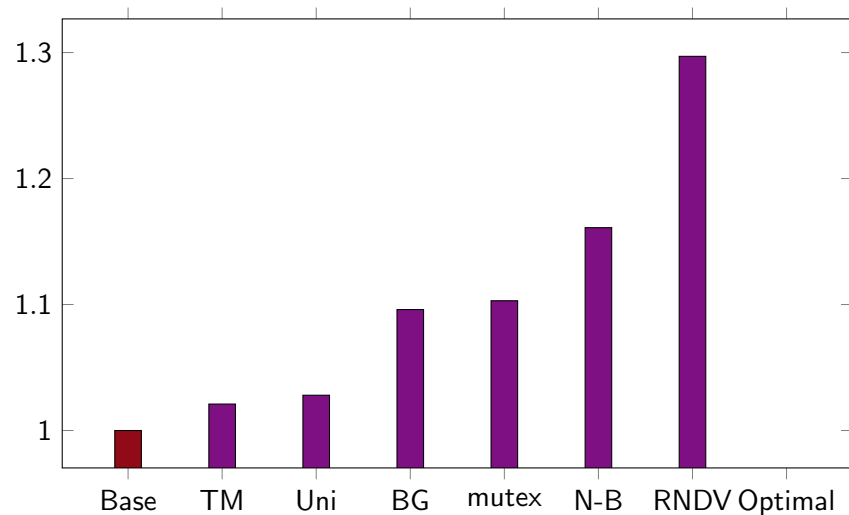
nevikw39

This is the baseline.



Bar graph of throughput speedup

Avg. of 10 iterations, small data set, Gadi Volta nodes



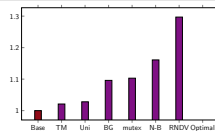
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Communications Performance with UCX

Conclusion

Bar graph of throughput speedup

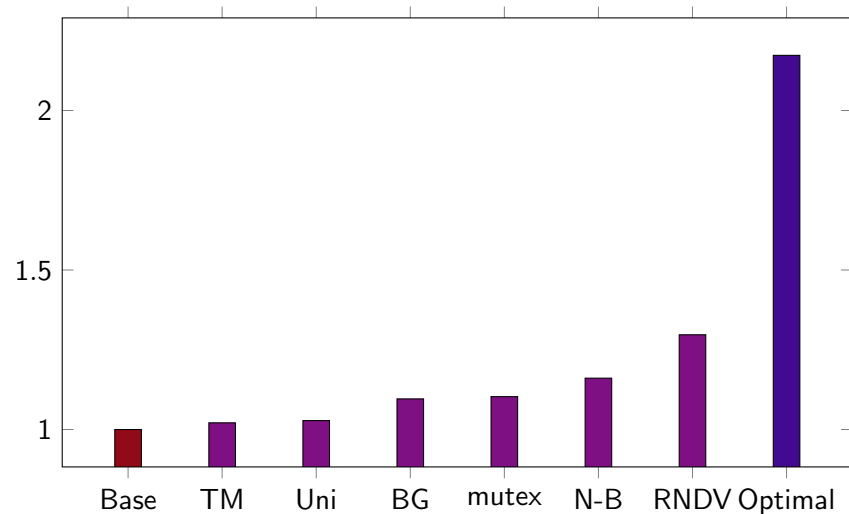


nevikw39

These are the speedup of a single option resp.

Bar graph of throughput speedup

Avg. of 10 iterations, small data set, Gadi Volta nodes



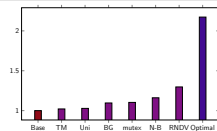
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Communications Performance with UCX

Conclusion

Bar graph of throughput speedup



nevikw39

As we can easily find, the optimized combination of configs give rise to as significant improvement of throughput.

Overall Throughput Result on DGX-A100 nodes

Avg. of 100 iterations on 16 GPUs over 2 Gadi DGX-A100 nodes

Table: Average throughput of 100 times (With DGX-A100s)

Chunk size	Default	Optimized Configurations
10^6	16.66 GiB/s	16.69 GiB/s
2.5×10^7	88.29 GiB/s	34.89 GiB/s ¹ 89.00 GiB/s ²

2022-10-24

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└ Communications Performance with UCX

└ Running on DGX-A100

└ Overall Throughput Result on DGX-A100 nodes

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Section 3

Deep-Learning-based DNA Sequence fast decoding

- 1 High Performance Computing with QUANTUM ESPRESSO
- 2 Communications Performance with UCX
- 3 Deep-Learning-based DNA Sequence fast decoding
 - Why do we choose this model?
 - Model structure
 - Tuning
 - Result

2022-10-24

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└ Deep-Learning-based DNA Sequence fast decoding

Section 3

Deep-Learning-based DNA Sequence fast decoding

• High Performance Computing with QUANTUM ESPRESSO

• Communications Performance with UCX

• Deep-Learning-based DNA Sequence fast decoding

• Why do we choose this model?

• Model structure

• Tuning

• Result

More accurate, more efficiency

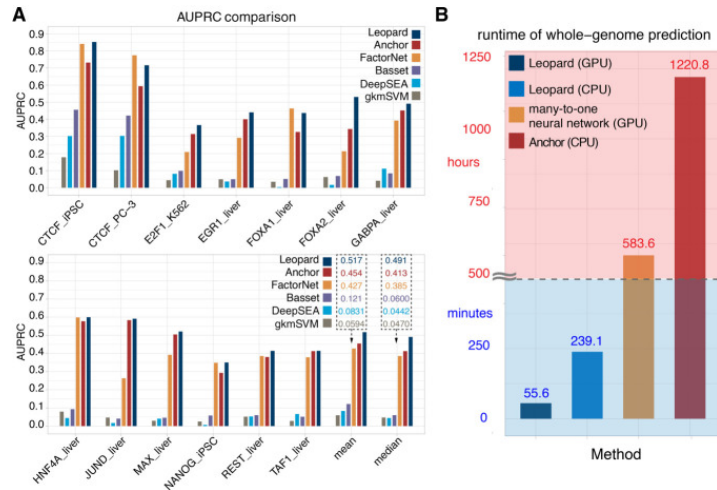


Figure: Model performance, adapted from the original paper

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Deep-Learning-based DNA Sequence fast decoding

Why do we choose this model?

More accurate, more efficiency

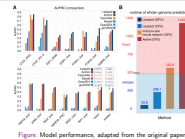


Figure: Model performance, adapted from the original paper

Main components

- Input
- Encoder (CCP blocks)
- Decoder (UCC blocks)
- Output

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└ Deep-Learning-based DNA Sequence fast decoding

└┐ Model structure

└┐ Main components

Main components

- Input
- Encoder (CCP blocks)
- Decoder (UCC blocks)
- Output

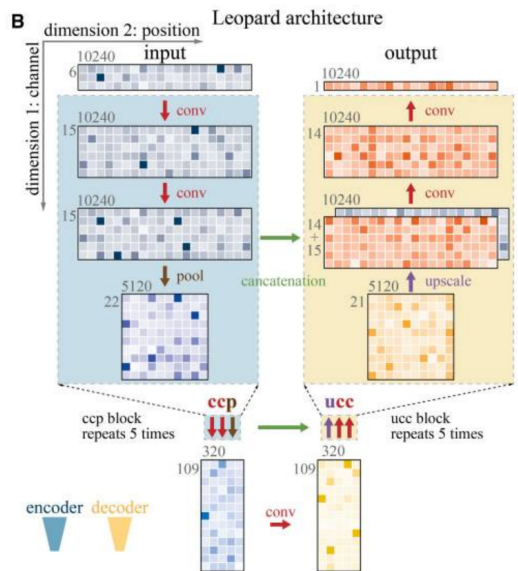


Figure: Model structure, adapted from the original paper

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Deep-Learning-based DNA Sequence fast decoding

Model structure

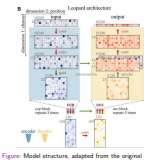


Figure: Model structure, adapted from the original paper

Brief summary

Some facts

- 61 layers
- 475969 parameters

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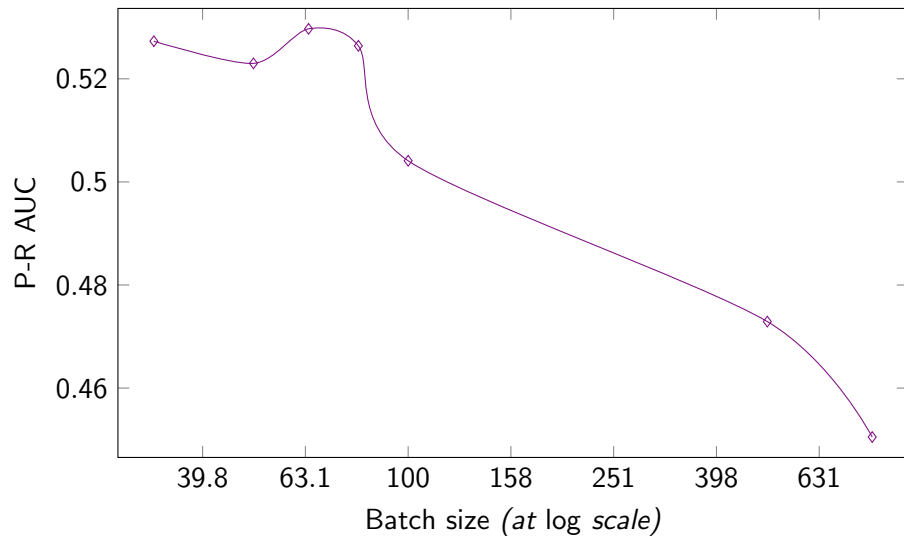
└ Deep-Learning-based DNA Sequence fast decoding

└└ Model structure

└└└ Brief summary

- 61 layers
- 475969 parameters

Maximum P-R AUC ever reached of various batch sizes



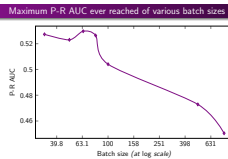
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Deep-Learning-based DNA Sequence fast decoding

Tuning

Maximum P-R AUC ever reached of various batch sizes



In our experiments, we follow a hierarchical manner; that is, we first tested **batch size**, then we adjusted **learning rate** for a particular **batch size**.

Batch sizes

- We tried batch size 32, 50, 80 and the default 100, yet their results were not optimal.

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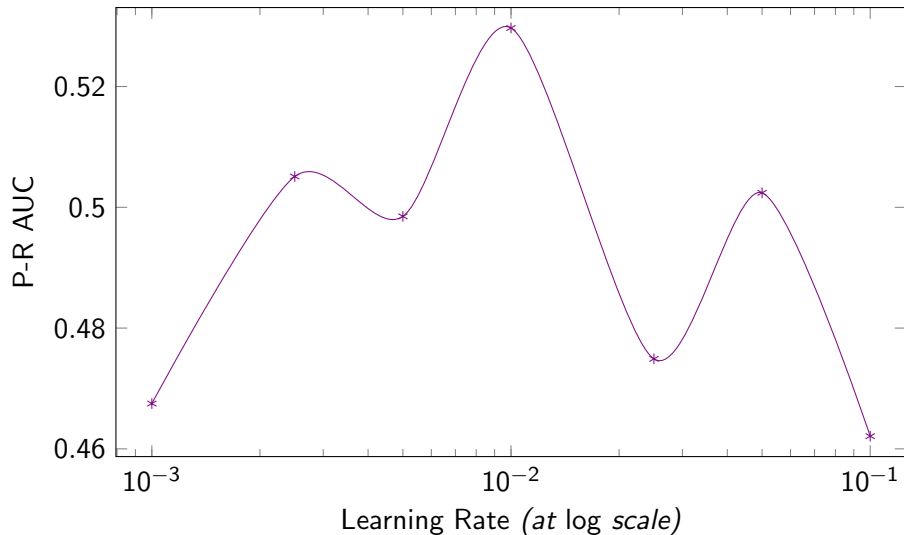
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- └ Deep-Learning-based DNA Sequence fast decoding
 - └ Tuning
 - └ Batch sizes

- We tried batch size 32, 50, 80 and the default 100, yet their results were not optimal.

Batch size 64

Maximum P-R AUC of several learning rates



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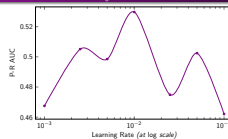
└ Deep-Learning-based DNA Sequence fast decoding

└ Tuning

└ Batch size 64

Batch size 64

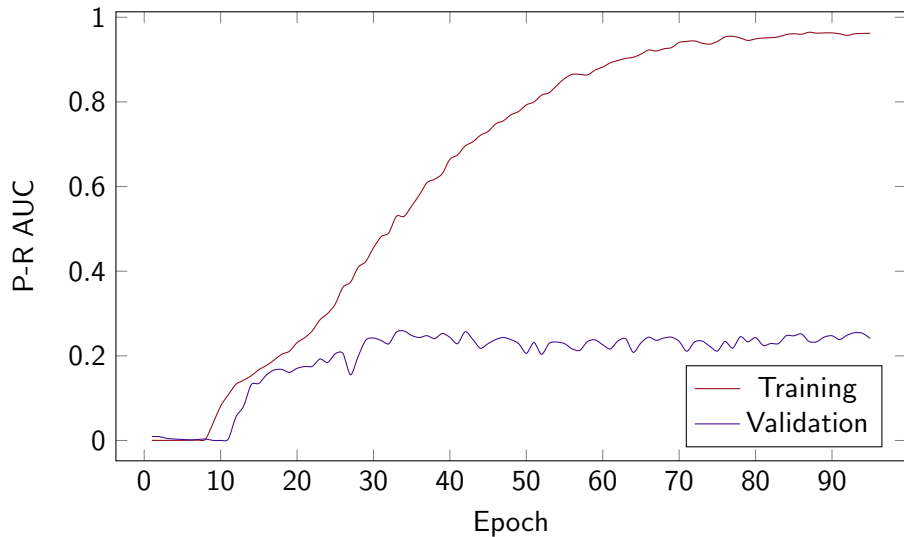
Maximum P-R AUC of several learning rates



This is the best **batch size** we have ever found. We tested several **learning rate**, such as 0.001, 0.0025, 0.005, 0.01, 0.025, 0.05, among of which 0.01 gave rise to optimal result.

Batch size 500

Overfitting



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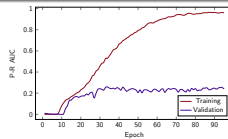
Deep-Learning-based DNA Sequence fast decoding

Tuning

Batch size 500

Batch size 500

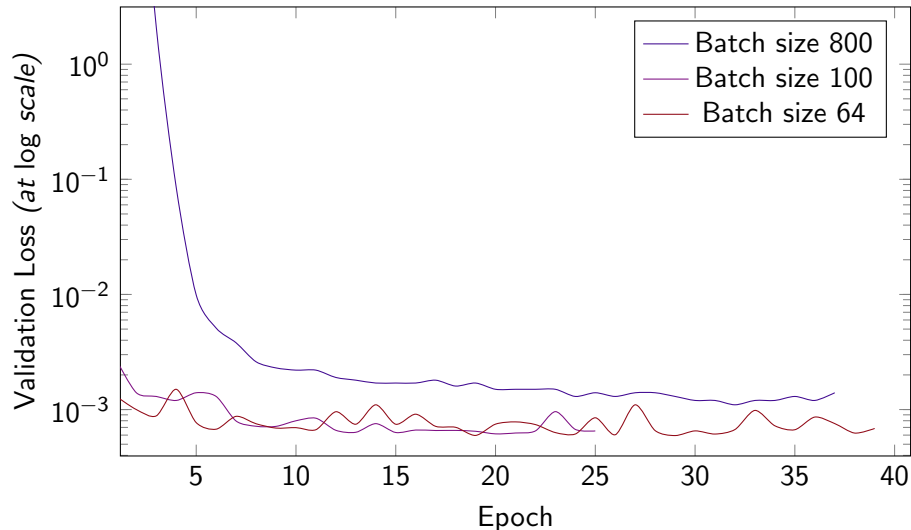
Overfitting



We encounter severe **overfitting** when it comes to this **batch size**; that is, P - R AUC could increase up to about 0.96 for the training set, whereas the ones for validation set were as low as 0.25. What's worse, since we increased the patience of early stop to 10, it exhausted the 2-hour wall time.

Batch size 800

Validation loss cannot converge to less than 10^{-3} (Note that y-axis is at log scale)



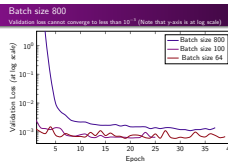
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Deep-Learning-based DNA Sequence fast decoding

Tuning

Batch size 800



The maximum **batch size** for V100 is 800 since it consumes about 31GB GPU memory. For this **batch size**, the converge rate of validation loss were quite slow despite of **learning rate**. As a consequence, the results were also not so good.

Batch size 1600, 2000, 2500

- On A100 only since memory usage would be over about 31GiB!
- Loss could hardly converge, similar with batch size 800

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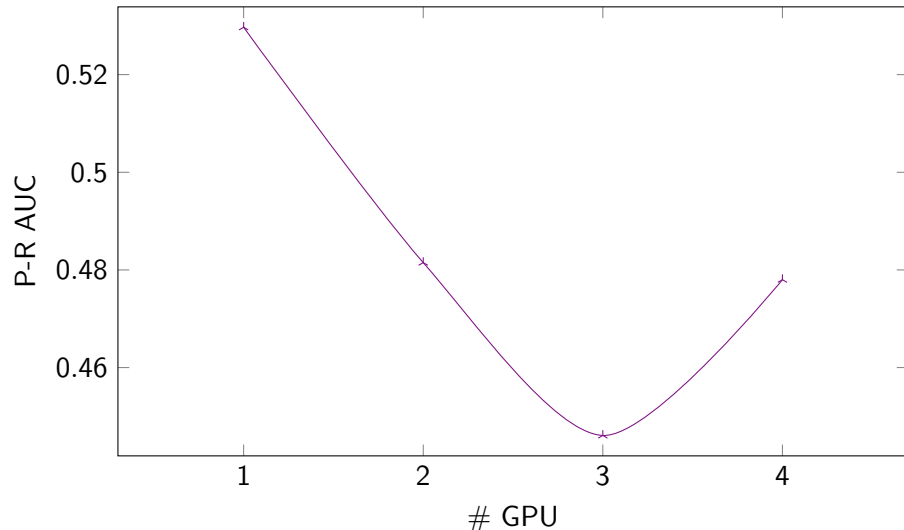
└ Deep-Learning-based DNA Sequence fast decoding

└ Tuning

└ Batch size 1600, 2000, 2500

Parallelization via Multiple GPUs

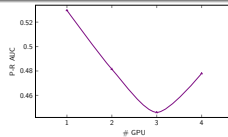
Performance always counts more!



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- Deep-Learning-based DNA Sequence fast decoding
 - Tuning
 - Parallelization via Multiple GPUs



We also managed to parallelize the training and utilized multiple GPUs. Nonetheless, the performance would decline a lot. Furthermore, the metrics would drop suddenly and dramatically after the number of GPU was over a value. We guessed that it might due to the simple, linear scale of **learning rate**, trying to find ad-hoc optimal **learning rate** for different number of GPU yet in vain.

Eventually, we decide to train on only a single GPU since we believe that the performance counts more. Still, we provide the job script to train across two A100s.

Volta and Ampère GPUs

- NVIDIA Volta V100: Main GPUs on Gadi
- NVIDIA Ampère A100: Faster and more memory

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└ Deep-Learning-based DNA Sequence fast decoding

└ Tuning

└ Volta and Ampère GPUs

- NVIDIA Volta V100: Main GPUs on Gadi
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Hyperparameters and environments

Batch Size 64

Learning Rate 0.01

GPU 1

2022-10-24

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└ Deep-Learning-based DNA Sequence fast decoding

└ Result

└ Hyperparameters and environments

Batch Size 64
Learning Rate 0.01
GPU 1

Table: Performance of Single GPU

GPU Type	Loss (<i>Binary Crossentropy</i>)	P-R AUC	Dice coeff.	Binary Int. of Union	Training Time [s]
V100	7.2768×10^{-4}	0.5297	0.3705	0.3625	3170.19
A100	7.3153×10^{-4}	0.5288	0.4109	0.3701	941.63

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└ Deep-Learning-based DNA Sequence fast decoding

└ Result

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