ExCALIBUR

CompBioMedX (CBMX) Computational Biomedicine at the

Exascale

Peter V. Coveney

Engineer's House, 11-12 October 2023



UK Research and Innovation

XUX, **UK** Atomic Energy Authority

Project Overview

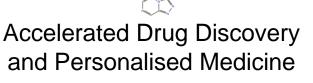
Key areas of computational biomedicine



Digital Twin of Human



Vascular Modelling © Crown Copyright, Met Office



Cardiac Simulations

Participants and partners



Project Status

HemeLB meet Frontier

- Lattice Boltzmann solver
- Massively paralleled highperformance code
- Available on both CPU and GPU (CUDA/Hipified)
- Designed for sparse geometry, ideal for hemodynamics simulations

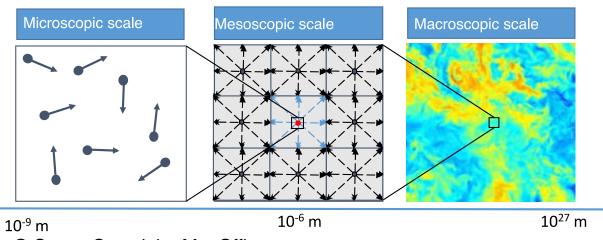


The world's only exascale machine. Access to it, a pathway that has gone via Titan, BlueWaters, and then Summit.

Frontier strong scaling plots

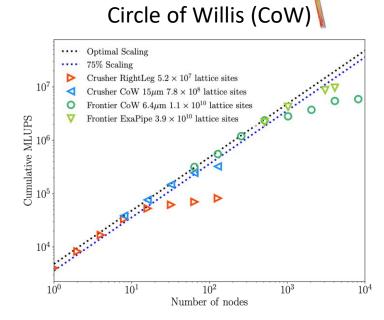
Full-human scale simulation requirements

- \circ 140 billion lattice sites (1.4 x 10¹⁰)
- Full deployment on Frontier (Exascale computing)
- A few cardio cycles to produce a highfidelity simulation



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The lattice Boltzmann method



Human Right leg Full-human scale arterial system



Project Status HemeLB_GPU: Towards a platform agnostic HemeLB_GPU from CUDA to HIP and oneAPI

HemeLB_GPU code – Port to oneAPI

- Single HemeLB collision-streaming CUDA kernel ported to Intel's oneAPI (SYCL/DPC++)
- $\circ~$ Ongoing efforts to port the full code to oneAPI
 - Deploy HemeLB_GPU on NVIDIA, AMD and Intel GPUs
- Preparing for Aurora (ALCF's forthcoming exascale system)

Port to oneAPI approach:

$\circ~$ Both with Intel DCPT Porting tool

- Testing on Sunspot (ALCF 2x Intel Xeon CPU Max Series (Sapphire Rapids) and 6x Intel Data Center GPU Max Series (codename Ponte Vecchio or PVC).
- Compiles Unstable... Debugging... Step by step approach Focus on Initialisation and then one kernel at a time...
- $\circ~$ Using factor based approach
 - Factor out the CUDA-specific parts of the code into back-ends:
 - Working for CUDA, HIP
 - SYCL/DPC++ up and running on Frontier (OLCF)
 - Unstable on Sunspot... Debugging in progress...

- Single source files – Reduce code duplication

- Simplifies code maintenance





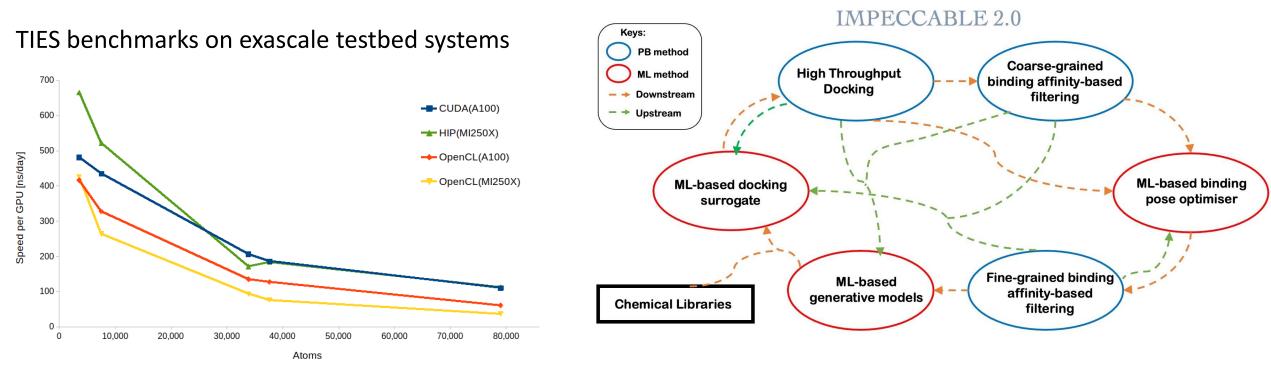


Data Parallel C++ Compatibility Tool

Project Status

Accelerated Drug Discovery and Personalised Medicine

IMPECCABLE 2.0 Workflow - Accelerating COVID-19 drug discovery



Performance comparison of TIES running on Polaris (A100) and Crusher (MI250X). All speed tests are performed with OpenMM 7.7.

Physics and machine learning based methods are used symbiotically to test drugs with required accuracy and efficiency.



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Current Challenges

• Technical challenges:

Implementation Challenge:

Full implementation of NAMD on Frontier

- Alchemical kernel not working on GPUs of Frontier (yet)
- Need one "srun" command for each task to a single GPU
- The number of "srun" commands in one submission is limited Implementation of complex and heterogeneous workflow
 - Workload: Task mix varies over campaign
 - Tasks: Run for varying duration

- **People barrier:** There is an insufficient number of people available in UK with the right training and skills.
- **Funding barrier:** There is insufficient funding available to sustain the threadbare efforts which we are currently undertaking.

Algorithm Challenge: HemeLB – it is challenging to resolve high Reynolds number blood flows coupling sparse geometry interacting with hemodynamic solver

Computing Challenge: Current status of Frontier is not fully stabilised yet (jobs may fail randomly after long queue)

Storage Challenge: Exascale computing is storage demanding (lack of storage space may lead to failure in running exascale jobs)



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