

MONT-BLANC

<http://www.montblanc-project.eu>



PharmaceleraTM

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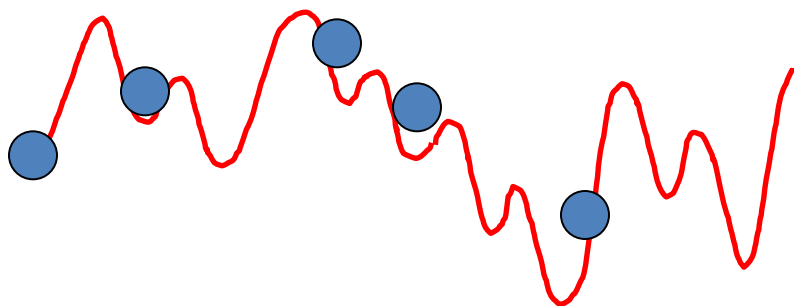
Pharmacelera in 5 Minutes

- Hardware and software solutions for scientific computations
- The team is a combination of complementary profiles
 - Management = 10+ years of management at Intel, 15+ years in entrepreneurship
 - Technical = 13+ years of software & hardware development at Intel, 33 patents, 26 technical publications
 - Scientific = 20+ years in drug discovery, 300+ publications
 - Commercial = 20+ years in pharma industry
- 3 main activity areas
 - Integrated hardware / software solutions for drug discovery
 - Hardware acceleration services
 - Established collaboration with Electronic and Atomic Protein Modelling (BSC)
 - Preferred H2020 partner for applied research and innovation
- More information at www.pharmacelera.com (info@pharmacelera.com)

PELE (Protein Energy Landscape Exploration)

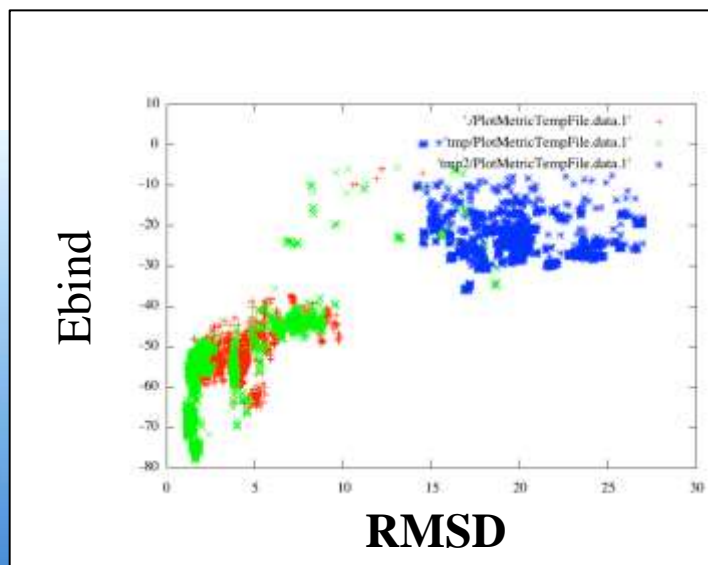
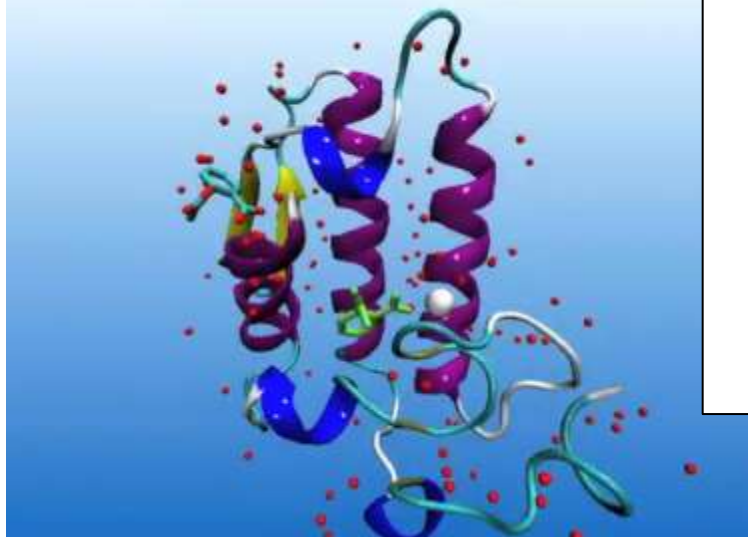
combining a Monte Carlo approach with protein structure prediction algorithms

* Software developed by the
Electronic and Atomic Protein Modelling group
(Víctor Guallar, BSC)



Provides a random walk along the
Energy Landscape

Example of ligand (aspirin)
search of the active site and
binding. The crystallographic
ligand is shown in green for
comparison



Interaction Energy (E_{bind}) allows identifying the best bound minima
(RMSD~1 Angstrom, analogous to the crystal)

Journal of Chemical Theory and Computation. 1 (6): NOV 2005

Tested application in Montblanc

- Molecular Solvent from PELE (molecular docking SW)
 - Primitive that accumulates 20%-30% of PELE's execution time
 - Molecular modeling for drug discovery
 - Programming language(s)
 - C, C++, OpenCL, ...
 - ~5000 LOC
 - Parallel programming model(s)
 - None so far
 - Accelerator programming model(s)
 - OpenCL
 - Libraries / Dependencies
 - Boost, OpenCL, stdc++

Resources required

- Memory requirement per node: ~4MB
- Storage required
 - Small
- Minimum number of nodes / CPU
 - 1 CPU + GPU

Molecular Solvent – OpenCL Parallelization

2 different inputs:

- Large: 4357 atoms → 19M pairs
- Medium: 31313 atoms → 980M pairs

```
for each atom i {  
  for each atom j {  
    if (i != j) {  
      compute interactions between atoms  
    }  
  }  
  update alpha field of atom i  
}
```

SCHEME 1: inner loop parallelization

```
for each atom i {  
  for each atom j {  
    if (i != j) {  
      compute interactions between atoms  
    }  
  }  
  update alpha field of i  
}
```

SCHEME 2: outer loop parallelization

```
for each atom i {  
  for each atom j {  
    if (i != j) {  
      compute interactions between atoms  
    }  
  }  
  update alpha field of i  
}
```

SCHEME 3: all pairs parallelization

N^2 pairs to expose max. parallelism



Reduction step

Assuming no shared memory for code portability (OpenCL 1.X....)

- Create memory buffers and copy data

Evaluated Systems – Performance Only

AMD FirePro W5100 (high-end GPU 500€) = WORKSTATION

Memory

4GB GDDR5 memory, 128-bit memory interface, up to 96 GB/s memory BW

Compute Performance

768 stream processors (PEs) (12 compute units) → 64 PEs per CU

1.43 TFLOPS peak single precision FP performance

89.2 GFLOPS peak double precision FP performance

CPU

Intel Xeon E3-1226 v3 (Haswell)

No shared memory between CPU and GPU

ARM MALI T-604 = MONTBLANC

Memory

256KB L2

Compute Performance

8 ALUs (PEs) (4 compute units) → 2 PEs per CU

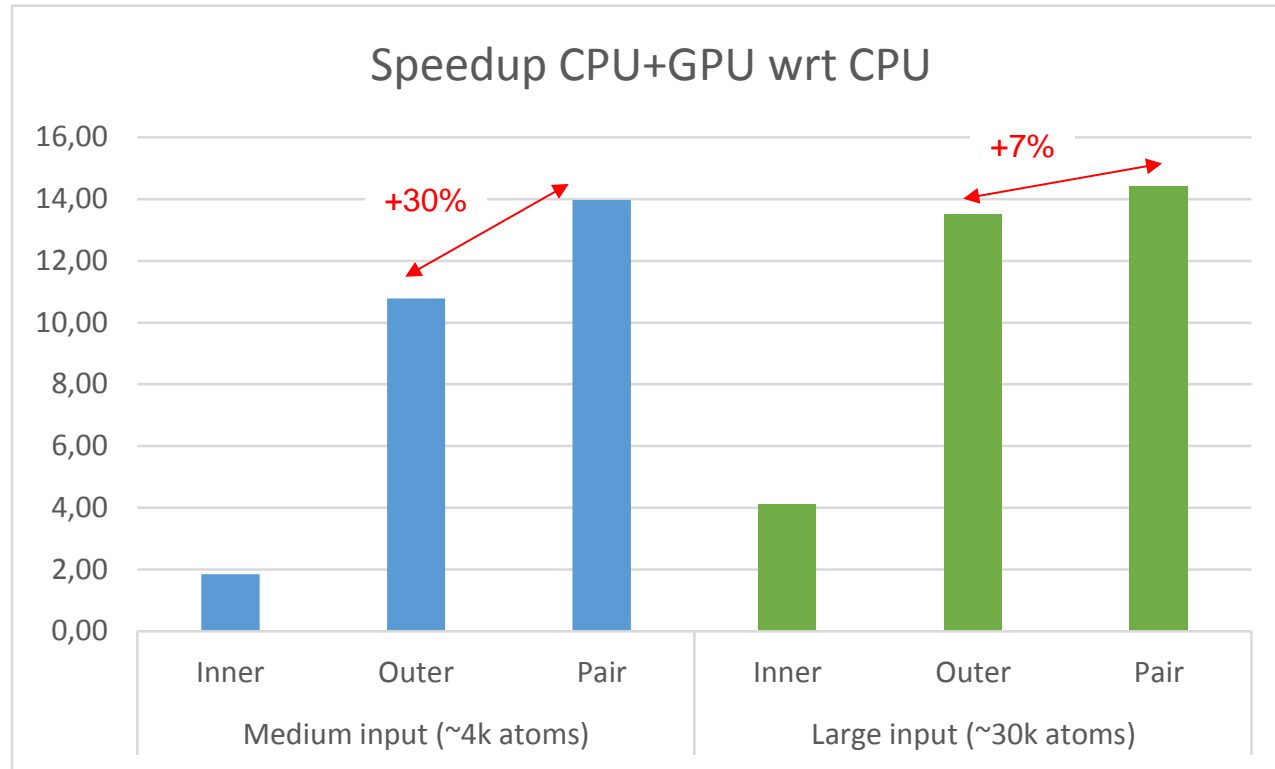
25.5 GFLOPS peak double precision FP performance (??)

CPU

ARM v7

Shared memory between CPU and GPU → we have not made use of SVM!

Performance Results on Workstation

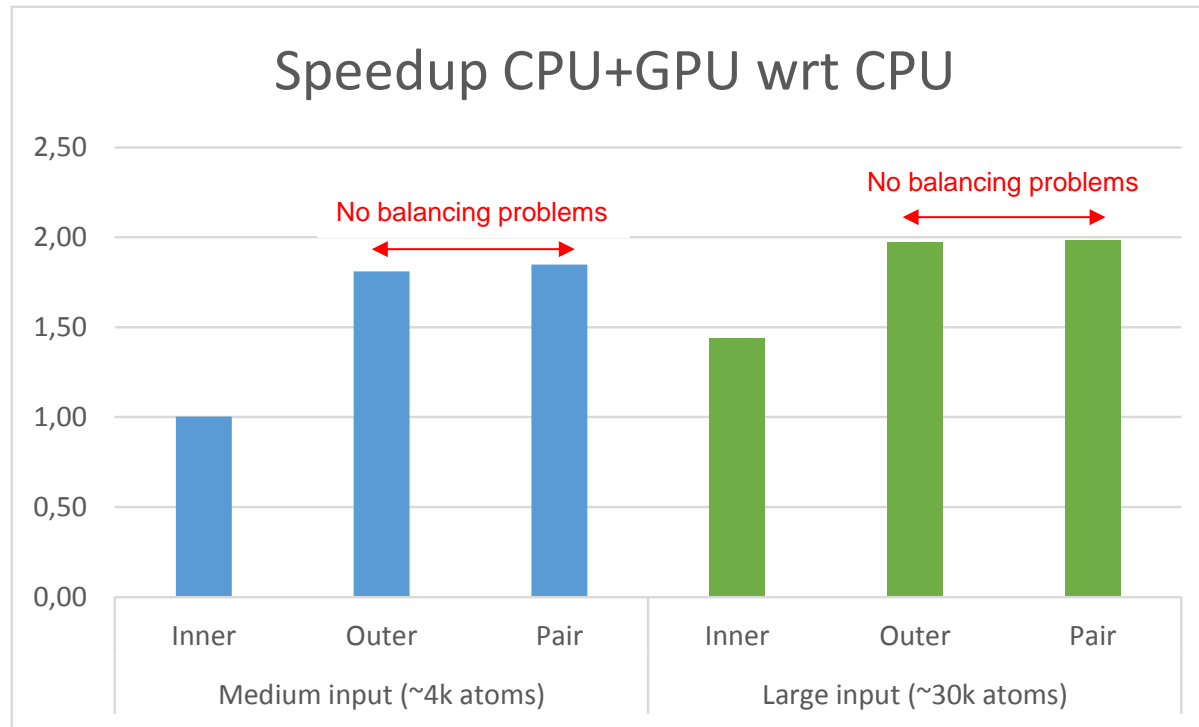


Baseline (CPU) execution times:

- Medium input = 1.13 seconds
- Large input = 52 seconds

Speedup severely impacted when work item group size is not max (256)

Performance Results on Montblanc



Baseline (CPU) execution times:

- Medium input = 4.30 seconds
- Large input = 226 seconds

Workstation vs Montblanc (Performance)

- Execution times in CPU
 - Workstation CPU between 3.8x and 4.3x better than Montblanc's
- Compiler role for CPU
 - Montblanc: 2.6x difference between `-O3` and `-O0`
 - Workstation: 1.6x difference between `-O3` and `-O0`
- Montblanc
 - Mobile GPU offers good performance (not outstanding)
 - Hidden support for shared memory in OpenCL 1.1 → not tested!
 - Lower amount of CEs → less prone to load unbalance

Feedback on platform usability

- Porting code: 1 hour effort!
 - Update paths: /apps/opencv_sdk/1.1.0/include, ...
 - Change routine that checks SVM availability (OpenCL 2.0)
 - Add '-lm' to Makefile
 - Change 'AMD' device by 'ARM' Device
 - Remove '-x spir' from clBuildProgram
- Any advantage / disadvantage of using our platforms?
 - IT support
 - Availability
 - Apparently some nodes going down suddenly
- No additional tools have been used

Ongoing Steps

- Pharmacelera
 - Use CodeXL in workstation to perform detailed GPU characterization
 - Parallelize the execution of non-bonding energy computations using OpenCL
- Electronic and Atomic Protein Modelling (BSC)
 - Full parallelization of PELE
 - MPI for inter-core
 - OpenMP for intra-core
 - Full characterization of MPI/OpenMP/OpenCL implementation