

# Performance Analysis of GPU-accelerated Applications with HPCToolkit

John Mellor-Crummey Rice University Oct 29-31, 2024

#### **Outline**

- Introduction to HPCToolkit performance tools
  - —Overview of HPCToolkit components and their workflow
  - —HPCToolkit's graphical user interfaces
- Analyzing the performance of GPU-accelerated codes with HPCToolkit
  - —GAMESS (OpenMP)
  - —Quicksilver (CUDA)
  - —PeleC (AMReX)
  - —LAMMPS at Exascale (Kokkos)
- Coming attractions
- Hands-on materials



#### **Hands-on Materials**

- Downloading and installing hpcviewer on your laptop
- Using hpcviewer on polaris
- Collecting performance data with HPCToolkit on turnkey examples
- Troubleshooting measurement and analysis with HPCToolkit



#### Linux Foundation's HPCToolkit Performance Tools

Collect profiles and traces of unmodified parallel CPU and GPU-accelerated applications

Understand where an application spends its time and why

call path profiles associate metrics with application source code contexts

analyze instruction-level performance within GPU kernels and attribute it to your source code

hierarchical traces to understand execution dynamics

Parallel programming models

across nodes: MPI, SHMEM, UPC++, ...

within nodes: OpenMP, Kokkos, RAJA, HIP, DPC++, Sycl, CUDA, OpenACC, ...

Languages

C, C++, Fortran, Python, ...

Hardware

CPU cores and GPUs within a node

CPU: x86 64, Power, ARM

GPU: NVIDIA, AMD, Intel

all of the nodes in Polaris



# Why HPCToolkit?

#### Measure and analyze performance of CPU and GPU-accelerated applications

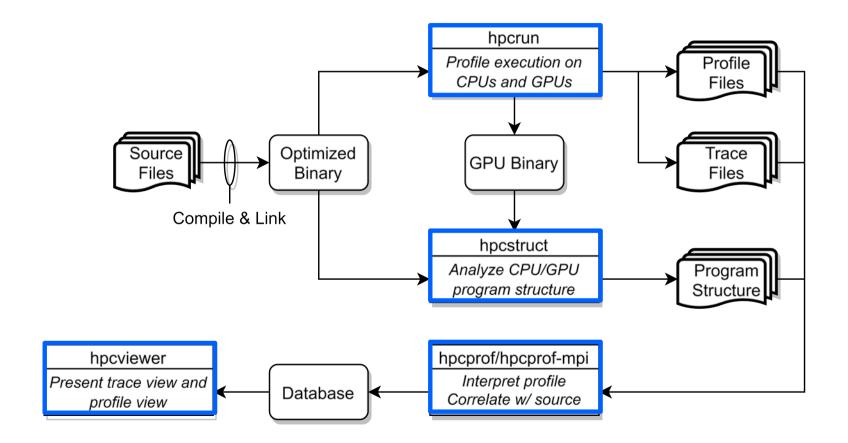
- Easy: profile unmodified application binaries
- Fast: low-overhead measurement
- Informative: understand where an application spends its time and why
  - —call path profiles associate metrics with application source code contexts
  - —optional hierarchical traces to understand execution dynamics
- Broad audience
  - —application developers
  - —framework developers
  - —runtime and tool developers
- Unlike vendor tools, works with a wide range of CPUs and GPUs



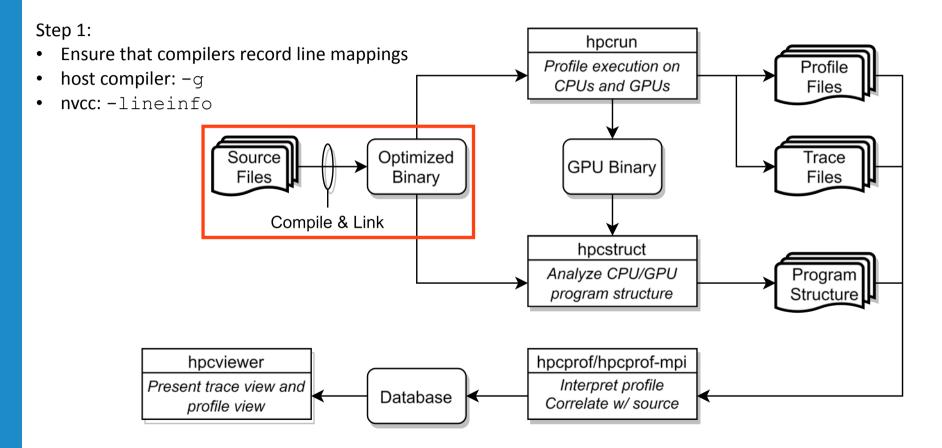
#### How does HPCToolkit Differ from NVIDIA's Tools?

- NVIDIA NSight Systems
  - —tracing of CPU and GPU streams
  - —analyze traces when you open them with the GUI
    - long running traces are huge and thus extremely slow to analyze, limiting scalability
  - —designed for measurement and analysis within a node
- NVIDIA NSight Compute
  - —detailed measurement of kernels with counters and execution replay
  - —very slow measurement
  - —flat display of measurements within GPU kernels
- HPCToolkit
  - —supports more scalable tracing than Nsight Systems
    - measure exascale executions across many GPUs and nodes
  - —scalable, parallel post-mortem analysis vs. non-scalable in-GUI analysis
  - —detailed reconstruction of estimates for calling context profiles within GPU kernels











#### Step 2: hpcrun hpcrun collects call path profiles (and Profile execution on **Profile** optionally, traces) of events of interest CPUs and GPUs **Files** Optimized Trace **GPU Binary** Files **Binary Files** Compile & Link hpcstruct Analyze CPU/GPU Program program structure Structure hpcprof/hpcprof-mpi hpcviewer Interpret profile Present trace view and Database Correlate w/ source profile view



# Measurement of CPU and GPU-accelerated Applications

- Sampling using Linux timers and hardware counter overflows on the CPU
- Callbacks when GPU operations are launched and (sometimes) completed
- Event stream for GPU operations
- PC Samples: NVIDIA (in progress: AMD, Intel)
- Binary instrumentation of GPU kernels on Intel GPUs for fine-grain measurement



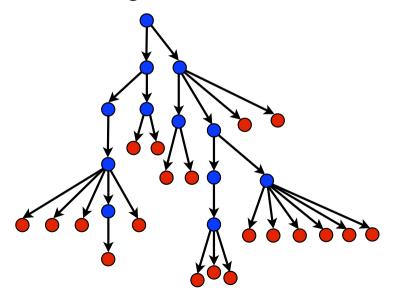
# **Call Stack Unwinding to Attribute Costs in Context**

- Unwind when timer or hardware counter overflows
  - —measurement overhead proportional to sampling frequency rather than call frequency
- Unwind to capture context for events such as GPU kernel launches

# Call path sample

return address
return address
return address
instruction pointer

#### Calling context tree



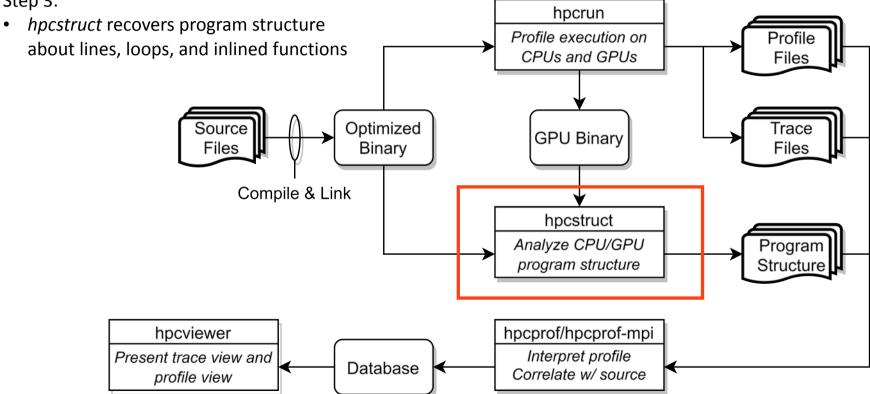


# hpcrun: Measure CPU and/or GPU activity

 GPU profiling —hpcrun -e qpu=xxx <app> .... xxx E {nvidia, amd, opencl, level0} GPU PC sampling (NVIDIA GPU only) —hpcrun -e qpu=nvidia,pc <app> CPU and GPU Tracing (in addition to profiling) —hpcrun -e CPUTIME -e qpu=xxx -tt <app> Use hpcrun with MPI on Polaris -mpiexec -n <ranks> ... hpcrun -e gpu=xxx <app>



#### Step 3:





#### hpcstruct: Analyze CPU and GPU Binaries Using Multiple Threads

Usage

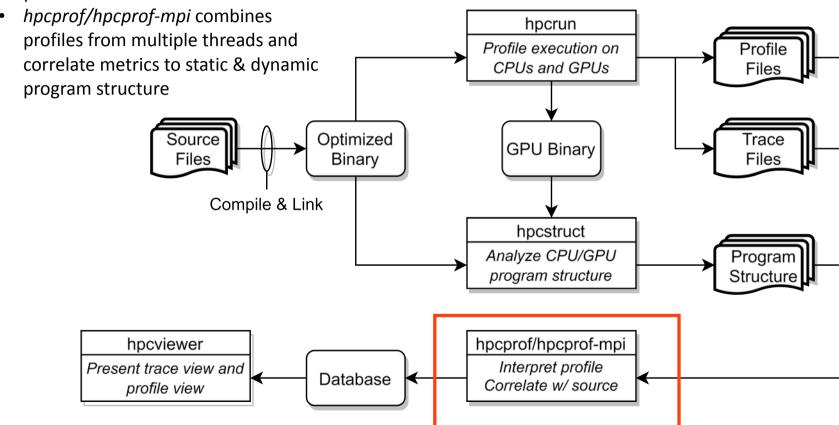
```
hpcstruct [--gpucfg yes] <measurement-directory>
```

- What it does
  - Recover program structure information
    - Files, functions, inlined templates or functions, loops, source lines
  - In parallel, analyze all CPU and GPU binaries that were measured by HPCToolkit
    - —typically analyze large application binaries with 16 threads
    - —typically analyze multiple small application binaries concurrently with 2 threads each
  - Cache binary analysis results for reuse when analyzing other executions

NOTE: --gpucfg yes needed only for analysis of GPU binaries for interpreting PC samples on NVIDIA GPUs



#### Step 4:





#### hpcprof/hpcprof-mpi: Associate Measurements with Program Structure

Analyze data from modest executions with multithreading (moderate scale)

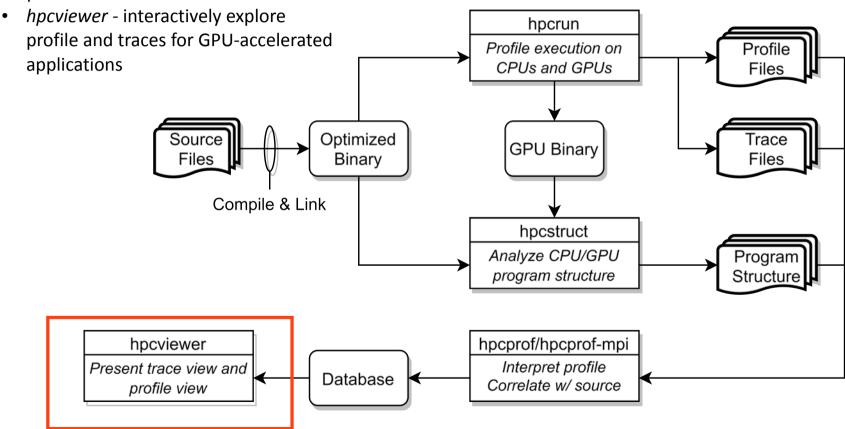
```
hpcprof <measurement-directory>
```

• Analyze data from large executions with distributed-memory parallelism + multithreading (large scale)

```
mpiexec -n ${NODES} --ppn 1 -depth=128 \
    hpcprof-mpi <measurement-directory>
```

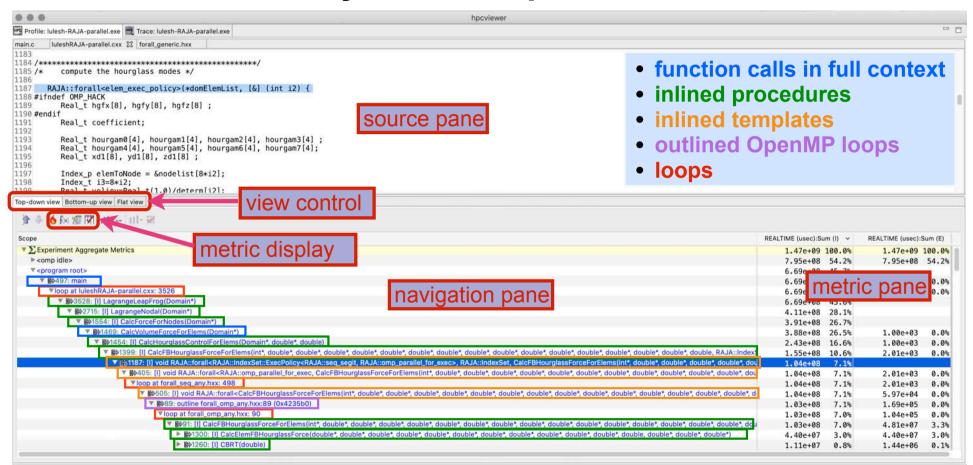


#### Step 4:





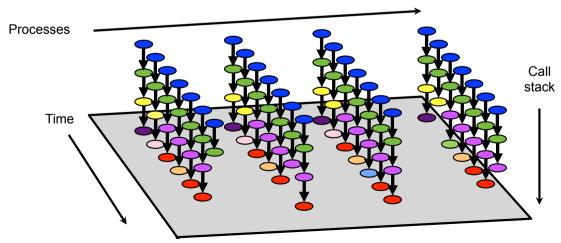
# **Code-centric Analysis with hpcviewer**





# **Understanding Temporal Behavior**

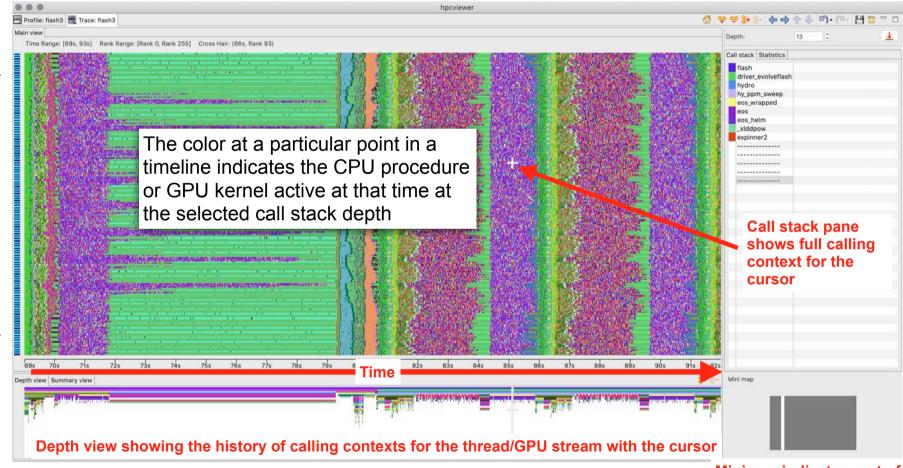
- Profiling compresses out the temporal dimension
  - —Temporal patterns, e.g. serial sections and dynamic load imbalance are invisible in profiles
- What can we do? Trace call path samples
  - —N times per second, take a call path sample of each thread
  - —Organize the samples for each thread along a time line
  - —View how the execution evolves left to right
  - —What do we view? assign each procedure a color; view a depth slice of an execution





# Pl ranks, OpenMP Threads, GPU streams

# Time-centric Analysis with hpcviewer





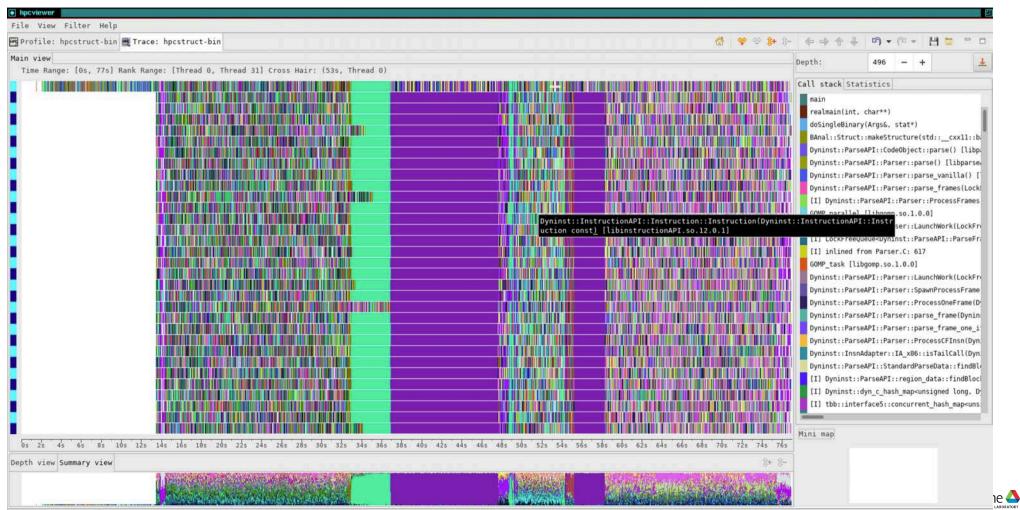
Argonne Leadership Compu

#### **Enhancements for Exascale**

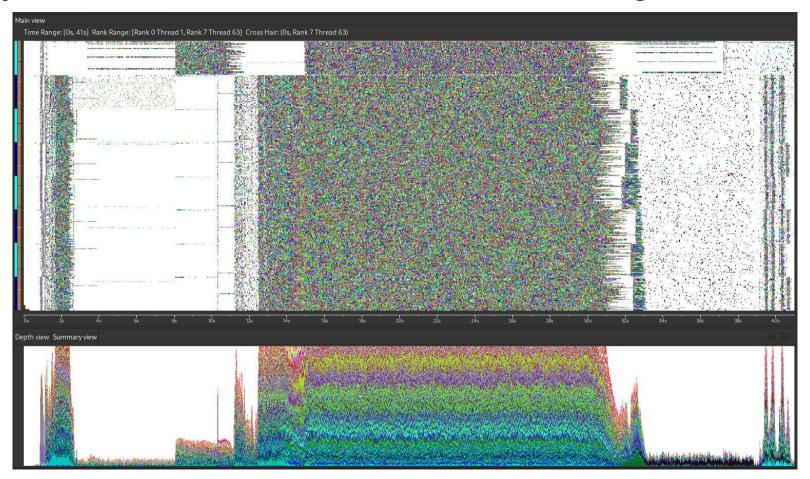
- Measurement
  - profile and trace GPU-accelerated applications on AMD, Intel, and NVIDIA GPUs
- Binary analysis
  - parallel analysis of CPU and GPU binaries to speed recovery of program structure
- Performance analysis and attribution
  - MPI + OpenMP highly parallel analysis of measurement data at exascale
  - sparse representations observed to reduce performance analysis results by > 1000x
  - detailed attribution of PC samples to rich calling contexts within GPU kernels
- Presentation
  - interactive display profiles and terabytes of traces from exascale executions



#### hpcstruct Example: Analyze 7.7GB TensorFlow library (170MB text) in 77s



#### Analyze 38.1GB data for 2K MPI ranks + 2K GPUs using 1K threads in 41s





#### **Case Studies**

- ExaWind
- GAMESS (OpenMP)
- Quicksilver (CUDA)
- PeleC (AMReX)
- LAMMPS (Kokkos) at exascale



### **ExaWind: Wakes from Three Turbines over Time**

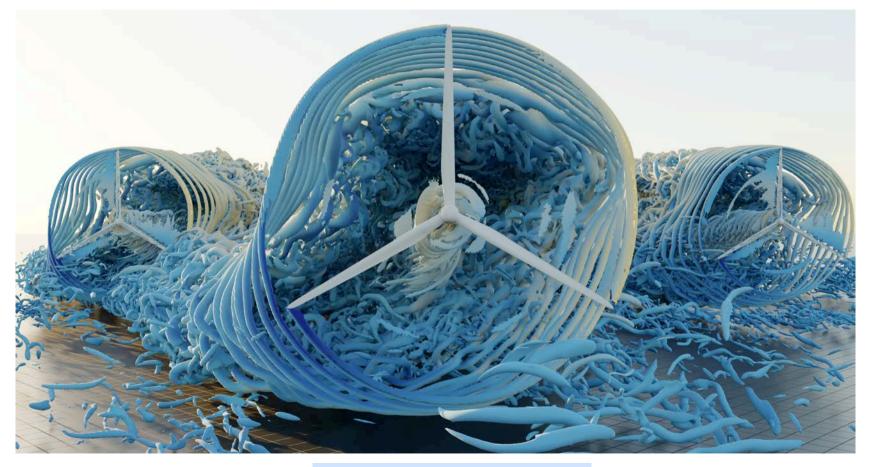




Figure credit: Jon Rood, NREL

#### **ExaWind: Visualization of a Wind Farm Simulation**





#### **ExaWind: Execution Traces on Frontier Collected with HPCToolkit**

Traces on roughly ~70K MPI ranks for ~17minutes

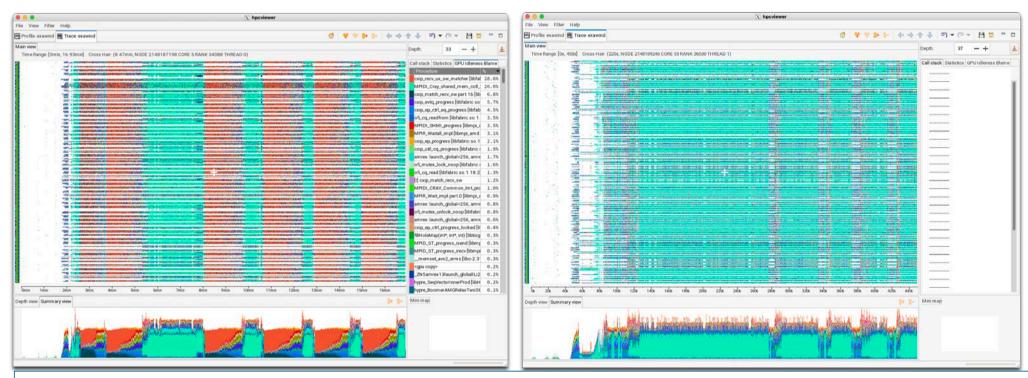


Figure credits: Jon Rood, NREL

\*replaced non-blocking send/recv with ialltoallv

#### **ExaWind Testimonials for HPCToolkit**

I just wanted to mention we've been using HPCToolkit a lot for our ExaWind application on Frontier, which is a hugely complicated code, and your profiler is one of the only ones we've found that really lets us easily instrument and then browse what our application is doing at runtime including GPUs. As an example, during a recent hackathon we had, we improved our large scale performance by 24x by understanding our code better with HPCToolkit and running it on 1000s of nodes while profiling. We also recently improved upon this by 10% for our total runtime.

- Jon Rood NREL (5/31/2024)

One big thing for us is that we can't overstate how complicated ExaWind is in general, and how complicated it is to build, so finding out that HPCToolkit could easily profile our entire application without a ton of instrumentation during the build process, and be able to profile it on a huge amount of Frontier with line numbers and visualizing the trace was really amazing to us.

- Jon Rood NREL (6/3/2024)



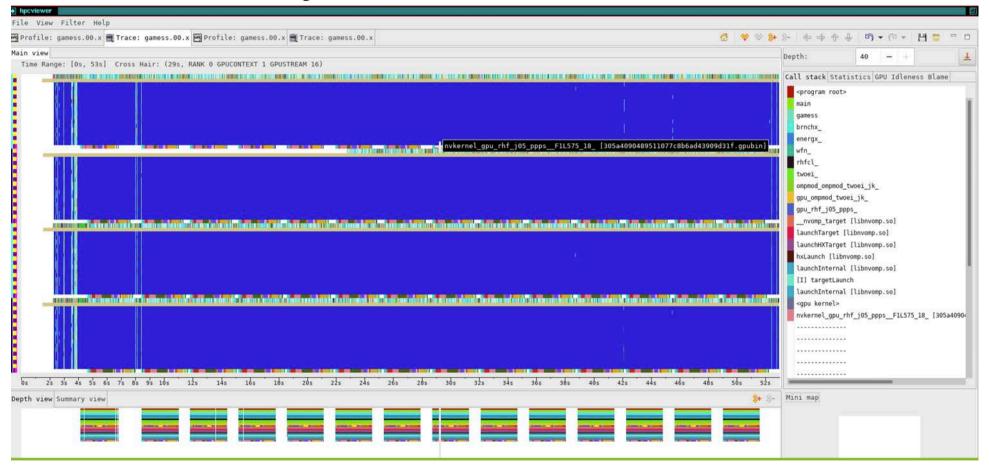
# **Case Study: GAMESS**

- General Atomic and Molecular Electronic Structure System (GAMESS)
  - —general *ab initio* quantum chemistry package
- Calculates the energies, structures, and properties of a wide range of chemical systems
- Experiments
  - GPU-accelerated nodes at a prior Perlmutter hackathon
    - Single node with 4 GPUs
    - Five nodes with 20 GPUs

Perlmutter node at a glance

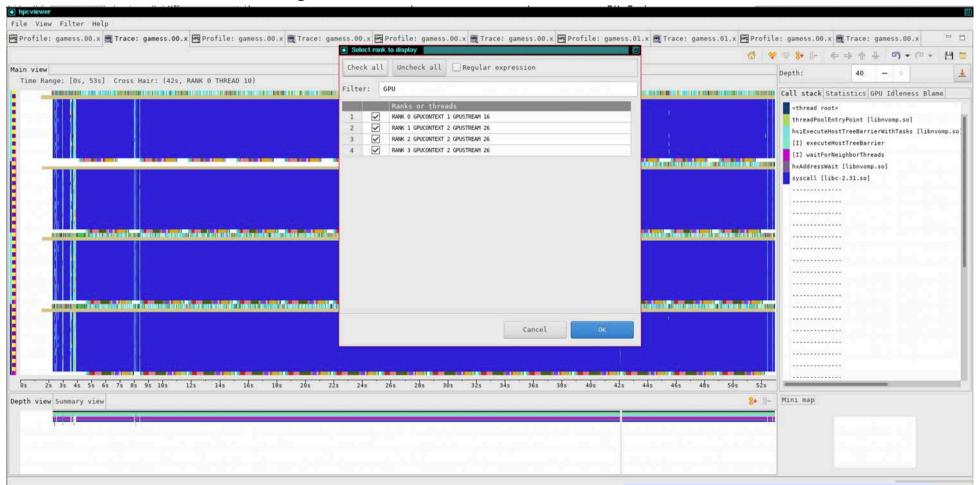
AMD Milan CPU 4 NVIDIA A100 GPUs 256 GB memory



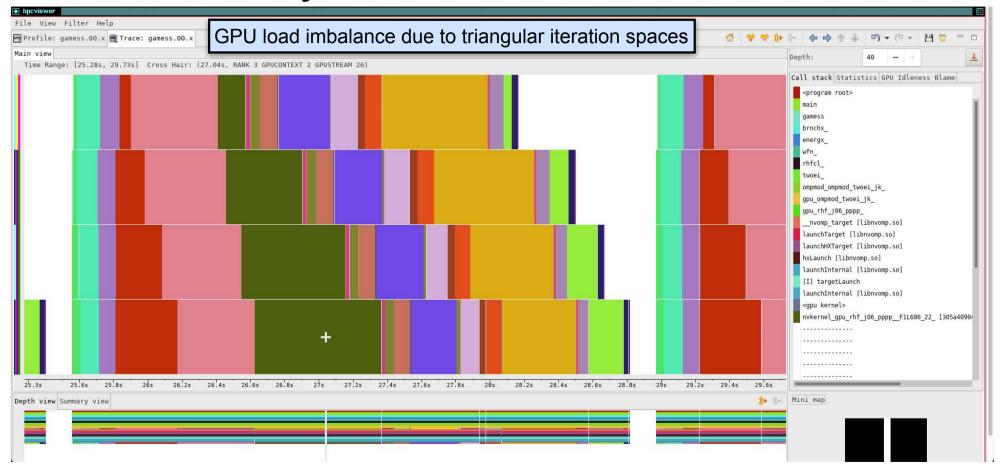




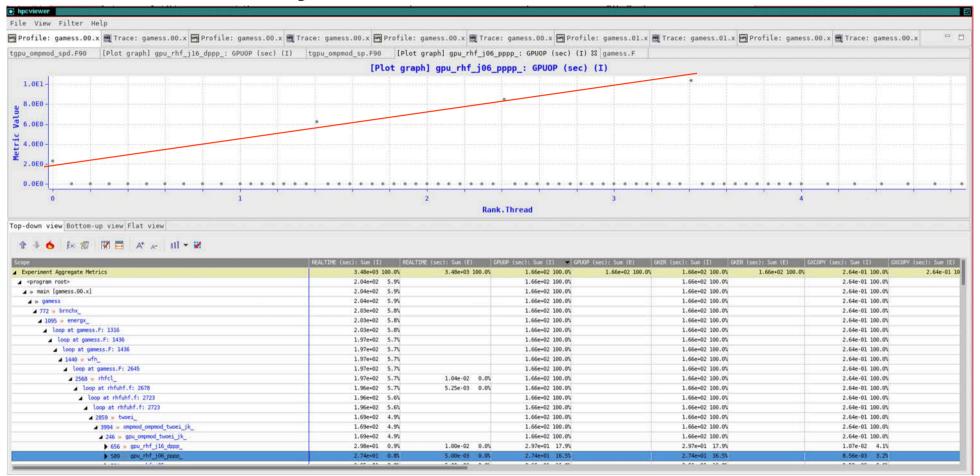
All CPU threads and GPU streams





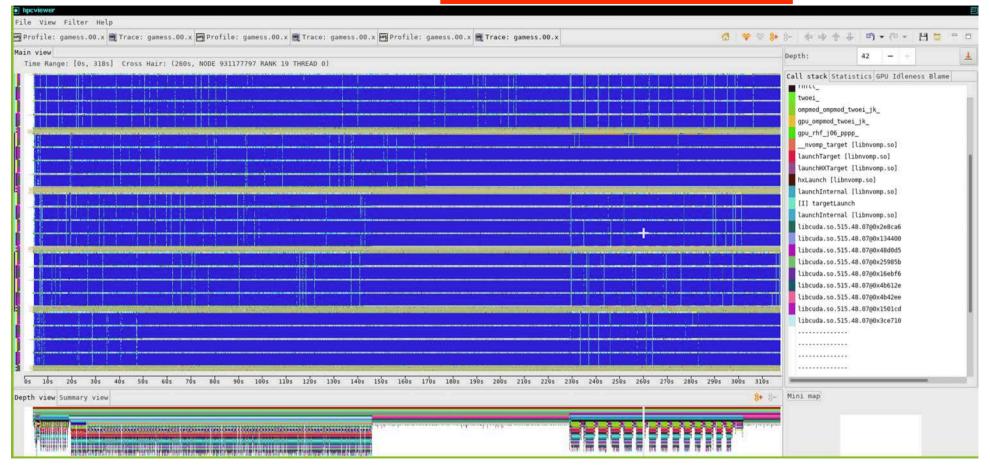


GPU streams: 1 iteration





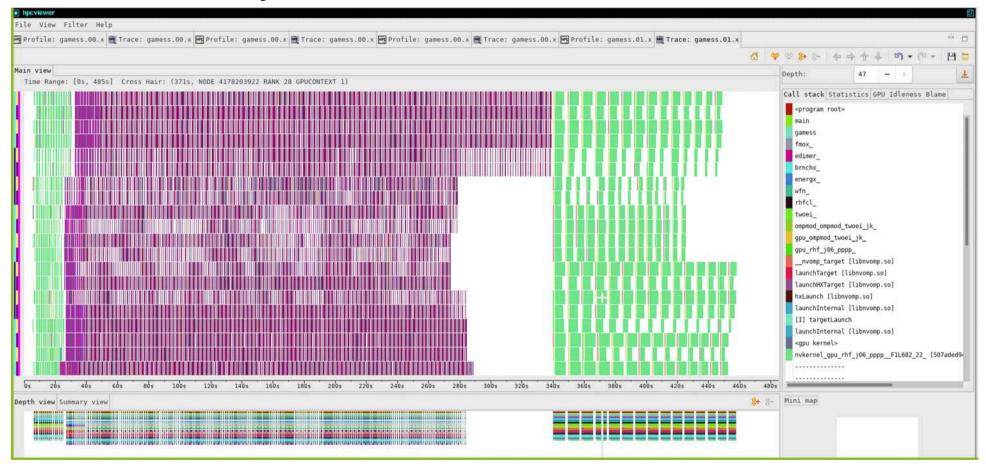
# Time-centric Analysis: GAMESS 5 nodes, 40 ranks, 20 GPUs on Perlmutter



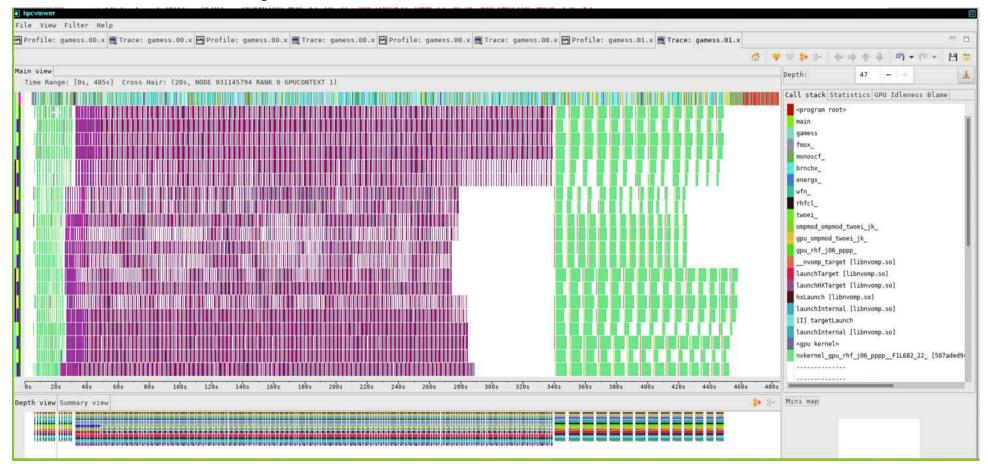
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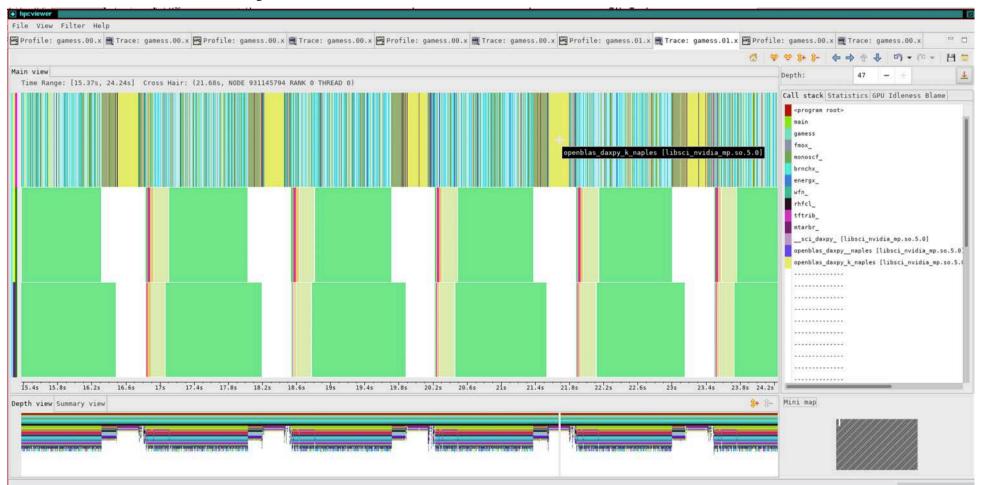






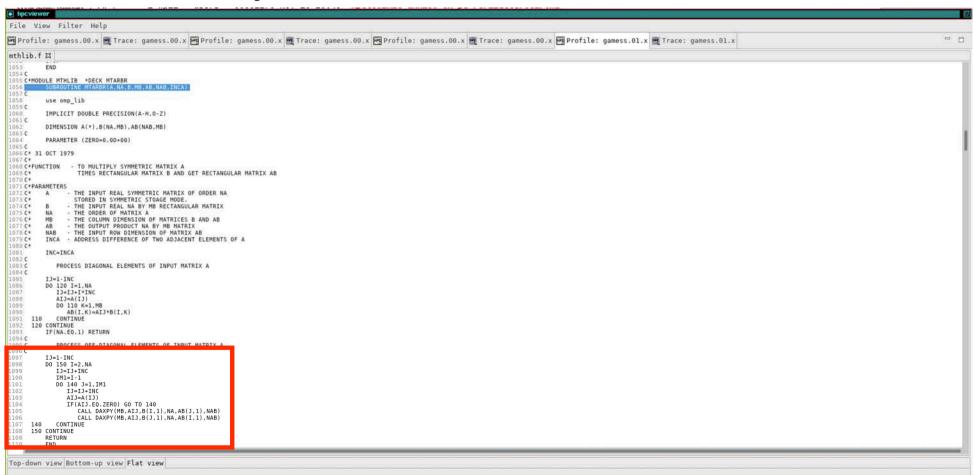




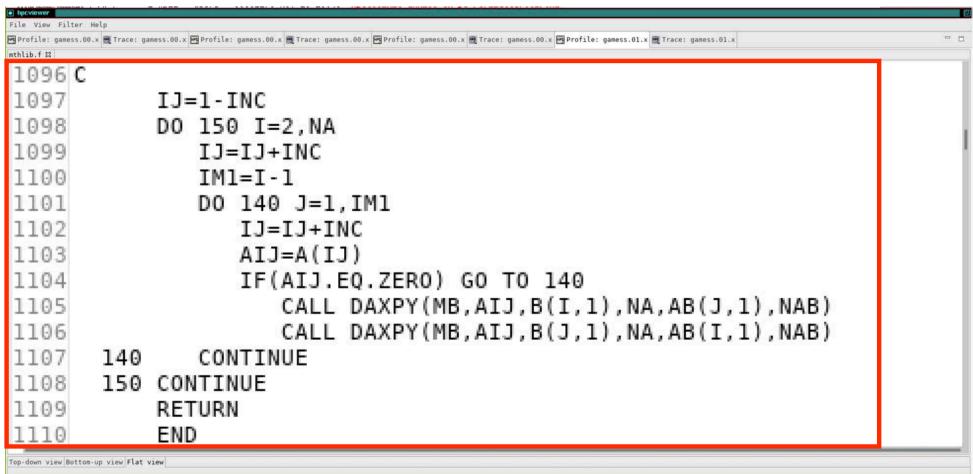




```
File View Filter Help
Profile: gamess.00.x Trace: gamess.00.x Profile: ga
 mthlib.f ₩
    1955 C*MODULE MTHLIB *DECK MTARBR
                         IMPLICIT DOUBLE PRECISION(A-H, 0-Z)
   1061 C
                         DIMENSION A(*), B(NA, MB), AB(NAB, MB)
   1063 C
                         PARAMETER (ZERO=0.0D+00)
   1966 C* 31 OCT 1979
   1067 C+
                                         - TO MULTIPLY SYMMETRIC MATRIX A
   1069 C*
                                                TIMES RECTANGULAR MATRIX B AND GET RECTANGULAR MATRIX AB
   1070 C*
    071 C*PARAMETERS
                                       - THE INPUT REAL SYMMETRIC MATRIX OF ORDER NA
                                              STORED IN SYMMETRIC STOAGE MODE.
                                         - THE INPUT REAL NA BY MB RECTANGULAR MATRIX
                                     - THE ORDER OF MATRIX A
                                     - THE COLUMN DIMENSION OF MATRICES B AND AB
                                       - THE OUTPUT PRODUCT NA BY MB MATRIX
                                    - THE INPUT ROW DIMENSION OF MATRIX AB
                         INCA - ADDRESS DIFFERENCE OF TWO ADJACENT ELEMENTS OF A
                         INC=INCA
    1082 C
                                 PROCESS DIAGONAL ELEMENTS OF INPUT MATRIX A
    984 C
                         IJ=1-INC
                          DO 120 I=1.NA
                                IJ=IJ+I*INC
                                  AIJ=A(IJ)
                                        AB(I,K)=AIJ*B(I,K)
                         IF(NA.EQ.1) RETURN
                                 PROCESS OFF-DIAGONAL ELEMENTS OF INPUT MATRIX A
                         IJ=1-INC
                         DO 150 I=2,NA
                                IJ=IJ+INC
                                 TM1=T-1
                                 DO 140 J=1, IM1
                                        AIJ=A(IJ)
                                        IF(AIJ.EQ.ZERO) GO TO 140
                                                CALL DAXPY(MB.AIJ.B(I.1),NA.AB(J.1),NAB)
                                                CALL DAXPY(MB, AIJ, B(J, 1), NA, AB(I, 1), NAB)
              150 CONTINUE
                         RETURN
  Top-down view Bottom-up view Flat view
```







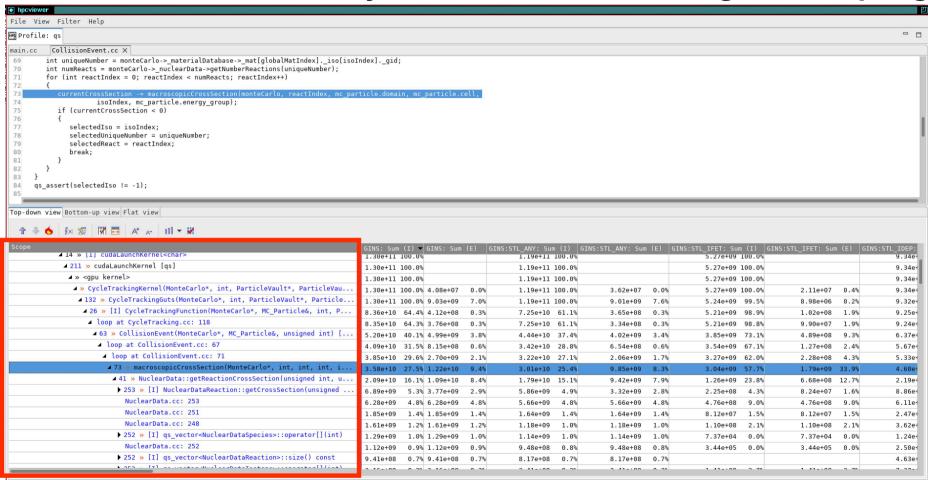


# Case Study: Quicksilver

- Proxy application that represents some elements of LLNL's Mercury workload
- Solves a simplified dynamic Monte Carlo particle transport problem
  - Attempts to replicate memory access patterns, communication patterns, and branching or divergence of Mercury for problems using multigroup cross sections
- Parallelization: MPI, OpenMP, and CUDA
- Performance Issues
  - load imbalance (for canned example)
  - latency bound table look-ups
  - a highly branchy/divergent code path
  - poor vectorization potential



### Quicksilver: Detailed analysis within a Kernel using PC Sampling



### Quicksilver: Detailed analysis within a Kernel using PC Sampling

```
■ 14 » [1] cudaLaunchKernet<char>

▲ 211 » cudaLaunchKernel [qs]

→ » <apu kernel>

   A » CycleTrackingKernel(MonteCarlo*, int, ParticleVault*, ParticleVau...

▲ 132 » CycleTrackingGuts(MonteCarlo*, int, ParticleVault*, Particle...
     ▲ 26 » [I] CycleTrackingFunction(MonteCarlo*, MC_Particle&, int, P...

▲ loop at CycleTracking.cc: 118

▲ 63 » CollisionEvent(MonteCarlo*, MC Particle&, unsigned int) [...

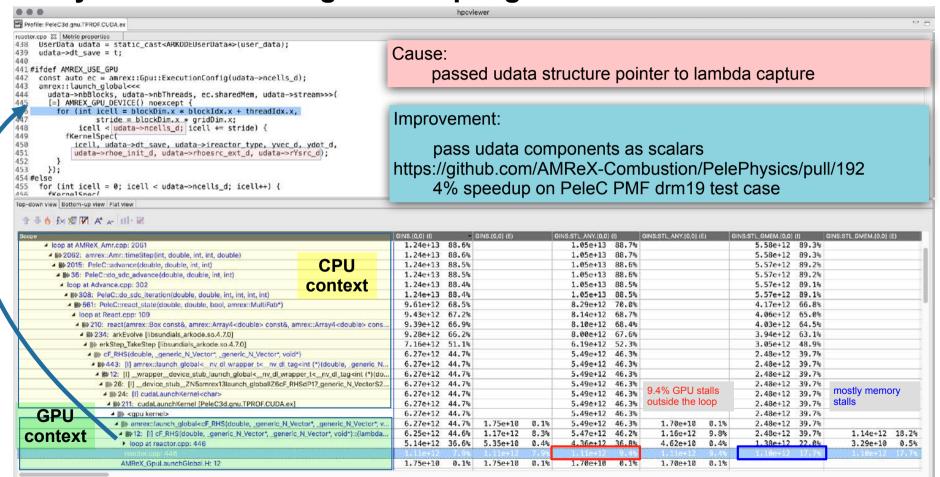
■ loop at CollisionEvent.cc: 67

■ loop at CollisionEvent.cc: 71
           4 73 » macroscopicCrossSection(MonteCarlo*, int, int, int, i...

▲ 41 » NuclearData::getReactionCrossSection(unsigned int, u...
              253 » [I] NuclearDataReaction::getCrossSection(unsigned ...
                NuclearData.cc: 253
                NuclearData.cc: 251
                NuclearData.cc: 248
              252 » [I] qs_vector<NuclearDataSpecies>::operator[](int)
                NuclearData.cc: 252
              252 » [I] qs vector<NuclearDataReaction>::size() const
```



### Analysis of PeleC using PC Sampling on an NVIDIA GPU



# **Key Metrics for GPU Kernels**

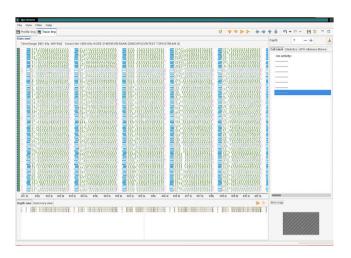
- GPUOP: GPU operation time (kernel launch, copies, etc.)
- GXCOPY:\* GPU copies of various kinds
- GKER: GPU kernel time
- GKER:FGP\_ACT: fine grain parallelism actual (active warps per SM)
- GKER:FGP\_MAX: maximum possible fine-grain parallelism (max warps per SM)
- GKER:BLK\_THR: threads per block
- GKER:BLK\_SM: block shared memory
- GKER:OCC\_THR: theoretical thread occupancy

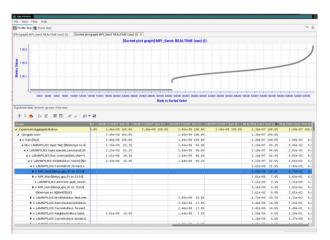


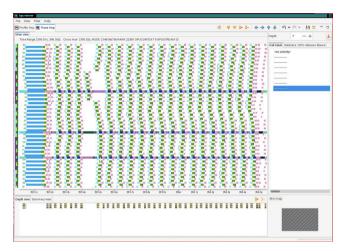
# Metrics for GPU Kernels with PC Samples

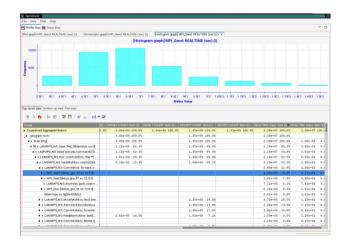
- GINS: GPU instructions
- GINS:STL\_ANY: GPU instruction stalls for any reason
- GINS:STL IFET: GPU instruction stalls for instruction fetch
- GINS:STL GMEM: GPU instruction stalls for global memory
- GINS:STL\_CMEM: GPU instruction stalls for constant memory
- GINS:STL\_IDEP: GPU instruction stalls for instruction dependences
- GINS:STL\_PIPE: GPU instruction pipeline stalls
- GINS:STL\_MTHR: GPU instruction stalls for memory throttling
- GSAMP:EXP: expected number of samples
- GSAMP:TOT: total number of samples recorded
- GSAMP:UTIL: GPU utilization = (PC samples expected) / (PC samples total)



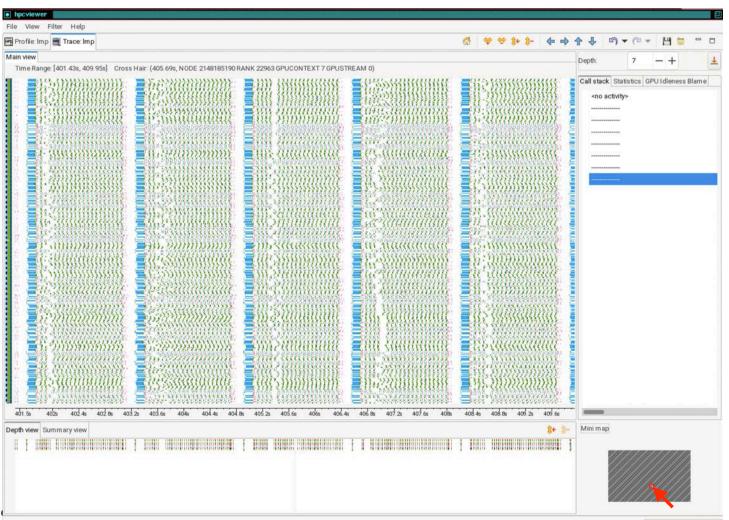




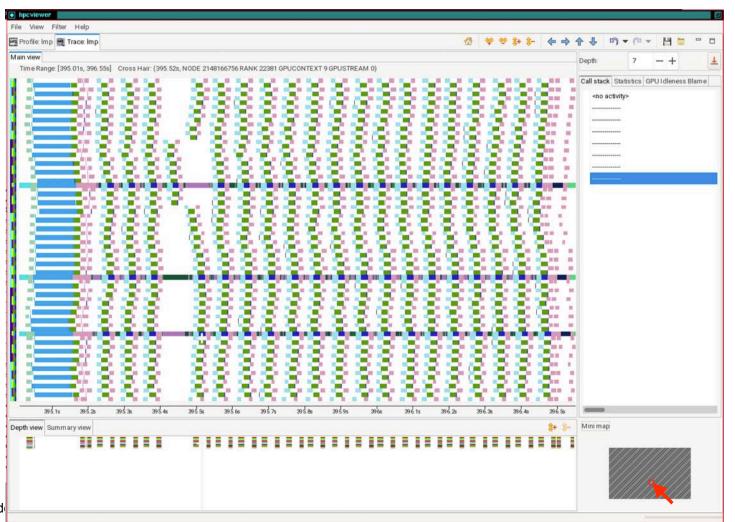




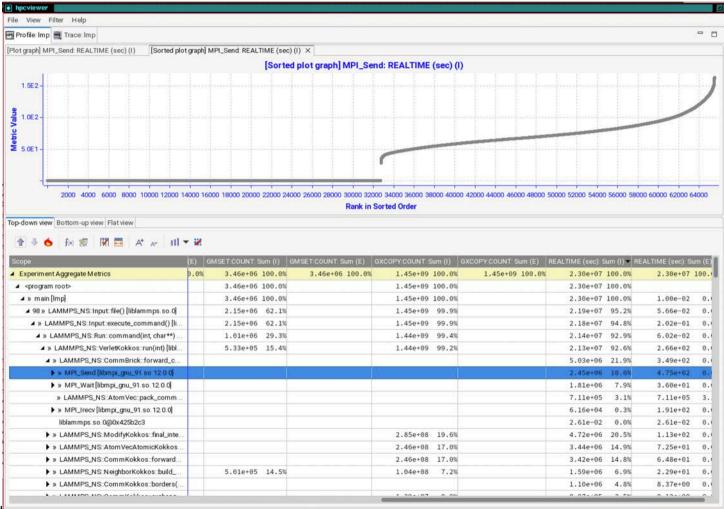




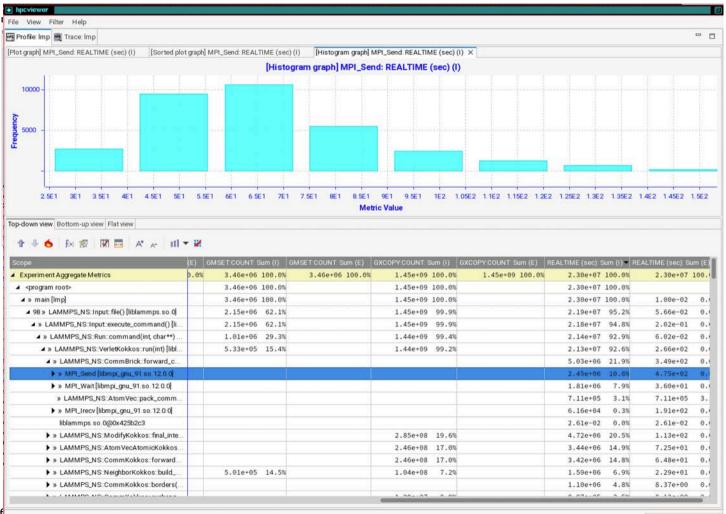








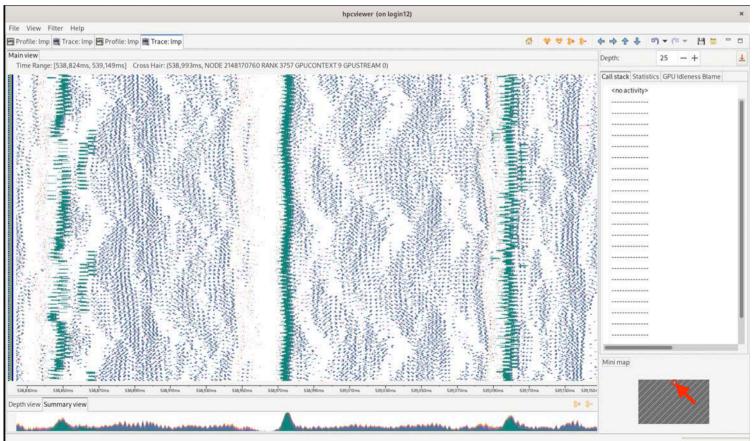






### LAMMPS on Frontier: 8K nodes, 64K MPI ranks + 64K GPU tiles

#### Kernel duration of microseconds





# **Coming Attractions**

- Integrated support for NVTX/ROCTX/Caliper/Kokkos Labels
- Python-based interface for analysis of performance results
- Support for instruction-level measurement and attribution on AMD and Intel GPUs



#### **HPCToolkit Resources**

- Documentation
  - —User manual
    - http://hpctoolkit.org/manual/HPCToolkit-users-manual.pdf
  - —Tutorial videos
    - http://hpctoolkit.org/training.html
    - recorded demo of GPU analysis of Quicksilver: https://youtu.be/vixa3hGDuGg
    - recorded tutorial presentation including demo with GPU analysis of GAMESS: https://vimeo.com/781264043
  - —Cheat sheet
    - https://gitlab.com/hpctoolkit/hpctoolkit/-/wikis/home
- Software
  - —Download hpcviewer GUI binaries for your laptop, desktop, cluster, or supercomputer
    - OS: Linux, Windows, MacOS
    - Processors: x86\_64, aarch64, ppc64le
    - http://hpctoolkit.org/download.html
  - —Install HPCToolkit on your Linux desktop, cluster, or supercomputer using Spack
    - http://hpctoolkit.org/software-instructions.html



# **Current Funding for HPCToolkit**

- Government
  - —Lawrence Livermore National Laboratory Subcontract B665301
  - —DOE Software Tools Ecosystem Project UT-Battelle Subcontract CW54422
  - —Argonne National Laboratory Subcontract 4F-60094
- Corporate
  - —Advanced Micro Devices
  - —TotalEnergies EP Research & Technology USA, LLC



# Downloading, Installing, and Using Hpcviewer on Your Laptop



### Hpcviewer Graphical User Interface on Your Laptop

### Prepare to explore performance data on your laptop

- Download and install hpcviewer: https://hpctoolkit.org/download.html
  - Select the right one for your laptop: MacOS (Apple Silicon, Intel), Windows, Linux
- User manual for hpcviewer: https://hpctoolkit.gitlab.io/hpcviewer





# **Viewing Performance Data**

- Copy a performance database directory to your laptop and open it locally
- Open a performance database on a remote system

Note: using a HPCViewer with a remote system presumes that hpcserver has already been installed on the remote system

hpcserver has been installed on Polaris





# **Configuring Hpcviewer Remote Access**

Run hpcviewer

From the file menu, select "Open remote database"

Fill in the hostname/IP address: polaris.alcf.anl.gov

Fill in your username on Polaris

Fill in the remote installation directory for hpcviewer's server: /soft/perftools/hpctoolkit/hpcserver

Select the authentication method: "Use password"

Click "OK"

Authenticate using your token as you normally do

Navigate to a database with the file chooser in /soft/perftools/hpctoolkit/examples: quicksilver, lammps

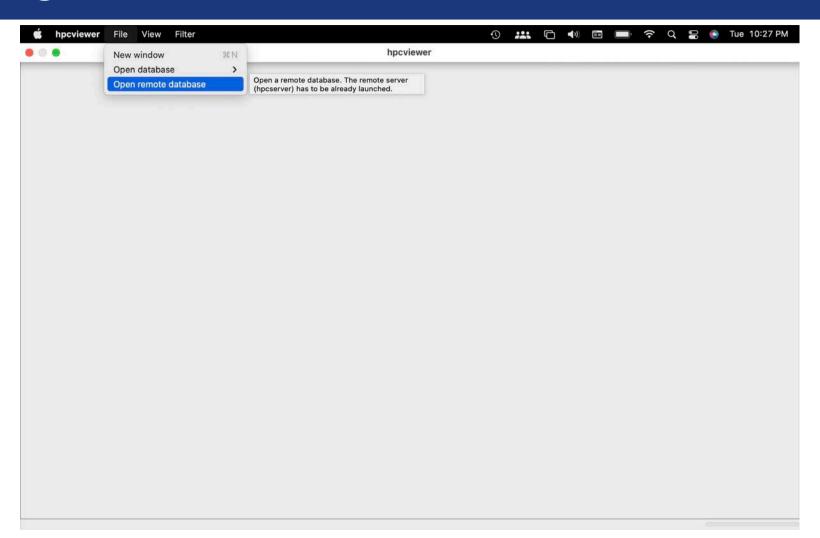
lammps: hpctoolkit-lmp.d hpctoolkit-lmp-pc.d

quicksilver: hpctoolkit-qs.d hpctoolkit-qs-pc.d

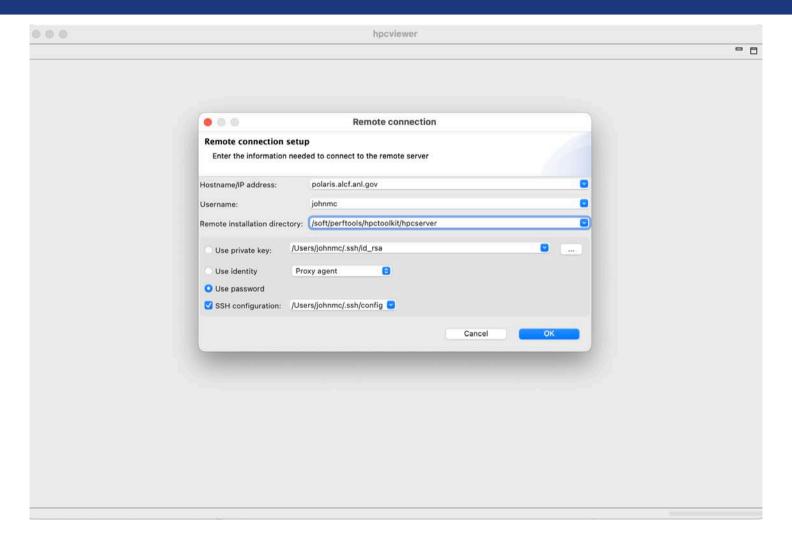




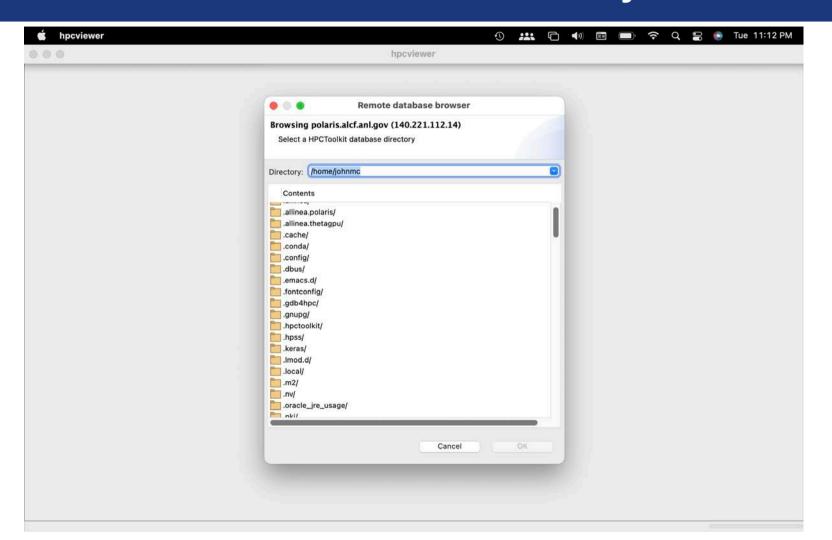
# **Opening a Remote Database**



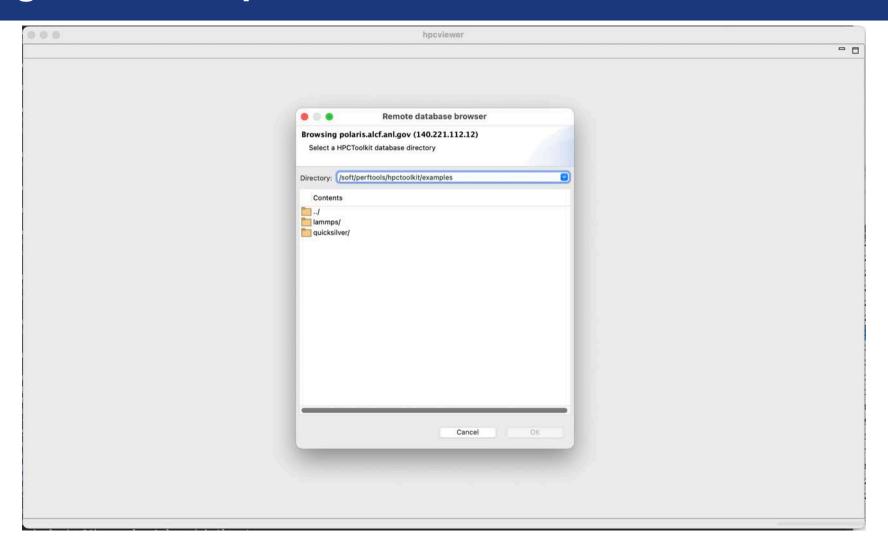
# **Configuring for use with Polaris**



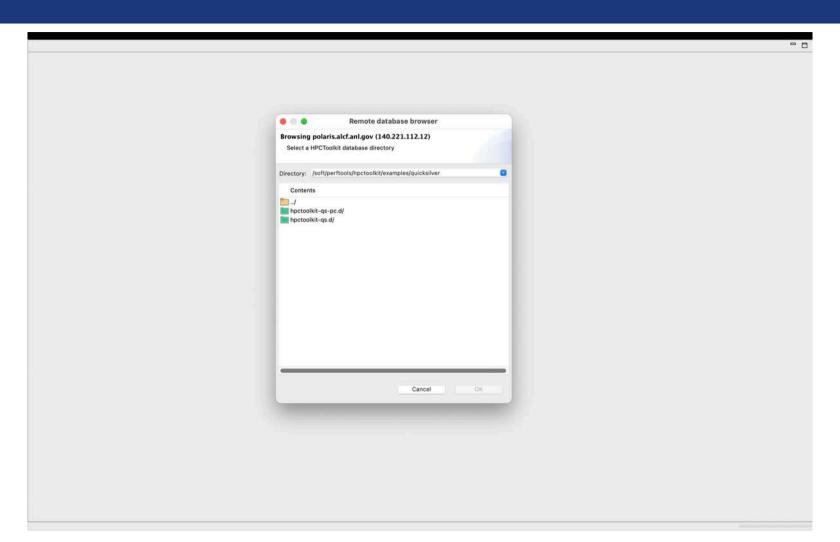
# **First View of Polaris: Your Home Directory**



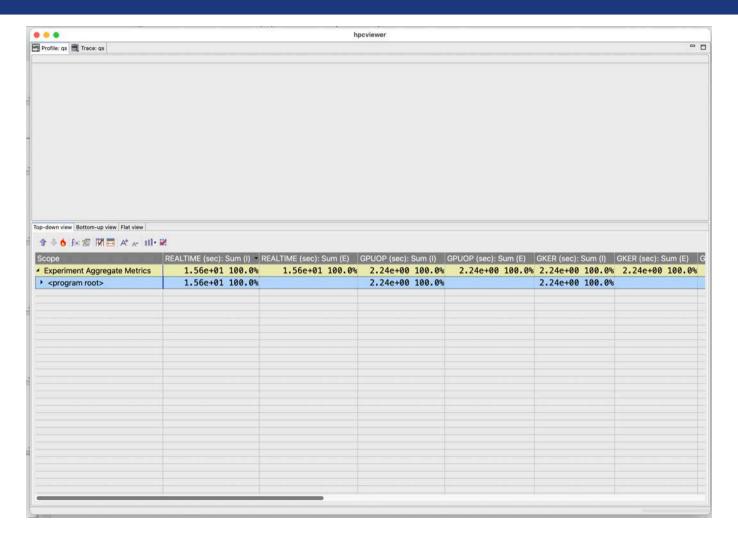
# **Navigate to Example Databases**



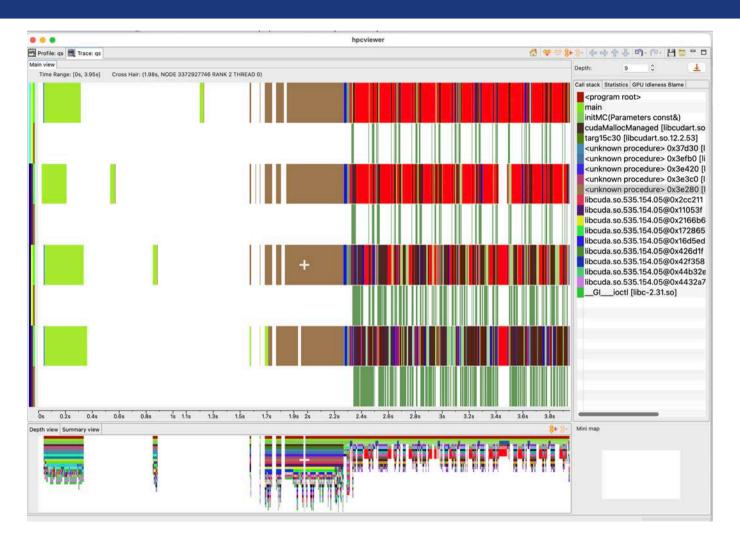
### **Select a Quicksilver Database with Traces**



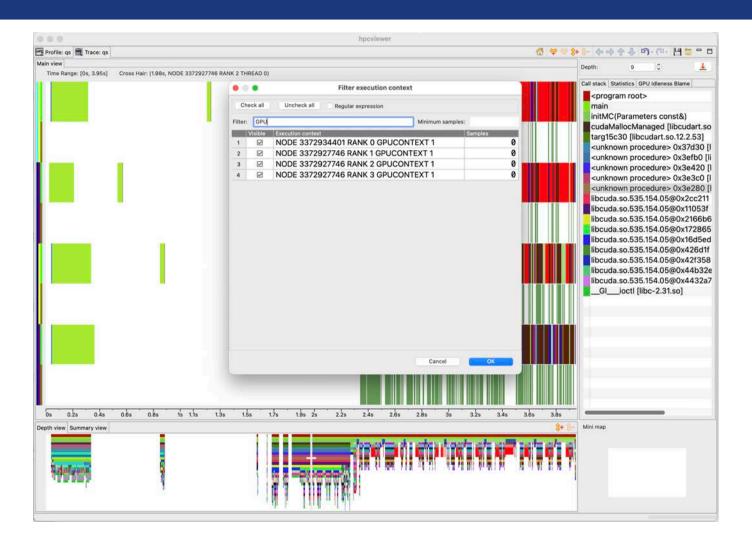
# After Selecting hpctoolkit-qs.d



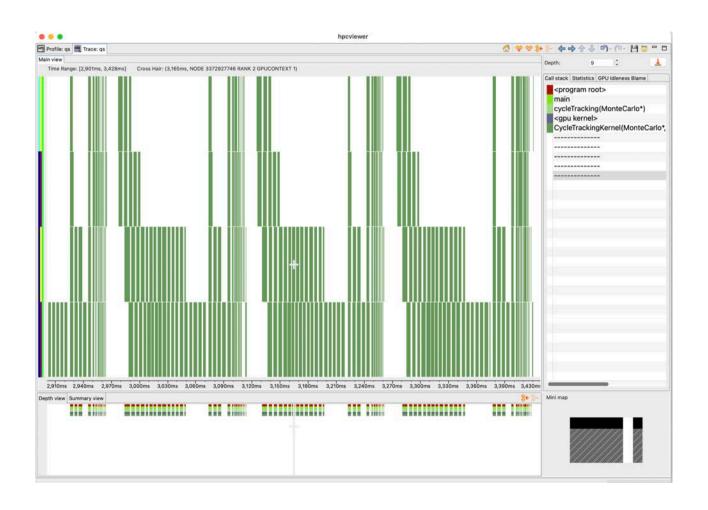
# Select the Tab "Trace: qs"



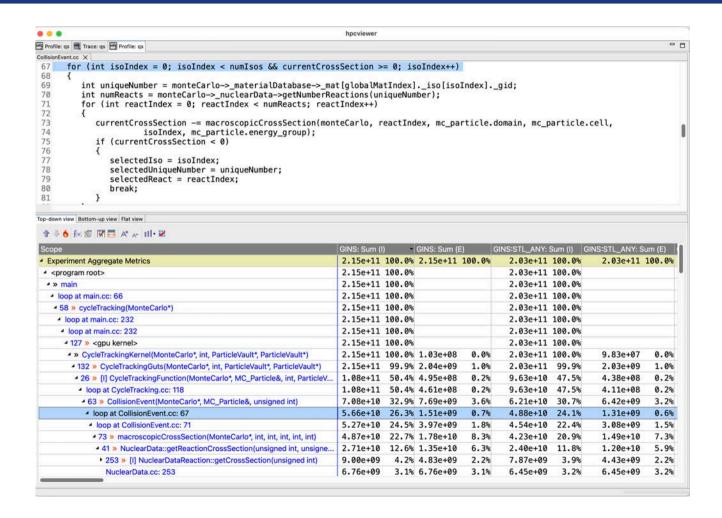
### Use the Filter to "Uncheck all" and Check "GPU" streams



### See Load Imbalance Across the Four GPUs



### The Profile View in the other "PC Sampling" Database



# **Using Hpcviewer on Polaris**



### Inspecting Precomputed Databases on Polaris

NOTE: Displaying performance results by running hpcviewer directly on Polaris requires you to be using an X11 desktop

Load hpctoolkit module to get hpcviewer on your path

```
module use /soft/perftools/hpctoolkit/modulefiles
module load hpctoolkit
```

- Use hpcviewer to open example database directories
  - Quicksilver

```
hpcviewer /soft/perftools/hpctoolkit/examples/quicksilver/hpctoolkit-qs.d hpcviewer /soft/perftools/hpctoolkit/examples/quicksilver/hpctoolkit-qs-pc.d
```

LAMMPS

```
hpcviewer /soft/perftools/hpctoolkit/examples/lammps/hpctoolkit-lmp.d hpcviewer /soft/perftools/hpctoolkit/examples/lammps/hpctoolkit-lmp-pc.d
```



# Collecting Performance Data with HPCToolkit: Turnkey Examples





### **Hands-on Tutorial Examples**

```
% git clone https://github.com/hpctoolkit/hpctoolkit-tutorial-examples
% cd hpctoolkit-tutorial-examples/gpu/nvidia
% ls
    arborx.kokkos lammps.kokkos quicksilver.cuda
```





### A Hands-on Example: Quicksilver

#### A LLNL proxy application for dynamic Monte Carlo particle transport (MPI + CUDA)

```
cd hpctoolkit-tutorial-examples/gpu/nvidia/guicksilver.cuda
source setup/polaris.sh
make build
make run
make run-pc
make view
make view-pc
```

#### **Notes**

- Running "make view" or "make view-pc" requires an X11 desktop to support the GUI
- Alternatively, you can use the hpcviewer's "open remote database" capability to view the databases
  - hpctoolkit-qs-gpu-cuda.d: profiles + traces
  - hpctoolkit-qs-qpu-cuda-pc.d: GPU PC samples





### **Analyzing Quicksilver Traces**

- Select the Trace tab "Trace: qs"
- Identifying the traces
  - Select a pixel on a trace line
  - Look at legend on the top of the display, which reports the location of the "cross hair"
  - Is this a CPU or GPU trace line?
  - Repeat this a few times to identify what each of the trace lines represents
- Notice that each time you select a colored pixel on a trace line, you will be shown the function call stack in the rightmost pane
- At the top of the pane is a "depth" indicator, that indicates what level in the call stack you are viewing. The selected level will also be highlighted
- You can change the depth of your view by using the depth up/down, typing a depth, or simply selecting a frame in the call stack at the desired depth
- You can select 
   above the call stack frame to show the call stacks at the deepest depth
  - If a sample doesn't have an entry at the selected depth, its deepest frame will be shown





### **Analyzing Quicksilver Traces**

- Zoom in on a region in a trace by selecting it in the trace display
- Use the back button is to undo a zoom
- Use the control buttons the top of the trace pane to
  - expand or contract the pane
  - move left, right, up, or down
- Keep an eye on the minimap in the lower right corner of the display to know what part of the trace you are viewing
- Use the home button to reset the trace view to show the whole trace





#### **Analyzing Quicksilver Traces**

- Select the Trace tab "Trace: qs"
- Configure filtering
  - Use the Filter menu to select Filter Execution Contexts
  - In the filtering menu, select "Uncheck all"
  - Now, in the empty box preceded by "Filter:", type "GPU" and then click "Check all"
  - Select "OK".
  - Now, the Trace View will show only trace lines for the GPUs.
- Inspect the trace data
  - Is the work load balanced across the GPUs? How can you tell?
  - Bring up the filter menu again. Select "Uncheck all". Type in "RANK 3" in the Filter box. Select thread
    0 and the GPU context. Select "OK".
  - Move the call stack to depth 2
    - What CPU function is Rank 3 thread 0 executing when the GPU is idle?
    - Does this suggest any optimization opportunities?





### **Analyzing the Quicksilver Summary Profile**

- Select the Profile Tab "Profile: qs"
- Use the column selector to deselect and hide the two REALTIME columns
- Select the GPU OPS column, which represents time spent in all GPU operations
- Select the 6 button to show the "hot path" according to the selected column
  - the hot path of parent will continue into a child as long as the child accounts for 50% or more of the parent's cost
- The hot path will select "CycleTrackingKernel" a GPU kernel that consumes 100% of the GPU cost in this profile
- Use the III button to graph "GPU OPS (I)" inclusive GPU operations across the profiles
  - Are the GPU operations balanced or not across the execution contexts (ranks)?





### **Analyzing the Quicksilver Summary Profile**

- You will notice that for quicksilver, HPCToolkit doesn't report any data copies between the host and device
  - The quicksilver code uses "unified memory" so that all of the data movement occurs between CPU and GPU using page faults rather than explicit copies
  - Today's GPU hardware doesn't support attribution of page faults to individual instructions
    - We could profile them, but not attribute them to code





### **Analyzing Quicksilver PC Samples**

#### Using a measurement database with traces that was collected \*with\* PC sampling enabled

Using the default top-down view of the profile

- Select the column "GINS (I)" to focus on the measurement of inclusive GPU Instructions
- Select use the flame button to look at where the instructions are executed
- In the call stack revealed, you will <gpu kernel> placeholder that separates CPU activity (above) from GPU kernel activity (below)
- Below the <gpu kernel> placeholder you will see the function calls, inlined functions, loops and statements in HPCToolkit's reconstruction of calling contexts within the CycleTrackingKernel
- Using the bottom-up view of the profile
  - Select the bottom-up tab of above the control pane
  - Select the GINS STL\_ANY (E) column, which will sort the functions by the exclusive GPU instruction stalls within that function
  - Scroll right to see which of the types of contributing types of stalls accounts for most of the STL\_ANY amount
  - Select the function that has the most exclusive stalls
  - Select the the hot path to see where this function is called from.
    - Where do the calls to the costly function come from?
    - Does there appear to be an opportunity to reduce the number of calls to this function?





### Filtering Tips to Hide Unwanted Implementation Details

- Filter "descendants-only" of CCT nodes with names \*MPI\* to hide the details of MPI implementation in profiles and traces
- Filter internal details of RAJA and SYCL templates to suppress unwanted detail using a "self-only" filter





#### A Hands-on Example: ArborX

#### Performance portable algorithms for geometric search MPI + Kokkos + OpenMP

```
cd hpctoolkit-tutorial-examples/gpu/nvidia/arborx.kokkos
source setup/polaris.sh
make build
make run
make run-pc
make view
make view-pc
```

#### **Notes**

- Running "make view" or "make view-pc" requires an X11 desktop to support the GUI
- Alternatively, you can use the hpcviewer's "open remote database" capability to view the databases
  - hpctoolkit-arborx-md.d: profiles + traces
  - hpctoolkit-arborx-md-pc.d: GPU PC samples





### **Analyzing ArborX Traces**

- Is the GPU active for most of the brief execution or not?
- Zoom in on the pair of trace lines that represents the GPU activity for a rank
  - You will see that there are two GPU trace lines per process
  - What happens on each?





### A Hands-on Example: LAMMPS

#### A molecular dynamics code with a focus on materials modeling (Kokkos + MPI)

```
cd hpctoolkit-tutorial-examples/gpu/nvidia/lammps.kokkos
source setup/polaris.sh
make build
make run
make run-pc
make view
make view-pc
```

#### **Notes**

- Running "make view" or "make view-pc" requires an X11 desktop to support the GUI
- Alternatively, you can use the hpcviewer's "open remote database" capability to view the databases
  - hpctoolkit-lmp.d: profiles and traces
  - hpctoolkit-Imp-pc.d: GPU PC samples





### **Analyzing LAMMPS Profiles, Traces, and PC Samples**

HPCToolkit can profile, trace, and collect PC samples for codes regardless of their complexity



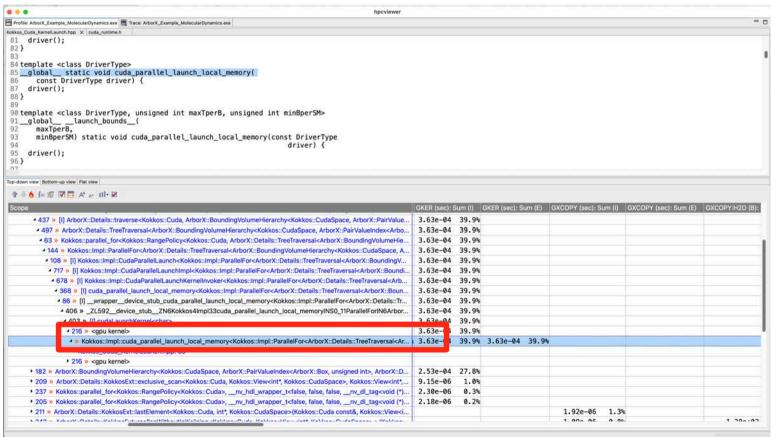


## Troubleshooting Measurement and Analysis with HPCToolkit



### **Troubleshooting: Only GPU kernel Name**

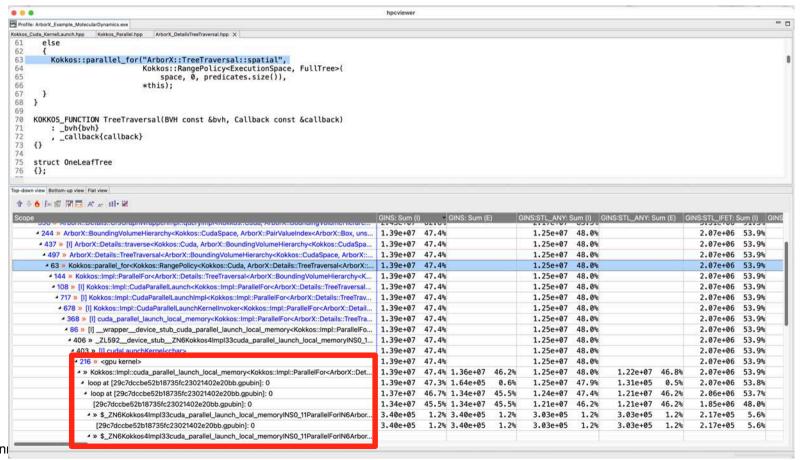
Need to measure with PC sampling to measure within GPU kernels





#### Troubleshooting: No GPU source code lines with PC sampling

If you don't see source code with PC sampling on NVIDIA GPUs: compile with "-lineinfo" option





#### Troubleshooting: Compiling ArborX with GPU Line Map Info

- ArborX cmake isn't set up to include GPU line mappings
- Force the compiler to record GPU line mappings

```
%cmake -DARBORX_ENABLE_EXAMPLES=true \
    -DCMAKE_INSTALL_PREFIX=`pwd`/../install \
    -DCMAKE_CXX_COMPILER=g++ \
    -DCMAKE_BUILD_TYPE=RelWithDebInfo \
    -DCMAKE_CXX_FLAGS_RELWITHDEBINFO="-O2 -g -DNDEBUG -lineinfo"
```

