Holoscan Flow Benchmarking

White Paper

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Document History

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Overview

Developing and optimizing the performance of a time-critical application is a challenging task. One needs to run an application with different configurations and evaluate the performance to figure out the desired production environment of an application. Holoscan is a real-time AI sensor-processing platform that enables developers to build real-time AI applications with intuitive interfaces. However, measuring the performance of a Holoscan application can require significant efforts by the application developers. This article introduces Holoscan flow benchmarking on HoloHub, which aims to make Holoscan applications performance measurements and analysis easy and scalable. Holoscan flow benchmarking can help evaluate different configurations before deploying a Holoscan application to production.

A key performance indicator (KPI) for real-time sensor processing applications is the end-to-end latency. There are many possible metrics on the end-to-end latency performance, including average end-to-end latency and maximum (worst-case) end-to-end latency. For a developer, these metrics indicate how well their application is performing in terms of responsiveness and efficiency. Holoscan SDK data flow tracking allows for precise measurement of the end-to-end latency of Holoscan applications. Holoscan flow benchmarking in Holohub leverages the data flow tracking of the Holoscan SDK.

Introduction to Holoscan Flow Benchmarking

Holoscan flow benchmarking allows developers to automate the benchmarking process and generate the necessary log files, which are analyzed later. This article demonstrates how to use Holoscan flow benchmarking to evaluate different configurations, applications and schedulers.

There are four steps to perform Holoscan flow benchmarking, which are summarized here. The following is a high-level overview:

1. **Patching an application:** Patch a Holoscan application to turn on data flow tracking.
2. **Building an application:** Compile the patched application with necessary header files.

3. **Running the benchmark:** Run the `benchmark.py` script with necessary parameters to evaluate the performance of the application in different configurations. This generates a number of log files that capture the result of the performance measurements in a raw format.
4. **Analyzing the result:** Retrieve the result of the benchmarking process using the generated log files and the `analyze.py` script. You can also export the results in a CSV file or generate graphs to visualize certain results.

The following sections will demonstrate some of the capabilities of Holoscan flow benchmarking.

Comparing performance for multiple instances of an application

In many cases, users may want to run multiple Holoscan applications in parallel on their systems. They want to know the performance implications of a particular configuration before developing a full-fledged system with more than one Holoscan application. Through Holoscan flow benchmarking, they can easily evaluate the performance of multiple instances of an application in parallel to compare the behavior of specific and curated use-cases. They can learn how many parallel instances of an application, representative of their own application, can safely run until the configuration cannot meet their expected end-to-end latency guarantees.

Suppose you want to evaluate the performance of running multiple instances of the endoscopy tool tracking application in parallel to understand end-to-end latency performance. After completing the first two steps specified in the **Introduction to Holoscan Flow** workflow, you can run the following command to evaluate how up to 5 concurrent instances of the endoscopy tool tracking application will perform.

```
$ python tutorials/benchmarking/benchmark.py -a endoscopy_tool_tracking --sched greedy -i <Number of Instances> -r 10 -m 1000 -d endoscopy_<Number of Instance>
```

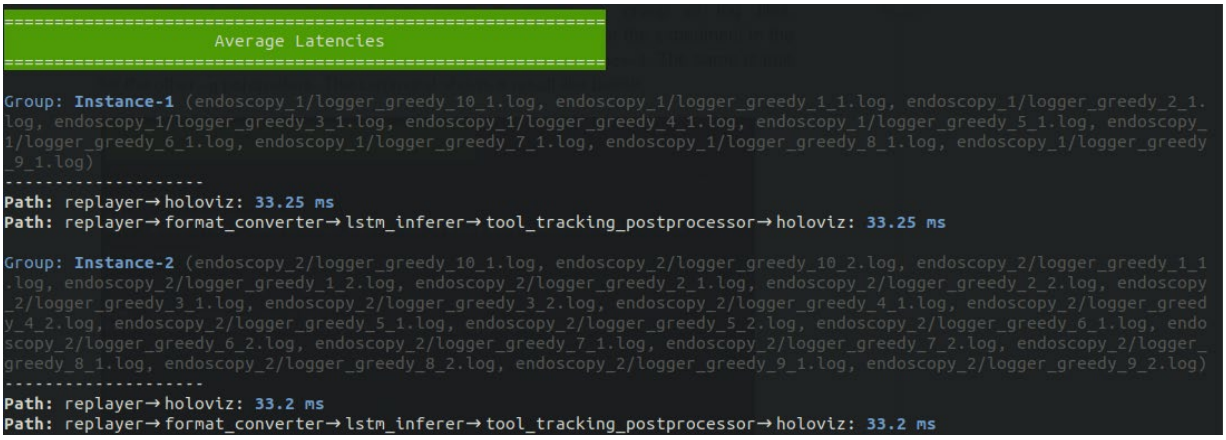
`Number of Instances` needs to be set to measure the performance of multiple concurrent instances of the endoscopy tool tracking applications. The above command tests the application against 1000 data frames (`-m 1000`) and repeats every experiment 10 times (`-r 10`) for the greedy scheduler (`--sched greedy`). The log files generated by the benchmarking process are stored in the `endoscopy_<Number of Instance>` directory, where `Number of Instance` varies from 1 to 5. The format of the filename for the data flow tracking log files is `logger_<scheduler>_<run_number>_<instance-id>.log`.

Retrieving the Result

After the benchmarking process is complete, you can analyze the result using the `analyze.py` script. If you want to know the average end-to-end latencies of the above experiment, the following command could be used:

```
$ python tutorials/holoscan_flow_benchmarking/analyze.py --avg -g
endoscopy_1/logger* Instance-1 -g endoscopy_2/logger* Instance-2 -g
endoscopy_3/logger* Instance-3 -g endoscopy_4/logger* Instance-4 -g
endoscopy_5/logger* Instance-5
```

In the above command, `--avg` is used to show the average end-to-end latency of each experiment. Every `-g` parameter is used to specify a group of log files. `endoscopy_1/logger*` specifies the data flow tracking log files for the experiment in the `endoscopy_1` directory. It is followed by a group name of `Instance-1`. The same is true for the other `-g` parameters. Executing the command shows a result similar to following:



Plotting the Data

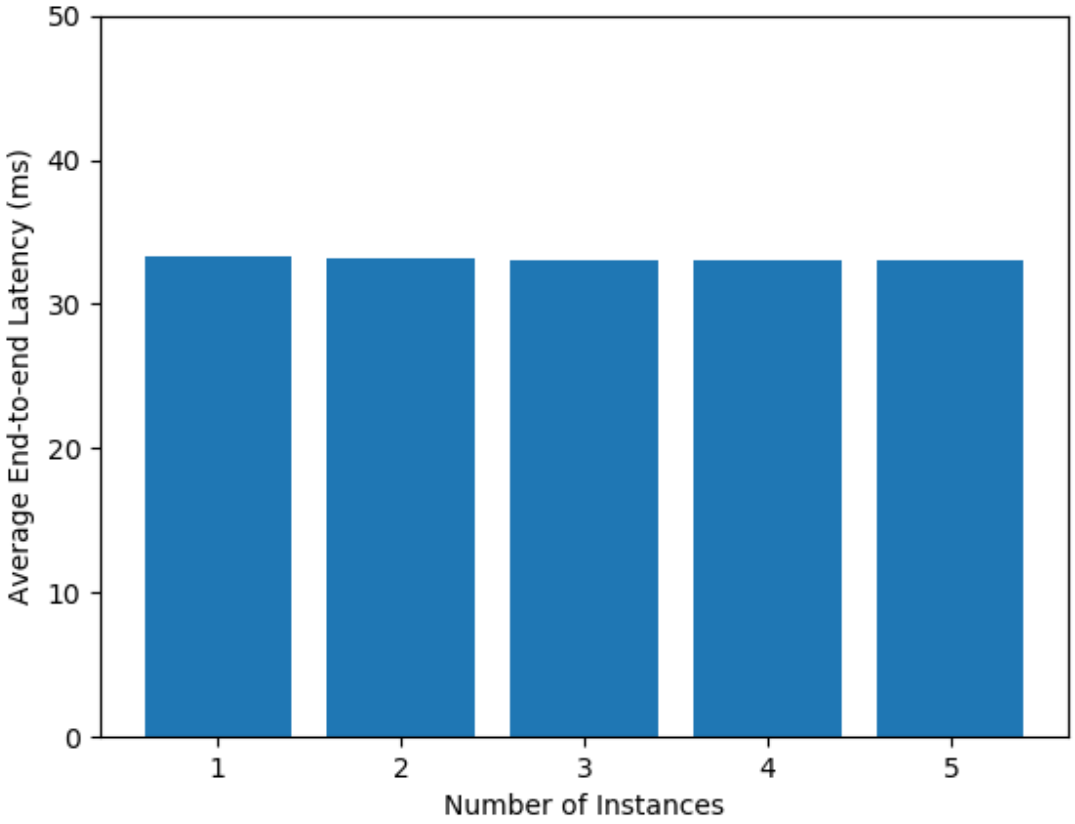
In addition to getting the analysis results, it is important to plot the result in a graph to better understand the trends in an evaluation result. The Holoscan flow benchmarking provides options to export the results in a CSV file to plot the data with your favorite plotting tool later on. Appending the `analyze.py` command with the `--save-csv` parameter enables saving the results in an `avg_values.csv` file in CSV format:

```
$ python tutorials/holoscan_flow_benchmarking/analyze.py --avg -g
endoscopy_1/logger* Instance-1 -g endoscopy_2/logger* Instance-2 -g
endoscopy_3/logger* Instance-3 -g endoscopy_4/logger* Instance-4 -g
endoscopy_5/logger* Instance-5 --save-csv
```

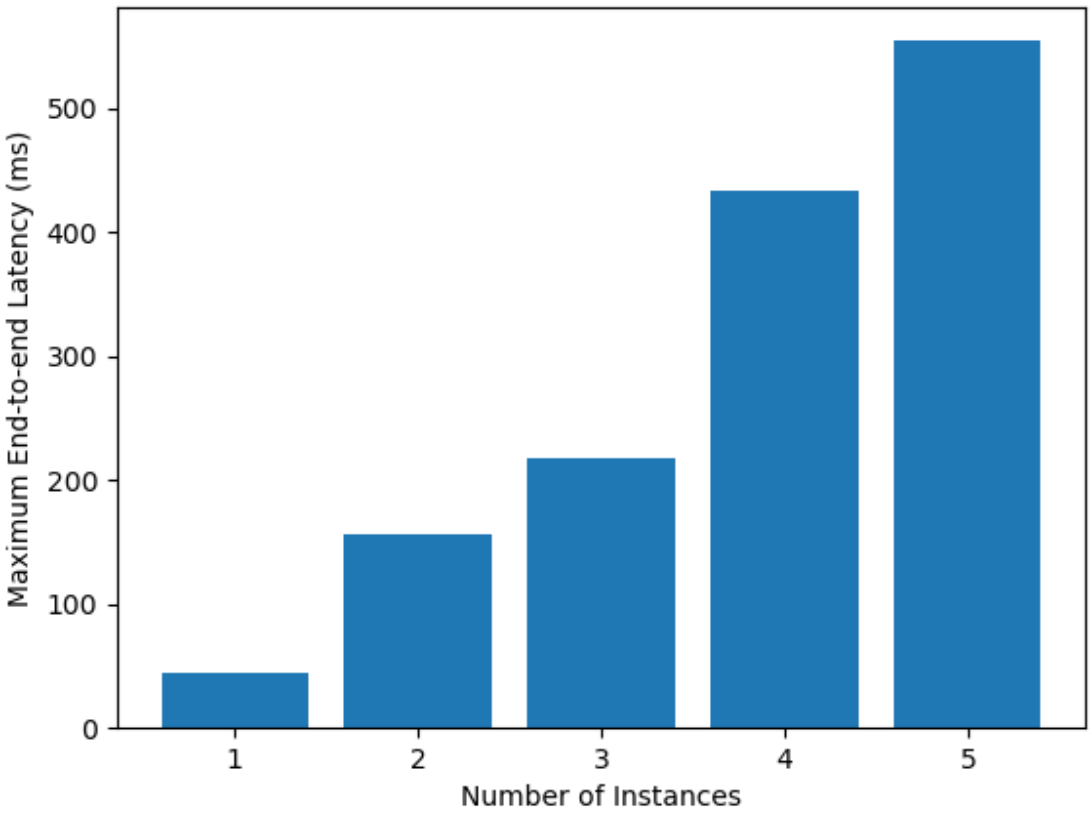
Then, the average values could be plotted with your preferred plotting tools. For example, the `matplotlib` Python library could be used to plot the average values in a bar-graph with the following code:

```
import matplotlib.pyplot as plt

with open('avg_values.csv', 'r') as f:
    lines = f.readlines()
    avg_values = [float(x) for x in lines[0].strip().split(',') if x]

plt.bar(range(1, 6), avg_values)
plt.xlabel('Number of Instances')
plt.ylabel('Average End-to-end Latency (ms)')
plt.savefig('avg_bar_graph.png')
```

The graph looks like the following:



Similar results can be obtained for the maximum end-to-end latencies as well if the above `analyze.py` command is supplied with the `--max` parameter. The bar-graph with the maximum end-to-end latency would look like the following graph, as the worst-case latency is affected by interferences from multiple instances:



The application developers can decide for their own applications the acceptable maximum or average end-to-end latency and, as a result, determine the following:

- How many parallel instances of an application they want to run on their system
- Whether they need to further optimize the pipeline
- Whether they need more compute resources

Including GPU Utilization in the Result

Understanding the impact of running multiple instances of an application on GPU utilization is crucial for optimizing performance. Holoscan flow benchmarking can also help measure the GPU utilization for every experiment. By appending `-u` to the above `benchmark.py` command, the GPU utilization is monitored and logged in a CSV file named `gpu_utilization_<scheduler>_<run_number>.csv`. For example, the final command for GPU utilization monitoring is as follows:

```
$ python tutorials/benchmarking/benchmark.py -a endoscopy_tool_tracking --sched greedy -i
<Number of Instances> -r 10 -m 1000 -d endoscopy_<Number of Instance> -u
```

In the analysis phase, the average GPU utilization result can be saved in a CSV file (`avg_gpu_utilization_values.csv`) using the `-u --save-csv` parameters:

```
$ python tutorials/holoscan_flow_benchmarking/analyze.py -g endoscopy_1/logger* Instance-
1 -u endoscopy_1/gpu* Instance-1-GPUUtil -u endoscopy_2/gpu* Instance-2-GPUUtil -u
endoscopy_3/gpu* Instance-3-GPUUtil -u endoscopy_4/gpu* Instance-4-GPUUtil -u
endoscopy_5/gpu* Instance-5-GPUUtil --save-csv
```

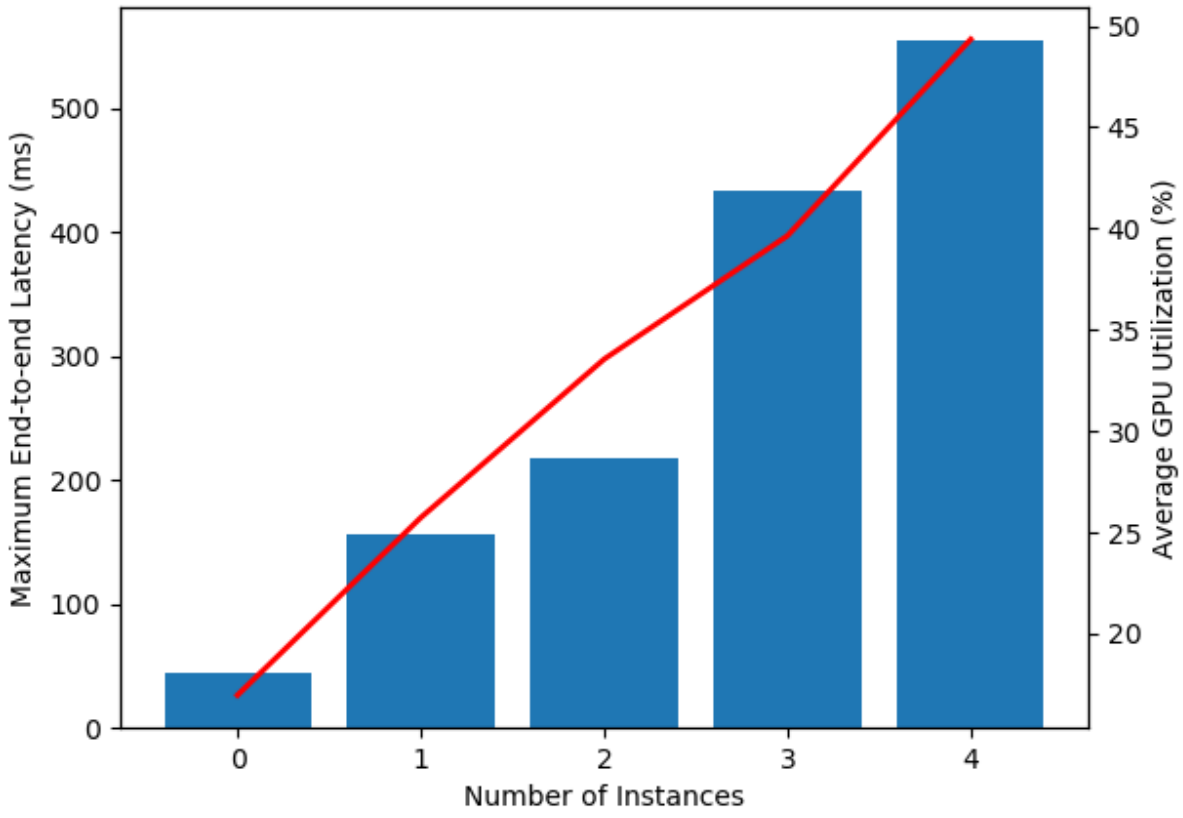
Each `-u` parameter specifies the group of GPU utilization log files (`endoscopy_1/gpu*`), with a last parameter that specifies the group name (`Instance-1-GPUUtil`). `-g endoscopy_1/logger* Instance-1` to satisfy the requirement of a mandatory `-g` parameter.

Suppose you want to plot the average GPU utilization, as well in the above bar-graph of maximum values. You can achieve that with the following code in Python:

```
import matplotlib.pyplot as plt

with open('max_values.csv', 'r') as f:
    lines = f.readlines()
    max_values = [float(x) for x in lines[0].strip().split(',') if x]

with open('avg_gpu_utilization_values.csv', 'r') as f:
    lines = f.readlines()
    avg_gpu_utilizations = [float(x) for x in lines[0].strip().split(',') if x]

fig, ax1 = plt.subplots()
ax1.bar(range(len(max_values)), max_values)
ax1.set_ylabel('Maximum End-to-end Latency (ms)')
ax1.set_xlabel('Number of Instances')
ax2 = ax1.twinx()
```

```
ax2.plot(range(len(avg_gpu_utilizations)), avg_gpu_utilizations, color='r',
linewidth=2.0)
ax2.set_ylabel('Average GPU Utilization (%)')
plt.savefig('max_bar_graph.png')
```

The generated graph looks like the following:

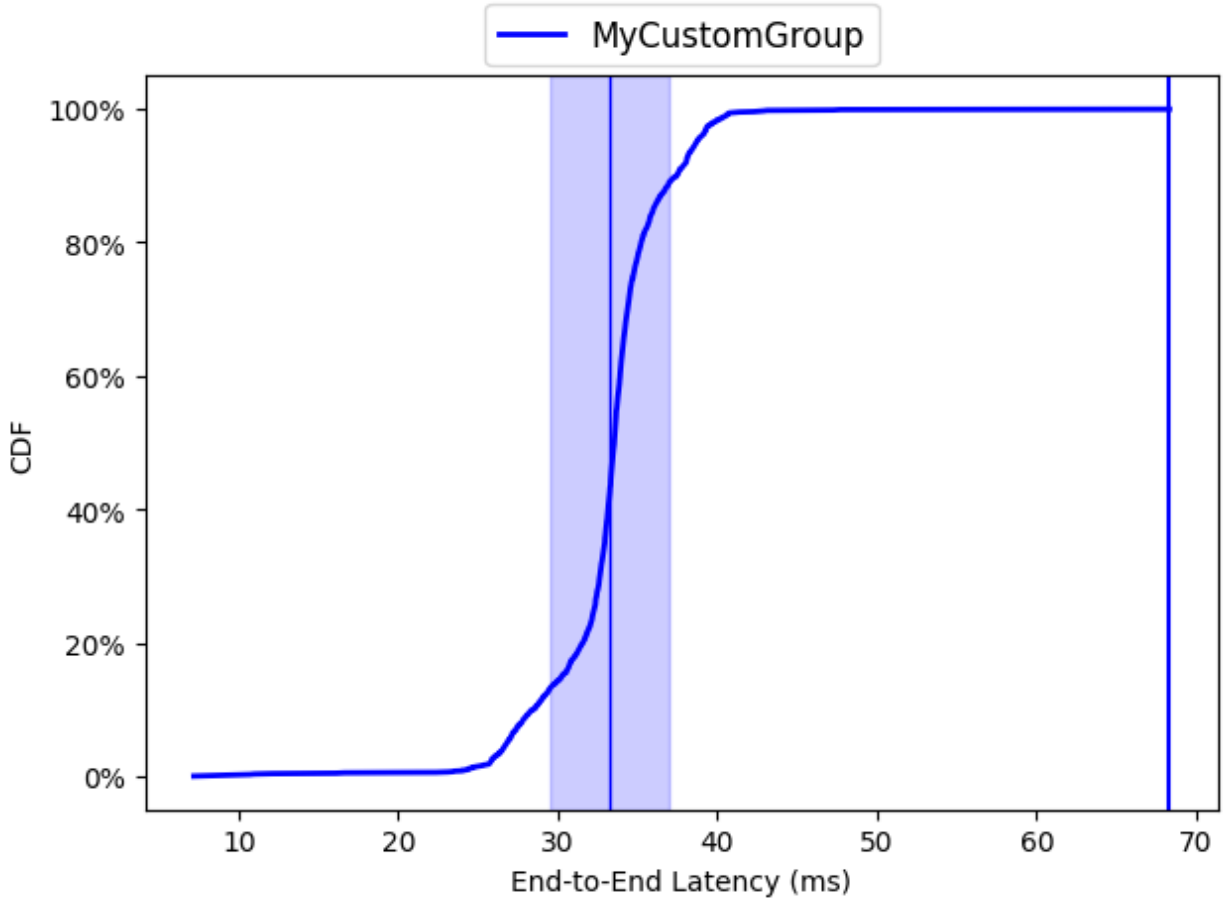


Generating a CDF Curve

Holoscan flow benchmarking can also be used to generate the graph of the Cumulative Distribution Function (CDF) of the observed end-to-end latencies. The CDF curve is a useful tool to understand how much the latencies of all the data frames passing through an application graph are distributed. The following command generates a CDF curve of the end-to-end latencies of the first path for the experiment with one instance:

```
$ python tutorials/holoscan_flow_benchmarking/analyze.py --draw-cdf single_path_cdf.png -g endoscopy_1/logger* MyCustomGroup --no-display-graphs
```

By default, the command also displays the graph in a separate window. The `--no-display-graphs` suppresses this option. The graph is saved as a `single_path_cdf.png` file; an example is shown below:



In addition to plotting the CDF curve of the first path, it is also possible to plot the CDF curves of all the paths of an application graph with the `--draw-cdf-paths` parameter.

Comparing Two Different Applications

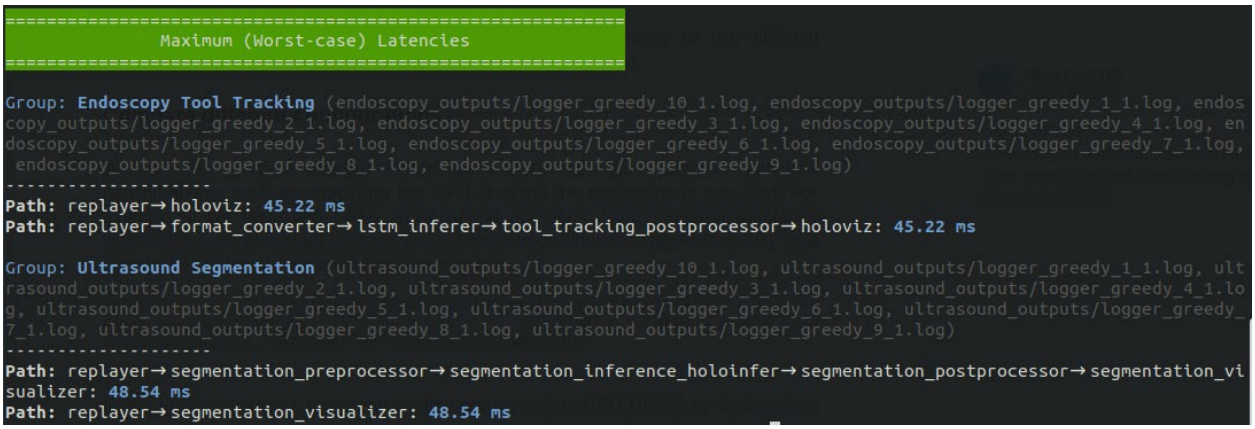
The `benchmark.py` script can be used to evaluate the performance of two different applications. The results can be analyzed and compared using the `analyze.py` script. For example, you can run the following two commands to run two different applications under the same settings:

```
$ python tutorials/holoscan_flow_benchmarking/benchmark.py -a endoscopy_tool_tracking -r 10 -i 1 -m 1000 --sched greedy -d endoscopy_outputs
$ python tutorials/holoscan_flow_benchmarking/benchmark.py -a ultrasound_segmentation -r 10 -i 1 -m 1000 --sched greedy -d ultrasound_outputs
```

The above commands run two experiments and save the corresponding log files in two different directories, `endoscopy_outputs` and `ultrasound_outputs`. We can analyze and compare their maximum end-to-end latencies with the following `analyze.py` command:

```
$ python tutorials/holoscan_flow_benchmarking/analyze.py --max -g endoscopy_outputs/logger* "Endoscopy Tool Tracking" -g ultrasound_outputs/logger* "Ultrasound Segmentation"
```

The result is as follows:



Such a command shows the maximum end-to-end latency of two different applications and helps the developers compare their performances.

Comparing Different Configurations

You can also compare different configurations of an application with Holoscan flow benchmarking, such as specifying the GPU in which the application is executed. For example, if you have two GPUs (RTX A6000 and RTX A4000) both available for visualization, you may want to know the performance of running an application on one of the GPUs only. You can run the following command:

```
$ python tutorials/holoscan_flow_benchmarking/benchmark.py -a endoscopy_tool_tracking -r 10 -i 1 -m 1000 --sched greedy -d endoscopy_outputs_<GPU Name> -g <Corresponding GPU UUID>
```

The above command requires a GPU UUID, which can be looked up using `nvidia-smi -L`, and the `<GPU Name>` can be used to save the outputs in different directories. The `-g <Corresponding GPU UUID>` parameter sets the `CUDA_VISIBLE_DEVICES` environment variable to the corresponding GPU UUID. It is important to note that this option does not override the application-specific GPU settings in the code--for example, via the GPU assignment in Inference operator (`device_map` option).

The results of the above experiment can be compared using the following command:

```
$ python tutorials/holoscan_flow_benchmarking/analyze.py <insert your metrics options> -g endoscopy_outputs_<GPU Name>/logger* "GPU1" -g endoscopy_outputs_<GPU Name>/gpu* "GPU2"
```

Comparing the Performance of Different Schedulers

It is also possible to compare different schedulers using Holoscan flow benchmarking. The following commands can be used to evaluate performance of the endoscopy tool tracking sample application under the Greedy scheduler and the Multithread scheduler:

```
$ python tutorials/holoscan_flow_benchmarking/benchmark.py -a endoscopy_tool_tracking -r
10 -i 1 -m 1000 --sched greedy -d endoscopy_greedy_outputs
$ python tutorials/holoscan_flow_benchmarking/benchmark.py -a endoscopy_tool_tracking -r
10 -i 1 -m
1000 --sched multithread -w 5 -d endoscopy_multithread_outputs
```

Then, the results can be analyzed and compared using the following command:

```
$ python tutorials/holoscan_flow_benchmarking/analyze.py <insert your metrics options> -g
endoscopy_greedy_outputs/logger* "Endoscopy (Greedy)" -g
endoscopy_multithread_outputs/logger* "Endoscopy (Multithread)"
```

Tail and Flatness of the CDF Curve

The `analyze.py` script provides options for calculating the tail and flatness of the CDF curve of the observed latencies using the `--tail` and `--flatness` parameters, respectively.

The tail of the CDF curve is the difference between the 95 percentile and 100 percentile values. It helps to understand how widely distributed the worst-case latencies of an application are. The lesser the value of the CDF curve tail, the better the application is performing in the far end of the latency distribution

The flatness of the CDF curve is the difference between the 10 percentile and 90 percentile values. It informs how much the observed latencies are distributed where most of the latencies are observed. A smaller value of the flatness of the CDF curve indicates the latencies are more concentrated, and the application is performing more deterministically.

Overall, it is preferable for both the tail and flatness of the CDF curve to be as small as possible.

Conclusion

Holoscan flow benchmarking is currently available for four HoloHub C++ applications:

- endoscopy_tool_tracking
- multiai_endoscopy
- multiai_ultrasound
- ultrasound_segmentation

We plan to add Holoscan flow benchmarking for other C++ and Python sample applications for HoloHub in the future.

Holoscan flow benchmarking allows developers to evaluate the performance of Holoscan applications at scale. The article demonstrates a few common use-cases. Please let us know how you are leveraging Holoscan flow benchmarking and if you are experiencing any gaps or blockers for your applications. Please feel free to file issues on Github or contribute directly to HoloHub.

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