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Parallel Analysis in MDAnalysis using the Dask Parallel Computing Library

Abstract

The analysis of biomolecular computer simulations has become a challenge because the amount of output data is now routinely in the terabyte range. We evaluate if this challenge can be met by a parallel map-reduce approach with the Dask parallel computing library for task-graph based computing coupled with our MDAnalysis Python library for the analysis of molecular dynamics (MD) simulations [Gowers2016]. We performed a representative performance evaluation, taking into account the highly heterogeneous computing environment that researchers typically work in together with the diversity of existing file formats for MD trajectory data. We found that the the underlying storage system (solid state drives, parallel file systems, or simple spinning platter disks) can be a deciding performance factor that leads to data ingestion becoming the primary bottle neck in the analysis work flow. However, the choice of the data file format can mitigate the effect of the storage system; in particular, the commonly used "Gromacs XTC" trajectory format, which is highly compressed, can exhibit strong scaling close to ideal due to trading a decrease in global storage access load against an increase in local per-core cpu-intensive decompression. Scaling was tested on single node and multiple nodes on national and local supercomputing resources as well as typical workstations. In summary, we show that, due to the focus on high interoperability in the scientific Python eco system, it is straightforward to implement map-reduce with Dask in MDAnalysis and provide an in-depth analysis of the considerations to obtain good parallel performance on HPC resources.

Keywords

MDAnalysis, High Performance Computing, Dask, Map-Reduce, MPI

Introduction

MDAnalysis is a Python library that provides users with access to raw simulation data that allows structural and temporal analysis of molecular dynamics (MD) trajectories generated by all major MD simulation packages [Gowers2016]. The size of these trajectories is growing as the simulation times is being extended from micro-seconds to milli-seconds and larger systems with increasing numbers of atoms are simulated. Thus the amount of data to be analyzed is growing rapidly (into the terabyte range) and analysis is increasingly becoming a bottleneck. Therefore, there is a need for high performance computing (HPC) approaches to increase the throughput. MDAnalysis does not yet provide a standard interface for parallel analysis; instead, various existing parallel libraries are currently used to parallelize MDAnalysis-based code. Here we evaluate performance for parallel map-reduce type analysis with the Dask parallel computing library for task-graph based distributed computing on HPC and local computing resources. As the computational task we perform an optimal structural superposition of the atoms of a protein to a reference structure by minimizing the RMSD of the Cα. A range of commonly used MD file formats (CHARMM/NAMD DCD, Gromacs XTC, Amber NetCDF) and different trajectory sizes are benchmarked on different HPC resources including national supercomputers (XSEDE TACC Stampede and SDSC Comet), university supercomputers (ASU Research computing center (Saguaro)), and local resources (Gigabit networked multi-core workstations). All resources architectures are parallel and heterogeneous with different CPUs, file systems, high speed networks and are suitable for high-performance distributed computing at various levels of parallelization. Such a heterogeneous environment creates a challenging problem for developing high performance programs without the effort required to use low-level, architecture specific parallel programming models for our domain-specific problem. Different storage systems such as solid state drives (SSDs), hard disk drives (HDDs), and the parallel Lustre file system (implemented on top of HDD) are also tested to examine effect of I/O on the performance. The benchmarks are performed both on a single node and across multiple nodes using the multiprocessing and distributed schedulers in Dask library. A protein system of N = 3341 atoms per frame but with different number of frames per trajectory which corresponds to different trajectory sizes of (50GB, 150GB, 300GB) for Dask multiprocessing and (100GB, 300GB, 600GB) for Dask distributed. All the results for Dask distributed are obtained across three nodes on different clusters. Results are compared across all file formats, trajectory sizes, and machines. Our results show strong dependency on the storage system because a key problem is competition for access to the same file from multiple processes. However, the exact data access pattern depends on the trajectory file format and a strong dependence on the actual data format arises. Some trajectory formats are more robust against storage system specifics than others. In particular, analysis with the Gromacs XTC format can show strong ideal scaling over multiple nodes because this highly compressed format effectively reduces (global) I/O at the expense of increasing (local) per-core work for decompression. Our results show that there can be other challenges aside from the I/O bottleneck for achieving good speed-up. For instance, with numbers of processes matched to the available cores, contention on the network may slow down individual tasks and lead to poor load balancing and poor overall performance. In order to identify the performance bottlenecks for our Map-Reduce Job, we have tested and examined several other factors including striping, oversubscribing, Dask Scheduler, and

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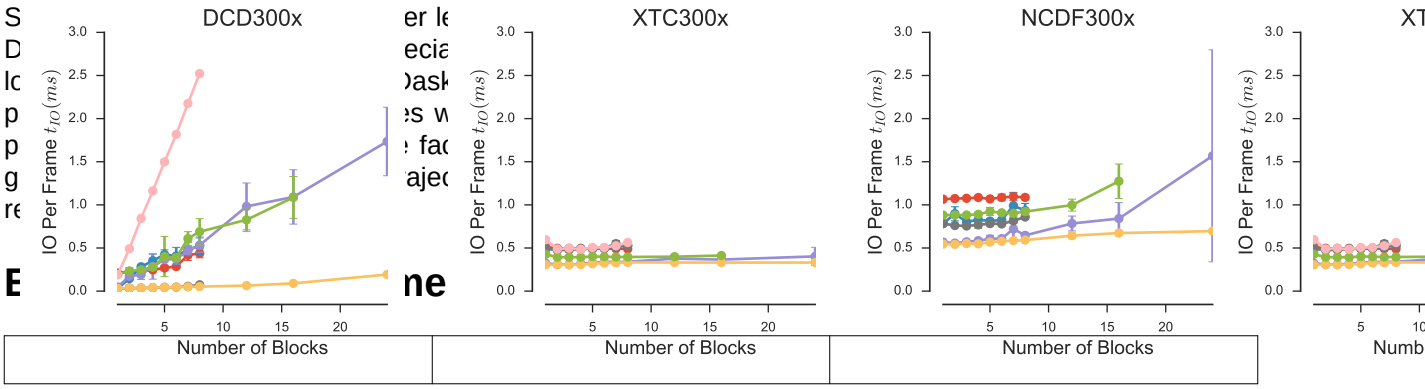

Effect of File Format

Challenges for Good HPC Performance

Performance Optimization

Effect of Striping

Effect of Oversubscribing

Effect of Scheduler Overhead

Scheduler Plugin Results

Comparison of Performance of Map-Reduce Job Between MPI for Python and Dask Frameworks

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