# Hyperscaling Internet Graph Analysis with D4M on the MIT SuperCloud

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Abstract—Detecting anomalous behavior in network traffic is a major challenge due to the volume and velocity of network traffic. For example, a 10 Gigabit Ethernet connection can generate over 50 MB/s of packet headers. For global network providers, this challenge can be amplified by many orders of magnitude. Development of novel computer network traffic analytics requires: high level programming environments, massive amount of packet capture (PCAP) data, and diverse data products for "at scale" algorithm pipeline development. D4M (Dynamic Distributed Dimensional Data Model) combines the power of sparse linear algebra, associative arrays, parallel processing, and distributed databases (such as SciDB and Apache Accumulo) to provide a scalable data and computation system that addresses the big data problems associated with network analytics development. Combining D4M with the MIT SuperCloud manycore processors and parallel storage system enables network analysts to interactively process massive amounts of data in minutes. To demonstrate these capabilities, we have implemented a representative analytics pipeline in D4M and benchmarked it on 96 hours of Gigabit PCAP data with MIT SuperCloud. The entire pipeline from uncompressing the raw files to database ingest was implemented in 135 lines of D4M code and achieved speedups of over 20,000.

## I. INTRODUCTION

The rapid rise of sophisticated cyber threats is well documented and a growing threat to our information systems [1], [2]. Understanding internet phenomenology is challenging due to the variety of new threats and volume of new data being generated. To demonstrate the variety challenges, there are approximately 250,000 new malware programs registered each day [3], and a majority of all web traffic comes from bots, many of which are malicious in nature [4]. These evolving vulnerabilities can lead to public safety concerns [5] and economic impact: it is estimated that cyber attacks will cost nearly \$2 trillion in 2019 [6].

Enhancing this data variety challenge is the massive scale of internet and cyber networks. These ubiquitous networks form the basis of worldwide communication and it is estimated that in 2018, there will be almost 37 Terabytes per second

(TB/s) of Internet Protocol (IP) traffic [7]. To underscore the volume challenge in a more specific instance, consider the task of collecting and analyzing network traffic data to detect and remove botnets, networks of malicious computers that are controlled as a group. Network traffic data is typically collected using a packet capture appliance that intercepts packets moving through a network. These packets can be analyzed to look for broad trends across a network using packet metadata such as IP addresses, protocol, packet lengths, etc. that are stored in the packet header. As described in [8], [9], there are a number of approaches to detecting botnets from network flow data such as anomaly detection algorithms that look for particular patterns in the movement of IP packets. For example, a large number of packets with source IP addresses communicating with particular destination IP addresses in a non-human pattern may indicate a botnet or commandand-control server. For large networks, capturing, storing and processing packet capture data can be a large challenge. Consider a 10 Gigabit Ethernet (10 GbE) link. Such a link can often have over 100,000 packets/second. With a header length of 40 bytes, this translates to nearly 50 MB/s of storage and processing of header information alone! Looking for patterns within such data rates can be quite a challenge. Of course, enterprises and internet service providers often have much larger network links and sustaining such rates is only possible with massive computing systems serviced by parallel filesystems and/or databases.

Development of novel computer network traffic analytics requires: high level programming environments, massive amount of packet capture (PCAP) data, and diverse data products for "at scale" algorithm pipeline development. In this article, we present our approach to developing a scalable internet analytics platform applied to a IP network data using the D4M (Dynamic Distributed Dimensional Data Model) [10] analytics environment and MIT SuperCloud [11] interactive computing environment. D4M combines the power of sparse linear algebra, associative arrays, parallel processing, and distributed databases (such as SciDB and Apache Accumulo) to provide a scalable data and computation system that addresses the big data problems associated with network analytics development. The MIT SuperCloud allows users to interactively process massive amounts of data in minutes using the software and environments most familiar to them.

As depicted in Figure 1, large enterprises typically develop

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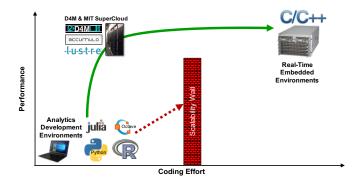


Fig. 1. D4M and MIT SuperCloud allows high performance without significantly compromising coding effort

analytics in environments such as Julia [12] or machine learning environments like TensorFlow [13] or Caffe [14]. While these have low coding effort and are useful for rapid analytic programming, they often come at the cost of lower relative performance. Deploying these algorithms to work at the scale of network traffic often implies translating these complex analytics into high performance languages such as C or C++ which requires significant coding effort. The time taken for this transition can be prohibitive for applications such as cyber analytics where there is a need for rapid deployment of analytics. Using MIT SuperCloud and D4M together allows cyber network analysts to overcome the scalability wall shown in Figure 1.

The rest of the article is organized as follows: Section II describes the tools used to develop a scalable network analysis pipeline, Section III details the implementation and Section IV describes scaling and analytic results. Finally, we conclude in Section V.

## II. Tools

The scalable architecture described in this article leverages prior work on D4M, Associative Arrays and the MIT Super-Cloud computing platform.

## A. D4M

The Dynamic Distributed Dimensional Data Model (D4M) is a software library developed at MIT Lincoln Laboratory that is used in a number of applications for processing large amounts of data. D4M is made up of three components:

- Support for a mathematical data object called associative arrays;
- A schema that is used to represent unstructured data as associative arrays; and
- 3) A library of software tools for connecting associative arrays with database management systems [15] such as Apache Accumulo, SciDB, mySQL, PostGRES.

The D4M library is currently written to work in the analytic environments of MATLAB, GNU Octave, Julia [16] and is currently being implemented as a Python toolbox. To connect to database engines, D4M can leverage high speed connectors or leverage existing connectors. D4M is a natural environment

to match the scaling requirements of network packet capture data and analytics.

## B. Associative Arrays

Associative Arrays generalize matrices to better match the intuitions of spreadsheets, databases, and tables, all while supporting the power of linear algebra. The indices of an associative array can range over arbitrary (though usually totally ordered and finite) sets, while the entries of an associative array may lie in an arbitrary semiring, which support addition and multiplication operations subject to most of the familiar field laws (associativity, commutativity, distributivity, identity, etc.).

This allows associative arrays to support many of the algebraic features of matrices, including element-wise addition and multiplication, as well as array multiplication and Kronecker products. By having its rows and columns meaningfully labeled, associative arrays also allow these operations to be well-defined between arrays of varying dimensions, unlike their matrix cousins.

Associative array algebra can provide a uniform mathematical framework to describe operations in SQL, noSQL and NewSQL databases [17]. For example, in Figure 2, we describe how one would express the same operation in three different styles of database systems.

## C. MIT SuperCloud

The MIT SuperCloud [11] is a high performance computing environment developed at the Massachusetts Institute of Technology. Unlike traditional supercomputing systems that are tuned for large-scale batch processing, the MIT SuperCloud is designed for data scientists interested in iterative analysis of machine learning and AI workloads. Specific technologies such as interactive databases [18], and high performance analytic IDEs such as Jupyter [19] provide a familiar environment for analysts. Figure 3 shows the IDE used by MIT SuperCloud users

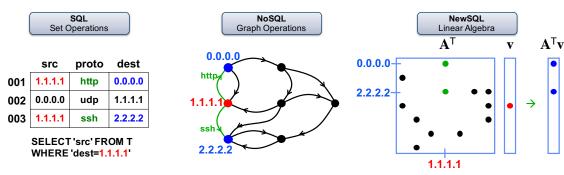
Scaling jobs to tens of thousands of cores on the SuperCloud is straightforward due to support for distributed computing paradigms such as Map-Reduce [20] and analytics development environments tuned for high performance distributed computing [21].

## III. DEVELOPING SCALABLE PIPELINE AND ANALYTICS

Developing network analytics involves developing a pipeline that can scale with the massive amount of data collected by packet capture devices. This section details the network data used and computational pipeline developed.

### A. IP Network Traces

IP network packets form the basic unit in which information is transmitted across the internet. An individual network packet consists of a header and payload. The header consists of typical information that one needs to correctly route a particular packet such as source IP, destination IP, etc. Headers are typically 40 bytes in size. The second part of the packet is the



Operation: finding 1.1.1.1's connections

Fig. 2. Different data management and computing systems naturally support different types of operations. In this graphic, all of the systems are performing the same operation - looking for connections to 1.1.1.1 - in the language native to their system. Associative arrays provide a uniform mathematical framework capable of representing these operations.

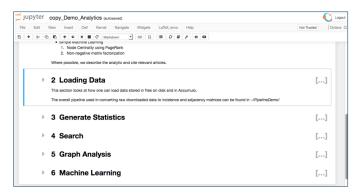


Fig. 3. Jupyter Notebook IDE available on the MIT SuperCloud.

payload or user data. This consists of the actual data payload of the packet. Payload information often consists of encrypted or sensitive user data and most network analytics focus on packet headers for their analysis. Listing III-A shows an example of the information (in associative array form) encapsulated by an individual packet's header.

```
(PacketID, frame.time_relative|0.000000000) 1
(PacketID, frame.time|2017 Apr 12 07:49:36.18828 EDT)

1
(PacketID, ip.dst|63.237.205.194) 1
(PacketID, ip.len|1500) 1
(PacketID, ip.proto|6) 1
(PacketID, ip.src|133.40.77.44) 1
(PacketID, tcp.dstport|55428) 1
(PacketID, tcp.flags|0x00000010) 1
(PacketID, tcp.srcport|80) 1
```

Using the packet header metadata, it is possible to determine clusters of similar network flows [22], important activity using centrality measures [23], and anomalous behavior based on clustering techniques [24]. We have also applied domain agnostic techniques such as dimensional analysis [25] and background modeling techniques for power-law data [26].

The MAWI Working Group (http://mawi.wide.ad.jp/mawi/) collects and shares a variety of network trace data collected on the WIDE network (http://www.wide.ad.jp/) backbone in Japan [27]–[29]. The working group has made a rich repository

of data available for researchers interested in analyzing trends in network traffic. The MAWI dataset provides a realistic view into data collected by global internet service providers.

## B. Computing Pipeline

Figure 4 describes the pipeline used to extract, store and process packet capture data described in Section III-A.

Each step of this pipeline is described below:

- Uncompress: Data from packet capture appliances is often written in a binary compressed format. In this step, we uncompress each of the binary packet capture files in parallel in order to make it readable for subsequent processing.
- 2) Split: In order to make processing large data files efficient on high performance computing systems, each uncompressed binary file is read by a packet analyzer such as topdump [30] and split into smaller files. This step ensures that further processing is amenable to parallelization.
- 3) Parse: In this step, each of the split files is run through a network analyzer such as tshark [31] in order to convert the packet capture (pcap) data into to a human readable format. For our implementation, each output file is stored in a tab-separated value (TSV) format.
- 4) **Sort**: Each TSV packet capture file is converted into a dense associative array that is similar to a dense table in a relational database.
- Sparse: Each dense array generated in the previous step is converted in an equivalent graph using the D4M schema.
- 6) **Ingest**: Each subgraph is inserted into a suitable database. For the purpose of our evaluation, we use the high-performance Apache Accumulo database [32].

In the following section, we describe specific settings and performance details of the above pipeline.

# IV. EXPERIMENTAL RESULTS

In order to test the pipeline of Figure 4, we use data products made available by the MAWI working group. The dataset we

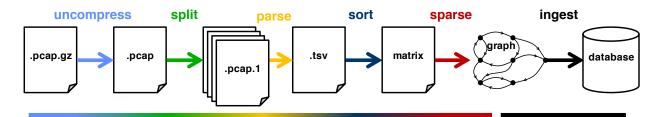


Fig. 4. Analytics pipeline used for processing network packet capture data.

use called a "Day in the Life" (DITL) internet traces, consists of 4 days (96 hours) of 1 Gigabit packet capture headers collected on two days in 2015 and two days in 2017.

In total, the raw data in compressed form, is approximately 700 GB. When converted to an analyst-friendly form by uncompressing, parsing, and sorting, the data expands to approximately 20 TB. Scaling performance analysis was performed on MIT Lincoln Laboratory Supercomputing Center's system. This system consists of 650 nodes with Intel Xeon 64-core processors and 180 nodes with 32-core AMD Opteron processors. For our scaling experiments, processing is performed on Xeon-64 nodes and databases are operated on AMD Opteron nodes. For the results presented below, the maximum processing size was performed on 385 Intel Xeon-64 nodes (24,640 cores) and the largest database instance was distributed across 128 AMD Opteron nodes.

In the subsections below, we described the implementation details of the pipeline presented in Section III-B.

# A. Step1: Uncompress Raw Data

In this step, we take 385 compressed input files (corresponding to the number of computing nodes used in the experiment) and convert them to 385 uncompressed output files. Each input and output file corresponds with roughly 15 minutes of network flows. Each 2GB file expands to 6GB after uncompressing which translates to an increase from 700GB to approximately 2.3 TB. The maximum speedup is largely impacted by the number of input files and eventually limited by the file system I/O speed.

The code snippet below shows the D4M code used to uncompress a single <code>.pcap</code> file. In this snippet, <code>dataDir</code> and <code>dataDOM</code> corresponds with file locations on the system and iFile corresponds to the compressed file to be processed by each node:

```
uncompressCommand = ['gunzip -k ' dataDIR dataDOM '/
    ' iFile '.pcap.gz']
system(uncompressCommand);
```

# B. Step 2: Split Uncompressed Files

Once the uncompressed output files are generated from the previous step, we split these files into smaller chunks in order to optimize later steps in the pipeline. We first use tcpdump to convert the 385 binary .pcap files into ASCII versions, then split these files into into approximately 500,000 smaller output .pcap files appended with a split ID. Similar to the

previous step, the maximum speedup is largely impacted by the number of input files (which should closely match the number of processing nodes) and eventually limited by file system I/O.

The code snippet below shows the code used to convert from binary to ASCII and split the input .pcap files. The splitSize was set to be 5 MB.

## C. Step 3: Parse Split Files

With the approximately 500,000 split and uncompressed .pcap files, we convert these files into a human readable format using a tool such as tshark [31]. Using tshark, we convert these .pcap into a tab separated value (TSV) format while also filtering the headers for the fields shown in Section III-A. Each output TSV file at this stage is approximately 5MB in size (for a total of 2.3 TB across all files) and each TSV file corresponds to rougly 1 second of network flow data. The maximum speedup of this step is limited by the number of cores available for parsing.

The code snippet below describes the D4M operations used for parsing the split files:

## D. Step 4: Dense Array Construction (Sort)

In order to convert the 500,000 files in the previous step to a format amenable for further processing, we use D4M to convert these TSV files into associative array format (which also sorts the data during construction). Each of the 5 MB input files expands to roughly 50 MB (total of 20 TB) during this step. At this point, data is human readable and ready to construct the network graph. At this stage, the maximum speedup is limited by the number of cores.

The code snippet below describes the D4M syntax to load the input files, restructure the time field, construct the associative array and save the resultant sorted array to disk.

## E. Step 5: Graph Construction (Sparse)

With the dense associative arrays from the previous step stored on disk, we can now, in parallel, generate the sparse version of the network graph. This sparse representation directly corresponds to the incidence matrix of the graph. Each of the 50 MB input associative array is converted to a sparse representation using the D4M schema. The resultant output file is saved to disk for database insertion. As in the previous step, the maximum speedup of this step is limited by the number of cores.

The code snippet below describes the D4M syntax for loading in the output array from Step 4 and converting it to a sparse representation:

```
load([parseDIR dataDOM '/' iFile '/' ijFile '.tsv.A.
     mat'],'A');
E = val2col(A,'|');
save([parseDIR dataDOM '/' iFile '/' ijFile '.tsv.A.
     mat.E.mat'],'E');
```

## F. Step 6: Ingest

With the sparse data products of the previous step, it is easy to use D4M to directly insert this data into Apache Accumulo. Our prior work has demonstrated that Accumulo is capable of extremely high ingest rates suitable for applications such as internet traffic analysis. In our experiment, we create various Accumulo instances with different configurations in order to test scalability. For our testing, we deploy Accumulo on 32-core AMD Opteron nodes. To test scalability, we use 1, 4, 16 node instances. For larger database instances, we found that running multiple database systems over 16 nodes was more efficient than larger Accumulo instance (i.e., 2, 4, 8 databases running in parallel each with 16 nodes rather than 32, 64, and 128 node instances).

Each of the 385 Xeon-64 nodes is responsible for loading a subset of the 500,000 sparse arrays from the previous step into an Accumulo instance (or a particular Accumulo instance in the case where we have multiple databases in parallel). The maximum speedup for this step is limited by the number of Accumulo cores available.

The code snippet below describes the D4M syntax for loading the incidence matrix file, inserting into a table called Tedge, generating the degree table and inserting it into TedgeDeg. Details about the general schema and table design can be found in [33].

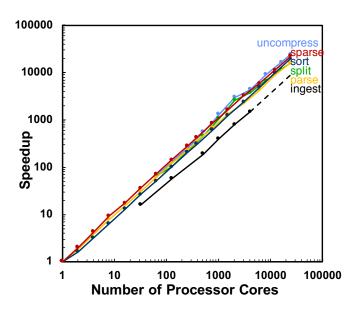


Fig. 5. Scaling Performance using D4M and MIT SuperCloud. The x-axis indicate the number of processing cores and the y-axis the resulting speedup.

```
load([parseDIR dataDOM '/' iFile '/' ijFile '.tsv.A.
    mat.E.mat'],'E');
put(Tedge,putVal(E,'1,'));
Edeg = putCol(sum(E.',2),'degree,');
put(TedgeDeg,num2str(Edeg));
```

## G. Performance Analysis

To assess the performance of each step, the D4M code included timers. For each of the first five steps of the pipeline, the time measured includes the time for reading the file from disk, performing the operation and writing the file back to disk. For the insertion step, we measure the time taken to load the file and insert into Accumulo. For each of the experiments, we fix the data size and compute the speedup relative to the time taken for a single core to perform the task.

Figure 5 describes the speedup associated with a varying number of processing cores for each of the steps of the processing pipeline. Each line in the figure is color coded according to the color of the step in Figure 4. The ingest line starts at 32 database cores and ends at 4096 database cores (corresponding to 8 x 16-node Accumulo databases).

As seen in Figure 5, for Steps 1-5 of the pipeline, increasing the number of cores leads to a near linear speedup. For the database ingest, the speedup is largely limited by the number of Accumulo cores available (4096 is the maximum number of Accumulo cores in our experiment). The entire pipeline from uncompressing the raw data to database ingest was implemented in approximately 135 lines of D4M code.

#### V. CONCLUSIONS

Network and cyber security of the future will largely rely on massive quantities of data. Internet network analysis will continue to be challenged by the fast pace of analytic changes coupled with massive quantities of data. In order to address these challenges, it is important that researchers leverage high level programming environments that simplify analytic development along with computing platforms that support high-performance analysis. In this article, we describe our approach to developing such a toolbox based on D4M and MIT SuperCloud. We describe our approach to using this infrastructure to develop a processing pipeline for IP traces collected by the MAWI working group. As is described in the article, our system allows researchers to develop scalable processing pipelines without compromising coding effort.

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