

A 3rd Party oneAPI Case Study: GROMACS



Andrey Alekseenko

KTH Royal Institute of Technology & SciLifeLab Stockholm, Sweden

GROMACS

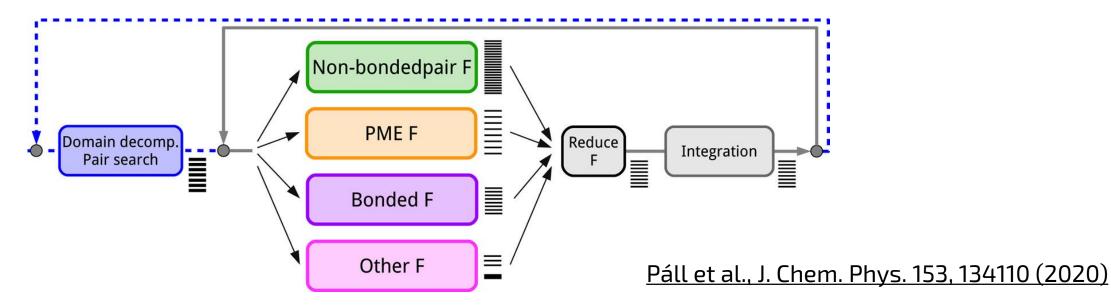
- Open source molecular dynamics engine
- One of the most used HPC codes worldwide
- High-performance for a wide range of modeled systems
- ... and on a wide range of platforms:
 - from supercomputers to laptops (Folding@Home)
 - x86, x86-64, ARM, POWER, SPARC, RISC-V
 - 11 SIMD backends
 - AMD, Apple, Intel, and NVIDIA GPUs; Intel Xeon Phi
 - Windows, MacOS, included in many Linux distros

GROMACS 2023 (upcoming)

- (Mostly) modern C++17 codebase
 - 449k lines of C++ code
 - With a bit of legacy (first release: 1991)
- MPI for inter-node parallelism
- OpenMP for multithreading
- SIMD for low-latency operations on CPU
- GPU offload for high-throughput operations
 - CUDA: NVIDIA
 - OpenCL: AMD, Apple, Intel, NVIDIA
 - SYCL: AMD, Intel, NVIDIA

Molecular dynamics

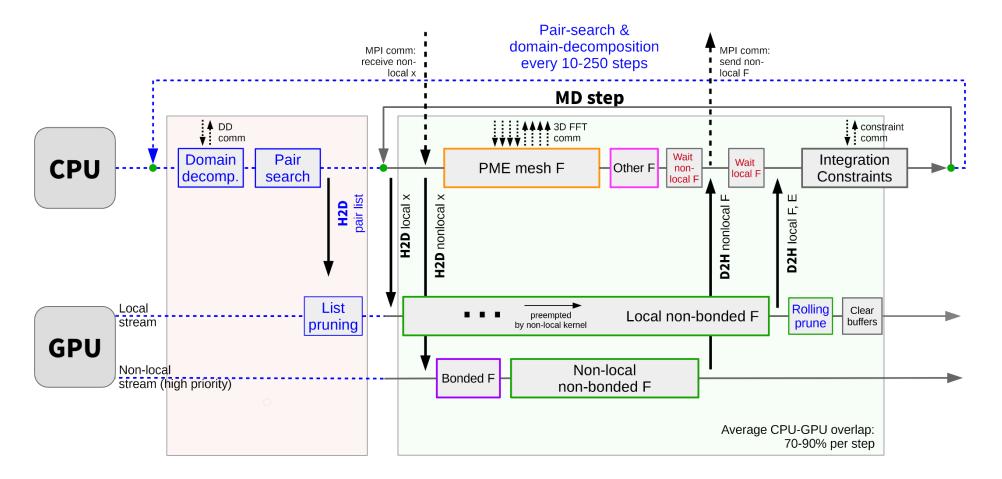
- Iterative problem
 - Like N-body, but with fancier physics
- One step ~1 fs, need to simulate μs to ms
 - 10⁹-10¹² steps



Heterogeneous parallelization

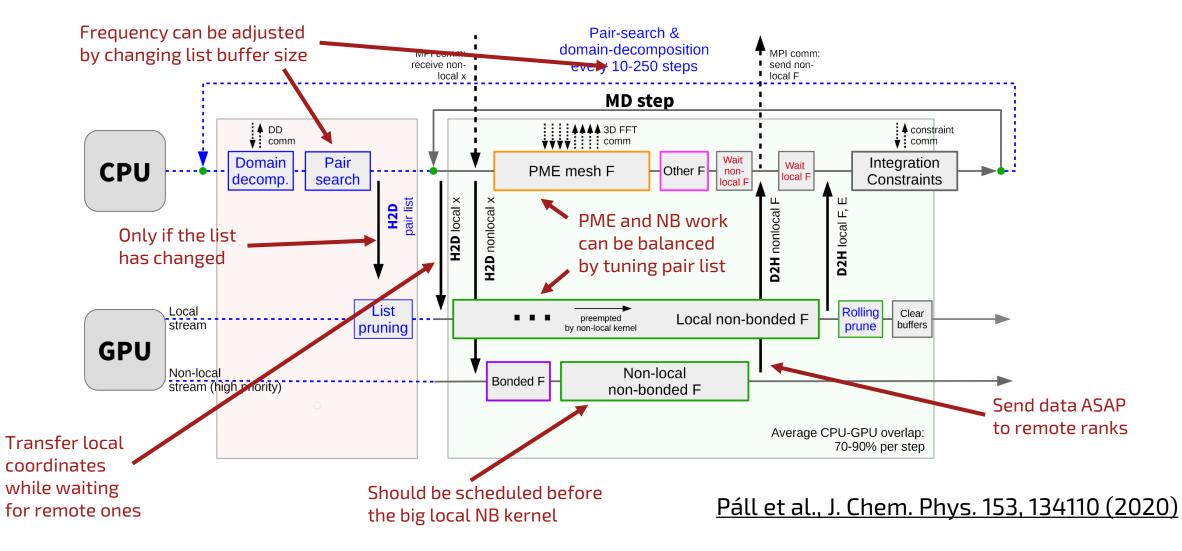
- Minimize latency
- Minimize CPU and GPU stalls
- Minimize data exchange between host and device
 - And between nodes
- Optimal offloading scheme depends on simulated system
 - And on available hardware
- Must be maintainable

Molecular dynamics: real schedule



Páll et al., J. Chem. Phys. 153, 134110 (2020)

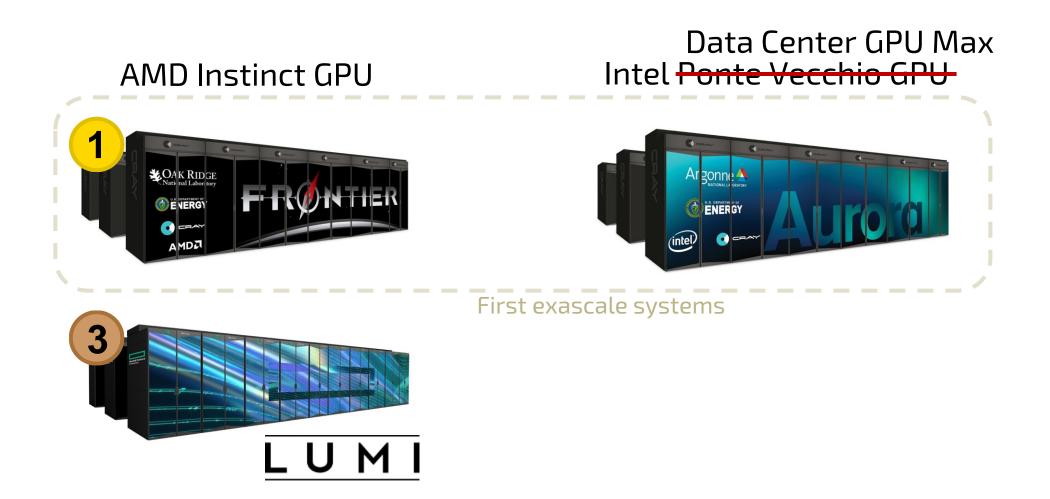
Molecular dynamics: real schedule



GPU feature support in GROMACS 2020

	NVIDIA . CUDA	OpenCL	
Non-bonded offload	√	\checkmark	
PME offload	\checkmark	\checkmark	
Update offload	\checkmark	Х	
Bonded offload	\checkmark	Х	
Direct GPU-GPU comm	\checkmark	Х	
Hardware support	NVIDIA	NVIDIA, AMD, Intel	

Why another GPU framework?



Why not OpenCL?

- \bullet OpenCL kernels are C99, the rest of GROMACS is C++17
 - C++ kernels are not widely supported
- Separate-source model
- Hard to maintain
- Supported by all vendors, preferred by none

Why SYCL?

- Open standard, free (libre) implementations
- Implemented on top of existing backend
 - Intel® oneAPI DPC++: OpenCL and LevelZero; CUDA; HIP
 - hipSYCL: CUDA, HIP; LevelZero (via DPC++)
 - Leverage existing profiling and debugging tools
 - And device compilers
- Standard C++ with a custom library
 - No need for extra support in linters, IDEs, etc.
- Logically similar to OpenCL
 - (Almost) no need to deeply modify existing code

SYCL enablement plan (late 2020)

- Step 1:
 - Target oneAPI DPC++ / Intel GPUs, but stay standard-compliant
 - Device detection and initialization
 - Remove code specific to CUDA/OpenCL
- Step 2:
 - Port kernels accounting for majority of run time
- Step 3:
 - Expand support to AMD GPUs
 - Port the rest of the kernels
 - Add support for GPU-aware MPI
 - Optimize kernels and runtime

SYCL enablement plan

- Step 1:
 - Target oneAPI DPC++ / Intel GPUs, but stay mostly standard-compliant
 - Device detection and initialization
 - Remove code specific to CUDA/OpenCL: still ongoing...
- Step 2:
 - Port kernels accounting for majority of run time
- Step 3:
 - Expand support to hipSYCL; AMD and NVIDIA GPUs
 - Port the rest of the kernels
 - Add support for GPU-aware MPI
 - Optimize kernels and runtime: we're here

Automatic conversion?

- We want to have both CUDA and SYCL in the same codebase
- Already have abstraction layer for Device, Queue, etc
 - Supports CUDA and OpenCL
 - CUDA kernels heavily optimized for NVIDIA
 - OpenCL kernels have Intel-optimized code paths
 - Rewriting kernels is ~trivial
- Conclusion: manual porting

	DVIDIA . CUDA	OpenCL	SYCL
Scheduling	in-order queue or explicit DAG	in-order and out-of-order queues	implicit DAG and in-order queues
Synchronization event	separate pseudo-task	associated with a task or a pseudo-task	associated with a task
Timing measurement	regions	of a single event	of a single event
Timing enablement	at event creation	at queue creation	at queue creation
Device selection	stateful per-thread	explicit in each call	explicit in each call
Native float3 size	12 bytes	16 bytes	16 bytes

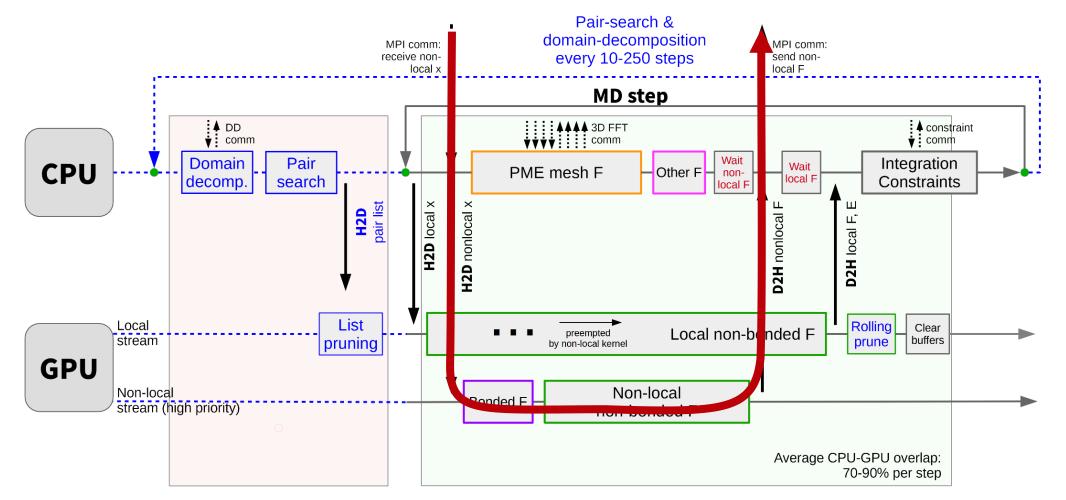
	We already had an abstraction layer		
	NVIDIA . CUDA	OpenCL	SYCL
	in-order queue	in-order and	implicit DAG and
Scheduling	or explicit DAG	out-of-order queues	in-order queues
		associated with a task	
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- Good: Prevent bugs and improve performance
- Bad: GROMACS is built around for in-order queues, with explicit barrier synchronizations:
 - Performance: synchronizing twice
 - Correctness: device-to-host copies
- Bad: Runtime must be smart
- Ugly: Additional divergence between backends

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• No, just use in-order queues and USM

- Bonus:
 - Accessors hard to optimize for compiler
 - Easier interop with GPU-aware MPI

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Synchronization Events

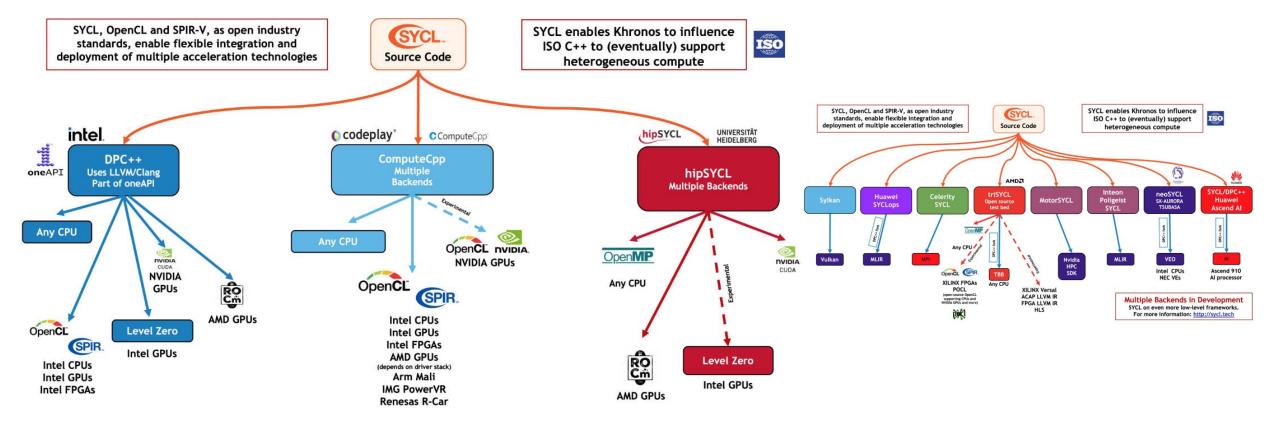
- Event can be recorded far from the last submission
 - Not easy to tell which operation should be used for synchronization
- Custom extensions to mark events:
 - oneAPIDPC++: SYCL_EXT_ONEAPI_ENQUEUE_BARRIER
 - hipSYCL: hipSYCL_enqueue_custom_operation to submit empty jobs acting as barriers
- hipSYCL's coarse-grained events

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Other differences to keep in mind

- Exceptions vs return codes
- Different and variable (for Intel) sub-group sizes
- Thread indexing order:
 - CUDA and OpenCL: thread (x, y, z) is adjacent to (x+1, y, z)
 - SYCL: thread (x, y, z) is adjacent to (x, y, z+1)
- No SYCL implementation is fully standard-compliant yet
 - Some standardized features still implemented as extensions
 - It's getting better
- No SYCL implementation is fully optimized
 - Less of an issue for compilers, more of an issue for the runtime

SYCL beyond oneAPI



https://www.khronos.org/sycl/

Portability in practice: FFT

- 3D real-to-complex, forward and backward FFT
- Intel GPUs: oneMKL
- AMD GPUs: rocFFT/vkFFT via HIPSYCL_EXT_ENQUEUE_CUSTOM_OPERATION
- NVIDIA GPUs: vkFFT via HIPSYCL_EXT_ENQUEUE_CUSTOM_OPERATION
- Future: HeFFTe to decompose FFT over multiple nodes

Portability in practice: hipSYCL

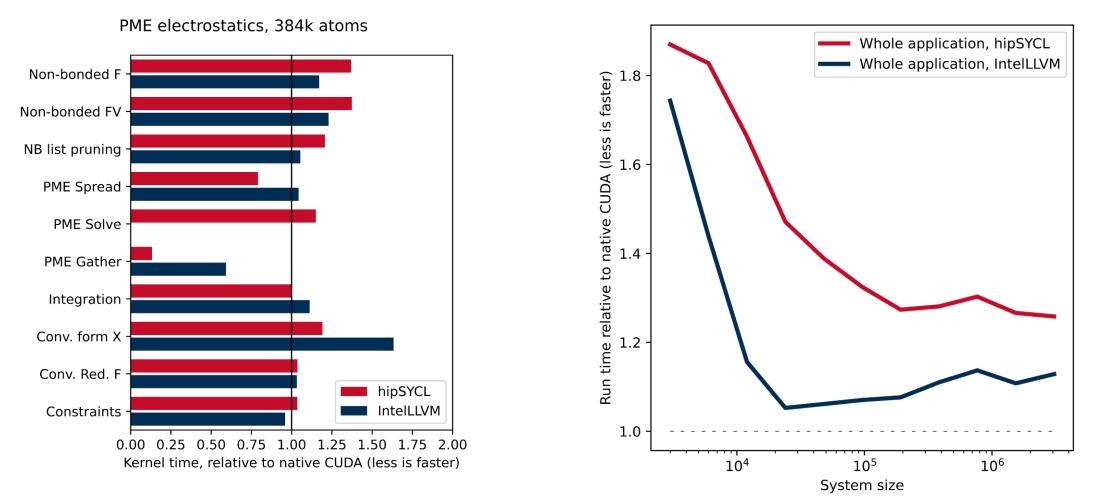
- At start, only Intel oneAPI DPC++ and Intel GPUs supported
 - hipSYCL added later to target AMD devices
- Effort:
 - Workarounds due to backend / compiler issues
 - Different parts of SYCL 2020 implemented
 - Fix a few bugs not triggered with oneAPI
 - CMake scripting
 - Kernel optimizations mostly ported from OpenCL
 - Still, some time with profiler was required
 - Runtime profiling/tuning
 - When the GPU FLOPS are not the bottleneck

Portability in practice: results

- GROMACS can use SYCL to run on:
 - Intel GPUs via oneAPI,
 - AMD and NVIDIA GPUs via oneAPI and hipSYCL
- Performance, compared to native CUDA/HIP/OpenCL:
 - Complex kernels are somewhat slower, require attention
 - Less complex kernels on par, sometimes faster
 - Extra runtime overhead
- Vendor-specific code
 - Sub-group-size-dependent algorithms
 - Workarounds for compiler issues
 - FFT invocation, a lot of related CMake scripting

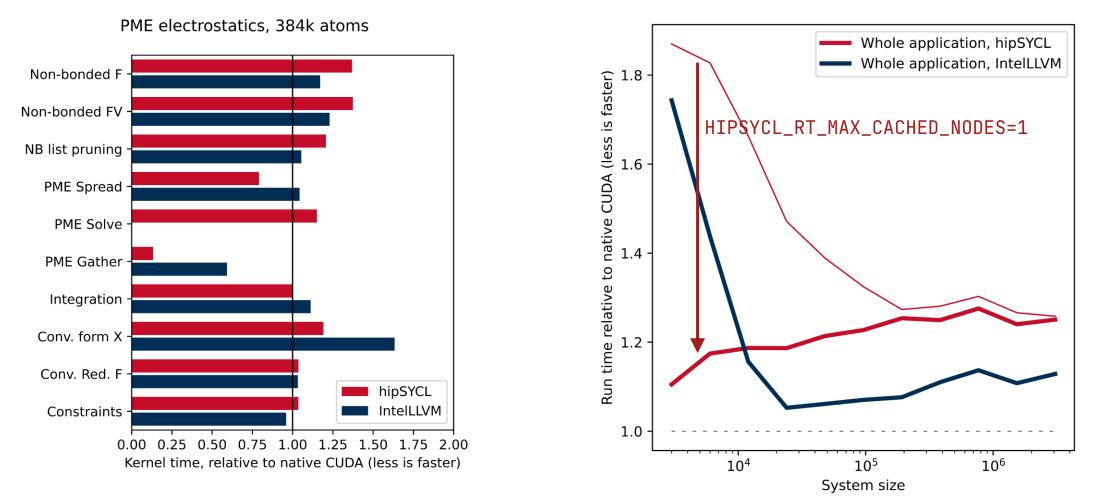
Performance: NVIDIA

V100, CUDA 11.5, hipSYCL develop and IntelLLVM vs CUDA



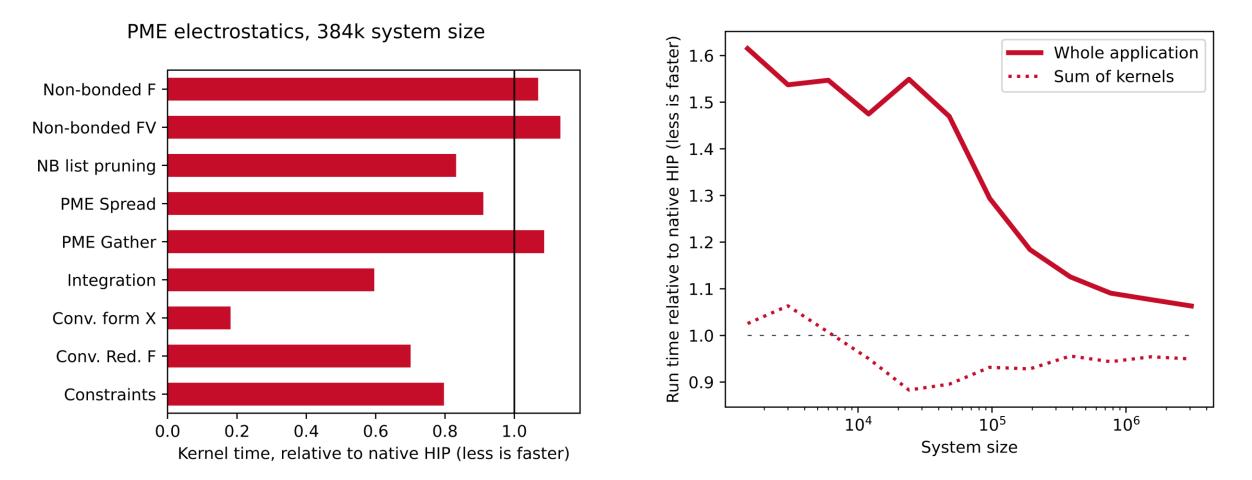
Performance: NVIDIA

V100, CUDA 11.5, hipSYCL develop and IntelLLVM vs CUDA



Performance: AMD

MI100, ROCm 4.5.2, hipSYCL 0.9.2 vs experimental HIP port by AMD/StreamHPC

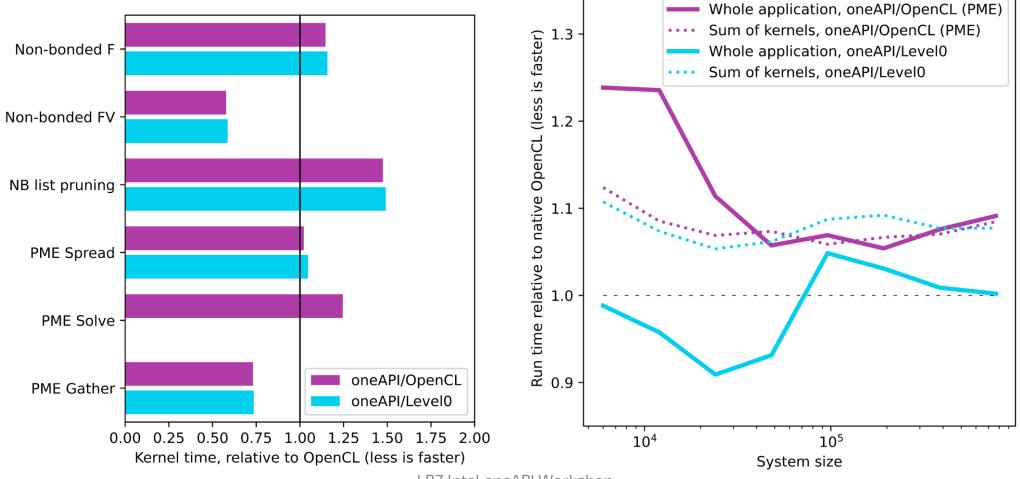


Performance: Intel

Xe MAX (DG1), oneAPI 2022.1, oneAPI (LevelZero, OpenCL) vs OpenCL

older GROMACS version, low-end GPU

PME electrostatics, 384k system size



LRZ Intel oneAPI Workshop

Missing features / Wishlist

- Queue/task priorities
- Fine control of host scheduling
- Hardware topology information
- Inter-node communication: Celerity?
- Libraries: oneMKL?
- Robustness: installation, error messages, ...

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PME offload	\checkmark	\checkmark	\checkmark
Update offload	\checkmark	Х	\checkmark
Bonded offload	\checkmark	Х	\checkmark
Direct GPU-GPU comm	\checkmark	Х	√*
Hardware support	NVIDIA	AMD, Intel, NVIDIA	AMD, Intel, NVIDIA

Conclusions

- "Write once, run anywhere" mostly works
 - Trivial changes to support all three major vendors with oneAPI and hipSYCL
- But running fast is not easy
 - Still need vendor-specific code branches to get high performance
 - Runtime might behave sub-optimally by default
- API is similar to OpenCL in spirit, but usually nicer
- The whole ecosystem is rapidly evolving

Acknowledgements

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- Aksel Alpay (Heidelberg University Computing Centre)
- GROMACS dev team, in particular Mark Abraham, Paul Bauer, Szilárd Páll, and Artem Zhmurov

Learn more

- <u>https://www.gromacs.org/</u>
- <u>https://gromacs.bioexcel.eu/</u>
- https://manual.gromacs.org/documentation/2022.3/index.html
- <u>Páll et al., J. Chem. Phys. 153, 134110 (2020)</u>
- If you have questions: andrey.alekseenko@scilifelab.se