

Parallel Applications And Tools For Cloud Computing Environments

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The main research focus of SALSA project is two-fold. First, we investigate new programming models of parallel multicore computing and Cloud/Grid computing. It aimed at developing and applying parallel and distributed Cyberinfrastructure to support large scale data analysis. Second, we develop user-friendly and integrated Cloud computing environments and tools to provide our parallel algorithms and Cloud infrastructures as services.

To fulfill our research objectives, we have researched various parallel applications and programming models, especially designed for real life computing-intensive data analysis. The most notable example is Twister [1], which is an iterative MapReduce parallel programming model developed for Cloud computing environments. In addition to those efforts, we have also developed integrated Cloud computing environments to extend our research efforts to real-life use cases. For this purpose, we have built a portal web service to integrate our various Cloud applications and tools along with convenient workflow engines.

We will demonstrate the following key research efforts of the SALSA project.

A. *AzureMapReduce*

AzureMapReduce is a distributed decentralized MapReduce runtime for Windows Azure cloud infrastructure developed by utilizing Azure cloud infrastructure services. Usage of cloud infrastructure services allows the AzureMapReduce implementation to take advantage of the scalability and the distributed nature of such services guaranteed by the cloud service providers. AzureMapReduce is able to overcome the latencies of the cloud services by the use of sufficiently coarser grained map and reduce tasks. We overcome the eventual consistency nature of cloud services in AzureMapReduce by designing the system not to rely on the immediate availability of data with the use of retrying. AzureMapReduce runtime currently uses Azure Queues for map/reduce task scheduling, Azure tables for metadata & monitoring data storage, Azure blob storage for input/output/intermediate data storage and Window Azure Compute worker roles to perform the computations.

Google MapReduce [2], Hadoop [3] as well as Twister [1] MapReduce computations are centrally controlled using a master node and assume master node failures to be rare. In these run times, the master node handles the fault tolerance, task assignment and monitoring of Map & Reduce tasks among other responsibilities. Cloud environments are known to be more brittle than the traditional compute clusters and the cloud applications should be developed to expect and withstand the failures. Hence AzureMapReduce is designed as a decentralized controlled system avoiding the possible single point of failures. AzureMapReduce also provides users with the capability to dynamically scale up or down the number of compute instances, even in middle of a MapReduce computation, as and when based on the needs of the user. The map & reduce tasks of the AzureMapReduce runtime are dynamically scheduled using a global queue. AzureMapReduce provides fault tolerance capabilities similar to the other MapReduce run times such as Hadoop by rerunning of the failed or slow tasks.

In this demo, we are going to demonstrate the usage of AzureMapReduce for scientific computations with the use of several Bioinformatics application use cases. We showcase the viability of AzureMapReduce and the ability of the underlying cloud infrastructure services to deliver comparable performance and efficiency with appropriately designed systems.

B. *Large-scale PageRank with Twister*

PageRank is a well-studied web graph ranking algorithm. As there is a data deluge in the internet, the study of appliance of PageRank in large graph is becoming increasingly popular. The main challenges of large scale PageRank processing we faced are 1) most distributed job execution engines do not support iterative map reduce well. 2) there is a significant amount of network traffic in large scale PageRank processing. We resolve this issue by implementing PageRank with Twister [1], a lightweight iterative map reduce execution engine. Further, we optimize the distribution of both Mappers and Reducers in Twister to decrease the communication cost among them. Result shows that our method outperforms tradition technology that process large scale PageRank job.

We evaluate Twister PageRank performance by using ClueWeb data set collected in January 2009. We built the adjacency matrix using this data set. The whole web graph are partitioned into few parts and stored in the format of sub adjacency matrix, which is called static data in Twister. During the computation, each partition of static data is cached in the memory; and it can be used multiple times by the iterative Map task. This strategy brings much benefit as it does not need reload the static data from disk to memory in every iteration.

C. SALS Portal and Biosequence Analysis Workflow

The advent and continued refinement of modern high-throughput sequencing techniques have led to a proliferation of raw biosequence data, as labs routinely generate millions of sequence reads in a matter of days. Analyzing these results is beyond the computational capacity of single-lab resources, necessitating the use of high-performance computing resources, which presents significant overhead in terms of manual data manipulation and job monitoring. To overcome this bottleneck, application pipelines are being developed in conjunction with a generalized service-based portal system to abstract the details of job creation and management. This infrastructure will eventually provide service interfaces to map-reduce technologies, leveraging the computing resources offered by traditional grids and clusters, as well as emerging Cloud platforms.

We demonstrate the design and implementation of a software package to automate the setup steps for a specific sequence analysis workflow and a generalized service-oriented architecture (SOA) to expose this pipeline and other analysis tools as web services. Then, a simple web interface for submitting and managing jobs on high-performance computing platforms is presented as an example of the flexibility in building applications afforded by web service composition.

D. PlotViz Visualization with parallel MDS/GTM

PlotViz is a 3D data point visualization tool for high-dimensional data analysis. It is developed to visualize results of our in-house high-performance parallel dimension reduction algorithms MDS (Multi-dimensional Scaling) and GTM (Generative Topographic Mapping) [4, 5], and their variants, such as interpolation algorithms for MDS and GTM.

With the use of PlotViz and parallel MDS and GTM, users can easily identify points of interests by colors or select a group of points distinguished by structural distribution in 3D space. Additional functions are included in browsing data by rotating,

zooming, or panning the 3D space to search for more details. Dynamic updating labels of points or adding new data points are also supported by integrating an external repository system, Chem2Bio2RDF, by using the standard web query language, SPARQL.

Our tool can help very large and high-dimensional data analysis, which is very common in many life science researches. As a result, we have been successfully used PlotViz and parallel MDS and GTM with our internal collaborators for analyzing large and high-dimensional life science data, including PubChem data analysis for drug discoveries and genetic data analysis.

We demonstrate the following key features of PlotViz.

- i) PlotViz which is a lightweight 3D data visualization client to browse large (up to a few millions) and high-dimensional data.
- ii) On-line data fetching by connecting a remote external system, Chem2Bio2RDF, which is an integrated repository of chemogenomic and systems chemical biology data.
- iii) Research results for drug discovery with mining cause-effect relationship between large number of chemical compounds and diseases

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