

Reproduced Computational Results Report for "Ginkgo: A Modern Linear Operator Algebra Framework for High Performance Computing"

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The article titled "Ginkgo: A Modern Linear Operator Algebra Framework for High Performance Computing" by Anzt et al. presents a modern, linear operator centric, C++ library for sparse linear algebra. Experimental results in the article demonstrate that Ginkgo is a flexible and user-friendly framework capable of achieving high-performance on state-of-the-art GPU architectures.

In this report, the Ginkgo library is installed and a subset of the experimental results are reproduced. Specifically, the experiment that shows the achieved memory bandwidth of the Ginkgo Krylov linear solvers on NVIDIA A100 and AMD MI100 GPUs is redone and the results are compared to what presented in the published article. Upon completion of the comparison, the published results are deemed reproducible.

CCS Concepts: • Software and its engineering \rightarrow Software creation and management; • Mathematics of computing \rightarrow Mathematical software; • Computing methodologies \rightarrow Massively parallel algorithms

Additional Key Words and Phrases: High performance computing, healthy software lifecycle, multicore and manycore architectures

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1 INTRODUCTION

In [2], Anzt et al. introduce a modern C++ library for sparse linear operator algebra, Ginkgo. To demonstrate flexibility and performance, the authors conduct several experiments on GPU architectures relevant to today's supercomputers and offer performance comparisons between the Ginkgo implementation of certain algorithms and GPU vendor implementations.

In this report, we focus on reproducing a subset of the results presented by Anzt et al. in [2]; specifically, we reproduce the solver memory bandwidth data and plots given in Figures 8 and 9. The results portrayed by Figure 8 of [2] are generated using an NVIDIA A100 GPU with 40 GB of

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memory and the CUDA programming model [5], while the results portrayed by Figure 9 of [2] are generated using an AMD MI100 GPU with 32 GB of memory and the HIP programming model [1]. The general steps we use to reproduce the experimental results are the same for both GPUs:

- (1) Install the ssget tool and prefetch test matrices from the SuiteSparse collection.
- (2) Download and build the Ginkgo library.
- (3) Generate the scripts needed to execute the experiments.
- (4) Upload the experiments to a git repository and use the Ginkgo Performance Explorer interactive website to generate the figures.

The published manuscript [2] utilized the Tulip early access system for the Frontier supercomputer to benchmark Ginkgo, but in this report, we utilize the Spock early access system sited at Oak Ridge National Laboratory [7]. The Spock system has AMD MI100 GPUs, like Tulip [2], so the results we generate will be comparable to the original. For reproducing the NVIDIA A100 results, we utilize the Guyot system hosted by the **Innovative Computing Laboratory** (**ICL**) at the University of Tennessee, Knoxville. While Guyot has NVIDIA A100 GPUs, they are slightly different from the A100 GPUs used in the published article. In particular, the Guyot A100 GPUs have 80 GB of memory instead of 40 GB and 2039 GB/s of memory bandwidth vs 1555 GB/s [6]. All of the other specifications of the A100 GPUs in Guyot match the A100 GPUs used to generate the published experimental data. Therefore, we should still be able to reproduce the results within a reasonable margin, and we only have one variable, the increased memory bandwidth, which we must account for in our analysis.

2 REPRODUCTION OF EXPERIMENTAL RESULTS

Anzt et al. provide detailed steps to reproduce Figures 8 and 9 and their relevant data in Annex A of the published article [2]. We follow the instructions exactly (including using the same software versions), except where noted, and as such, we only summarize most of the steps below. Steps that differ for the A100 and MI100 experiments are also noted.

2.1 Preparing to Execute the Experiments

2.1.1 Clone the ssget Tool. The ssget tool is cloned from the git repository https://github.com/ ginkgo-project/ssget to \$HOME/TOMS-gko-reproduce. The ARCHIVE_LOCATION variable on line 39 of the ssget.sh script is set to be \$HOME/TOMS-gko-reproduce on Guyot. On Spock, the variable is set to a directory, /gpfs/alpine/<projid>/scratch/<username>, that resides on the Spock parallel file system. We add the location of the ssget script to our \$PATH variable.

2.1.2 Use ssget to Download the SuiteSparse Matrices Needed for the Experiments. Following the author-provided instructions, we create a file with a list of 10 relevant matrix IDs from the SuiteSparse Matrix Collection [3]. The ssget script is then used to fetch each of the matrices.

2.1.3 Clone and Build Ginkgo. On Guyot, we follow the author-provided instructions to clone Ginkgo from https://github.com/ginkgo-project/ginkgo.git and build it. We change line 3 of Listing 13 in the published article to load the equivalent modules on Guyot. We also omit line 15 of Listing 13, since Guyot does not require us to submit a job through a job scheduler. The available CUDA version on Guyot is a slightly newer version than used by Anzt et al. (CUDA 11.0.221 instead of 11.0.194). With these modifications, we successfully built Ginkgo on Guyot and all unit tests run by make test passed.

On Spock, first, we modified Listing 13 for HIP use as the authors instructed. The exact script we use is given in Listing 1. On the Spock system, the ROCM version used by Anzt et al., 4.0.20496, is not available. Instead, we utilize ROCM 4.1.0, which requires us to modify line 157 of the CMake-

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Lists.txt in the root directory of the Ginkgo source code. Specifically, we change the line to read if (GINKGO_HIP_PLATFORM MATCHES "hcc|amd"). After these steps were completed, running make -j10 successfully compiled Ginkgo, and all tests run by make test passed as well.

```
ginkgo_source=$HOME/TOMS-gko-reproduce/ginkgo
   ginkgo_build=/gpfs/alpine/<projid>/scratch/<username>/TOMS-gko-reproduce/
2
       ginkgo-build
   module load craype-accel-amd-gfx908 rocm cmake git
3
4
   # For every new session, the previous setup is required
5
6
   # git clone https://github.com/ginkgo-project/ginkgo.git ${ginkgo_source} --
       branch master
7
   mkdir -p ${ginkgo_build} && cd ${ginkgo_build}
   cmake -DGINKGO_BUILD_CUDA=off -DGINKGO_BUILD_HIP=ON -DGINKGO_BUILD_OMP=off -
8
       DGINKGO_BUILD_EXAMPLES=off -DGINKGO_BUILD_TESTS=on -DGINKGO_DEVEL_TOOLS=
       off -DCMAKE_CXX_COMPILER=$(which hipcc) ${ginkgo_source}
9
   # Compilation can happen either directly or through a job depending on the
10
   # system policies.
11
   srun -N 1 -A <projid> -p <partition> --gres=gpu:1 --time=3:00:00 --export=ALL
12
        make -j10
   make -j10 # afterwards, ensure everything is compiled
13
14
   make test
   # Everything should run without failure. If cuda tests fail logging
15
16
  # in again might solve some issue, this could be due to the hardware
  # restrictions on summit after 4 hours of login time
17
```

Listing 1. A script to download and build the Ginkgo library to reproduce the M1100 experiments on Spock with HIP.

2.1.4 Clone and Build BabelStream. Since the NVIDIA A100 GPUs on Guyot have a higher theoretical memory bandwidth than the A100 GPUs utilized by Anzt et al. in [2], we need to run the BabelStream [4] TRIAD benchmark on Guyot. We clone the BabelStream git repository (https://github.com/UoB-HPC/BabelStream.git) to \$HOME/TOMS-gko-reproduce/babelstream and then follow the documentation to build it with CUDA enabled. After building, we end up with the cuda-stream script in the \$HOME/TOMS-gko-reproduce/babelstream/build directory.

2.2 Executing the Experiments

To execute the A100 experiments on Guyot, we do not need to use a SLURM batch script like the authors instructed in the article (so we skip the steps in Listings 14 and 15 of [2]). Instead, we execute the benchmarks directly by navigating to the directory \${ginkgo_build}/benchmark, where \${ginkgo_build} is the directory where Ginkgo was built earlier, and then running the command sh run_all_benchmarks.sh. As in the published article, the experiments employ a single NVIDIA A100 GPU.

For the MI100 experiments that we run on Spock, a SLURM batch script is required. We utilize Listing 14 of [2] as a guide to create the batch script. Due to the queue limitations, we cannot run all of the experiments as a single batch job. As such, we split the experiments into two jobs by splitting the matrices list file from Section 2.1.2 into two files, each with five matrix IDs. Our exact batch script is given in Listing 2. Note that each batch job uses a single AMD MI100 GPU for the experiments.

In addition to the Ginkgo experiments, we also run the BabelStream TRIAD benchmark on Guyot. To do this, we navigate to \$HOME/TOMS-gko-reproduce/babelstream/build, execute the

command ./cuda-stream $\,$ --triad-only, and then note the output bandwidth (1721 GB/s) for later use.

```
1
   #!/bin/bash
   #SBATCH --nodes=1
2
   #SBATCH --ntasks=1
3
   #SBATCH --exclusive
4
5
   #SBATCH --gres=gpu:1
   #SBATCH --time=3:00:00
6
7
   #SBATCH --account=<account>
   #SBATCH --partition=<partition>
8
   #SBATCH --export=ALL
9
10
   cd ${ginkgo_build}/benchmark
11
12
   make -j10
13
   chmod +x run_all_benchmarks.sh
   # choose which part of the experiment to run in this job
14
   export MATRIX_LIST_FILE=$HOME/TOMS-gko-reproduce/matrices.list.part1
15
   #export MATRIX_LIST_FILE=$HOME/TOMS-gko-reproduce/matrices.list.part2
16
   export SOLVERS_PRECISION=1e-200
17
18
   export SYSTEM_NAME=MI100_solvers
19
   export EXECUTOR=hip
   export BENCHMARK=solver
20
   export FORMATS="coo"
21
   exec ./run_all_benchmarks.sh
22
```

Listing 2. The SLURM batch script we utilize to launch the MI100/HIP experiments on Spock.

2.3 Evaluating the Reproduced Results

The result of the experiment batch jobs is a set of JSON files, one for each test matrix, containing timing information for five of the different Krylov linear solver methods available in Ginkgo: BiCGSTAB, CG, CGS, FCG, and GMRES. To evaluate the reproduced results and recreate Figures 8 and 9 of [2], we utilize the **Ginkgo Performance Explorer** (**GPE**) plotting tool (https://ginkgo-project.github.io/gpe/) as discussed by Anzt et al. in Annex A.4 of their article.

Continuing to follow the authors' instructions, we first fork the ginkgo-data (https://github.com/ ginkgo-project/ginkgo-data) git repository. To publish the results, we use Listing 16 from [2] with one change: For the A100 results from Guyot, we publish the files to the TOMS-interface branch of our ginkgo-data fork (https://github.com/balos1/ginkgo-data), but for the MI100 results from Spock, we publish the files to a branch named TOMS-interface-hip. After publishing, we use the GPE to inspect our reproduced results. Again, we simply follow the instructions of Anzt et al. to load the reproduced results into the GPE.

In order to recreate the plot with the MI100 results, we modify the plotting script plots/solver-bandwidth.plot.jsonata in our fork of ginkgo-data on the TOMS-interface-hip branch so that MI100 results are plotted instead of the A100 results. We provide the exact changes needed as a diff in Listing 3.

Upon inspection of the results generated from Guyot, we note that the achieved memory bandwidth for the thermal2, atmosmodj, and StocF1465 matrices are comparable to the results generated by Anzt et al [2]. However, for the other matrices, we note that our reproduced results achieve a memory bandwidth that is approximately 15% higher than original results. As we pointed out in Section 1, the NVIDIA A100 GPU available on Guyot has a higher peak memory bandwidth than the NVIDIA A100 GPU utilized by Anzt et al. Indeed, our run of the BabelStream TRIAD benchmark indicated that the Guyot A100 could achieve a 19% higher memory bandwidth than the other

A100 (1,732 GB/s vs 1,399 GB/s). Furthermore, the vectors associated with the first three matrices are small enough to fit into the cache of the Guyot A100, which is the same size as the cache of the A100 used in the published article (so the increased memory bandwidth has a limited effect) [2]. Therefore, the discrepancy with the seven larger matrices is not surprising, and we look at performance as a percentage of the STREAM bandwidth instead. When we do this comparison, we see that the published results and newly generated results are similar as both achieve between 65% and 85% of the STREAM bandwidth recorded for their respective version of the A100.

```
diff --git a/plots/solver-bandwidth.plot.jsonata b/plots/solver-bandwidth.
1
        plot.jsonata
   index 09af1c0580..bdc349de70 100644
2
   --- a/plots/solver-bandwidth.plot.jsonata
3
   +++ b/plots/solver-bandwidth.plot.jsonata
4
   @@ -2,7 +2,7 @@
5
    $data_hip := content[dataset.executor="hip" and dataset.system="
6
        MI100_solvers"];
    $data_cuda := content[dataset.executor="cuda" and dataset.system="
7
       A100_solvers"];
8
   -$solvers := $data_cuda.solver~>$keys();
9
   +$solvers := $data_hip.solver~>$keys();
10
11
    $matrices := [
12
    "thermal2"
13
14
   @@ -46,7 +46,7 @@ $memops := function($name, $n, $nnz, $it, $k, $vtype,
       $itype) {
15
    $plot := $solvers~>$map(function($v, $i) {{
16
    "label": $v,
17
   - "data": $data_cuda.{
18
19
   + "data": $data_hip.{
    "x": problem.name,
20
    "y": $memops($v, problem.rows, problem.nonzeros, (solver~>$lookup($v)).apply
21
        .iterations, 100, 8, 4) / ((solver~>$lookup($v)).apply.time/100000000)
22
    },
   @@ -58,7 +58,7 @@ $plot := $solvers~>$map(function($v, $i) {{
23
24
    }});
25
    $bw := $matrices~>$map(function($v, $i) {
26
   - $get_bandwidth("cuda")
27
   + $get_bandwidth("hip")
28
29
    });
30
31
    {
   @@ -82,7 +82,7 @@ $bw := $matrices~>$map(function($v, $i) {
32
    },
33
    "title": {
34
   "display": true,
35
   - "text": "Bandwidth of selected problems for Ginkgo solvers on A100(CUDA)",
36
   + "text": "Bandwidth of selected problems for Ginkgo solvers on MI100(Hip)",
37
    "fontSize": 20
38
39
    },
    "tooltips": {
40
```

Listing 3. A diff showing the changes made to the ginkgo-data plotting script in order to plot the M100/HIP results.



Fig. 1. Reproduction of Figure 8 from Anzt et al. [2] using the Guyot system. The plot shows the memory efficiency of Ginkgo's Krylov solvers on an NVIDIA A100 GPU. The matrices are sorted by number of rows. When compared to the published results, the new ones are similar once the increased memory bandwidth of the Guyot A100 GPU is accounted for.



Bandwidth of selected problems for Ginkgo solvers on MI100(hip)

Fig. 2. Reproduction of Figure 9 from Anzt et al. [2] using the Spock system. The plot shows the memory efficiency of Ginkgo's Krylov solvers on the AMD MI100 GPU. The matrices are sorted by number of rows. These newly reproduced results are nearly identical to the published results.

Examining the reproduced results we generated with an AMD MI100 GPU on Spock, we see that they are nearly identical to the memory bandwidth values presented by Anzt et al. in [2]. For all of the matrices, roughly 50% of the STREAM bandwidth is achieved.

Figures 1 and 2 show our reproductions of Figures 8 and 9 of [2]. Since both the results generated with the NVIDIA A100 GPU and AMD MI100 GPU are comparable to the published results, we consider the published results successfully reproduced.

3 CONCLUSION

Anzt et al. present Ginkgo, a modern C++ sparse linear operator algebra framework that targets GPU accelerators, in [2]. Using the instructions provided by the authors in Annex A of [2], we were able to install all of the software needed on two different computers: Guyot and Spock. We utilized Guyot for experiments that require CUDA and an NVIDIA A100 GPU and Spock for experiments that required HIP and an AMD MI100 GPU. All of the software was freely and openly available. Once the software was installed, we were able to continue using the instructions provided by the authors, with only a few deviations, to reproduce the experimental data. Finally, we utilized the Ginkgo Performance Explorer plotting tool to recreate the plots in Figures 8 and 9 of the published article [2]. After analyzing the newly generated results and comparing them to the published results, the reviewer deems the published results to be reproducible.

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